Slc30a9 Cas9-KO Strategy

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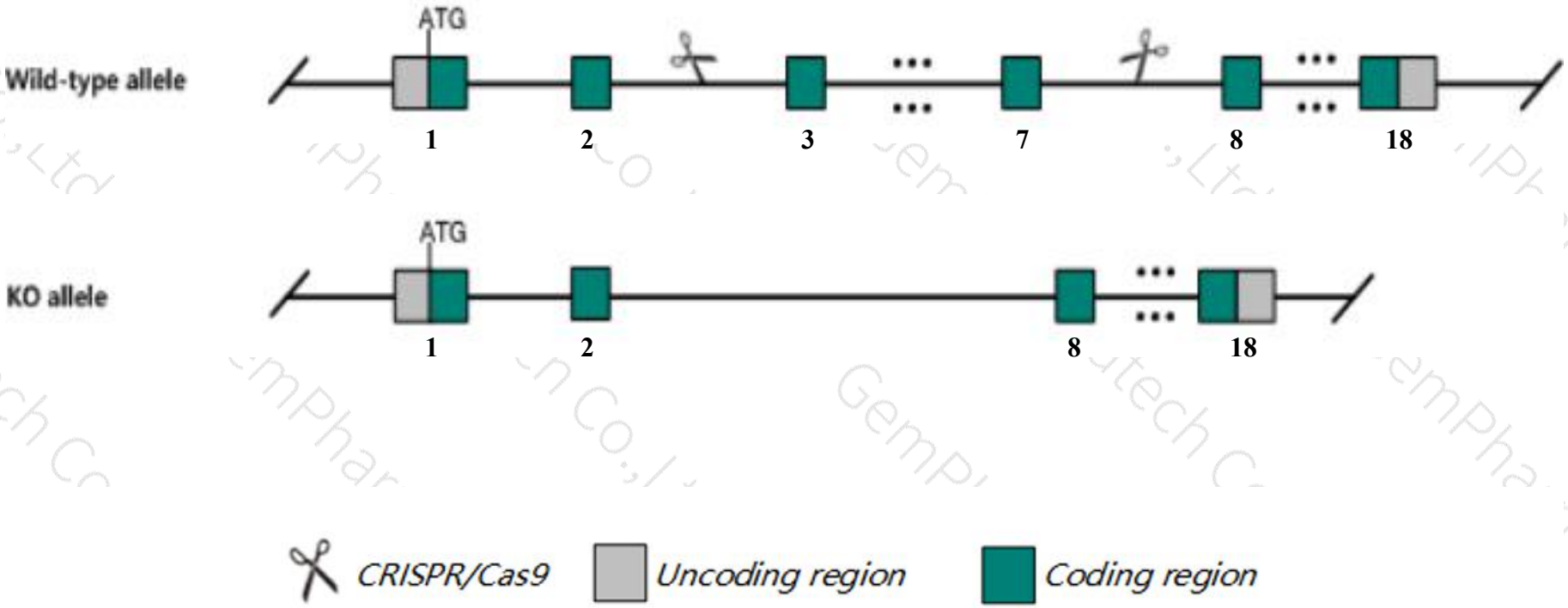
Project Overview

Project Name	***Slc30a9***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc30a9* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc30a9* gene has 8 transcripts. According to the structure of *Slc30a9* gene, exon3-exon7 of *Slc30a9-204* (ENSMUST00000162372.7) transcript is recommended as the knockout region.The region contains 395bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc30a9* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- The *Slc30a9* gene is located on the Chr5. 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）

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Slc30a9 solute carrier family 30 (zinc transporter), member 9 [Mus musculus (house mouse)]

Gene ID: 109108, updated on 13-Mar-2020

Summary

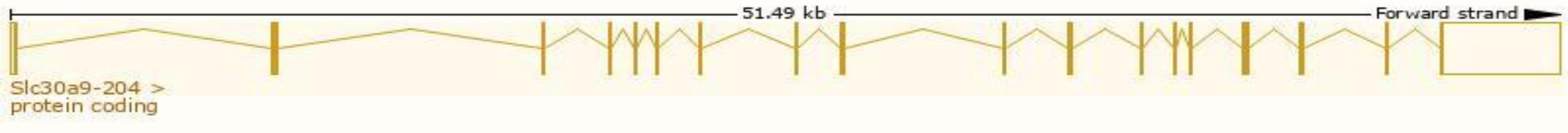
Official Symbol	Slc30a9 provided by MGI
Official Full Name	solute carrier family 30 (zinc transporter), member 9 provided by MGI
Primary source	MGI:MGI:1923690
See related	Ensembl:ENSMUSG00000029221
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310024J23Rik, AL024256, GAC63, HUEL, znT-9
Expression	Ubiquitous expression in cerebellum adult (RPKM 23.5), frontal lobe adult (RPKM 21.7) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

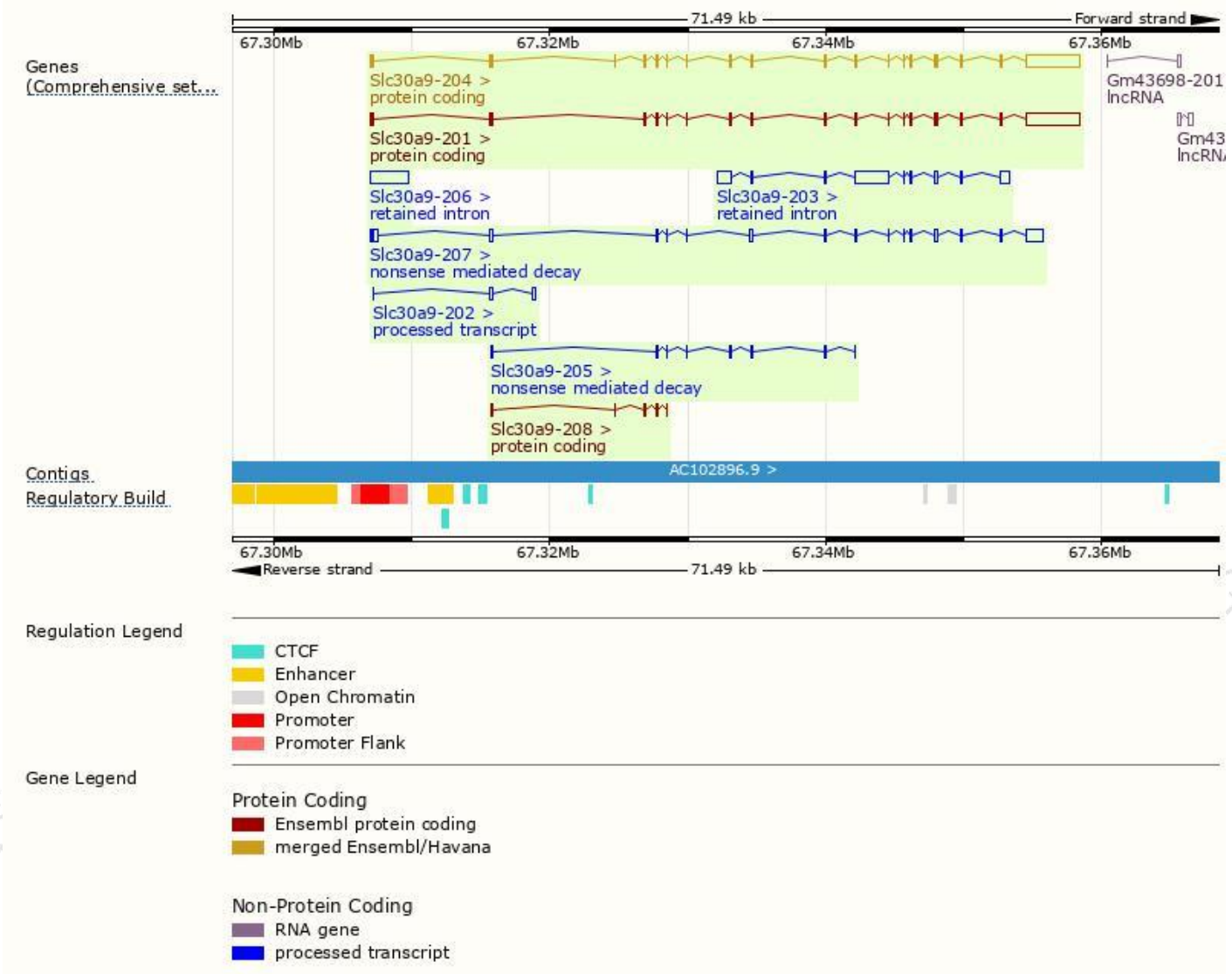
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc30a9-204	ENSMUST00000162372.7	5711	567aa	Protein coding	CCDS39103	Q5IRJ6	TSL:1 GENCODE basic APPRIS P3
Slc30a9-201	ENSMUST00000113676.5	5648	547aa	Protein coding	CCDS80294	F8WHL1	TSL:1 GENCODE basic APPRIS ALT2
Slc30a9-208	ENSMUST00000202770.1	425	142aa	Protein coding	-	A0A0J9YVB0	CDS 5' and 3' incomplete TSL:3
Slc30a9-207	ENSMUST00000202521.3	3272	36aa	Nonsense mediated decay	-	A0A0J9YU90	TSL:5
Slc30a9-205	ENSMUST00000200734.3	678	51aa	Nonsense mediated decay	-	A0A0J9YV89	CDS 5' incomplete TSL:3
Slc30a9-202	ENSMUST00000159907.2	383	No protein	Processed transcript	-	-	TSL:5
Slc30a9-203	ENSMUST00000161169.2	4838	No protein	Retained intron	-	-	TSL:2
Slc30a9-206	ENSMUST00000201173.1	2791	No protein	Retained intron	-	-	TSL:NA

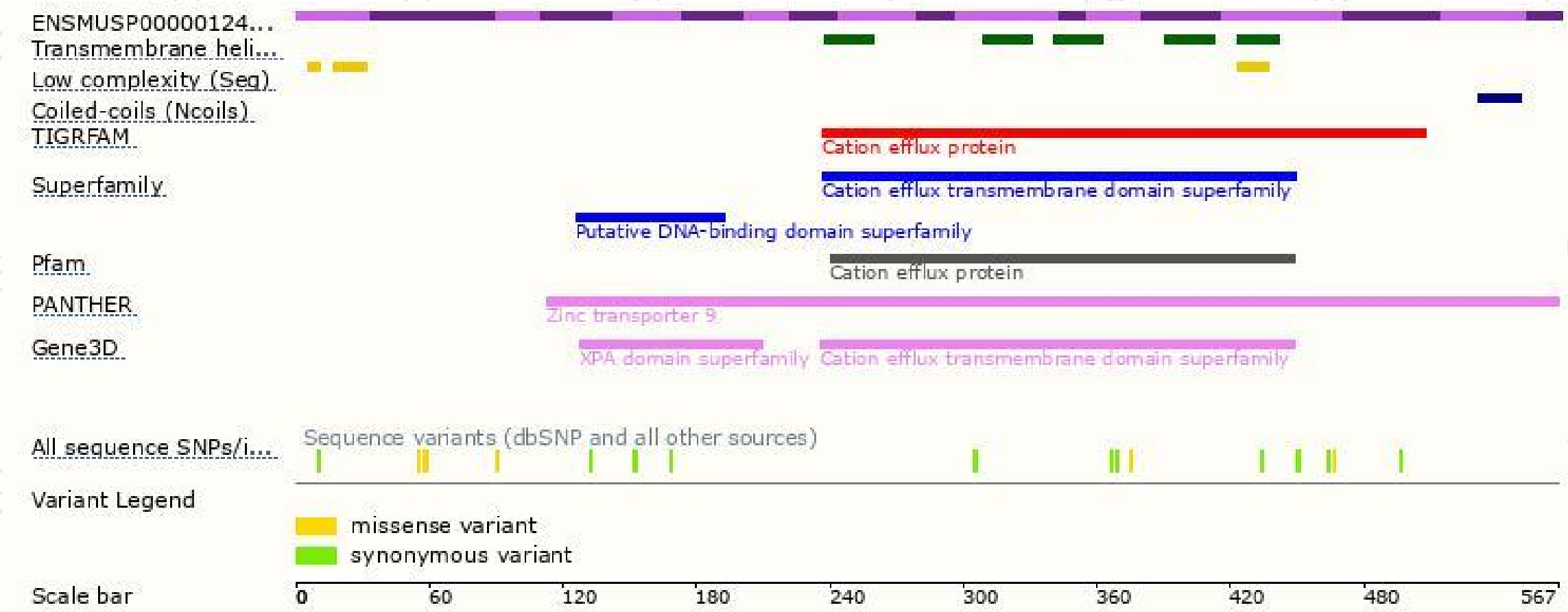
The strategy is based on the design of *Slc30a9-204* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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