

***Zfp57* Cas9-CKO Strategy**

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Project Overview

Project Name

Zfp57

Project type

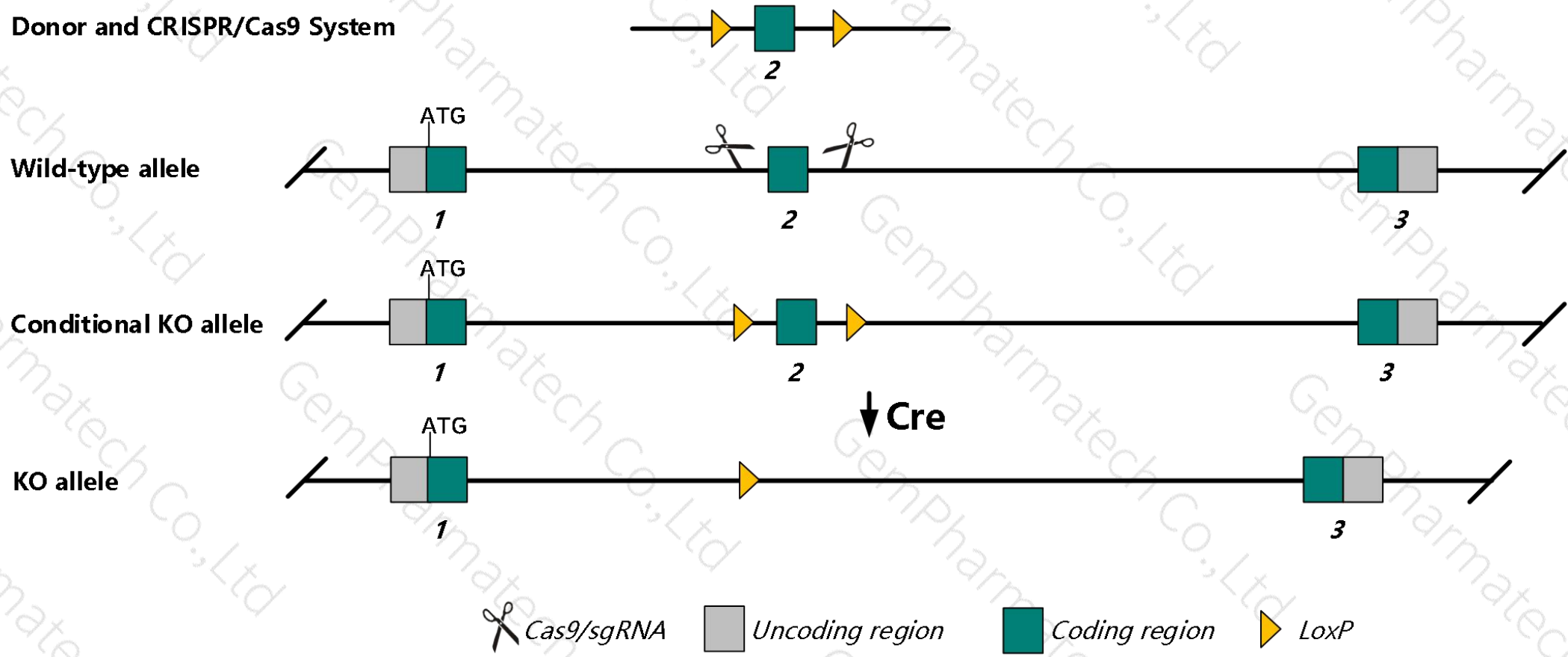
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp57* gene. The schematic diagram is as follows:



- The *Zfp57* gene has 13 transcripts. According to the structure of *Zfp57* gene, exon2 of *Zfp57-212* (ENSMUST00000174672.1) transcript is recommended as the knockout region. The region contains 145bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp57* 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

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit some postnatal lethality with abnormal imprinting and fetal lethality observed in the homozygous offspring of homozygous females.
- Transcripts 205,207,208,213 are incomplete and effects are unknown.
- The *Zfp57* gene is located on the Chr17. 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)

Zfp57 zinc finger protein 57 [*Mus musculus* (house mouse)]

Gene ID: 22715, updated on 10-Oct-2019

Summary

Official Symbol	Zfp57 provided by MGI
Official Full Name	zinc finger protein 57 provided by MGI
Primary source	MGI:MGI:99204
See related	Ensembl:ENSMUSG00000036036
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	G19; Zfp-57
Expression	Biased expression in CNS E18 (RPKM 66.8), CNS E14 (RPKM 62.8) and 8 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

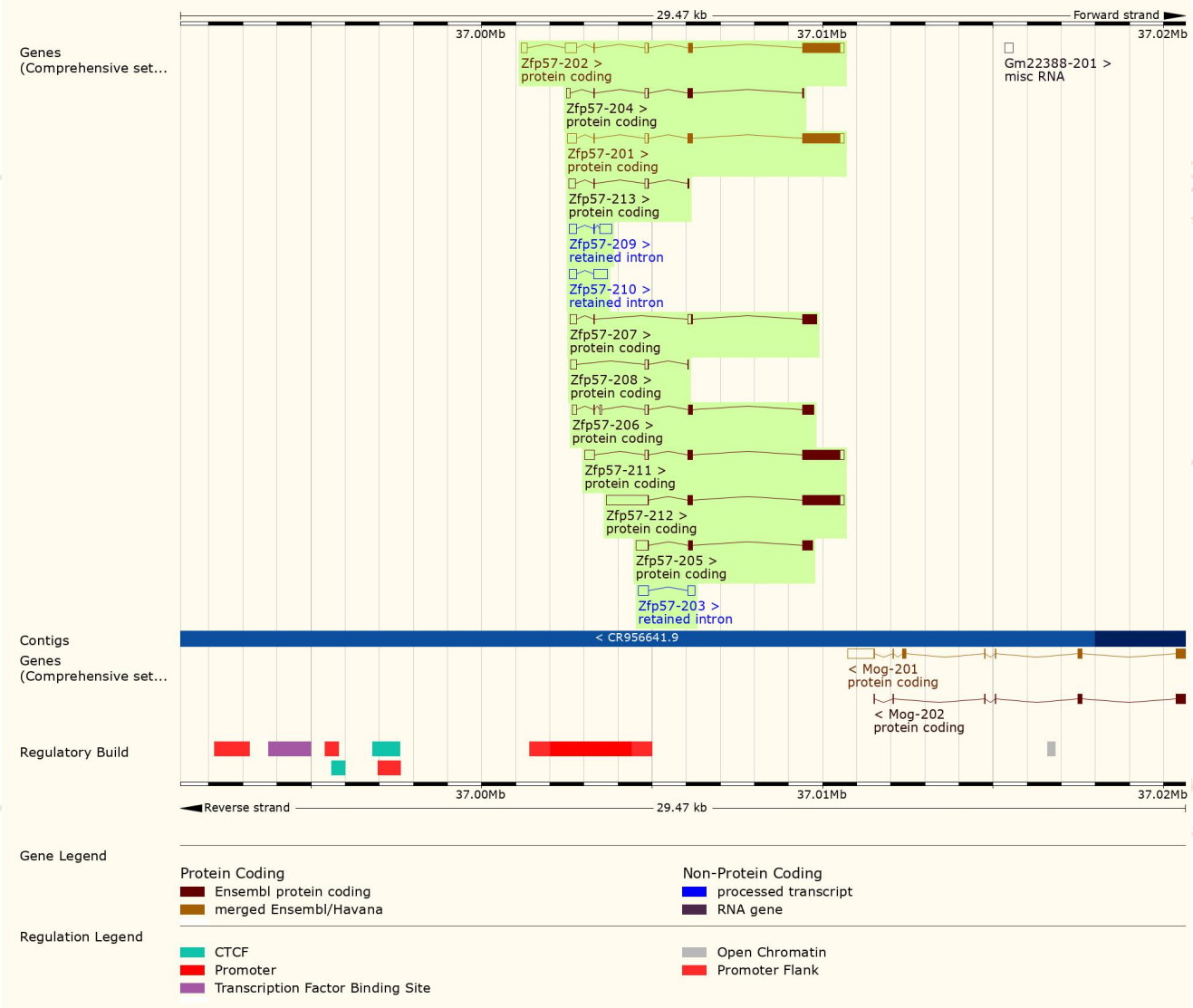
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp57-212	ENSMUST00000174672.1	2597	421aa	Protein coding	CCDS28733	Q8C6P8	TSL:1 GENCODE basic APPRIS P3
Zfp57-202	ENSMUST00000089968.12	1991	418aa	Protein coding	CCDS50106	Q8C6P8	TSL:1 GENCODE basic APPRIS ALT2
Zfp57-201	ENSMUST00000069250.13	1749	421aa	Protein coding	CCDS28733	Q8C6P8	TSL:1 GENCODE basic APPRIS P3
Zfp57-211	ENSMUST00000174524.7	1747	421aa	Protein coding	CCDS28733	Q8C6P8	TSL:1 GENCODE basic APPRIS P3
Zfp57-205	ENSMUST00000172540.1	815	150aa	Protein coding	-	G3UYC1	CDS 3' incomplete TSL:2
Zfp57-206	ENSMUST00000172580.7	763	160aa	Protein coding	-	G3UY05	CDS 3' incomplete TSL:3
Zfp57-207	ENSMUST00000173588.7	762	146aa	Protein coding	-	H3BL53	CDS 3' incomplete TSL:3
Zfp57-204	ENSMUST00000172527.7	425	62aa	Protein coding	-	G3UYK1	CDS 3' incomplete TSL:5
Zfp57-213	ENSMUST00000174747.7	375	16aa	Protein coding	-	G3UWX4	CDS 3' incomplete TSL:5
Zfp57-208	ENSMUST00000173921.7	290	11aa	Protein coding	-	G3UX77	CDS 3' incomplete TSL:5
Zfp57-210	ENSMUST00000174470.1	608	No protein	Retained intron	-	-	TSL:2
Zfp57-209	ENSMUST00000174016.7	590	No protein	Retained intron	-	-	TSL:3
Zfp57-203	ENSMUST00000172502.1	500	No protein	Retained intron	-	-	TSL:2

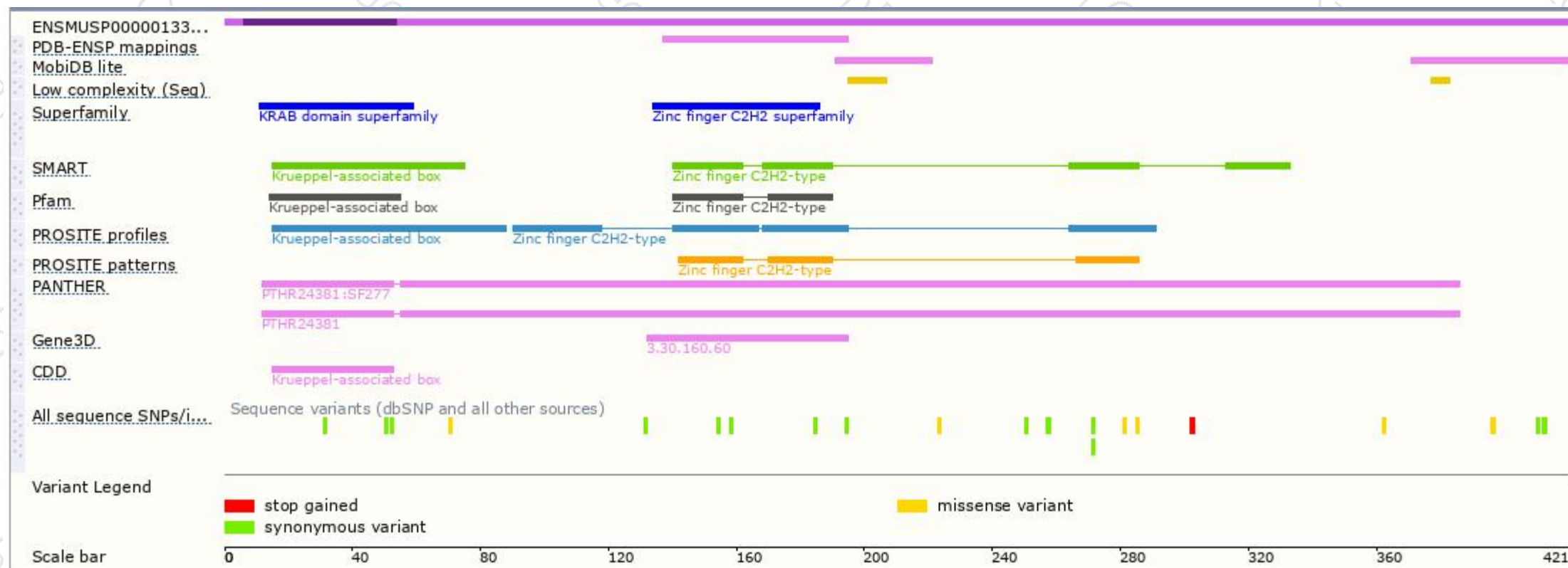
The strategy is based on the design of *Zfp57-212* transcript,The transcription is shown below



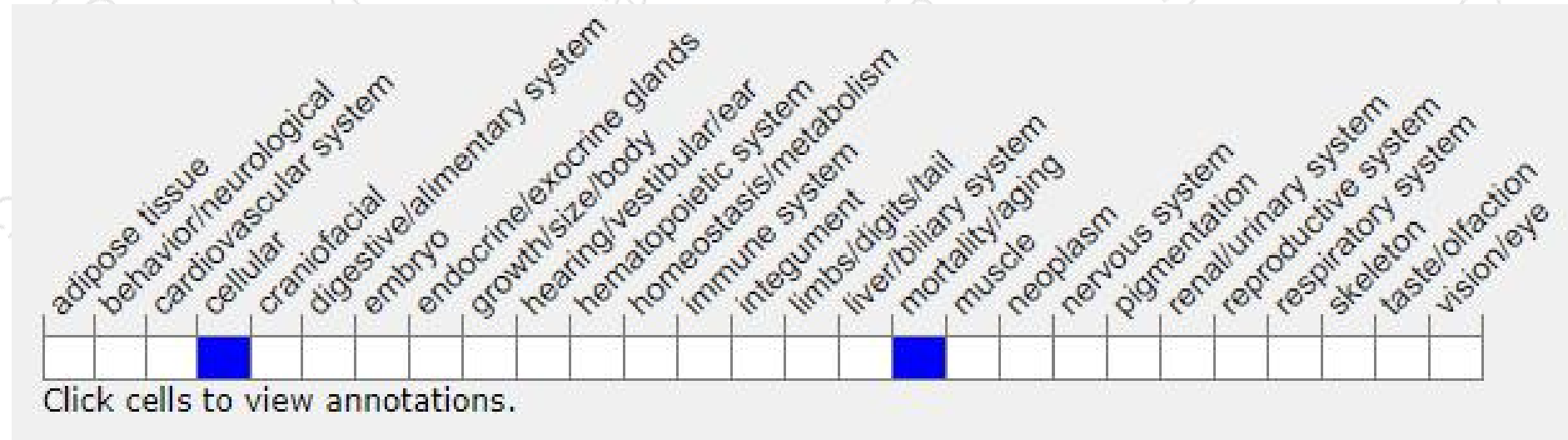
Genomic location distribution



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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