**Supplementary Information 2 –** **Free Mg2+ concentration error analysis**

The Metabolome Weakens RNA Thermodynamic Stability and   
Strengthens RNA Chemical Stability

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*Free Mg2+ concentration error analysis*

It is important to understand the error in the free Mg2+ concentration reported in artificial cytoplasm, and the impact of such errors to appropriately assess the results presented in the main text. In this supplement, we first analyze the precision of the free Mg2+ concentration determination using HQS, then provide a conservative estimate for the uncertainty in the free Mg2+ concentration reported in artificial cytoplasm. Lastly, we consider if errors in the free Mg2+ concentration could explain the results presented in the main text.

The biological free Mg2+ concentration range of 0.5 to 3.0 mM is within the linear range of the HQS calibration curve (Figure S2-1A). Propagation of the errors from the calibration curve fit used to determine the free Mg2+ concentration indicate that errors are minimized in the biological free Mg2+ concentration range, less than 5% of the calculated value (Figure S2-1B). The HQS assay is less precise outside of this range of free Mg2+ concentrations because large changes in Mg2+ concentrations only lead to small changes in HQS emission. For example, in the absence of chelators, 200 mM Mg2+ produces the same fluorescence emission as 100 mM Mg2+ (Figure S2-1A) because HQS is already completely bound at 100 mM Mg2+. Thus, the HQS assay is precise, with an uncertainty less than 5% of the measured free Mg2+ concentration within the biological free Mg2+ range, but not as precise outside of the biological free Mg2+ range.

It may appear that the free Mg2+ concentration is changing rapidly with the total Mg2+ concentration near 2 mM free Mg2+ in Figure 1E in the main text because there is almost no change at lower total concentrations and the linear y-axis/log10 transformed x-axis. However, the actual slope for this region is not large, at 0.08 mM free Mg2+ for each 1 mM increase in total Mg2+. This buffering is evidence that the free Mg2+ is constant near 2 mM given errors in the total Mg2+.

The true uncertainty for the free Mg2+ concentration in our experiments is hard to calculate, but 10%, or twice the propagated uncertainty from the fit in the biological free Mg2+ range (Figure S2-1B), is a conservative value. At 2 mM free Mg2+, this would be an uncertainty of 0.2 mM. A free Mg2+ concentration error of 0.2 mM would require an exceptionally large total Mg2+ error of 2.5 mM, given the buffering by Eco80 of 0.08 mM free Mg2+ for each 1 mM change in total Mg2+.

A Mg2+ concentration error of 0.2 mM is unlikely to impact our results. For example, we applied a tightly bound ion (TBI) theoretical model for mixed Na+ and Mg2+ solutions to calculate the change in free energy change (ΔΔG°37) from a 380 mM Na+ 2 mM free Mg2+ reference state as a function of the free Mg2+ concentration (Figure S2-1C).1 Accordingly, errors in the free Mg2+ concentration are unlikely to cause the free energy changes we observed in Figure 2, notably, the +0.69±0.12 kcal/mol we observed in Eco80. Indeed, a 1 mM free Mg2+ concentration error (an error of 50%) would be required to cause even a 0.25 kcal/mol fluctuation in the ΔG°37. A 1 mM free Mg2+ concentration error would require our estimate for the total Mg2+ required to provide 2 mM free Mg2+ in Eco80 to be off by 12.5 mM, given the free Mg2+ buffering capacity of Eco80. In summary, given the free Mg2+ buffering capacity of artificial cytoplasm and the precision of the HQS assay in the biological free Mg2+ range, our results cannot be explained by errors in the free Mg2+ concentration alone.

Chart

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**Figure S2-1** Analysis of free Mg2+ concentration errors in Eco80. **(A)** Figure 1B modified with a linear x-axis to show that the biological free Mg2+ range is within the linear range of the HQS calibration curve. **(B)** Uncertainty in the free Mg2+ concentration calculated from HQS emission, estimated by propagating uncertainty in the calibration fit coefficients, as a function of the free Mg2+ concentration calculated from HQS emission. **(C)** TBI theoretical model prediction of the ΔΔG°37 as a function of the free Mg2+ concentration for an 8 nucleotide helix. The reference state (380 mM Na+ and 2 mM Mg2+) approximates the 2 mM free Mg2+ condition in this manuscript (240 mM Na+, 140 mM K+, and 2 mM Mg2+).

*Supplemental information 2 references*

(1) Tan, Z.-J.; Chen, S.-J. RNA Helix Stability in Mixed Na+/Mg2+ Solution. *Biophys. J.* **2007**, *92* (10), 3615–3632. https://doi.org/10.1529/biophysj.106.100388.