SUPPORTING INFORMATION

HILIC-MS for Untargeted Profiling of the Free Glycation Product Diversity

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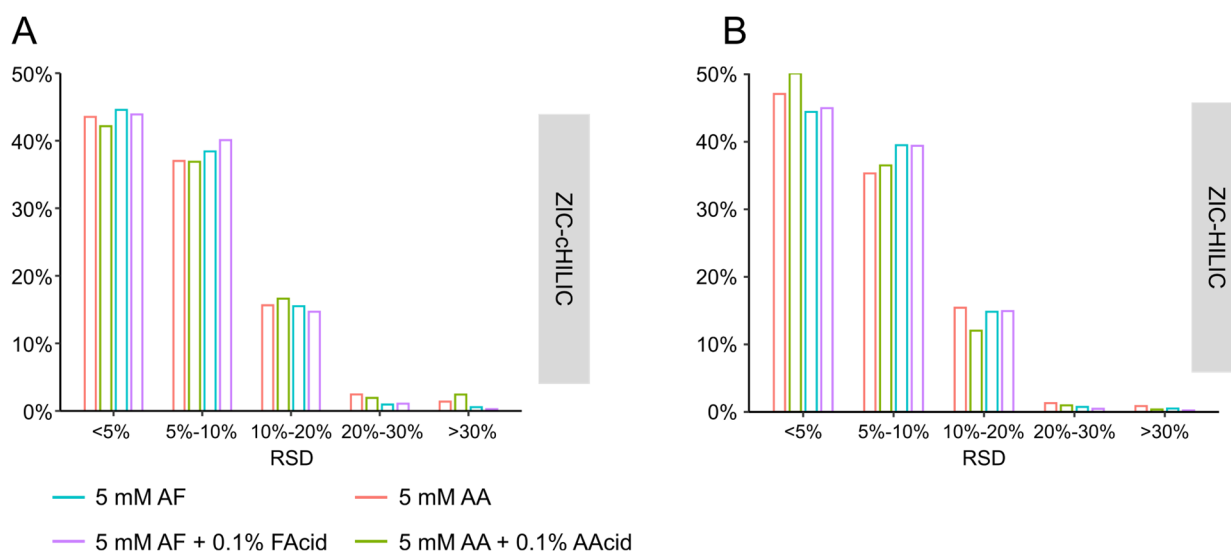
Figure S1. Relative standard derivation (RSD) distribution of all feature intensities detected by ZIC-cHILIC column (A) and ZIC-HILIC column (B) using different mobile phases.
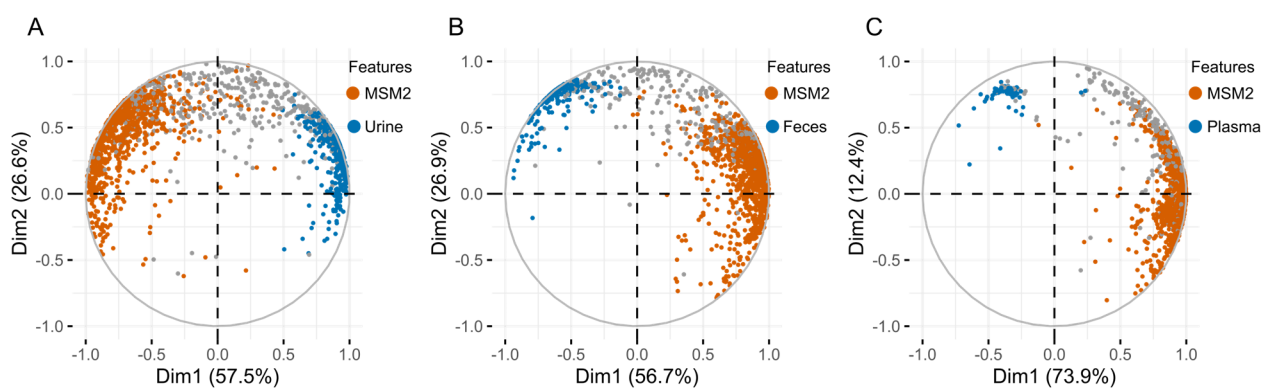

Figure S2. Principal component analysis (PCA) loading plots. Each loading plot corresponds to a PCA score plot in Figure 6A. In the loading plots, each point represents a feature with unique *m/z* and retention time. Points in blue refer to features that were only detected in biological samples: urine (A), feces (B) and plasma (C). Features in orange were only detected in model system mixture samples (lysine and arginine; MSM2).
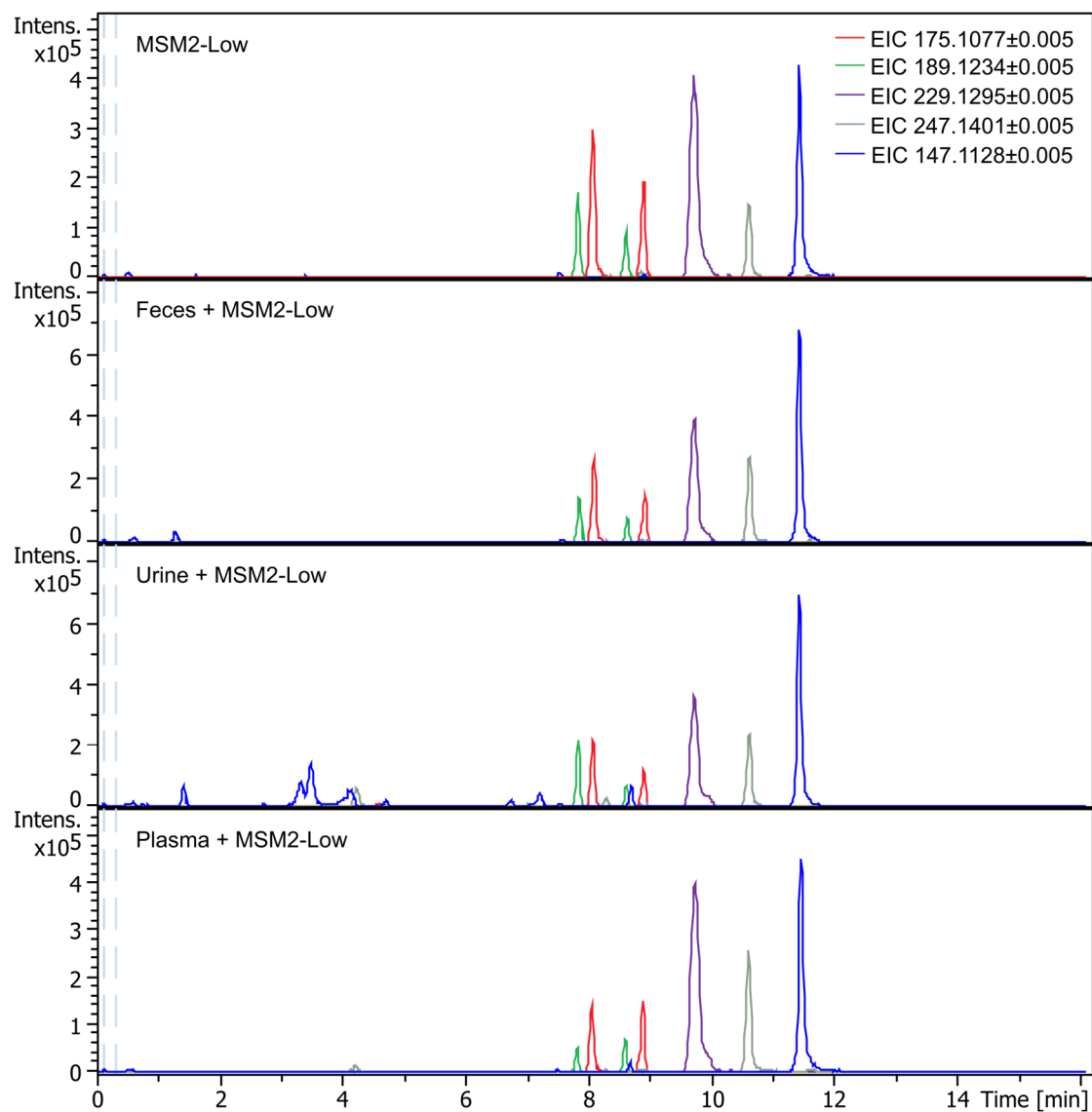
Figure S3. Representative extracted ion chromatograms (EICs) of amino acids and putative advanced glycation end products in the 25 times diluted model system mixture (lysine and arginine; MSM2), and model system-spiked biological samples; from top to bottom: model system mixture MSM2, MSM2 spiked feces, urine and plasma. EICs correspond to: formyllysine ($[M + H]^+$ = 175.1077, red), acetyllysine ($[M + H]^+$ = 189.1234, green), methylglyoxal hydroimidazolones ($[M + H]^+$ = 229.1295, purple), carboxyethylarginine ($[M + H]^+$ = 247.1401, grey), lysine ($[M + H]^+$ = 147.1128, blue).