

498 **Microfluidic Cell-phoresis Enabling High-throughput Analysis of Red Blood**
499 **Cell Deformability and Biophysical Screening of Antimalarial Drugs**

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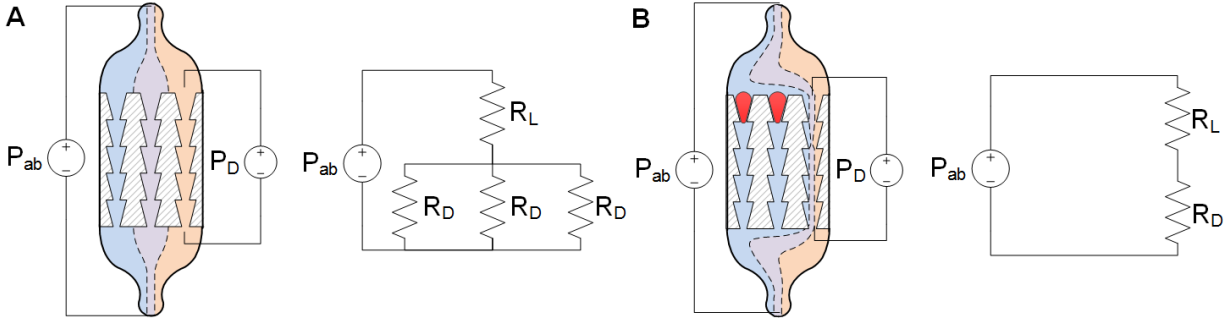
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507 **SUPPLEMENTAL MATERIALS**

508 **Supplemental 1: Multiplexing Error (E_M)**

509 The key design challenge in multiplexing cellular microfluidic cell-phoresis is to ensure a
510 consistent pressure is applied across each deformation microchannel independent from the number of
511 deformation microchannels occupied with cells. The pressure applied across the deformation
512 microchannels (P_D) varies with the number of deformation microchannels occupied with cells
513 (**Supplemental 1**). This phenomenon could be explained by considering the fluid flow in the loading and
514 deformation microchannels in the following two situations: 1) When the deformation microchannels
515 contain no cells, fluid streamlines in the loading microchannels are evenly distributed across the
516 deformation microchannels (**Supplemental 1A**). 2) When one or more of the deformation microchannels
517 are occupied with cells, the fluid flow is blocked in that channel. Consequently, fluid streamlines in the
518 loading microchannel are skewed into the remaining unblocked deformation microchannels
519 (**Supplemental 1B**). The difference between these two situations results in an inconsistency in the flow
520 inside the deformation microchannels, and the resulting deformation pressure, P_D . An equivalent
521 hydrodynamic circuit of these two cases is shown in **Supplemental 1**, where:

- 522
- P_{ab} : Pressure across loading and bypass microchannels.
 - 523 • P_D : Deformation pressure.
 - 524 • R_D : Hydrodynamic resistance of individual deformation microchannel.
 - 525 • R_L : Hydrodynamic resistance of loading microchannels.



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527 **Supplemental 1:** Graphic representation of fluid streamlines in the loading and deformation microchannels and its
528 associated hydrodynamic circuit when: (A) All deformation microchannels are unoccupied with cells and (B) only
529 one deformation microchannel is unoccupied.

530 To estimate the potential error due to microchannel occupancy on the pressure across the
531 deformation microchannels (P_D) for a device with N deformation microchannels, the worst-case
532 pressure difference is considered, which occurs when the deformation microchannels are occupied with
533 a single cell and when the deformation microchannels are completely occupied with cells, which can be
534 estimated as follows:

535 Deformation microchannels occupied with a single cell:

$$P_{D,1} \approx P_{ab} \left(\frac{R_D}{R_D + (N - 1)2R_L} \right) \quad \text{Equation 1}$$

536 Deformation microchannels completely occupied:

$$P_{D,N} = P_{ab} \quad \text{Equation 2}$$

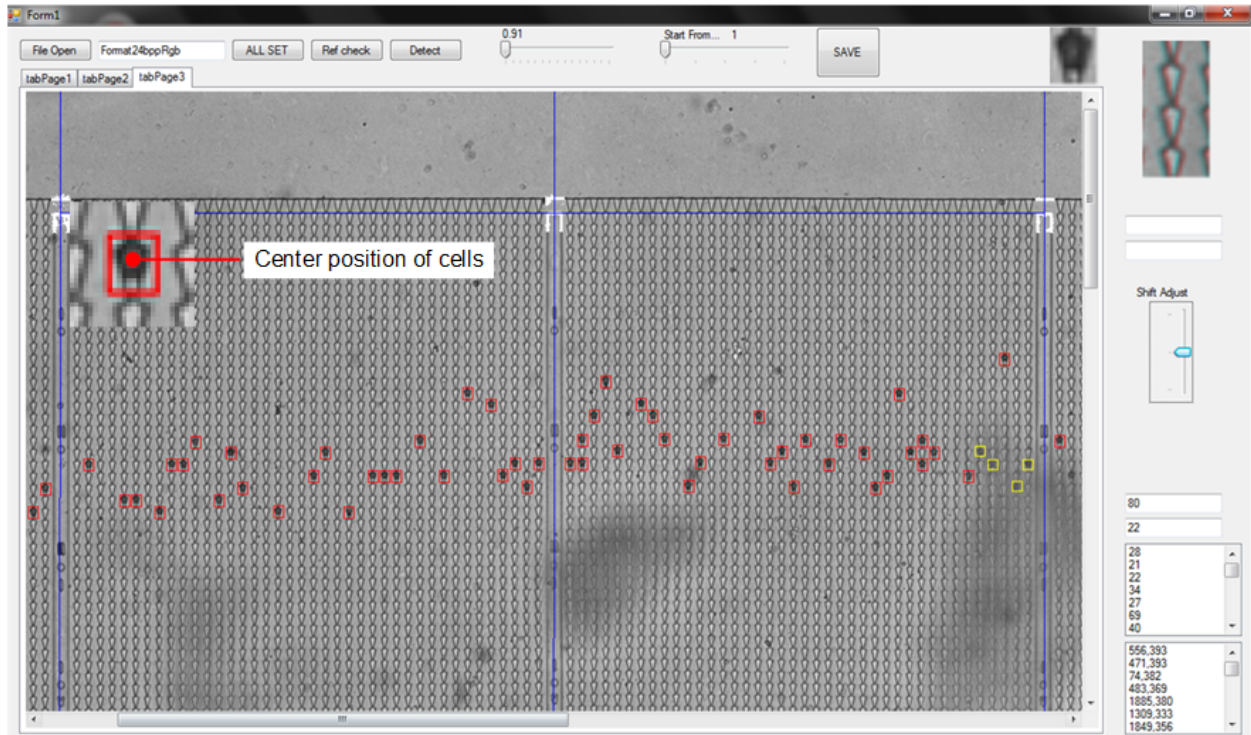
537 The multiplexing error (E_M) is evaluated as the pressure difference between these two extreme
538 cases (Equation 3) and can be minimized by maximizing the ratio of R_D/R_L based on a target N .

$$E_M = \frac{P_{D,N}}{P_{D,1}} - 1 = (N - 1) \frac{2R_L}{R_D} \quad \text{Equation 3}$$

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540 **Supplemental 2: Video of the RBC Deformation Process**

541 **Supplemental 3: Image Analysis Software**



542 **Supplemental 3:** Image processing software used to automatically detect RBCs. Red squares indicate automatic
 543 detection by the software while yellow squares indicate manual selection by the user. (Inset) The center position
 544 of the cell determines its position within the deformation microchannel.
 545

546 **Supplemental 4: Detailed Device Geometries**

547 Supplemental 4: Details of device geometries based on the target cells

Target Cells	Normal RBCs	<i>P. falciparum</i> ring-stage iRBCs	<i>P. falciparum</i> late-stage iRBCs	Antimalarial drug-treated iRBC
Manifold	4	8	8	8
Number of funnels in a deformation microchannel (N_F)	100	$N_{F1}: 75$ $N_{F2}: 75$	$N_{F1}: 75$ $N_{F2}: 75$	$N_{F1}: 75$ $N_{F2}: 75$
Pressure attenuator ratio (α)	500	500	500	300
Pore Size, W (μm)	1.7	$W_1: 1.5$ $W_2: 1.2$	$W_1: 2.0$ $W_2: 1.5$	$W_1: 2.4$ $W_2: 1.9$
Thickness of deformation microchannel H_F (μm)	3.8 ± 0.1	3.7 ± 0.1	3.9 ± 0.1	4.4 ± 0.1
R_D (Pa.s/m ³)	$3.91\text{E}+17$	$6.57\text{E}+17$	$4.12\text{E}+17$	$2.15\text{E}+17$
R_L (Pa.s/m ³)	$7.12\text{E}+13$	$8.41\text{E}+13$	$8.41\text{E}+13$	$4.40\text{E}+13$
R_B (Pa.s/m ³)	$4.26\text{E}+12$	$1.07\text{E}+13$	$1.07\text{E}+13$	$6.48\text{E}+12$
E_M	4.36%	3.06%	4.87%	4.90%

548 **Supplemental 5: Data Analysis**

549 Due to inherent variability in donors, each experiment was normalized to a sample, which was
 550 designated as the control of that experiment (**Supplemental 5**). Data normalization is performed by
 551 dividing the position (indicating the deformability) of each cell to the mean and median of the control
 552 sample. Samples were normalized to the mean of the control when the expected distribution of the cells
 553 is Gaussian, such as with the device validation experiments in **Figure 3**. Parasitized RBCs were also
 554 normalized to the mean-value since iRBCs form a very small subpopulation in the sample, resulting in an
 555 overall Gaussian distribution. However, iRBCs treated with antimalarials was normalized to the median
 556 of the control since the expected population distribution is not Gaussian. This normalized deformability
 557 measurement is usually denoted as normalized position of the cells along the deformation
 558 microchannel.

559 **Supplemental 5:** Summary of data analysis process for each experiment.

Figure	Experiment	Sample Designated as Control	Normalized To
Figure 3A	Repeated deformations	2 minutes at 20 Pa	Mean-value
Figure 3B	Multiplexing error	Nearly empty	Mean-value
Figure 3C	Oxidatively damaged RBCs	Untreated RBCs	Mean-value
Figure 3D	Applied pressure waveform	Untreated RBCs at 5 Pa	Mean-value
Figure 4	<i>Plasmodium falciparum</i> iRBCs	Uninfected RBCs	Mean-value
		Individual sample to produce the cumulative distribution	Mean-value
Figure 5A	Antimalarial-treated iRBCs	DMSO-treated late-stage iRBCs	Median-value

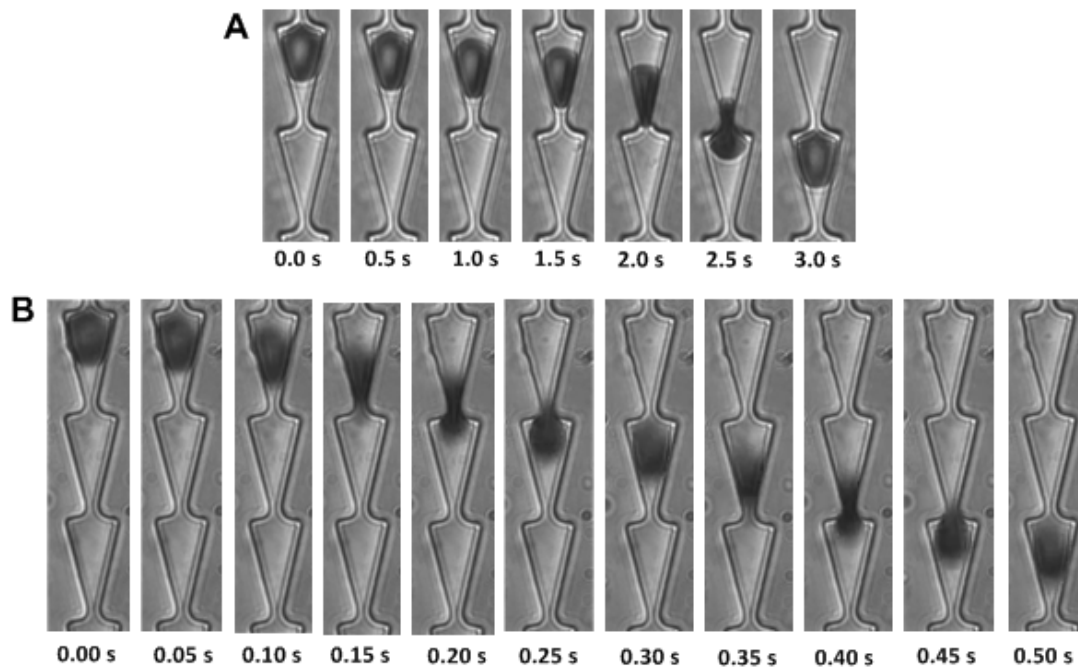
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561 The small subpopulation of malaria-iRBCs (unsynchronized or ring-stage) becomes progressively
 562 stiffer as the parasites mature and also causes bystander injury on the uninfected, exposed RBCs. Hence,
 563 to capture the effect of this key subpopulation and to eliminate the effect of uninfected RBCs in the
 564 deformability measurement, each sample was normalized to the mean of individual sample, after which
 565 the least deformable subpopulation was emphasized in the data analysis by sorting the cells according
 566 to its normalized position. The mean of 1% to 100% of the least deformable population fraction was
 567 then plotted to obtain a cumulative distribution profile of each sample, which is referred to as the
 568 deformability profile of that sample.

569 When more than two groups of samples were investigated, an ANOVA (Analysis of Variance)
 570 test was performed, after which an unpaired t-test was used to compare two groups of interest. Mean

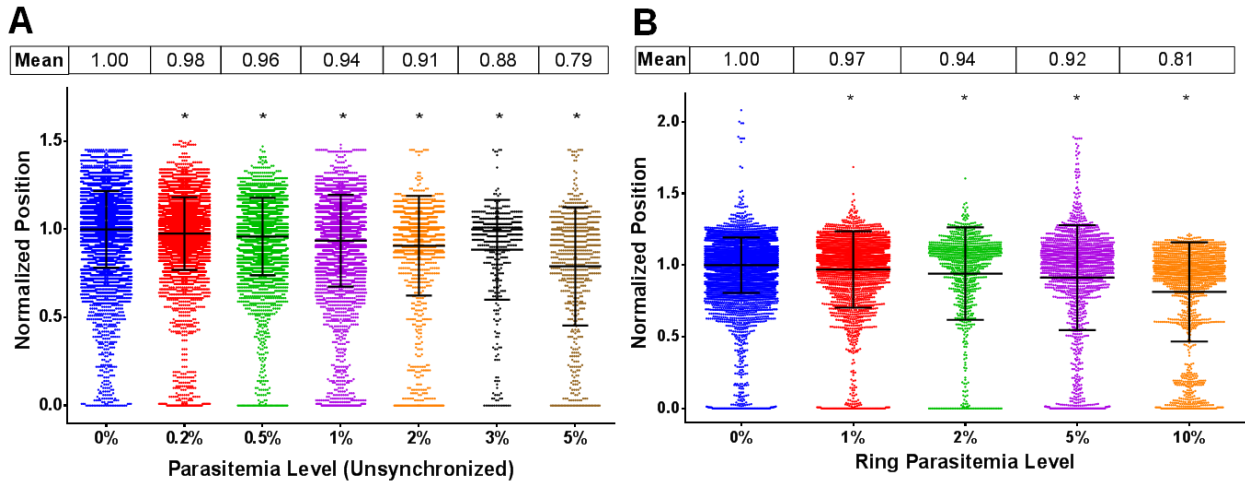
571 with the standard deviation (SD) was plotted for healthy and oxidatively damaged RBCs while median
572 with interquartile range (IQR) was plotted for parasitized RBCs and trophozoites treated with DMSO or
573 drugs. Linear regression was used in **Figure 3A** and **Figure 4D** while non-linear regression was used in
574 section **Figure 3D** to determine the relationship between two parameters. The coefficient of
575 determination (r^2 for linear regression and R^2 for non-linear regression) was used to indicate how good
576 the data fits the statistical model. All statistical analysis was done using GraphPad Prism v6 software
577 (Graphpad Software, US).

578 **Supplemental 6: Effect of Speed on RBCs Shape**



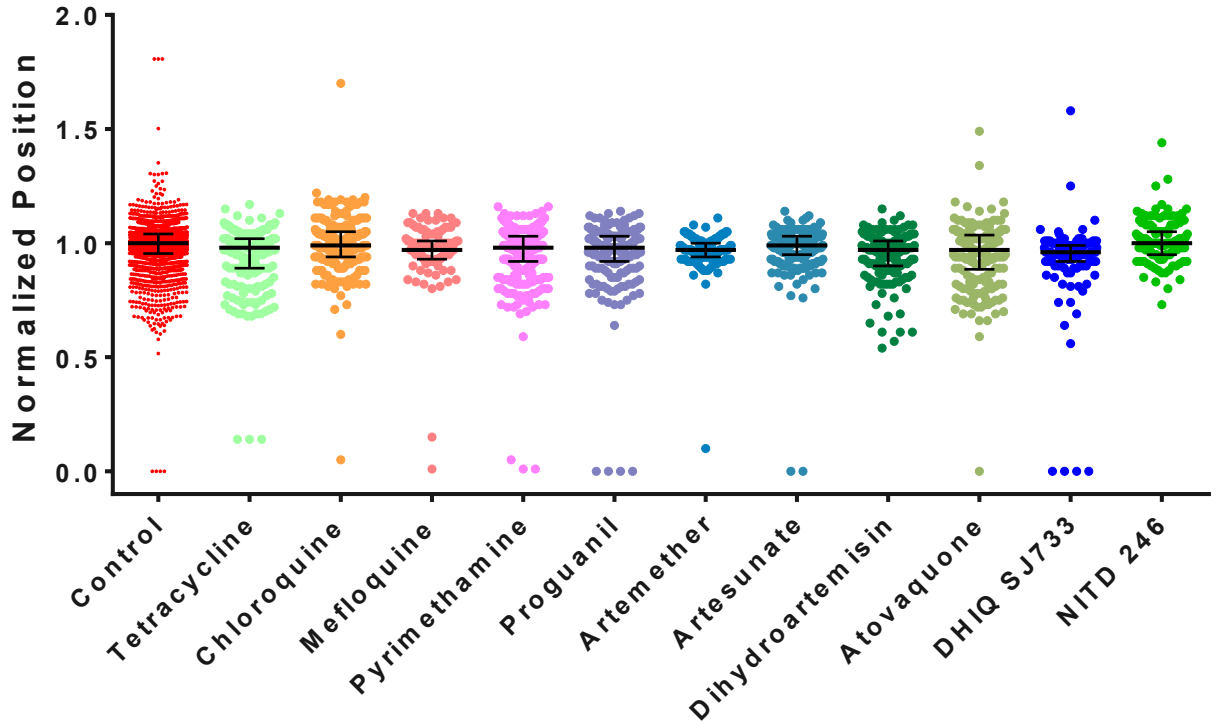
579 **Supplemental 6:** Shape of an RBC during deformation process: (A) at 15 Pa, the RBC goes back to its normal discoid
580 shape after each deformation; (B) at 120 Pa, the RBC remains in its deformed, “bullet” shape, resulting in a loss of
581 device capability to resolve the difference in RBC deformability.
582

583 Supplemental 7: Malaria data



584 **Supplemental 7: (A)** The deformability patterns of RBCs parasitized with unsynchronized *P. falciparum*. Each
 585 sample is normalized to the mean of the control. The normalized mean of the sample decreases with increasing
 587 parasitemia level, with $p < 0.0001$ for (*) with respect to control ($n = 8575$ for control and an $n \geq 500$ for 3%
 588 parasitemia level). **(B)** The deformability patterns of RBCs parasitized with synchronized *P. falciparum* at ring-stage
 589 show decreased mean normalized position occurring with increasing parasitemia level with $p < 0.0001$ for (*)
 590 ($n = 9074$ for control and an $n \geq 978$ for 2% parasitemia level).

591 **Supplemental 8: Antimalarials negative control using uninfected RBCs**



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593 **Supplemental 8:** Deformability of normal RBCs treated with $\geq 4 \times EC_{50}$ concentration of antimalarial drugs showing
594 no appreciable difference relative to control.

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High-throughput Analysis of Red Blood Cell Deformability

596 **Supplemental 9: Detailed result for antimalarial drug treatments**

597 **Supplemental 9:** Individual concentrations and normalized deformability values for various antimalarial drug
 598 treatments (n=616 for control and n≥100 for iRBCs)

Drug Name	Concentration (≥ 4 × EC50)	Number of RBCs	Median	% decrease vs. DMSO	p-value
Tetracycline	100 μM	245	1.00	0	0.54
Chloroquine	1 μM	502	0.66	34	<0.0001
Mefloquine	1 μM	281	0.67	33	<0.0001
Pyrimethamine	20 nM	267	0.55	45	<0.0001
Proguanil	100 μM	205	0.59	41	<0.0001
Arthemether	8 nM	364	0.24	76	<0.0001
Artesunate	10 nM	270	0.82	18	<0.0001
Dihydroartemisinin	20 nM	233	0.61	39	<0.0001
Atovaquone	250 nM	100	0.56	44	<0.0001
(+)-SJ733	1.08 μM	307	0.01	100	<0.0001
(-)-SJ733	1.08 μM	153	1.02	-2%	0.1
NITD246	3.6 nM	369	0.00	100	<0.0001

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