Supplementary information - Polymer conformation during flow of viscoelastic solution in a porous media

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- 1. Two movies, SM-1 and SM-2 are included in the supplementary information. Both these movies show one instance of DNA chain (marked with dotted circle) approaching the pillar. The DNA chains coil at the tip of DZ and as it enters the DZ it stretches and rotates in a direction perpendicular to the flow. $\dot{\gamma}_{app} = 3.3 \text{ s}^{-1}$, $C_s = 0 \text{ mM}$ NaCl, Wi = 290.98, Ma = 0.95, Re $\ll 1$.
- 2. Table S1, we summarize the mean DNA fractional extension, μ and skewness, s.
- 3. In fig. S1 we show the stead-shear rheology of 0.2 gL^{-1} PAA solutions at $22 \degree \text{C}$ in DI water ($C_s = 0 \text{ mM}$) and in presence of salt ($C_s = 6 \text{ mM}$).
- 4. In fig. S2 we show the results from pressure drop measurement across the periodic array. In fig. S2a the standard deviation (std) of the ΔP fluctuations in the microfluidic device. The sampling period for Newtonian fluid flow is 120 s and for polymer solution flow is 600 s. All three solid are obtained by fitting power law equation of type $y = ax^b$ through experimental data. For Newtonian data, regression is performed over all data points. For polymer solution data, regression is performed for data beyond $\dot{\gamma}_{app} = 10 \text{ s}^{-1}$. The onset point is obtained as the intersection of polymer solution lines with the Newtonian data lines. In fig. S2b, the apparent viscosity as calculated by Darcy's law is shown. Error bars are calculated based on std(ΔP).
- 5. In fig. S3 we show the probability distribution of DNA orientation angle, θ as Wi number increases. The DNA samples were located inside the DZ.
- 6. Fig. S4 shows schematic explaining the molecular parameters extracted from DNA-imaging. The end-to-end vector, \vec{R} is measured manually using ImageJ. The DNA extension, $\langle \vec{R} \rangle$ is the magnitude of \vec{R} , whereas the DNA orientation angle, θ is the angle of \vec{R} . θ is 0° in the direction of flow (*x*-axis), whereas it is 90° in the direction perpendicular to the flow (along the microfluidic device width, *y*-axis).
- 7. Fig. S5 shows the velocity field for flow of the 200 ppm PAA solution (in DI Water) through pillared array at $\dot{\gamma}_{app} = 0.07 \,\text{s}^{-1}$ (Wi = 5.8). We can see the dead zone formation in the left figure. The velocity field appears not to be time dependent. Details of the PIV calculations are the PIV vector calculation was performed using LaVision DaVis 8.4.0 (LaVision inc, England). The background noise was subtracted by subtracting the average intensity of the raw images (in time)

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	$C_s = 0 \mathrm{mM}$		$C_s = 6 \mathrm{mM}$	
	Coil	Stretch	Coil	Stretch
$\dot{\gamma}_{app}=3.3s^{-1}$	$\mu = 0.18 \pm 0.12$ s = 3.08	$\mu = 0.30 \pm 0.15$ s = 0.69	$\mu = 0.09 \pm 0.02$ s = 0.84	$\mu = 0.15 \pm 0.07$ s = 1.00
$\dot{\gamma}_{app}=33s^{-1}$	$\mu = 0.21 \pm 0.04 \\ s = 0.14$	$\mu = 0.53 \pm 0.18$ s = 1.04	$\mu = 0.11 \pm 0.03$ s = 0.38	$\mu = 0.22 \pm 0.1$ s = 1.21

Table S1: DNA fractional extension mean, μ and skewness, *s* at the DZ tip (coil) and close to pillar (stretch).

Table S2: Summary of DNA fractional extension inside DZ, local De and DNA velocity inside DZ. The standard deviation of De_{loc} and v_{DNA} values is based on an ensemble of 20 individual DNA tracking velocimetry measurements, whereas the standard deviation of DNA fractional extension is based on the number of DNA molecules measured as shown in fig. 5c

DNA fractional extension (-)	Deloc (-)	$v_{\rm DNA}~(\mu m{ m s}^{-1})$
0.15 ± 0.07	0.59 ± 0.28	78.48 ± 27.43
0.22 ± 0.10	4.76 ± 1.45	497.19 ± 174.17
0.30 ± 0.15	15.55 ± 5.00	19.28 ± 5.24
0.53 ± 0.18	735.60 ± 250.20	573.29 ± 202.09

from each raw image. The pillars were then masked out using geometric masks. Vector were obtained using multipass FFT based cross correlation with window sizes from 64x64 px (50%, 2 pass) to 16x16 px (50%, 3 pass). Spurious vectors were removed using a median filter. Sub-pixel interpolation was done using a 3 point Gaussian estimator. Final presented results are average of 100 instantaneous vector fields (average in time). The peak standard deviation in velocity is around $5.25 \times 10^{-5} \,\mathrm{m\,s^{-1}}$ (at zones with high velocity). Calibration was done with pillar diameter. The other derived parameters were based on the average velocity field using in built functions.

- 8. Fig.S6 shows the ratio of the polymer apparent viscosity to the steady shear viscosity calculated at the apparent shear rate, η_{app} plotted against the Wi number.
- 9. Table S2 shows the DNA fractional extension inside DZ, local Deborah number, De_{loc} and the DNA velocity, v_{DNA} inside the DZ.



Figure S1: (b) Steady-state shear rheology of 0.2 gL^{-1} PAA solutions at 22 °C in DI water ($C_s = 0 \text{ mM}$ NaCl, filled-circle symbol) and in presence of salt ($C_s = 6 \text{ mM}$ NaCl, filled-square symbol). The solid line is a Carreau model fit (eqn. ??) to the shear rheology.



Figure S2: (a) Standard deviation (std) of the ΔP fluctuations. The dotted curve is fitted to the data. (b) The apparent viscosity as calculated from Darcy's law. The solid lines are spline fit to the data, shown as a guide to the reader's eye. Error bars are based on std(ΔP).



Figure S3: Probability distribution of DNA orientation angle, θ as Wi number increases. *N* is the number of samples measured and all the samples are located inside the DZ.



Figure S4: Schematic showing DNA chain end-to-end vector, \vec{R} and the orientation angle, θ .



Figure S5: (a) Streamline snapshots and the (b-c) the velocity field calculated by PIV at Wi = 5.8 or $\dot{\gamma}_{app} = 0.07 \,\text{s}^{-1}$. The fluid is 200 ppm PAA in DI water. Flow direction is from right to left. (c) shows a zoomed-in image of the velocity field in the DZ.



Figure S6: Figure showing ratio of the apparent viscosity, η_{app} and the steady-shear viscosity, η_{Sh} at the apparent shear rate, $\dot{\gamma}_{app}$ as a function of the Wi number.