Amyotrophic lateral sclerosis (ALS) is motor neurodegenerative neuromuscular disease. ALS cases are classified as” sporadic” ALS (sALS) or “familial” ALS (fALS). With the fALS form, the disease is inherited. It has been reported that mutations of genes have been associated with fALS. And for this model, we will focus on the mutated FUS gene on chromosome 16. The C-terminal end of the FUS gene is involved in protein and RNA. It appears in double-strand break sites for repair of DNA damages. Mutations in the FUS NLS (Nuclear localization sequence) impairs the poly (ADP-ribose) polymerase (PARP)-dependent DNA damage response[[1]](#footnote-1). This impairment leads to FUS aggregate formation which is a common pathologic hallmark for ALS.

**AIM**: Mutation in the FUS nuclear localization sequence (NLS) induces impairment of DNA repair and cytoplasmic FUS mislocalization leads to FUS aggregate formation.

**Methodology**

**Patient selection**

R521C and R521H mutations are the most prevalent mutations within the NLS region of FUS. In addition of normal patients, fALS patients carrying diverse NLS mutations will be selected.

**Line cells**

Line cells will be established from biopsies (skin or hair cells) obtained after consent from the fALS patients and healthy individuals. The fibroblast lines will be plated in a media, and reprogrammed into human induced pluripotent stem cells (hiPSCs) using “Yamanake-factors”. These vectors could be transfected into the cells with a transfection agent. These cell lines, then can be constantly regenerated in subcultures and will be monitored until colonies will develop enough.

**CRISPR/Cas9 genome editing**

To increase the significance of the research, mutations which have been linked to ALS will be performed using CRISPR/Cas9 vector and guide RNAs (gRNA) to create double strand break at the target site and insert the mutated sequence in the C-terminal nuclear localization sequence (NLS) of the gene[[2]](#footnote-2). These proteins will be GFP-tagged.

**Study**

Electrophysiology of motor neurons will be performed to check the presence of voltage-gated Na+ and K+ channels, action potentials and intracellular calcium. After extended maturation of the cultures, we will look for an increase of FUS aggregates and will compare DNA double strand breaks in mutated lines to normal cells from healthy patients.

**Motivations for the specifics of the methodology**

The reasons to select patients of mutated FUS gene is to compare their cells with the cells with the same mutated gene using CRISP and acts as an additional validation step. Because it a genetic disease study, CRISP-Cas9 seems the natural choice for this gene editing.

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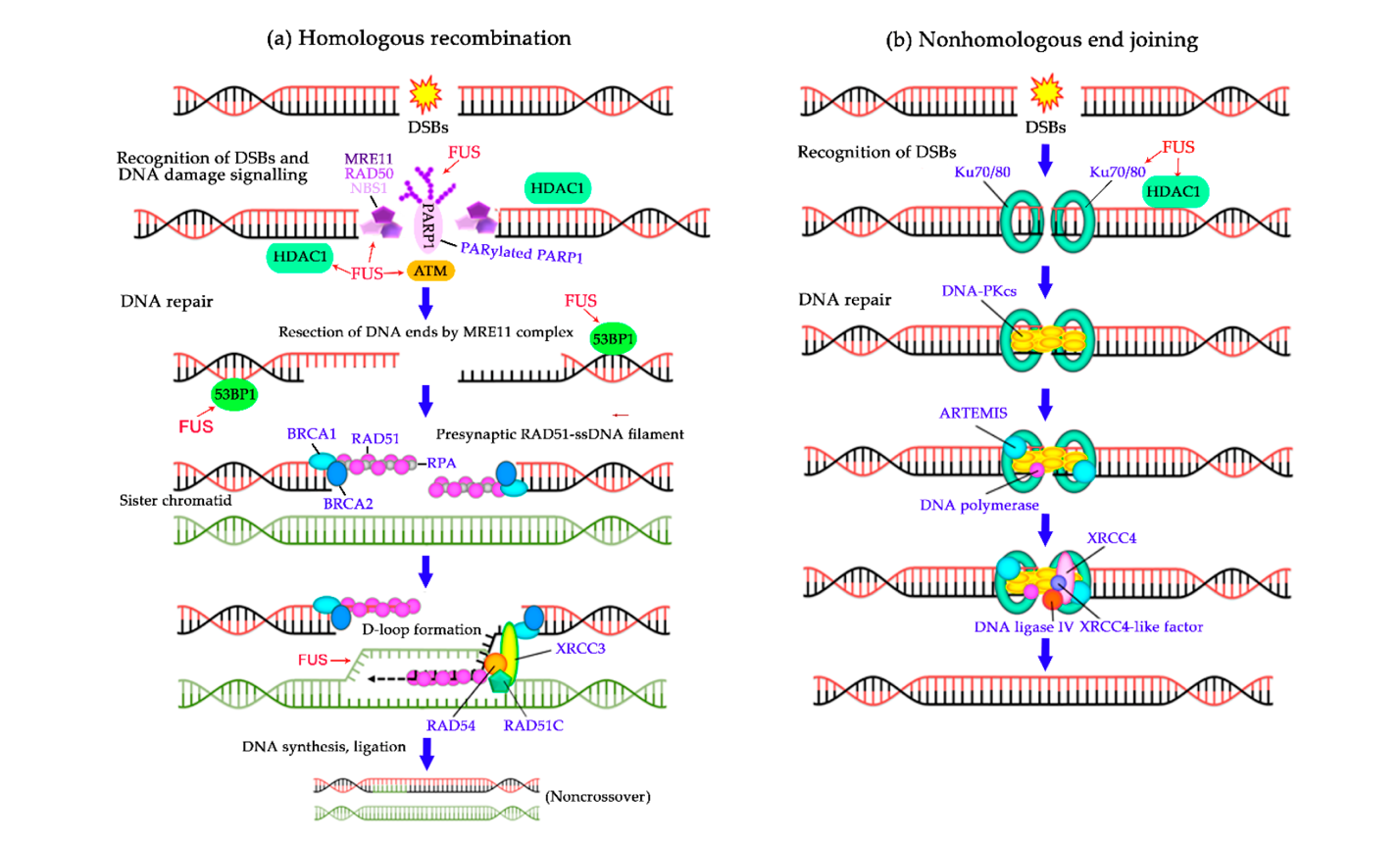
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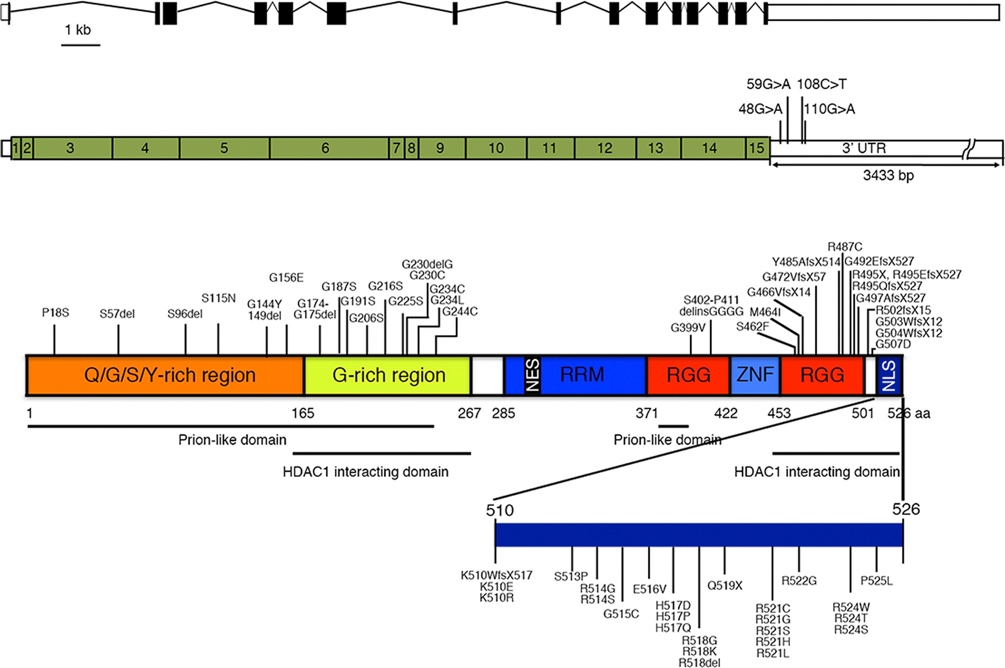
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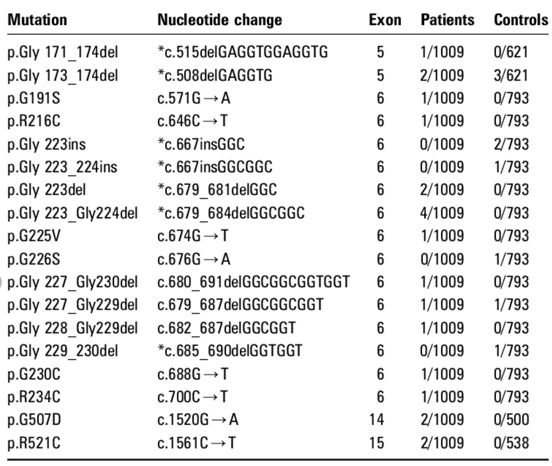
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**Fig 1. FUS DNA Repair mechanism**



**Fig 2. FUS NLS mutations**



**Fig 3. R521C nucleotide change: C->T**

1. See figure 1 [↑](#footnote-ref-1)
2. See figure 2 and 3 [↑](#footnote-ref-2)