Satb2 Cas9-KO Strategy

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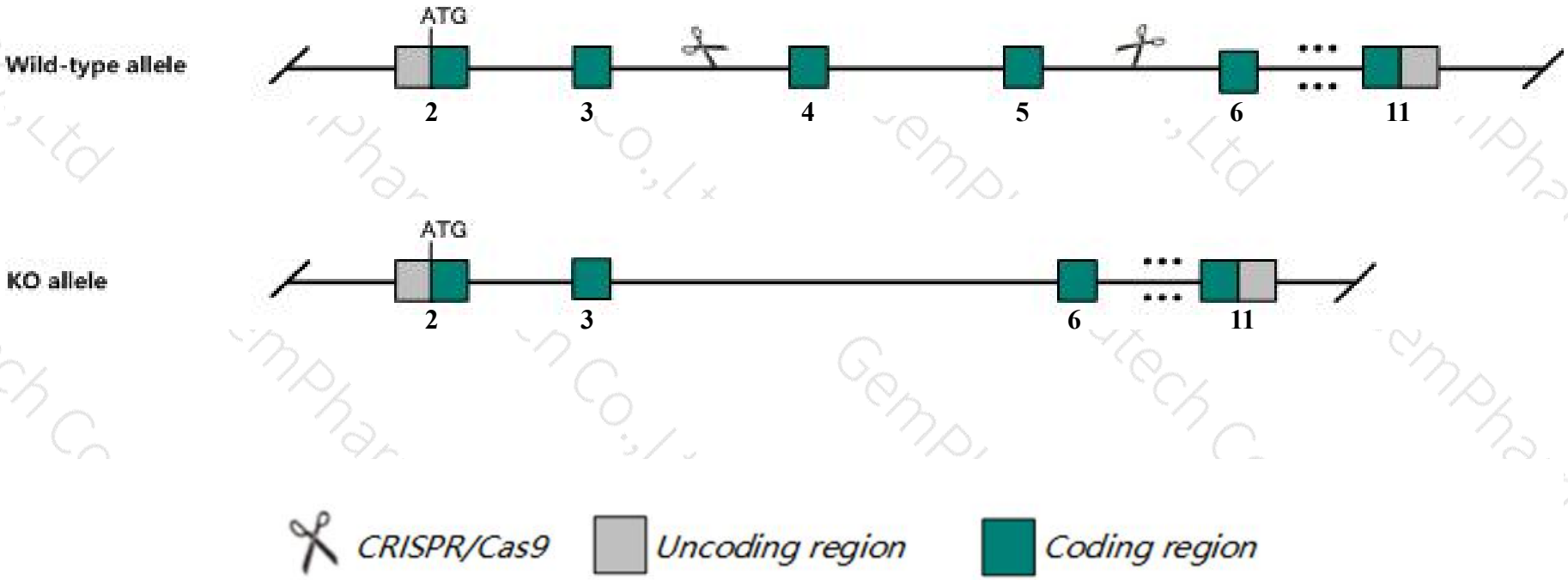
Project Overview

Project Name	***Satb2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Satb2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Satb2* gene has 5 transcripts. According to the structure of *Satb2* gene, exon4-exon5 of *Satb2-202* (ENSMUST00000114415.9) transcript is recommended as the knockout region.The region contains 251bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Satb2* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Homozygous inactivation of this gene causes complete perinatal lethality and craniofacial anomalies, such as cleft palate, micrognathia, microcephaly, decreased tongue size, absent incisors and nasal capsule hypoplasia, and leads to short limbs and defects in osteoblast differentiation and function.
- Transcript *Satb2-203,204,205* may not be affected.
- The *Satb2* 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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Satb2 special AT-rich sequence binding protein 2 [*Mus musculus* (house mouse)]

Gene ID: 212712, updated on 17-Sep-2019

Summary

Official Symbol	Satb2 provided by MGI
Official Full Name	special AT-rich sequence binding protein 2 provided by MGI
Primary source	MGI:MGI:2679336
See related	Ensembl:ENSMUSG00000038331
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	BAP002; mKIAA1034
Expression	Biased expression in colon adult (RPKM 11.8), CNS E18 (RPKM 11.0) and 8 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

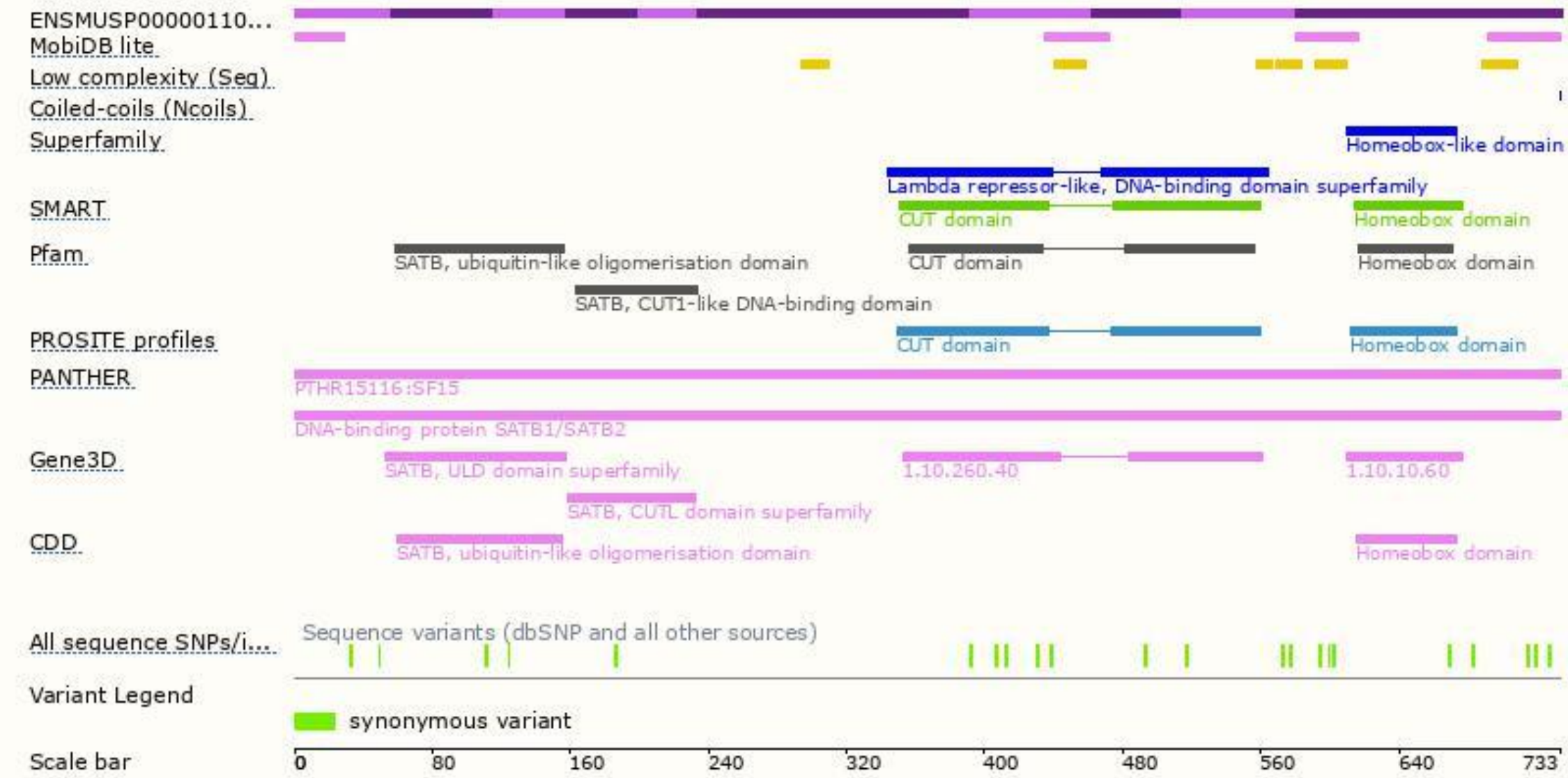
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Satb2-202	ENSMUST00000114415.9	5805	733aa	Protein coding	CCDS14965	Q546B3 Q8VI24	TSL:1 GENCODE basic APPRIS P1
Satb2-201	ENSMUST00000042857.13	6277	674aa	Protein coding	-	Q8VI24	TSL:1 GENCODE basic
Satb2-205	ENSMUST00000177424.1	4694	615aa	Protein coding	-	H3BKH3	TSL:5 GENCODE basic
Satb2-204	ENSMUST00000177282.1	454	27aa	Protein coding	-	H3BKV4	CDS 3' incomplete TSL:3
Satb2-203	ENSMUST00000176759.1	331	104aa	Protein coding	-	H3BJX4	CDS 3' incomplete TSL:3

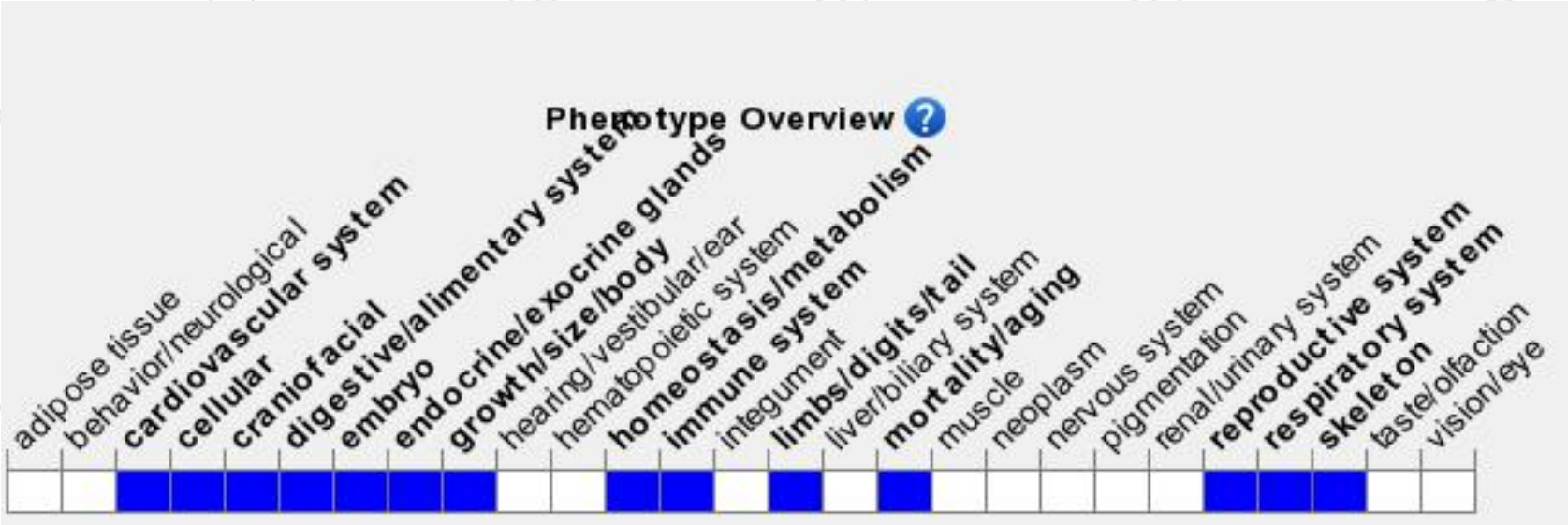
The strategy is based on the design of *Satb2-202* transcript,The transcription is shown below

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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