Smyd5 Cas9-CKO Strategy

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Project Overview

Project Name	***Smyd5***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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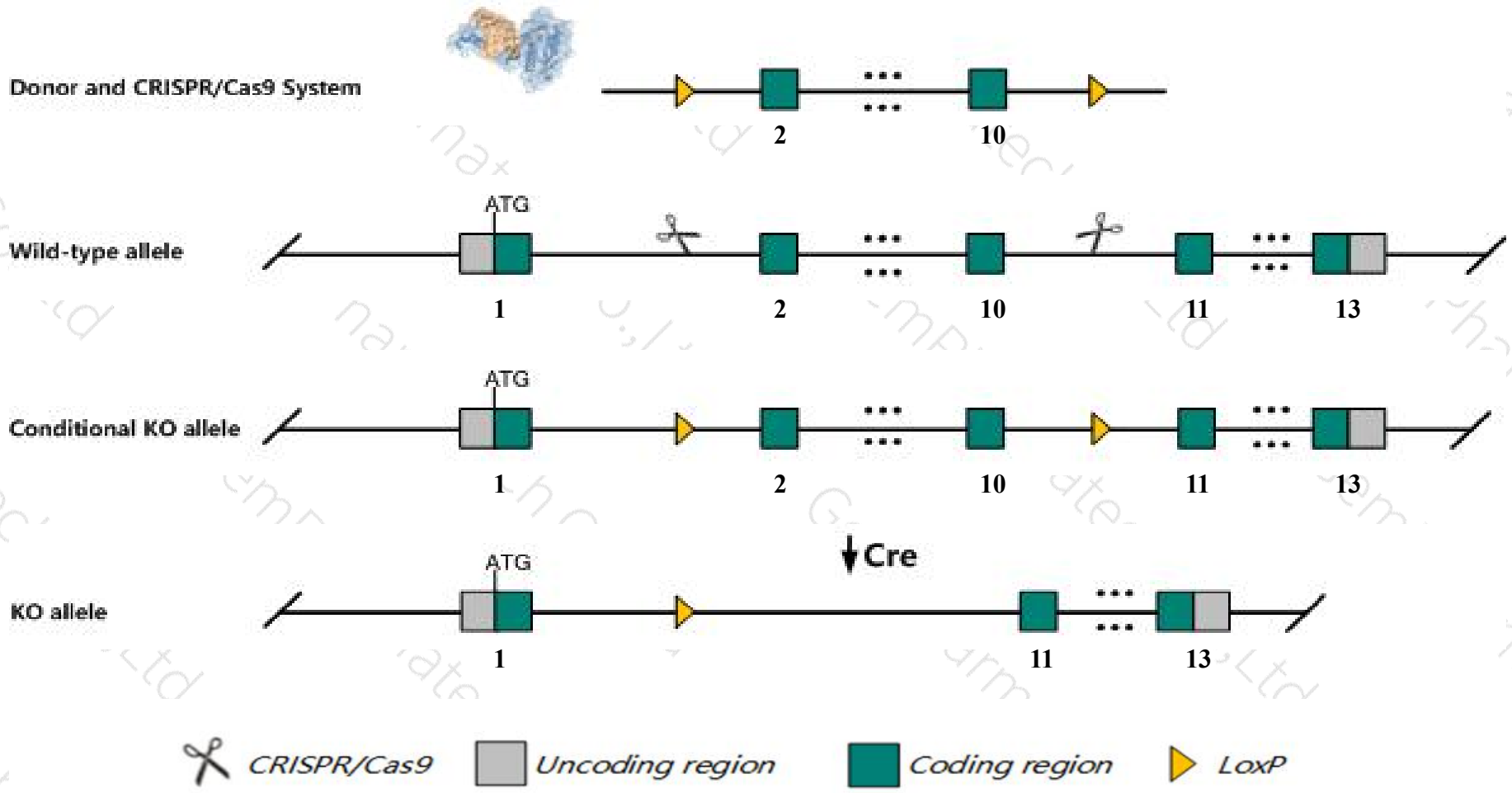
This model will use CRISPR/Cas9 technology to edit the *Smyd5* gene. The schematic diagram is as follows:



Technical routes

- The *Smyd5* gene has 8 transcripts. According to the structure of *Smyd5* gene, exon2-exon10 of *Smyd5-201* (ENSMUST00000045693.7) transcript is recommended as the knockout region.The region contains 841bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Smyd5* 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

- The *Smyd5* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Smyd5 SET and MYND domain containing 5 [Mus musculus (house mouse)]

Gene ID: 232187, updated on 13-Mar-2020

Summary

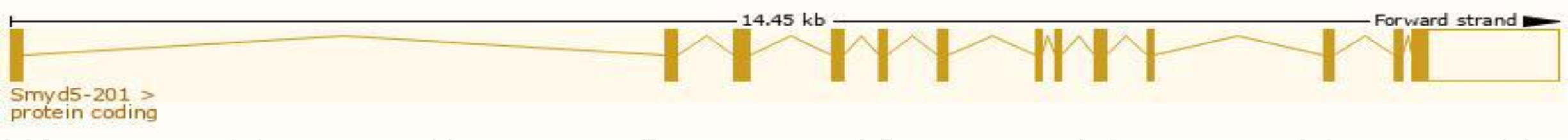
Official Symbol	Smyd5 provided by MGI
Official Full Name	SET and MYND domain containing 5 provided byMGI
Primary source	MGI:MGI:108048
See related	Ensembl:ENSMUSG00000033706
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW536703, NN8-4AG, Rai15, Rrg1
Expression	Ubiquitous expression in CNS E18 (RPKM 20.8), limb E14.5 (RPKM 19.3) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

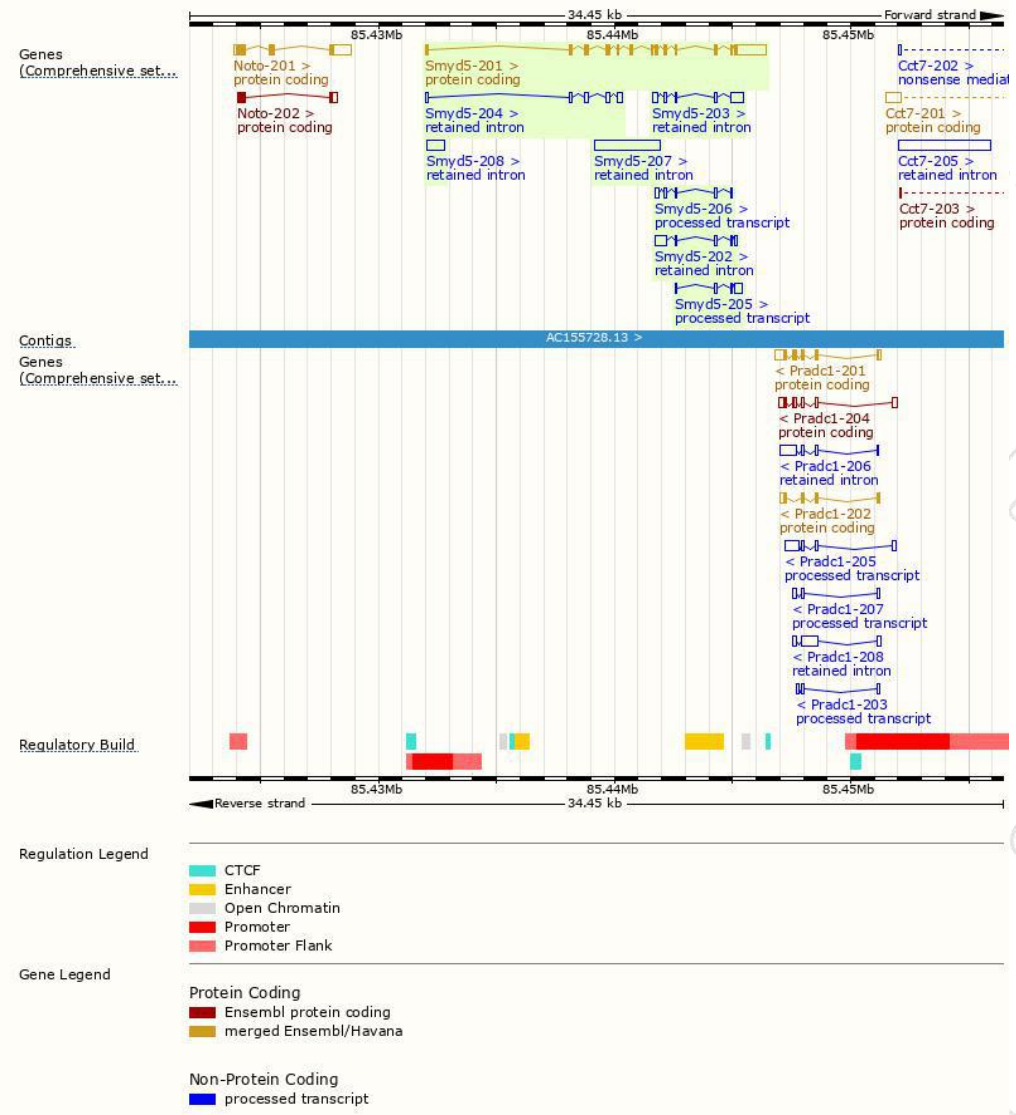
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Smyd5-201	ENSMUST00000045693.7	2486	416aa	Protein coding	CCDS51827	Q3TYX3	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Smyd5-205	ENSMUST00000153749.1	613	No protein	Processed transcript	-	-	TSL:2
Smyd5-206	ENSMUST00000156322.7	477	No protein	Processed transcript	-	-	TSL:3
Smyd5-207	ENSMUST00000204428.1	2812	No protein	Retained intron	-	-	TSL:NA
Smyd5-203	ENSMUST00000134405.7	964	No protein	Retained intron	-	-	TSL:5
Smyd5-202	ENSMUST00000130928.7	830	No protein	Retained intron	-	-	TSL:2
Smyd5-208	ENSMUST00000204615.1	746	No protein	Retained intron	-	-	TSL:NA
Smyd5-204	ENSMUST00000152218.1	704	No protein	Retained intron	-	-	TSL:2

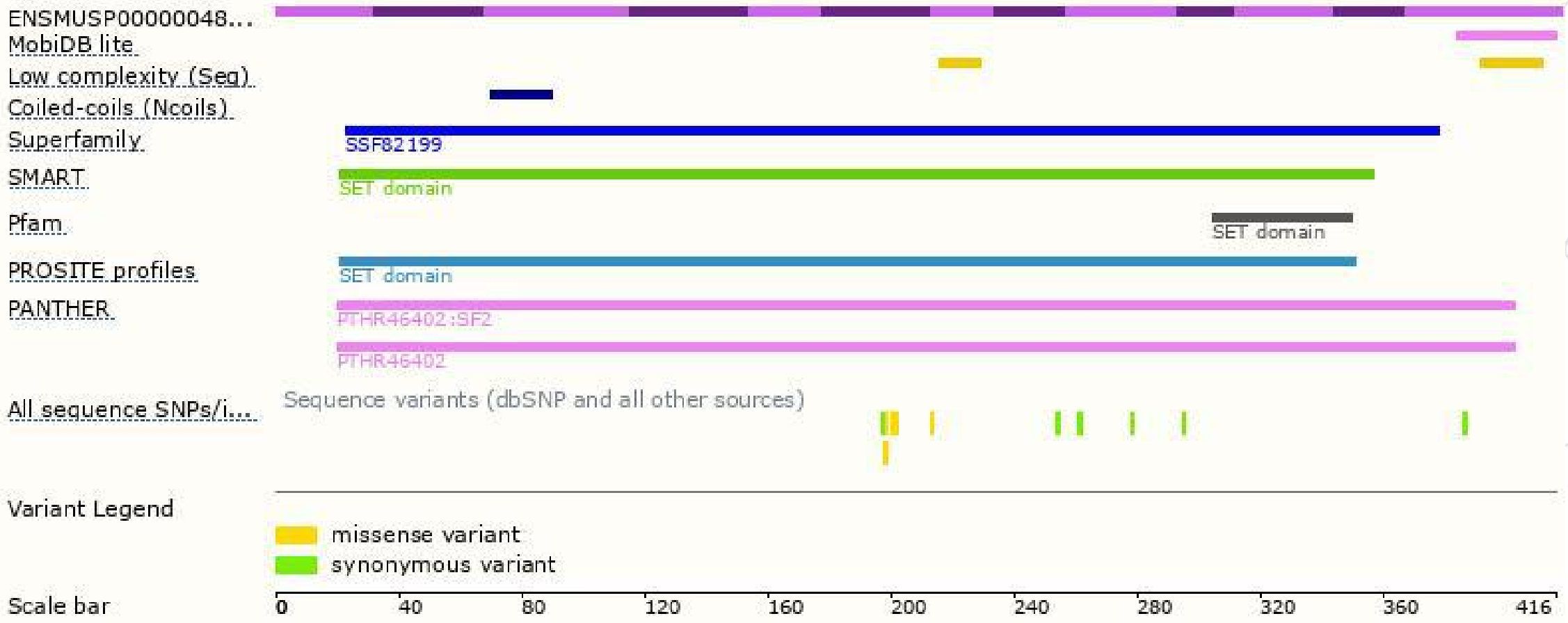
The strategy is based on the design of *Smyd5-201* transcript,the transcription is shown below



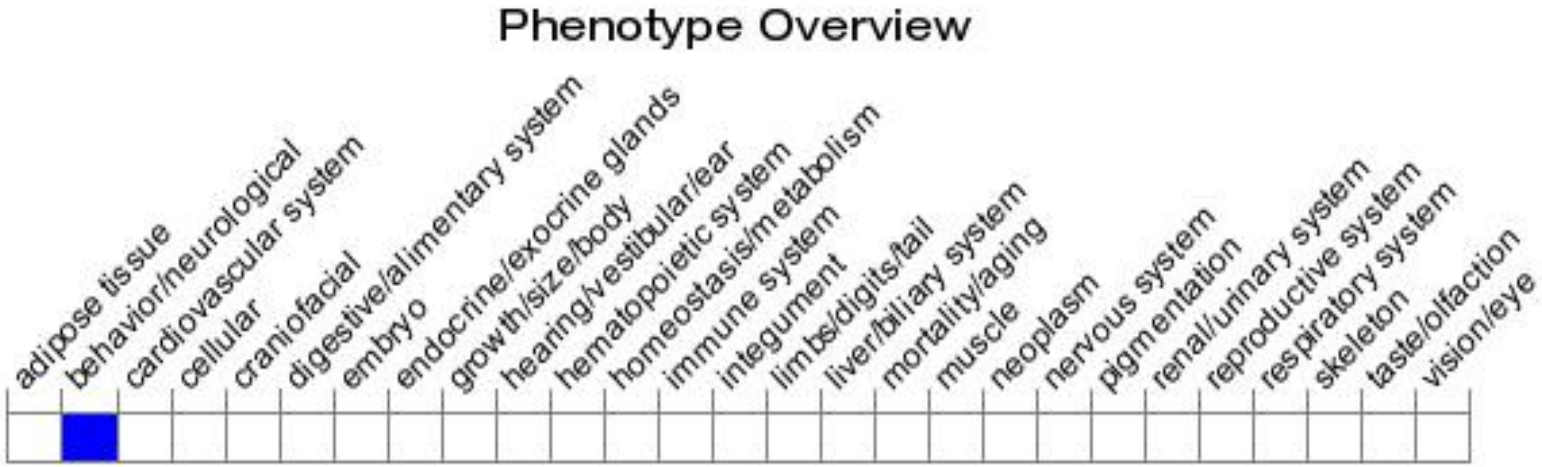
Genomic location distribution



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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