

# *Rtkn* Cas9-KO Strategy

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# Project Overview

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**Project Name**

*Rtkn*

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**Project type**

**Cas9-KO**

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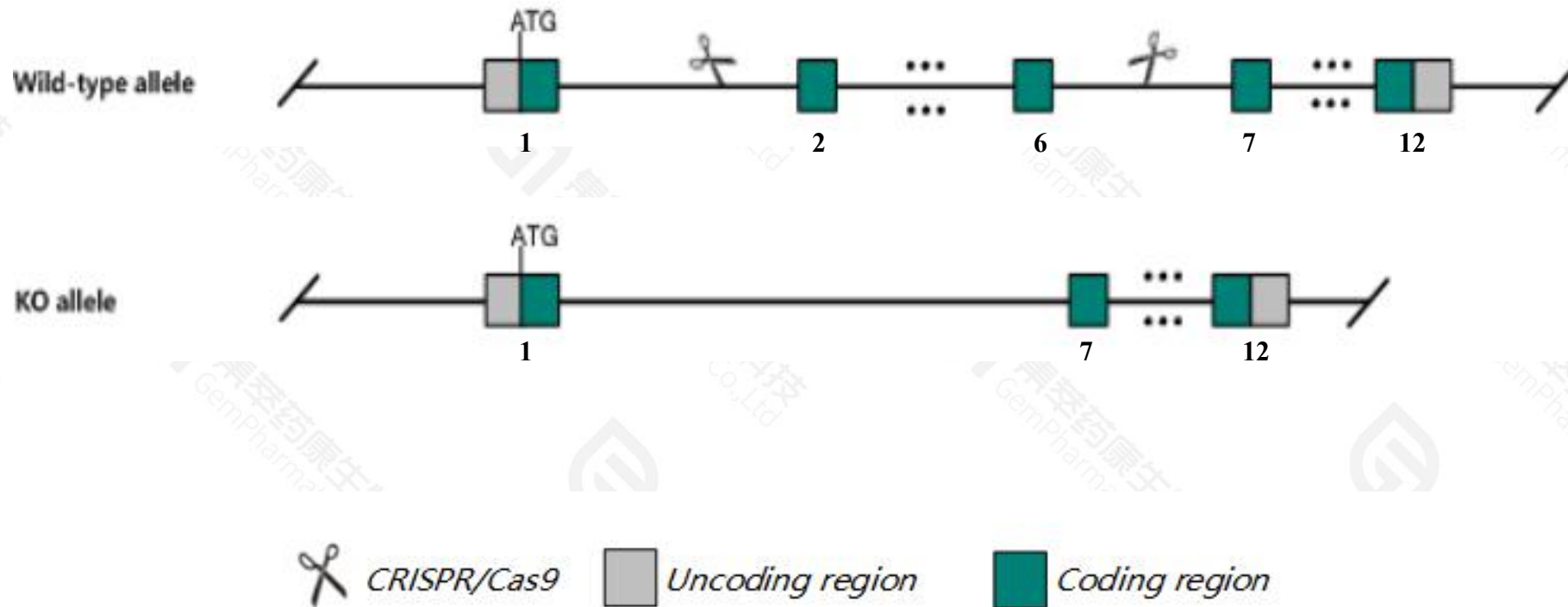
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

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



- The *Rtkn* gene has 9 transcripts. According to the structure of *Rtkn* gene, exon2-exon6 of *Rtkn*-201(ENSMUST00000065512.11) transcript is recommended as the knockout region. The region contains 644bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rtkn* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.



- Transcript *Rtkn*-209 may not be affected.
- The *Rtkn* gene is located on the Chr6. 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)

## Rtnr rhotekin [Mus musculus (house mouse)]

Gene ID: 20166, updated on 13-Mar-2020

### Summary

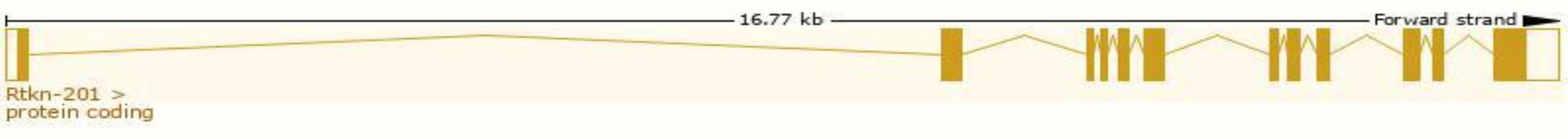
Official Symbol	Rtnr provided by <a href="#">MGI</a>
Official Full Name	rhotekin provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:107371</a>
See related	<a href="#">Ensembl:ENSMUSG00000034930</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Ubiquitous expression in limb E14.5 (RPKM 11.3), duodenum adult (RPKM 8.2) and 27 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

The gene has 9 transcripts,all transcripts are shown below:

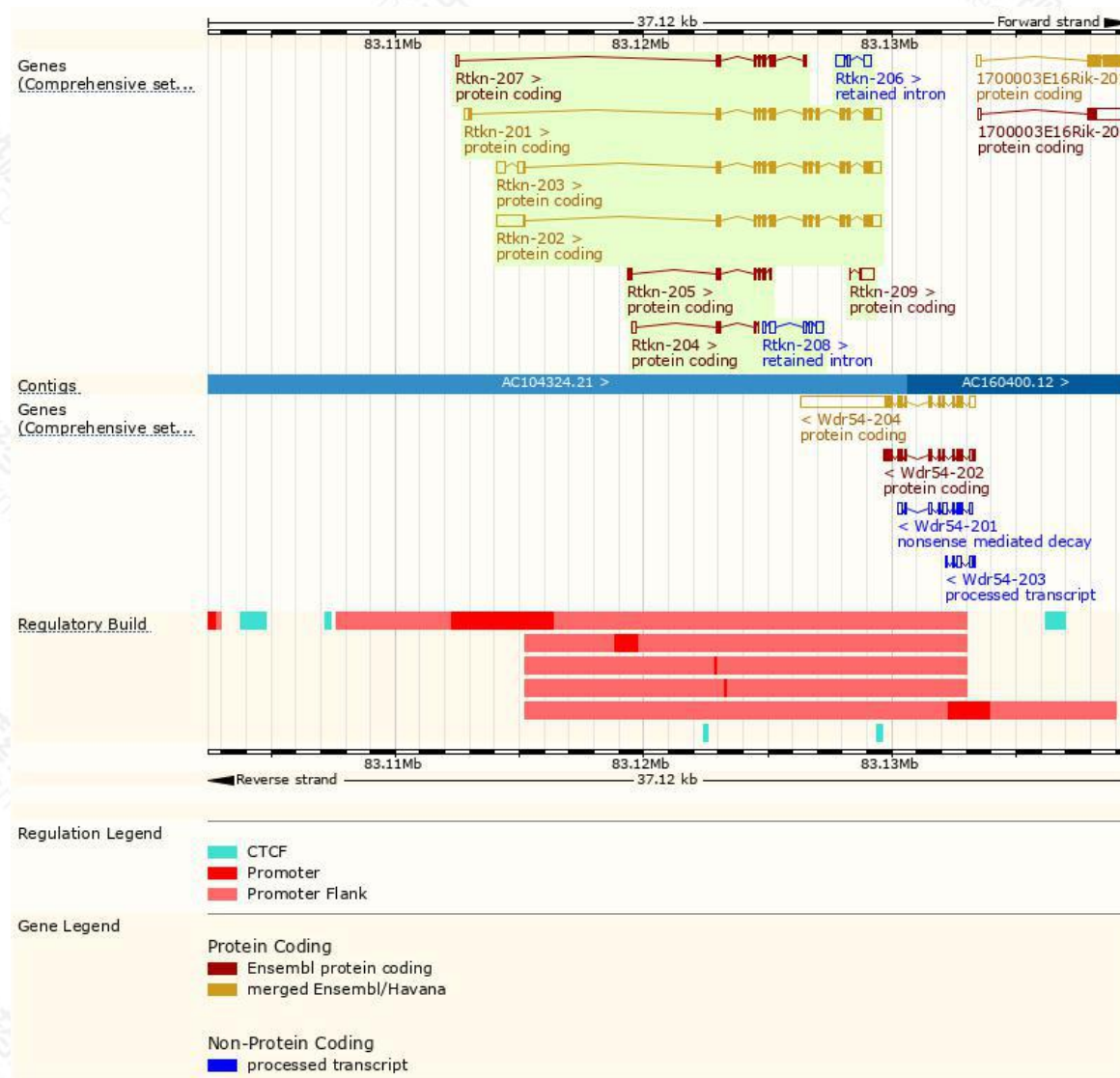
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rtkn-202	<a href="#">ENSMUST00000087938.10</a>	3080	<a href="#">551aa</a>	Protein coding	<a href="#">CCDS20274</a>	<a href="#">Q8C6B2</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Rtkn-203	<a href="#">ENSMUST00000121093.7</a>	2597	<a href="#">551aa</a>	Protein coding	<a href="#">CCDS20274</a>	<a href="#">Q8C6B2</a>	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 P3
Rtkn-201	<a href="#">ENSMUST00000065512.10</a>	2191	<a href="#">564aa</a>	Protein coding	<a href="#">CCDS51817</a>	<a href="#">Q8C6B2</a>	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 ALT2
Rtkn-207	<a href="#">ENSMUST00000135490.7</a>	862	<a href="#">233aa</a>	Protein coding	-	<a href="#">D3Z7S7</a>	CDS 3' incomplete TSL:5
Rtkn-205	<a href="#">ENSMUST00000130622.7</a>	653	<a href="#">217aa</a>	Protein coding	-	<a href="#">D3Z4N1</a>	CDS 3' incomplete TSL:3
Rtkn-209	<a href="#">ENSMUST00000213056.1</a>	608	<a href="#">48aa</a>	Protein coding	-	<a href="#">A0A1D5RLJ9</a>	CDS 5' incomplete TSL:3
Rtkn-204	<a href="#">ENSMUST00000129316.1</a>	434	<a href="#">82aa</a>	Protein coding	-	<a href="#">D3YXC9</a>	CDS 3' incomplete TSL:3
Rtkn-208	<a href="#">ENSMUST00000203183.1</a>	792	No protein	Retained intron	-	-	TSL:3
Rtkn-206	<a href="#">ENSMUST00000133226.1</a>	750	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Rtkn-201* transcript,the transcription is shown below:



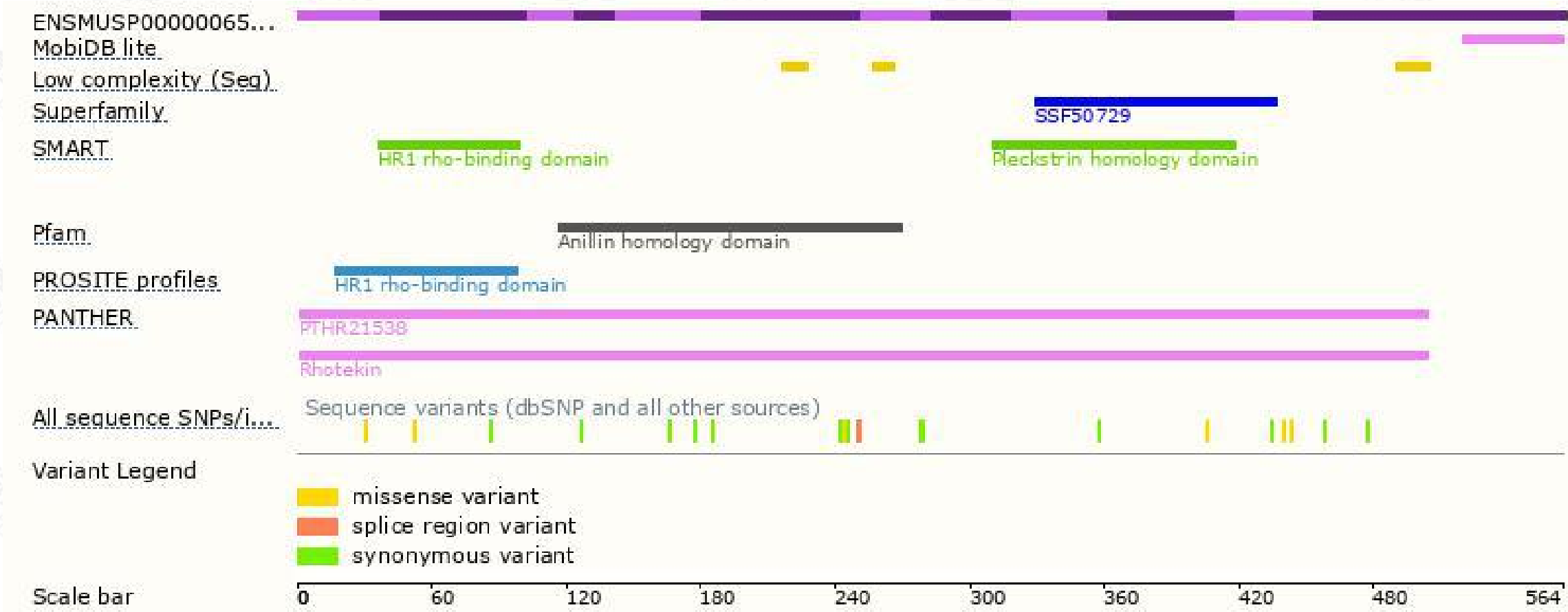


# Genomic location distribution





# Protein domain



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