

***Anks6* Cas9-KO Strategy**

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Reviewer:

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Design Date:

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Project Overview

Project Name

Anks6

Project type

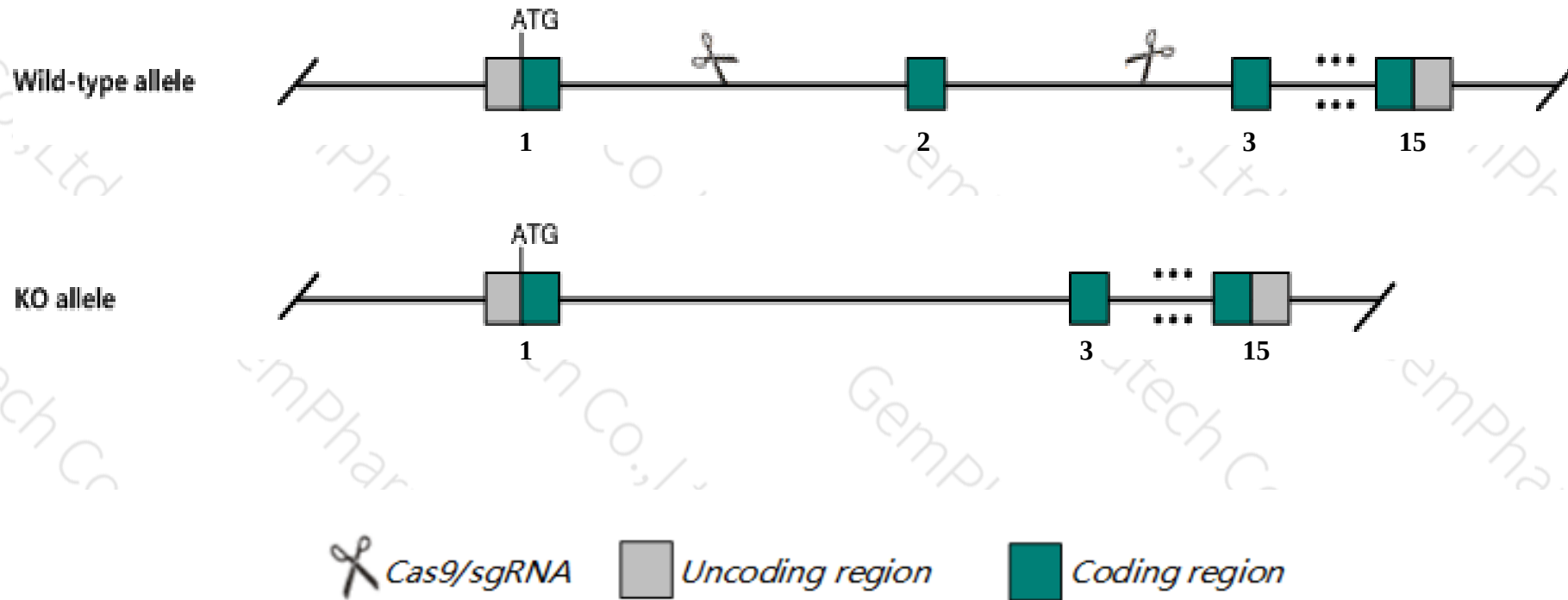
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Anks6* gene. The schematic diagram is as follows:



- The *Anks6* gene has 5 transcripts. According to the structure of *Anks6* gene, exon2 of *Anks6*-201(ENSMUST00000084616.2) transcript is recommended as the knockout region. The region contains 503bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Anks6* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, mice homozygous for an ENU-induced mutation exhibit complex congenital heart defects including TGA, DORV and septal defects associated with heterotaxy.
- The *Anks6* gene is located on the Chr4. 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)

Anks6 ankyrin repeat and sterile alpha motif domain containing 6 [Mus musculus (house mouse)]

Gene ID: 75691, updated on 13-Mar-2020

Summary



Official Symbol	Anks6 provided by MGI
Official Full Name	ankyrin repeat and sterile alpha motif domain containing 6 provided by MGI
Primary source	MGI:MGI:1922941
See related	Ensembl:ENSMUSG00000066191
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	2210417J20Rik, Ankrd14, Gm635, SamCystin, Samd6, b2b1801.1Clo
Expression	Ubiquitous expression in ovary adult (RPKM 4.2), CNS E18 (RPKM 3.6) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

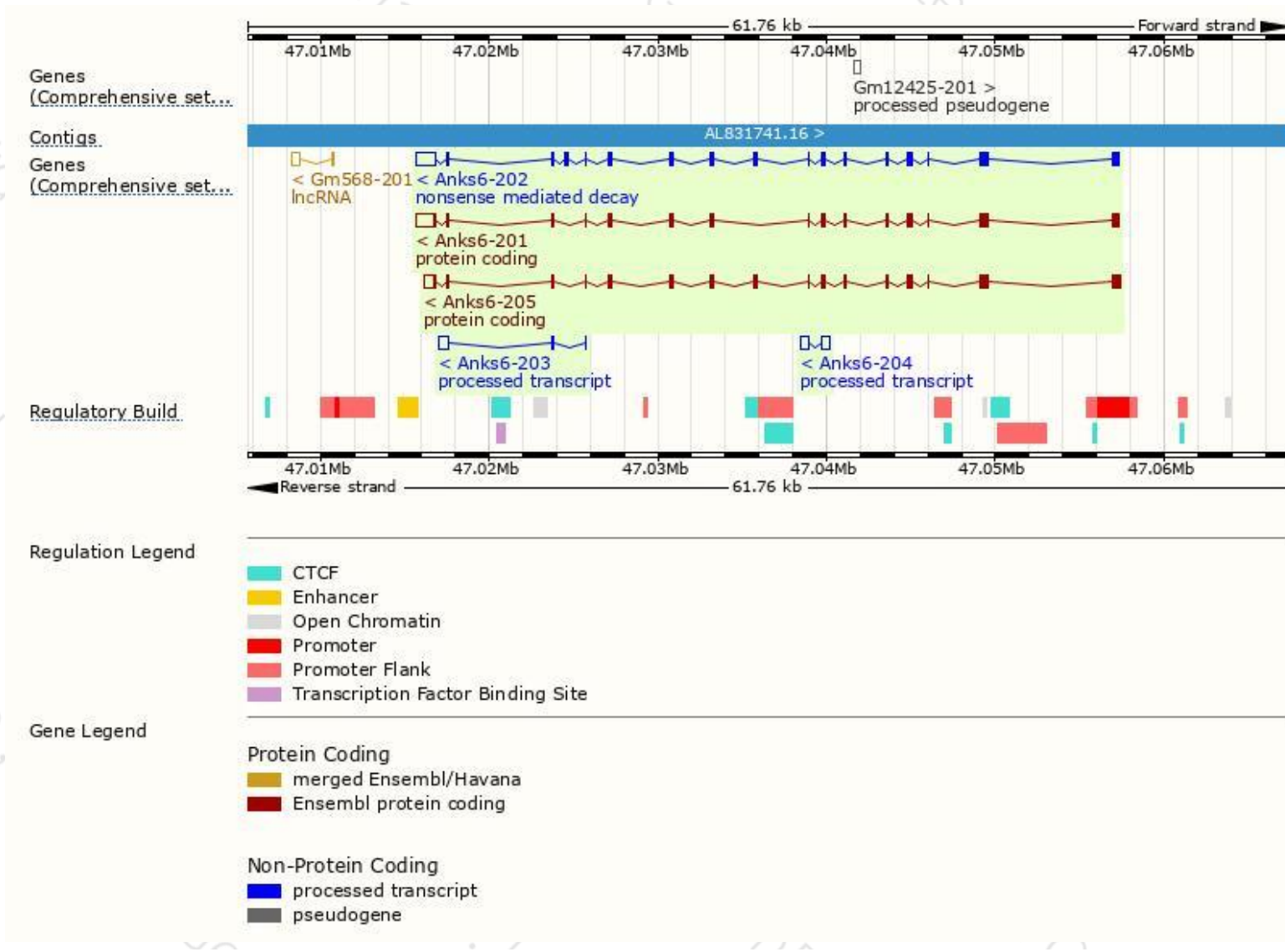
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Anks6-201	ENSMUST00000084616.2	3552	815aa	Protein coding	CCDS18157	E9PUD3	TSL:5 GENCODE basic APPRIS P2
Anks6-205	ENSMUST00000229609.1	3438	883aa	Protein coding	-	Q6GQX6	GENCODE basic APPRIS ALT2
Anks6-202	ENSMUST00000107747.7	3980	815aa	Nonsense mediated decay	-	A2ANT9	TSL:1
Anks6-204	ENSMUST00000154664.1	1013	No protein	Processed transcript	-	-	TSL:2
Anks6-203	ENSMUST00000152479.1	762	No protein	Processed transcript	-	-	TSL:5

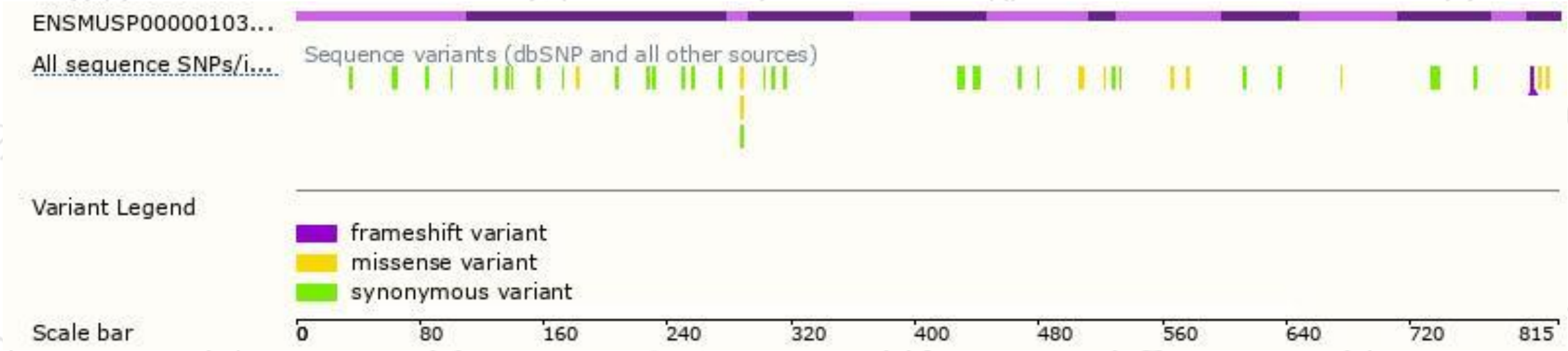
The strategy is based on the design of *Anks6-201* transcript,the transcription is shown below:



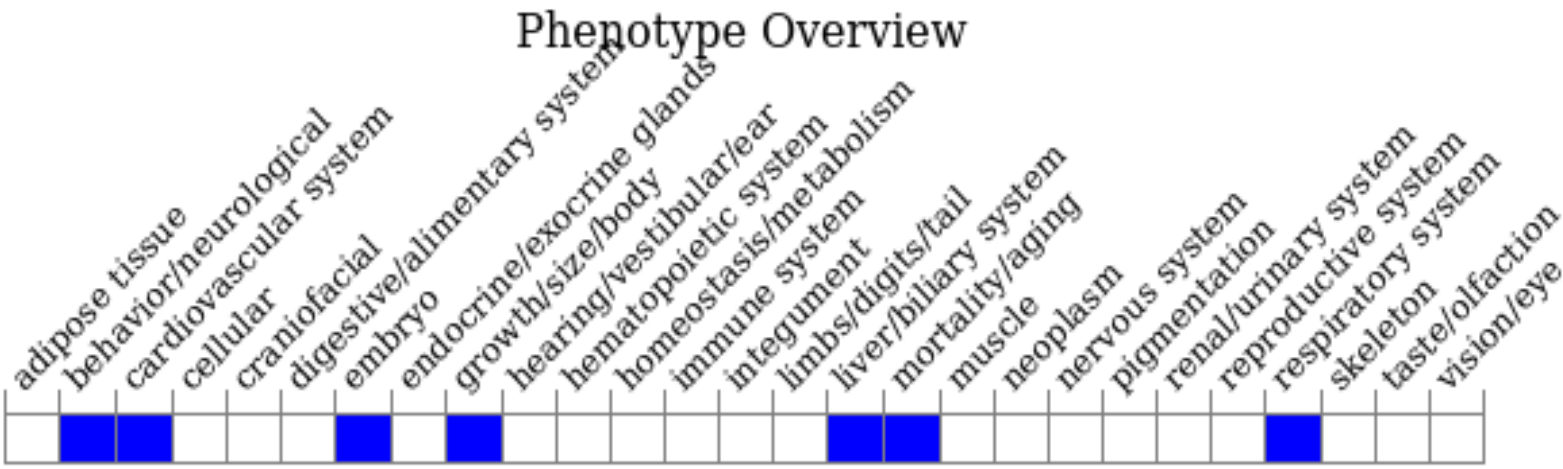
Genomic location distribution



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,mice homozygous for an ENU-induced mutation exhibit complex congenital heart defects including TGA, DORV and septal defects associated with heterotaxy.

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

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