**Supplementary Figures for**

**HuR Stabilizes *HTT* mRNA via Interacting with Its Exon 11 in a Mutant HTT-Dependent Manner**

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**Supplementary Figure 1. Western-blot validation of the knock-down efficiency of HuR and Mapk11 siRNAs**

1. A representative Western-blot of HuR in HD mouse striatal cells (STHdhQ7/Q111) transfected with the siRNAs targeting HuR (HuR\_siRNA 1 and HuR\_siRNA 2) or Mapk 11, or with the non-targeting control siRNA (Neg\_siRNA) for 72 hours to test the knockdown efficiency of siRNAs. β-Tubulin and Lamin A/C were blotted as loading controls.
2. Similar to A), but in wild-type mouse striatal cells (STHdhQ7/Q7)
3. Similar to A), but in immortalized human HD (Q47) fibroblasts.
4. Similar to A), but in immortalized human wildtype (Q16) fibroblasts.

**Supplementary Figure 2. RT-qPCR validation of *HTT* mRNA level in HuR knock-down human patient fibroblasts**

RT-qPCR measurements of *HuR* and *HTT* mRNA level in immortalized human HD (Q45 & Q68) fibroblasts transfected with the siRNAs targeting *HuR* (HuR\_siRNA 1 and HuR\_siRNA 2) or with the non-targeting control siRNA (Neg\_siRNA) for 48 hours (12 technical replicates from 3 biological replicates). All signals were normalized to the averaged signal of Neg\_siRNA transfected controls. For all plotted data, error bars represent mean and SEM. The statistical analysis was performed by one-way ANOVA and post-hoc Dunnett’s tests. \*\*\*\*P < 0.0001.

**Supplementary Figure 3. The Coomassie blue staining of purified HuR protein.**

The Coomassie blue staining for HuR-MBP.His protein purification samples from transfected HEK293T cells. The final purification product and the flow-through fraction were loaded and stained. The HuR-MBP.His band is consistent with the expected molecular weight (79.11 kD).

**Supplementary Figure 4. A schematic model illustrating the transgene and reporter constructs.**

**Supplementary Figure 5. The standard curves of qPCR primers.**

Ct values of serial diluted cDNA samples (human cDNAs from immortalized Q47 fibroblasts and mouse cDNAs from STHdhQ7/Q111 cells). The initial quantity indicates the initial template concentration normalized to the original cDNA samples. The Ct values were fitted with linear curves and the efficiency was calculated based on the assumption of doubling the qPCR product in each cycle.