Improved Single Cell Proteome Coverage Using Narrow-Bore Packed NanoLC Columns and Ultrasensitive Mass Spectrometry

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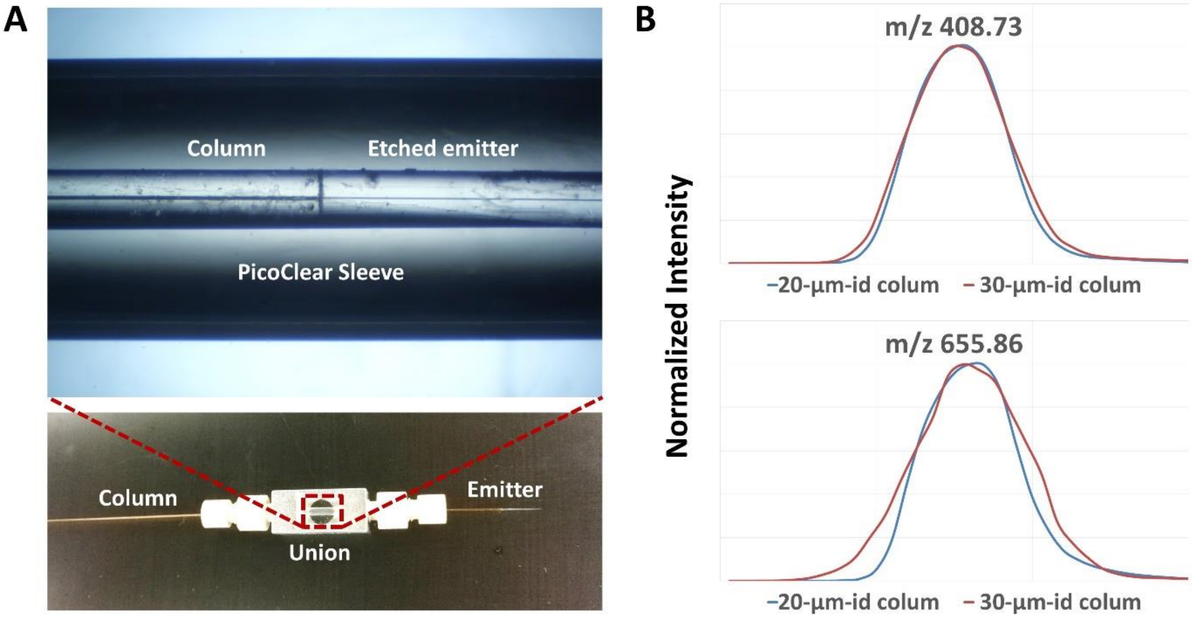

Figure S1. (A) Zero-dead-volume connection between 20-µm-i.d. column and 10-µm-i.d. etched emitter. Polyimide capillary coating was removed to show a clear connection. (B) Similar peak widths achieved using the 20-µm-i.d. column with connected emitter and 30-µm-i.d. column with integrated emitter.

Table S1. Number of Unique peptides and protein groups identified from samples using 20 µm i.d. column and Eclipse.

	Identification	100 Hela cells	20 Hela cells	Single cell 1	Single cell 2	Single cell 3	Single cell 4 (Large Hela cell)	Blank
Unique peptides	By MS/MS	9615	7261	1260	1021	1551	3062	12
	By MS/MS+MBR	9839	7908	3657	3661	3059	5865	95
Protein groups	By MS/MS	1646	1386	351	334	402	704	6
	By MS/MS+MBR	1664	1478	910	934	778	1292	88

Raw data files corresponding to Table S1 are available at the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD016921.