Chrnd Cas9-KO Strategy

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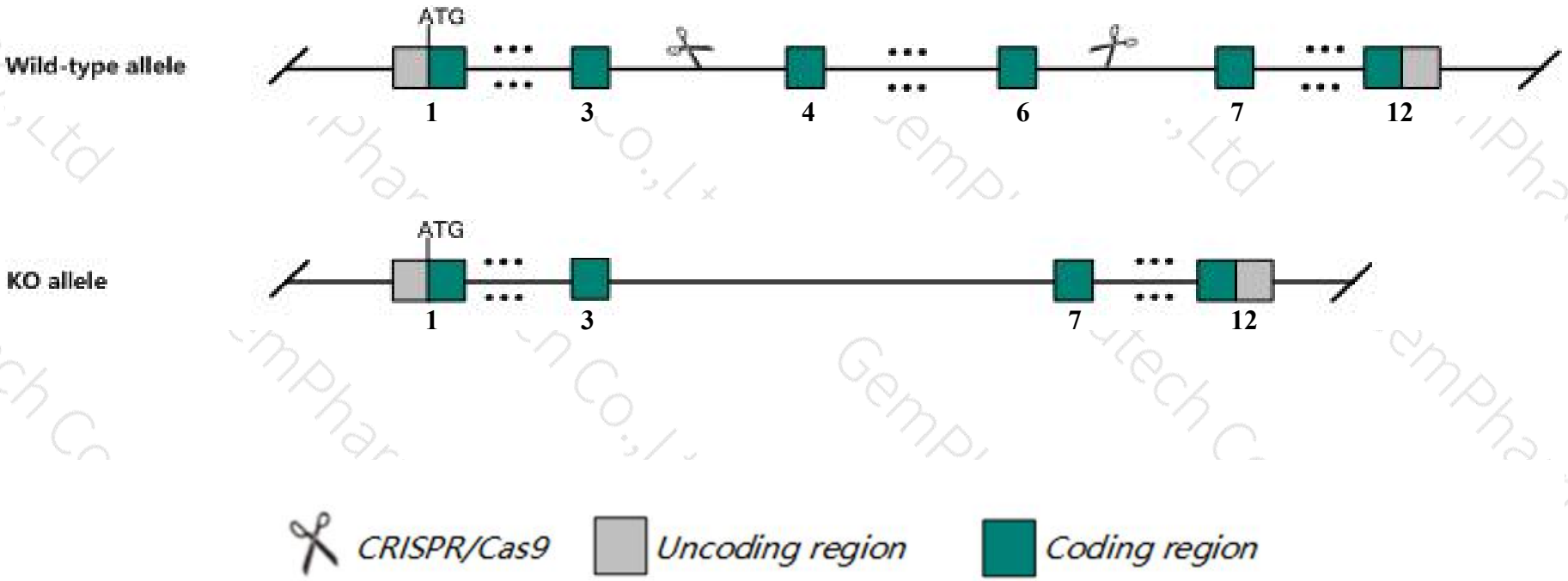
Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Chrnd* gene has 3 transcripts. According to the structure of *Chrnd* gene, exon4-exon6 of *Chrnd-201* (ENSMUST00000073252.8) transcript is recommended as the knockout region.The region contains 376bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

➢ The *Chrnd* gene is located on the Chr1. 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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Chrnd cholinergic receptor, nicotinic, delta polypeptide [*Mus musculus* (house mouse)]

Gene ID: 11447, updated on 12-Aug-2019

Summary

Official Symbol	Chrnd provided by MGI
Official Full Name	cholinergic receptor, nicotinic, delta polypeptide provided by MGI
Primary source	MGI:MGI:87893
See related	Ensembl:ENSMUSG00000026251
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Acrd; Achr-4; L10076
Summary	This gene encodes the delta subunit of the muscle-derived nicotinic acetylcholine receptor, a pentameric neurotransmitter receptor and member of the ligand-gated ion channel superfamily. The delta subunit together with the alpha subunit forms the ligand-binding site. [provided by RefSeq, Nov 2012]
Expression	Biased expression in limb E14.5 (RPKM 2.7), ovary adult (RPKM 0.2) and 1 other tissue See more
Orthologs	human all

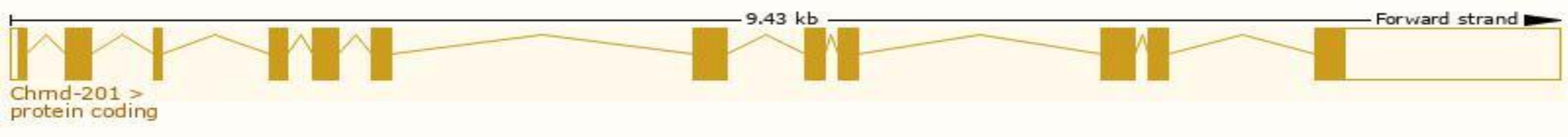
Chromosome 1 - NC_000067.6

Transcript information（Ensembl）

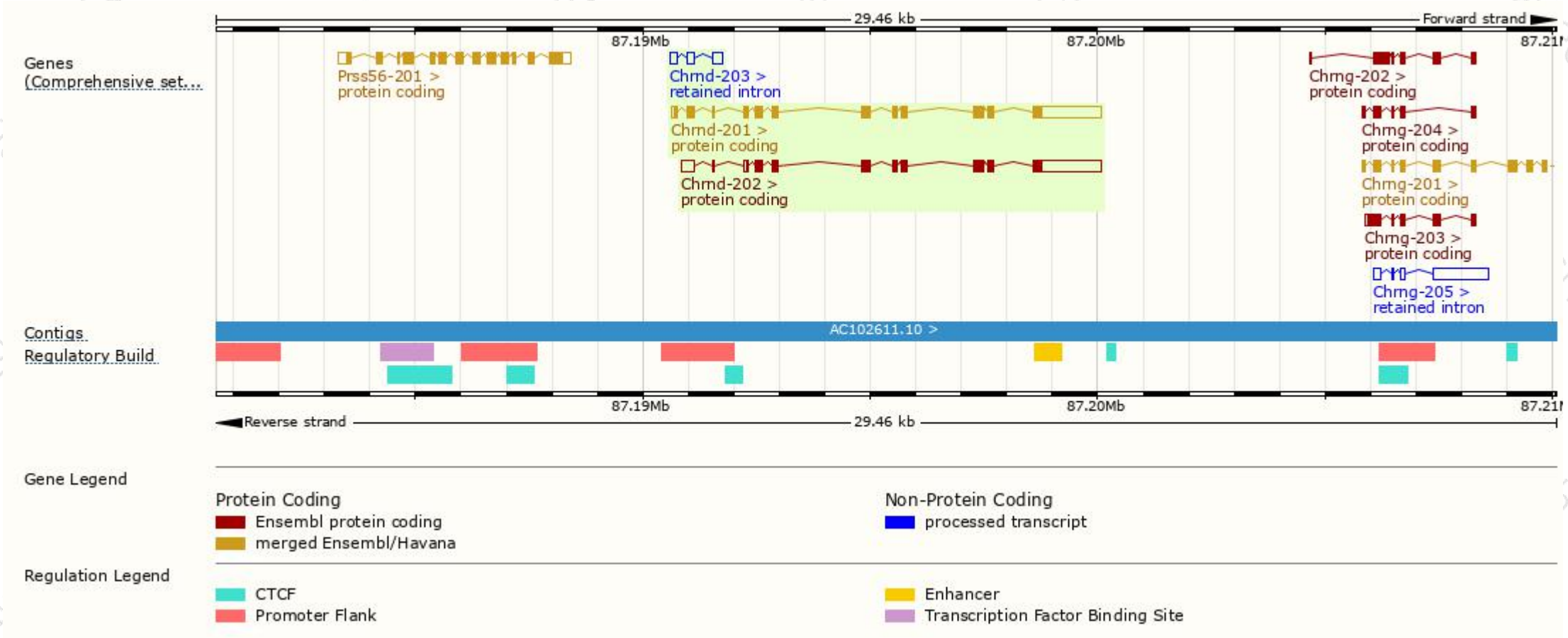
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Chrnd-201	ENSMUST00000073252.8	2925	520aa	Protein coding	CCDS15129	P02716 Q80VZ5	TSL:1 GENCODE basic APPRIS P1
Chrnd-202	ENSMUST00000186373.1	2949	411aa	Protein coding	-	A0A087WNX8	TSL:1 GENCODE basic
Chrnd-203	ENSMUST00000189970.1	538	No protein	Retained intron	-	-	TSL:2

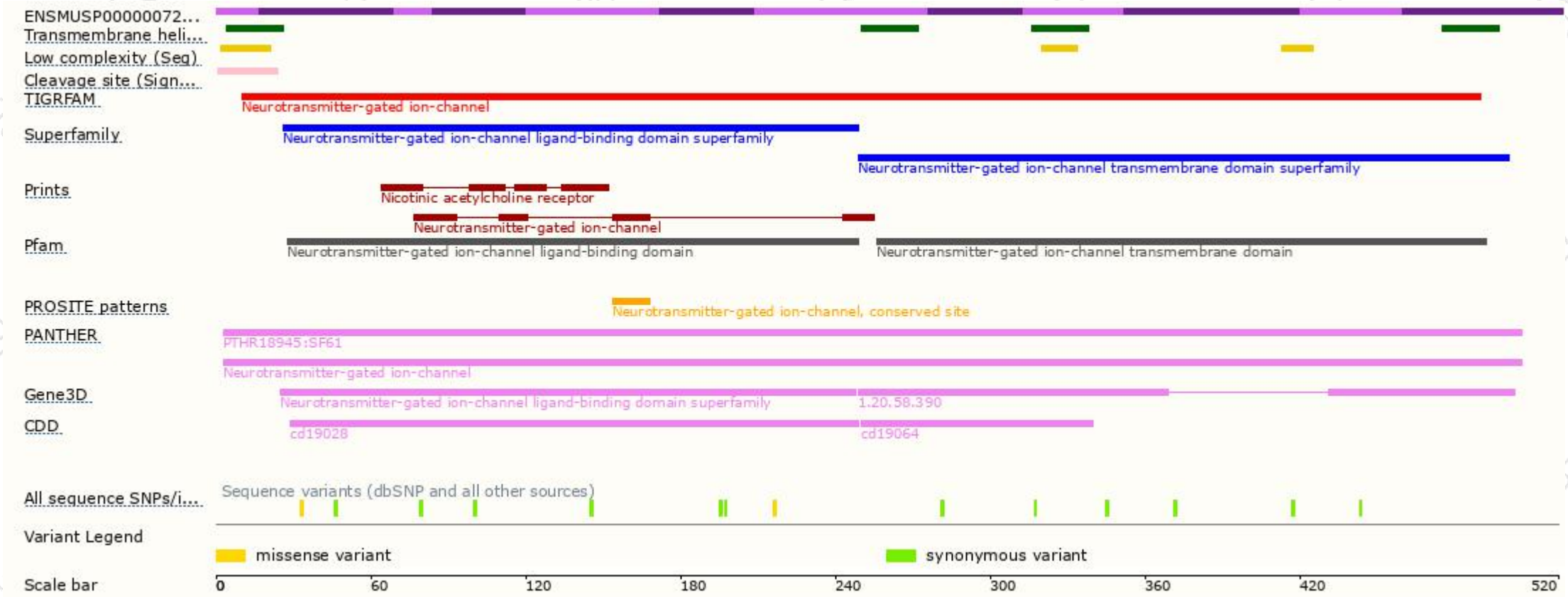
The strategy is based on the design of *Chrnd-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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