Slc29a2 Cas9-KO Strategy

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Design Date:	**2020-3-24**

Project Overview

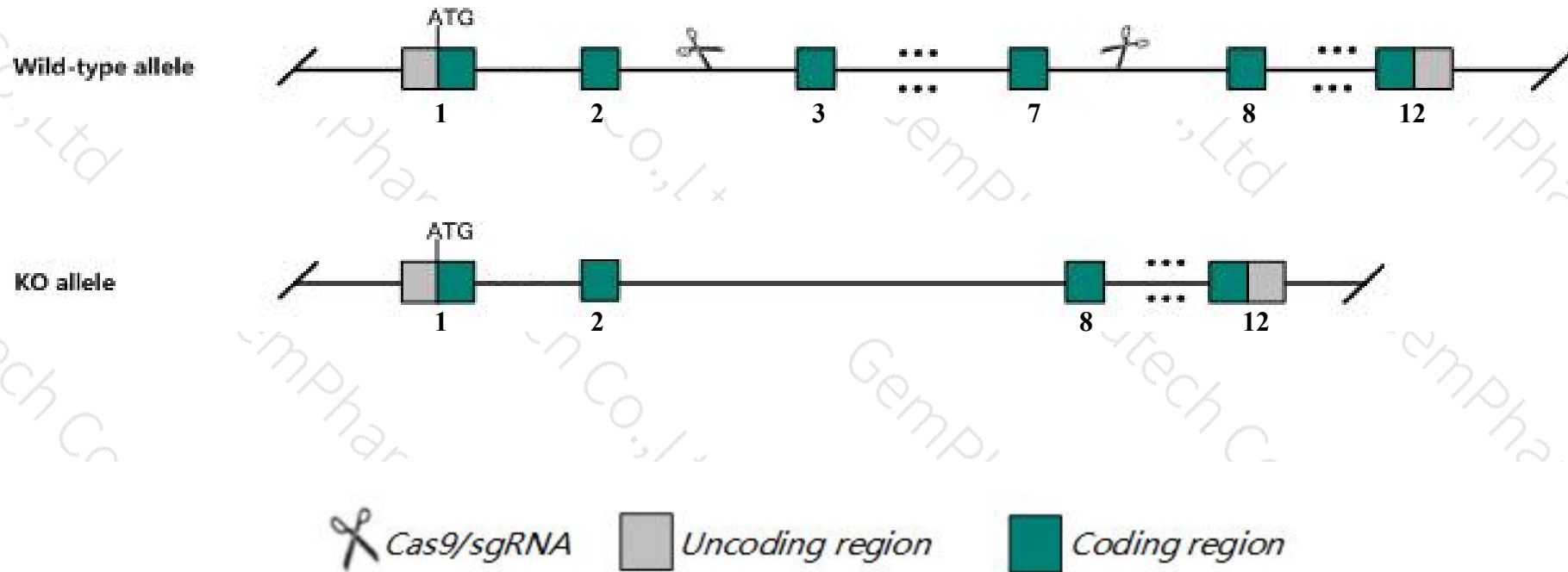|	
Project Name	***Slc29a2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc29a2* gene. The schematic diagram is as follows:

Technical routes

➤ The *Slc29a2* gene has 6 transcripts. According to the structure of *Slc29a2* gene, exon3-exon7 of *Slc29a2-204* (ENSMUST00000236152.1) transcript is recommended as the knockout region. The region contains 619bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Slc29a2* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

➢ According to the existing MGI data, mice homozygous for a gene trap allele exhibit normal adenosine uptake in erythrocytes and protection from acute lung injury.

➢ The *Slc29a2* gene is located on the Chr19. 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）

Slc29a2 solute carrier family 29 (nucleoside transporters), member 2 [*Mus musculus* (house mouse)]

Gene ID: 13340, updated on 13-Mar-2020

▲ Summary

Official Symbol	Slc29a2 provided by MGI
Official Full Name	solute carrier family 29 (nucleoside transporters), member 2 provided by MGI
Primary source	MGI:MGI:1345278
See related	Ensembl:ENSMUSG00000024891
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	Ent2; Der12; Hnp36
Expression	Ubiquitous expression in CNS E18 (RPKM 8.0), heart adult (RPKM 7.3) and 28 other tissues See more
Orthologs	human all

▲ Genomic context

Location: 19; 19 A

See Slc29a2 in Genome Data Viewer

Exon count: 13

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	19	NC_000085.6 (5019057..5031972)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	19	NC_000085.5 (5024006..5031972)

Chromosome 19 - NC_000085.6

[4962152 ▶

[5041134 ▶

Mrpl11

Npas4

Slc29a2

n-TS9ct6

Gm30581

B4gmt1
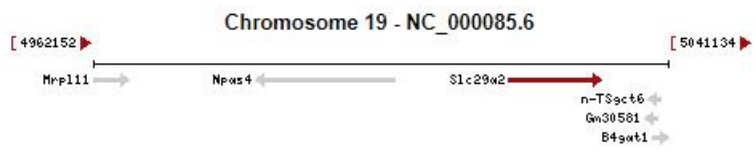
Transcript information（Ensembl）

The gene has 6 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc29a2-204	ENSMUST00000236152.1	2619	456aa	Protein coding	CCDS50354	Q61672	GENCODE basic APPRIS P1
Slc29a2-201	ENSMUST00000025826.6	2401	427aa	Protein coding	-	A0A498WFQ1	TSL:1 GENCODE basic
Slc29a2-206	ENSMUST00000237371.1	2362	404aa	Protein coding	-	A0A494BAC3	GENCODE basic
Slc29a2-202	ENSMUST00000235416.1	784	228aa	Protein coding	-	A0A494BAD2	CDS 3' incomplete
Slc29a2-205	ENSMUST00000237267.1	750	No protein	Retained intron	-	-	-
Slc29a2-203	ENSMUST00000235933.1	440	No protein	Retained intron	-	-	-

The strategy is based on the design of *Slc29a2-204* transcript, the transcription is shown below:
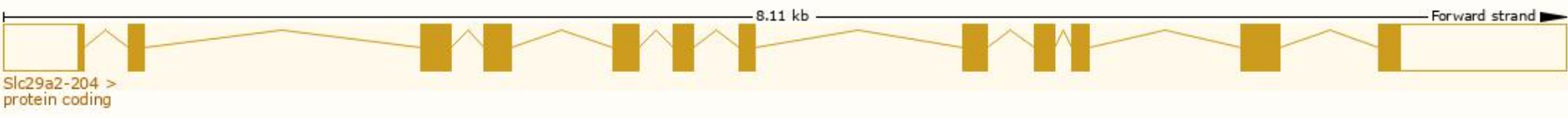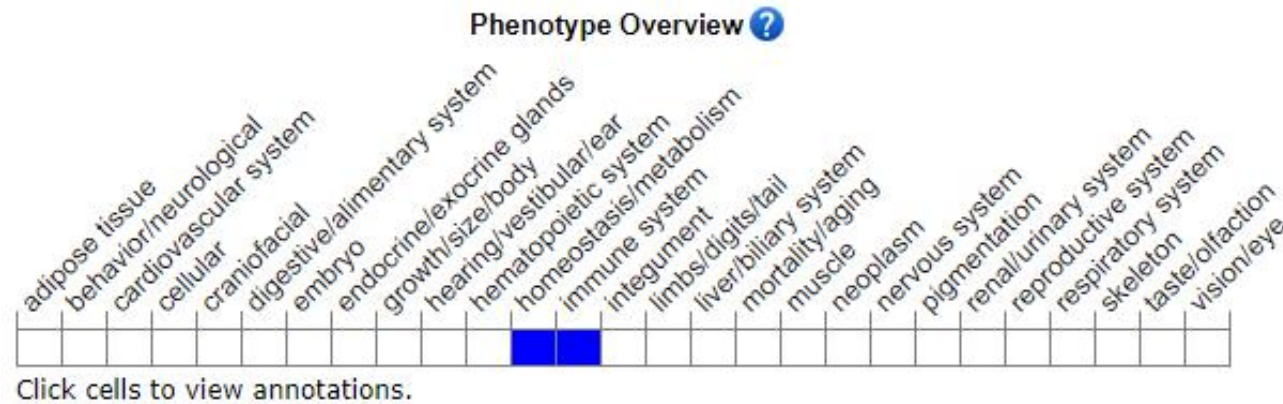
Genomic location distribution
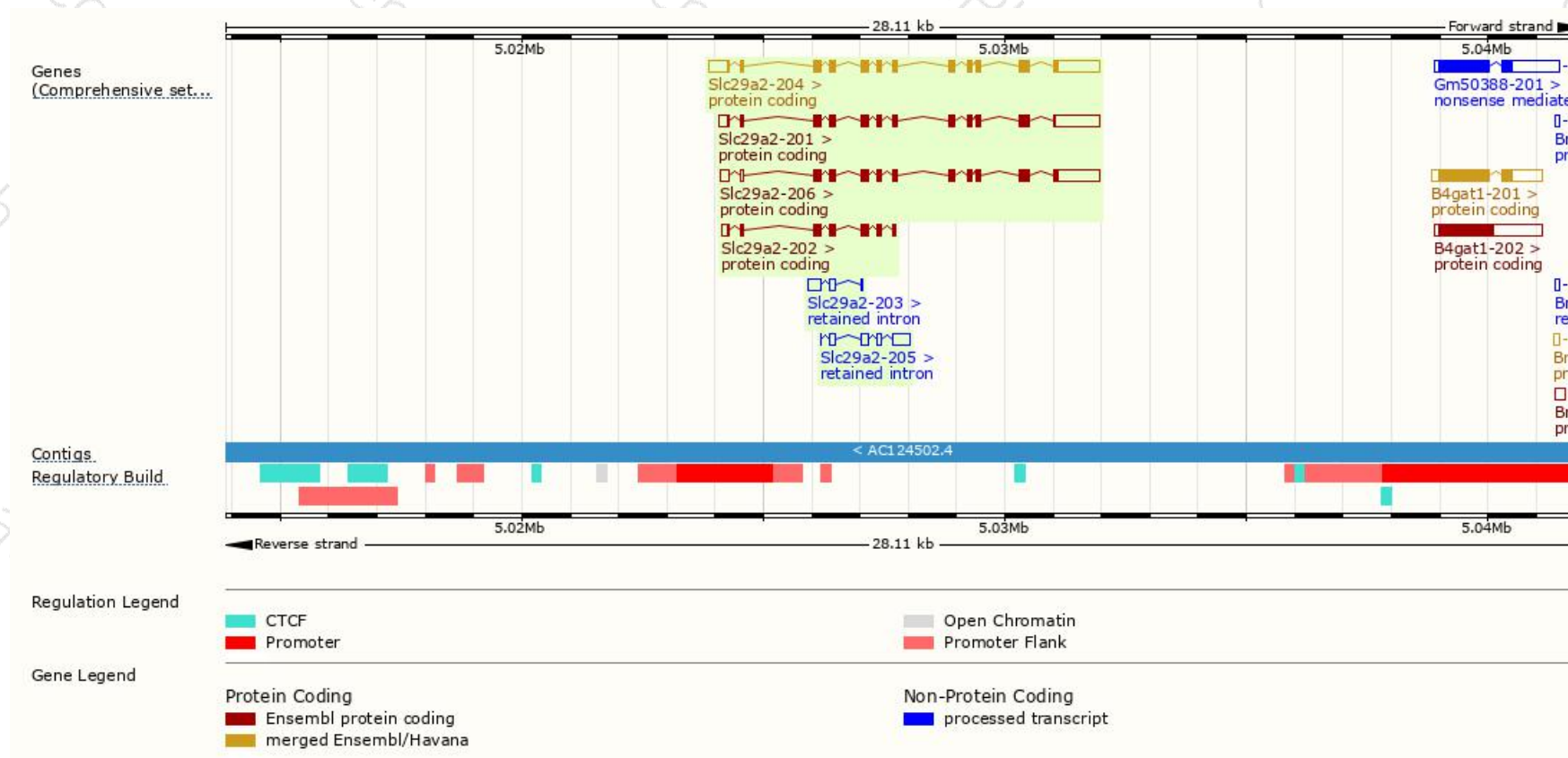
Protein domain
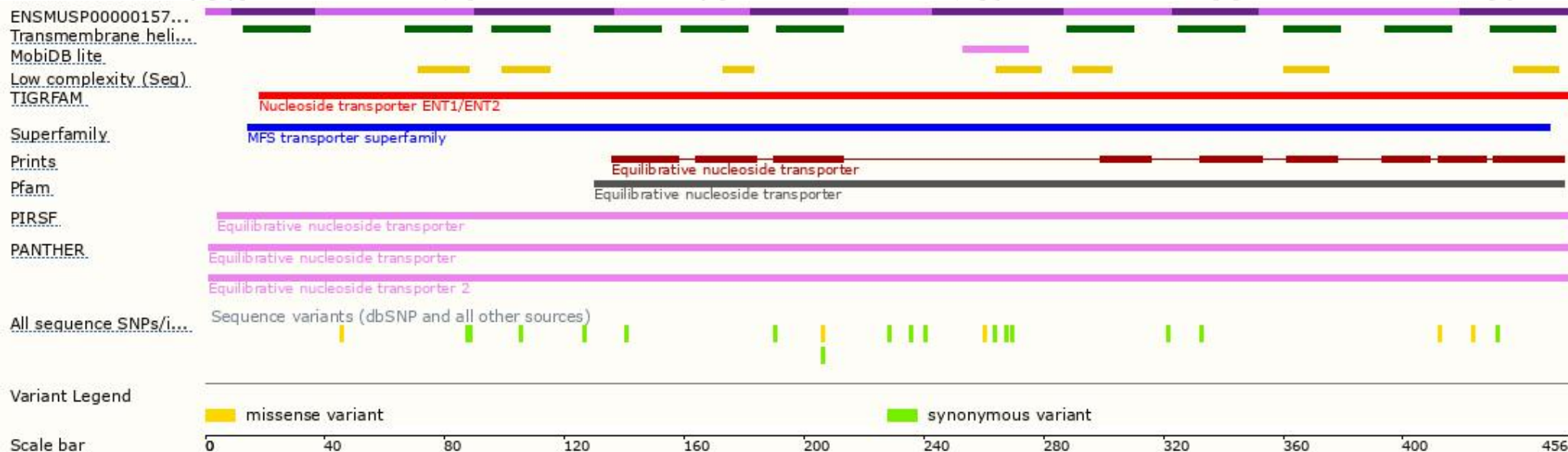
Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data, Mice homozygous for a gene trap allele exhibit normal adenosine uptake in erythrocytes and protection from acute lung injury.

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