Scnn1a Cas9-KO Strategy

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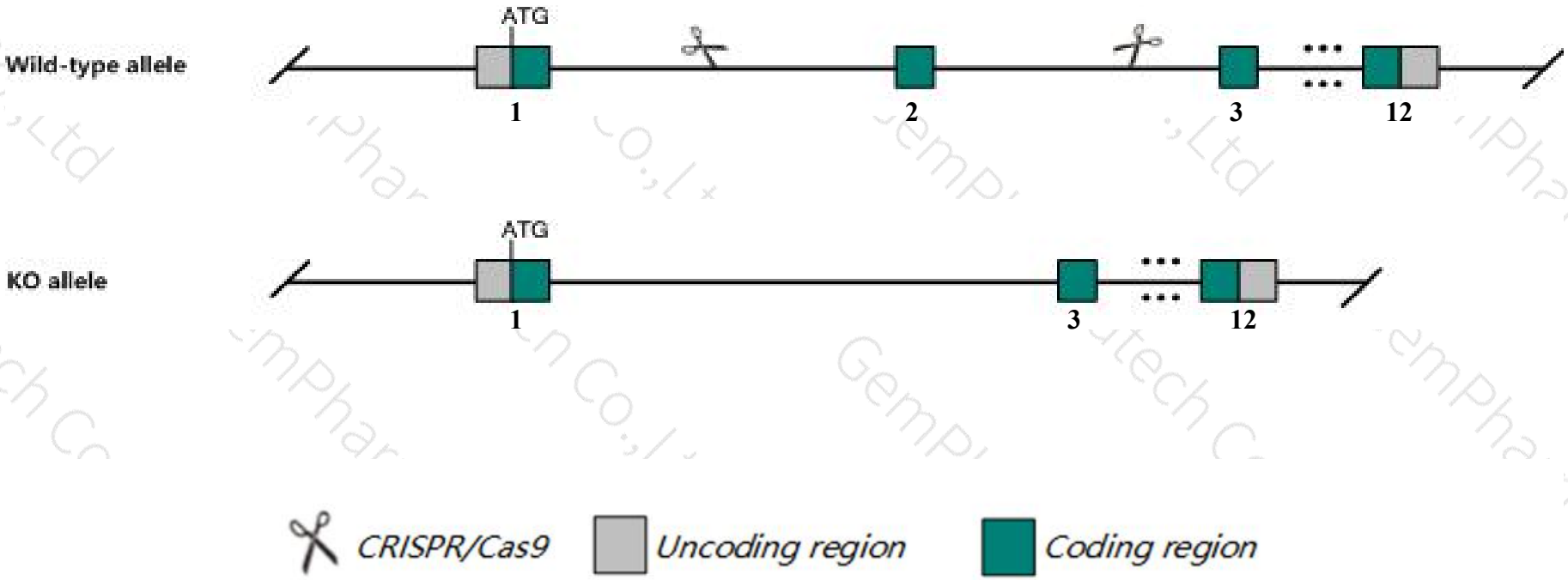
Project Overview

Project Name	***Scnn1a***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Scnn1a* gene. The schematic diagram is as follows:



Technical routes

➢ The *Scnn1a* gene has 7 transcripts. According to the structure of *Scnn1a* gene, exon2 of *Scnn1a-201* (ENSMUST00000081440.13) transcript is recommended as the knockout region.The region contains 274bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Scnn1a* gene. The brief process is as follows: CRISPR/Cas9 syster

Notice

➢ According to the existing MGI data,Homozygotes for targeted null mutations exhibit skin with epithelial hyperplasia, abnormal nuclei, premature lipid secretion, and abnormal keratohyaline granules. Mutants die within 40 hours of birth due to inability to clear their lungs of liquid.

➢ The *Scnn1a* gene is located on the Chr6. 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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Scnn1a sodium channel, nonvoltage-gated 1 alpha [Mus musculus (house mouse)]

Gene ID: 20276, updated on 19-Mar-2019

Summary

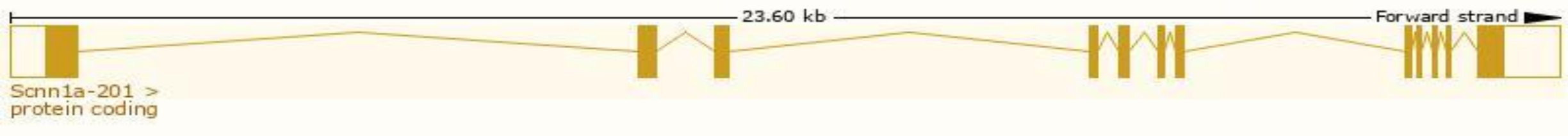
Official Symbol	Scnn1a provided by MGI
Official Full Name	sodium channel, nonvoltage-gated 1 alpha provided by MGI
Primary source	MGI:MGI:101782
See related	Ensembl:ENSMUSG00000030340
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ENaC, SCNEA, Scnn1, mENaC
Expression	Biased expression in lung adult (RPKM 90.9), colon adult (RPKM 43.3) and 8 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

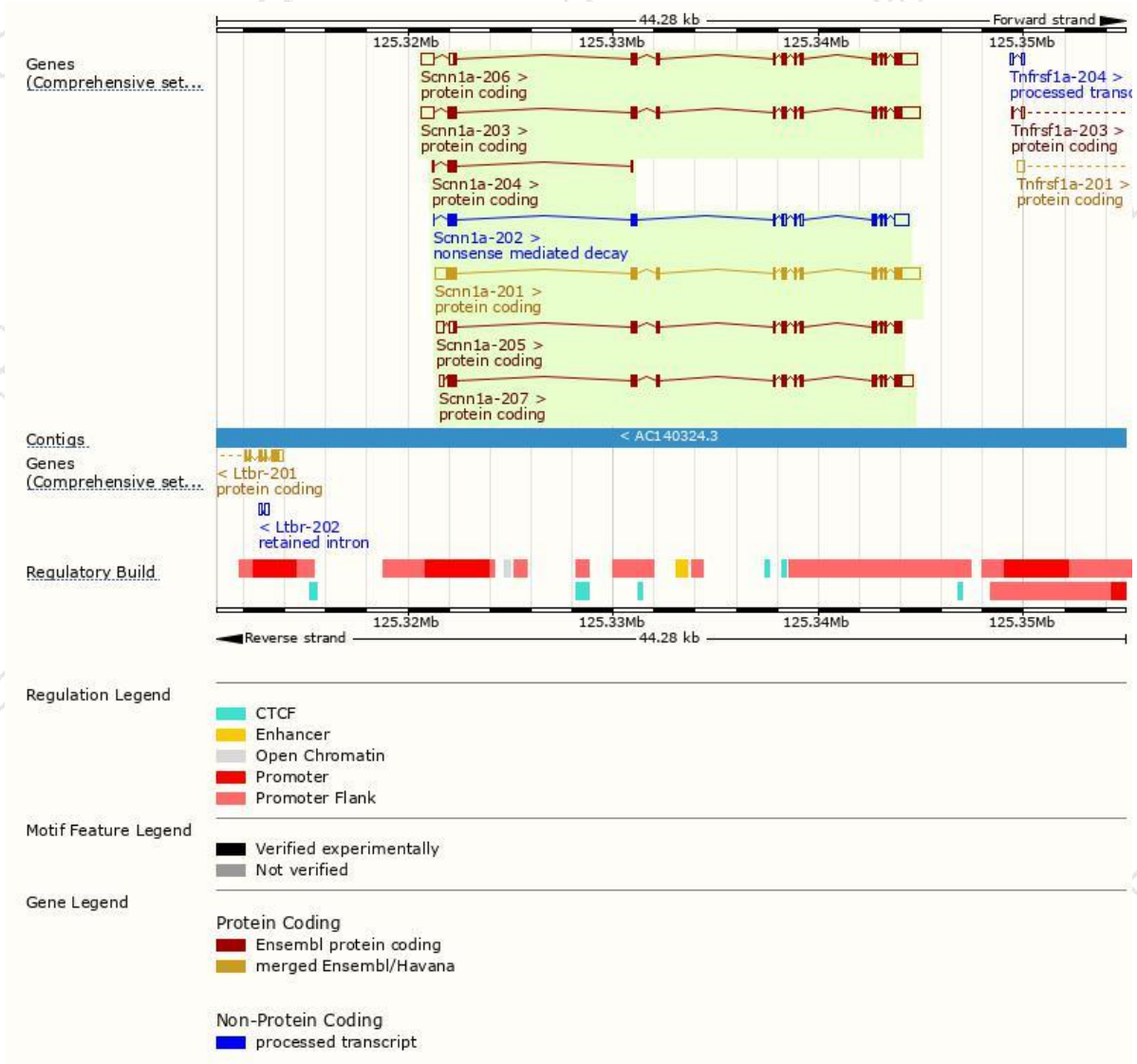
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Scnn1a-201	ENSMUST00000081440.13	3499	700aa	Protein coding	CCDS39641	Q3USG4	TSL:1 GENCODE basic APPRIS P2
Scnn1a-203	ENSMUST00000176110.7	3494	674aa	Protein coding	-	H3BJC3	TSL:5 GENCODE basic APPRIS ALT2
Scnn1a-206	ENSMUST00000176655.7	3354	593aa	Protein coding	-	H3BLI2	TSL:5 GENCODE basic
Scnn1a-207	ENSMUST00000177329.1	2807	674aa	Protein coding	-	H3BJC3	TSL:5 GENCODE basic APPRIS ALT2
Scnn1a-205	ENSMUST00000176442.7	2323	591aa	Protein coding	-	H3BKC4	CDS 3' incomplete TSL:5
Scnn1a-204	ENSMUST00000176365.1	560	143aa	Protein coding	-	H3BKP2	CDS 3' incomplete TSL:5
Scnn1a-202	ENSMUST00000175966.7	2154	275aa	Nonsense mediated decay	-	H3BKW1	TSL:5

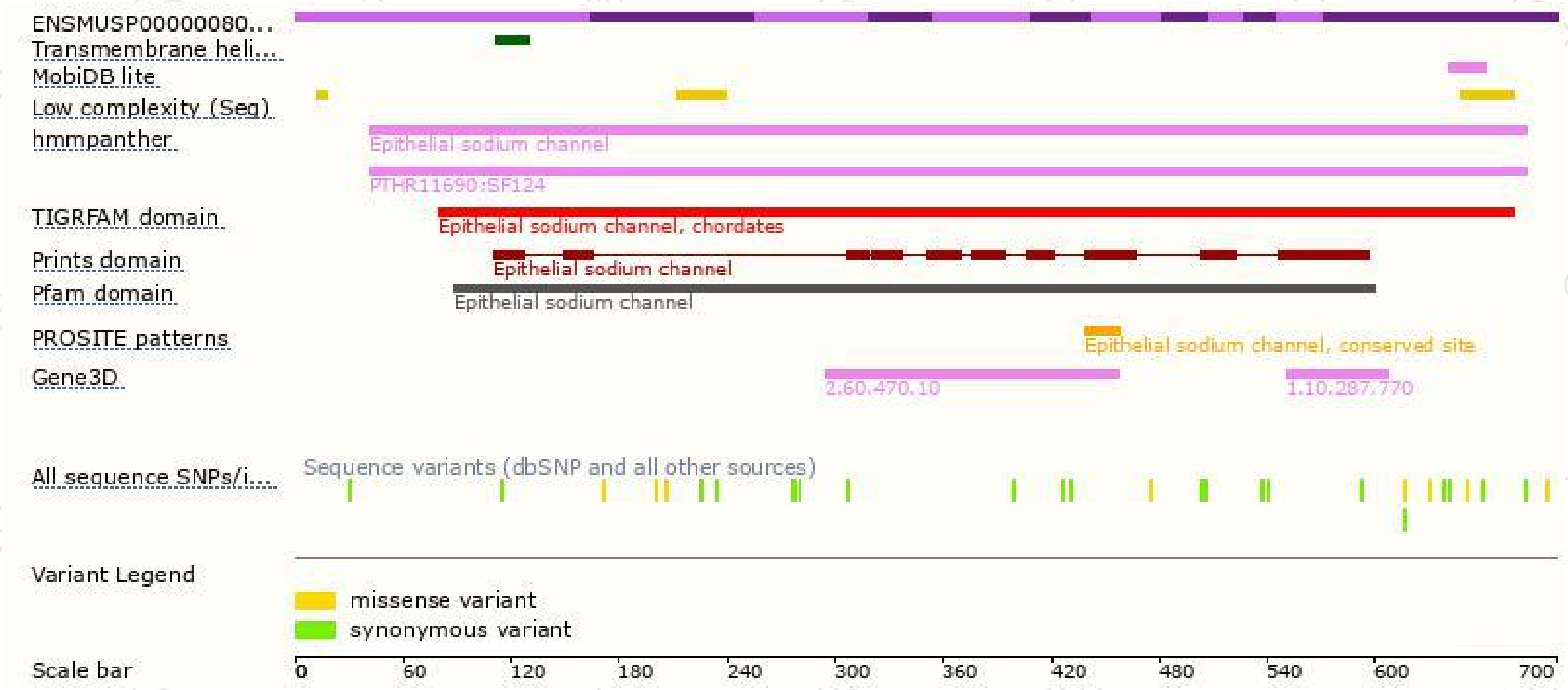
The strategy is based on the design of *Scnn1a-201* transcript,The transcription is shown below



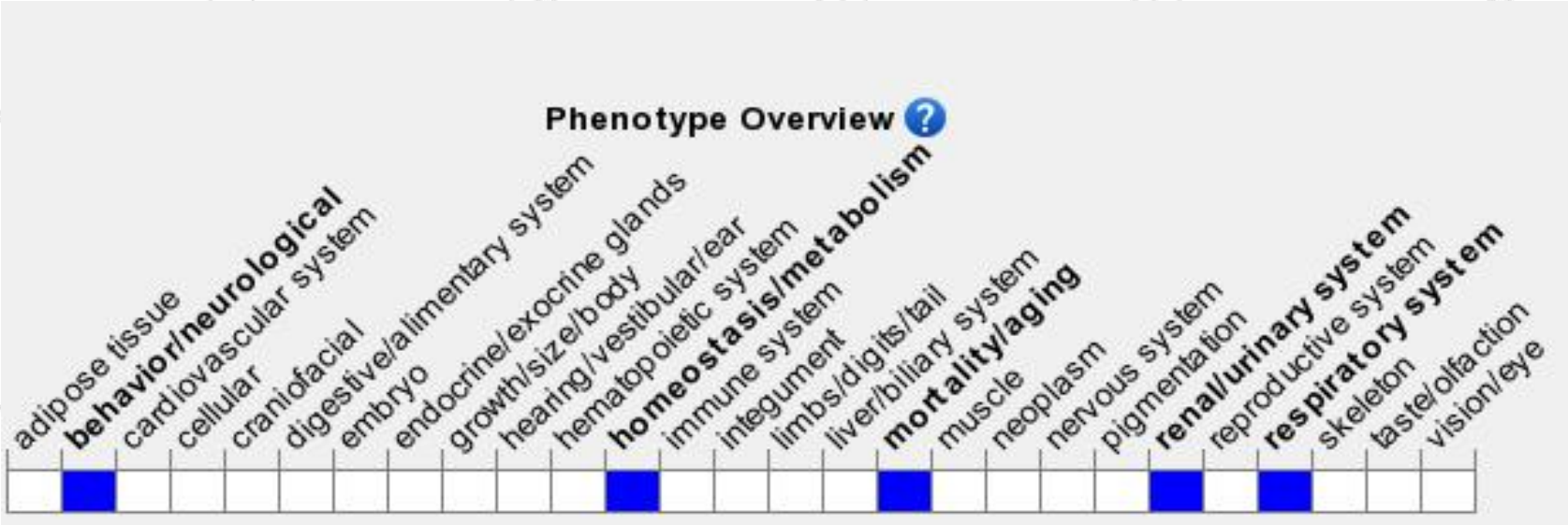
Genomic location distribution



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

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