

Supporting Information for:

The role of context in RNA structure: flanking sequences reconfigure CAG motif folding in *huntingtin* exon 1 transcripts

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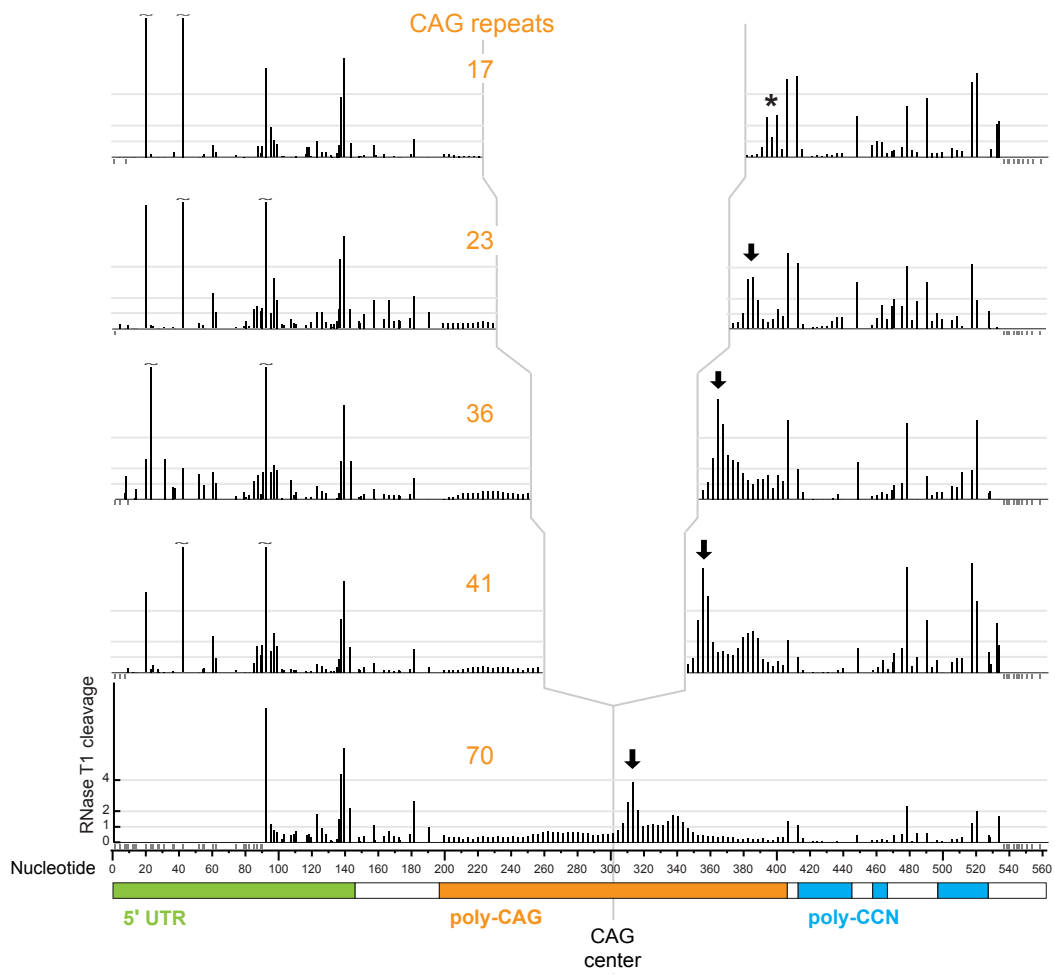
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Supplementary Figure 1. RNA structure probing profiles using RNase T1. In the context of complete *huntingtin* exon 1 sequences, RNase T1 cleavage supports a model in which the CAG hairpin is positioned asymmetrically relative to the center of the sequence (emphasized with solid arrows), consistent with base pairing between CAG sequences and 3' flanking sequences. Nucleotides for which no data is available are marked with gray boxes at the x-axis.

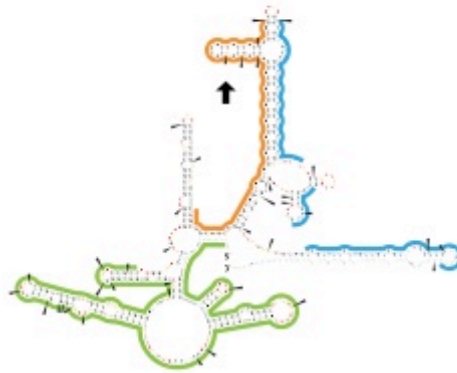
Supplementary Figure 2. Secondary structure models for 23, 36, and 70-CAG repeat length *huntingtin* exon 1 transcripts. Structure and reactivity annotation scheme is the same as shown in Fig. 2.

Supplementary Figure 3. Plausible competing structures for long CAG repeat sequences. Representative structures are shown in the context of the 41-CAG transcript.

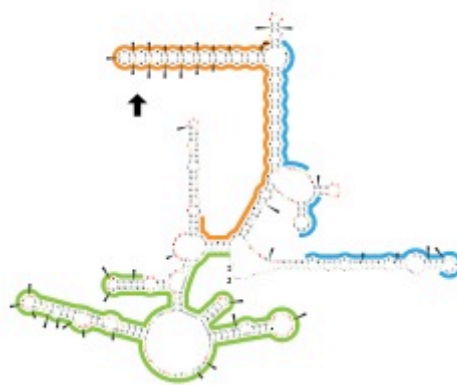


Busan / Supporting Figure 1

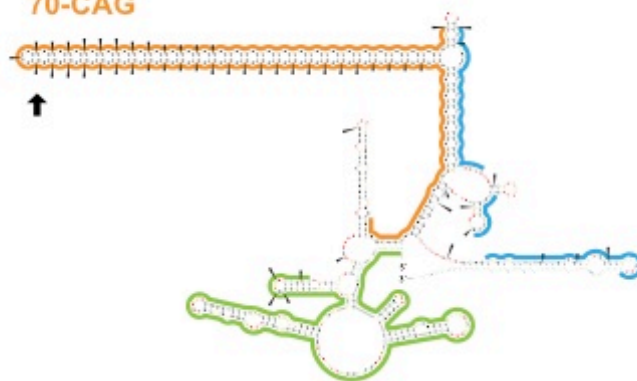
23-CAG



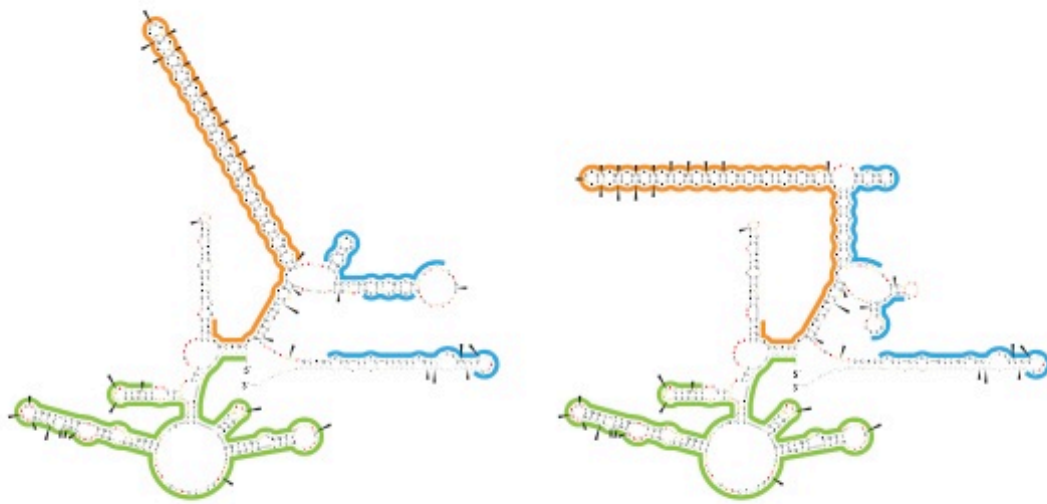
36-CAG



70-CAG



Busan / Supporting Figure 2



Busan / Supporting Figure 3