

***Bud13* Cas9-KO Strategy**

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Project Overview

Project Name

Bud13

Project type

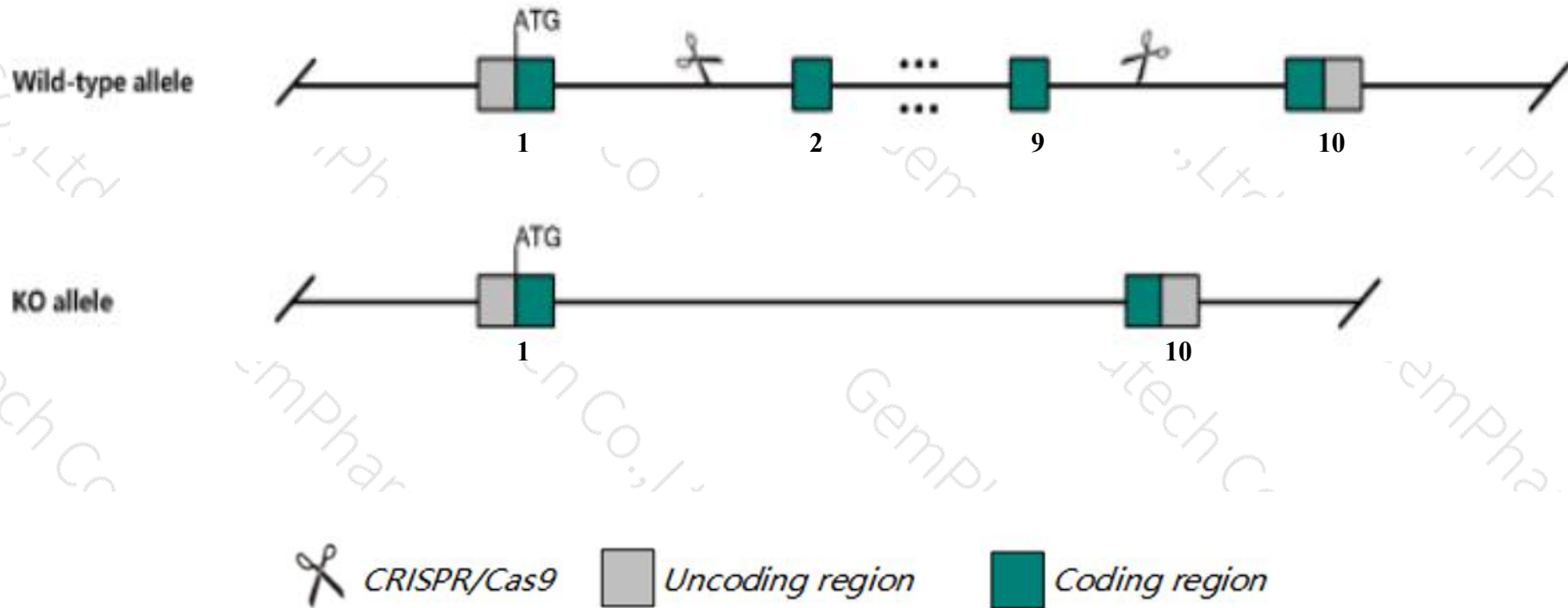
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bud13* gene. The schematic diagram is as follows:



- The *Bud13* gene has 6 transcripts. According to the structure of *Bud13* gene, exon2-exon9 of *Bud13-201* (ENSMUST00000074957.4) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bud13* gene. The brief process is as follows: CRISPR/Cas9 system

- The effect on transcript *Bud13*-206 is unknown.
- The *Bud13* gene is located on the Chr9. 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)

Bud13 BUD13 homolog [Mus musculus (house mouse)]

Gene ID: 215051, updated on 13-Mar-2020

Summary



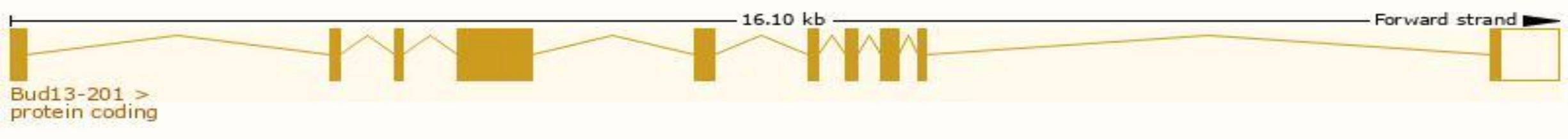
Official Symbol	Bud13 provided by MGI
Official Full Name	BUD13 homolog provided by MGI
Primary source	MGI:MGI:2443443
See related	Ensembl:ENSMUSG00000032077
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AV305342, D030060M11Rik
Expression	Ubiquitous expression in thymus adult (RPKM 7.4), whole brain E14.5 (RPKM 6.9) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

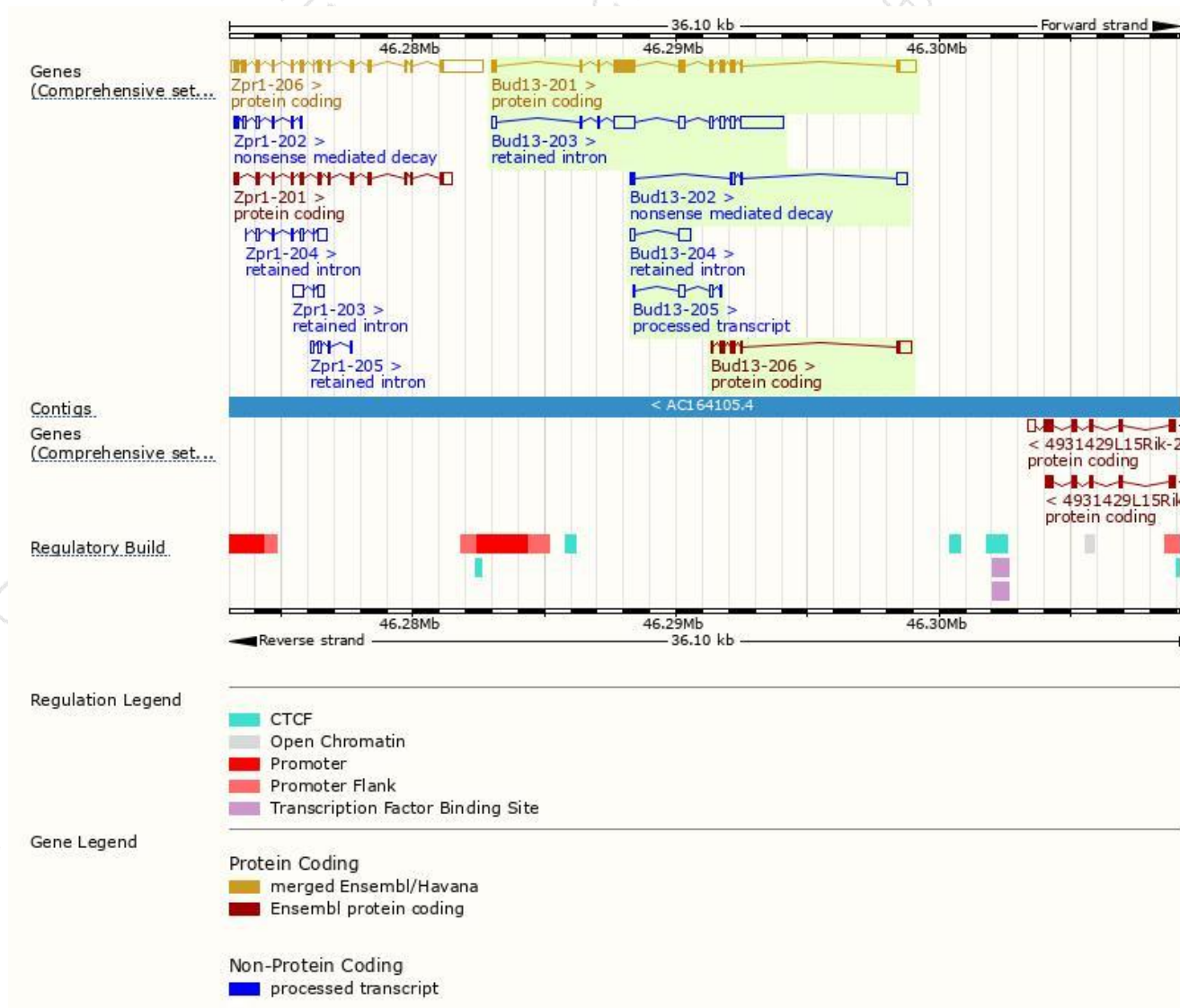
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bud13-201	ENSMUST00000074957.4	2539	637aa	Protein coding	CCDS23145	Q8R149	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
Bud13-206	ENSMUST00000213932.1	978	185aa	Protein coding	-	A0A1L1SSX5	CDS 5' incomplete TSL:3
Bud13-202	ENSMUST00000124887.1	825	74aa	Nonsense mediated decay	-	F6ZBW5	CDS 5' incomplete TSL:5
Bud13-205	ENSMUST00000213338.1	436	No protein	Processed transcript	-	-	TSL:5
Bud13-203	ENSMUST00000138498.1	3413	No protein	Retained intron	-	-	TSL:1
Bud13-204	ENSMUST00000154247.1	583	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Bud13-201* transcript,the transcription is shown below



Genomic location distribution



Protein domain



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

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