Celsr2 Cas9-KO Strategy

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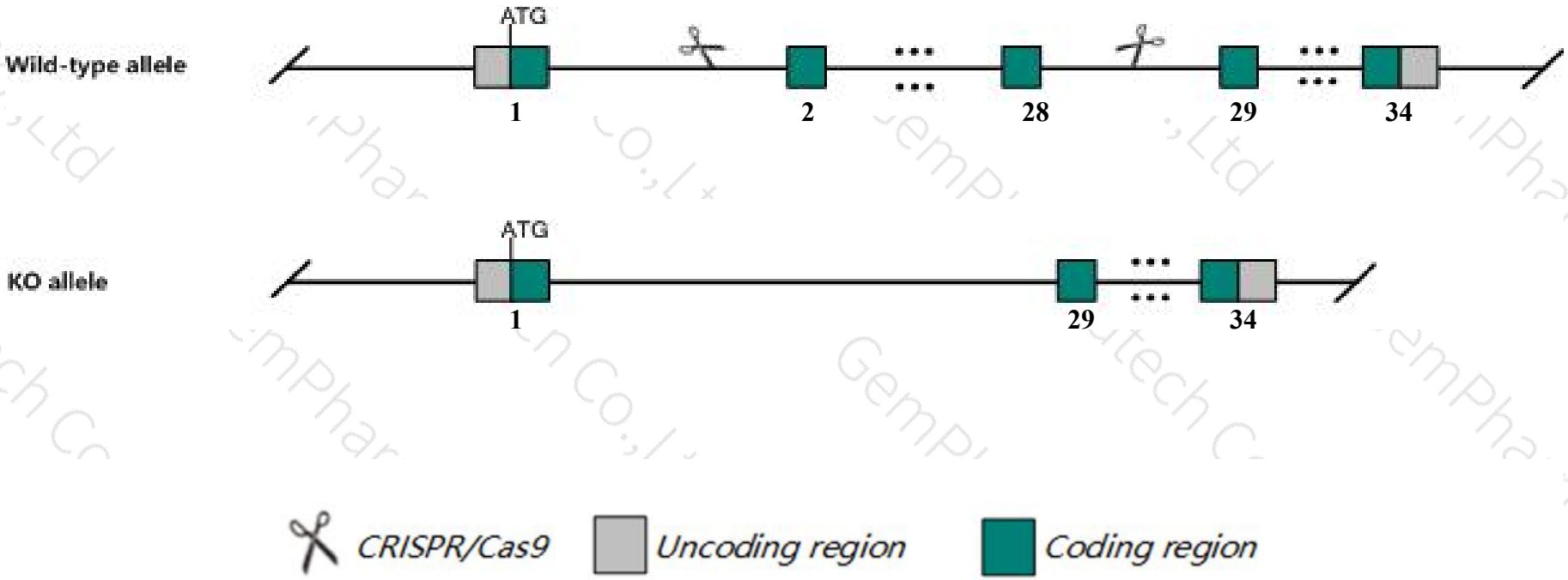
Project Overview

Project Name	***Celsr2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Celsr2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Celsr2* gene has 7 transcripts. According to the structure of *Celsr2* gene, exon2-exon28 of *Celsr2-201* (ENSMUST00000090558.9) transcript is recommended as the knockout region.The region contains 4616bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Celsr2* 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 disruptions in this allele have mild to moderately dilated lateral ventricles in the brain but are otherwise normal.

- The *Celsr2* gene is located on the Chr3. 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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Celsr2 cadherin, EGF LAG seven-pass G-type receptor 2 [*Mus musculus* (house mouse)]

Gene ID: 53883, updated on 14-Aug-2019

Summary

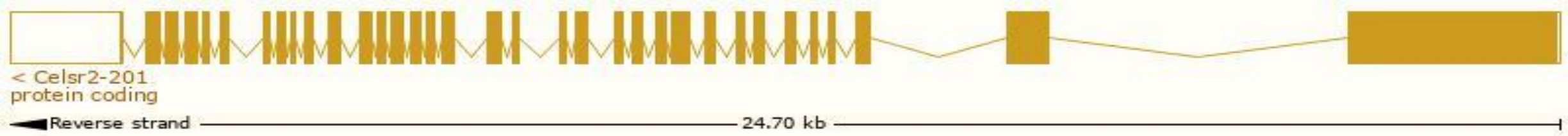
Official Symbol	Celsr2 provided by MGI
Official Full Name	cadherin, EGF LAG seven-pass G-type receptor 2 provided by MGI
Primary source	MGI:MGI:1858235
See related	Ensembl:ENSMUSG00000068740
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	EGFL2; mfmi1; Adgrc2; flamingo; Flamingo1; mKIAA0279
Expression	Broad expression in CNS E11.5 (RPKM 14.7), kidney adult (RPKM 13.4) and 22 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

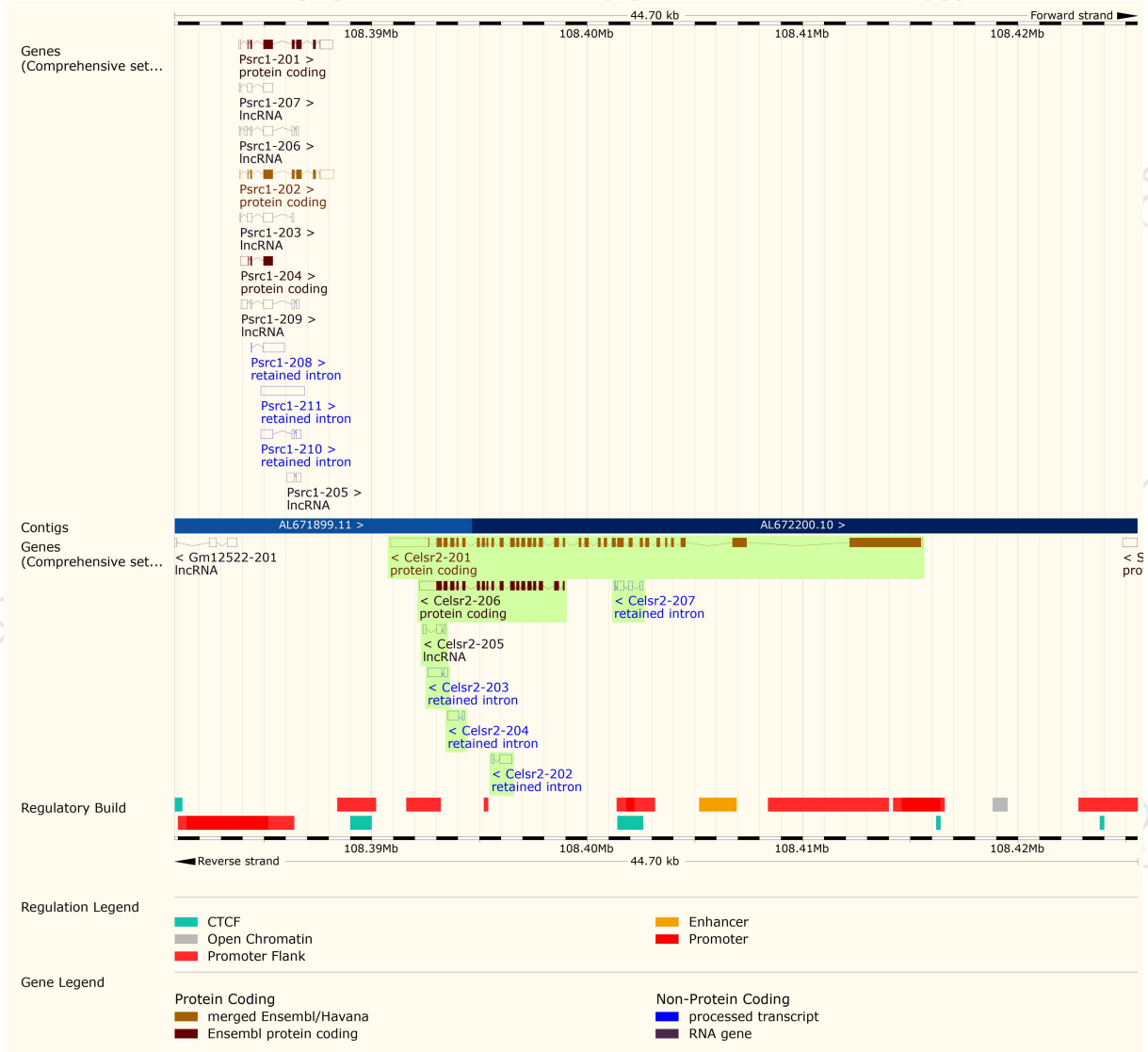
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Celsr2-201	ENSMUST00000090558.9	10598	2919aa	Protein coding	CCDS17759	A2AEE7	TSL:1 GENCODE basic APPRIS P1
Celsr2-206	ENSMUST00000147251.1	3486	900aa	Protein coding	-	F7BHW1	CDS 5' incomplete TSL:1
Celsr2-205	ENSMUST00000133216.1	467	No protein	Processed transcript	-	-	TSL:2
Celsr2-203	ENSMUST00000126935.1	831	No protein	Retained intron	-	-	TSL:2
Celsr2-202	ENSMUST00000126349.1	664	No protein	Retained intron	-	-	TSL:2
Celsr2-207	ENSMUST00000147565.2	658	No protein	Retained intron	-	-	TSL:3
Celsr2-204	ENSMUST00000130941.1	580	No protein	Retained intron	-	-	TSL:5

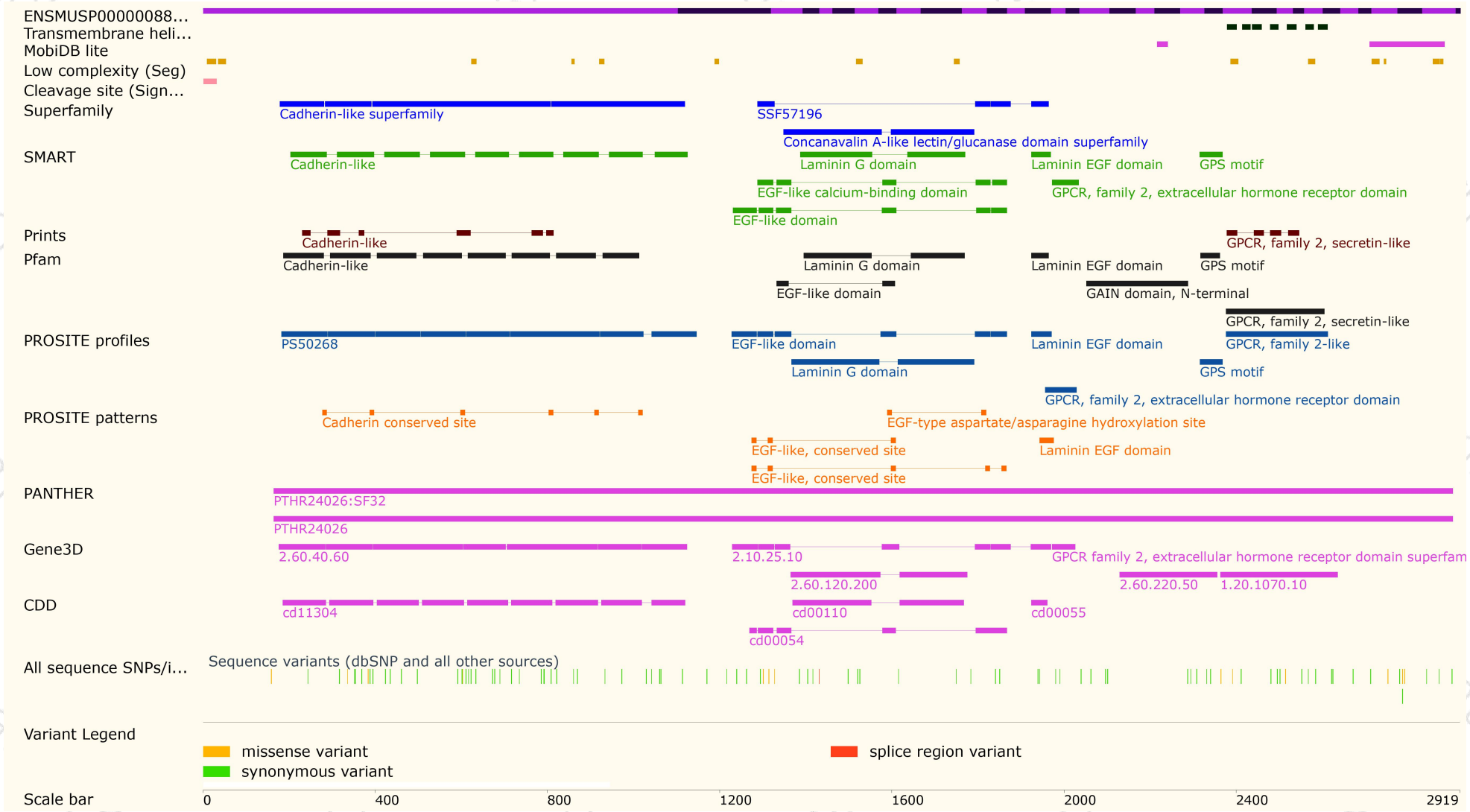
The strategy is based on the design of *Celsr2-201* transcript,The transcription is shown below



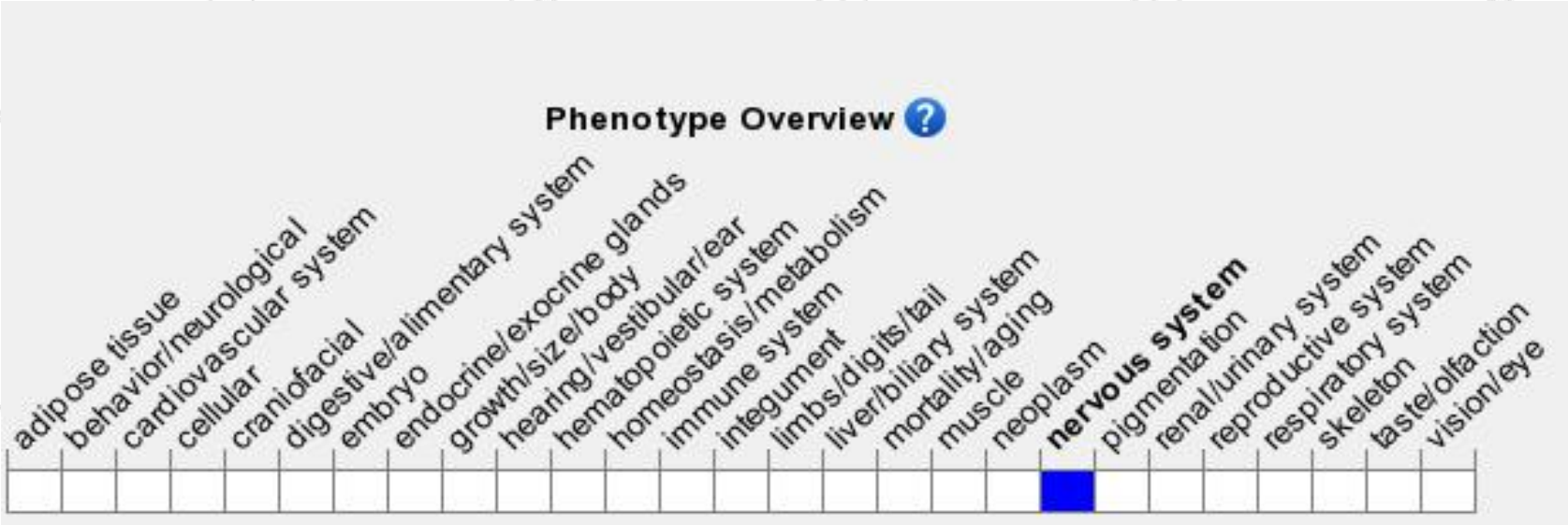
Genomic location distribution



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/).

According to the existing MGI data,Mice homozygous for disruptions in this allele have mild to moderately dilated lateral ventricles in the brain but are otherwise normal.

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

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