Ccnj Cas9-CKO Strategy

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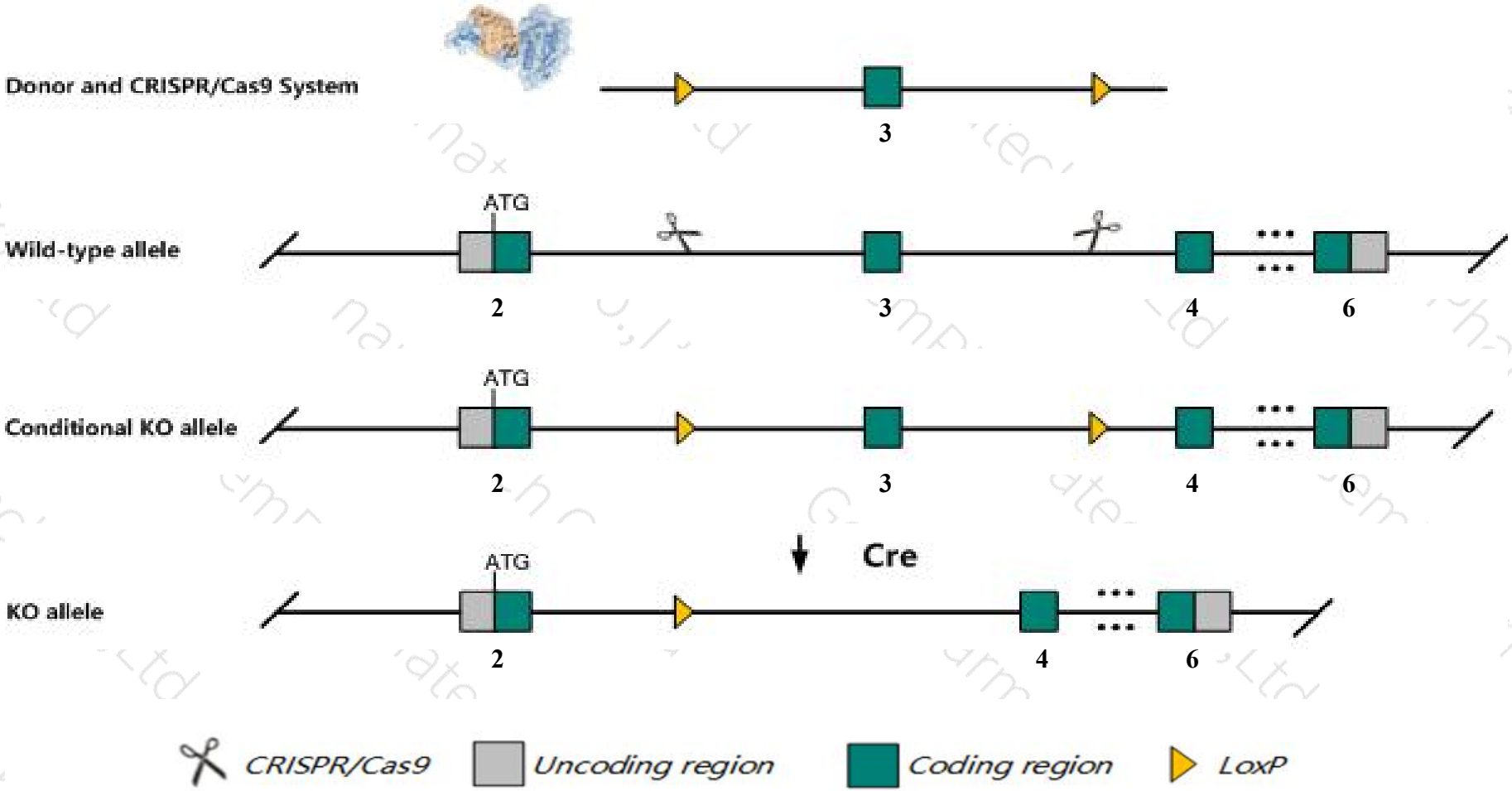
Design Date: 2020-4-15

Project Overview

Project Name	***Ccnj***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

- The *Ccnj* gene has 2 transcripts. According to the structure of *Ccnj* gene, exon3 of *Ccnj-201* (ENSMUST00000025983.12) transcript is recommended as the knockout region.The region contains 211bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Ccnj* gene. The brief process is as follows:CRISPR/Cas9 system and Donor 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.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

➢ The *Ccnj* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Ccnj cyclin J [Mus musculus (house mouse)]

Gene ID: 240665, updated on 13-Mar-2020

Summary

Official Symbol	Ccnj provided by MGI
Official Full Name	cyclin J provided byMGI
Primary source	MGI:MGI:2443297
See related	Ensembl:ENSMUSG00000025010
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	D430039C20Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 10.4), whole brain E14.5 (RPKM 8.0) and 28 other tissuesSee more
Orthologs	human all

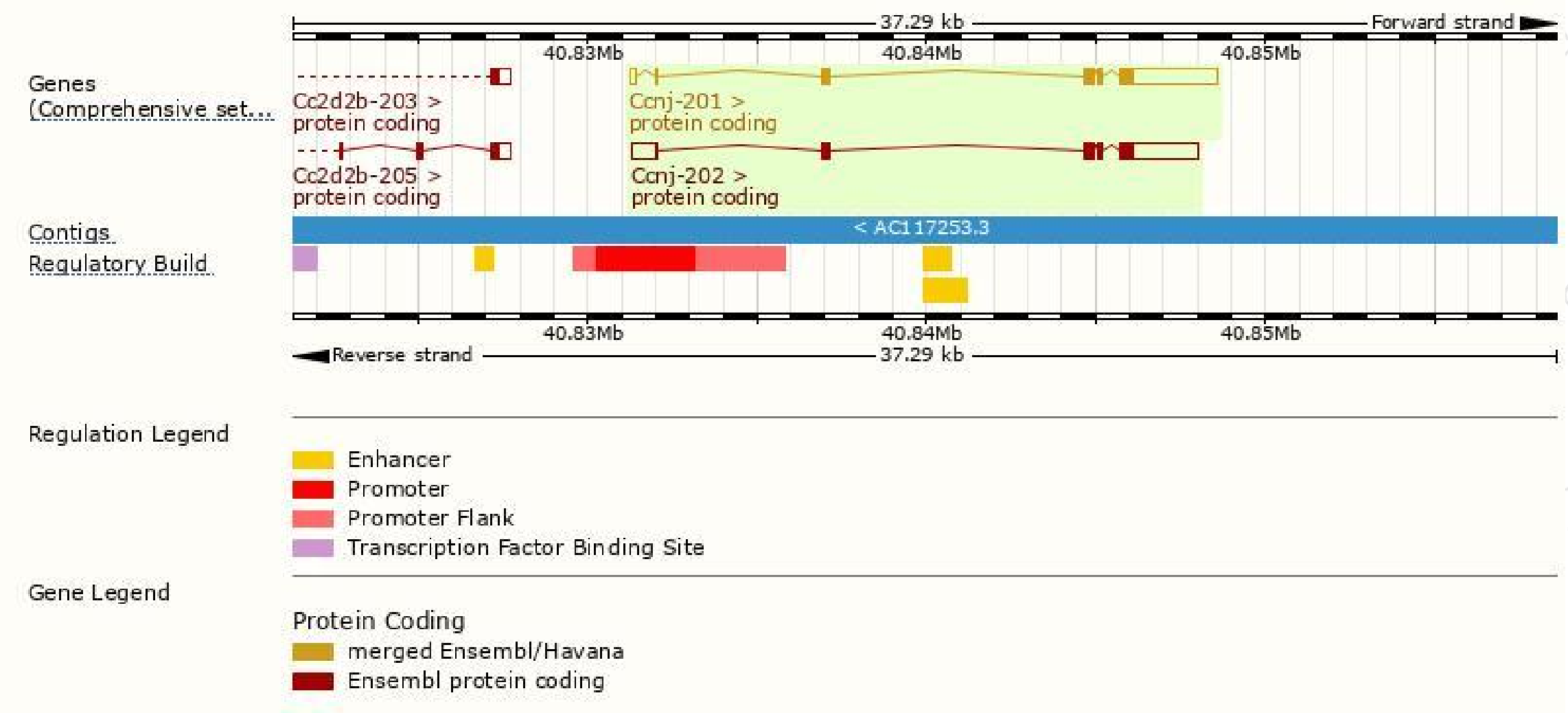
Transcript information（Ensembl）

The gene has 2 transcripts,all transcripts are shown below:

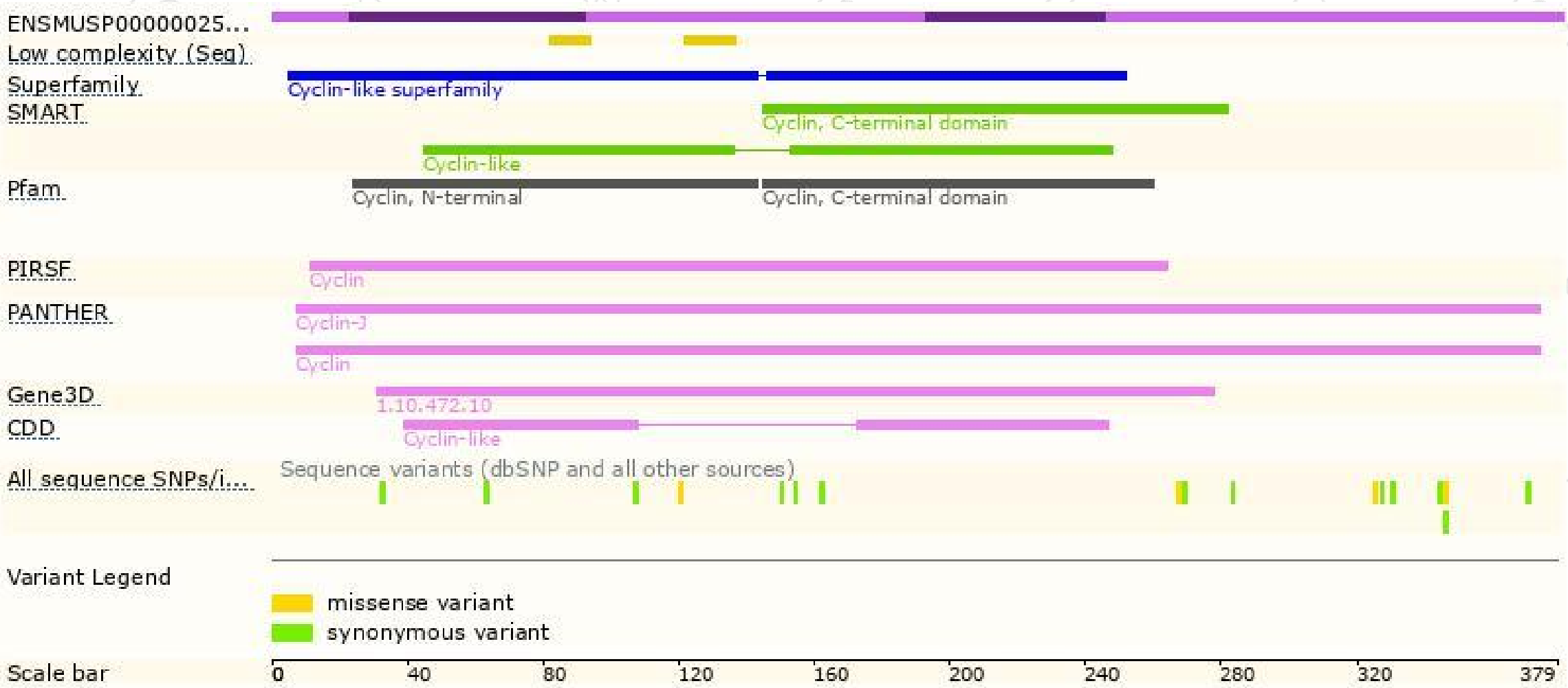
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccnj-201	ENSMUST00000025983.12	3819	379aa	Protein coding	CCDS29806	Q3TZI6	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Ccnj-202	ENSMUST00000119316.1	3763	379aa	Protein coding	CCDS29806	Q3TZI6	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

The strategy is based on the design of *Ccnj-201* 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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