

***Zfp37* Cas9-KO Strategy**

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Project Overview

Project Name

Zfp37

Project type

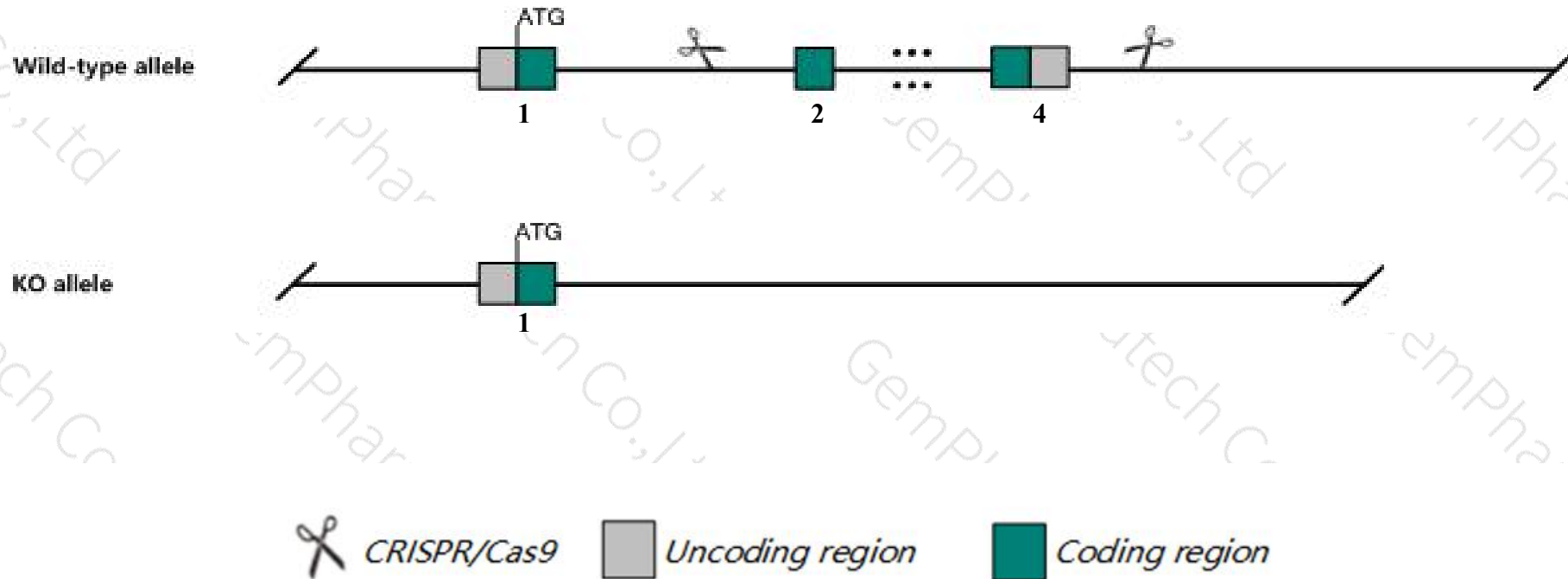
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp37* gene. The schematic diagram is as follows:



- The *Zfp37* gene has 7 transcripts. According to the structure of *Zfp37* gene, exon2-exon4 of *Zfp37-201* (ENSMUST00000068822.3) 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 *Zfp37* gene. The brief process is as follows: CRISPR/Cas9 system

- The effect on transcript *Zfp37*-203 is unknown.
- The *Zfp37* 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)

Zfp37 zinc finger protein 37 [*Mus musculus* (house mouse)]

Gene ID: 22696, updated on 24-Oct-2019

Summary

- Official Symbol** Zfp37 provided by MGI
- Official Full Name** zinc finger protein 37 provided by MGI
- Primary source** MGI:MGI:99181
- See related** Ensembl:ENSMUSG00000028389
- 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** Tzn; Zfp-37
- Expression** Biased expression in testis adult (RPKM 14.6), CNS E11.5 (RPKM 4.2) and 9 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 4 B3; 4 33.04 cM See Zfp37 in [Genome Data Viewer](#)

Exon count: 5

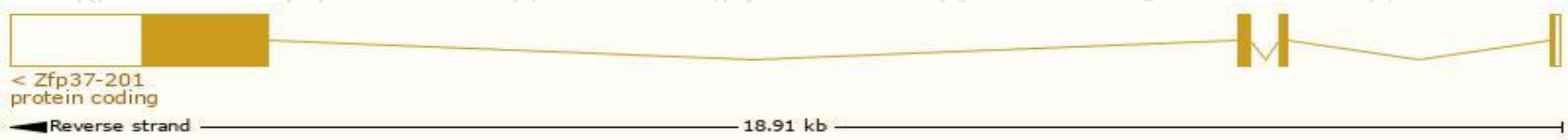
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	4	NC_000070.6 (62189537..62209129, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (61850577..61869580, complement)

Transcript information (Ensembl)

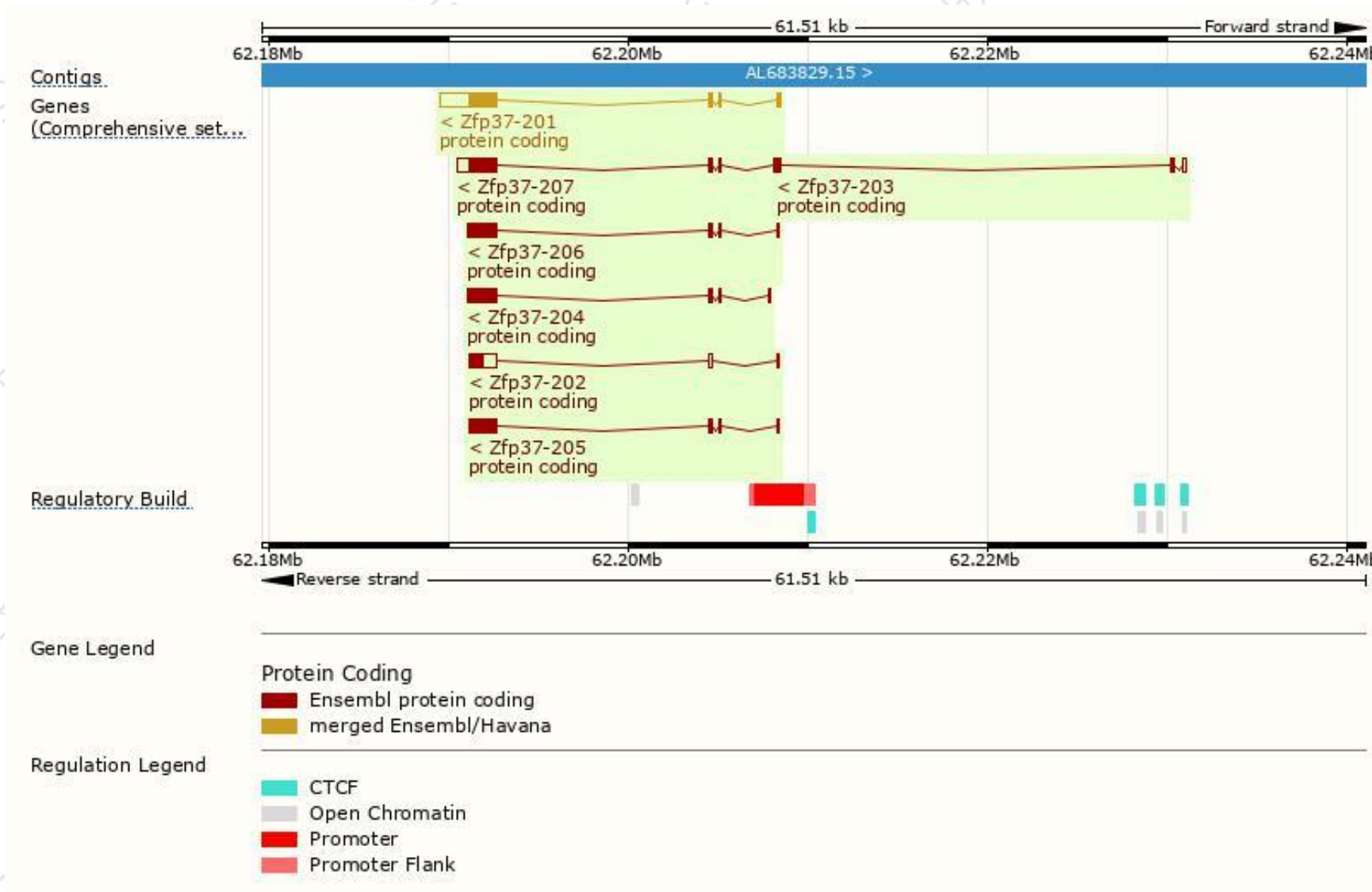
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp37-201	ENSMUST00000068822.3	3494	594aa	Protein coding	CCDS71400	P17141	TSL:1 GENCODE basic APPRIS P2
Zfp37-207	ENSMUST00000222748.1	2564	553aa	Protein coding	-	A0A1Y7VJF3	TSL:2 GENCODE basic APPRIS ALT2
Zfp37-206	ENSMUST00000222050.1	2017	590aa	Protein coding	-	Q6P3Z4	TSL:1 GENCODE basic APPRIS ALT2
Zfp37-204	ENSMUST00000220873.1	1985	553aa	Protein coding	-	A0A1Y7VJF3	TSL:5 GENCODE basic APPRIS ALT2
Zfp37-205	ENSMUST00000221329.1	1776	591aa	Protein coding	-	A0A1Y7VLM5	TSL:2 GENCODE basic APPRIS ALT2
Zfp37-202	ENSMUST00000129511.2	1691	240aa	Protein coding	-	A0A1Y7VJ69	TSL:5 GENCODE basic
Zfp37-203	ENSMUST00000212325.1	521	100aa	Protein coding	-	A0A1D5RLS9	CDS 3' incomplete TSL:5

The strategy is based on the design of *Zfp37-201* 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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