Zfp106 Cas9-CKO Strategy

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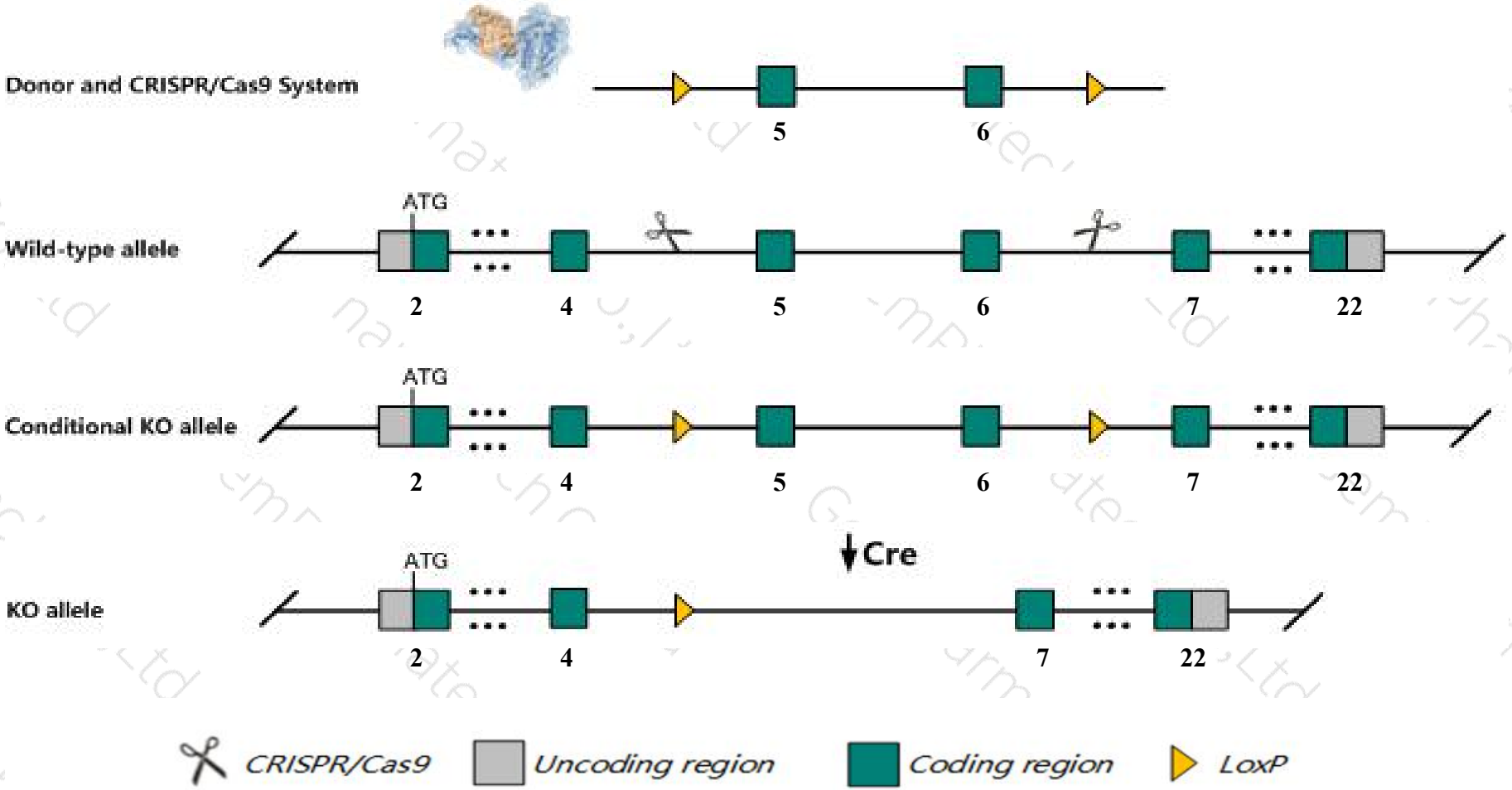
Project Overview

Project Name	***Zfp106***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp106* gene. The schematic diagram is as follows:



Technical routes

➢ The *Zfp106* gene has 11 transcripts. According to the structure of *Zfp106* gene, exon5-exon6 of *Zfp106-201*(ENSMUST00000055241.12) transcript is recommended as the knockout region.The region contains 2797bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Zfp106* 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 null allele exhibit an abnormal gait, progressive motor deficits, kyphosis, weight loss, severe adult-onset degenerative sensory-motor axonopathy, mitochondrial dysfunction, and premature death.

➢Transcript *Zfp106-208* is incomplete, so the effect on it is unknown.

➢ The *Zfp106* gene is located on the Chr2. 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）

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Zfp106 zinc finger protein 106 [*Mus musculus* (house mouse)]

Gene ID: 20402, updated on 26-Jun-2020

Summary

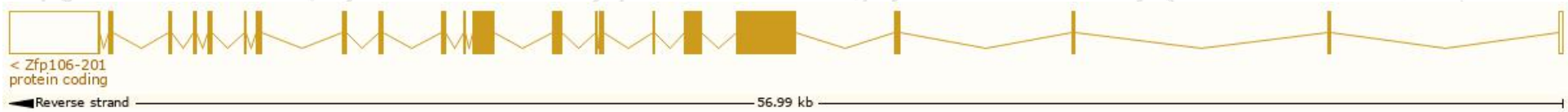
Official Symbol	Zfp106 provided by MGI
Official Full Name	zinc finger protein 106 provided by MGI
Primary source	MGI:MGI:1270153
See related	Ensembl:ENSMUSG00000027288
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	H3a; Cd-1; sirm; Sh3bp3; Znf106; D2Dcr28; zfp-106; EyeLinc12
Expression	Ubiquitous expression in heart adult (RPKM 47.5), frontal lobe adult (RPKM 16.8) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

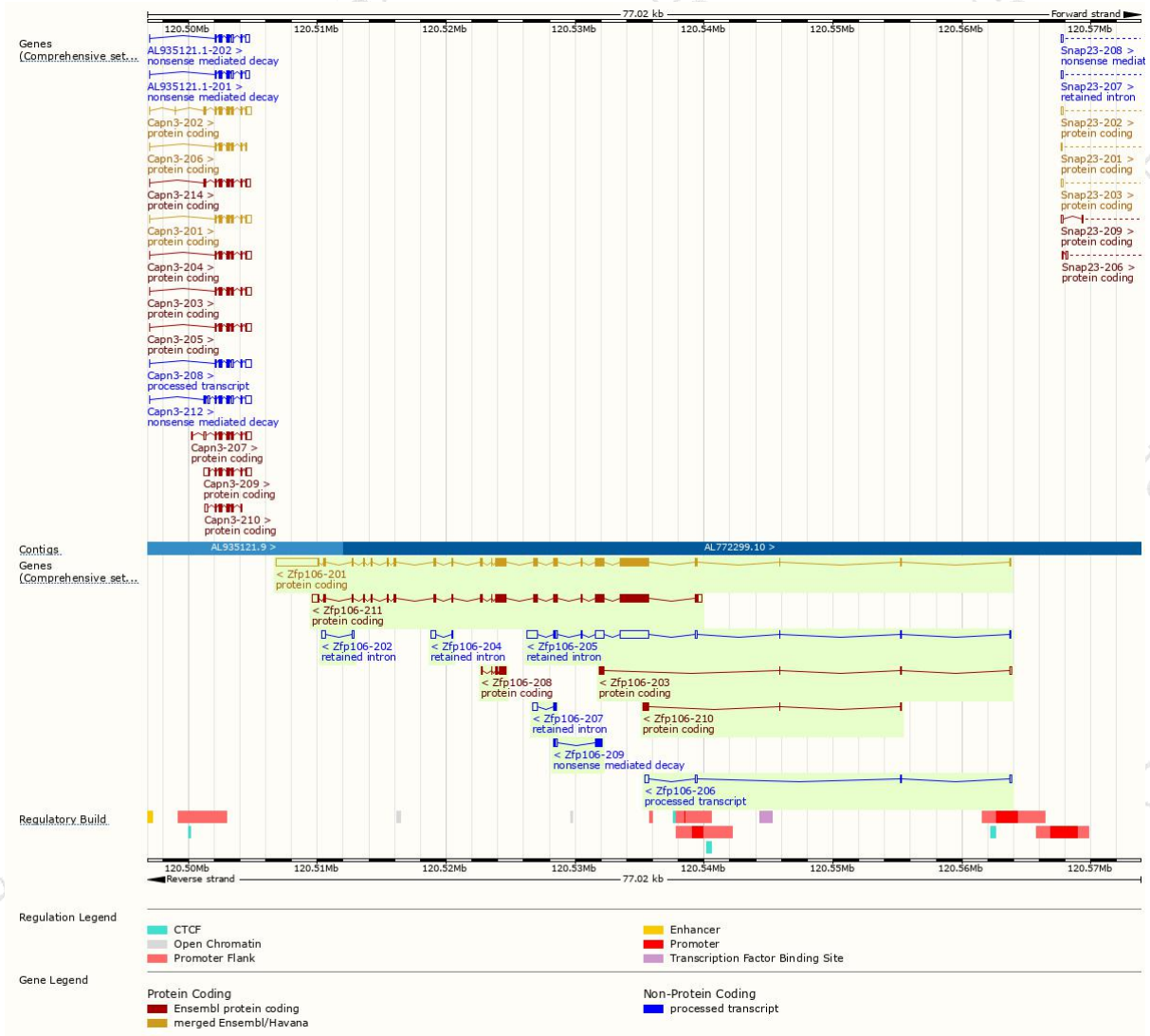
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein ▲	Biotype	CCDS	UniProt	Flags
Zfp106-203	ENSMUST00000135625.7	641	151aa	Protein coding	-	E9PVH6	CDS 3' incomplete TSL:2
Zfp106-209	ENSMUST00000163384.1	677	163aa	Nonsense mediated decay	-	F6QFS1	CDS 5' incomplete TSL:2
Zfp106-210	ENSMUST00000167241.1	505	168aa	Protein coding	-	F6SID8	CDS 5' and 3' incomplete TSL:3
Zfp106-208	ENSMUST00000152347.1	794	264aa	Protein coding	-	F6UL00	CDS 5' and 3' incomplete TSL:5
Zfp106-211	ENSMUST00000171215.7	6391	1865aa	Protein coding	-	E9Q7S1	TSL:5 GENCODE basic
Zfp106-201	ENSMUST00000055241.12	9085	1888aa	Protein coding	CCDS16621	R4GML0	TSL:5 GENCODE basic APPRIS P1
Zfp106-206	ENSMUST00000147353.1	691	No protein	Processed transcript	-	-	TSL:3
Zfp106-205	ENSMUST00000141874.7	4375	No protein	Retained intron	-	-	TSL:1
Zfp106-204	ENSMUST00000139942.1	467	No protein	Retained intron	-	-	TSL:3
Zfp106-207	ENSMUST00000149210.1	460	No protein	Retained intron	-	-	TSL:2
Zfp106-202	ENSMUST00000130303.1	458	No protein	Retained intron	-	-	TSL:5

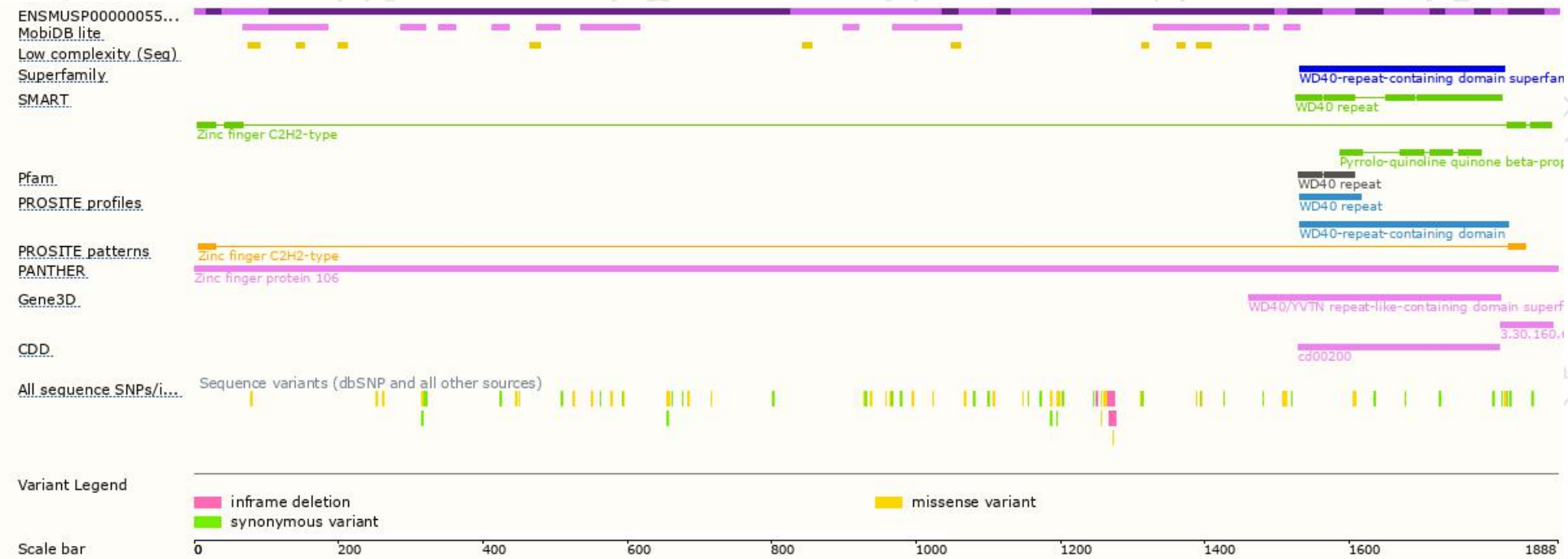
The strategy is based on the design of *Zfp106-201* transcript,the transcription is shown below:



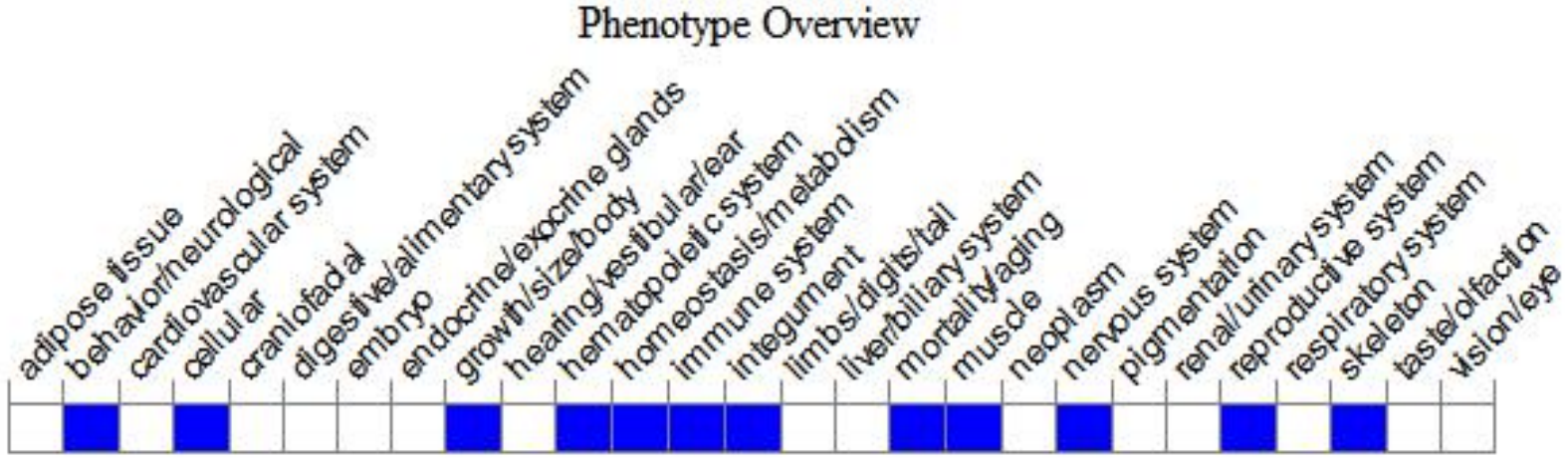
Genomic location distribution



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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