

Nfia Cas9-CKO Strategy

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Project Overview

Project Name

Nfia

Project type

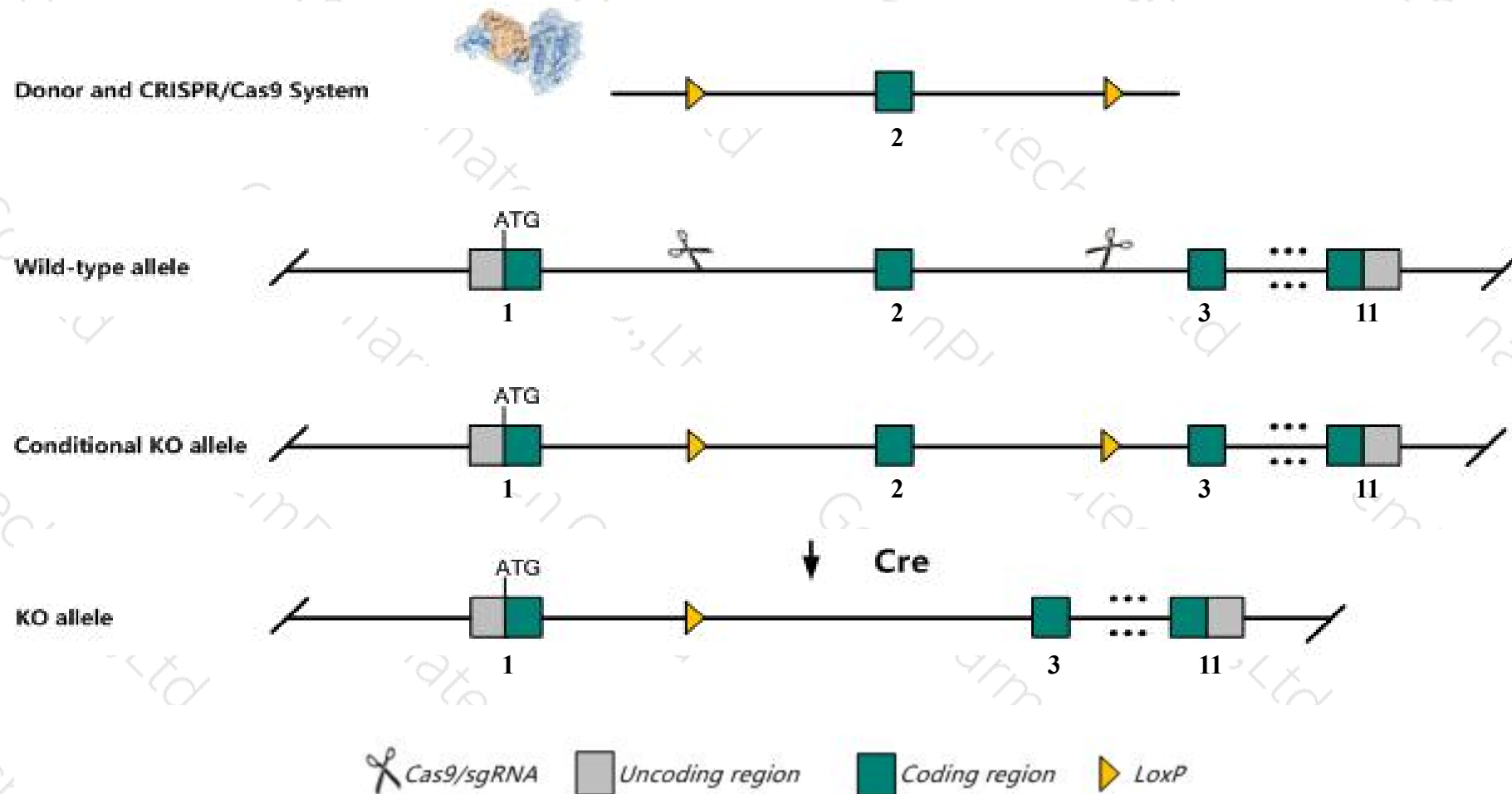
Cas9-CKO

Strain background

C57BL/6J

Conditional Knockout strategy

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



- The *Nfia* gene has 8 transcripts. According to the structure of *Nfia* gene, exon2 of *Nfia-202* (ENSMUST00000075448.12) transcript is recommended as the knockout region. The region contains 532bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nfia* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA and Donor were microinjected into the fertilized eggs of C57BL/6J mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6J mice.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Homozygous null mice display perinatal lethality, hydrocephalus, agenesis of the corpus callosum and hippocampal commissure. Fertility of surviving homozygotes is compromised. A decrease in the number of heterozygous animals is associated with a maternal effect.
- The *Nfia* gene is located on the Chr4. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Nfia nuclear factor I/A [Mus musculus (house mouse)]

Gene ID: 18027, updated on 12-Mar-2019

Summary



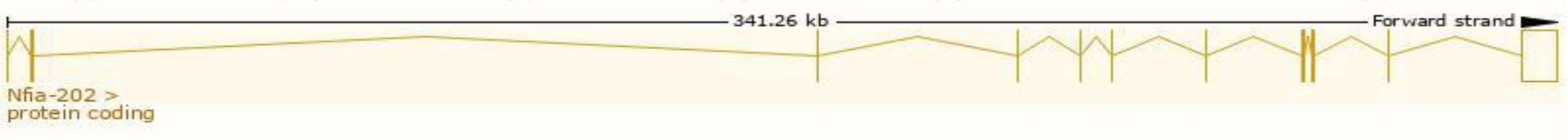
Official Symbol	Nfia provided by MGI
Official Full Name	nuclear factor I/A provided by MGI
Primary source	MGI:MGI:108056
See related	Ensembl:ENSMUSG00000028565
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110047K16Rik, 9430022M17Rik, CTF, NF1-A, NF1A
Expression	Ubiquitous expression in limb E14.5 (RPKM 8.7), CNS E14 (RPKM 7.7) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nfia-202	ENSMUST00000075448.12	9526	509aa	Protein coding	CCDS18373	Q02780	TSL:1 GENCODE basic APPRIS P2
Nfia-203	ENSMUST00000092532.12	9382	466aa	Protein coding	CCDS51234	Q02780	TSL:1 GENCODE basic
Nfia-201	ENSMUST00000052018.11	9249	487aa	Protein coding	-	B1AUB9	TSL:5 GENCODE basic
Nfia-205	ENSMUST00000107062.8	9239	498aa	Protein coding	-	B1AUC0	TSL:5 GENCODE basic APPRIS ALT 1
Nfia-204	ENSMUST00000107057.7	8913	380aa	Protein coding	-	B1AUB8	TSL:5 GENCODE basic
Nfia-208	ENSMUST00000152023.7	851	225aa	Protein coding	-	B1AUB6	CDS 3' incomplete TSL:5
Nfia-207	ENSMUST00000148930.2	821	274aa	Protein coding	-	E7CDR2	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
Nfia-206	ENSMUST00000133011.1	1649	No protein	Processed transcript	-	-	TSL:1

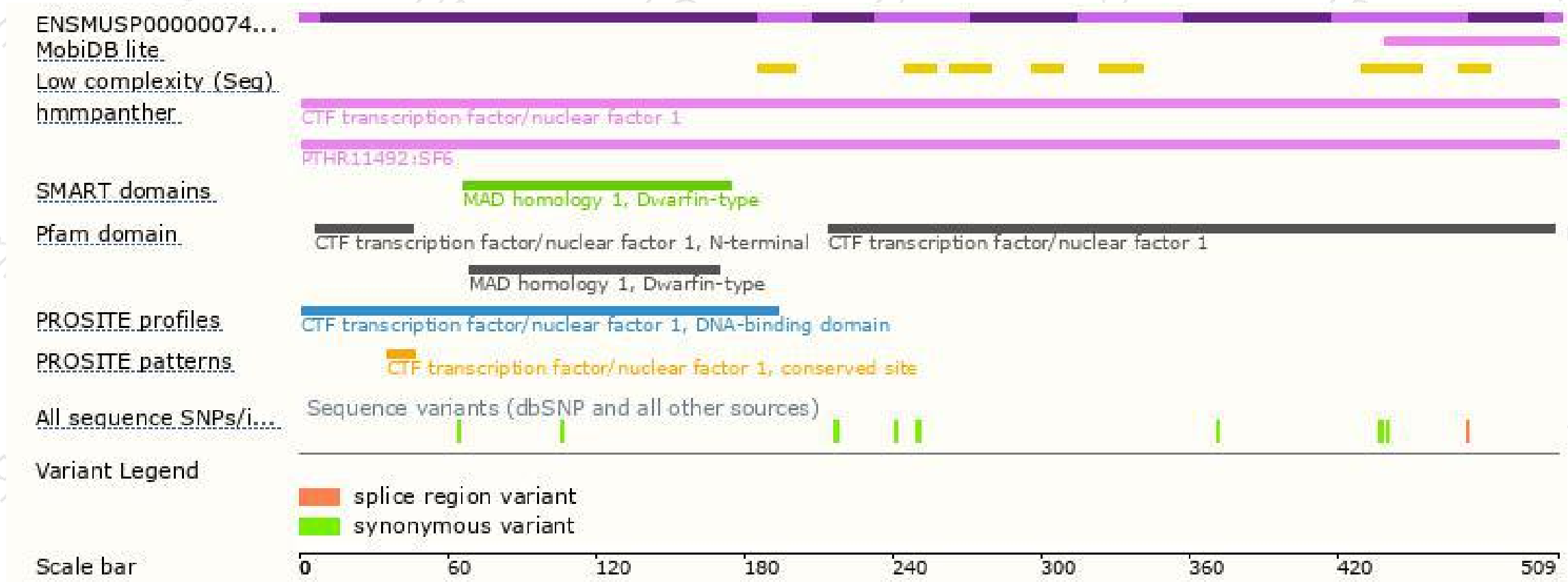
The strategy is based on the design of *Nfia-202* transcript,The transcription is shown below



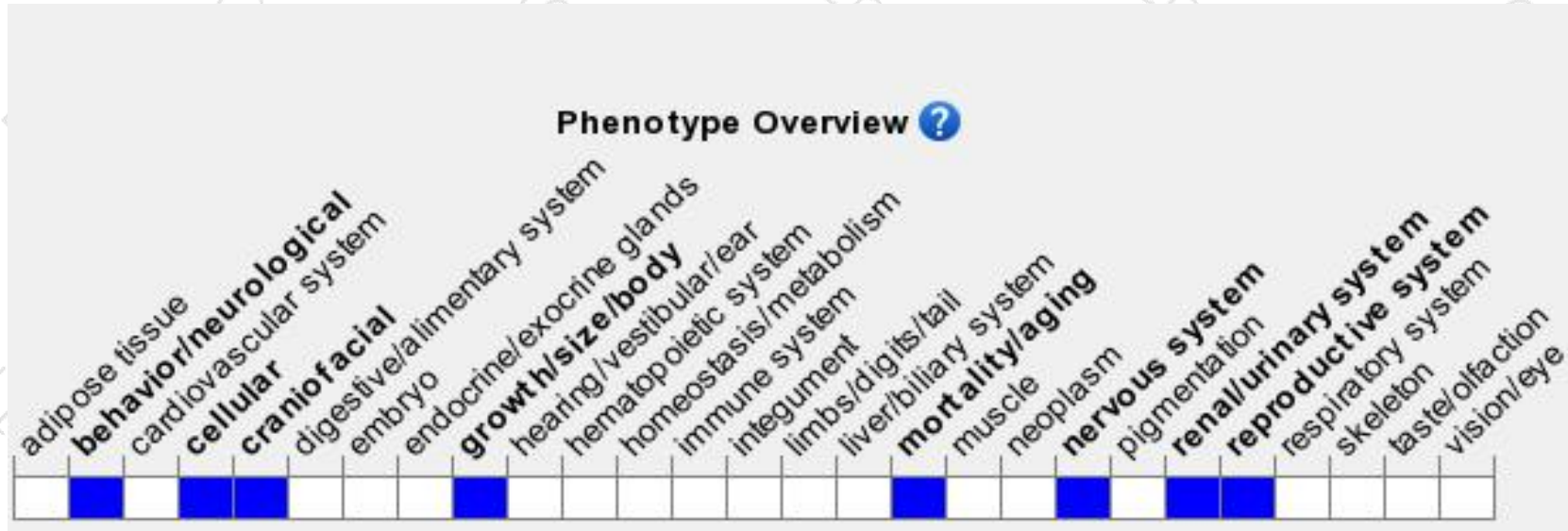
Genomic location distribution



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/>).

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

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