Ncaph Cas9-CKO Strategy

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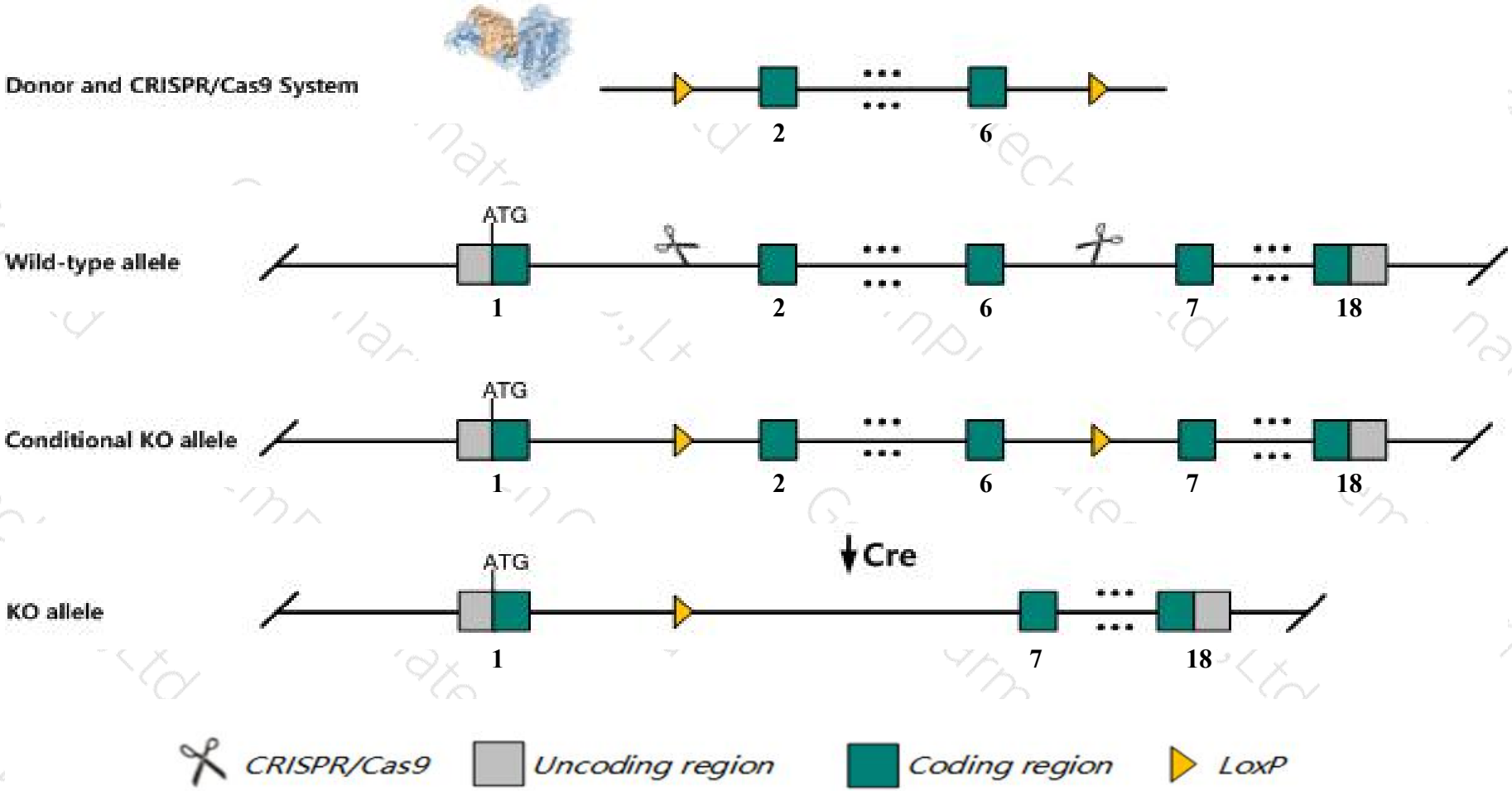
Project Overview

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

Conditional Knockout strategy

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



Technical routes

- The *Ncaph* gene has 6 transcripts. According to the structure of *Ncaph* gene, exon2-exon6 of *Ncaph-201* (ENSMUST00000110387.3) transcript is recommended as the knockout region.The region contains 683bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Ncaph* 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

➢ According to the existing MGI data,Homozygous null mice die before E12.5.

➢ The *Ncaph* gene is located on the Chr2. 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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Ncaph non-SMC condensin I complex, subunit H [Mus musculus (house mouse)]

Gene ID: 215387, updated on 31-Jan-2019

Summary

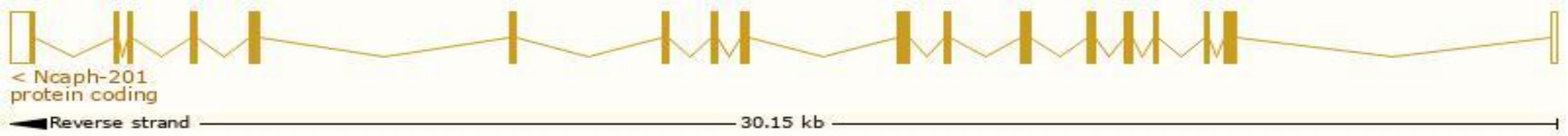
Official Symbol	Ncaph provided by MGI
Official Full Name	non-SMC condensin I complex, subunit H provided by MGI
Primary source	MGI:MGI:2444777
See related	Ensembl:ENSMUSG00000034906
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A730011O11Rik, Brrn1, CAP-H, HCAP-H, mCAP-H
Expression	Biased expression in CNS E11.5 (RPKM 23.0), liver E14 (RPKM 21.6) and 10 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

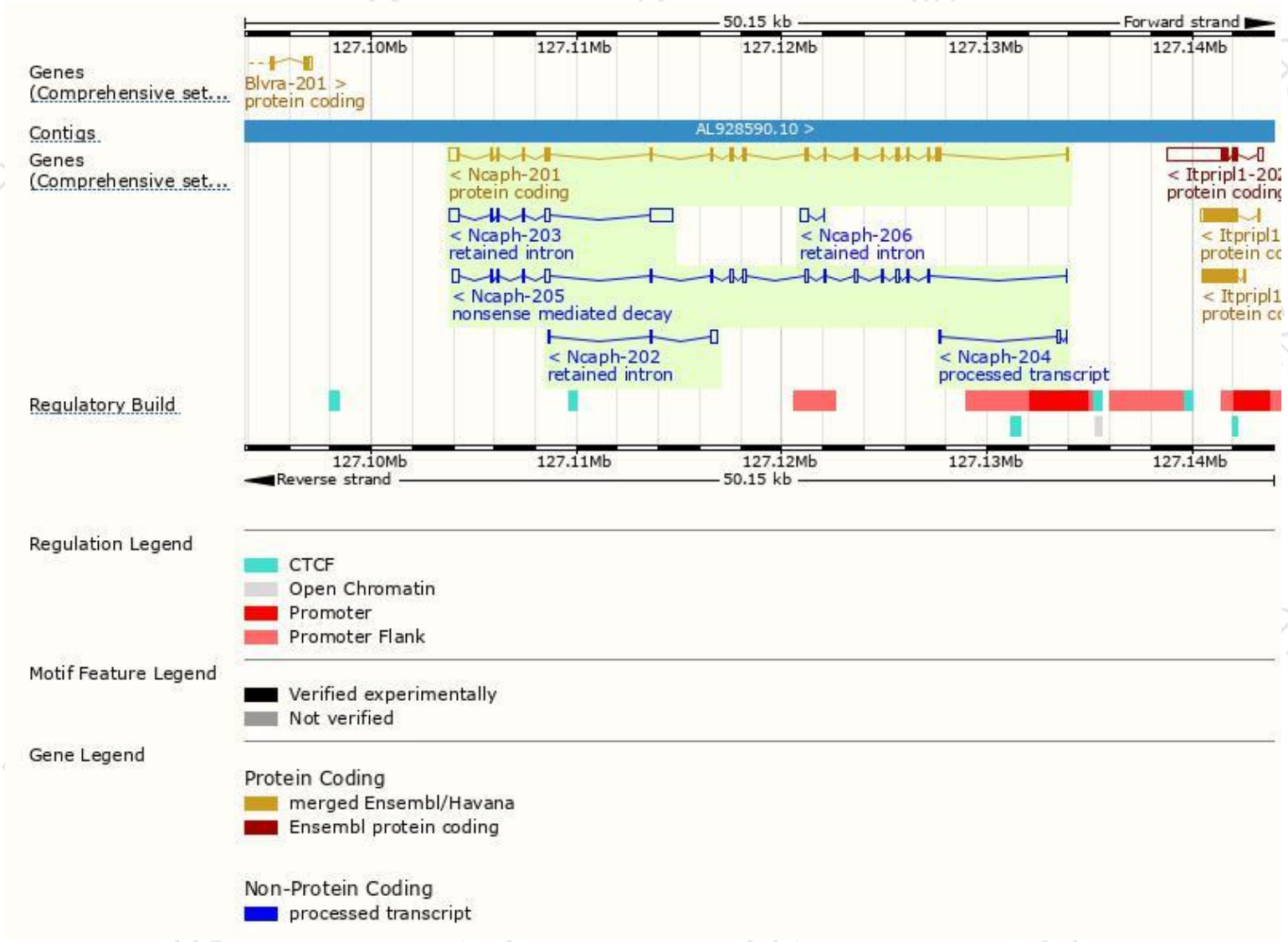
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ncaph-201	ENSMUST00000110387.3	2695	731aa	Protein coding	CCDS16693	Q8C156	TSL:1 GENCODE basic APPRIS P1
Ncaph-205	ENSMUST00000175885.7	2264	60aa	Nonsense mediated decay	-	H3BL21	CDS 5' incomplete TSL:5
Ncaph-204	ENSMUST00000156625.2	283	No protein	Processed transcript	-	-	TSL:5
Ncaph-203	ENSMUST00000152806.7	2024	No protein	Retained intron	-	-	TSL:2
Ncaph-202	ENSMUST00000146142.1	540	No protein	Retained intron	-	-	TSL:2
Ncaph-206	ENSMUST00000177191.1	426	No protein	Retained intron	-	-	TSL:1

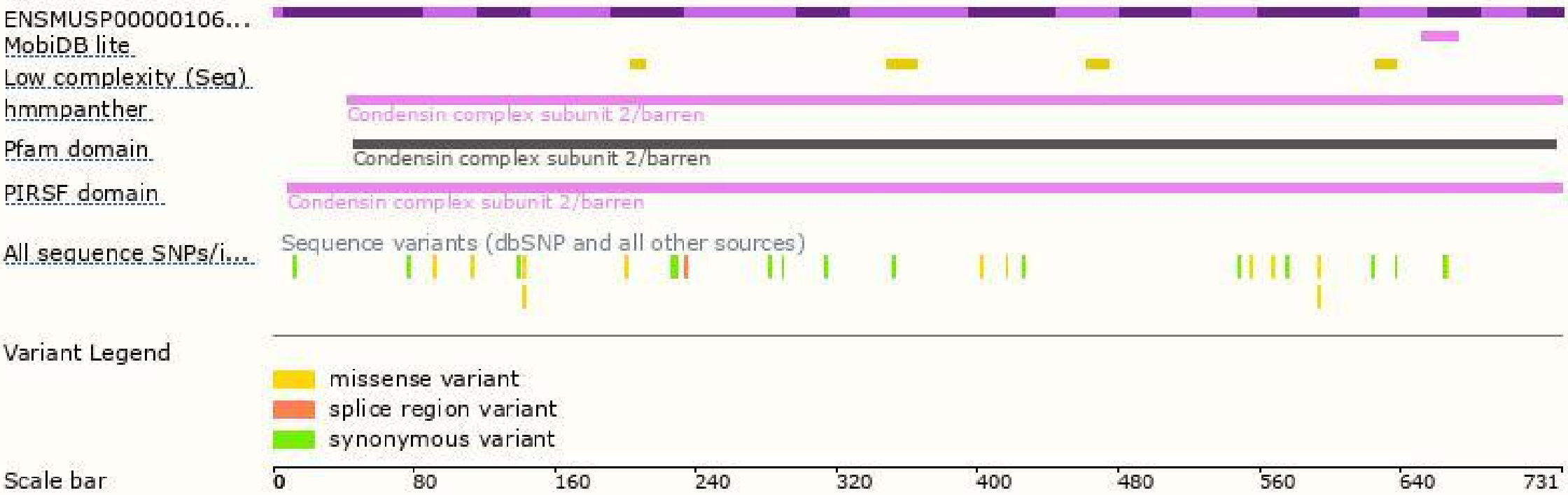
The strategy is based on the design of *Ncaph-201* transcript,The transcription is shown below



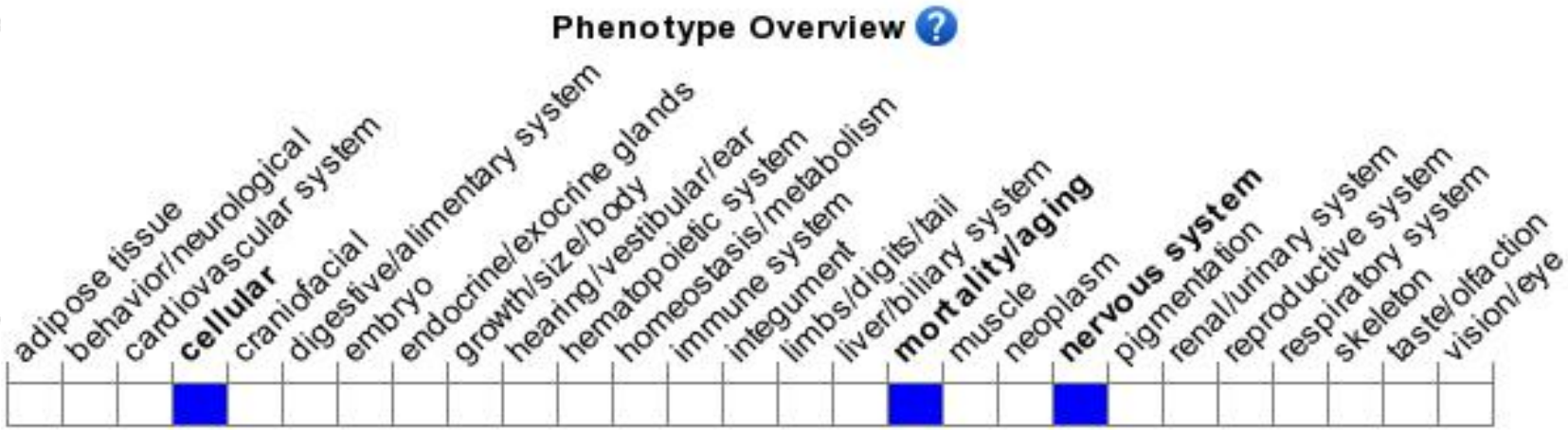
Genomic location distribution



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,Homozygous null mice die before E12.5.

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

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