

***Gabbr1* Cas9-KO Strategy**

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Project Overview

Project Name

Gabbr1

Project type

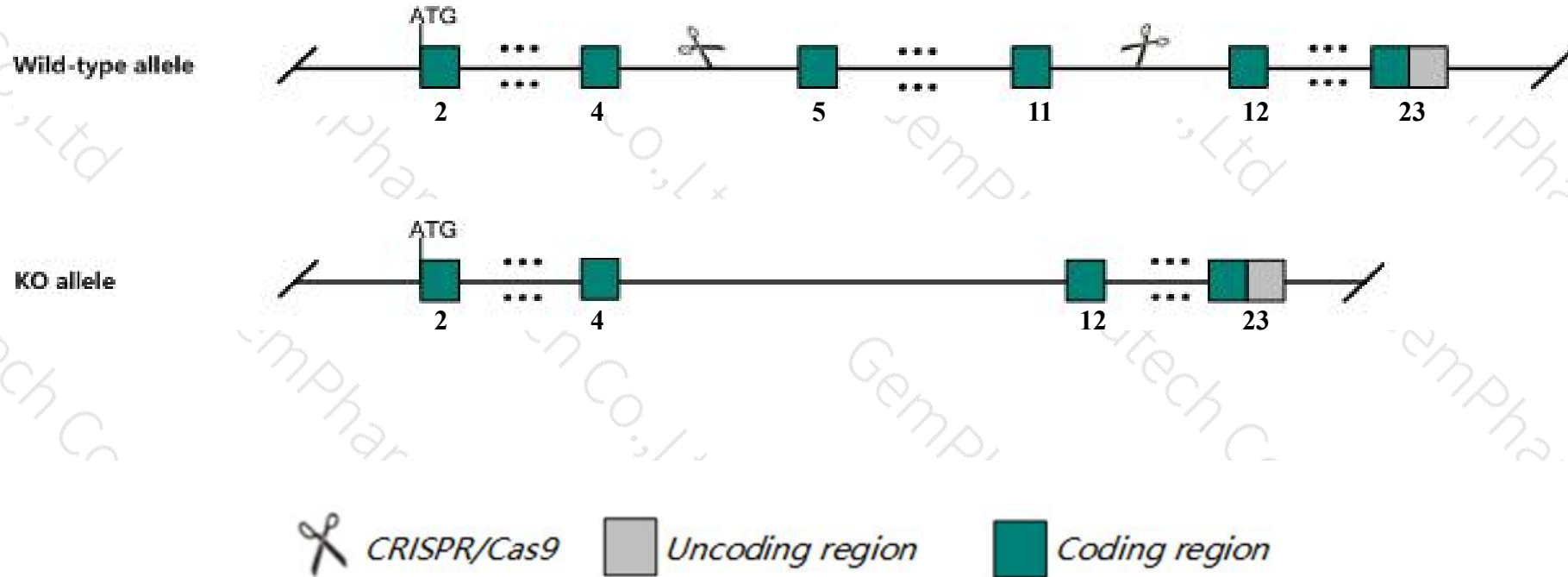
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gabbr1* gene. The schematic diagram is as follows:



- The *Gabbr1* gene has 11 transcripts. According to the structure of *Gabbr1* gene, exon5-exon11 of *Gabbr1-201* (ENSMUST00000025338.15) transcript is recommended as the knockout region. The region contains 848bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gabbr1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Phenotypes of null mice vary depending on strain background and allele. Homozygous null mice may display seizures, premature death, and abnormal nervous system electrophysiology.
- The *Gabbr1* gene is located on the Chr17. 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)

Gabbr1 gamma-aminobutyric acid (GABA) B receptor, 1 [Mus musculus (house mouse)]

Gene ID: 54393, updated on 19-Mar-2019

Summary



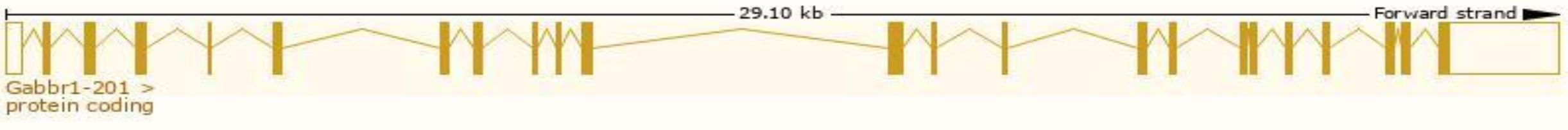
Official Symbol	Gabbr1 provided by MGI
Official Full Name	gamma-aminobutyric acid (GABA) B receptor, 1 provided by MGI
Primary source	MGI:MGI:1860139
See related	Ensembl:ENSMUSG00000024462
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	GABAB1, GABAbR1, bM573K1.1
Expression	Broad expression in cortex adult (RPKM 73.7), frontal lobe adult (RPKM 72.2) and 20 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

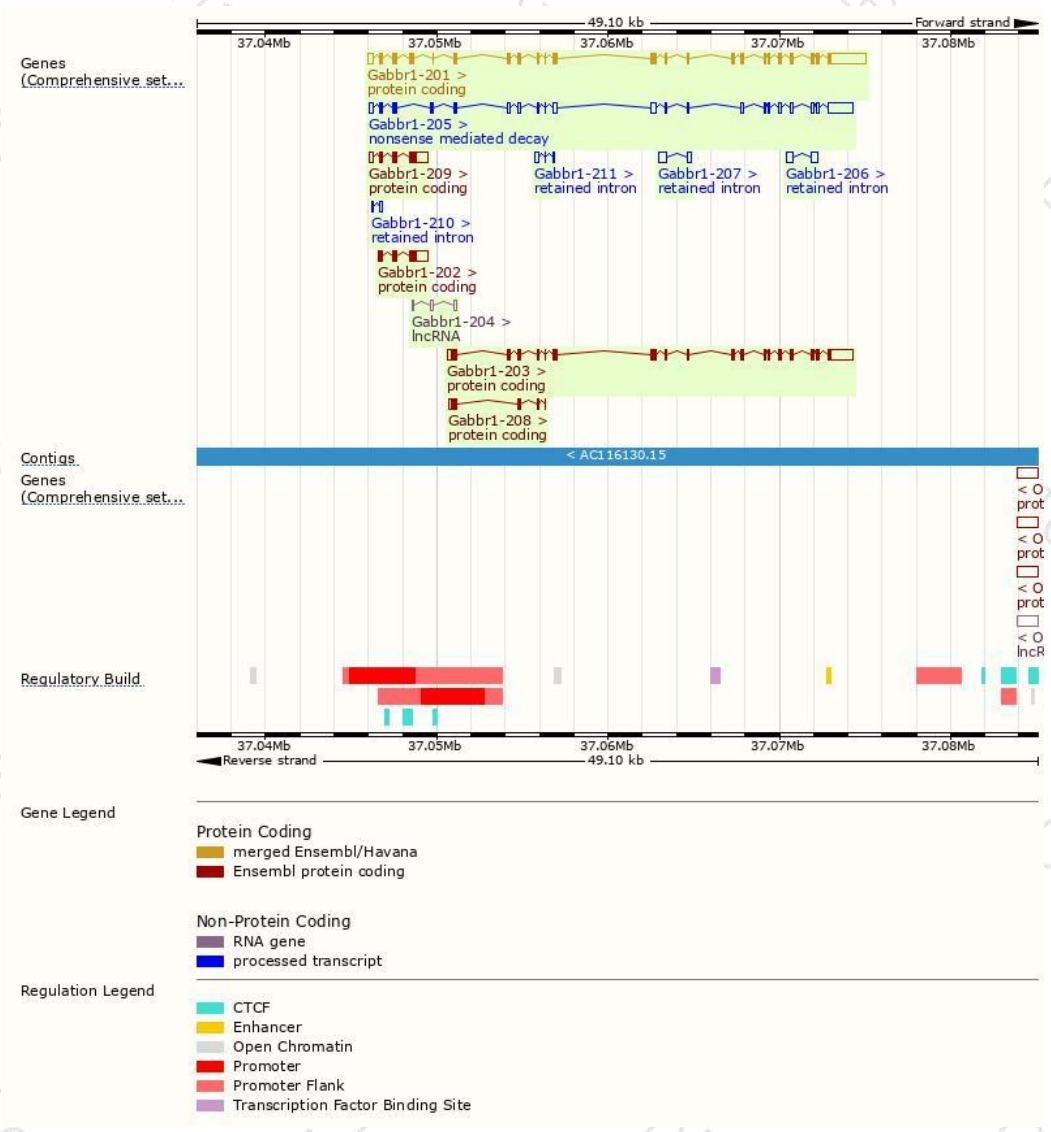
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gabbr1-201	ENSMUST00000025338.15	5248	960aa	Protein coding	CCDS37616	Q9WV18	TSL:1 GENCODE basic APPRIS P1
Gabbr1-203	ENSMUST00000172792.7	4036	844aa	Protein coding	-	Q9WV18	TSL:1 GENCODE basic
Gabbr1-209	ENSMUST00000174456.7	1595	229aa	Protein coding	-	Q3TWR2	TSL:1 GENCODE basic
Gabbr1-202	ENSMUST00000172789.1	1460	229aa	Protein coding	-	Q3TWR2	TSL:1 GENCODE basic
Gabbr1-208	ENSMUST00000174347.1	821	213aa	Protein coding	-	G3UZ52	CDS 3' incomplete TSL:5
Gabbr1-205	ENSMUST00000173823.7	4204	177aa	Nonsense mediated decay	-	G3UXR6	TSL:1
Gabbr1-206	ENSMUST00000174071.1	716	No protein	Retained intron	-	-	TSL:3
Gabbr1-207	ENSMUST00000174181.1	608	No protein	Retained intron	-	-	TSL:2
Gabbr1-211	ENSMUST00000174866.1	378	No protein	Retained intron	-	-	TSL:5
Gabbr1-210	ENSMUST00000174826.1	237	No protein	Retained intron	-	-	TSL:2
Gabbr1-204	ENSMUST00000173564.1	303	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Gabbr1-201* transcript,The transcription is shown below



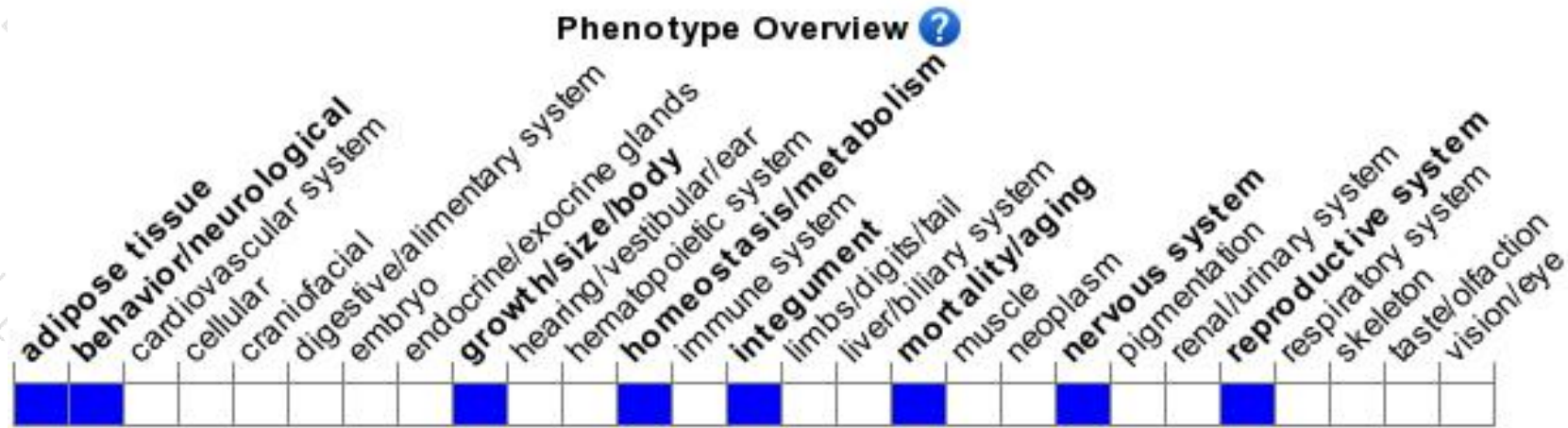
Genomic location distribution



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/>).

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

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