

***Fus* Cas9-KO Strategy**

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Project Overview

Project Name

Fus

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fus* gene. The schematic diagram is as follows:



- The *Fus* gene has 16 transcripts. According to the structure of *Fus* gene, exon2-exon6 of *Fus-203* (ENSMUST00000106251.9) transcript is recommended as the knockout region. The region contains 730bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fus* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygotes for targeted null mutations exhibit impaired lymphocyte development, chromosomal instability, increased cellular radiation sensitivity, high neonatal mortality, and male sterility associated with lack of chromosomal pairing.
- The *Fus* gene is located on the Chr7. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Fus fused in sarcoma [Mus musculus (house mouse)]

Gene ID: 233908, updated on 7-Apr-2019

Summary



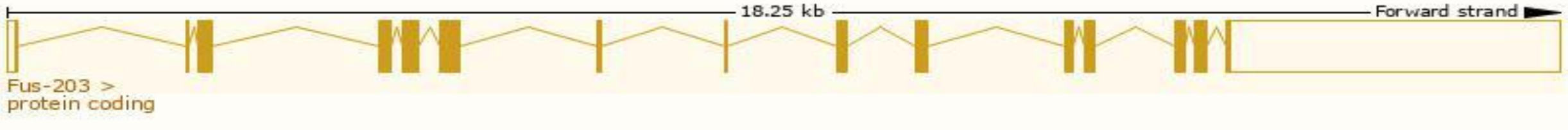
Official Symbol	Fus provided by MGI
Official Full Name	fused in sarcoma provided by MGI
Primary source	MGI:MGI:1353633
See related	Ensembl:ENSMUSG00000030795
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	D430004D17Rik, D930039C12Rik, Fus1, Tls
Expression	Ubiquitous expression in limb E14.5 (RPKM 160.0), CNS E11.5 (RPKM 159.5) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

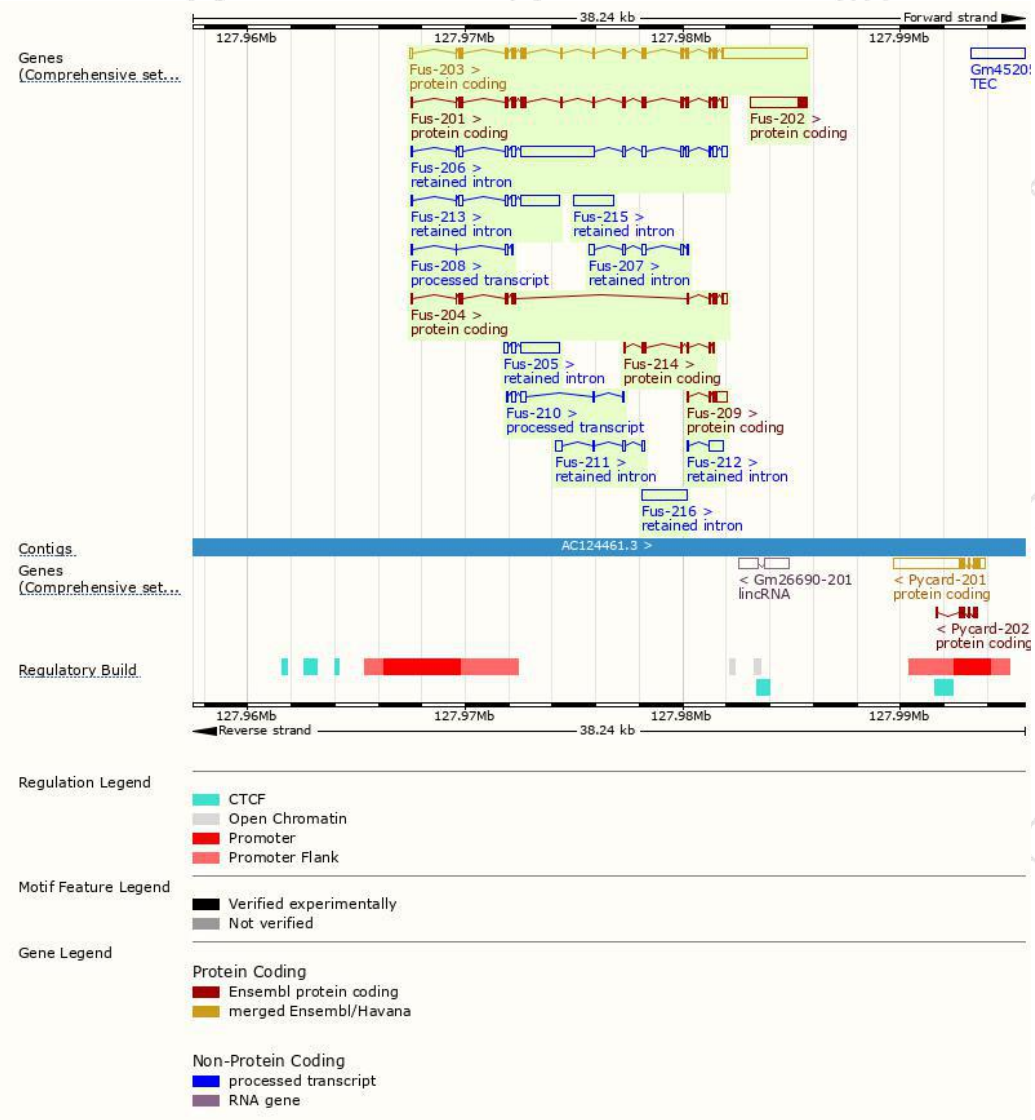
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fus-203	ENSMUST00000106251.9	5536	518aa	Protein coding	CCDS21886	P56959 Q564D0	TSL:1 GENCODE basic APPRIS P3
Fus-201	ENSMUST00000077609.11	1831	517aa	Protein coding	CCDS85425	Q8CFQ9	TSL:1 GENCODE basic APPRIS ALT2
Fus-202	ENSMUST00000079045.2	2623	122aa	Protein coding	-	Q8BNR3	TSL:NA GENCODE basic
Fus-204	ENSMUST00000121616.8	1102	280aa	Protein coding	-	Q91VQ2	TSL:1 GENCODE basic
Fus-209	ENSMUST00000141997.1	761	104aa	Protein coding	-	G3UZD2	CDS 5' incomplete TSL:2
Fus-214	ENSMUST00000174632.7	390	130aa	Protein coding	-	G3UXT7	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Fus-210	ENSMUST00000154843.7	600	No protein	Processed transcript	-	-	TSL:3
Fus-208	ENSMUST00000137464.6	354	No protein	Processed transcript	-	-	TSL:5
Fus-206	ENSMUST00000128851.7	4909	No protein	Retained intron	-	-	TSL:5
Fus-213	ENSMUST00000174196.7	2374	No protein	Retained intron	-	-	TSL:1
Fus-205	ENSMUST00000123151.7	2158	No protein	Retained intron	-	-	TSL:1
Fus-216	ENSMUST00000205351.1	2055	No protein	Retained intron	-	-	TSL:NA
Fus-215	ENSMUST00000205261.1	1859	No protein	Retained intron	-	-	TSL:NA
Fus-212	ENSMUST00000172755.1	670	No protein	Retained intron	-	-	TSL:5
Fus-207	ENSMUST00000136289.1	600	No protein	Retained intron	-	-	TSL:3
Fus-211	ENSMUST00000155941.7	516	No protein	Retained intron	-	-	TSL:3

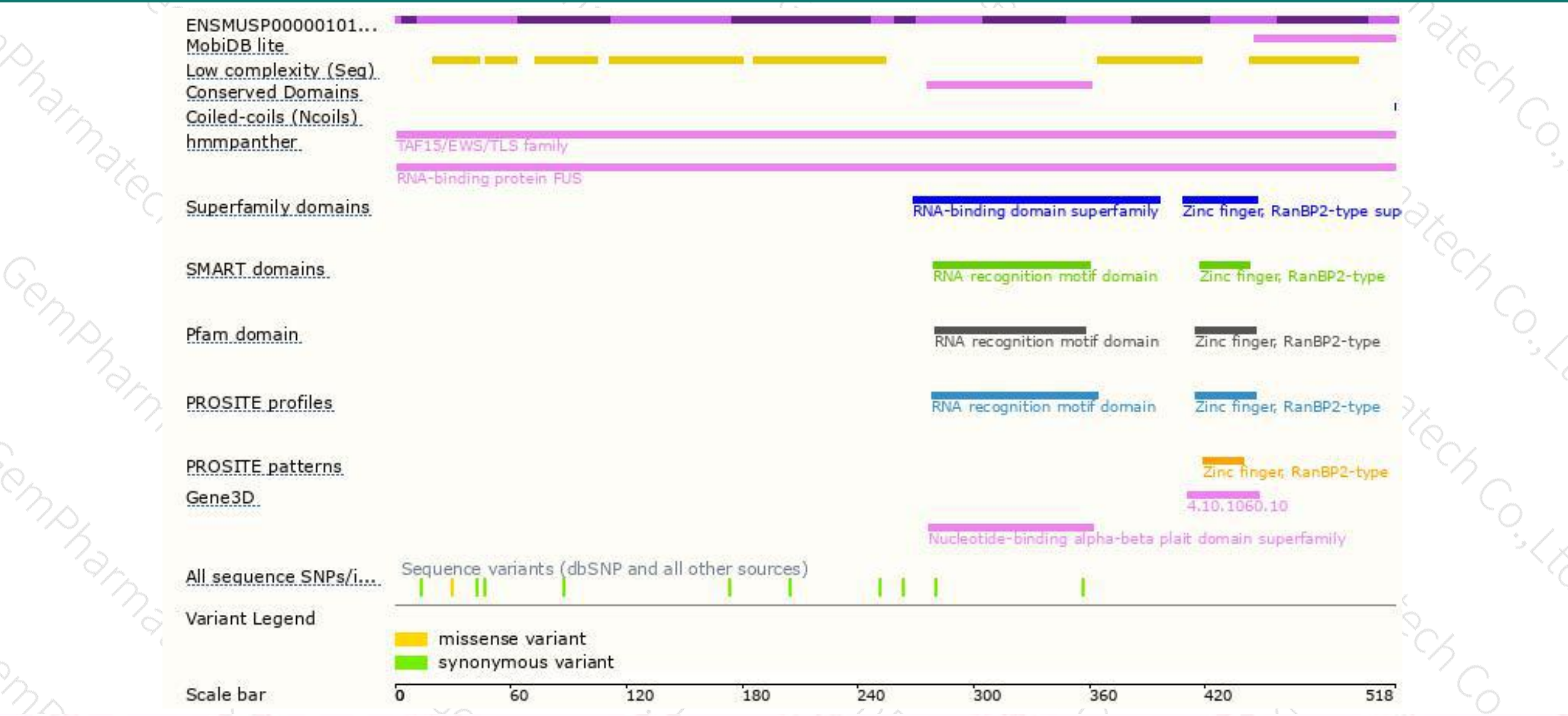
The strategy is based on the design of *Fus-203* transcript,The transcription is shown below



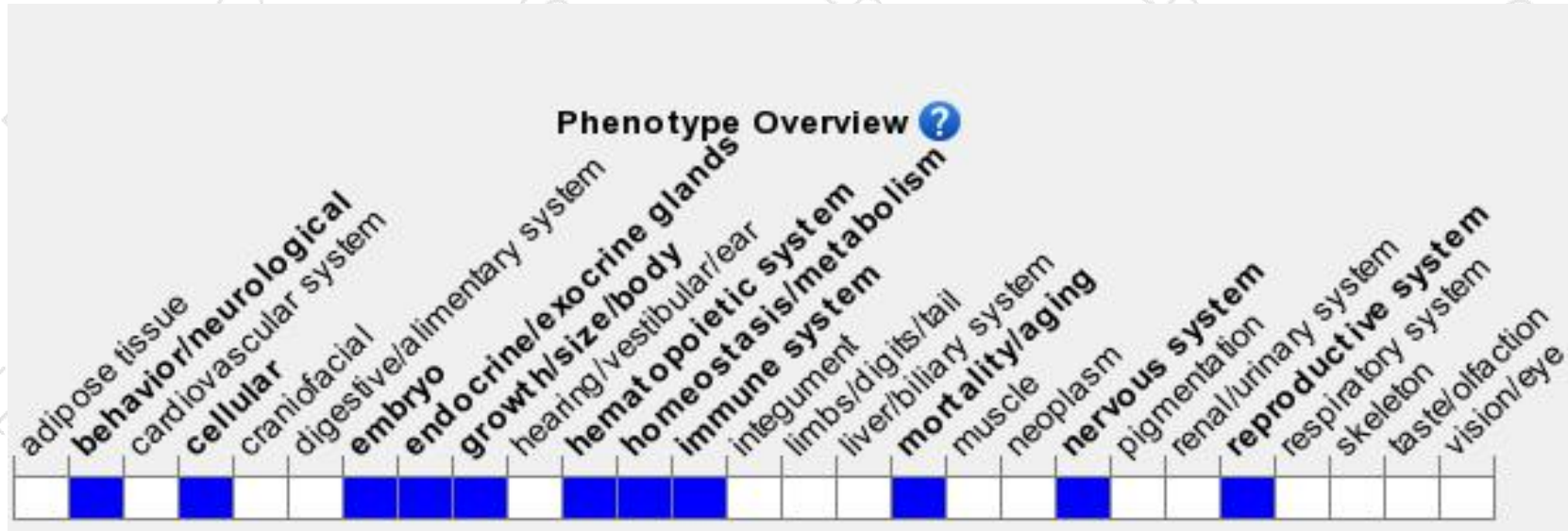
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, Homozygotes for targeted null mutations exhibit impaired lymphocyte development, chromosomal instability, increased cellular radiation sensitivity, high neonatal mortality, and male sterility associated with lack of chromosomal pairing.

If you have any questions, you are welcome to inquire.

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