Klf12 Cas9-CKO Strategy

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Project Overview

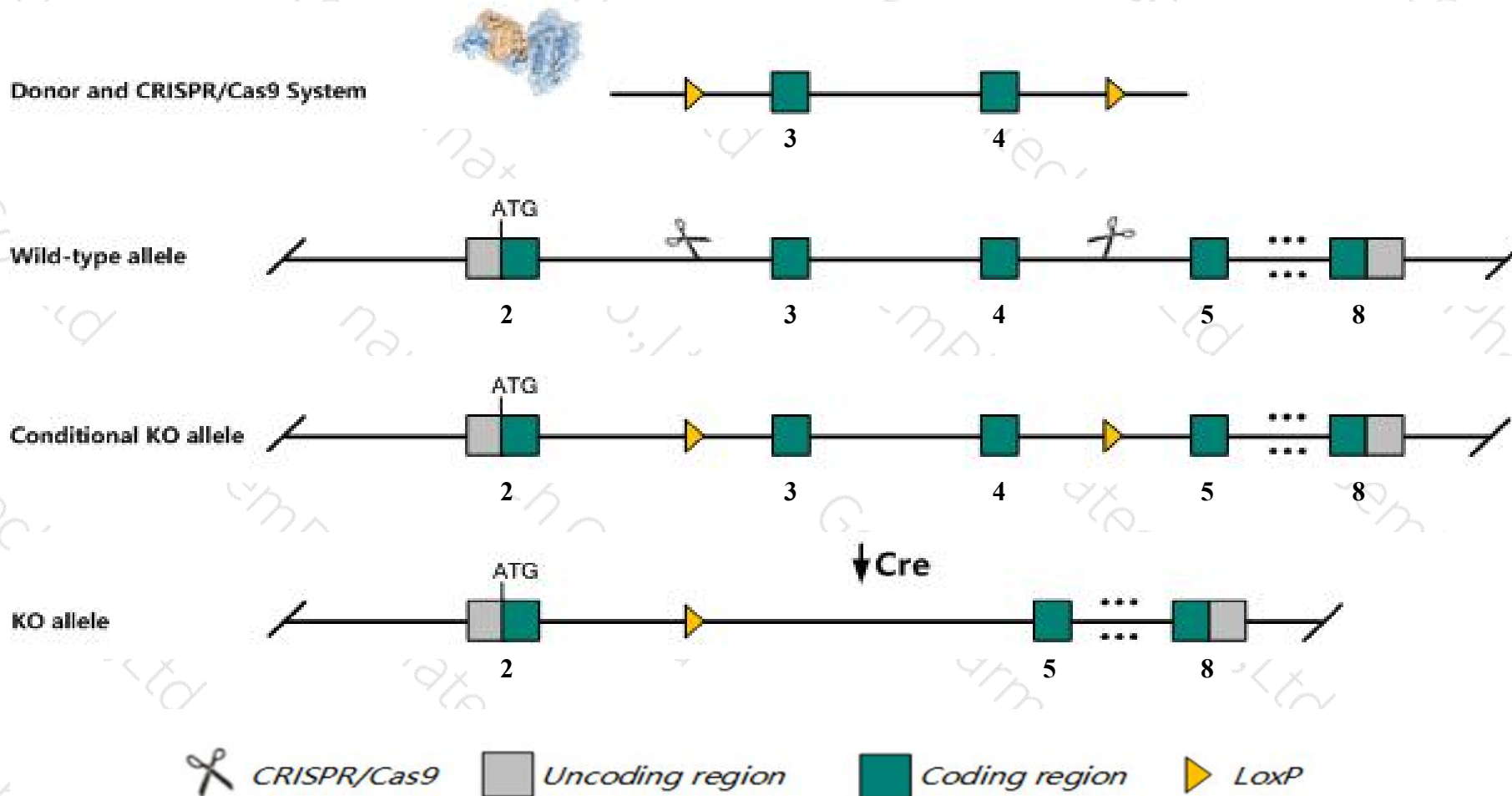|	
Project Name	*Klf12*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Klf12* gene. The schematic diagram is as follows:

➤ The *Klf12* gene has 6 transcripts. According to the structure of *Klf12* gene, exon3-exon4 of *Klf12-205* (ENSMUST00000228216.1) transcript is recommended as the knockout region.The region contains Ens 637bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Klf12* 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

➢ The *Klf12* gene is located on the Chr14. 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）

Klf12 Kruppel-like factor 12 [Mus musculus (house mouse)]

Gene ID: 16597, updated on 13-Mar-2020

▲ Summary

Official Symbol	Klf12 provided by MGI
Official Full Name	Kruppel-like factor 12 provided byMGI
Primary source	MGI:MGI:1333796
See related	Ensembl:ENSMUSG00000072294
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	2700063E05Rik, AI225908, AI315654, AP-2rep, B130052C06Rik, D530033K05Rik
Expression	Broad expression in whole brain E14.5 (RPKM 4.9), CNS E14 (RPKM 4.0) and 22 other tissuesSee 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
Klf12-205	ENSMUST00000228216.1	5890	402aa	Protein coding	CCDS36998	O35738	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
Klf12-201	ENSMUST00000097079.4	1856	402aa	Protein coding	CCDS36998	O35738	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
Klf12-204	ENSMUST00000226774.1	719	153aa	Protein coding	-	A0A2I3BQ01	CDS 3' incomplete
Klf12-203	ENSMUST00000226544.1	832	No protein	Processed transcript	-	-	
Klf12-202	ENSMUST00000226205.1	213	No protein	Processed transcript	-	-	
Klf12-206	ENSMUST00000228612.1	1137	No protein	Retained intron	-	-	

The strategy is based on the design of *Klf12-205* transcript,the transcription is shown below:

< Klf12-205
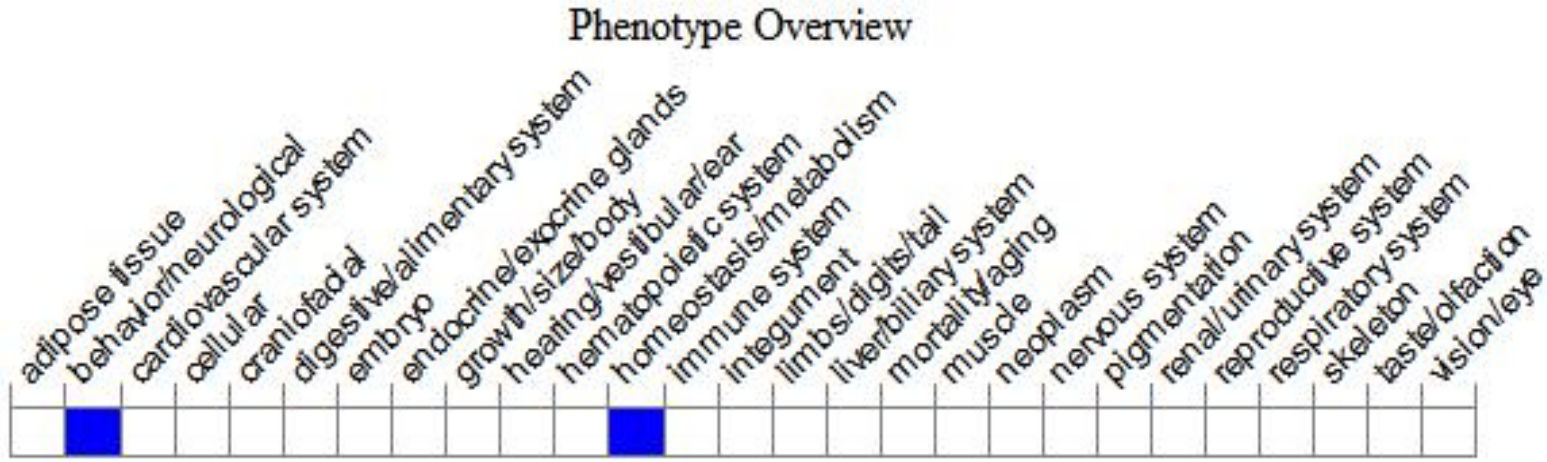protein coding

◄ Reverse strand

414.05 kb

Genomic location distribution
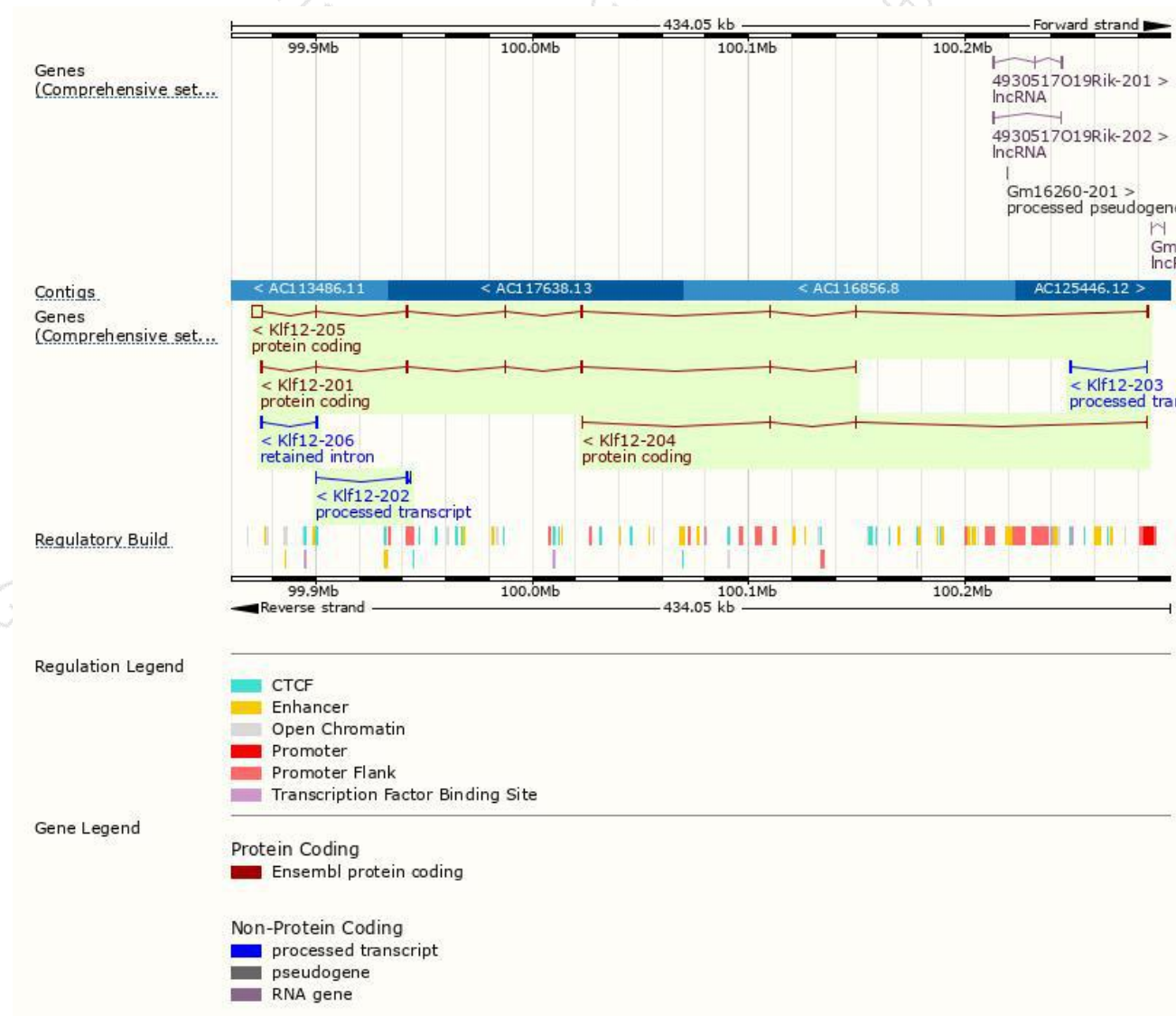
Protein domain
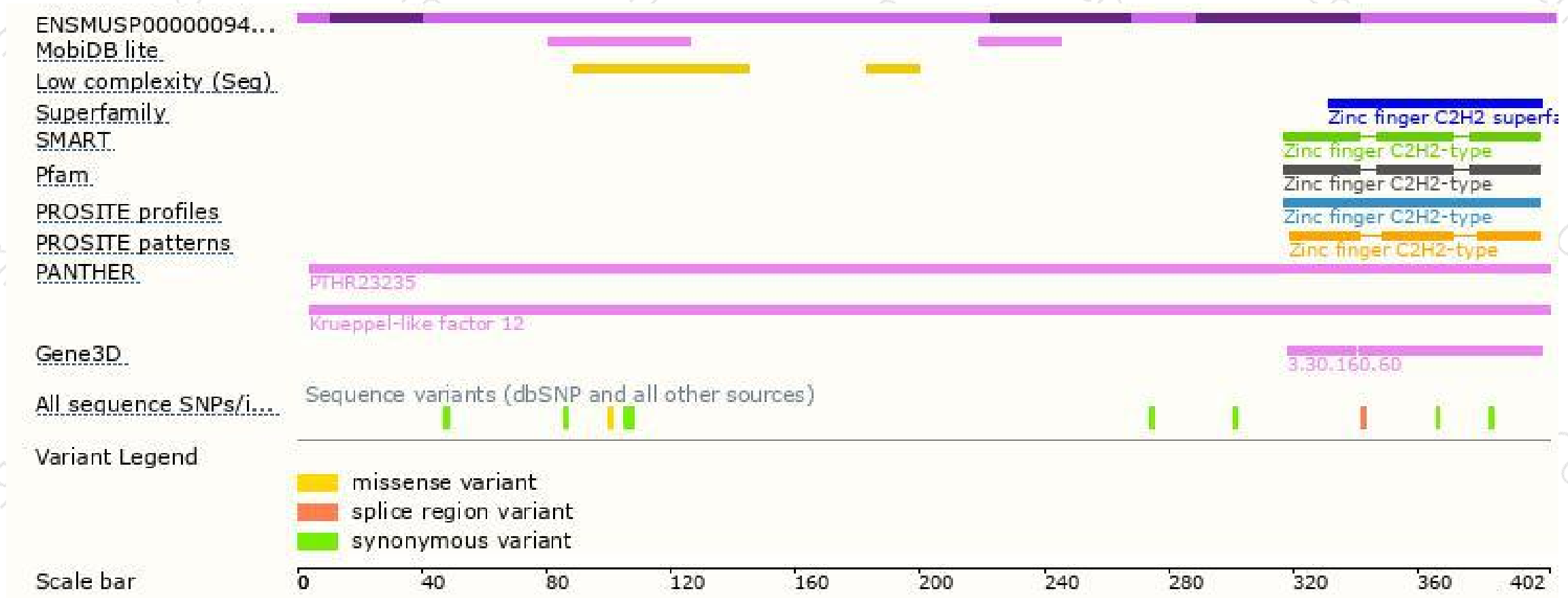
Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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