Snap29 Cas9-KO Strategy

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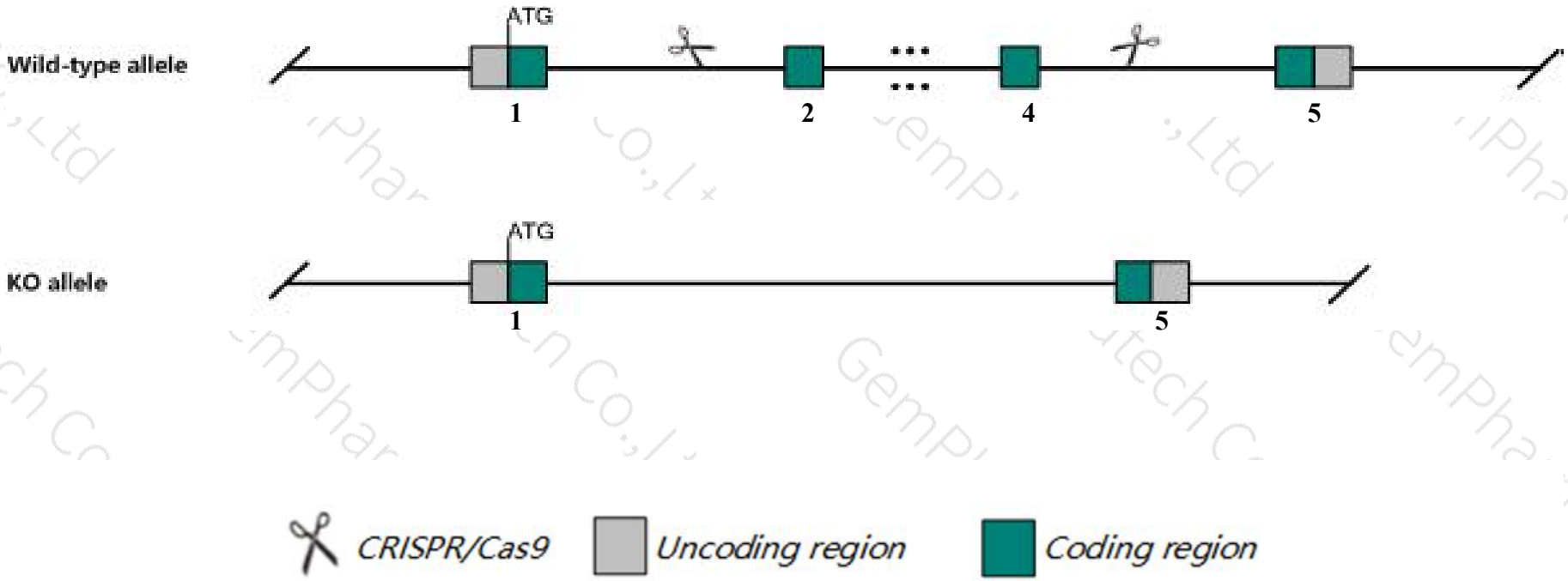
Project Overview

Project Name	***Snap29***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Snap29* gene. The schematic diagram is as follows:



Technical routes

➢ The *Snap29* gene has 1 transcript. According to the structure of *Snap29* gene, exon2-exon4 of *Snap29-201* (ENSMUST00000023449.10) transcript is recommended as the knockout region.The region contains 388bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Snap29* 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 knock-out allele exhibit slightly reduced birth body size and a congenital ichtyotic phenotype associated with scaly and tight skin, hyperkeratosis, acanthosis, abnormalities in epidermal differentiation and autophagy, and increased endoplasmic reticulum stress.

➢ The *Snap29* gene is located on the Chr16. 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

Snap29 synaptosomal-associated protein 29 [*Mus musculus* (house mouse)]

Gene ID: 67474, updated on 12-Aug-2019

Summary

Official Symbol	Snap29 provided by MGI
Official Full Name	synaptosomal-associated protein 29 provided by MGI
Primary source	MGI:MGI:1914724
See related	Ensembl:ENSMUSG00000022765
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	Gs32; AI891940; AU020222; BB131856; 1300018G05Rik
Expression	Ubiquitous expression in placenta adult (RPKM 6.2), CNS E18 (RPKM 4.5) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 16; 16 A3

See Snap29 in Genome Data Viewer

Exon count: 5

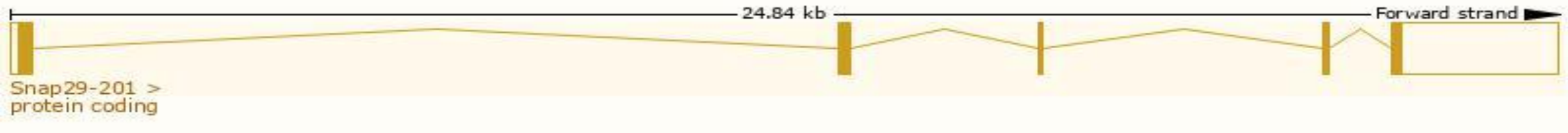
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	16	NC_000082.6 (17406000..17430826)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	16	NC_000082.5 (17406093..17430919)

Transcript information（Ensembl）

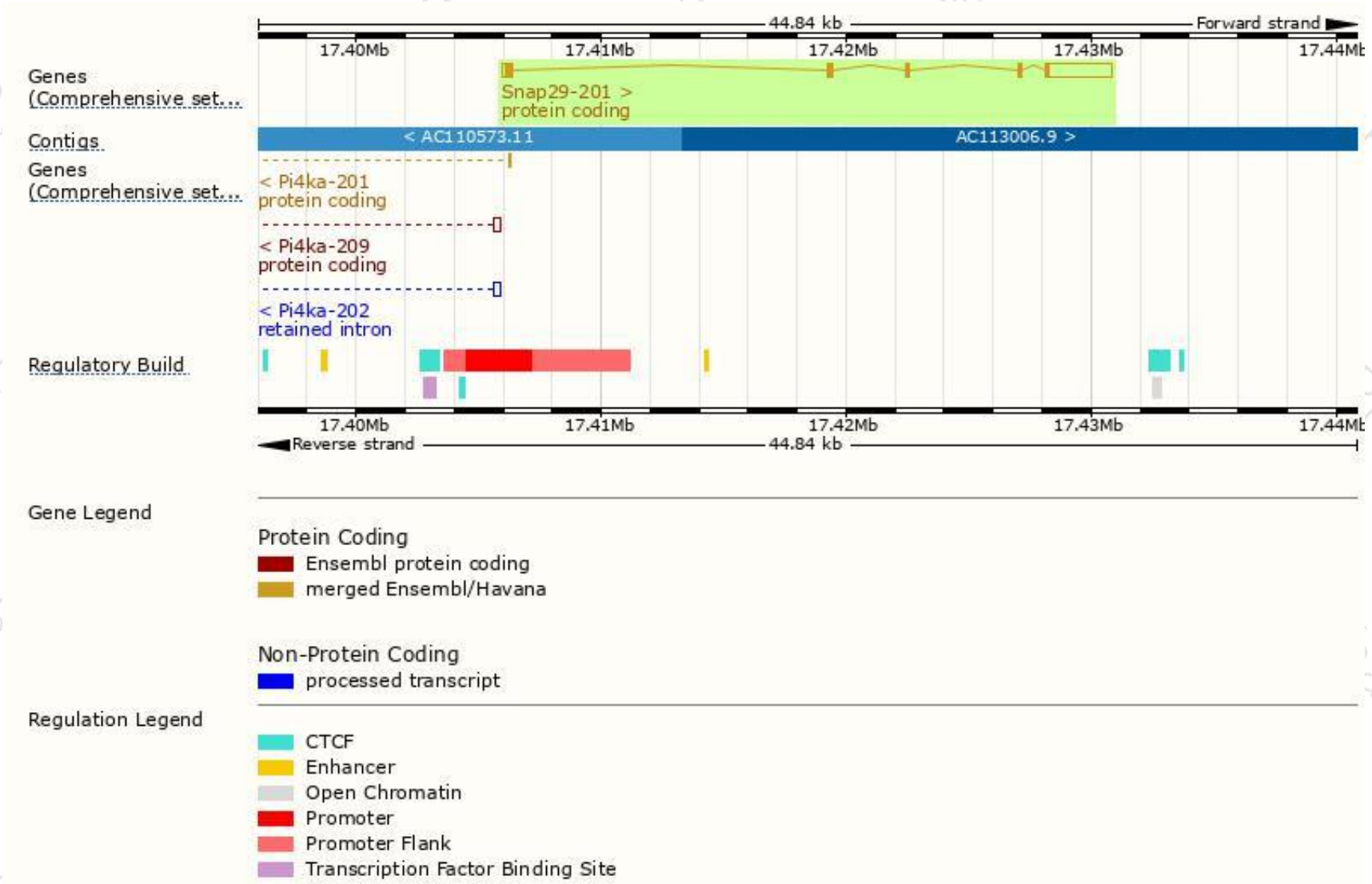
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Snap29-201	ENSMUST00000023449.10	3447	260aa	Protein coding	CCDS28001	Q9ERB0	TSL:1 GENCODE basic APPRIS P1

The strategy is based on the design of *Snap29-201* transcript,The transcription is shown below

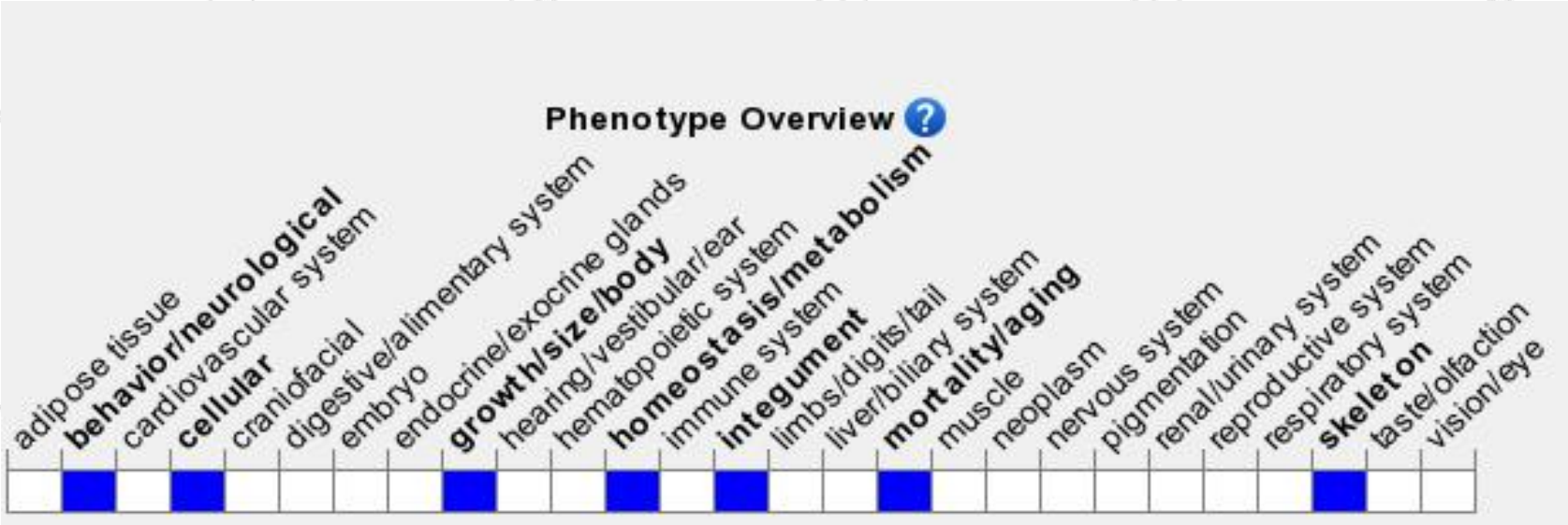


Genomic location distribution



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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