



Figure S1. RNA structural similarity vs the length of RNA. The length of RNA is plotted against RMscore with a different compensation (a is 0.1, b is 0.3, d is 0.6 and d is 0.9) to smooth the average RMscore at a smaller length, in random pairs 0.3M. RNA alignment is accomplished by needle in EMBOSS package. Raw-RMscore means that d0 is assigned to 5 angstrom in RMscore definition. The compensation is chosen as 0.6 that will result in the smoothest curver.