SUPPLEMENTARY MATERIAL

Structural determinants of the SINE B2 element embedded in the long non-coding RNA activator of translation AS *Uchl1*

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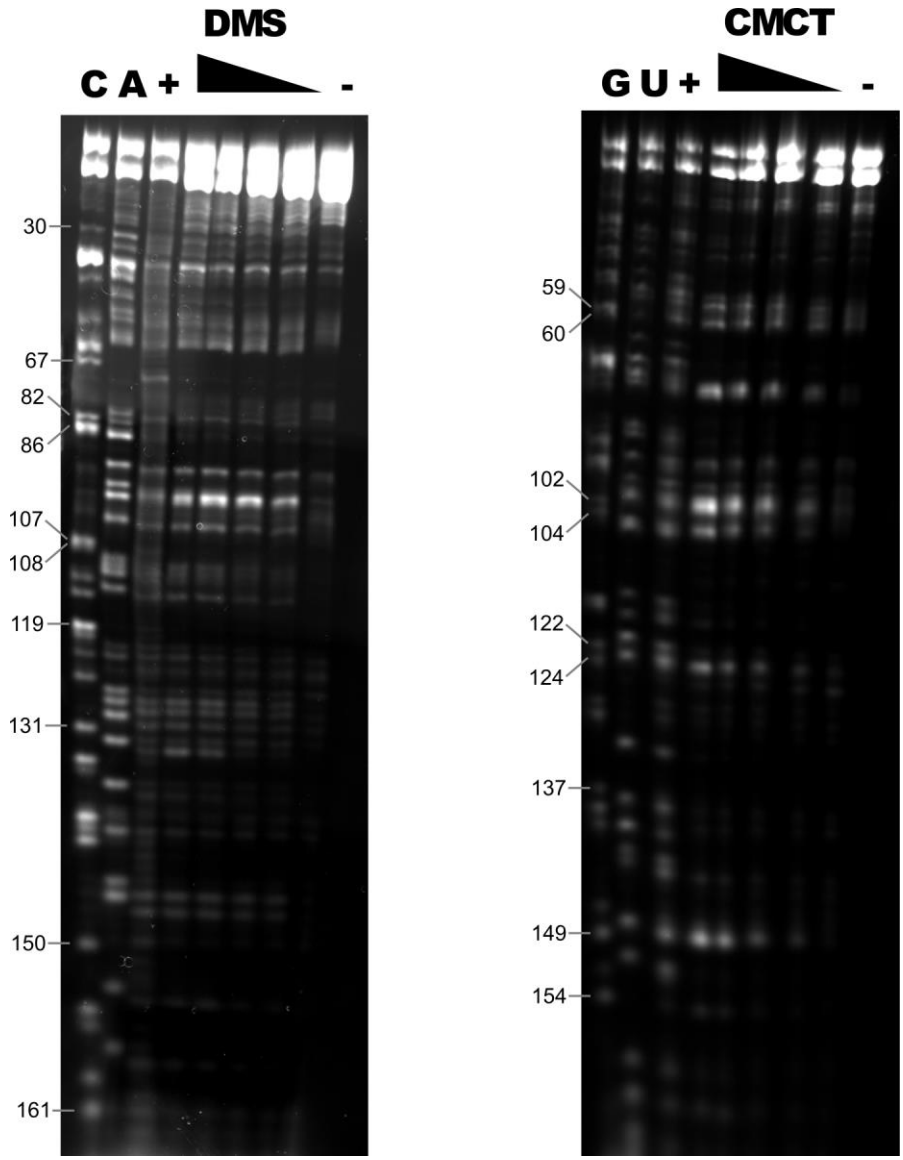

Figure S1 Chemical footprinting of the invSINEB2/183 RNA construct. (left) A fluorescent gel with C and A sequencing lanes with nucleotide numbering. DMS lanes with invSINEB2/183 RNA treated with increasing DMS concentrations with positive (+) and negative (-) controls. (right) A fluorescent gel with G and U sequencing lanes with nucleotide numbering. CMCT lanes with invSINEB2/183 RNA treated with increasing CMCT concentrations with positive (+) and negative (-) controls.

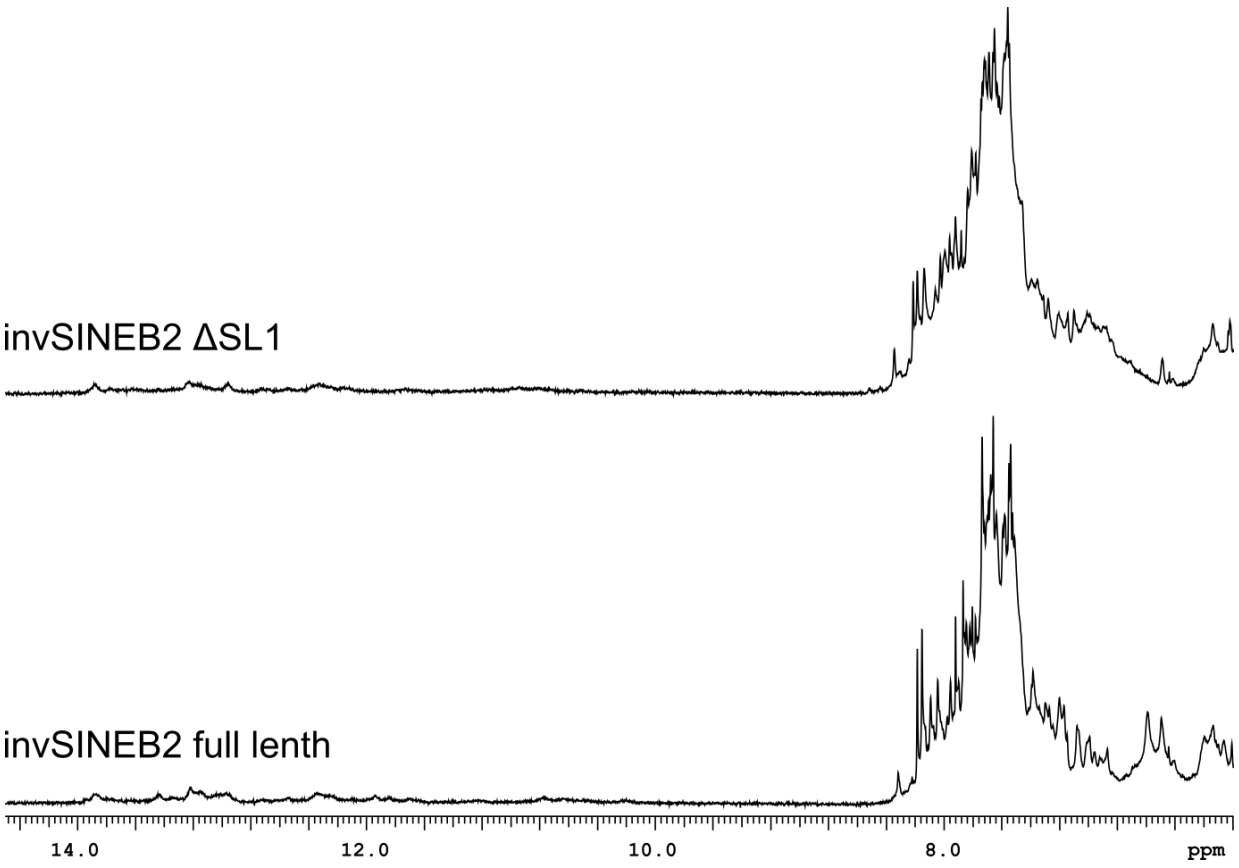

Figure S2 Imino and aromatic regions of ^{1}H NMR spectra of full length invSINEB2 RNA (183 nt) and the ΔSL1 construct (173 nt) in 5% 2H2O/95% H2O acquired at 25 °C.

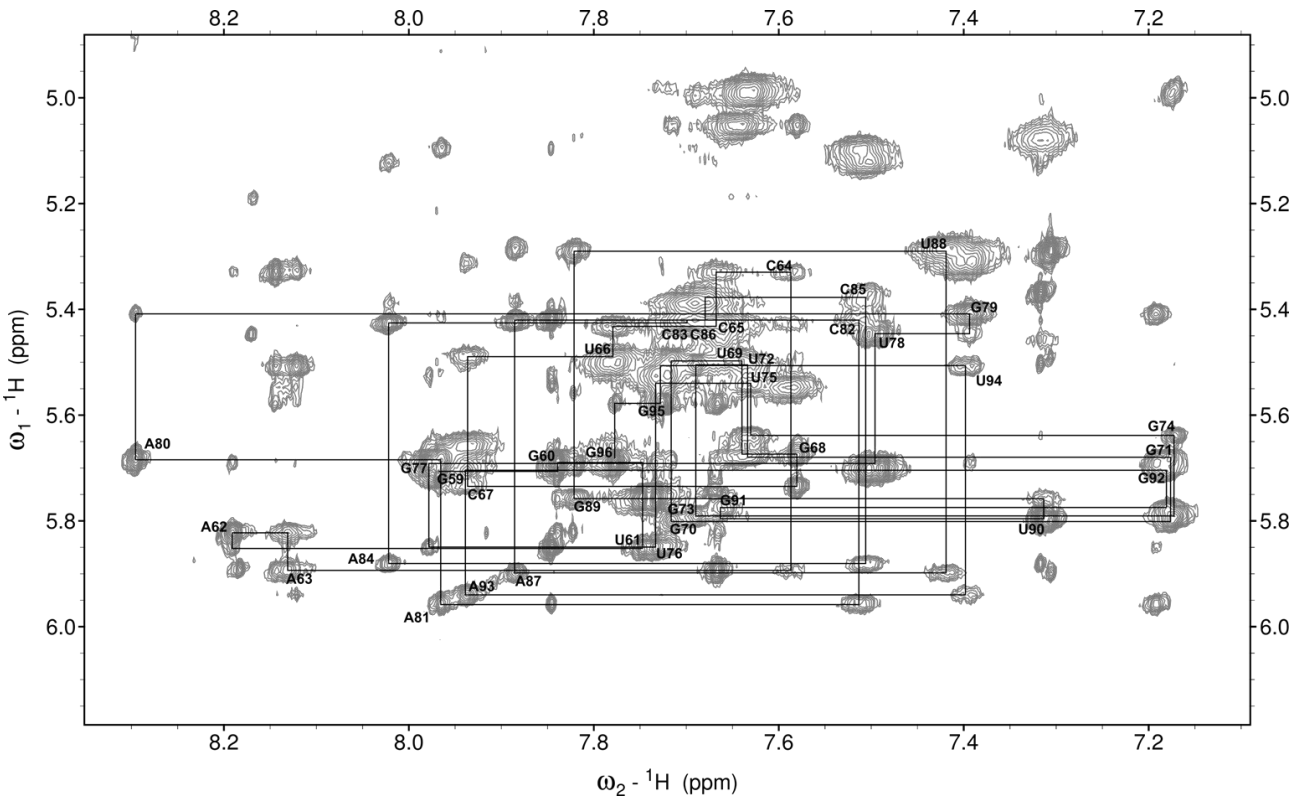

Figure S3 Assignment of relevant resonances. Aromatic-anomeric region of a 2D NOESY NMR spectrum (τ_m=250 ms) of invSINEB2/38. The sequential walk is depicted as a black line.

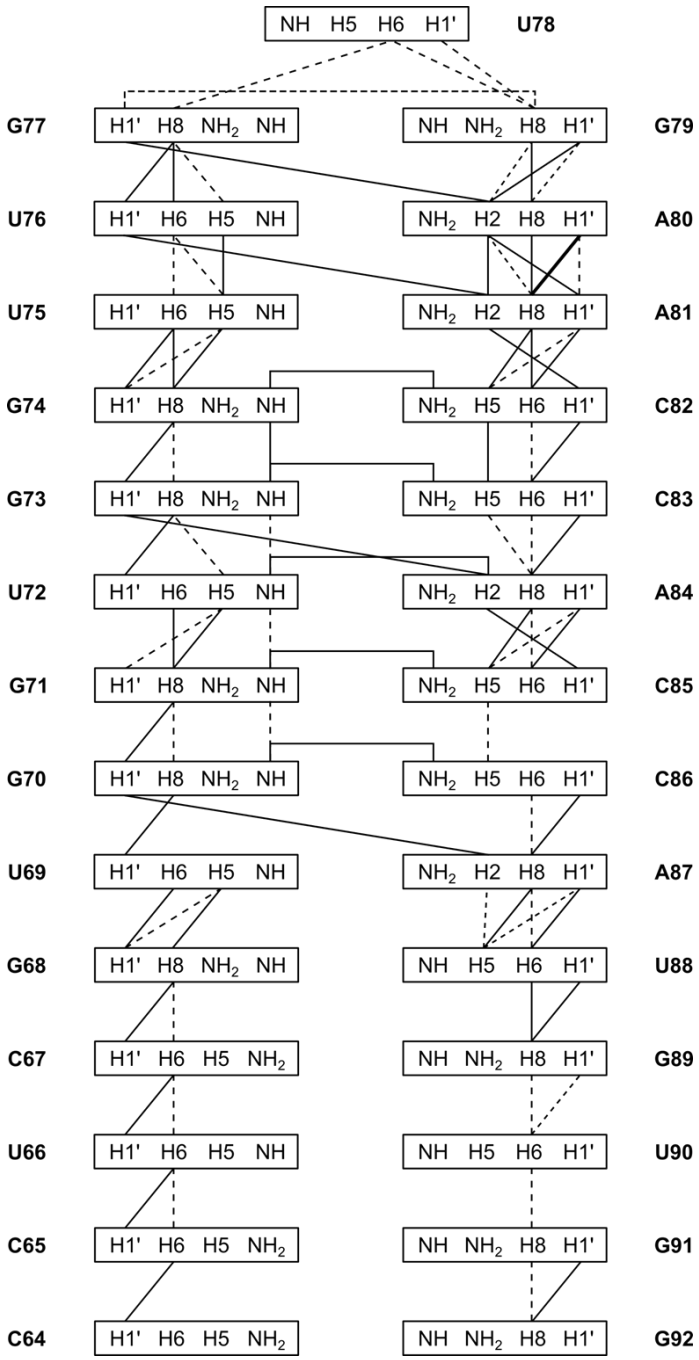

Figure S4 A diagram of strong (bold line) medium (solid line) and weak (dashed line) NOE connectivities for the invSINEB2/38 molecule.

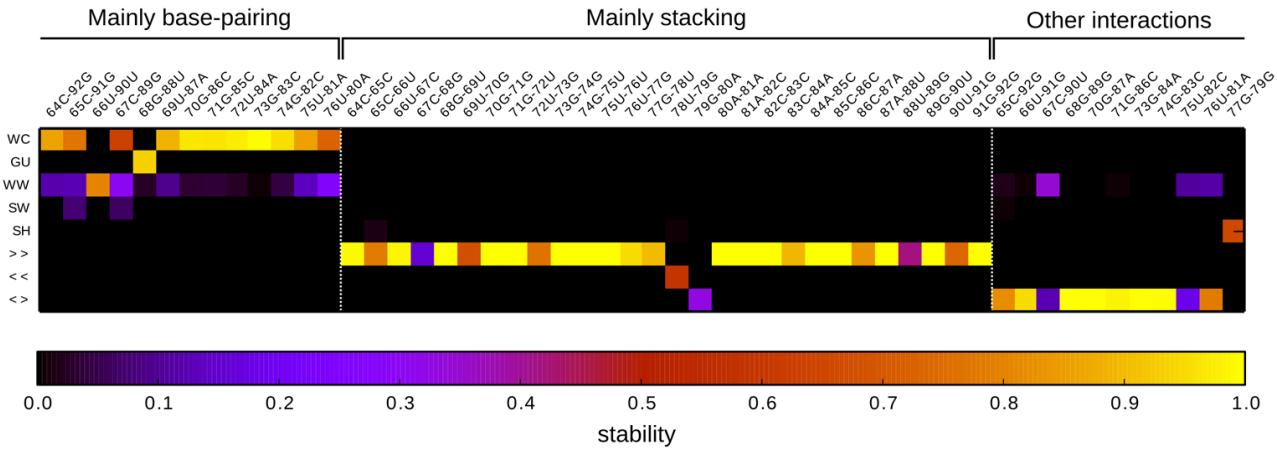

Figure S5 Stability of annotations per pair of bases, calculated with baRNAba (53) from the MD simulation. WC, GU and WW are interactions between the Watson-Crick edges of both bases. SW is a sugar-edge Watson-Crick-edge interaction, SH is a sugar-edge Hogsteen-edge interaction. >>, << and <> are stackings, in particular >> is the upward stacking found in a canonical double strand, << the downward stacking, and in <> the outward stacking.