Insc Cas9-CKO Strategy

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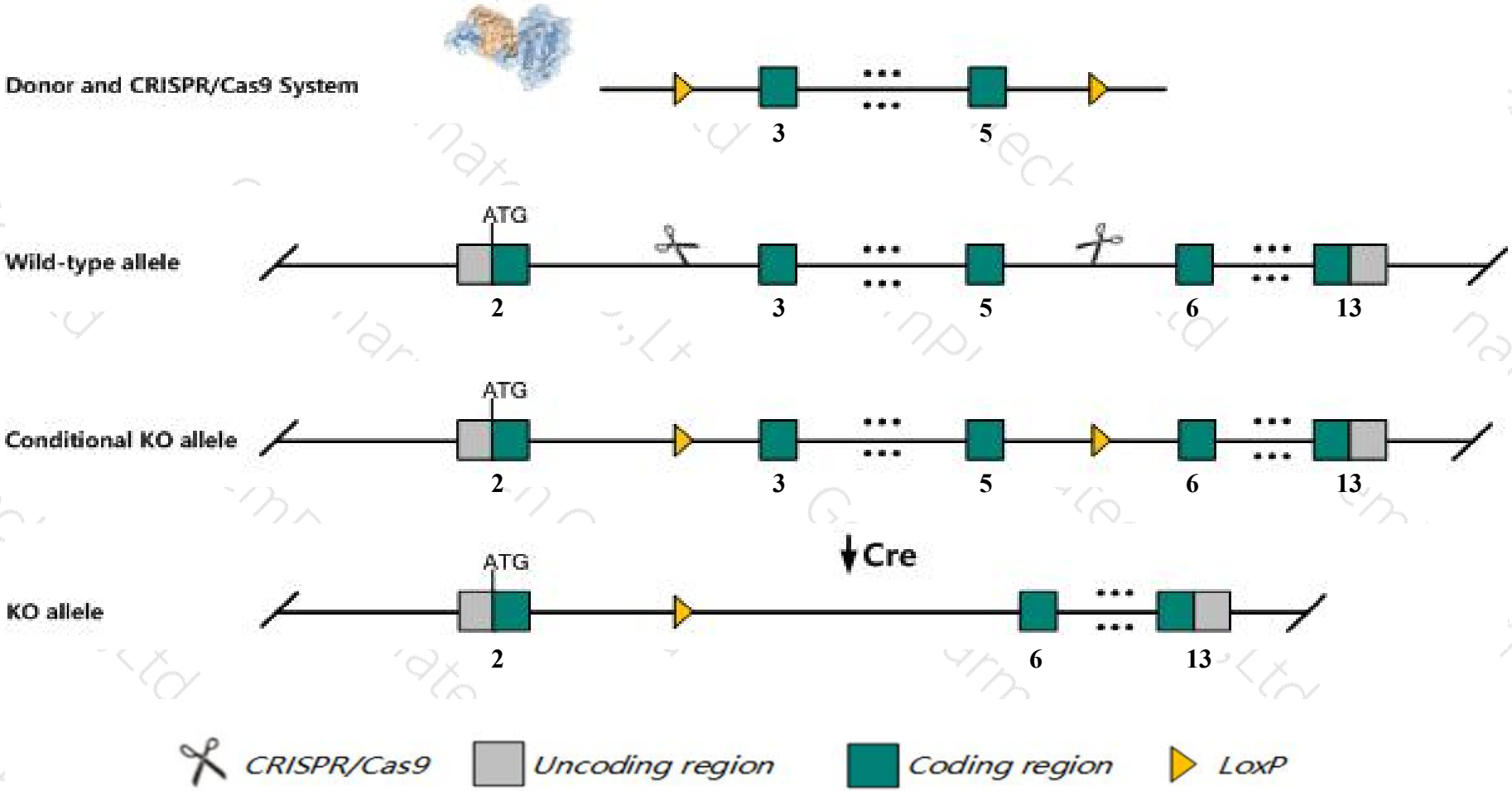
Project Overview

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

Conditional Knockout strategy

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



Technical routes

- The *Insc* gene has 9 transcripts. According to the structure of *Insc* gene, exon3-exon5 of *Insc-208* (ENSMUST00000169913.7) transcript is recommended as the knockout region.The region contains 523bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Insc* 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 inactivation of this gene leads to abnormal cochlear hair cell morphology.

- The *Insc* gene is located on the Chr7. 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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Insc INSC spindle orientation adaptor protein [*Mus musculus* (house mouse)]

Gene ID: 233752, updated on 17-Dec-2019

Summary

Official Symbol	Insc provided by MGI
Official Full Name	INSC spindle orientation adaptor protein provided by MGI
Primary source	MGI:MGI:1917942
See related	Ensembl:ENSMUSG00000048782
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	C730020D23; 3830422K02Rik
Expression	Broad expression in liver adult (RPKM 5.3), liver E18 (RPKM 3.5) and 21 other tissues See more
Orthologs	human all

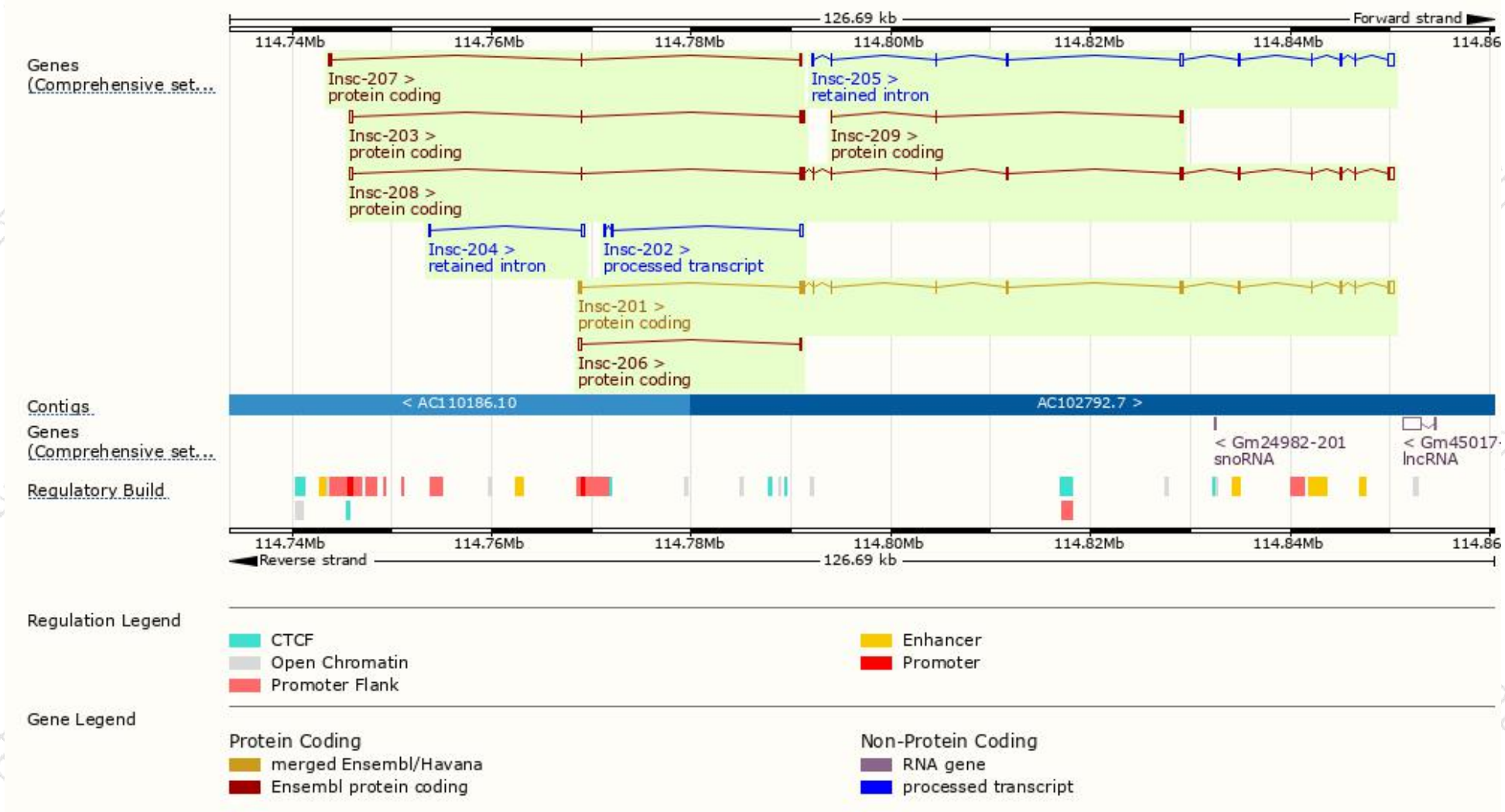
Transcript information（Ensembl）

The gene has 9 transcripts,all transcripts are shown below:

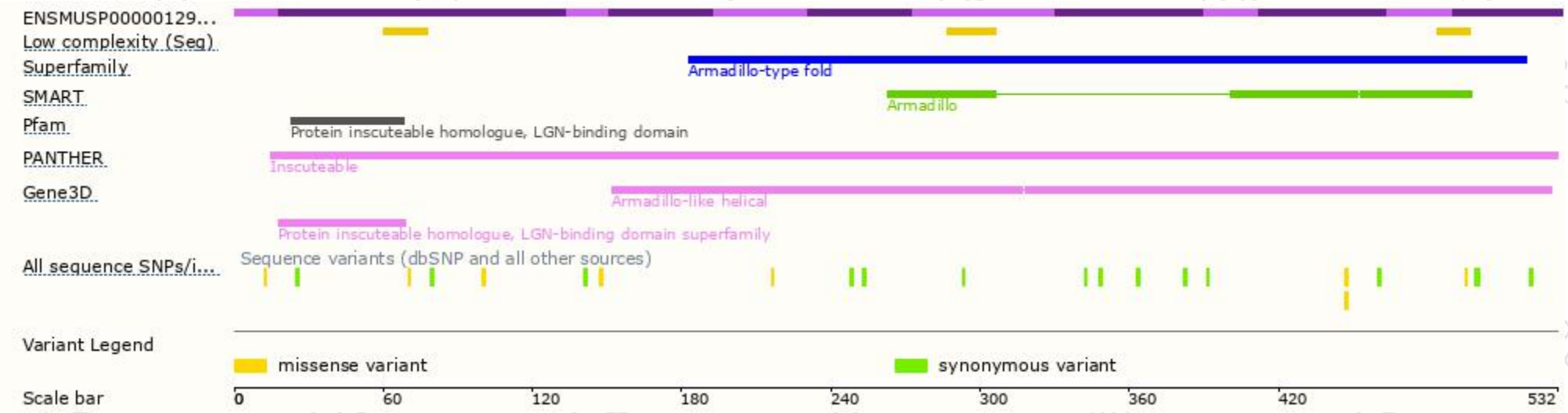
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Insc-208	ENSMUST00000169913.7	2321	532aa	Protein coding	CCDS40095	G3UW77	TSL:5 GENCODE basic APPRIS P1
Insc-201	ENSMUST00000117543.2	2170	532aa	Protein coding	CCDS40095	G3UW77	TSL:5 GENCODE basic APPRIS P1
Insc-203	ENSMUST00000136645.7	713	133aa	Protein coding	-	D3Z267	CDS 3' incomplete TSL:2
Insc-207	ENSMUST00000161800.1	451	88aa	Protein coding	-	E0CXR9	CDS 3' incomplete TSL:5
Insc-209	ENSMUST00000206274.1	405	135aa	Protein coding	-	A0A0U1RNN4	CDS 5' and 3' incomplete TSL:3
Insc-206	ENSMUST00000151464.1	363	53aa	Protein coding	-	D3Z5D7	CDS 3' incomplete TSL:1
Insc-202	ENSMUST00000136347.1	439	No protein	Processed transcript	-	-	TSL:1
Insc-205	ENSMUST00000150991.2	1826	No protein	Retained intron	-	-	TSL:1
Insc-204	ENSMUST00000139670.1	600	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Insc-208* transcript,The transcription is shown below

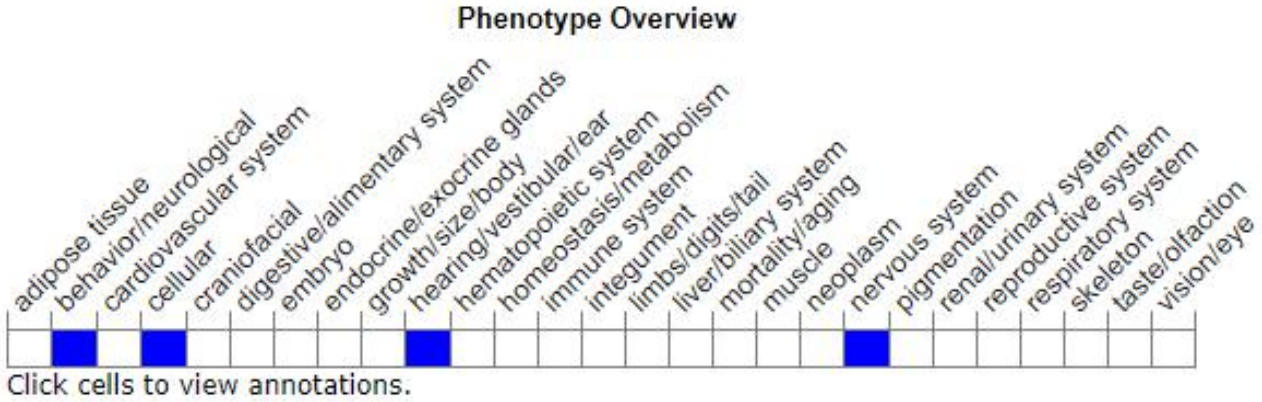
Genomic location distribution



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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