

***Pias2* Cas9-CKO Strategy**

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Project Overview

Project Name

Pias2

Project type

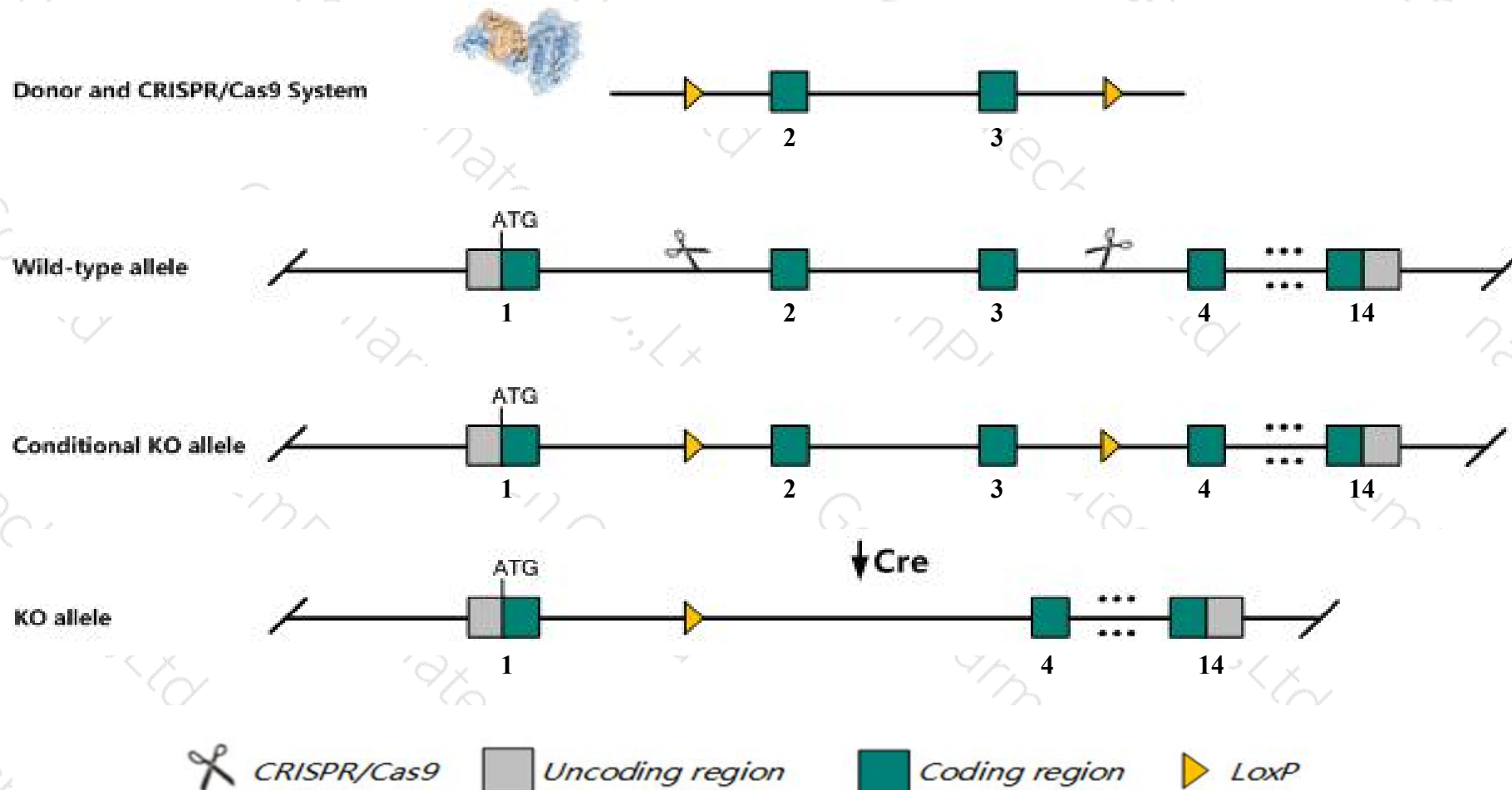
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pias2* gene. The schematic diagram is as follows:



- The *Pias2* gene has 4 transcripts. According to the structure of *Pias2* gene, exon2-exon3 of *Pias2*-202 (ENSMUST00000114777.9) transcript is recommended as the knockout region. The region contains 560bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pias2* 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.

- According to the existing MGI data, An uncharacterized gene trap insertion does not result in an obvious phenotype although abnormalities are reported in the testes.
- The *Pias2* gene is located on the Chr18. 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)

Pias2 protein inhibitor of activated STAT 2 [*Mus musculus* (house mouse)]

Gene ID: 17344, updated on 12-Nov-2019

Summary

Official Symbol	Pias2 provided by MGI
Official Full Name	protein inhibitor of activated STAT 2 provided by MGI
Primary source	MGI:MGI:1096566
See related	Ensembl:ENSMUSG00000025423
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Dib; Miz1; SIZ2; ARIP3; PIASxb; AI462206; AU018068; PIASxbeta; PIASxalpha; 6330408K17Rik
Expression	Broad expression in testis adult (RPKM 36.6), CNS E14 (RPKM 8.7) and 22 other tissues See more
Orthologs	human all

Genomic context

Location: 18; 18 E3

See Pias2 in [Genome Data Viewer](#)

Exon count: 16

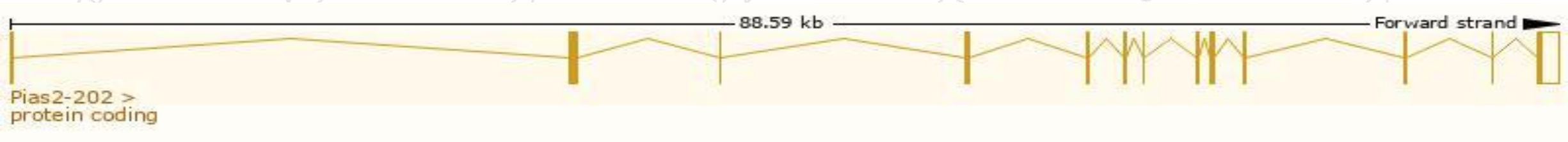
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	18	NC_000084.6 (77065176..77155710)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	18	NC_000084.5 (77303947..77394447)

Transcript information (Ensembl)

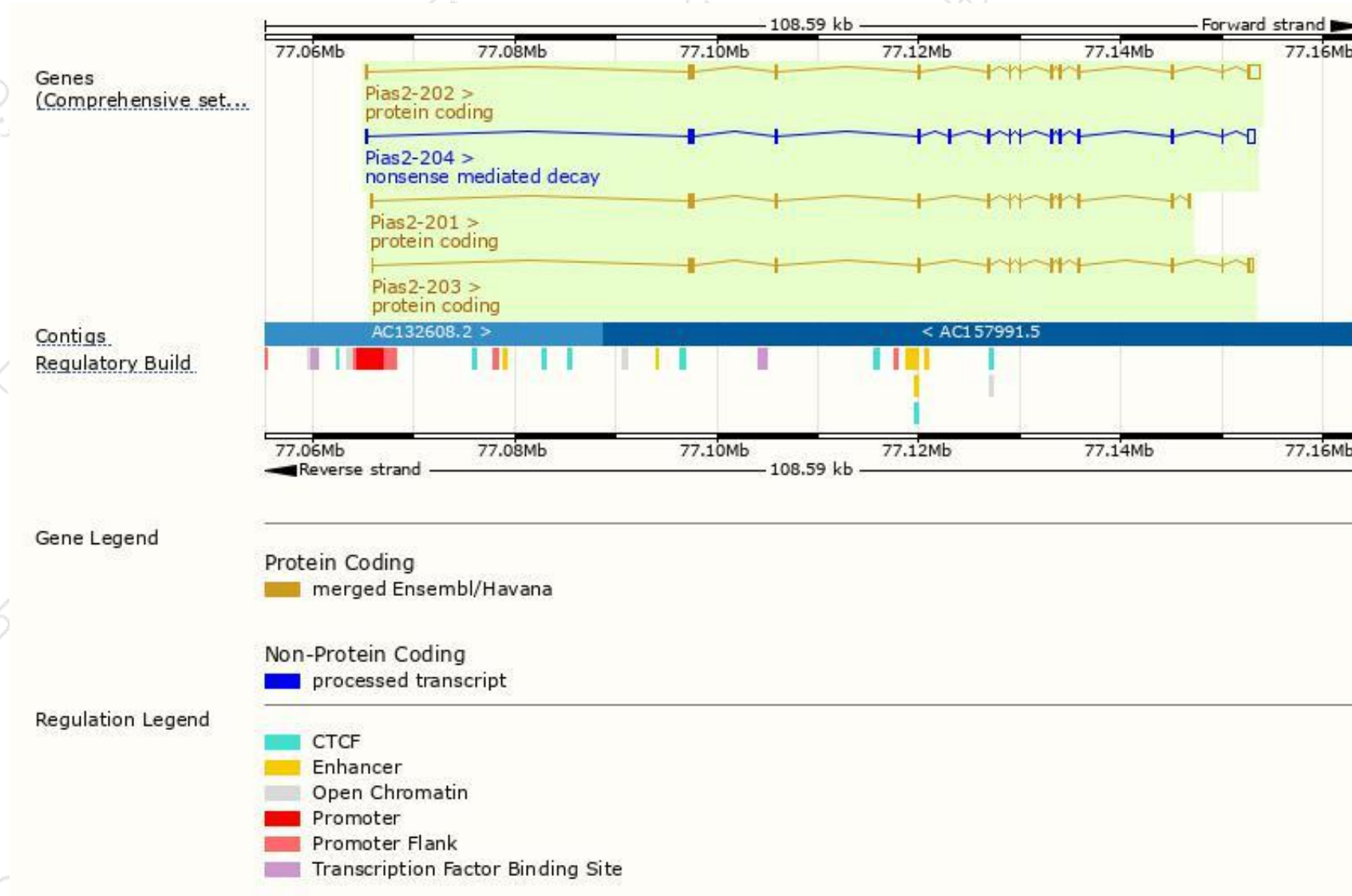
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pias2-202	ENSMUST00000114777.9	3060	621aa	Protein coding	CCDS37866	Q8C5D8	TSL:1 GENCODE basic APPRIS P3
Pias2-203	ENSMUST00000168882.8	2254	614aa	Protein coding	CCDS50324	G3UWE3	TSL:1 GENCODE basic APPRIS ALT 1
Pias2-201	ENSMUST00000114776.3	2077	565aa	Protein coding	CCDS50323	F8WHS8	TSL:1 GENCODE basic
Pias2-204	ENSMUST00000235135.1	2633	252aa	Nonsense mediated decay	-	-	

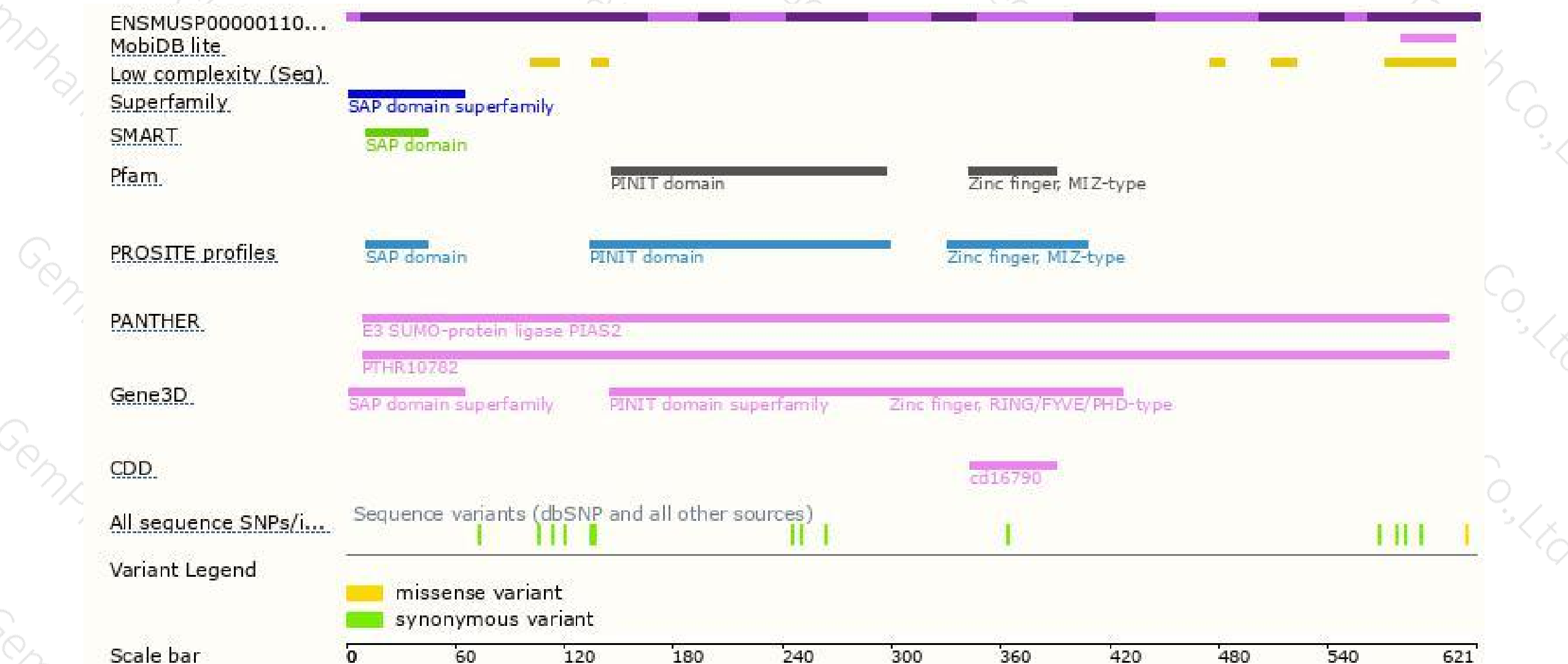
The strategy is based on the design of *Pias2-202* transcript,The transcription is shown below



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/>).

According to the existing MGI data, An uncharacterized gene trap insertion does not result in an obvious phenotype although abnormalities are reported in the testes.

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

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