WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote:
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment." 7sk_dkc1 X04236.1/1-328 7sk_consensus_structure HEXIM1 binding site U – A – HEXIM1 binding site HEXIM1 binding site HEXIM1 binding site 7sk_ivt X04236.1/1-328 7sk_mettl3 X04236.1/1-328 U = A HEXIM1 binding site HEXIM1 binding site - HEXIM1 binding site ACAG GG CUC 0 A - C C C C G - C C U-A-100
G-C C
U G
A-U C
G-C 110
5'-A U G U G C G
G-C 170
G-C G-C C G G U C U U C G G U C A A G G G U A U A C G A G U A
U
U
U
U
G-C G-C C
C-G
G-C C-G
G-C C-G
G-C C-G
G-C C-G G A A C C C C U - A C C - G A A - U C - G CG OU CO OU