

***2210408I21Rik* Cas9-KO Strategy**

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Project Overview

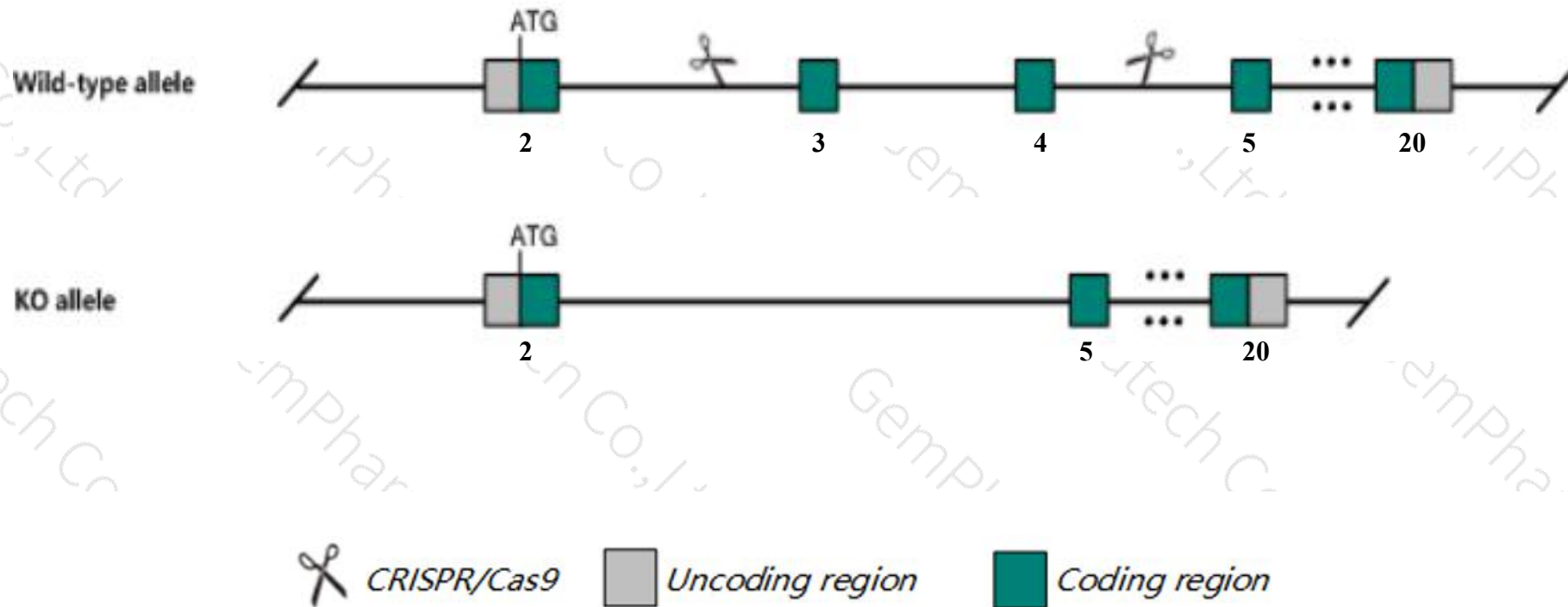
Project Name	<i>2210408I21Rik</i>
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Project type	Cas9-KO
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Strain background	C57BL/6JGpt
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Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *2210408I21Rik* gene. The schematic diagram is as follows:



- The *2210408I21Rik* gene has 5 transcripts. According to the structure of *2210408I21Rik* gene, exon3-exon4 of *2210408I21Rik-201* (ENSMUST00000168779.2) transcript is recommended as the knockout region. The region contains 839bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *2210408I21Rik* gene. The brief process is as follows: CRISPR/Cas

- The *2210408I21Rik* gene is located on the Chr13. 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)

2210408I21Rik RIKEN cDNA 2210408I21 gene [Mus musculus (house mouse)]

Gene ID: 72371, updated on 13-Mar-2020

Summary



Official Symbol	2210408I21Rik provided by MGI
Official Full Name	RIKEN cDNA 2210408I21 gene provided by MGI
Primary source	MGI:MGI:1919621
See related	Ensembl:ENSMUSG00000071252
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
Expression	Broad expression in testis adult (RPKM 2.4), CNS E18 (RPKM 0.9) and 18 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

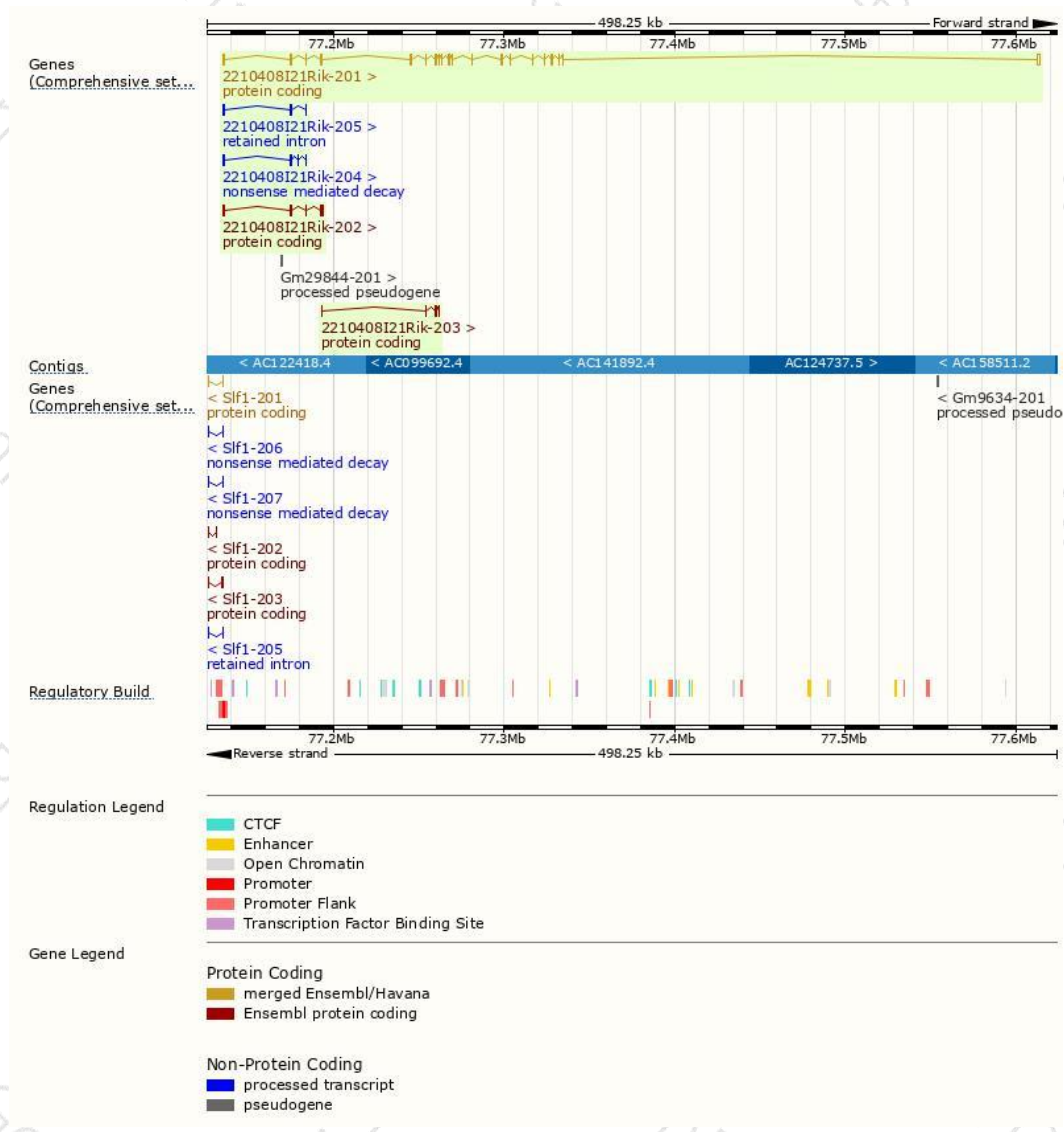
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
2210408I21Rik-201	ENSMUST00000168779.2	5051	1272aa	Protein coding	CCDS49316	Q3UPC7	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
2210408I21Rik-202	ENSMUST00000225605.1	1539	324aa	Protein coding	-	Q3UPC7	GENCODE basic
2210408I21Rik-203	ENSMUST00000225760.1	594	198aa	Protein coding	-	A0A286YD44	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
2210408I21Rik-204	ENSMUST00000225960.1	522	46aa	Nonsense mediated decay	-	A0A286YDQ9	
2210408I21Rik-205	ENSMUST00000225992.1	616	No protein	Retained intron	-	-	

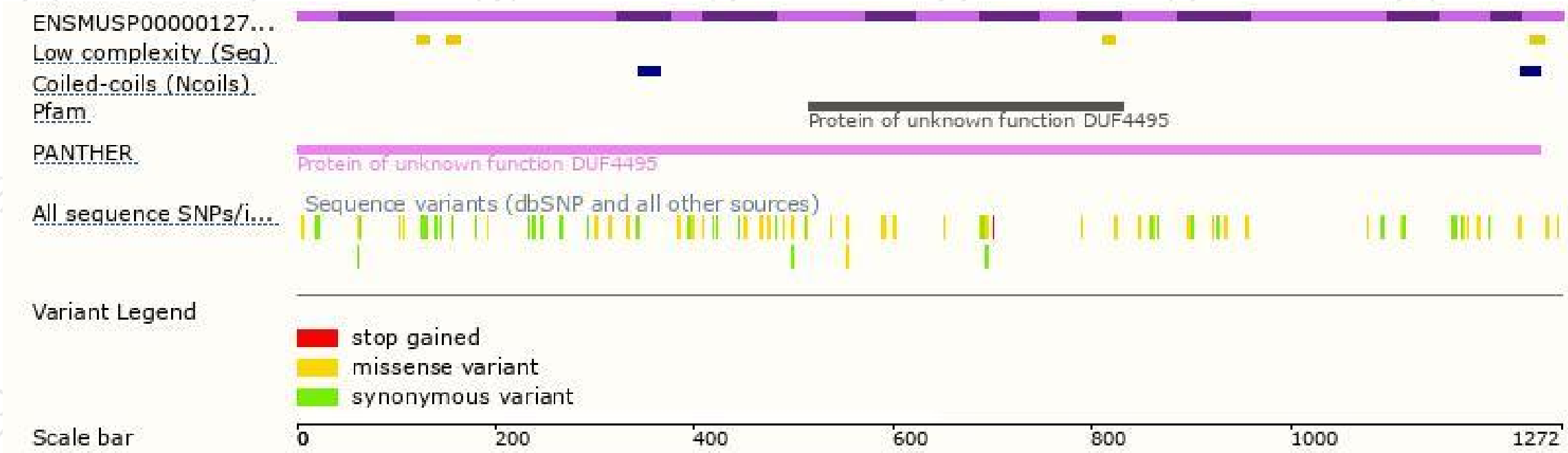
The strategy is based on the design of 2210408I21Rik-201 transcript,The transcription is shown below



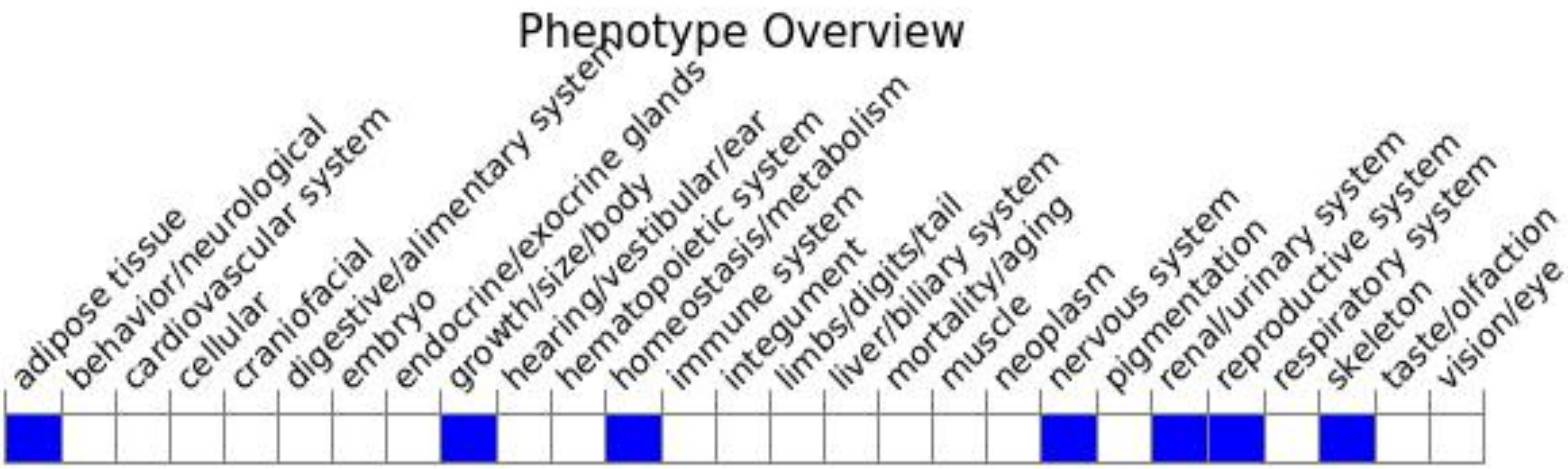
Genomic location distribution



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/>).

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

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