

# *Rora* Cas9-KO Strategy

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# Project Overview

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**Project Name**

***Rora***

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**Project type**

**Cas9-KO**

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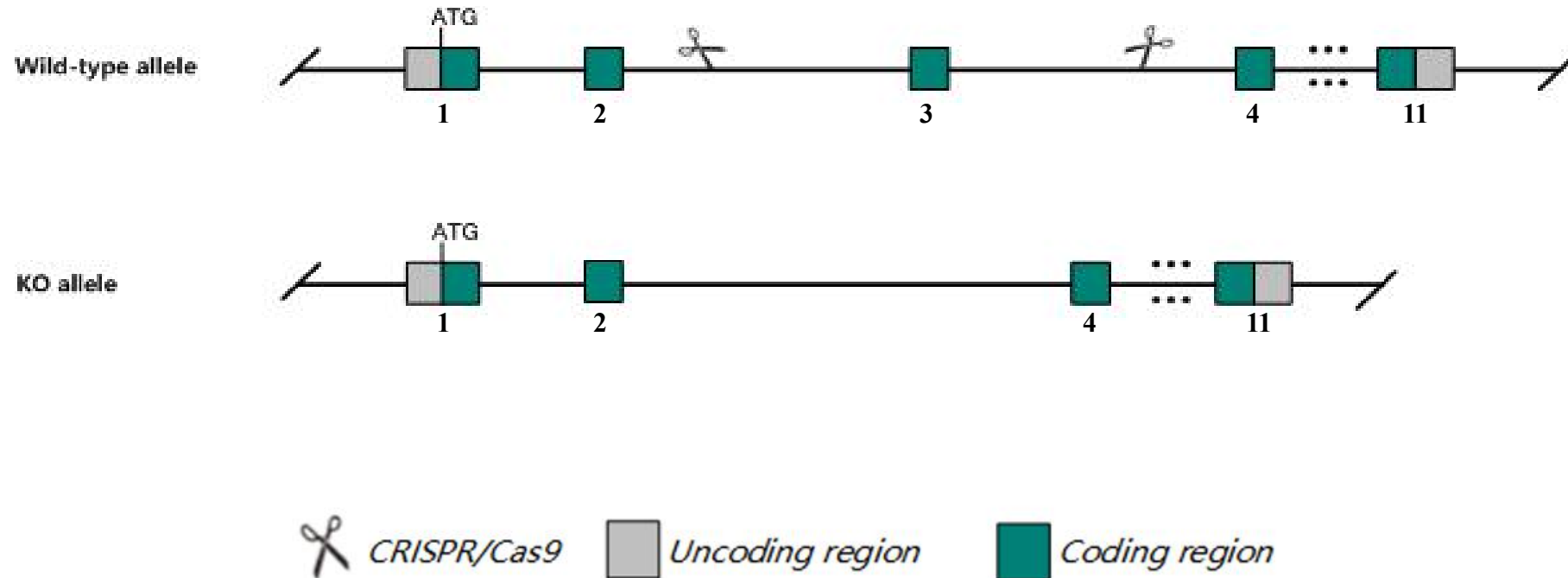
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

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



The *Rora* gene has 6 transcripts. According to the structure of *Rora* gene, exon3 of *Rora-201* (ENSMUST00000034766.13) transcript is recommended as the knockout region. The region contains 86bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Rora* gene. The brief process is as follows: CRISPR/Cas9 system v

According to the existing MGI data, Homozygotes for null mutations exhibit ataxia, cerebellar dysgenesis, impaired Purkinje and granule cell development, olfactory defects, hypoalphalipoproteinemia, and death around 4 weeks. Heterozygotes show slow Purkinje cell dendritic atrophy and loss.

The *Rora* gene is located on the Chr9. 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.

## Rora RAR-related orphan receptor alpha [Mus musculus (house mouse)]

Gene ID: 19883, updated on 26-Feb-2019

### Summary



<b>Official Symbol</b>	Rora provided by <a href="#">MGI</a>
<b>Official Full Name</b>	RAR-related orphan receptor alpha provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:104661</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000032238</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	9530021D13Rik, Nr1f1, ROR1, ROR2, ROR3, nmf267, sg, staggerer, tmgc26
<b>Summary</b>	The protein encoded by this gene is a member of the NR1 subfamily of nuclear hormone receptors. It can bind as a monomer or as a homodimer to hormone response elements upstream of several genes to enhance the expression of those genes. The encoded protein has been shown to interact with NM23-2, a nucleoside diphosphate kinase involved in organogenesis and differentiation, as well as with NM23-1, the product of a tumor metastasis suppressor candidate gene. Also, it has been shown to aid in the transcriptional regulation of some genes involved in circadian rhythm. Three transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Feb 2014]
<b>Expression</b>	Broad expression in cerebellum adult (RPKM 8.5), cortex adult (RPKM 3.0) and 19 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information      Ensembl

The gene has 6 transcripts,all transcripts are shown below:

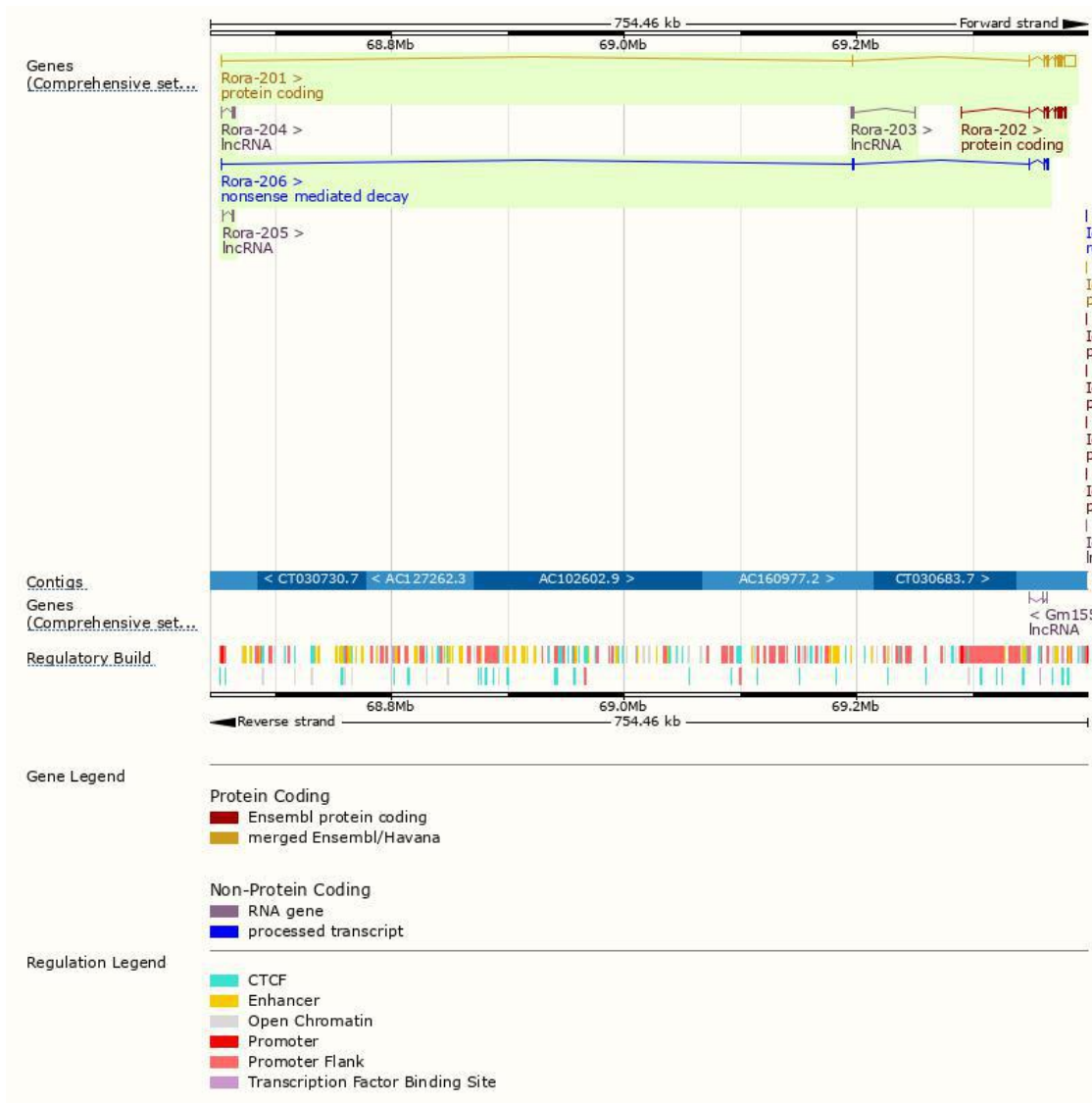
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rora-201	<a href="#">ENSMUST00000034766.13</a>	10878	<a href="#">523aa</a>	Protein coding	<a href="#">CCDS23314</a>	<a href="#">P51448</a>	TSL:1 GENCODE basic
Rora-202	<a href="#">ENSMUST00000113624.2</a>	2591	<a href="#">467aa</a>	Protein coding	<a href="#">CCDS72268</a>	<a href="#">P51448 Q3U1P4</a>	TSL:1 GENCODE basic APPRIS P1
Rora-206	<a href="#">ENSMUST00000174296.1</a>	751	<a href="#">62aa</a>	Nonsense mediated decay	-	<a href="#">G3UZ02</a>	CDS 5' incomplete TSL:5
Rora-204	<a href="#">ENSMUST00000140351.7</a>	1422	No protein	lncRNA	-	-	TSL:3
Rora-203	<a href="#">ENSMUST00000132355.1</a>	561	No protein	lncRNA	-	-	TSL:2
Rora-205	<a href="#">ENSMUST00000143507.1</a>	508	No protein	lncRNA	-	-	TSL:5

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



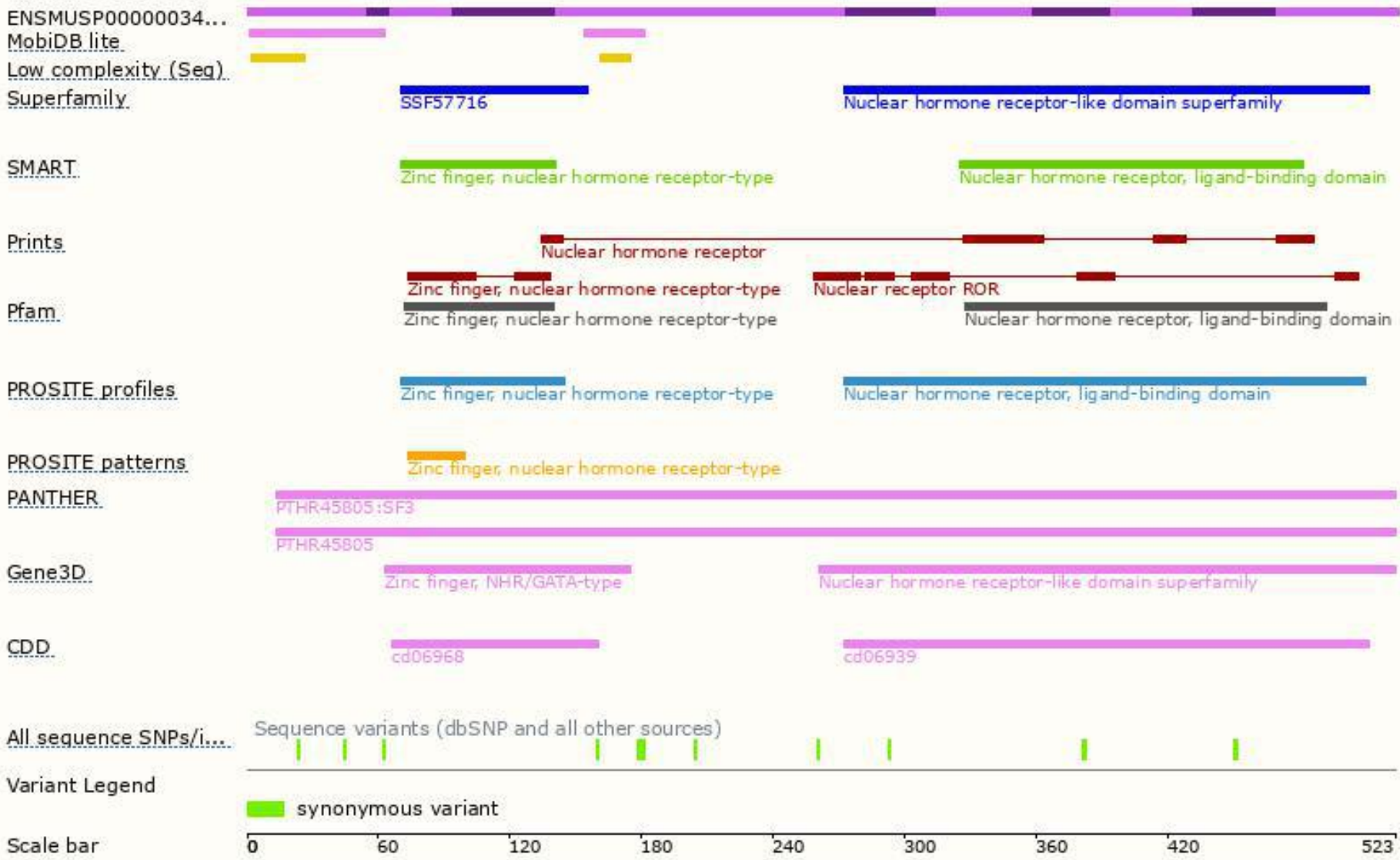


# Genomic location distribution

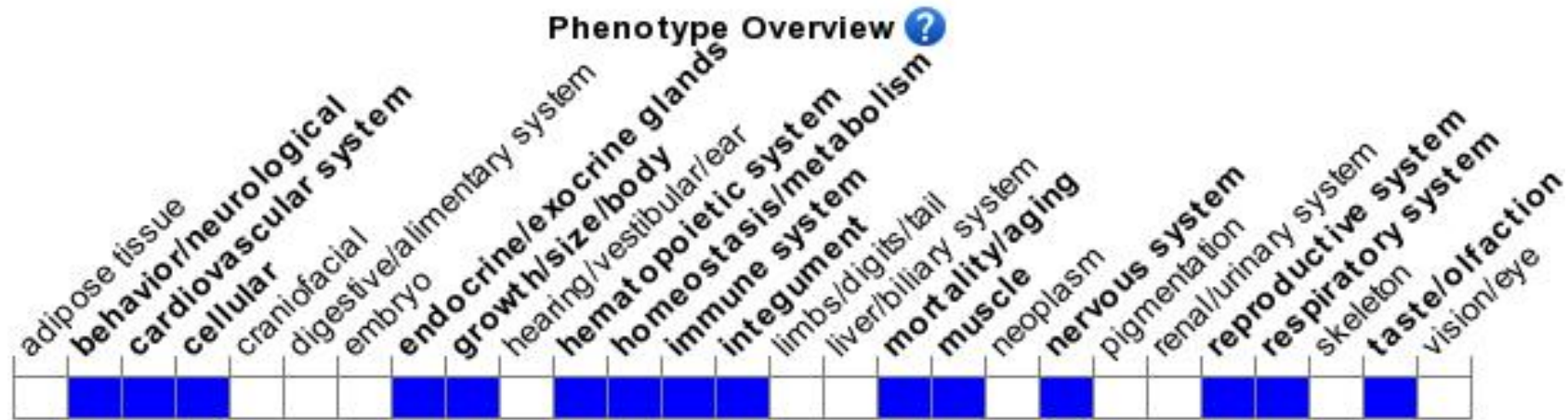




# Protein domain



# Mouse phenotype description(MGI )



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

According to the existing MGI data, Homozygotes for null mutations exhibit ataxia, cerebellar dysgenesis, impaired Purkinje and granule cell development, olfactory defects, hypoalphalipoproteinemia, and death around 4 weeks. Heterozygotes show slow Purkinje cell dendritic atrophy and loss.

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