Legends for Supplemental figures.

Supplemental figure 1: Characterization of G-quadruplex motif in mouse and human Anxa2 sequence. **A)** Analysis of the mouse and human Anxa2 sequence by QGRS mapper revealed potential G-quadruplex forming sequences (Highlighted in yellow). The ATG and STOP codons are shown in black boxes. The G-motifs are boxed in red. **B)** The motifs found in the mouse and human Anxa2 sequences are sorted by their position, length and G-scoring. Gs potentially involved in the G quadruplex are underlined.

Supplemental figure 2: Anxa2 RNA does not harbor a G quadruplex forming sequence. The formation of G quadruplex structure, that is stabilized in the presence of K+, was assessed by folding the RNA and performing fluorescent primer extension in the presence various cations. The fluorescent cDNA were separated by capillary electrophoresis and the electrophoregrams were analyzed with the QuShape software. In the presence of K+ (red traces), no specific RT stop was observed for Anxa2 RNA in the predicted G quadruplex forming sequences (shown in red at the bottom) whereas strong stops are observed in the well characterized N19 fragment from the Fmr1 RNA.

Supplemental figure 3: The G-motif region of human Anxa2 mRNA is important for axonal localization. **A)** The indicated fragments of the human Anxa2 mRNA were cloned into the pcDNA3-LacZ-24xMS2 vector containing the LacZ gene and 24 MS2 binding sites. The names of the plasmids are indicated on the left and the localization of the reporter RNA in axons of differentiated NSC-34 cells is shown on the right. **B)** FISH was performed using LacZ probes after 3 days of differentiation of human SH-SY5Y cells carrying the indicated reporter gene. Scale bar, 10 μm. Insets on the right are enlarged images of boxed sections. **C)** Quantitative analysis of localization of reporter RNAs in axons is illustrated by scatter plots showing the number of mRNA spots localized in the distal segment of axons with the indicated constructs. Mean and SEM are shown. **:$p<0.002$ (n=9)

Supplemental figure 4: Reporter mRNA are expressed at similar levels in differentiated NSC-34 cells. **A)** RT-qPCR analysis of the different reporters mRNAs using LacZ specific primers was performed on RNA together with primers specific to beta2 Microglobulin mRNA. Quantitative analysis were performed using MXpro software (Agilent), FL-wt reporter was

selected as a calibrator. **B)** RNA was prepared from non-induced control cells (NI) and from cells after induction of shSMN in order to obtain SMN depletion in differentiated NSC-34 cells. RT-PCR experiments were performed as in **A**. FL-wt and G-motif+3'UTR reporters (NI) serve as the calibrator for treated samples (I sh-SMN). Mean and SEM are shown. Statistical significance was calculated using the Student t test (ns: not statistically significant).

Supplemental Figure 5: Quantitation analysis showing that SMN depletion does not affect the length of axons in differentiated cells (**A**) but decreases the number of spots containing SMN in distal axons (**B**).