

# ***Gata2a*** Cas9-KO Strategy

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# Project Overview

**Project Name**

***Gatad2a***

**Project type**

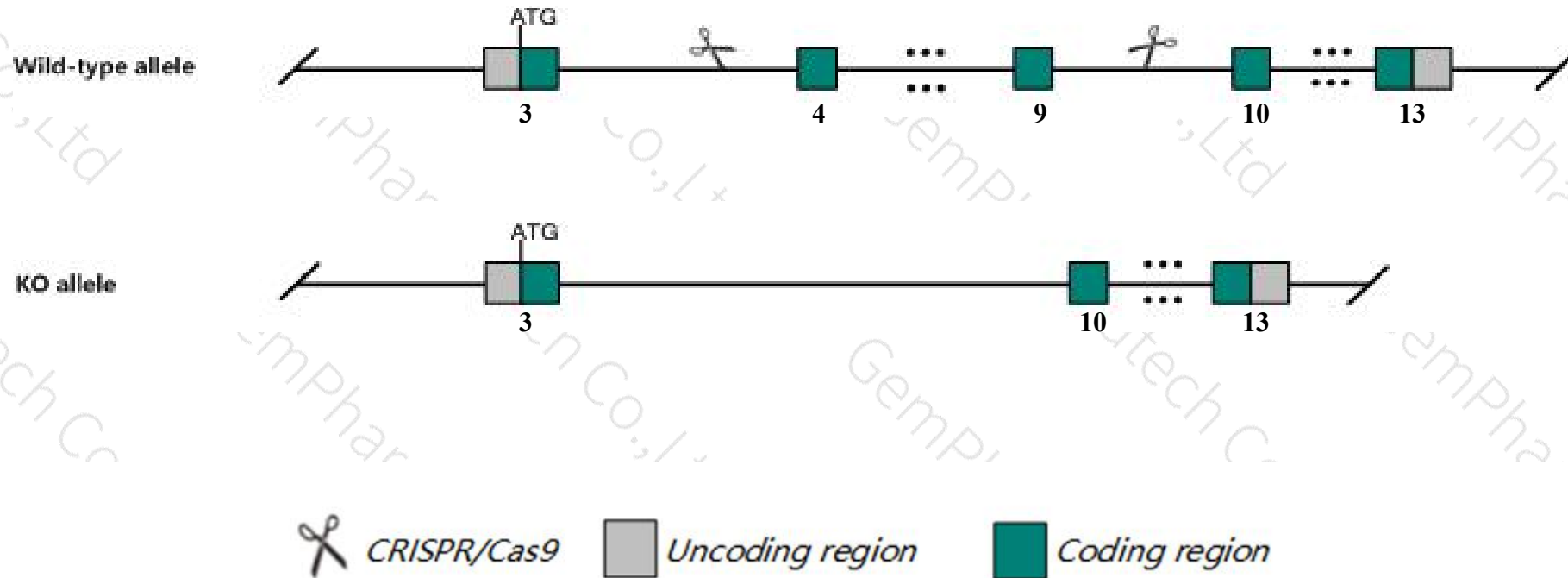
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gatad2a* gene. The schematic diagram is as follows:



- The *Gatad2a* gene has 6 transcripts. According to the structure of *Gatad2a* gene, exon4-exon9 of *Gatad2a-201* (ENSMUST00000065169.11) transcript is recommended as the knockout region. The region contains 935bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gatad2a* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele die around E9.5 displaying variable developmental defects, including malformed or unfused neural folds, failure of closure of anterior neuropore, missing or excessively large blood vessels in the yolk sac, abnormal embryo turning, and embryonic growth arrest.
- The *Gatad2a* gene is located on the Chr8. 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)

## Gatad2a GATA zinc finger domain containing 2A [Mus musculus (house mouse)]

Gene ID: 234366, updated on 19-Mar-2019

### Summary



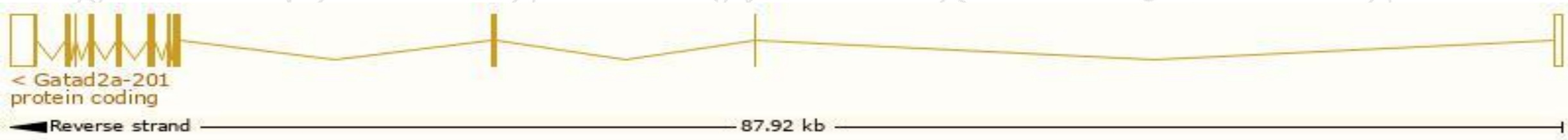
<b>Official Symbol</b>	Gatad2a provided by <a href="#">MGI</a>
<b>Official Full Name</b>	GATA zinc finger domain containing 2A provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2384585</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000036180</a>
<b>Gene type</b>	protein 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>	1110066C11Rik, BC031407, C80248
<b>Expression</b>	Ubiquitous expression in adrenal adult (RPKM 31.4), ovary adult (RPKM 26.7) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

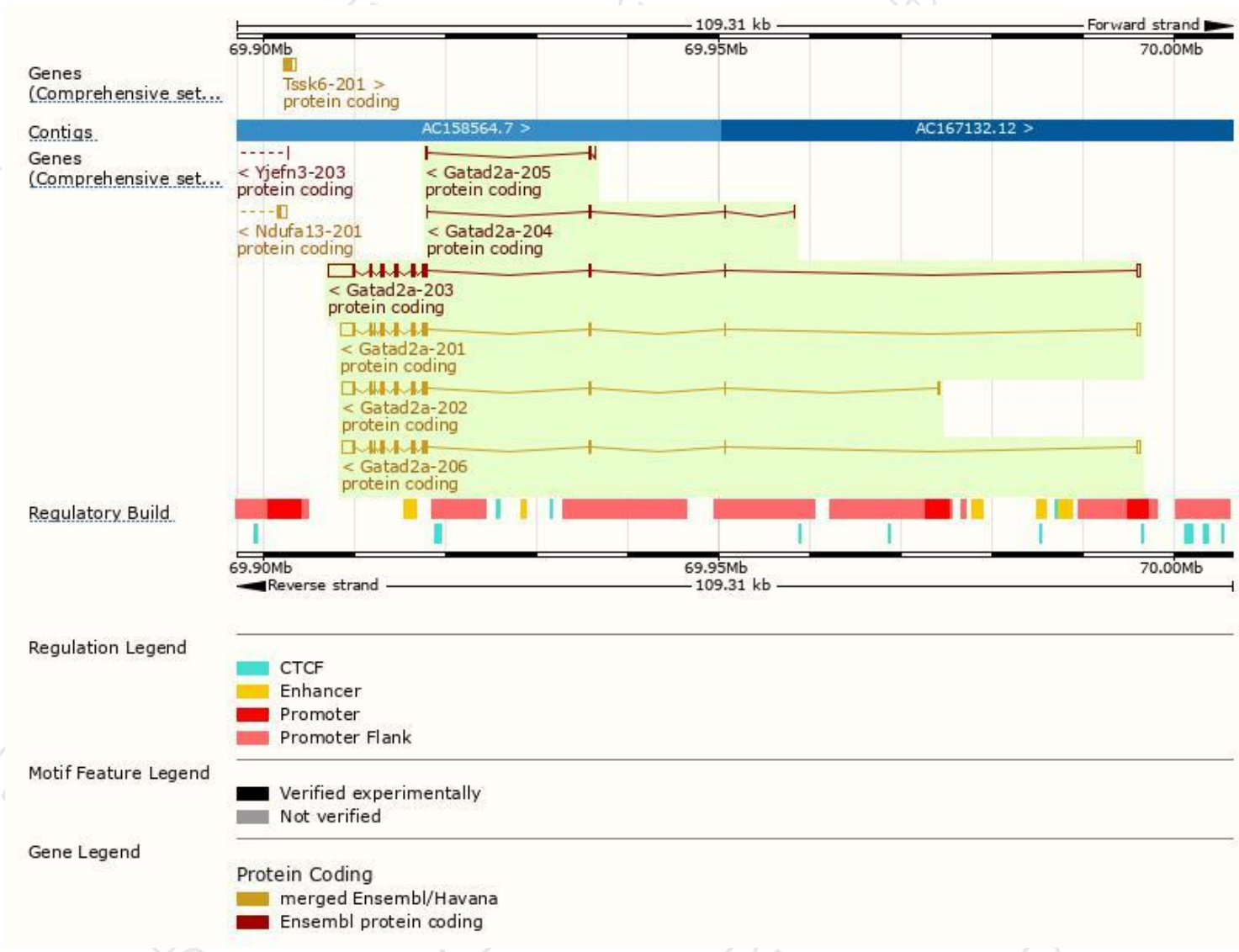
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gatad2a-201	<a href="#">ENSMUST00000065169.11</a>	3812	<a href="#">630aa</a>	Protein coding	<a href="#">CCDS22355</a>	<a href="#">E9QMN5</a>	TSL:1 GENCODE basic APPRIS P3
Gatad2a-206	<a href="#">ENSMUST00000212478.1</a>	3622	<a href="#">629aa</a>	Protein coding	<a href="#">CCDS52567</a>	<a href="#">Q8CHY6</a>	TSL:5 GENCODE basic APPRIS ALT2
Gatad2a-202	<a href="#">ENSMUST00000116463.3</a>	3363	<a href="#">629aa</a>	Protein coding	<a href="#">CCDS52567</a>	<a href="#">Q8CHY6</a>	TSL:1 GENCODE basic APPRIS ALT2
Gatad2a-203	<a href="#">ENSMUST00000177851.8</a>	5007	<a href="#">614aa</a>	Protein coding	-	<a href="#">A0A1I7Q4G8</a>	TSL:5 GENCODE basic APPRIS ALT2
Gatad2a-205	<a href="#">ENSMUST00000212277.1</a>	551	<a href="#">161aa</a>	Protein coding	-	<a href="#">A0A1D5RM58</a>	CDS 3' incomplete TSL:3
Gatad2a-204	<a href="#">ENSMUST00000211960.1</a>	507	<a href="#">99aa</a>	Protein coding	-	<a href="#">A0A1D5RM07</a>	CDS 3' incomplete TSL:3

The strategy is based on the design of *Gatad2a-201* transcript,The transcription is shown below

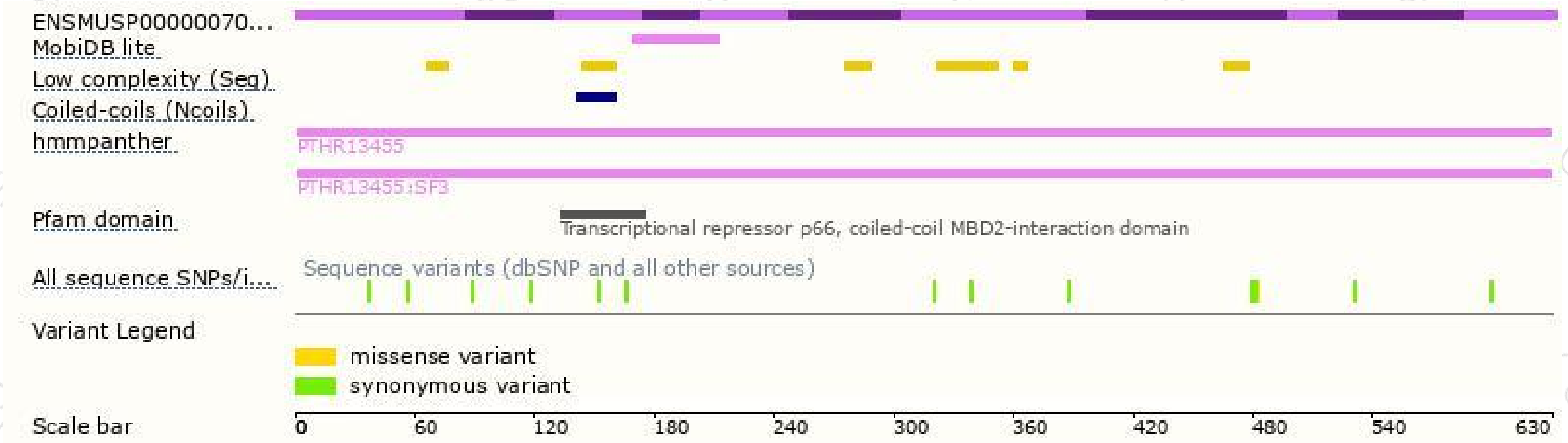


# Genomic location distribution

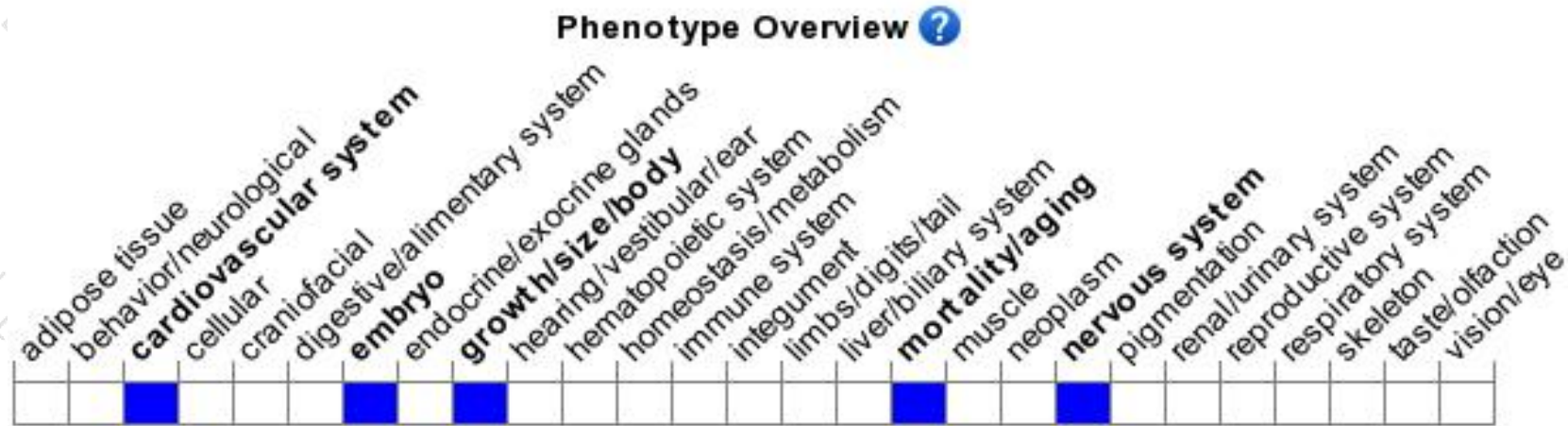




# Protein domain



# 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, Mice homozygous for a knock-out allele die around E9.5 displaying variable developmental defects, including malformed or unfused neural folds, failure of closure of anterior neuropore, missing or excessively large blood vessels in the yolk sac, abnormal embryo turning, and embryonic growth arrest.

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

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