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 seguences, or from alignments of seguences 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. To disable this warning, run r2r with --disable-usage-warning"

subfam\_weight=1

AdoCbl-variant-pknot1.cons

note: R2R does not box arbitrary regions, so you'll need to do this in a drawing program. See the published figure.

U **–** A

AdoCbl-variant-p7.cons

subfam\_weight=0.11505

12% G-C C - G

AdoCbl-variant-pknot2.consAdoCbl-variant.cons

