

# ***Slc12a4* Cas9-KO Strategy**

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# Project Overview

**Project Name**

*Slc12a4*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc12a4* gene. The schematic diagram is as follows:



- The *Slc12a4* gene has 5 transcripts. According to the structure of *Slc12a4* gene, exon2-exon3 of *Slc12a4-201* (ENSMUST00000034370.16) transcript is recommended as the knockout region. The region contains 227bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc12a4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a constitutively active mutation display microcytosis and hypochromic anemia.
- Transcript *Slc12a4*-204 may not be affected.
- The knockout region is near to the N-terminal of *Mir7074* gene, this strategy may influence the regulatory function of the N-terminal of *Mir7074* gene.
- The *Slc12a4* 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)

## Slc12a4 solute carrier family 12, member 4 [ *Mus musculus* (house mouse) ]

Gene ID: 20498, updated on 10-Dec-2019

### Summary

- Official Symbol** Slc12a4 provided by [MGI](#)
- Official Full Name** solute carrier family 12, member 4 provided by [MGI](#)
- Primary source** [MGI:MGI:1309465](#)
- See related** [Ensembl:ENSMUSG00000017765](#)
- Gene type** protein coding
- RefSeq status** VALIDATED
- Organism** [Mus musculus](#)
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as** KCC1; RBCKCC1; AW546649
- Expression** Ubiquitous expression in ovary adult (RPKM 36.4), lung adult (RPKM 32.8) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

### Genomic context

**Location:** 8 D3; 8 53.06 cM See Slc12a4 in [Genome Data Viewer](#)

**Exon count:** 24

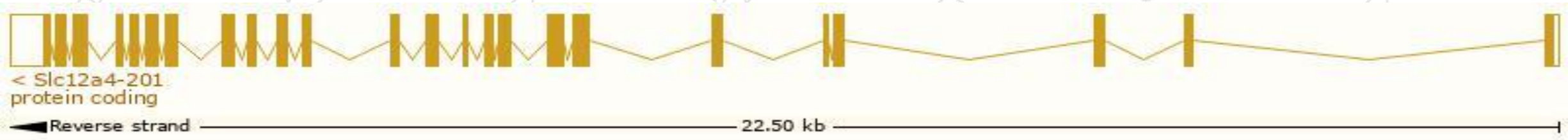
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	8	NC_000074.6 (105943590..105966149, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	8	NC_000074.5 (108467493..108489939, complement)

# Transcript information（Ensembl）

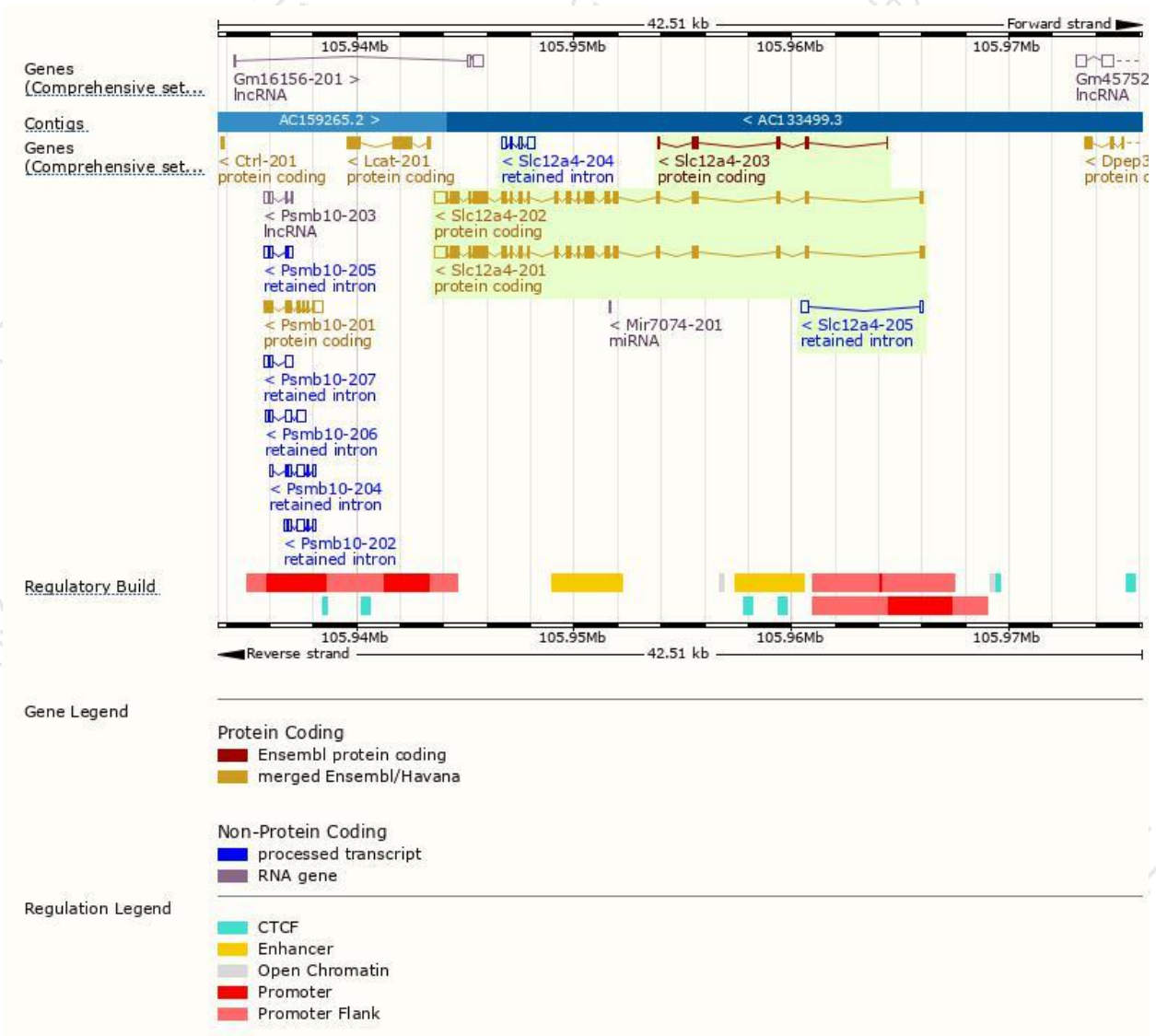
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc12a4-201	<a href="#">ENSMUST00000034370.16</a>	3811	<a href="#">1087aa</a>	Protein coding	<a href="#">CCDS57642</a>	<a href="#">F8WIJ0</a>	TSL:1 GENCODE basic APPRIS ALT 1
Slc12a4-202	<a href="#">ENSMUST00000116429.8</a>	3755	<a href="#">1085aa</a>	Protein coding	<a href="#">CCDS22623</a>	<a href="#">Q3TWZ6 Q9JIS8</a>	TSL:1 GENCODE basic APPRIS P3
Slc12a4-203	<a href="#">ENSMUST00000132231.1</a>	512	<a href="#">171aa</a>	Protein coding	-	<a href="#">F6TQE2</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Slc12a4-204	<a href="#">ENSMUST00000141326.1</a>	715	No protein	Retained intron	-	-	TSL:3
Slc12a4-205	<a href="#">ENSMUST00000143381.1</a>	461	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Slc12a4-201* transcript,The transcription is shown below



# Genomic location distribution

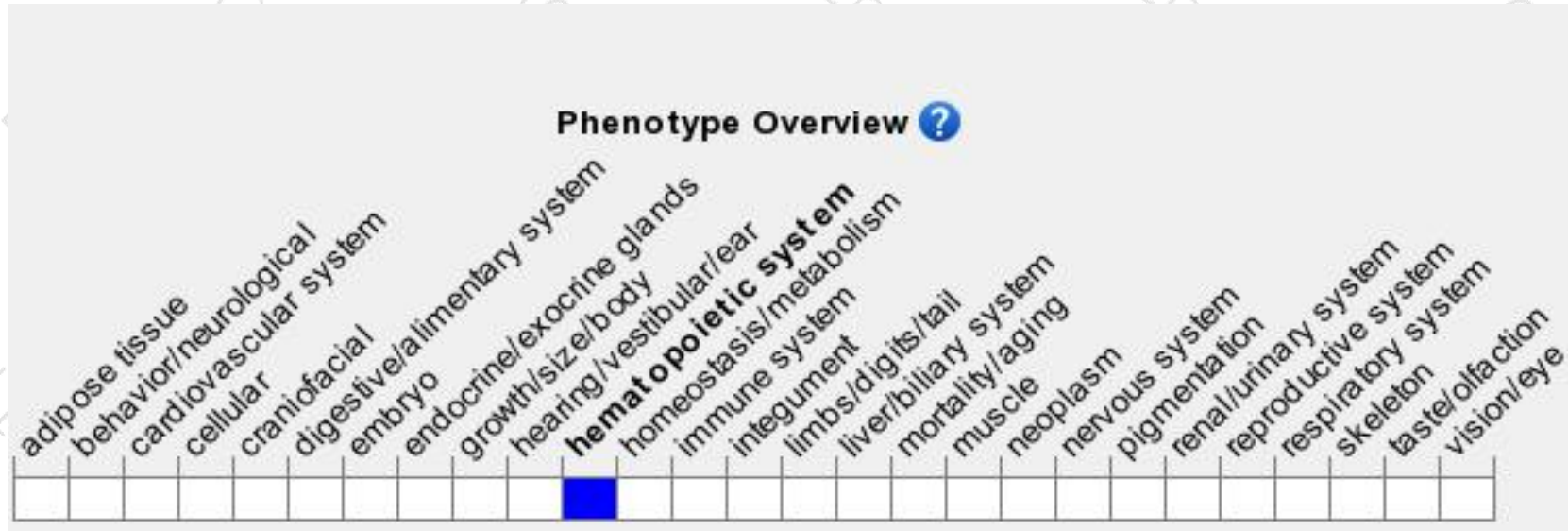




# Protein domain



# 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 constitutively active mutation display microcytosis and hypochromic anemia.

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

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