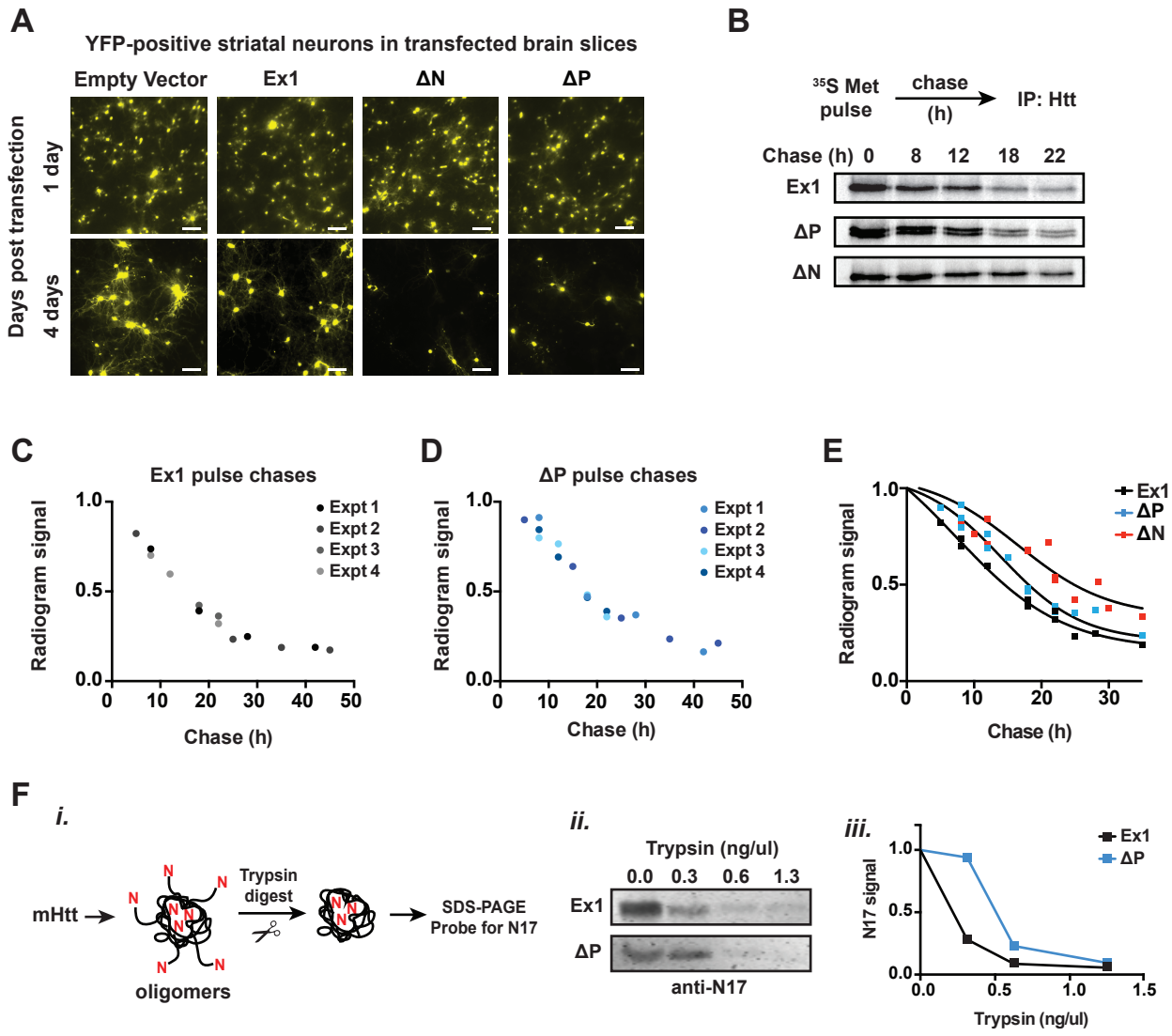

Figure 8 - figure supplement 1: Impact of polyQ flanking regions on mHtt degradation and proteolysis

A. Fluorescence images of MSNs co-transfected with the mHtt variants, YFP, and CCT1. Images were taken 1 day (top row) and 4 days (bottom row) after transfection. Data are representative of at least three independent experiments. Scale bar is 20 μm.

B. Radiogram gels of ^{35}S pulse-chase measuring soluble protein degradation of mHtt-Ex1 variants in transfected ST14a cells.

C. – D. Quantified data of Ex1 and ΔP degradation from four independent experiments each, demonstrating the robust degradation data.

E. Quantification of protein degradation of mHtt variants. Data compiled from four independent experiments each. Data fitted with GraphPad Prism software using the non-linear regression fit.

F. ***i.*** Schematic of trypsin digestion experiment: Ex1 and ΔP oligomers were generated *in vitro*, then digested with increasing concentrations of trypsin protease. Protease-digested reactions were run in an SDS-PAGE gel and probed for N17. ***ii.*** SDS-PAGE gel of trypsin-digested Ex1 and ΔP oligomers immunoprobed for N17. ***iii.*** Quantification of N17 signal intensity from SDS PAGE gel in (*ii*).