

**Supporting Information for**  
**Digital PCR on a SlipChip**

*Feng Shen, Wenbin Du, Jason E. Kreutz, Alice Fok, and Rustem F. Ismagilov*

Department of Chemistry and Institute for Biophysical Dynamics, The University of Chicago,

929 E 57th St, Chicago, Illinois 60637

**Derivation of Equation 1 to estimate template concentration:**

The Poisson equation (Equation S1),

$$p = (\lambda^k \cdot e^{-\lambda}) / k! \quad (\text{S1})$$

simplifies to  $\mathbf{p} = \mathbf{e}^{-\lambda}$  when  $\mathbf{k} = \mathbf{0}$ , where  $\mathbf{p}$  is the probability of having  $\mathbf{k}$  particles in a well given  $\lambda$ , the average concentration of particles per well. The average concentration is different at each dilution factor, but  $\lambda$  can be found using the expression  $\lambda = \mathbf{c} \cdot \mathbf{x}$ , where  $\mathbf{x}$  is the dilution factor of the original concentration,  $\mathbf{c}$ . Using  $\mathbf{s}/\mathbf{n}$  as an estimator of  $\mathbf{p}$ , where  $\mathbf{s}$  is the number of negative wells,  $\mathbf{f}$  is the number of positive wells, and  $\mathbf{n}$  is the total number of wells (so  $\mathbf{s} = \mathbf{n} - \mathbf{f}$ ), then Equation S2 is generated:

$$\frac{(n - f)}{n} = e^{-c \cdot x} \quad (\text{S2})$$

This equation can be linearized by taking the natural logarithm (ln) of both sides to give Equation S1 (also Equation 1 in the main text)

$$Y = \ln(n - f) = -c \cdot x + \ln n \quad (\text{S3, 1})$$

The y-intercept then gives the number of wells, so can be used to test the suitability of the equation, or used to constrain the fit based on the known  $\mathbf{n}$ . The slope then gives the negative concentration in terms of particles/well.

**Table S1. Number of positive wells in each quadrant of the SlipChip for various concentrations of genomic DNA and agreement with the 95% CI.**

	Number of positive wells in quadrant				Average # per quadrant	Score based 95% CI range		Rounded 95% CI	
	Upper Left	Upper Right	Lower Left	Lower Right		Lower limit	Upper limit	Lower limit	Upper limit
<b>1 fg/<math>\mu</math>L</b>									
Trial 1	0	1	1	1	0.75	0.11	5.17	0	5
Trial 2	0	2	0	0	0.50	0.05	4.73	0	5
Trial 3	0	0	1	0	0.25	0.01	4.28	0	4
Trial 4	0	0	1	1	0.50	0.05	4.73	0	5
<b>10 fg/<math>\mu</math>L</b>									
Trial 1	3	5	5	4	4.25	1.70	10.49	2	10
Trial 2	5	4	3	0*	3.00	1.02	8.70	1	9
Trial 3	5	3	3	0*	2.75	0.90	8.33	1	8
<b>100 fg/<math>\mu</math>L</b>									
Trial 1	24	21	22	16	20.75	13.66	31.14	14	31
Trial 2	18	22	19	26	21.25	14.06	31.73	14	32
Trial 3	19	13	15	24	17.75	11.28	27.59	11	28
<b>1 pg/<math>\mu</math>L</b>									
Trial 1	154	159	159	151	155.75	138.38	173.22	138	173
Trial 2	151	145	135	140	142.75	125.63	160.28	126	160
Trial 3	131	140	152	148	142.75	125.63	160.28	126	160

\*These values fell outside the CI.