

Supplementary Information

2D Separations on a 1D Chip: Gradient Elution Moving Boundary Electrophoresis – Chiral Capillary Electrophoresis

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Figure S1

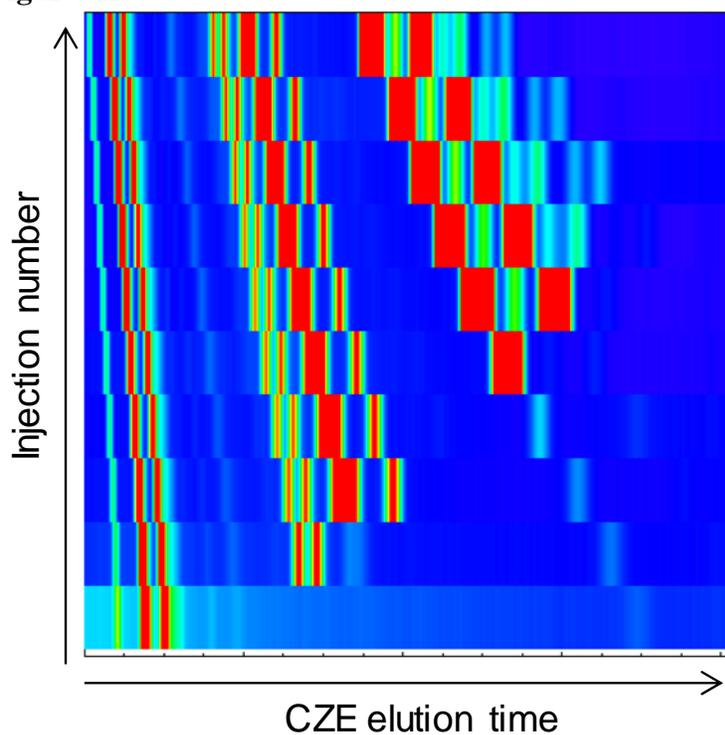


Figure S1. Raw data for 2D separation shown in Figure 3

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Figure S2

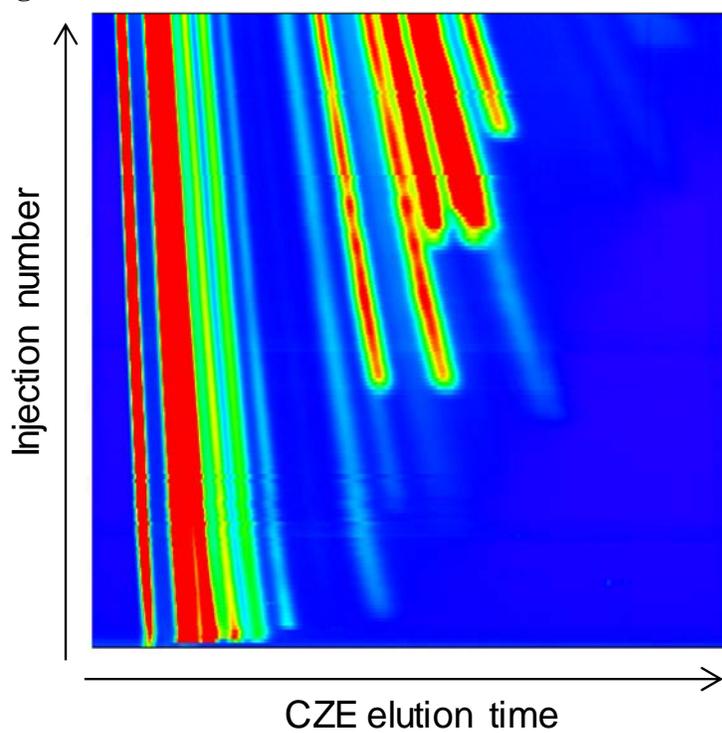


Figure S2. Raw data for 2D separation shown in Figure 4

Figure S3

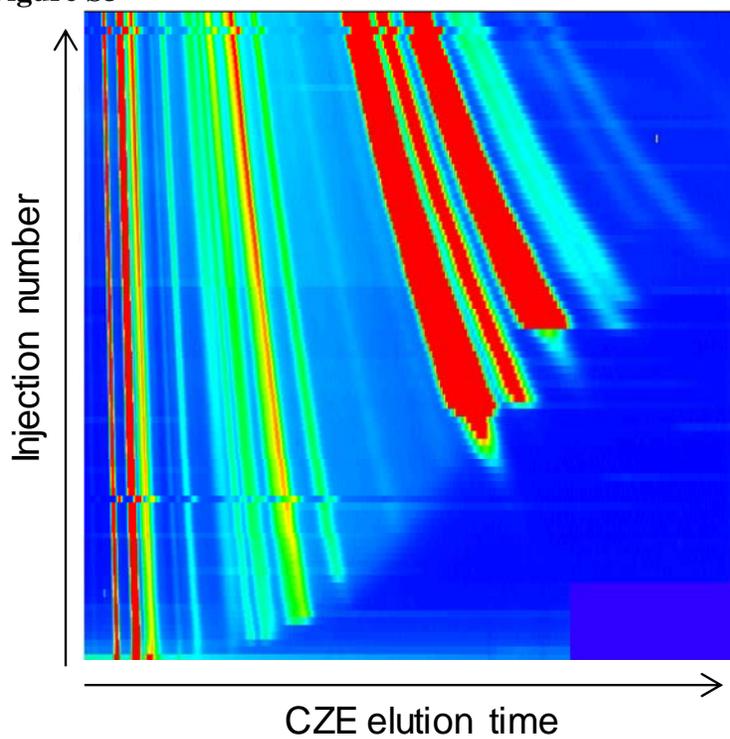


Figure S3. Raw data for 2D separation shown in Figure 5

Figure S4

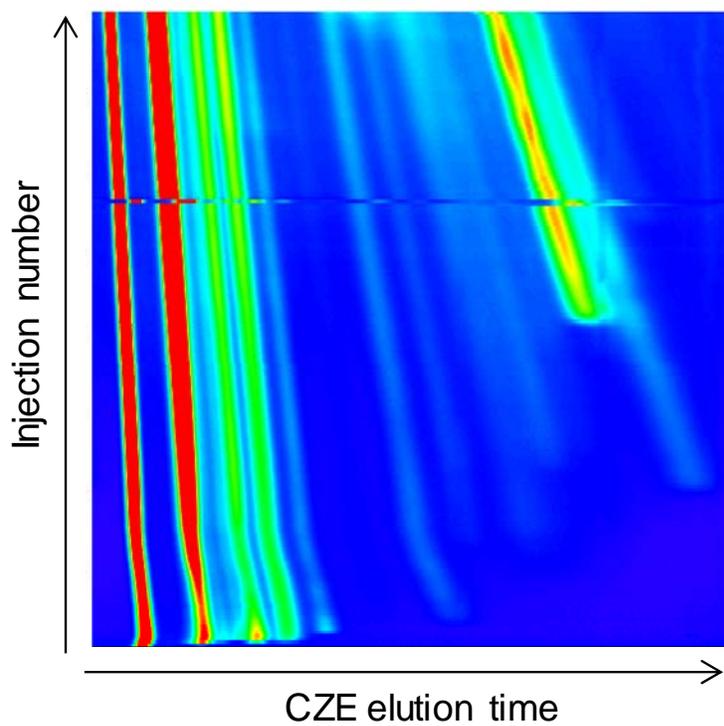


Figure S4. Raw data for 2D separation shown in Figure 7

Figure S5

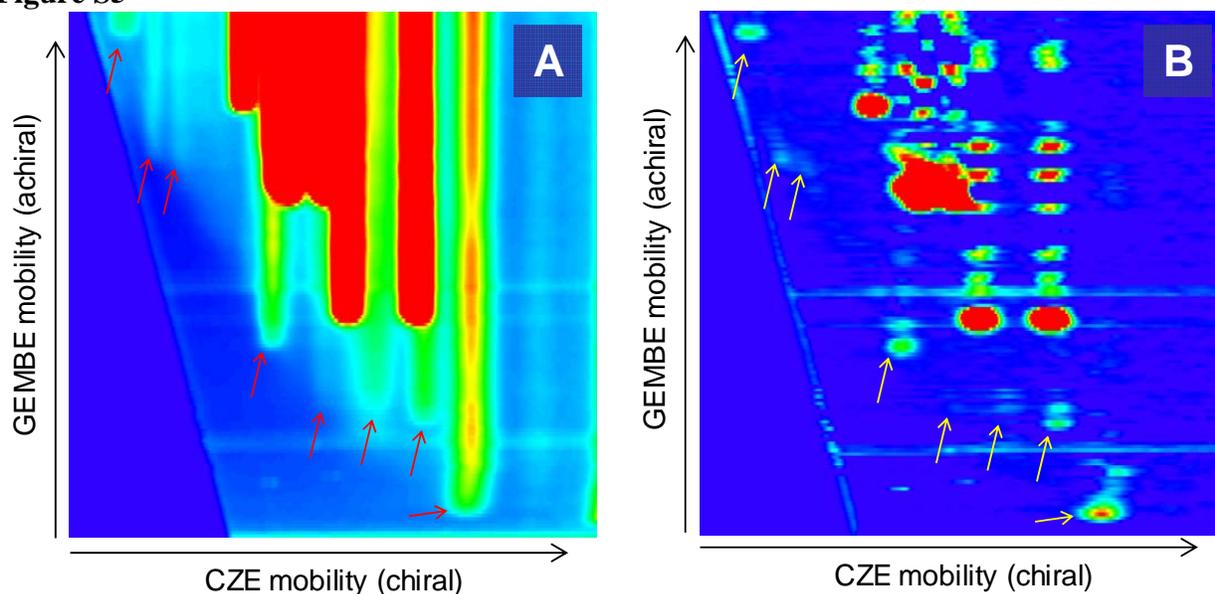


Figure S5. Re-plotting of data from Figure 4 (2D separation result for 190 nmol/L amino acid analysis) with false color scale set to show low-intensity unknown contaminants. False color images with red corresponding to higher concentration. Each known amino acid enantiomer was present in the sample at 190 nmol/L.

(A) High resolution 2D “stripe” plot of neutral amino acid region. Each stripe in the plot corresponds to a fluorescently labeled amine or amino acid. The position of the line along the x-axis indicates that amine’s mobility in the chiral CZE separation, and the start point of each stripe along the y-axis indicates the amine’s mobility in the achiral GEMBE separation. Arrows indicate the start point of several low-intensity detected stripes.

(B) High resolution 2D derivative plot. Each amino acid corresponds to a spot on the derivative plot, though there are extra spots from fluctuations in the measured intensity of the higher concentration stripes shown in (A).