Nptn Cas9-CKO Strategy

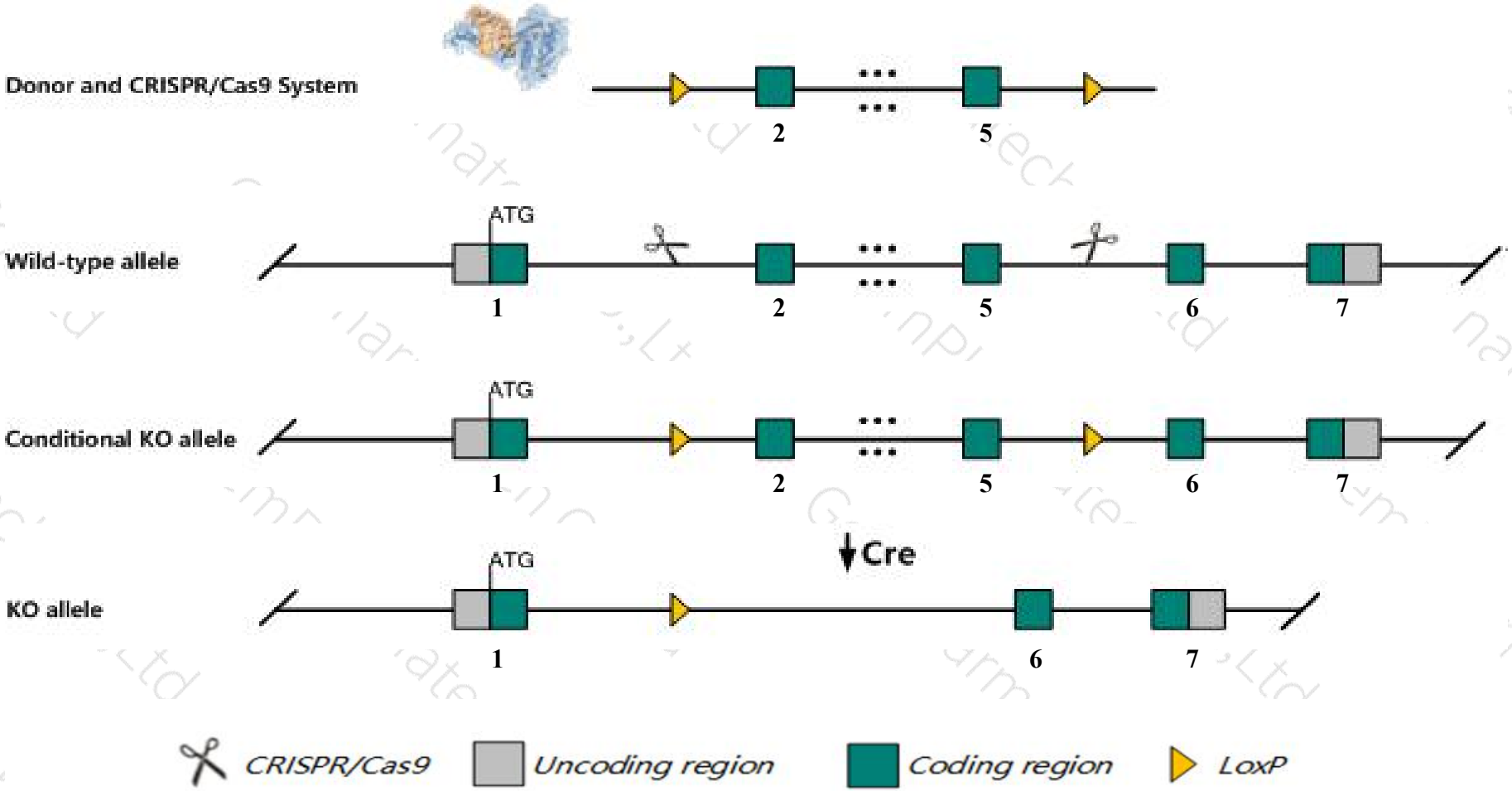
Designer: Yanhua Shen

Project Overview

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

Conditional Knockout strategy

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



Technical routes

- The *Nptn* gene has 13 transcripts. According to the structure of *Nptn* gene, exon2-exon5 of *Nptn-201* (ENSMUST00000085651.11) transcript is recommended as the knockout region.The region contains most of the coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Nptn* 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,Mice homozygous for a knock-out allele exhibit abnormal dendritic spine morphology, decreased CNS synapse formation, abnormal CNS synaptic transmission and impaired hearing.

- Non-coding transcripts 209 and 210 are unaffected.

- The *Nptn* gene is located on the Chr9. 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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Nptn neuroplastin [Mus musculus (house mouse)]

Gene ID: 20320, updated on 7-Apr-2019

Summary

Official Symbol	Nptn provided by MGI
Official Full Name	neuroplastin provided by MGI
Primary source	MGI:MGI:108077
See related	Ensembl:ENSMUSG00000032336
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	AW554172, SDR-1, Sdfr1
Expression	Ubiquitous expression in cortex adult (RPKM 131.7), cerebellum adult (RPKM 131.6) and 28 other tissues See more
Orthologs	human all

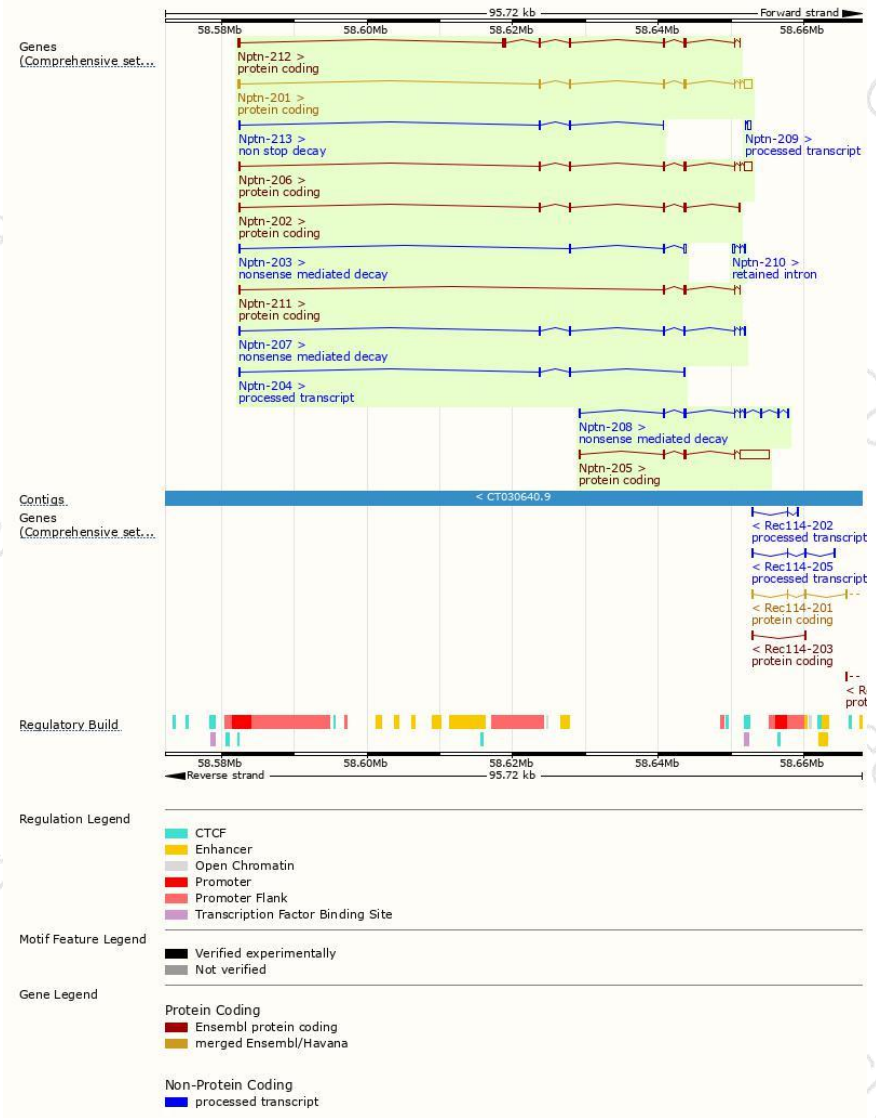
Transcript information（Ensembl）

The gene has 13 transcripts,all transcripts are shown below:

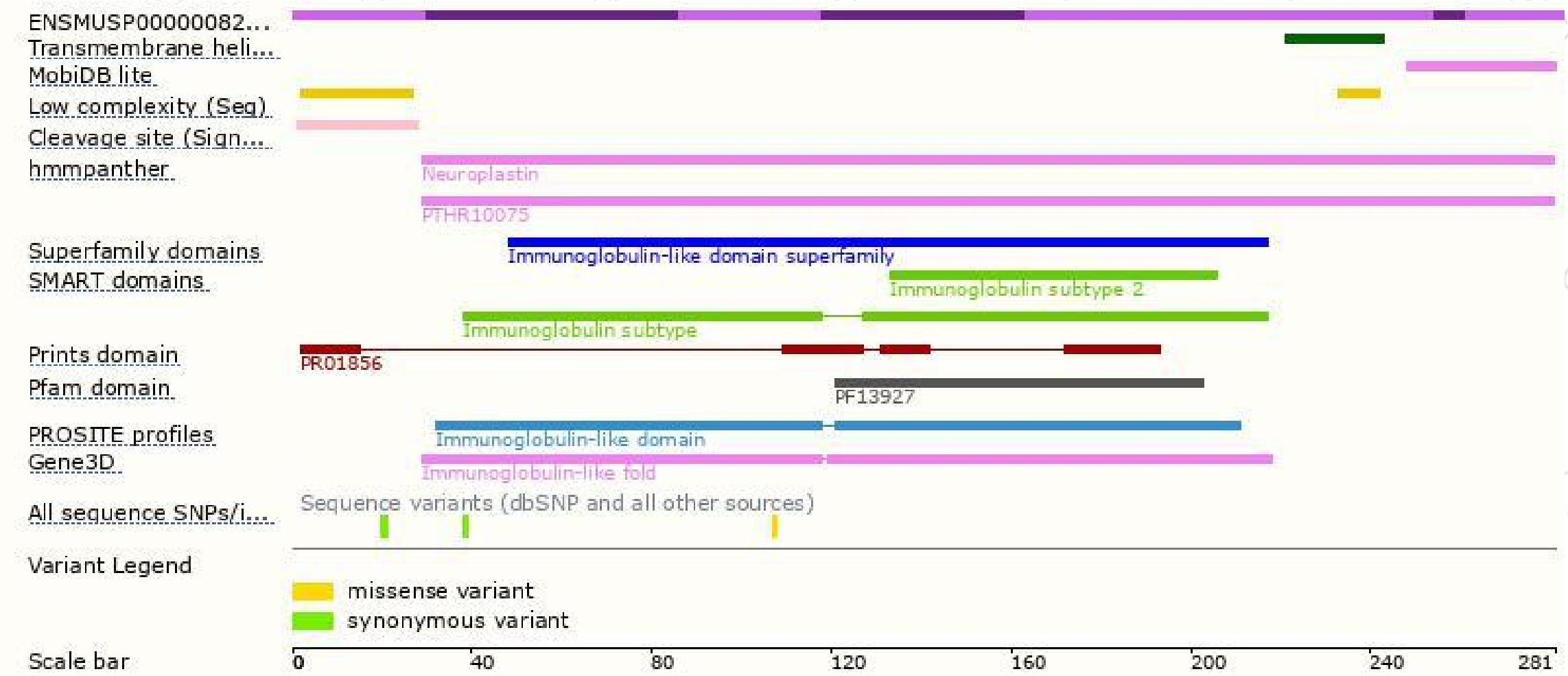
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nptn-201	ENSMUST00000085651.11	2024	281aa	Protein coding	CCDS23245	P97300	TSL:1 GENCODE basic
Nptn-206	ENSMUST00000176557.7	1898	277aa	Protein coding	CCDS81009	P97300	TSL:1 GENCODE basic
Nptn-205	ENSMUST00000176250.1	4531	171aa	Protein coding	-	P97300	TSL:1 GENCODE basic
Nptn-212	ENSMUST00000177292.7	1390	397aa	Protein coding	-	P97300	TSL:5 GENCODE basic APPRIS P1
Nptn-202	ENSMUST00000114121.10	863	277aa	Protein coding	-	Z4YLB7	TSL:5 GENCODE basic
Nptn-211	ENSMUST00000177064.7	582	193aa	Protein coding	-	H3BKA7	TSL:5 GENCODE basic
Nptn-213	ENSMUST00000177380.7	429	122aa	Non stop decay	-	A0A0A0MQN8	TSL:2
Nptn-208	ENSMUST00000176916.7	1401	171aa	Nonsense mediated decay	-	P97300	TSL:1
Nptn-207	ENSMUST00000176896.7	841	221aa	Nonsense mediated decay	-	H3BIX4	CDS 5' incomplete TSL:5
Nptn-203	ENSMUST00000175945.6	627	60aa	Nonsense mediated decay	-	H3BKY2	TSL:3
Nptn-204	ENSMUST00000176126.1	487	No protein	Processed transcript	-	-	TSL:3
Nptn-209	ENSMUST00000177020.1	486	No protein	Processed transcript	-	-	TSL:3
Nptn-210	ENSMUST00000177021.1	594	No protein	Retained intron	-	-	TSL:2

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

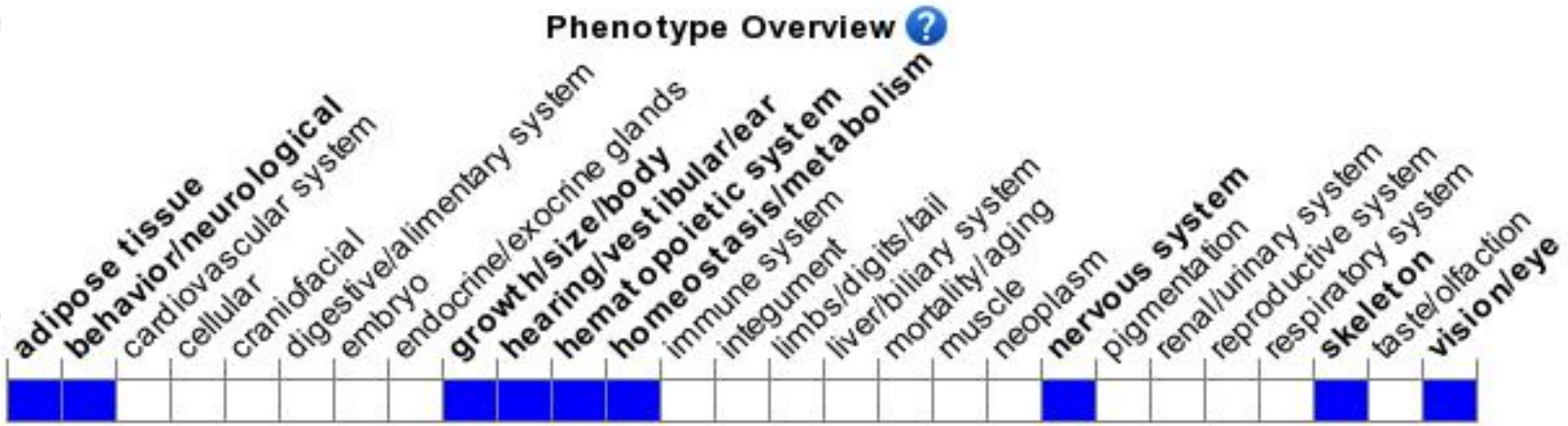
Genomic location distribution



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/).

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集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd