

# *Cul4a* Cas9-KO Strategy

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# Project Overview

**Project Name**

***Cul4a***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cul4a* gene. The schematic diagram is as follows:



- The *Cul4a* gene has 8 transcripts. According to the structure of *Cul4a* gene, exon3-exon8 of *Cul4a-201* (ENSMUST00000016680.13) transcript is recommended as the knockout region. The region contains 584bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cul4a* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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.

- According to the existing MGI data, Mice homozygous for one knock-out allele exhibit reduced female fertility, male infertility, impaired spermatogenesis, and impaired DNA repair.
- Transcript *Cul4a*-204&206&208 may not be affected.
- The knockout region is near to the N-terminal of *Pcid2* gene, this strategy may influence the regulatory function of the N-terminal of *Pcid2* gene.
- The *Cul4a* 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)

## Cul4a cullin 4A [ *Mus musculus* (house mouse) ]

Gene ID: 99375, updated on 12-Aug-2019

### Summary

Official Symbol	Cul4a provided by <a href="#">MGI</a>
Official Full Name	cullin 4A provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1914487</a>
See related	<a href="#">Ensembl:ENSMUSG000000031446</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
Also known as	AW495282; 2810470J21Rik
Expression	Ubiquitous expression in liver E14 (RPKM 25.1), adrenal adult (RPKM 24.4) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

### Genomic context

Location: 8; 8 A1.1

See Cul4a in [Genome Data Viewer](#)

Exon count: 20

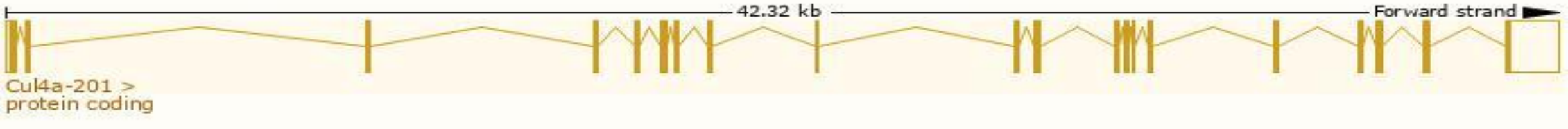
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	8	NC_000074.6 (13105623..13147940)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	8	NC_000074.5 (13105721..13147940)

# Transcript information (Ensembl)

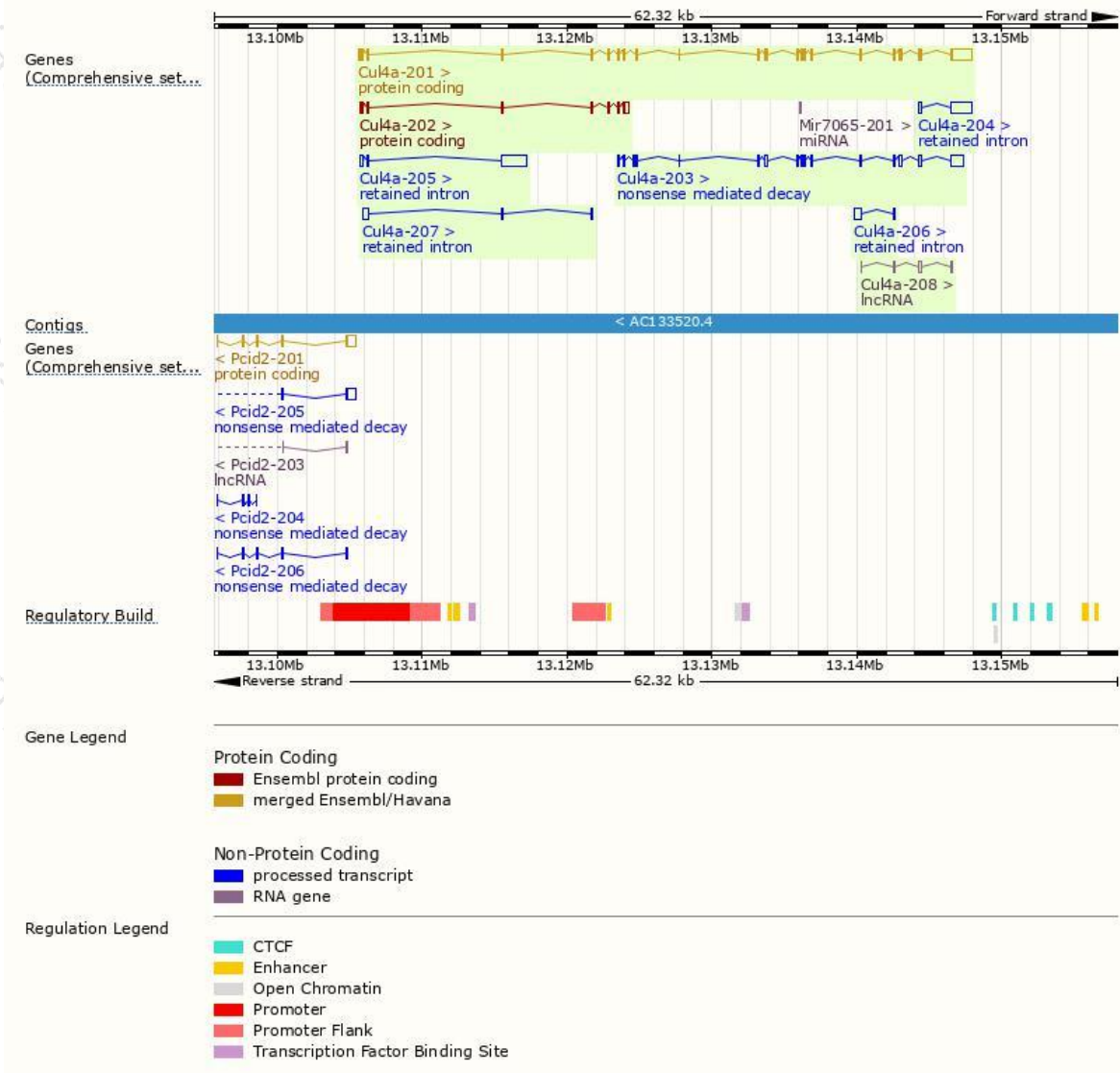
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cul4a-201	<a href="#">ENSMUST00000016680.13</a>	3728	<a href="#">759aa</a>	Protein coding	<a href="#">CCDS52485</a>	<a href="#">Q3TCH7</a>	TSL:1 GENCODE basic APPRIS P1
Cul4a-202	<a href="#">ENSMUST00000121426.1</a>	1044	<a href="#">265aa</a>	Protein coding	-	<a href="#">E9PXT5</a>	TSL:1 GENCODE basic
Cul4a-203	<a href="#">ENSMUST00000125514.7</a>	2570	<a href="#">87aa</a>	Nonsense mediated decay	-	<a href="#">F6UV36</a>	CDS 5' incomplete TSL:1
Cul4a-205	<a href="#">ENSMUST00000135371.1</a>	2006	No protein	Retained intron	-	-	TSL:1
Cul4a-204	<a href="#">ENSMUST00000125646.1</a>	1614	No protein	Retained intron	-	-	TSL:1
Cul4a-206	<a href="#">ENSMUST00000139316.1</a>	574	No protein	Retained intron	-	-	TSL:3
Cul4a-207	<a href="#">ENSMUST00000141315.1</a>	548	No protein	Retained intron	-	-	TSL:3
Cul4a-208	<a href="#">ENSMUST00000142700.1</a>	357	No protein	lncRNA	-	-	TSL:1

The strategy is based on the design of *Cul4a-201* transcript,The transcription is shown below



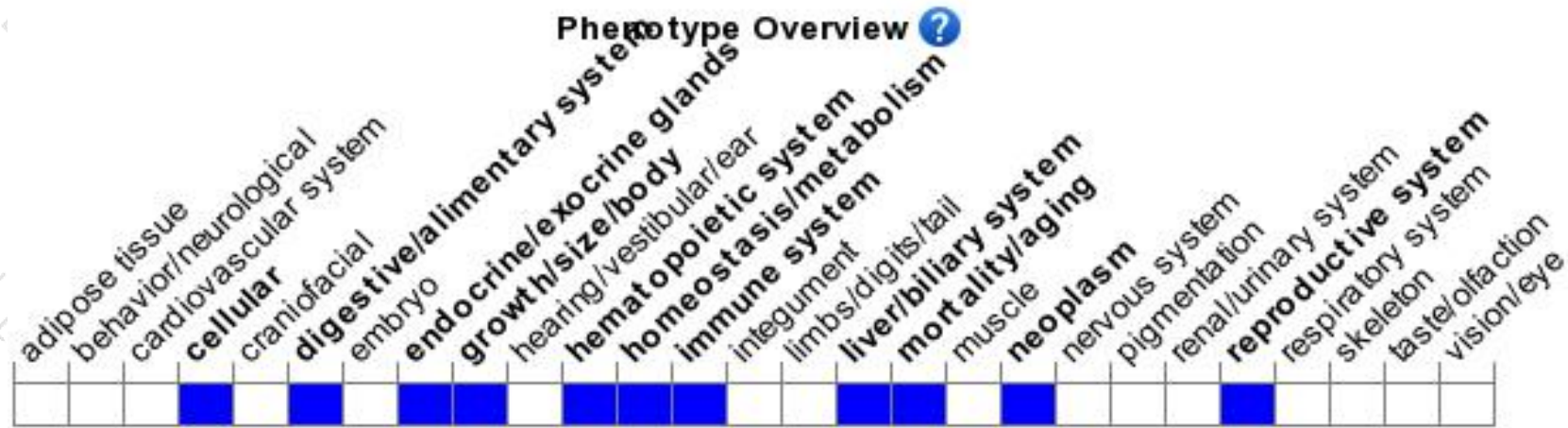
# Genomic location distribution



# 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 one knock-out allele exhibit reduced female fertility, male infertility, impaired spermatogenesis, and impaired DNA repair.

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

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