

# *Glr1* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Glr1***

**Project type**

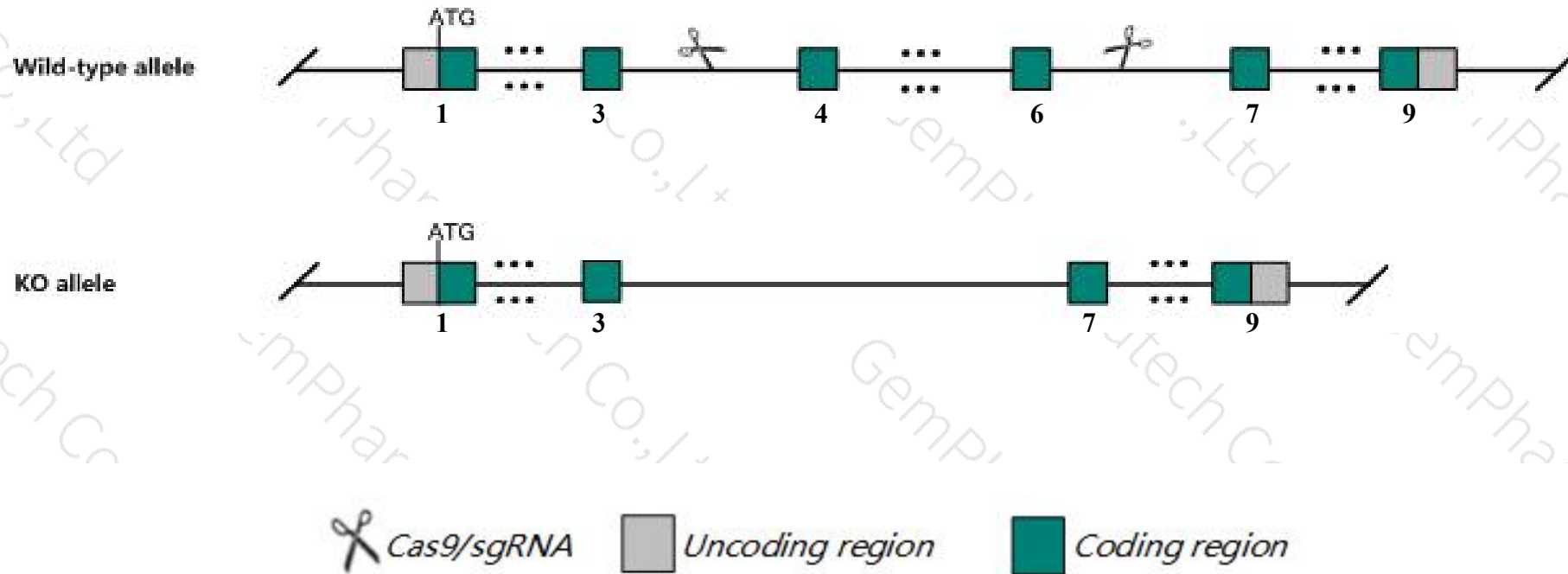
**Cas9-KO**

**Strain background**

**C57BL/6J**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Glr1* gene. The schematic diagram is as follows:



- The *Glra1* gene has 3 transcripts. According to the structure of *Glra1* gene, exon4-exon6 of *Glra1-201* (ENSMUST00000075603.4) transcript is recommended as the knockout region. The region contains 445bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Glra1* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Mutations in this gene result in neurological defects for all alleles reported. Specific alleles also show affects on viability, reproductive performance, and/or eye and respiratory physiology.
- The *Glr1* gene is located on the Chr11. 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)

## Glr1 glycine receptor, alpha 1 subunit [ *Mus musculus* (house mouse) ]

Gene ID: 14654, updated on 12-Aug-2019

### Summary

**Official Symbol** Glr1 provided by [MGI](#)  
**Official Full Name** glycine receptor, alpha 1 subunit provided by [MGI](#)  
**Primary source** [MGI:MGI:95747](#)  
**See related** [Ensembl:ENSMUSG00000000263](#)  
**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** ot; spd; nmf11; spasmodic; oscillator  
**Expression** Biased expression in cerebellum adult (RPKM 5.8), CNS E11.5 (RPKM 0.5) and 1 other tissue [See more](#)  
**Orthologs** [human](#) [all](#)

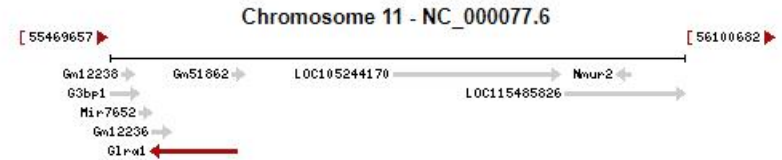
### Genomic context

Location: 11 B1.3; 11 33.12 cM

[See Glr1 in Genome Data Viewer](#)

Exon count: 9

Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	11	NC_000077.6 (55514239..55608198, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	11	NC_000077.5 (55328315..55421292, complement)

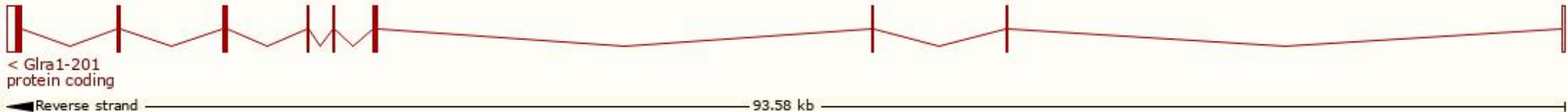


# Transcript information (Ensembl)

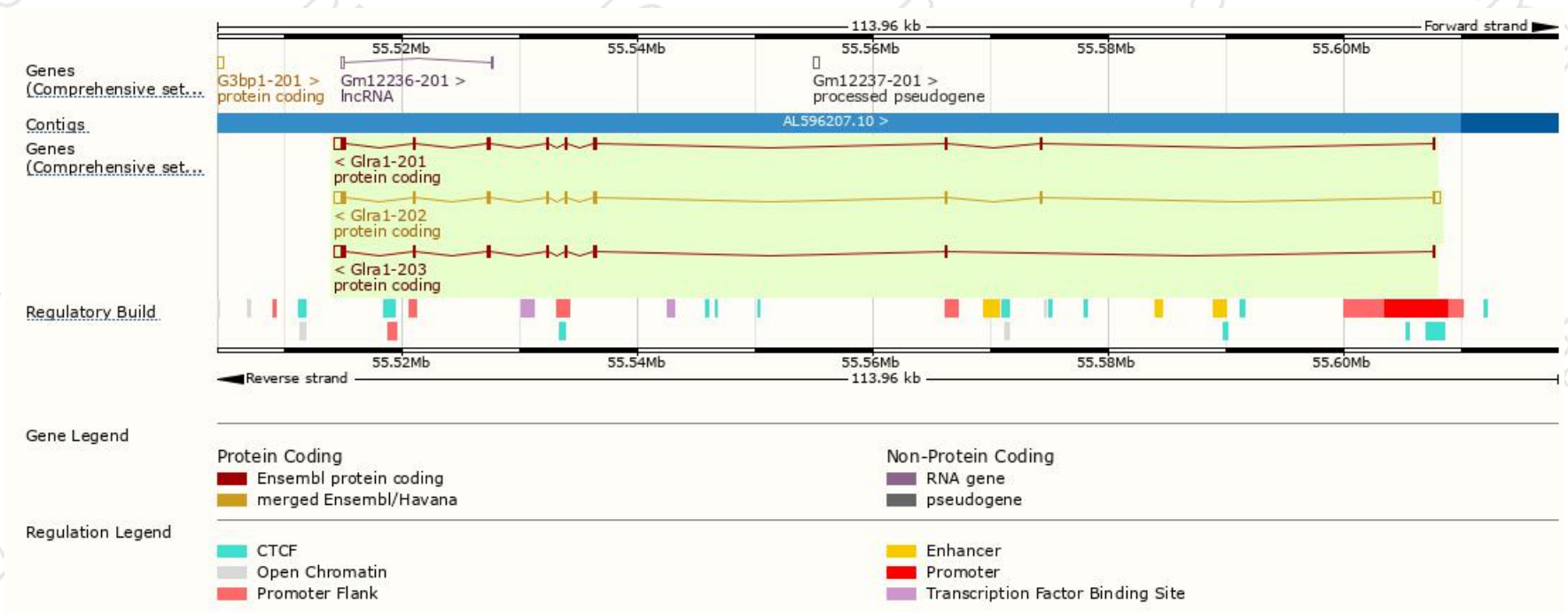
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Glra1-202	<a href="#">ENSMUST00000102716.9</a>	2390	<a href="#">449aa</a>	Protein coding	<a href="#">CCDS24715</a>	<a href="#">Q5NCT9</a> <a href="#">Q64018</a>	TSL:1 Gencode basic APPRIS P3
Glra1-201	<a href="#">ENSMUST00000075603.4</a>	2037	<a href="#">457aa</a>	Protein coding	<a href="#">CCDS70190</a>	<a href="#">Q64018</a>	TSL:1 Gencode basic APPRIS ALT1
Glra1-203	<a href="#">ENSMUST00000108853.7</a>	1797	<a href="#">366aa</a>	Protein coding	-	<a href="#">Q5NCU0</a>	TSL:5 Gencode basic

The strategy is based on the design of *Glra1-201* transcript,The transcription is shown below



# Genomic location distribution

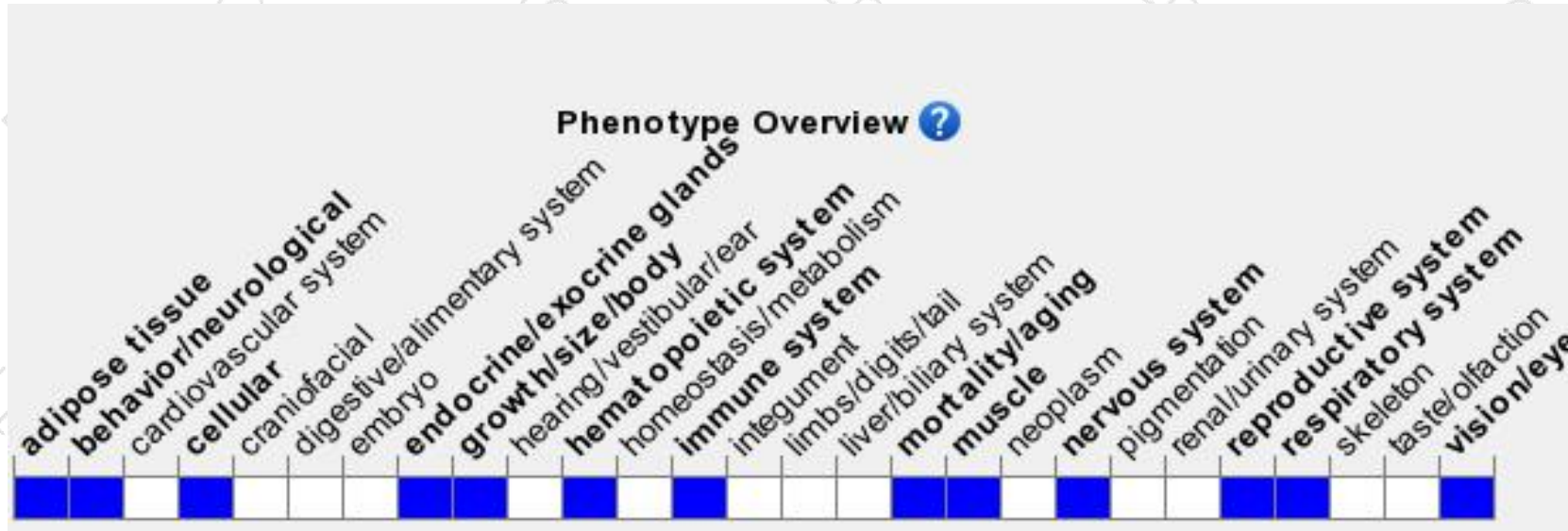




# Protein domain



# 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, Mutations in this gene result in neurological defects for all alleles reported.

Specific alleles also show affects on viability, reproductive performance, and/or eye and respiratory physiology.

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

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