Slc29a1 Cas9-KO Strategy

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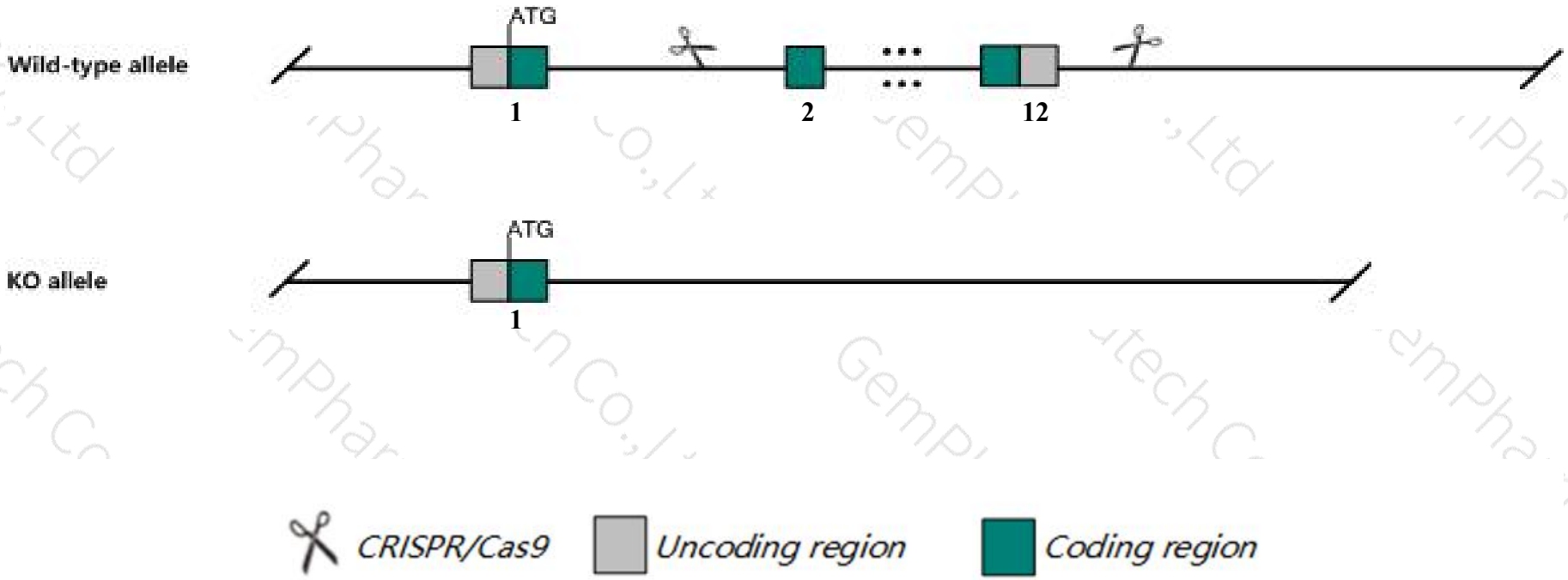
Project Overview

Project Name	***Slc29a1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc29a1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc29a1* gene has 25 transcripts. According to the structure of *Slc29a1* gene, exon2-exon12 of *Slc29a1-204* (ENSMUST00000163492.7) transcript is recommended as the knockout region.The region contains most of the coding sequence Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc29a1* 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.

Notice

- According to the existing MGI data,Mice homozygous for a targeted null allele exhibit a slightly decreased body weight, increased alcohol preference and alcohol consumption, and reduced hypnotic and ataxic responses to ethanol associated with a reduction in adenosine tone. Adenosine uptake is almost completely abolished in mice homozygous for a knock-out allele.
- *Gm17080* gene will be deleted together in this strategy.
- The *Slc29a1* 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）

集萃药康 GemPharmatech

Slc29a1 solute carrier family 29 (nucleoside transporters), member 1 [*Mus musculus* (house mouse)]

Gene ID: 63959, updated on 24-Oct-2019

Summary

Official Symbol	Slc29a1 provided by MGI
Official Full Name	solute carrier family 29 (nucleoside transporters), member 1 provided by MGI
Primary source	MGI:MGI:1927073
See related	Ensembl:ENSMUSG00000023942
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	ENT1; AA407560; 1200014D21Rik
Expression	Ubiquitous expression in liver adult (RPKM 135.7), adrenal adult (RPKM 95.4) and 26 other tissues See more
Orthologs	human all

Genomic context

Location: 17; 17 B3

See Slc29a1 in Genome Data Viewer

Exon count: 19

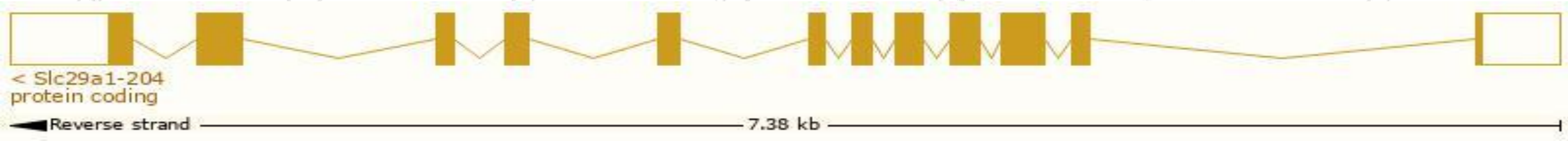
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	17	NC_000083.6 (45585200..45599618, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	17	NC_000083.5 (45722171..45729342, complement)

Transcript information（Ensembl）

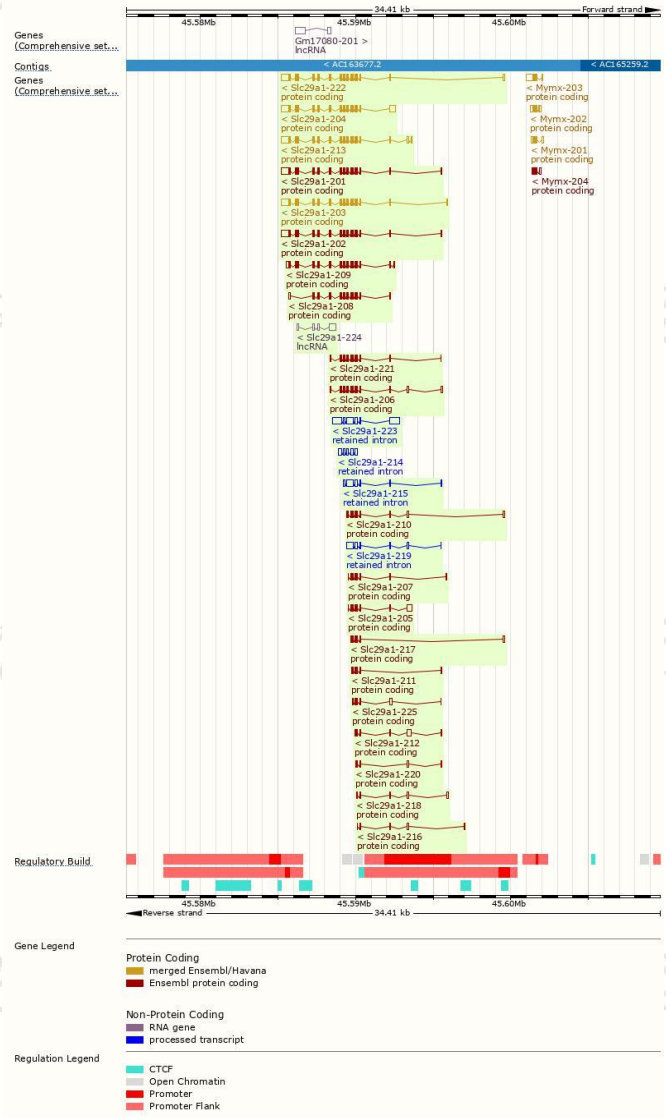
The gene has 25 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc29a1-204	ENSMUST00000163492.7	2216	458aa	Protein coding	CCDS28813	Q3TCZ2 Q9JIM1	TSL:1 GENCODE basic APPRIS P3
Slc29a1-213	ENSMUST00000167692.7	2092	460aa	Protein coding	CCDS57096	Q9JIM1	TSL:1 GENCODE basic APPRIS ALT2
Slc29a1-222	ENSMUST00000171847.7	2033	458aa	Protein coding	CCDS28813	Q3TCZ2 Q9JIM1	TSL:1 GENCODE basic APPRIS P3
Slc29a1-201	ENSMUST00000051574.12	1996	460aa	Protein coding	CCDS57096	Q9JIM1	TSL:5 GENCODE basic APPRIS ALT2
Slc29a1-202	ENSMUST00000064889.12	1988	458aa	Protein coding	CCDS28813	Q3TCZ2 Q9JIM1	TSL:1 GENCODE basic APPRIS P3
Slc29a1-203	ENSMUST00000097317.9	1931	460aa	Protein coding	CCDS57096	Q9JIM1	TSL:1 GENCODE basic APPRIS ALT2
Slc29a1-209	ENSMUST00000166119.7	1598	460aa	Protein coding	CCDS57096	Q9JIM1	TSL:5 GENCODE basic APPRIS ALT2
Slc29a1-208	ENSMUST00000164769.7	1226	358aa	Protein coding	-	E9PXM6	TSL:1 GENCODE basic
Slc29a1-206	ENSMUST00000164217.7	1062	262aa	Protein coding	-	E9PWY7	CDS 3' incomplete TSL:5
Slc29a1-210	ENSMUST00000166633.7	873	195aa	Protein coding	-	E9PXQ6	CDS 3' incomplete TSL:3
Slc29a1-221	ENSMUST00000171081.7	862	262aa	Protein coding	-	E9PWY7	CDS 3' incomplete TSL:5
Slc29a1-205	ENSMUST00000163905.7	837	160aa	Protein coding	-	E9PZV0	CDS 3' incomplete TSL:2
Slc29a1-212	ENSMUST00000167332.7	626	93aa	Protein coding	-	E9Q221	CDS 3' incomplete TSL:5
Slc29a1-207	ENSMUST00000164618.7	598	162aa	Protein coding	-	E9PVH9	CDS 3' incomplete TSL:3
Slc29a1-217	ENSMUST00000169729.7	543	114aa	Protein coding	-	E9Q3D1	CDS 3' incomplete TSL:3
Slc29a1-225	ENSMUST00000172301.7	520	121aa	Protein coding	-	E9PWD6	CDS 3' incomplete TSL:5
Slc29a1-211	ENSMUST00000167195.7	459	105aa	Protein coding	-	E9Q503	CDS 3' incomplete TSL:3
Slc29a1-218	ENSMUST00000170113.7	403	56aa	Protein coding	-	E9Q5E9	CDS 3' incomplete TSL:5
Slc29a1-216	ENSMUST00000168274.1	357	41aa	Protein coding	-	E9Q0Q5	CDS 3' incomplete TSL:3
Slc29a1-220	ENSMUST00000170488.7	348	39aa	Protein coding	-	E9Q7R8	CDS 3' incomplete TSL:5
Slc29a1-223	ENSMUST00000171876.7	2007	No protein	Retained intron	-	-	TSL:5
Slc29a1-215	ENSMUST00000167863.7	944	No protein	Retained intron	-	-	TSL:5
Slc29a1-219	ENSMUST00000170425.7	907	No protein	Retained intron	-	-	TSL:2
Slc29a1-214	ENSMUST00000167748.1	769	No protein	Retained intron	-	-	TSL:1
Slc29a1-224	ENSMUST00000171978.1	736	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Slc29a1-204* transcript,The transcription is shown below

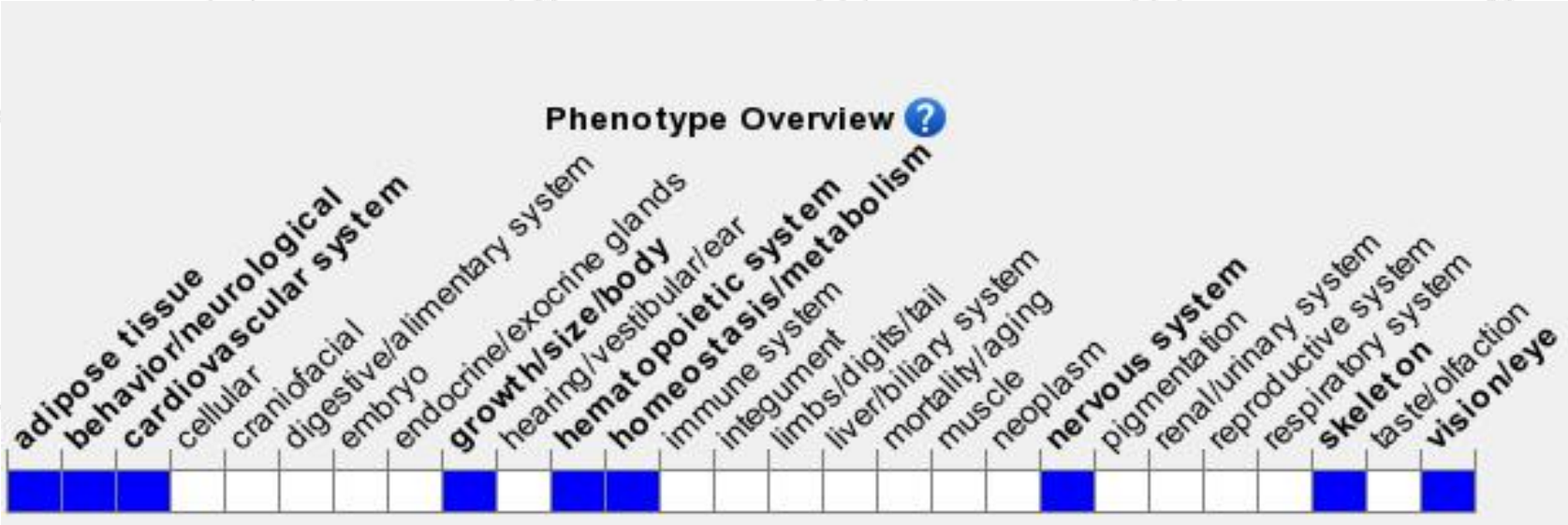


Genomic location distribution



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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