## SUPPLEMENTARY DATA

## Structural insights into synthetic ligands targeting A-A pairs in disease-related CAG RNA repeats

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**Figure S1.** The rearrangement of the RNA chain (orange) as a result of flipping out of the 4G and 5C residues and C2'*-endo* conformation of the 3A ribose (stereo view). The hydrogen bond between 2'OH group of 3A and oxygen atom of 5C is marked as dashed line.



**Figure S2.** Higher order interactions in the crystal lattice of RNA-CMBL complexes. **a**, Extruded 4G and 5C residues (*purple*) are integrated into the pseudo-infinite helix in the crystal lattice of the CAG-CMBL4 structure. **b**, A complex interaction involving four RNA duplexes, including Watson-Crick pairing (*purple*) triplex (*navy*) and stacking (*green*), in the CAG(Se)-CMBL3a model. **c**, An i-motif like (*blue*) in the CAG-CMBL3a(I) structure.



**Figure S3.** Thermal denaturation profiles of the CAG-containing RNA. **a**, (UCAACAGUUGA)<sub>2</sub> and **b**, (GCAGCAGC)<sub>2</sub>. Dashed and bold lines represent the melting curve without and with CMBL3a, respectively.



**Figure S4.** Biochemical analysis of CMBL3a interacting with CNG RNA repeats using Surface Plasmon Resonance. (**A-D**) SPR response as CMBL3a is added at increasing concentrations to immobilized RNA.



**Figure S5.** Conformation of the longer linker in the CMBL ligands. Left panel, The  $2F_o$ - $F_c$  electron density map of the CMBL ligands countered at  $1\sigma$  (grey). Right panel, Superposition of the structures of CMBL ligands showing differences in the conformation of the longer linker.