## Toward Artifacts-Free Data in Hadamard Transform-based Double Multiplexing of Ion

Mobility – Orbitrap Mass Spectrometry.

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Data plots in Figure 5 mapped into a single plot. Note that the actual peak is preserved in sign and position while the peaks corresponding to the artifacts have negative or zero values in at least one of the child sequences.





(A) Part of the double multiplexed data (m/z 777.5-778.0) for a mixture of Enolase and BSA tryptic digests. (B) Data demultiplexed using the algorithm reported previously<sup>26</sup> and (C) data demultiplexed using the current algorithm.

Figure S3



(A) Part of the data (m/z 928.3-928.7) for a mixture of Enolase and BSA tryptic digests collected in the signal averaging mode. (B) Total ion chromatogram.