

# *Cit* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Cit*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Cit* gene has 19 transcripts. According to the structure of *Cit* gene, exon2 of *Cit-201* (ENSMUST00000051704.14) transcript is recommended as the knockout region. The region contains 142bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cit* gene. The brief process is as follows: CRISPR/Cas9 system we

- According to the existing MGI data, Homozygotes for a null mutation are 20% smaller than wild-type and exhibit tremors, ataxia, and fatal seizures. Brains of mutant mice show a 50% size reduction with abnormalities in the hippocampus, cerebellum, and olfactory lobes. Mutant males show aberrant cytokinesis of spermatogenic precursors.
- The *Cit* gene is located on the Chr5. 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)

## Cit citron [Mus musculus (house mouse)]

Gene ID: 12704, updated on 31-Jan-2019

### Summary



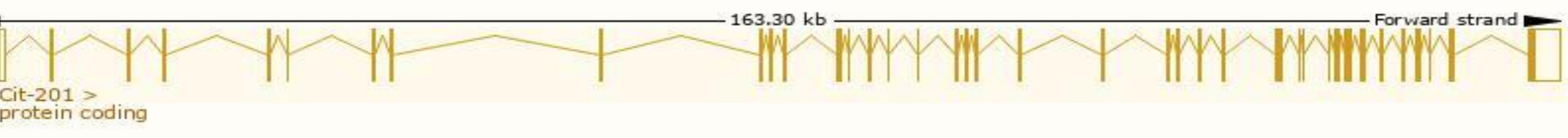
<b>Official Symbol</b>	Cit provided by <a href="#">MGI</a>
<b>Official Full Name</b>	citron provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:105313</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000029516</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<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>	C030025P15Rik, CRIK, CRIK-SK, Cit-k
<b>Expression</b>	Broad expression in cortex adult (RPKM 9.3), frontal lobe adult (RPKM 8.3) and 24 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

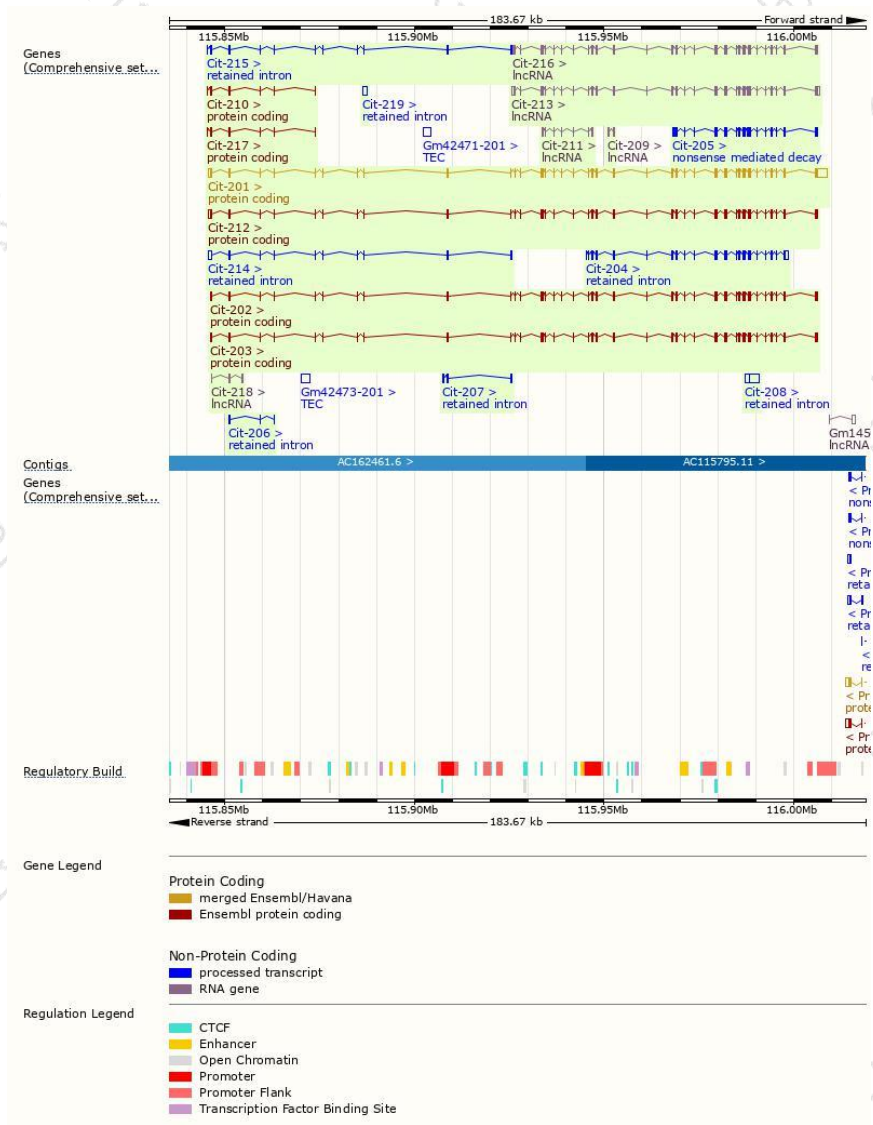
The gene has 19 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cit-201	<a href="#">ENSMUST00000051704.14</a>	9514	<a href="#">2055aa</a>	Protein coding	<a href="#">CCDS19597</a>	<a href="#">E9QL53</a>	TSL:1 GENCODE basic APPRIS P2
Cit-212	<a href="#">ENSMUST00000141101.4</a>	6794	<a href="#">2013aa</a>	Protein coding	-	<a href="#">F6SBR5</a>	TSL:5 GENCODE basic
Cit-202	<a href="#">ENSMUST00000102560.6</a>	6213	<a href="#">2070aa</a>	Protein coding	-	<a href="#">D3YU89</a>	TSL:5 GENCODE basic APPRIS ALT1
Cit-203	<a href="#">ENSMUST00000112008.8</a>	6087	<a href="#">2028aa</a>	Protein coding	-	<a href="#">D3Z1U0</a>	TSL:5 GENCODE basic APPRIS ALT2
Cit-217	<a href="#">ENSMUST00000148245.7</a>	651	<a href="#">181aa</a>	Protein coding	-	<a href="#">D3Z1K6</a>	CDS 3' incomplete TSL:5
Cit-210	<a href="#">ENSMUST00000137952.7</a>	571	<a href="#">175aa</a>	Protein coding	-	<a href="#">D3Z477</a>	CDS 3' incomplete TSL:5
Cit-205	<a href="#">ENSMUST00000123736.1</a>	3487	<a href="#">23aa</a>	Nonsense mediated decay	-	<a href="#">H3BJ74</a>	CDS 5' incomplete TSL:1
Cit-204	<a href="#">ENSMUST00000122877.7</a>	4398	No protein	Retained intron	-	-	TSL:1
Cit-208	<a href="#">ENSMUST00000134609.1</a>	3456	No protein	Retained intron	-	-	TSL:1
Cit-214	<a href="#">ENSMUST00000146387.7</a>	2335	No protein	Retained intron	-	-	TSL:1
Cit-215	<a href="#">ENSMUST00000147330.7</a>	1671	No protein	Retained intron	-	-	TSL:1
Cit-219	<a href="#">ENSMUST00000202734.1</a>	1184	No protein	Retained intron	-	-	TSL:NA
Cit-207	<a href="#">ENSMUST00000128702.1</a>	756	No protein	Retained intron	-	-	TSL:3
Cit-206	<a href="#">ENSMUST00000127976.2</a>	561	No protein	Retained intron	-	-	TSL:3
Cit-213	<a href="#">ENSMUST00000145363.7</a>	5974	No protein	lncRNA	-	-	TSL:5
Cit-216	<a href="#">ENSMUST00000147479.7</a>	5016	No protein	lncRNA	-	-	TSL:1
Cit-211	<a href="#">ENSMUST00000139881.7</a>	699	No protein	lncRNA	-	-	TSL:3
Cit-218	<a href="#">ENSMUST00000153407.1</a>	293	No protein	lncRNA	-	-	TSL:5
Cit-209	<a href="#">ENSMUST00000136780.1</a>	287	No protein	lncRNA	-	-	TSL:5

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



# Genomic location distribution

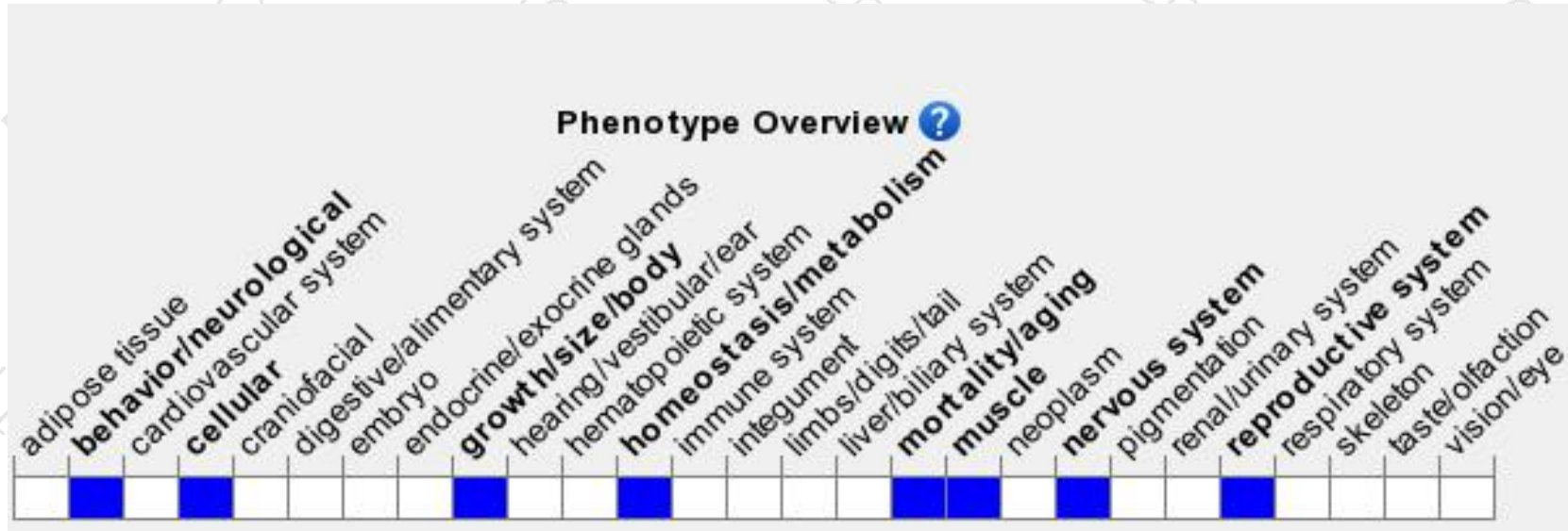




# Protein domain



# 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 a null mutation are 20% smaller than wild-type and exhibit tremors, ataxia, and fatal seizures. Brains of mutant mice show a 50% size reduction with abnormalities in the hippocampus, cerebellum, and olfactory lobes. Mutant males show aberrant cytokinesis of spermatogenic precursors.

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

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