

# Using Transgenic Mouse Models to Track DNA Repeat **Expansion of Friedreich's Ataxia Patients**

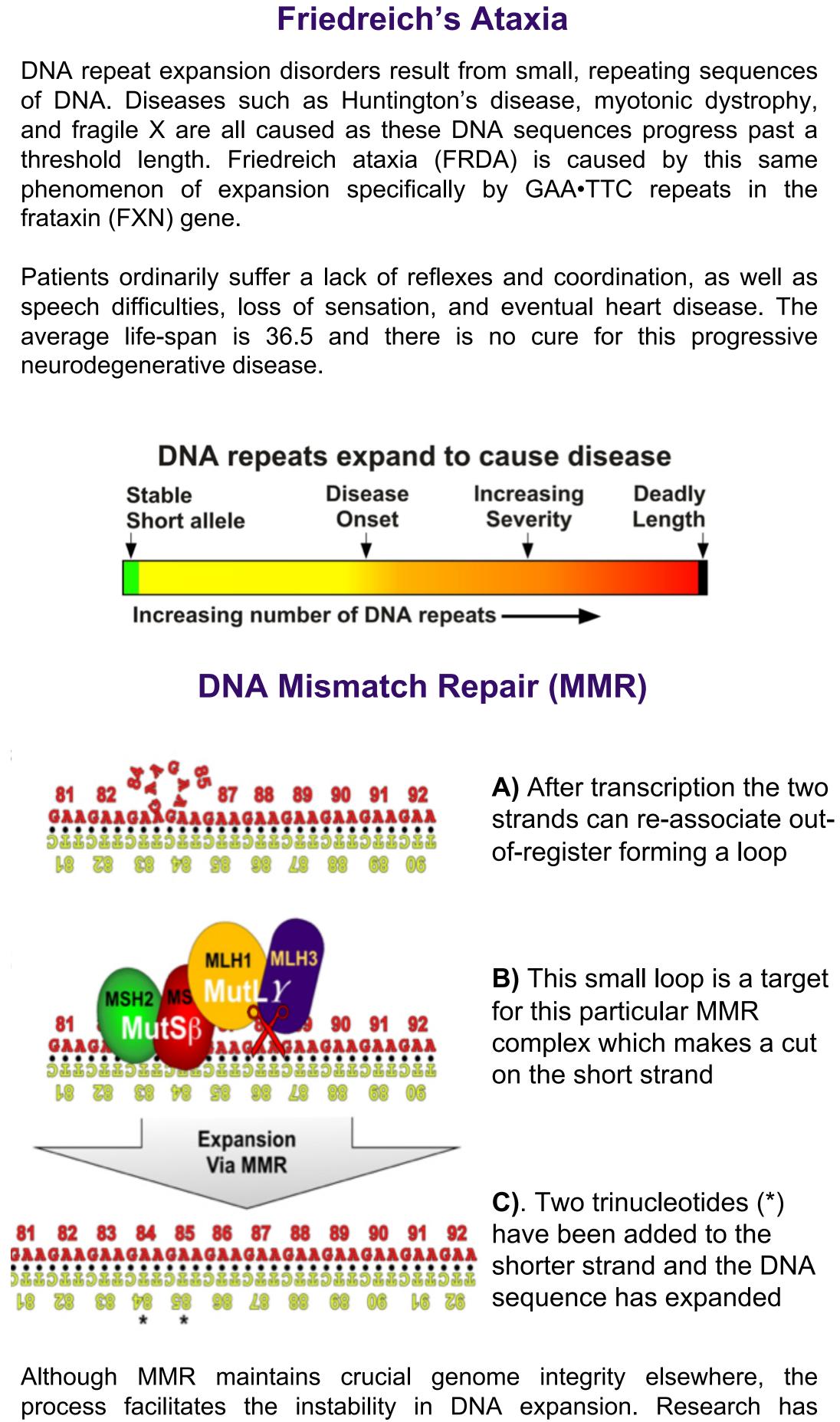
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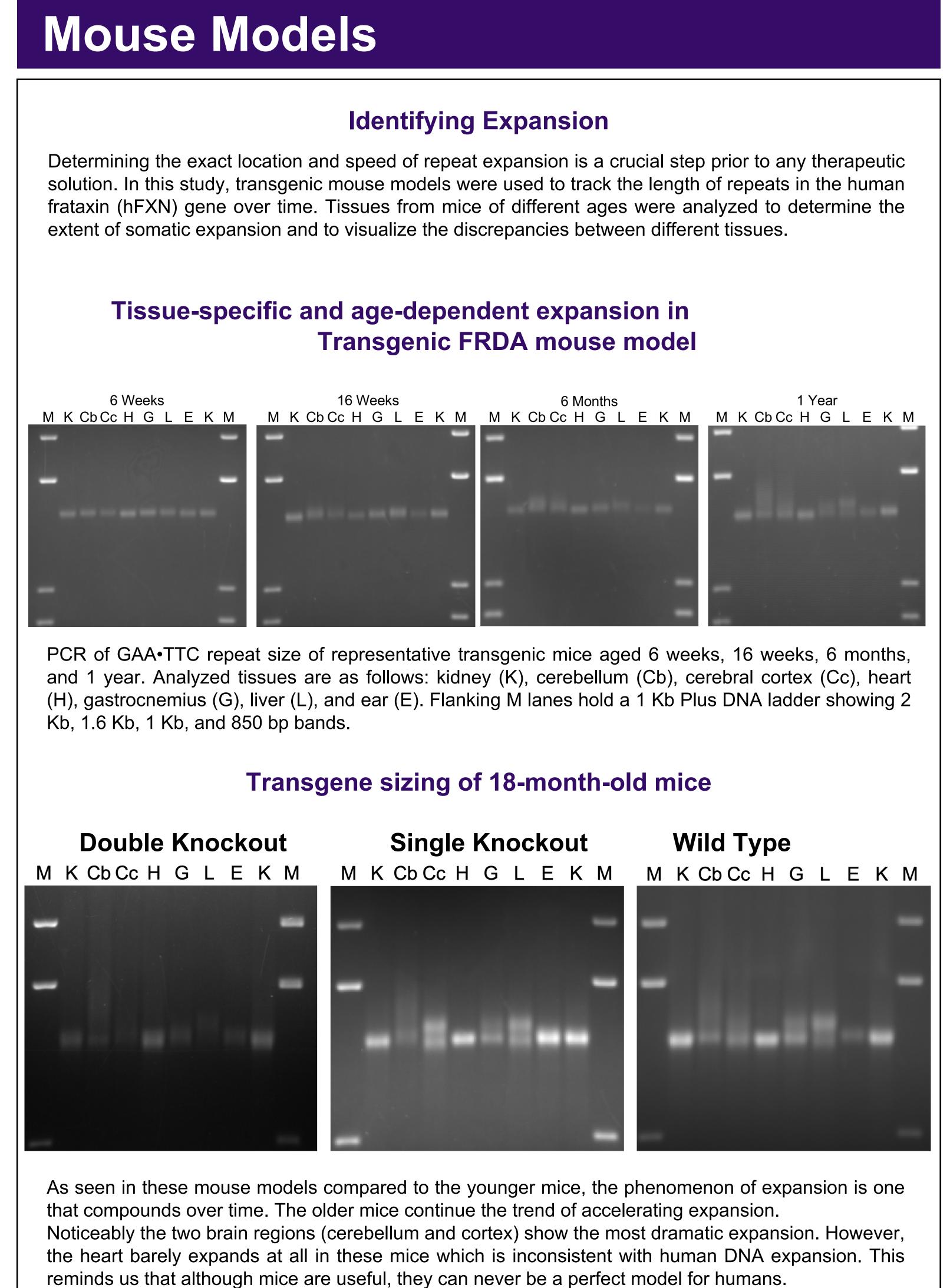
### Introduction



identified the role of MMR molecule MLH3 in the expansion of GAA•TTC repeats in the FXN gene. Importantly, one isoform of MLH3 does not cause repeat expansion. Because of this unique property, MLH3 is the target of our therapeutic answers to FRDA.

> This research project was supported by grant # 1659752 through the National Science Foundation (NSF), **Research Experiences for Undergraduates (REU) Program**

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### Method

### **DNA Extraction & PCR**

Three male 18-month old mice were dissected and each tissue was placed in a boil-proof tube with Proteinase K to digest proteins and remove contamination from the sample. Additionally stainless-steel beads were used to homogenize tissues prior to extraction.

Once the DNA of each tissue was isolated, the FXN gene could be selectively cut with primers and amplified via PCR. Finally a gel electrophoresis was run to image the length of expanded DNA fragments.



Each of the three 18-month old mice represent a different genotype of the mouse FXN gene: one with both copies, one missing one copy, and one lacking both copies. This last type, the "double knockout" had to rely completely on the hFXN transgene to produce frataxin since it had no FXN gene of its own

### **Conclusions / Next Steps**

### Hope for a Cure?

As hypothesized, there is no unexpected change in expansion in older mice. Although the rate of expansion increases to dangerous levels, this pattern is expected based on trends in younger mice. Because of this predictable progression of the disease and the compounding nature of expansion, an early delay or even a halt to expansion can be life changing for FRDA patients.

### **Further Questions?**

Are any discrepancies in expansions due to the different mouse frataxin genotyping?

Since the double knockout mouse genotype must transcribe from the hFXN gene for all its frataxin production, would expansion be accelerated in these cells?



# ntrocucton

## **Friedreich's Ataxia**

DNA repeat expansion disorders result from small, repeating sequences of DNA. Diseases such as Huntington's disease, myotonic dystrophy, and fragile X are all caused as these DNA sequences progress past a threshold length. Friedreich ataxia (FRDA) is caused by this same phenomenon of expansion specifically by GAA.TTC repeats in the frataxin (FXN) gene.



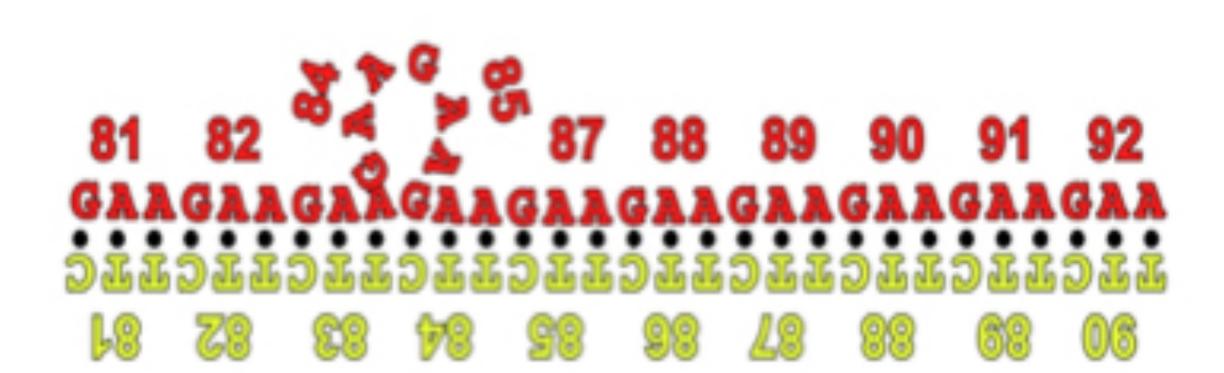
Patients ordinarily suffer a lack of reflexes and coordination, as well as speech difficulties, loss of sensation, and eventual heart disease. The average life-span is 36.5 years and there is no cure for this progressive neurodegenerative disease.

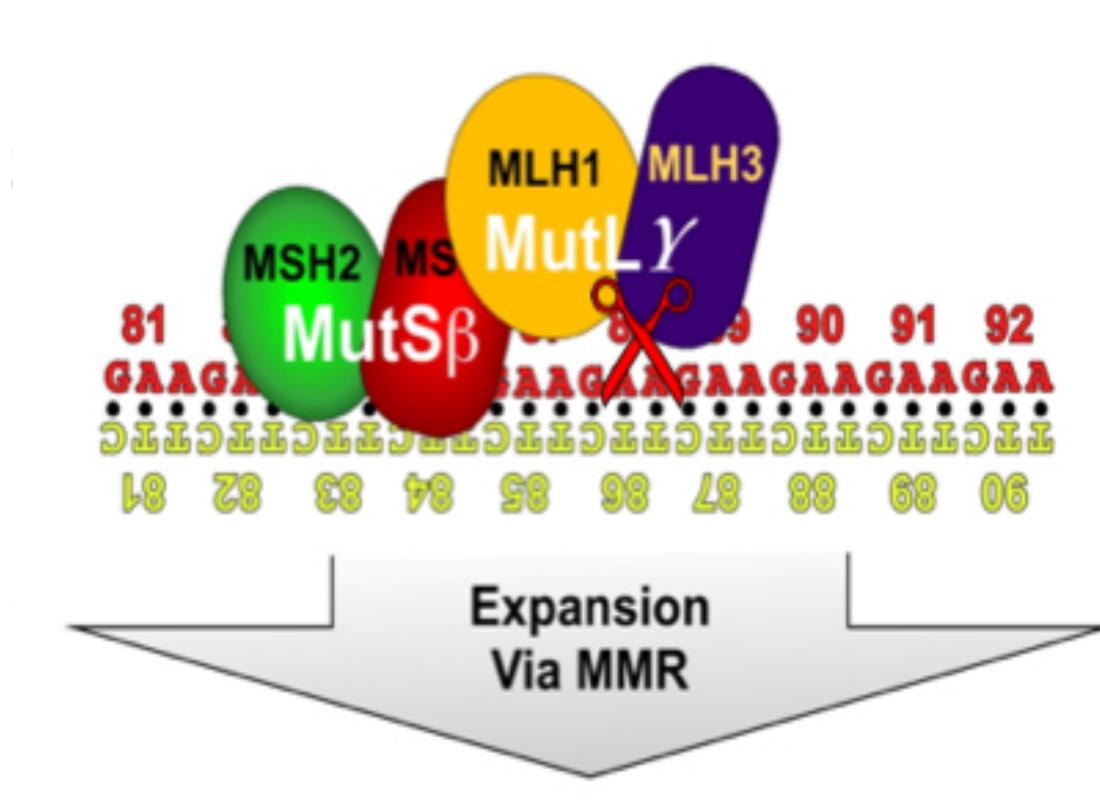
### **DNA repeats expand to cause disease** Increasing Disease Stable Severity Onset Short allele Increasing number of DNA repeats —



# ntrocuction

# **DNA Mismatch Repair (MMR)**







out-of-register forming a loop

C). Two trinucleotides (\*) have been added to the shorter strand and the DNA sequence has expanded

Although MMR maintains crucial genome integrity elsewhere, the process facilitates the instability in DNA expansion. Research has identified the role of MMR molecule MLH3 in the expansion of GAA-TTC repeats in the FXN gene. Importantly, one isoform of MLH3 does not cause repeat expansion. Because of this unique property, MLH3 is the target of our therapeutic answers to FRDA.

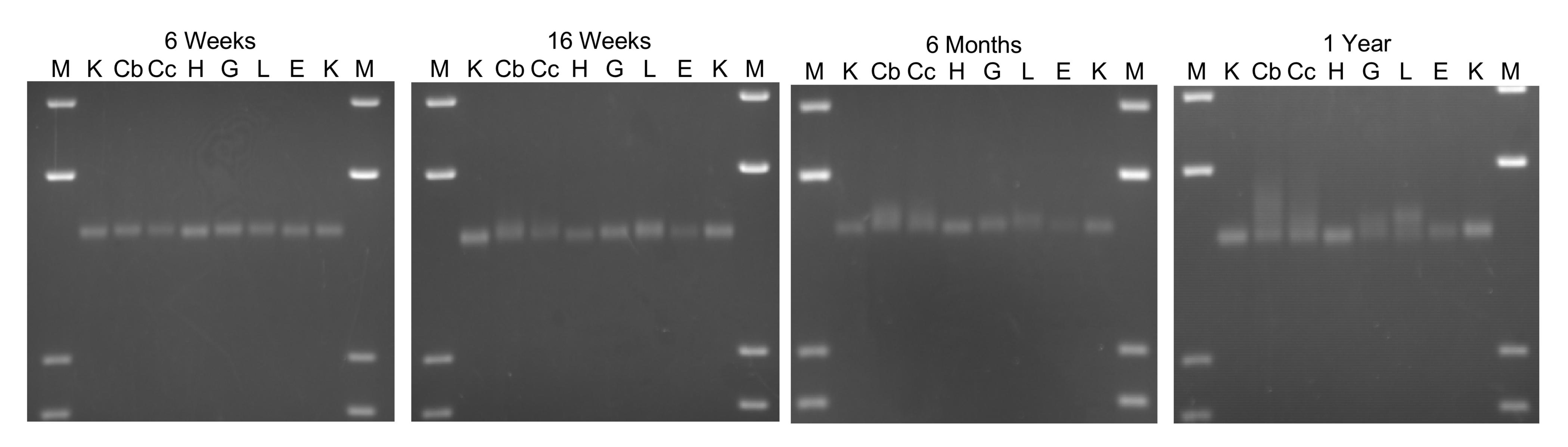
# A) After transcription the two strands can re-associate

B) This small loop is a target for this particular MMR complex which makes a cut on the short strand

# **NOUSE NOCES**

# Identifying Expansion

Determining the exact location and speed of repeat expansion is a crucial step prior to any therapeutic solution. In this study, transgenic mouse models were used to track the length of repeats in the human frataxin (hFXN) gene over time. Tissues from mice of different ages were analyzed to determine the extent of somatic expansion and to visualize the discrepancies between different tissues.

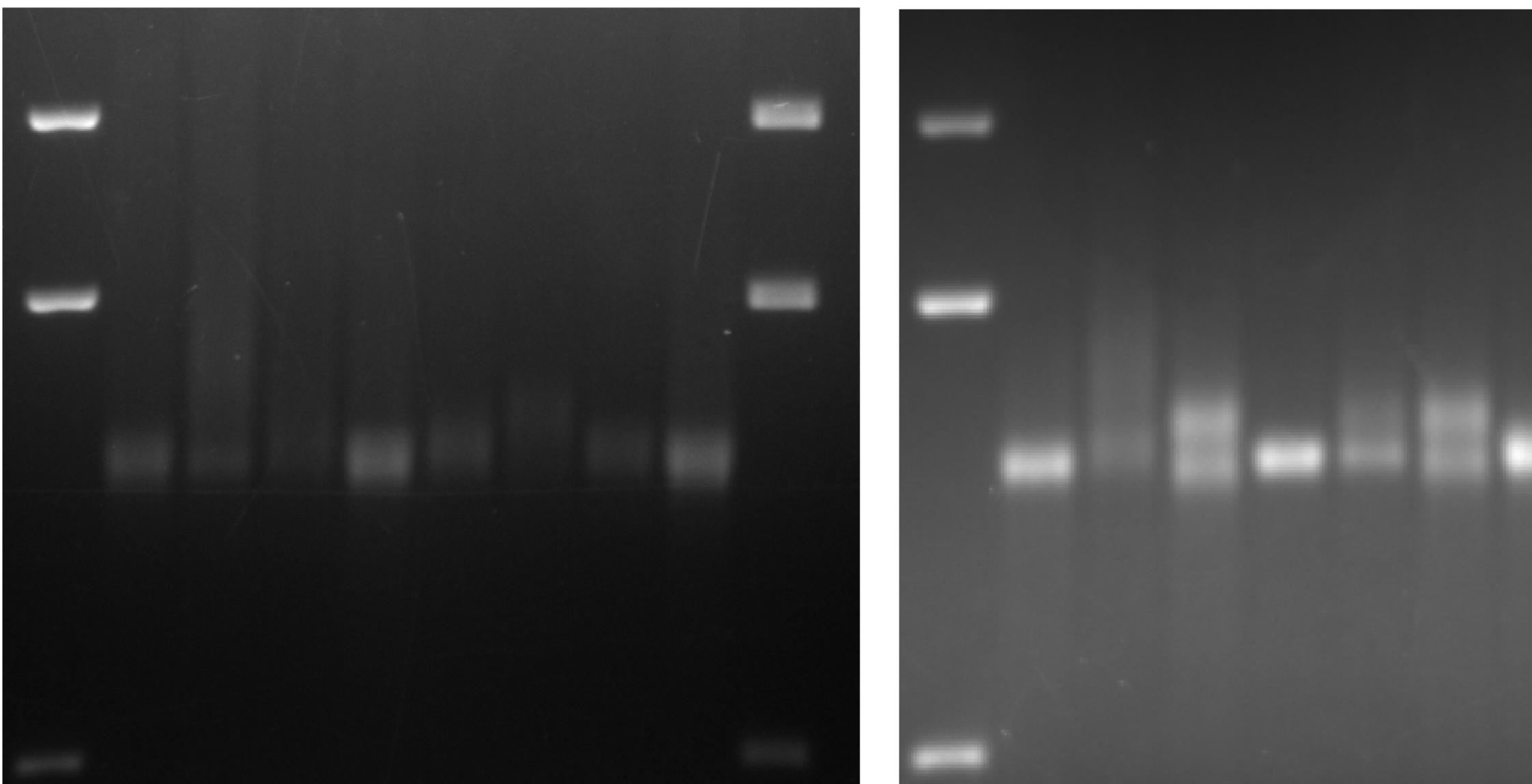


PCR of GAA•TTC repeat size of representative transgenic mice aged 6 weeks, 16 weeks, 6 months, and 1 year. Analyzed tissues are as follows: kidney (K), cerebellum (Cb), cerebral cortex (Cc), heart (H), gastrocnemius (G), liver (L), and ear (E). Flanking M lanes hold a 1 Kb Plus DNA ladder showing 2 Kb, 1.6 Kb, 1 Kb, and 850 bp bands.



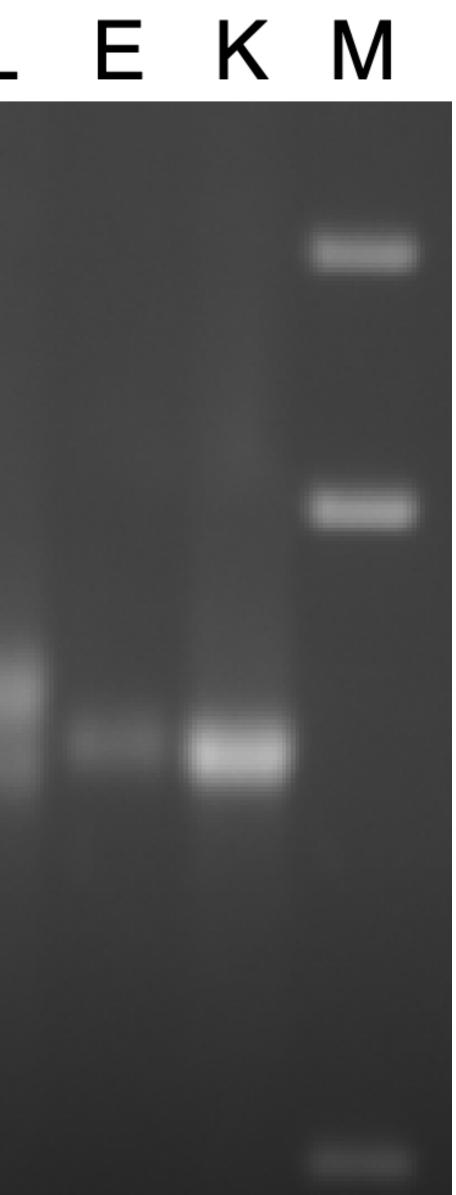
## **Transgene sizing of 18 month old mice**

### Single Knockout **Double Knockout** M K Cb Cc H G L E K M M K Cb Cc H G L E K M



As seen in these mouse models compared to the younger mice, the phenomenon of expansion is one that compounds over time. The older mice continue the trend of accelerating expansion. Noticeably the two brain regions (cerebellum and cortex) show the most dramatic expansion. However, the heart barely expands at all in these mice which is inconsistent with human DNA expansion. This reminds us that although mice are useful, they can never be a perfect model for humans.

# Wild Type M K Cb Cc H G L E K M







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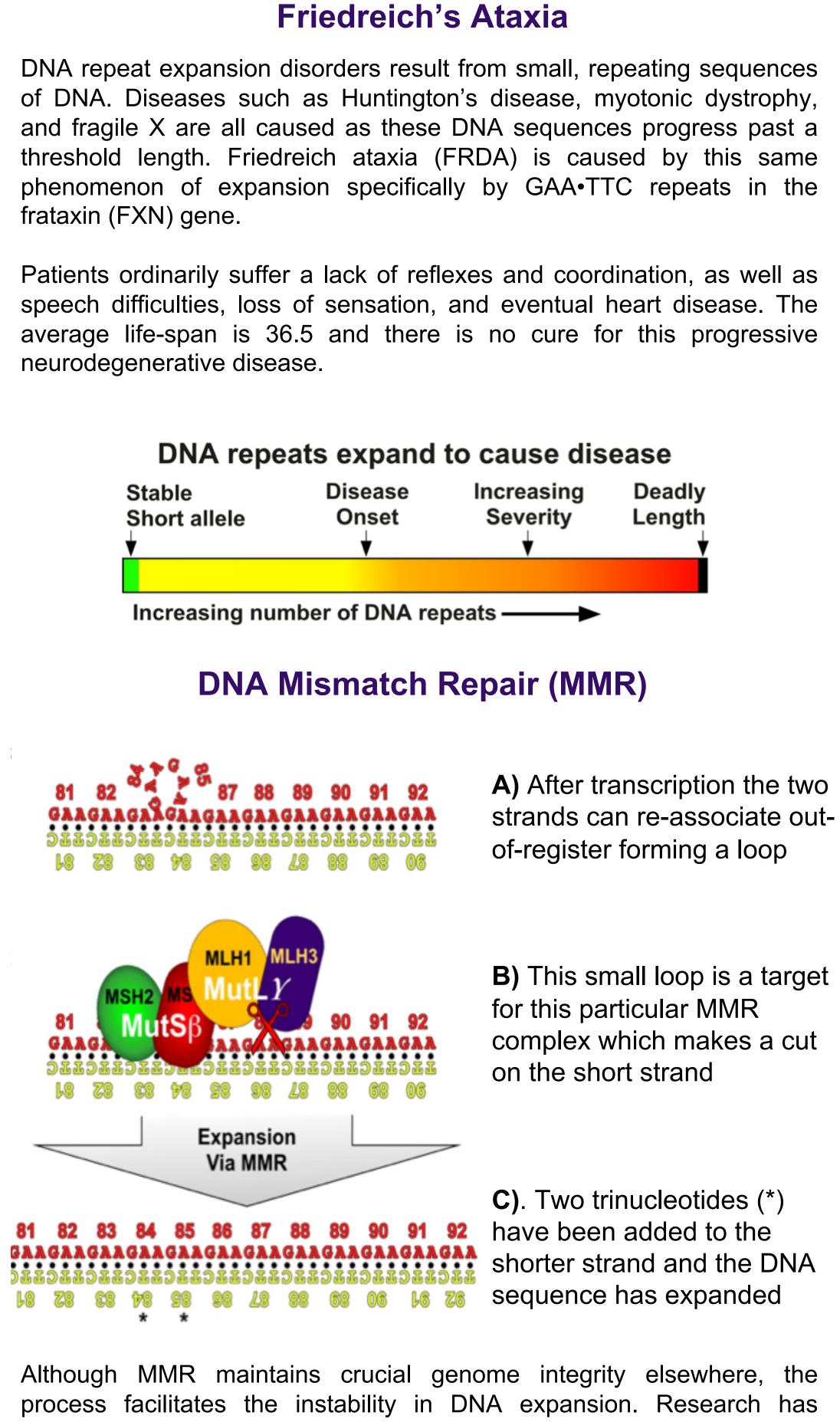
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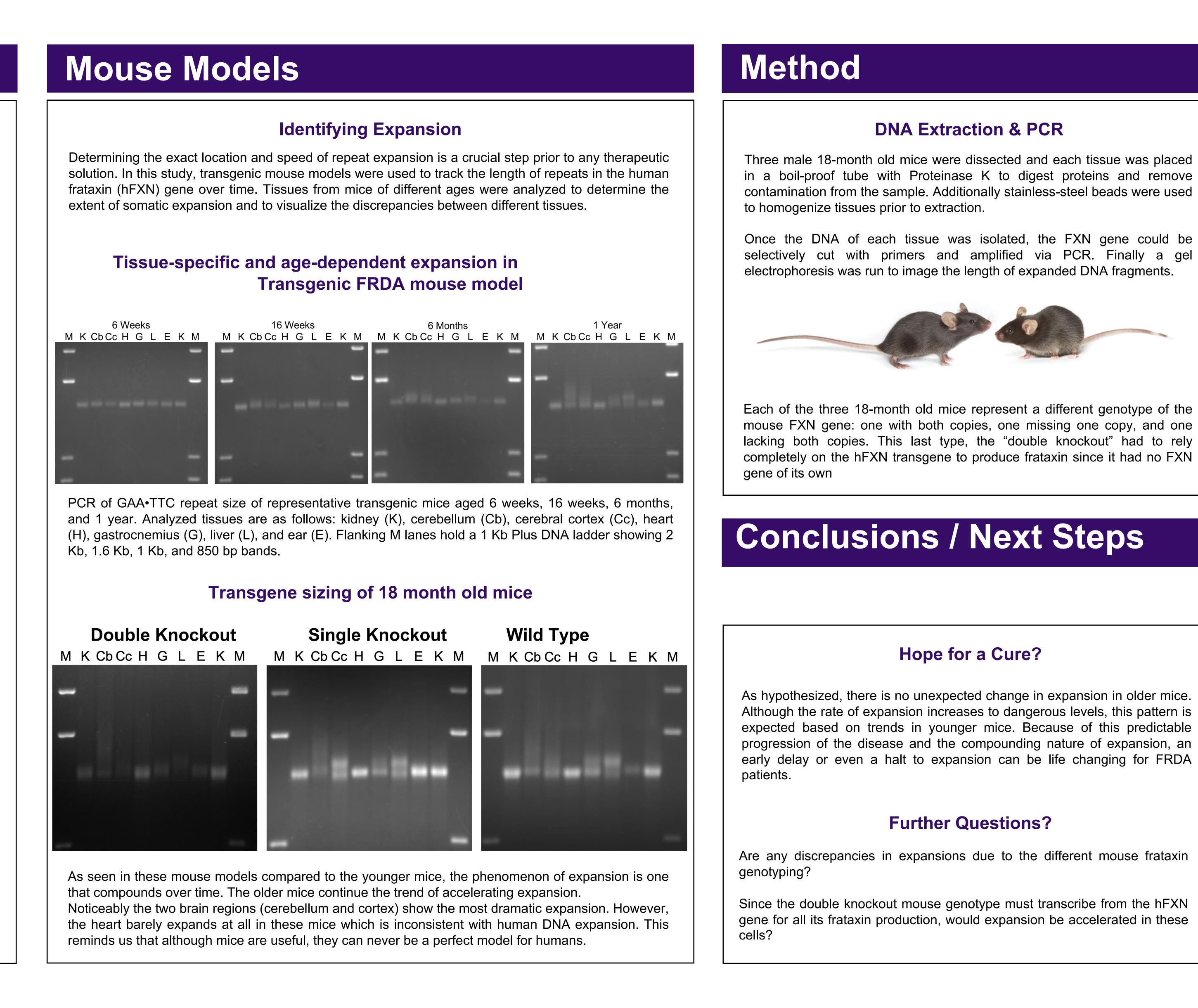
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