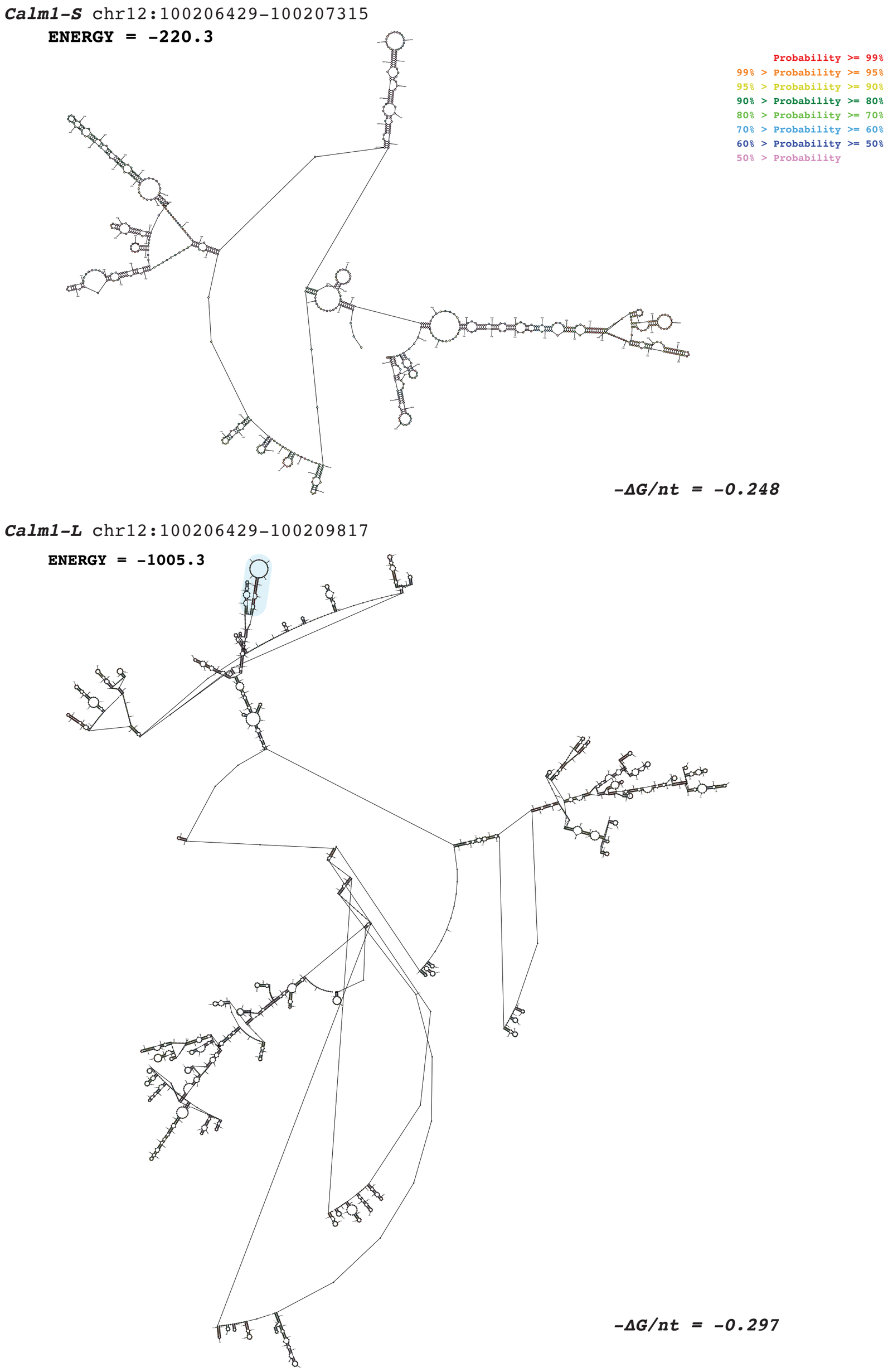
Supplemental Figure 6



Supplemental Figure 6. Secondary structure analysis of *Calm1-S* and *Calm1-L*. Prediction of secondary structure using the RNAstructure software (Bellaousov et al. 2013) estimated the free energy of folding for *Calm1-S* and *Calm1-L*, -220.3 and -1005.3 kcal/mol, respectively. The length-normalized minimum thermodynamic free energy (-∆G/nt) of predicted structures estimates the structural complexity of the 3′ UTRs in *Calm1-S* and *Calm1-L*. The value for *Calm1-L* 3′ UTR (-∆G/nt = - 0.297) compared to the *Calm1-S* 3′ UTR (-∆G/nt = - 0.248) suggested *Calm1-L* is more structured. Color reflects base-pairing probability. Blue shaded region is predicted as an AU-rich element uniquely found in the *Calm1-L*.