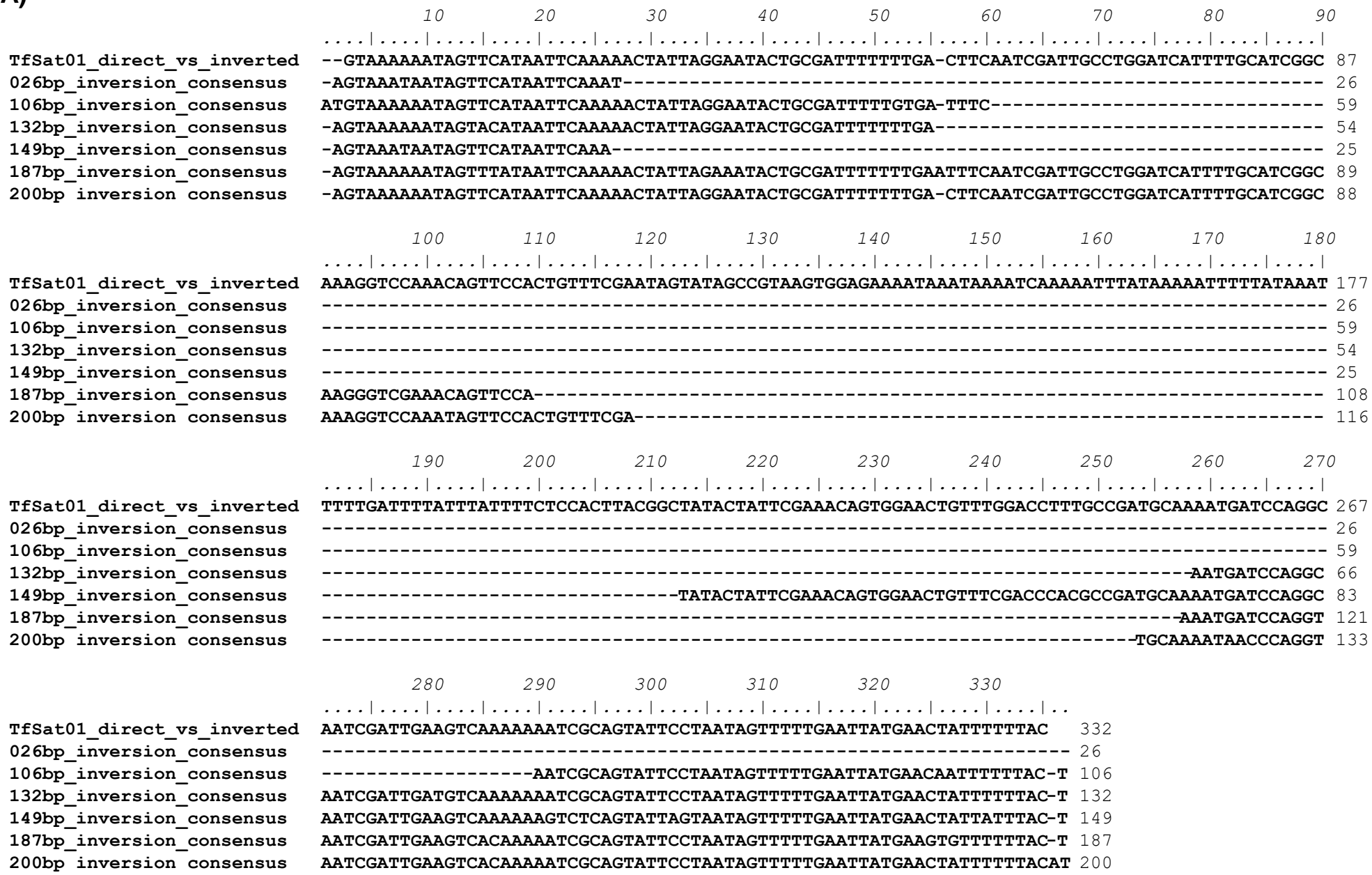
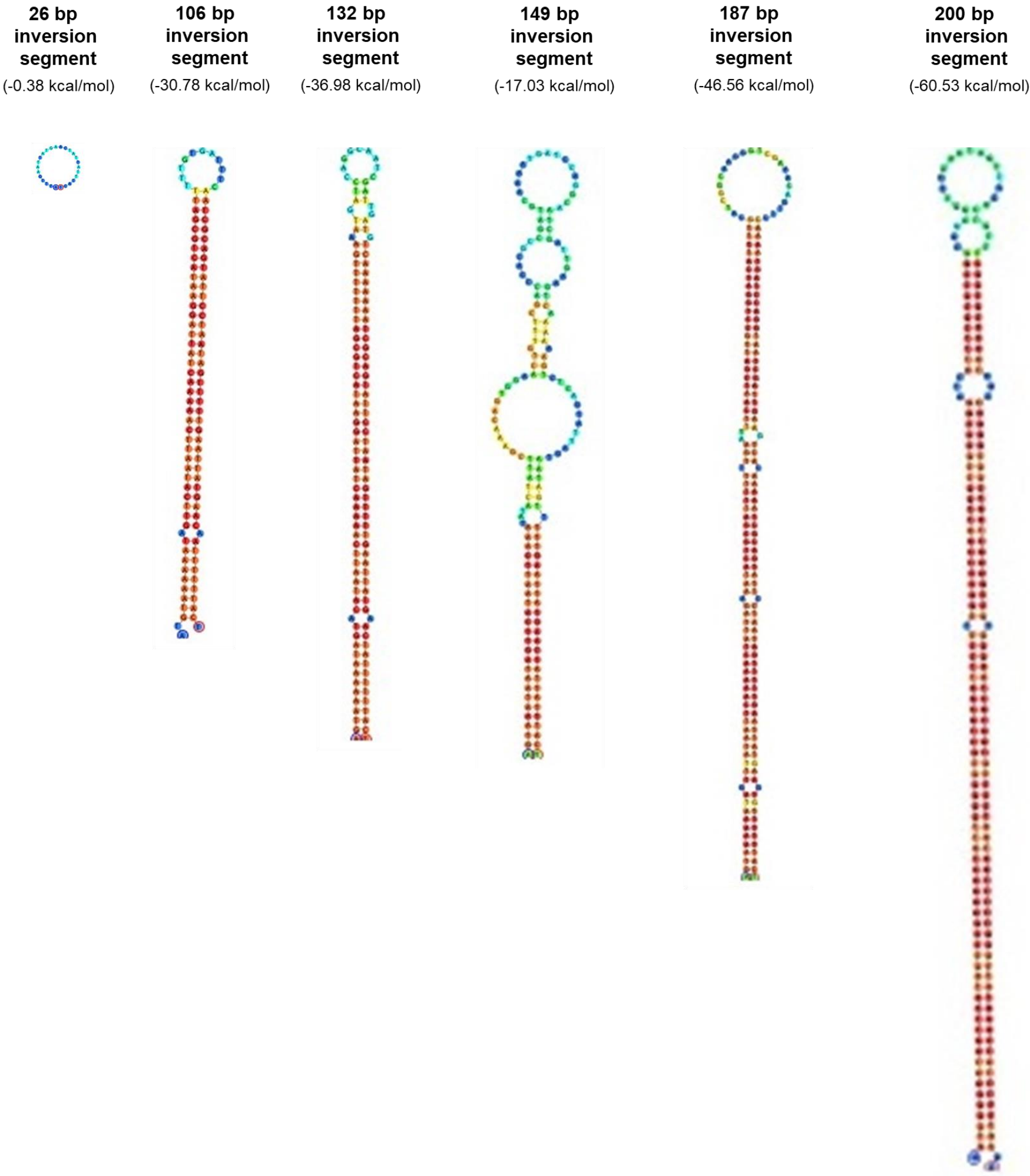


A)



B)



**Supplemental Figure S7.** The six most frequent inversion segments (26 bp, 106 bp, 132 bp, 149 bp, 187 bp, and 200 bp long) in which *TfSat01* monomers change their orientation within *TfSat01* arrays. **A)** Alignment of the truncated *TfSat01* monomers in the inversion segments. The sequence "*TfSat01\_direct\_vs\_inverted*" represents directly and inversely oriented *TfSat01* consensus monomers, according to which the truncated monomers of the inversion site are aligned. **B)** Potential secondary structures of the six inversion segments predicted by the RNAfold tool (Lorenz et al. 2011) using DNA Matthews 1999 energy model. The minimum free energies of the structures are given in parentheses.