Rab1b Cas9-KO Strategy

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Design Date: **2020-4-26**

Project Overview

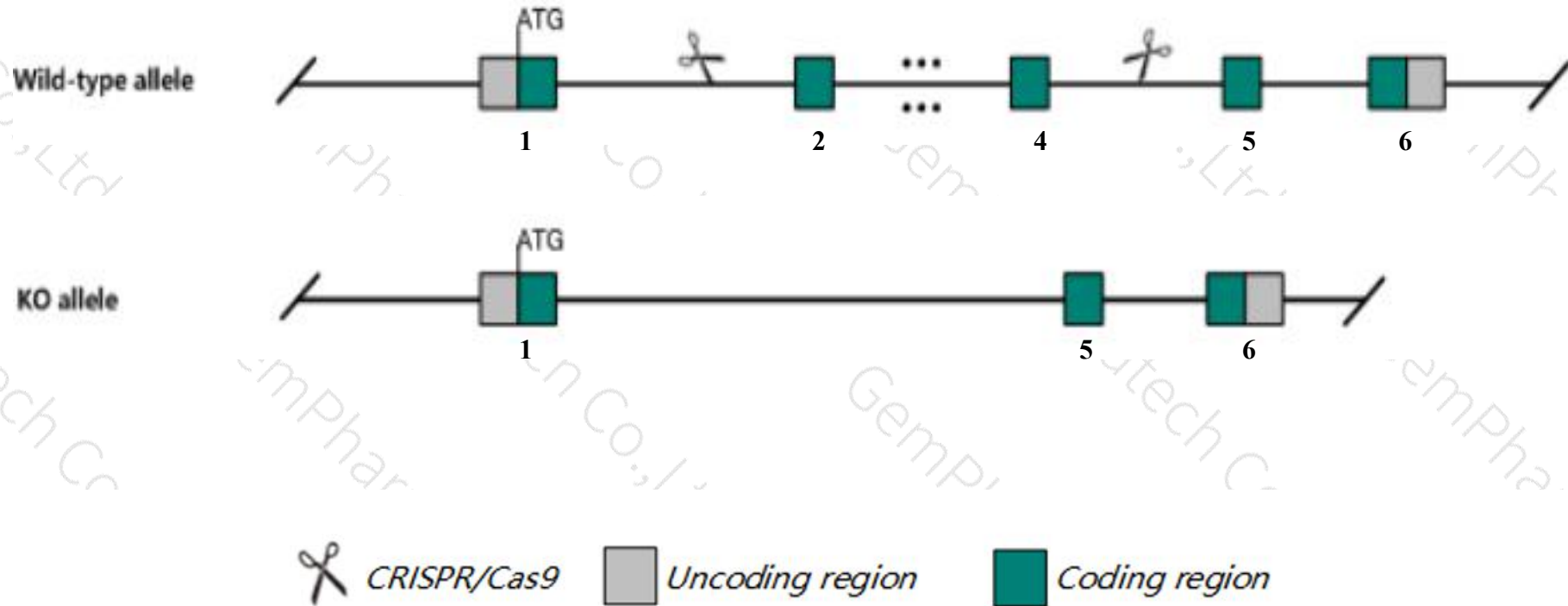|	
Project Name	*Rab1b*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rab1b* gene. The schematic diagram is as follows:

Technical routes

➢ The *Rab1b* gene has 4 transcripts. According to the structure of *Rab1b* gene, exon2-exon4 of *Rab1b-201* (ENSMUST00000025804.6) transcript is recommended as the knockout region.The region contains 265bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rab1b* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,mice homozygous for a gene trap insertion do not exhibit a detectable mutant phenotype.

➢ The *Rab1b* gene is located on the Chr19. 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）

Rab1b RAB1B, member RAS oncogene family [Mus musculus (house mouse)]

Gene ID: 76308, updated on 13-Mar-2020

Summary

|	
Official Symbol	Rab1b provided by MGI
Official Full Name	RAB1B, member RAS oncogene family provided by MGI
Primary source	MGI:MGI:1923558
See related	Ensembl:ENSMUSG00000024870
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	1110011F09Rik
Expression	Ubiquitous expression in subcutaneous fat pad adult (RPKM 59.5), genital fat pad adult (RPKM 55.0) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rab1b-201	ENSMUST00000025804.6	1913	201aa	Protein coding	CCDS29452	Q0PD66 Q9D1G1	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
Rab1b-203	ENSMUST00000237201.1	826	254aa	Protein coding	-	A0A494B945	CDS 3' incomplete
Rab1b-202	ENSMUST00000236149.1	757	189aa	Protein coding	-	A0A494BBL7	GENCODE basic
Rab1b-204	ENSMUST00000237438.1	657	182aa	Protein coding	-	A0A494BA38	GENCODE basic

The strategy is based on the design of *Rab1b-201* transcript,the transcription is shown below:

< Rab1b-201
protein coding

◄ Reverse strand

7.87 kb
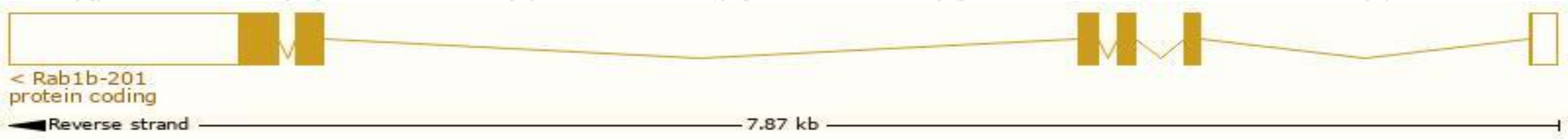
Genomic location distribution
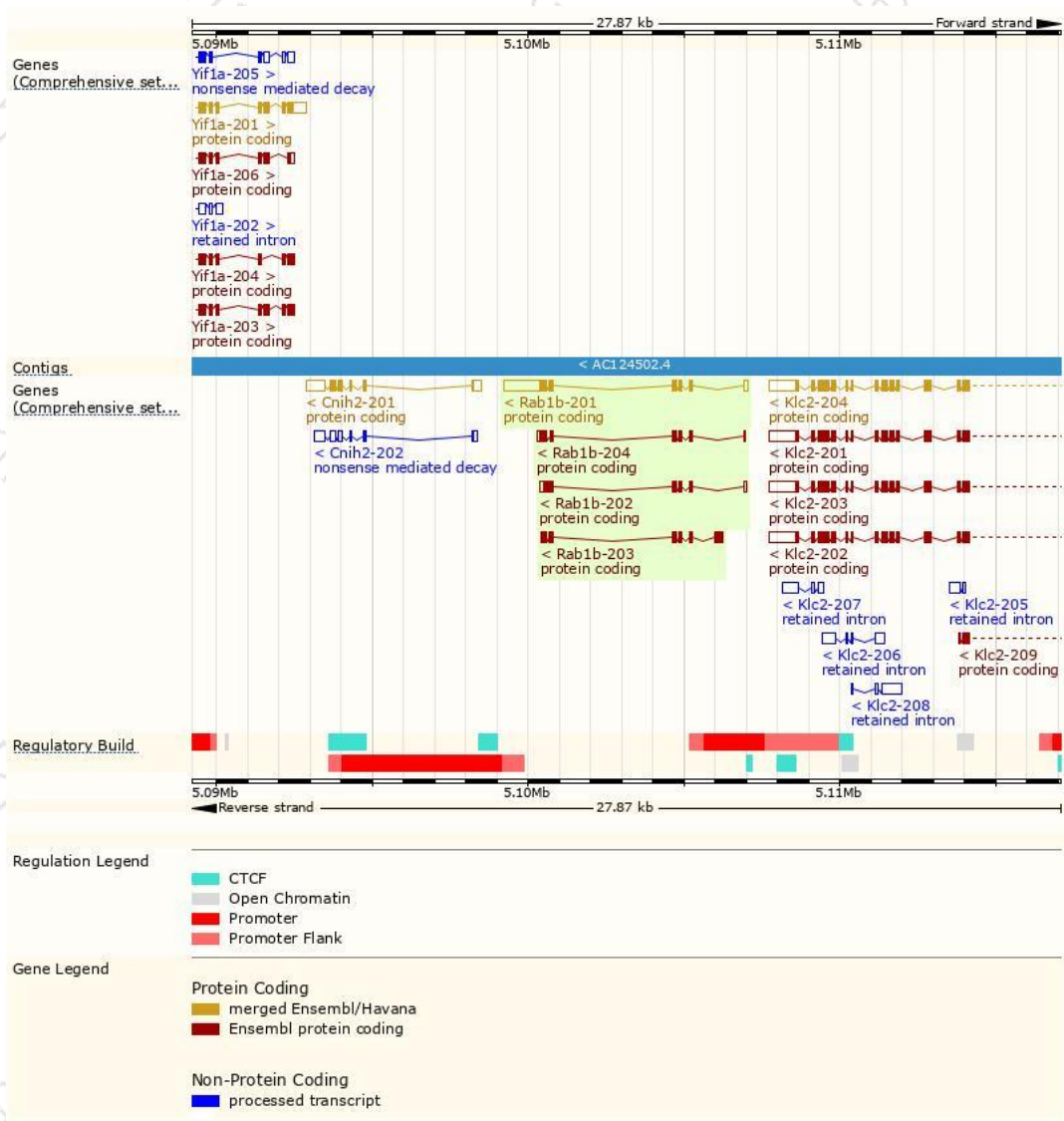
Protein domain

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