Electronic Supplementary Material (ESI) for Analyst.

Supporting Information

Ferguson analysis of protein electromigration during single-cell electrophoresis in an open microfluidic device

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Figure S1. Additional false-color fluorescence micrographs and intensity plots of electromigration for PTBP1, HSP90, SFPQ, and Vinculin protein targets

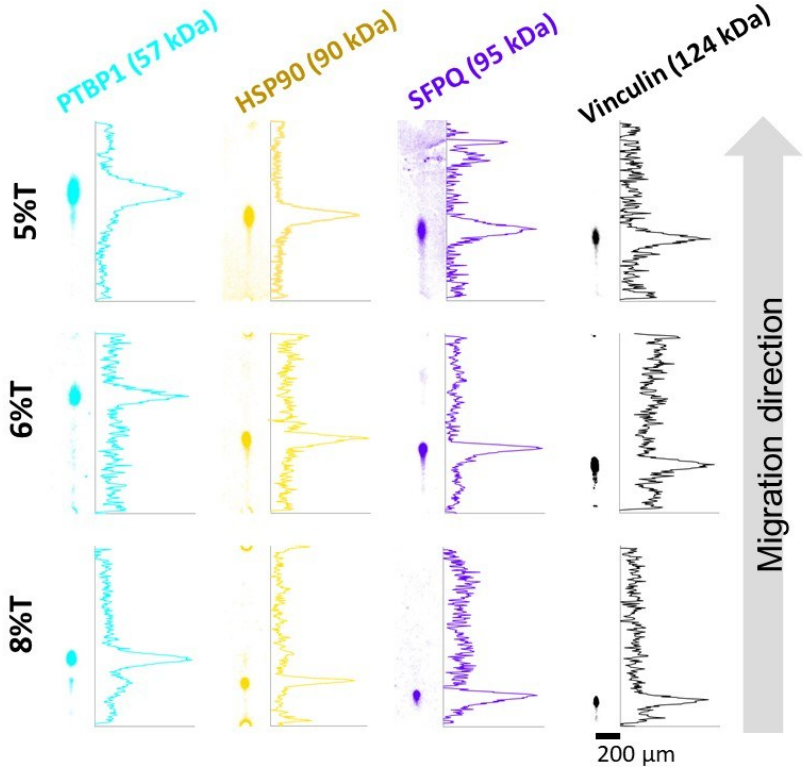

Figure S1 False-color fluorescence micrographs and corresponding intensity plots of additional protein targets: PTBP1 (57 kDa, above limit of detection in 6/9 gels tested), HSP90 (90 kDa), SFPQ (95 kDa), and Vinculin (124 kDa) from lysed MCF-7 cells assayed in all three gel conditions (5%, 6%, and 8%T).

Figure S2. Percent of the peaks that pass QC in the MATLAB scripts and have SNR ≥ 3

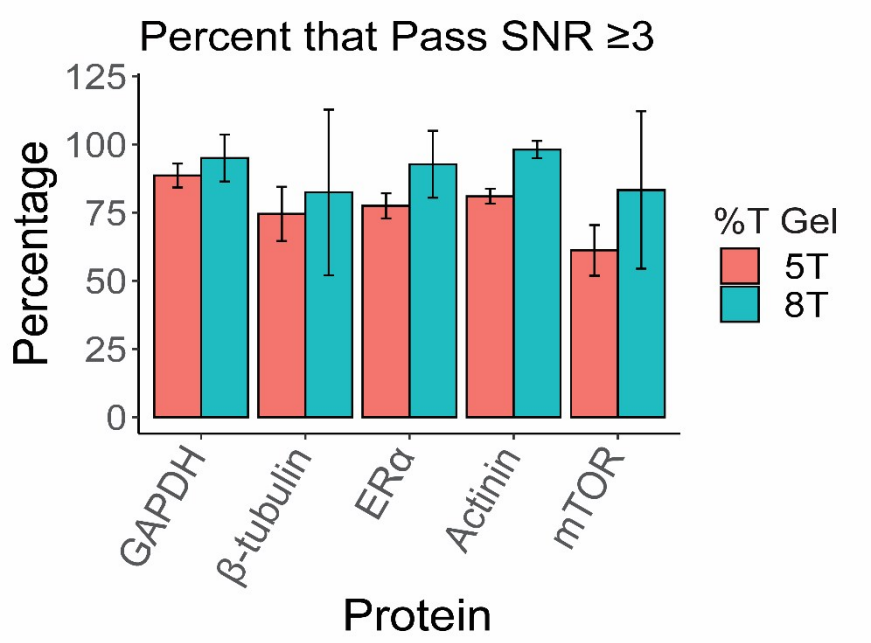

Figure S2. Percentage of protein peaks that have SNR ≥ 3 out of total number of protein peaks that passed initial quality control in the custom MATLAB scripts and for each protein comparing large pore size gel (5%T) to small pore size gel (8%T). Each bar represents the average percentage of 3 replicate devices with the error bars representing standard deviation.

$$\text{Percent that Pass SNR} \geq 3 = \frac{Peaks\ with\ SNR \geq 3}{All\ Peaks\ that\ Pass\ QC\ (R^2 \geq 0.7\ and\ visual)}$$

To compare the percentage of detected protein peaks that can be analyzed (SNR ≥ 3), the percentage of detected protein peaks that pass all quality control steps was calculated. The in-house MATLAB (R2018b) scripts used to quantify fluorescence signal from immunoblots identifies all the peaks that are detected and pass initial QC (Gaussian fit R^2-value ≥ 0.7 and visual inspection). Further screening is then performed to only accept intensity profiles containing peaks with SNR ≥ 3 (the numerator). The percent of peaks with an SNR ≥ 3 was calculated for each replicate device across all protein targets for the highest and lowest gel concentration. The mean and standard deviation of the three replicate devices is plotted to show that in general, we are able to recover a higher percent of detected peaks for the 8%T gel condition across all five protein targets. However, with a small *n* we cannot make significant conclusions.