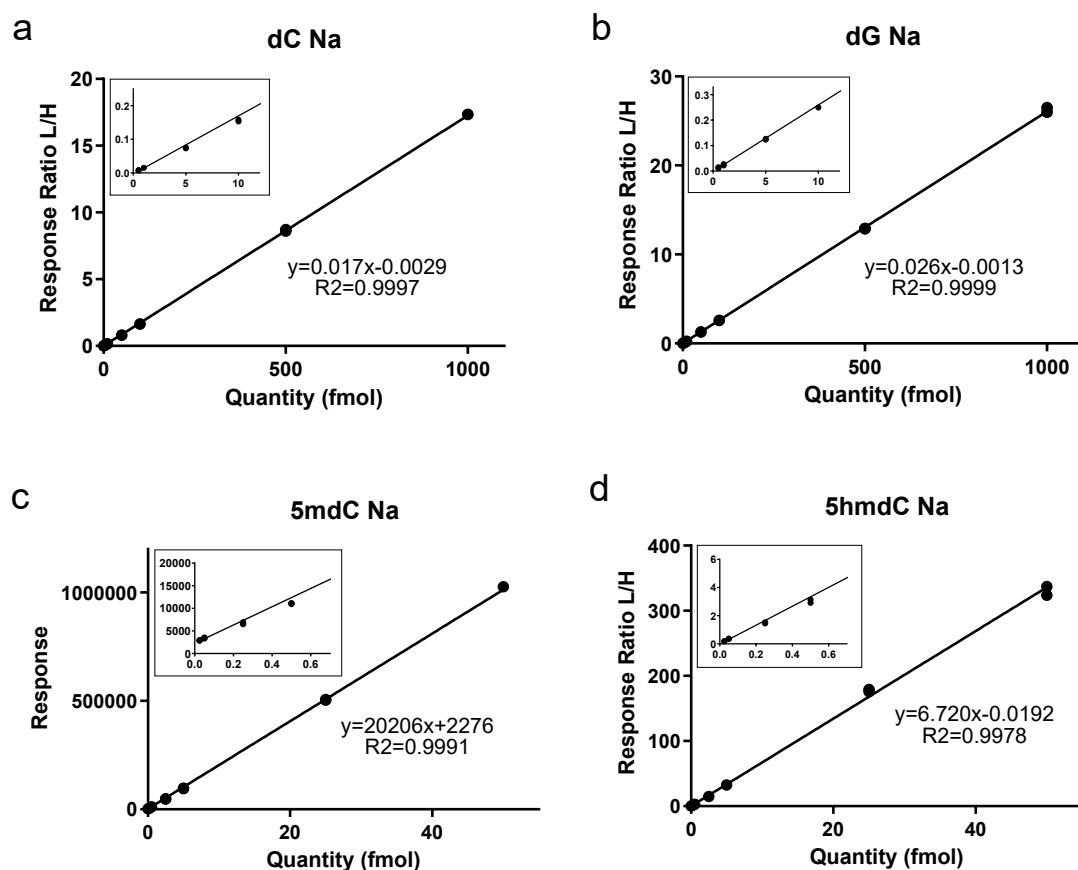
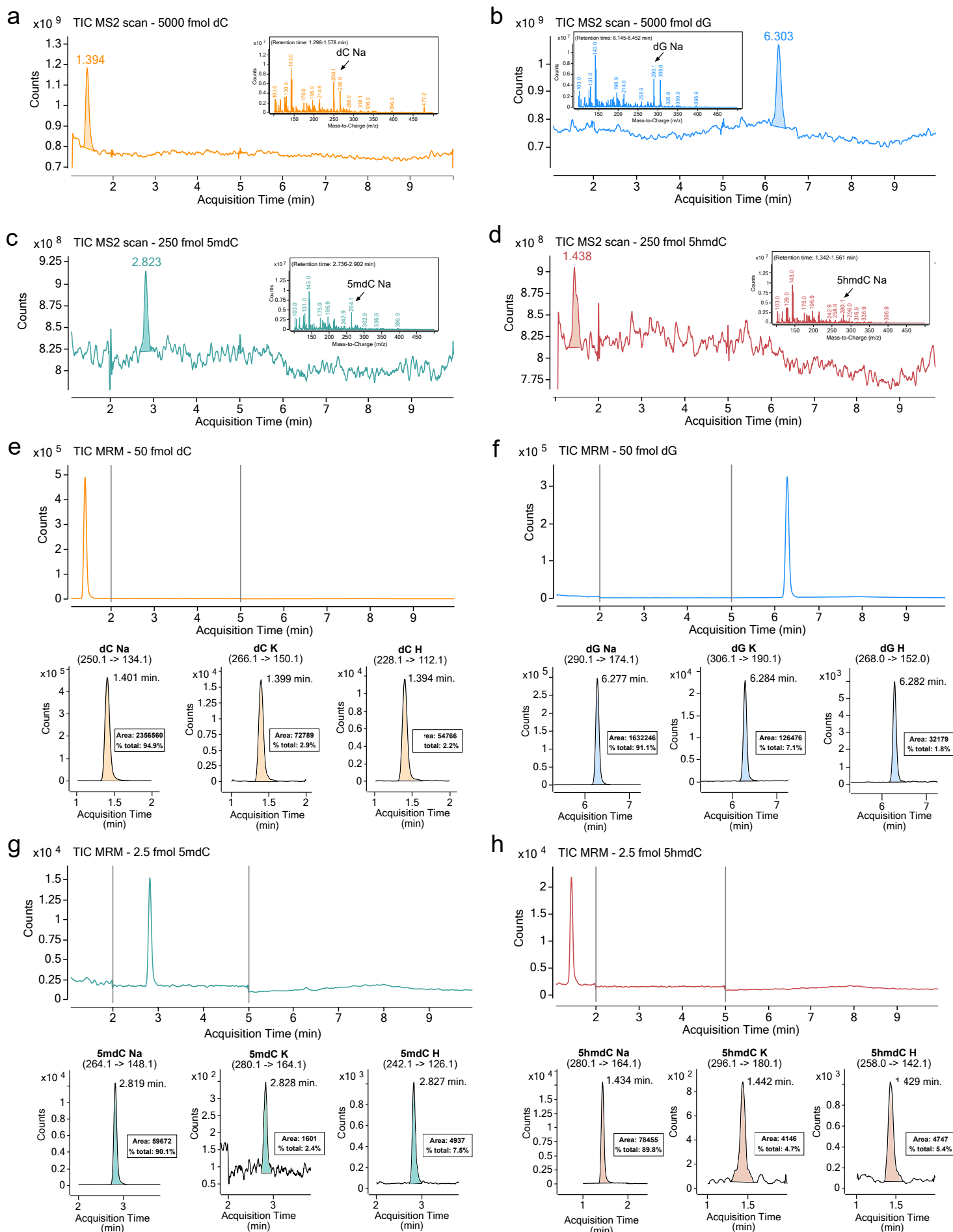


Quantifying propagation of DNA methylation and hydroxymethylation with iDEMS

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Supplementary Figure 1. Standard curves for the LC-MS/MS nucleoside quantification method for a) dC, b) dG, c) 5mdC and d) 5hmdC. The response for the different quantities of standards in femtomoles is represented as calculated by the mass spectrometry analysis. L/H: “Light” standards/“Heavy” isotope-labelled internal standards.



Supplementary Figure 2. Mass spectrometry assessment of nucleoside standards and the generated adducts. Total ionchromatograms (TIC) and inserted the MS2 scan from 100 to 500 m/z for a) dC, b) dG, c) 5mdC and d) 5hmdC. TIC for the standards in MRM mode and the main adducts detected are shown below for e) dC f) dG g) 5mdC h) 5hmdC.