

# Evaluation of RNA *trans*-splicing as a therapeutic strategy for spinocerebellar ataxia type 1

## Introduction

- Spinocerebellar ataxia type 1 (SCA1) is caused by an expanded polyglutamine (polyQ) tract in the protein ataxin-1 encoded by the *ATXN1* gene
- Phosphorylation at S776 is critical for its neurotoxicity and acts synergistically with the polyQ tract in the pathogenic mechanism<sup>1</sup>
- We are evaluating the potential therapeutic value of substituting S776 for alanine using spliceosome-mediated RNA *trans*-splicing (SMaRT)
- SMaRT creates a hybrid mRNA through a *trans*-splicing reaction between an endogenous target pre-mRNA and an exogenously delivered pre-*trans*-splicing molecule (PTM)<sup>2</sup>

## Aim

- To reprogramme *ATXN1* RNA using SMaRT

## Methods

- Wild-type and mutant PTMs (for mouse [S752] and human [S776]) were designed and constructed using traditional cloning into pcDNA3.1 or a lentiviral vector co-expressing GFP
- SH-SY5Y cells were transfected with a human *ATXN1* minigene and/or PTM
- Embryonic mouse cortical neurones were transduced with lentiviral vector co-expressing GFP and PTM
- Trans*-splicing was assessed by RT-PCR using a target specific forward primer and a PTM-specific reverse primer

## Results

PTMs successfully induced *trans*-splicing of:

- A human *ATXN1* minigene in SH-SY5Y cells (**Figure 1**)
- Endogenous human *ATXN1* in SH-SY5Y cells (**Figure 2**)
- Endogenous mouse *Atxn1* in wild type embryonic mouse cortical neurones transduced with a lentiviral vector co-expressing GFP (**Figure 3**)

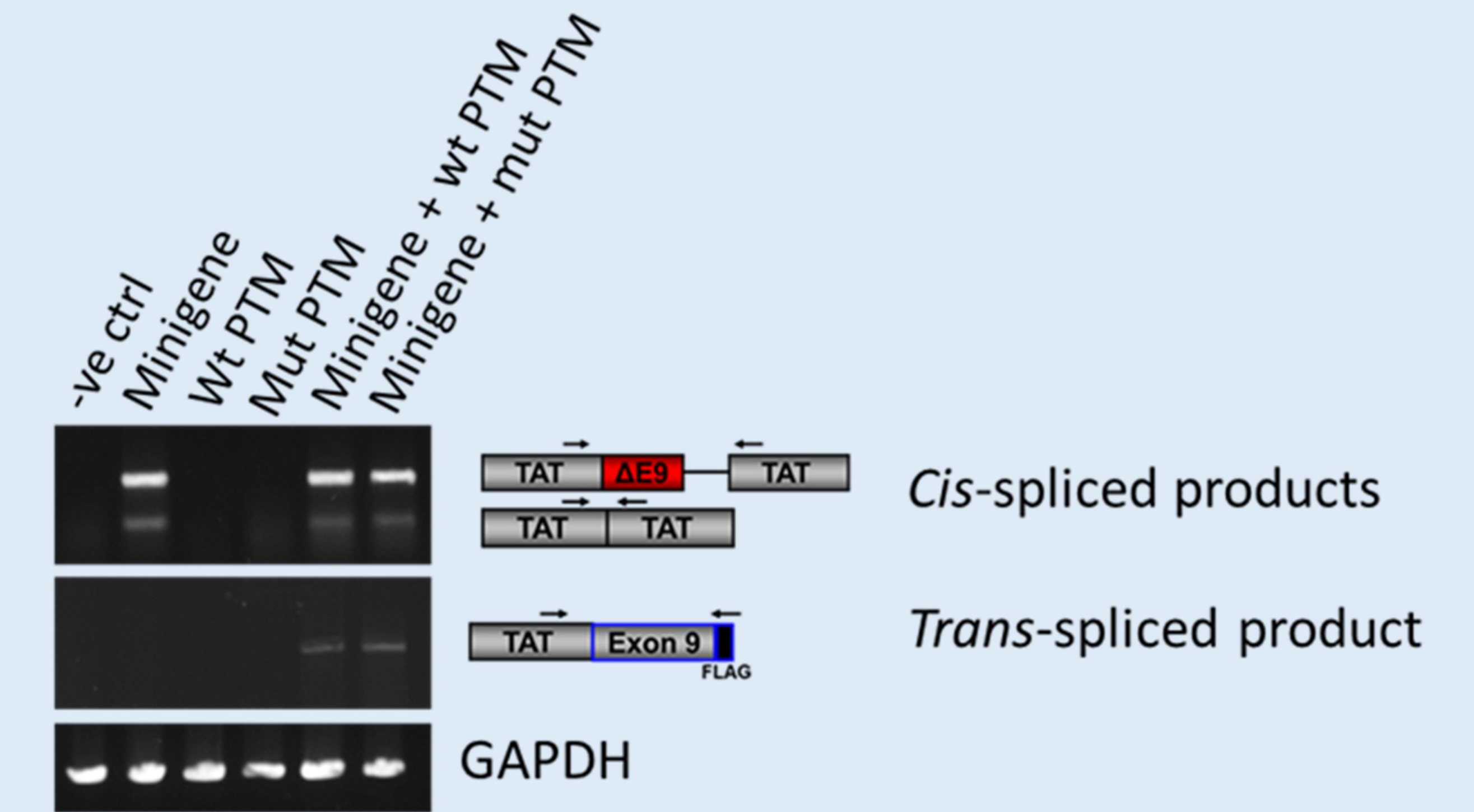


Figure 1.

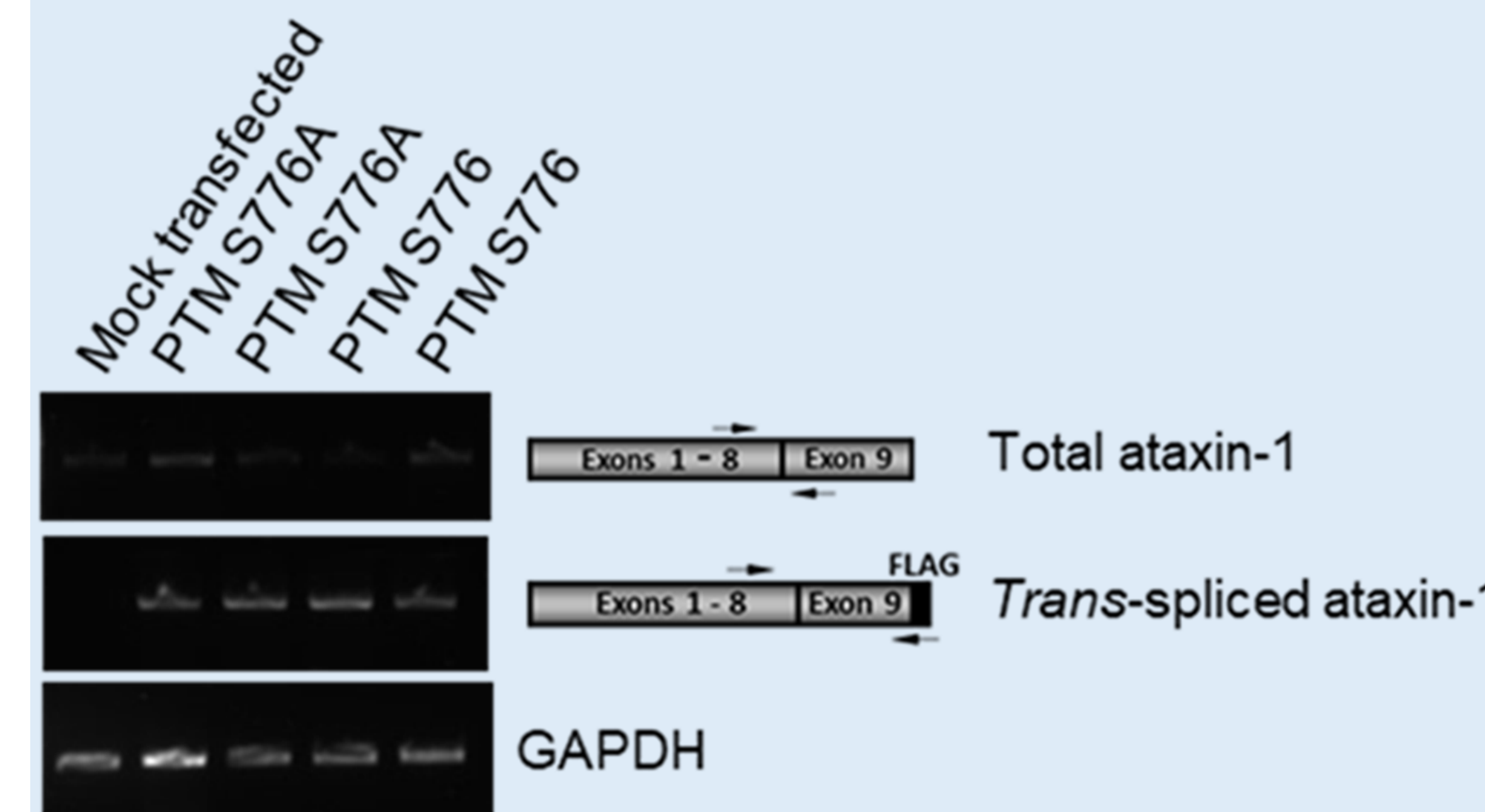
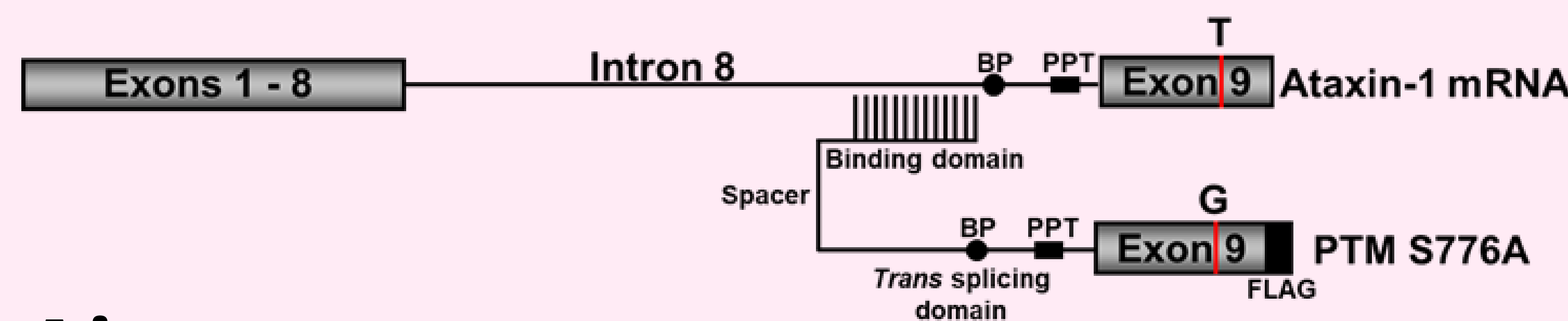


Figure 2.

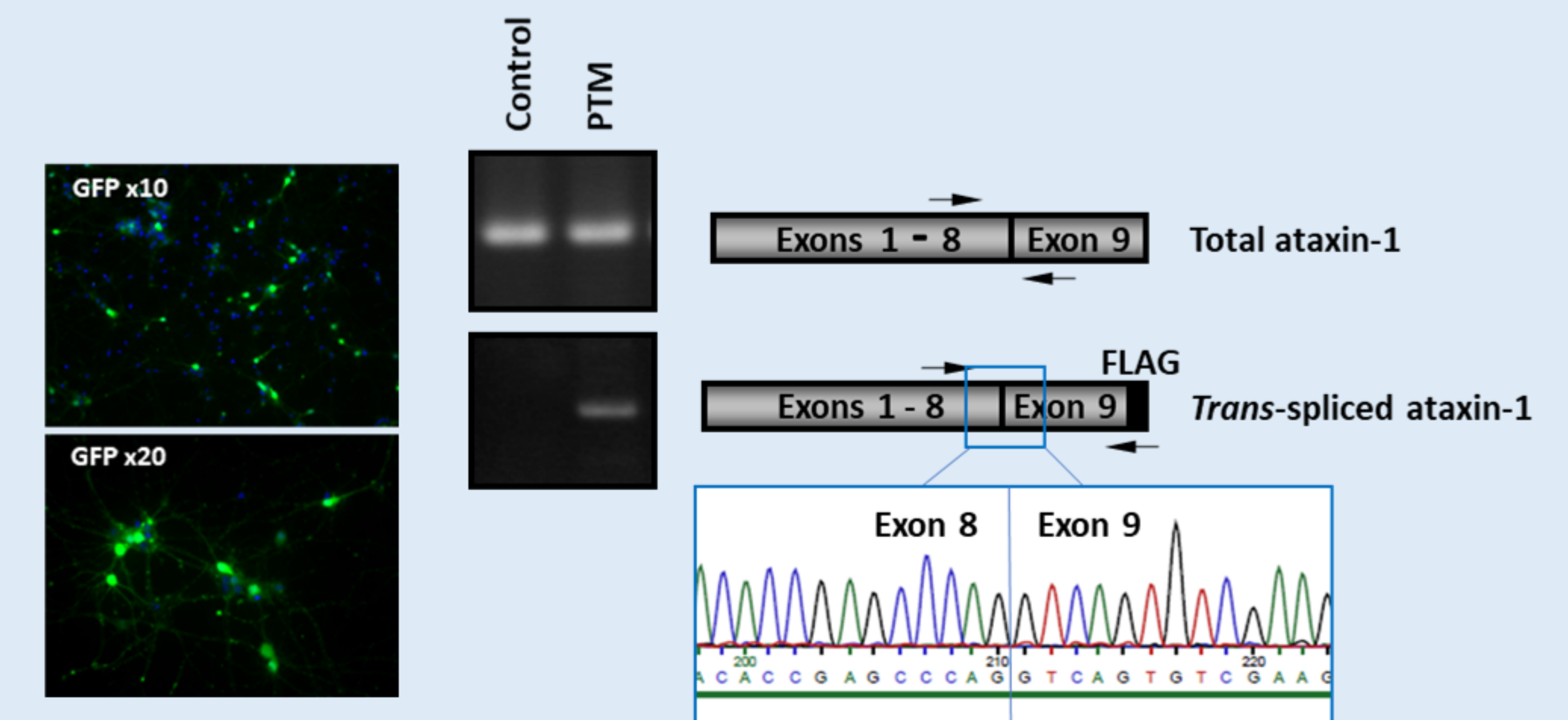


Figure 3.

All results in Figures 1 – 3 were verified by Sanger sequencing

## Discussion

- Ongoing work aims to confirm a change in phosphorylation status and test the effect of SMaRT on validated phenotypes of SCA1 patient-derived iPSC cell models<sup>3</sup>
- SMaRT can theoretically repair any mutation downstream of the PTM binding site and is suited for the dominant gain-of-function mutations of SCAs