Supplementary Materials

Modifying Protocol for HPLC-MS/MS

The UHPLC-MS/MS used in the assay we described may not be available to all researchers interested in this method. Tandem mass spectrometers have become widely available at many research institutions, while UHPLC equipment is less common. Built-in converter software applications are readily available to convert UHPLC methods to conventional HPLC methods, and vice versa, with concise instructions provided to the users. Such software and instructions are routinely available from the LC or MS vendors on request. Further, a literature search will reveal a number of publications on the topic of migrating UHPLC to HPLC and vice versa, such as Novakova et al. (2011). We selected UHPLC for the described assay, because it provides significant reduction in analysis time without loss in peak resolution.

Nováková L, Veuthey JL, Guillarme D. 2011. Practical method transfer from high performance liquid chromatography to ultra-high performance liquid chromatography: The importance of frictional heating. J Chromatogr A. **1218:** 7971– 7981

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Figure S1: Chromatograms of each nucleobase showing the elution order of a 1:1:1:1:1 mixture (1.0 ng each) of commercially supplied (a) cytosine, (b) adenine, (c) guanine, (d) uracil and (e) thymine. The blue line corresponds to the MRM trace of the ^{12}C species of each nucleobase, while red corresponds to the $MRM_{C12+1.}$ The cross-talk of signals from uracil into the cytosine channel (a, red and green lines) is due to the overlapping *m/z* of fragments.

Figure S2: Quantitation of ^{13}C-enriched RNA in CsTFA gradient fractions as a proportion of total RNA recovered (A) and by degree of enrichment (B). N.A. refers to the average % atom ^{13}C in unlabeled RNA.

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Figure S1

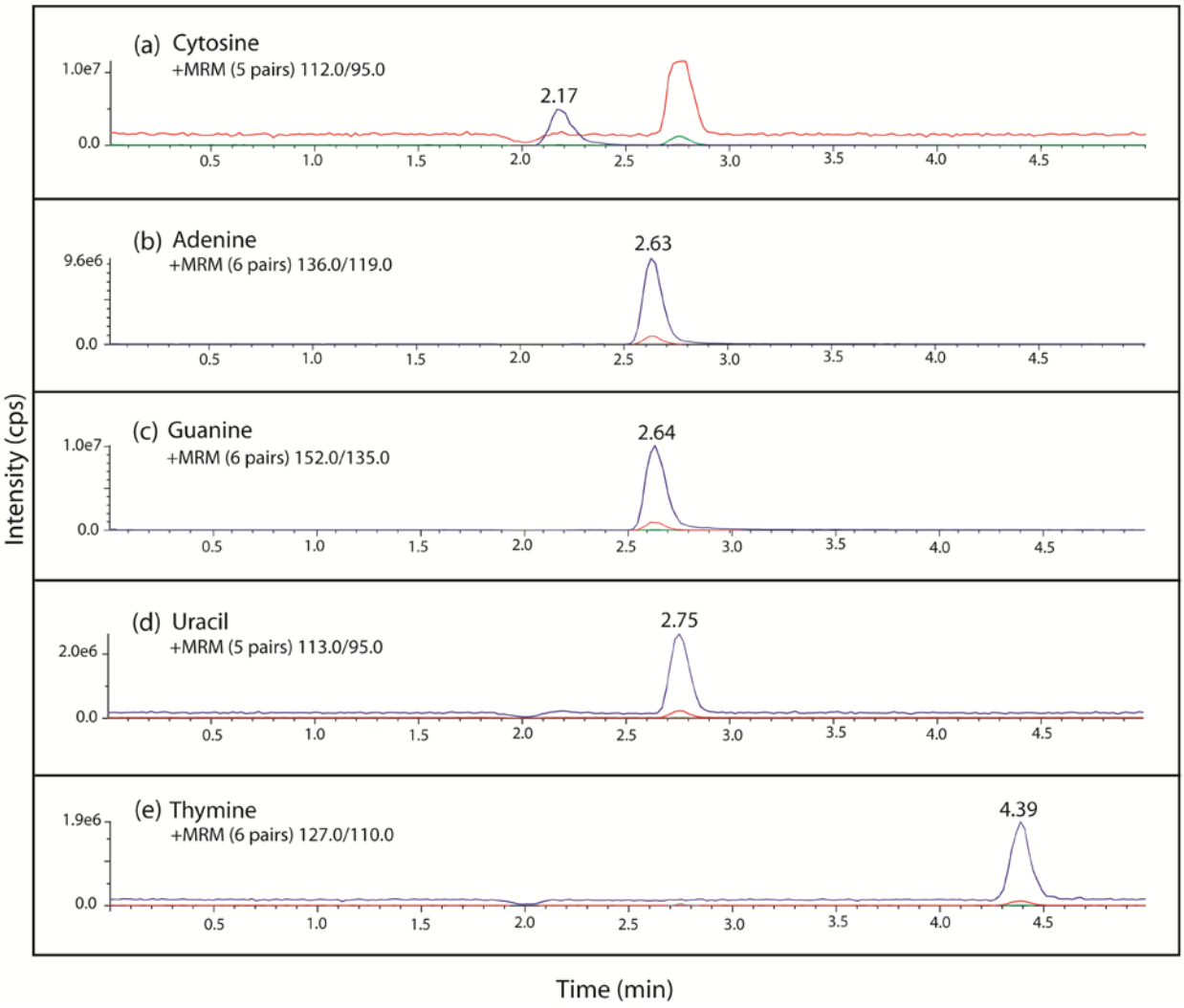

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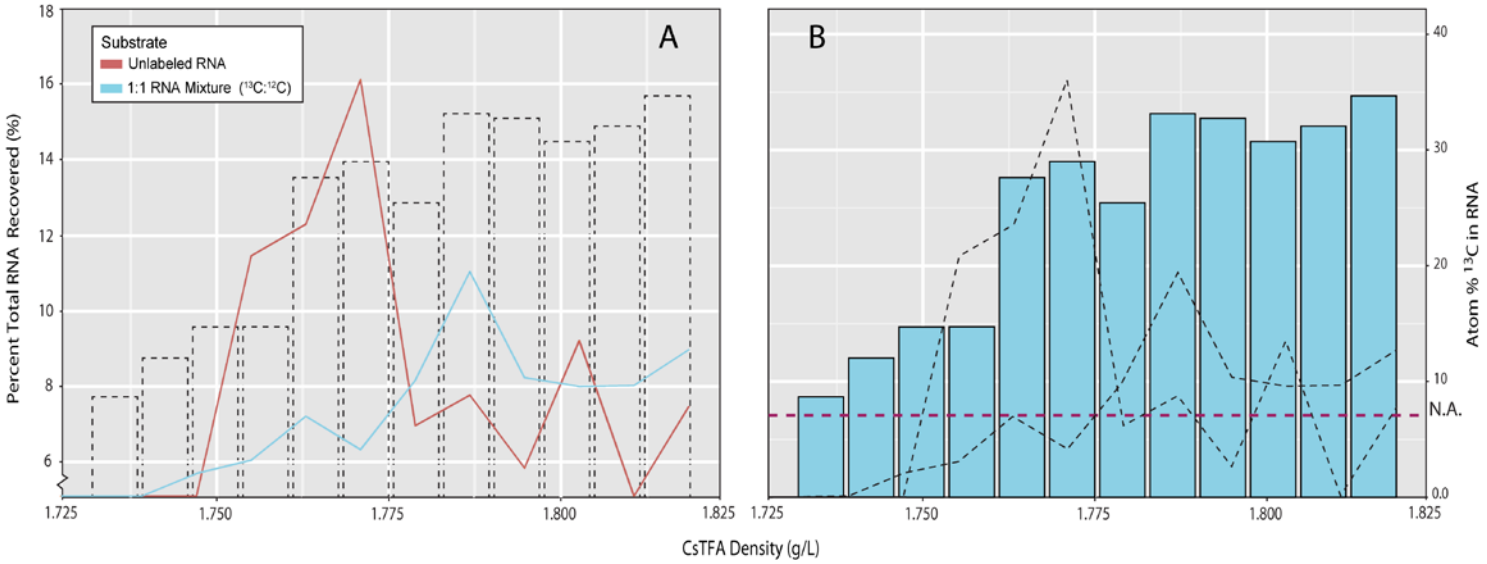
Figure S2



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