Supporting material I

Single-shot proteomics using capillary zone electrophoresis-electrospray ionization-tandem mass spectrometry produces more than 1,250 *E. coli* peptide identifications in a 50-minute separation

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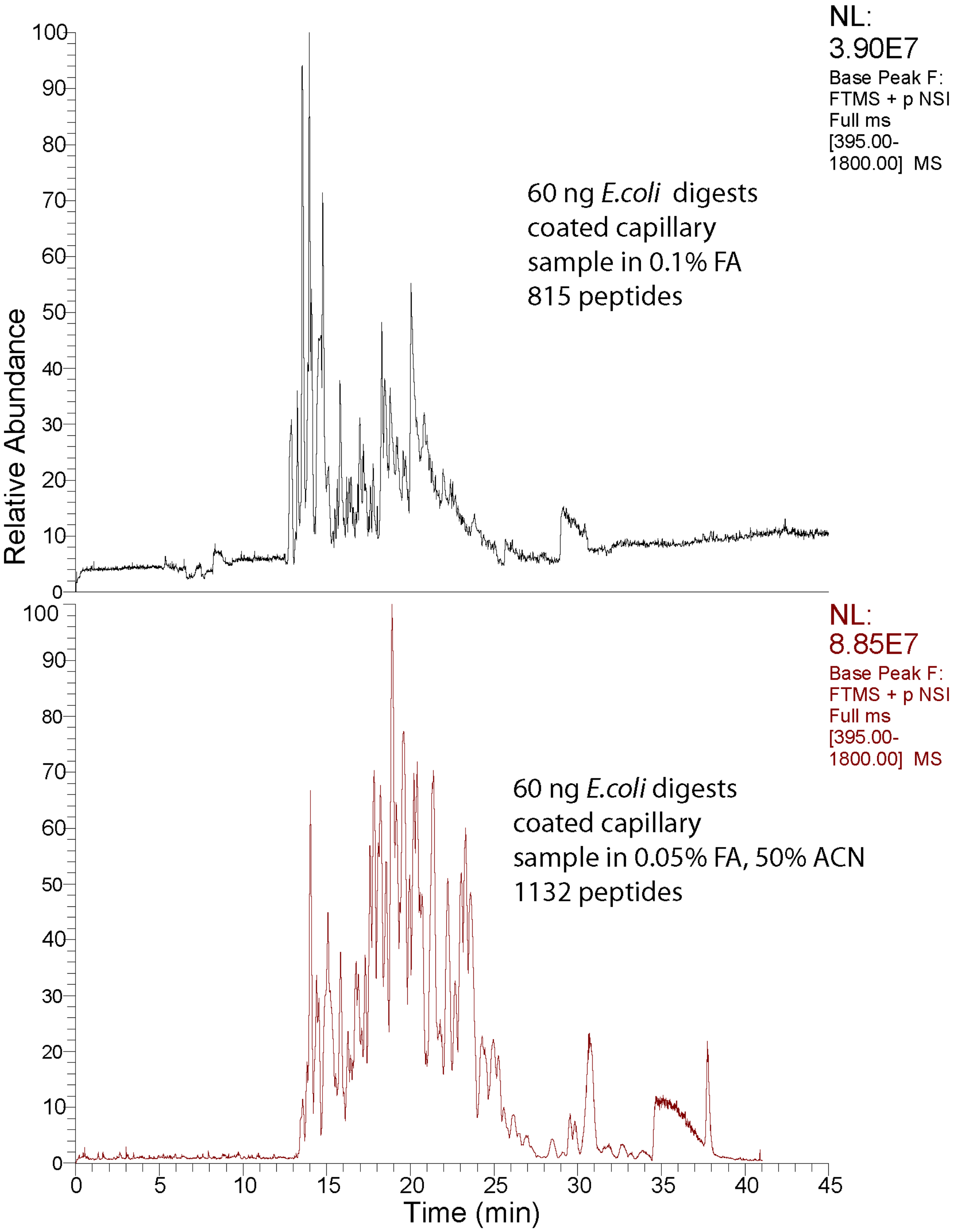
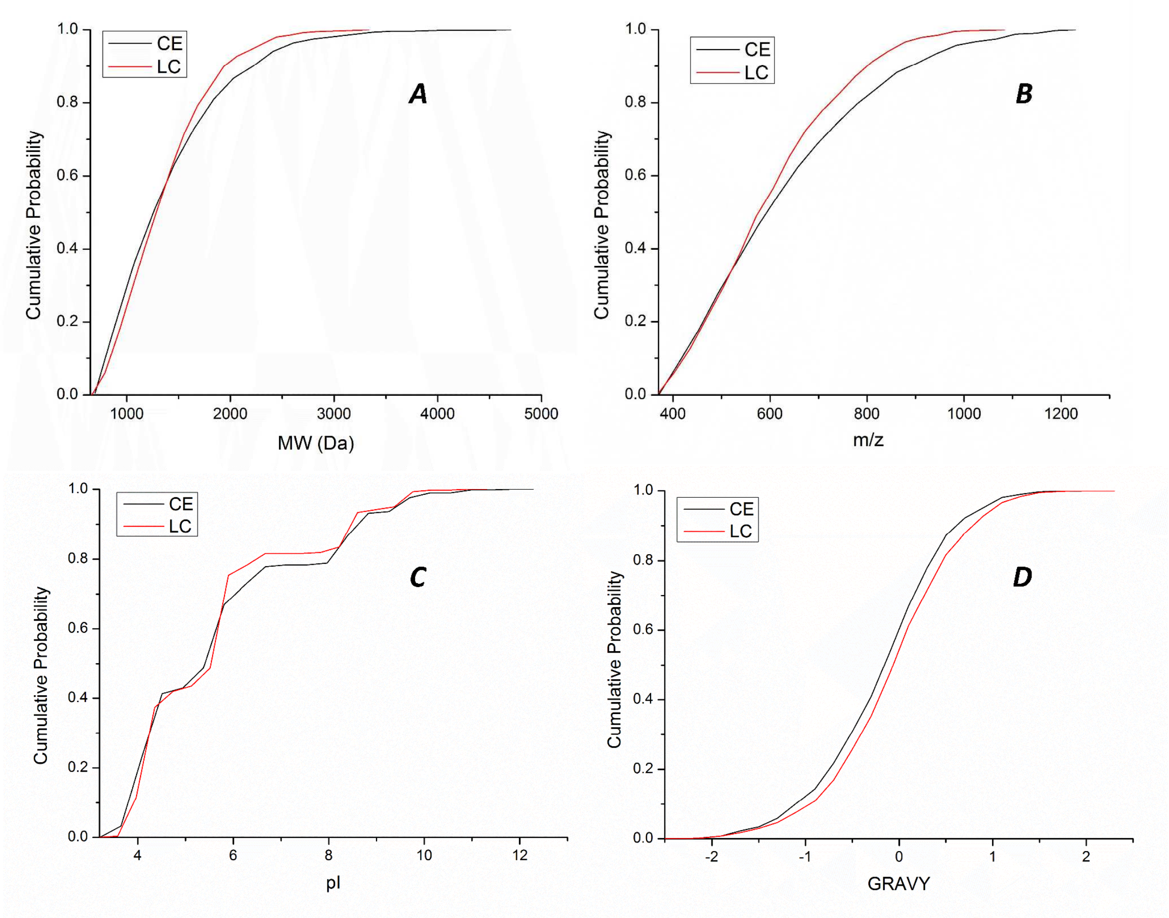
S-Table 1 Peak intensities of five selected peptides produced by CZE-ESI-MS/MS and UPLC-ESI-MS/MS for the analysis of 1 ng *E. coli* tryptic digest

	CZE-ESI-MS/MS		UPLC-ESI-MS/MS	
	Peak intensity	RSD	Peak intensity	RSD
ELLSQYDFPGDDTPIVR(m/z 982.9840)	(8.8 ± 1.3)E5	15%	(4.59 ± 0.25)E4	5.5%
AGENVGVLLR (m/z 514.2988)	(3.9 ± 0.9)E6	23%	(3.7 ± 1.4)E5	37%
SNTGLVIDPYFSGTK(m/z 799.9069)	(4.1 ± 0.8)E5	19%	(4.4 ± 0.7)E4	15%
EADKLGYNLVVLDSQNNPAK(m/z 730.0469)	(3.18 ± 0.14)E5	4.3%	(1.74 ± 0.09)E4	5.2%
VIELQGIAGTSAAR (m/z 693.3914)	(1.35 ± 0.16)E6	12%	(1.4 ± 0.6)E5	42%



S-Figure 1 Base peak spectra of 60 ng *E.coli* digests dissolved in 0.1% FA and 0.05% FA with 50% ACN analyzed by CZE-ESI-MS/MS.



S- Figure 2 Cumulative distribution of molecular weight(A), m/z(B),pI values(C) and GRAVY values(D) of identified peptides in CZE-ESI-MS/MS (black) and UPLC-ESI-MS/MS (red) for 10 ng sample loading amount.