Mmp16 Cas9-CKO Strategy

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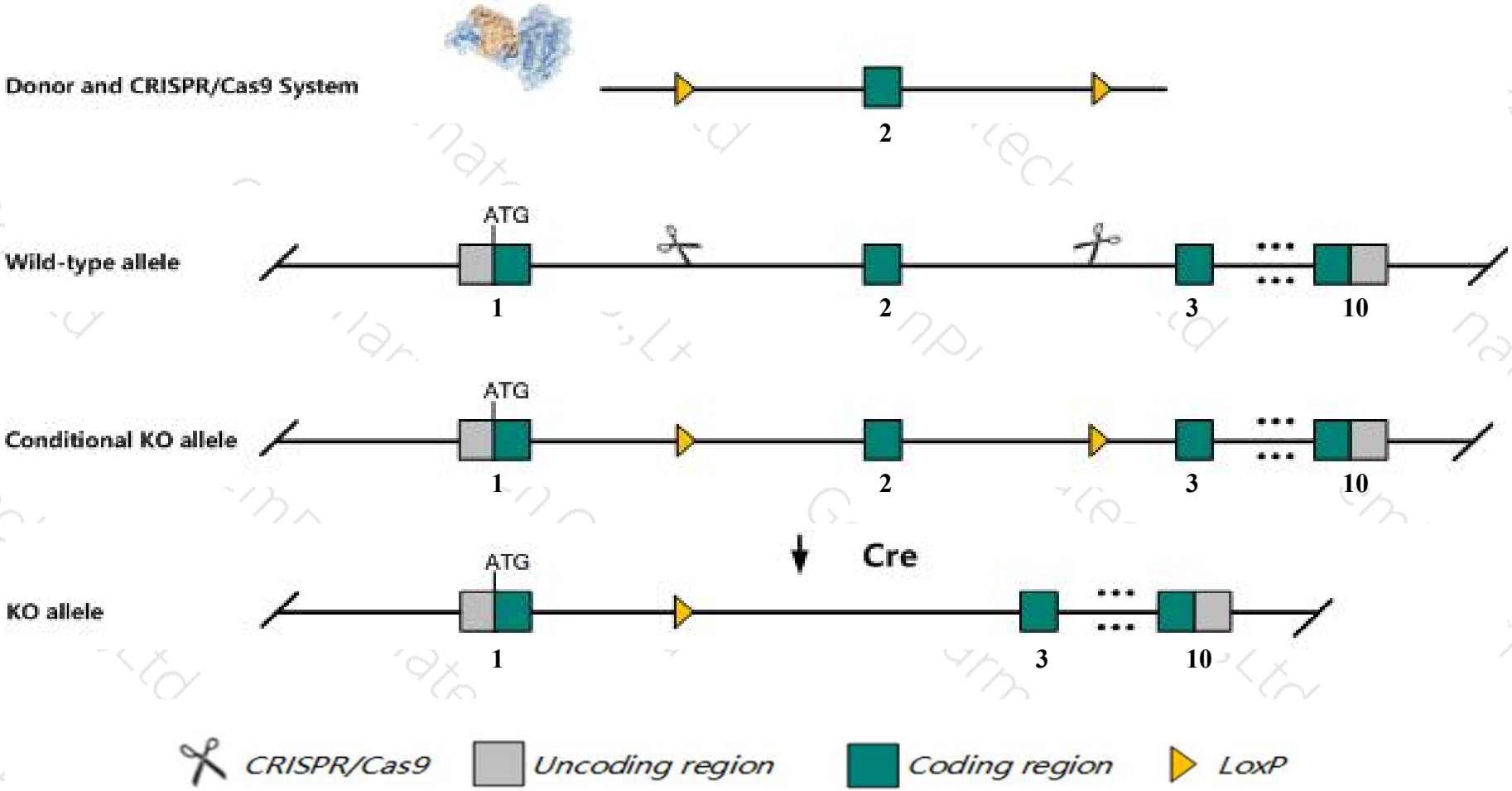
Project Overview

Project Name	***Mmp16***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mmp16* gene. The schematic diagram is as follows:



Technical routes

- The *Mmp16* gene has 6 transcripts. According to the structure of *Mmp16* gene, exon2 of *Mmp16-201* (ENSMUST00000029881.9) transcript is recommended as the knockout region.The region contains 149bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Mmp16* 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 gene disruption display normal morphology, clinical chemistry, hematology, and behavior. Mice homozygous for a null allele exhibit reduced skeletal growth.

- The *Mmp16* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Mmp16 matrix metallopeptidase 16 [Mus musculus (house mouse)]

Gene ID: 17389, updated on 31-Jan-2019

Summary

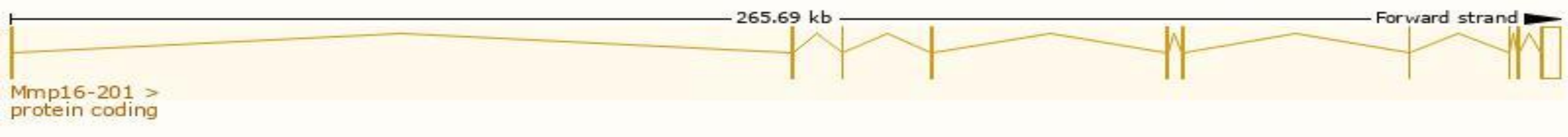
Official Symbol	Mmp16 provided by MGI
Official Full Name	matrix metallopeptidase 16 provided by MGI
Primary source	MGI:MGI:1276107
See related	Ensembl:ENSMUSG00000028226
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MT-MMP 3, MT3-MMP, Mt3mmp
Summary	This gene encodes a member of the matrix metalloproteinase family of extracellular matrix-degrading enzymes that are involved in tissue remodeling, wound repair, progression of atherosclerosis and tumor invasion. The encoded preproprotein undergoes proteolytic processing to generate a mature, zinc-dependent endopeptidase enzyme. Mice lacking the encoded protein exhibit retarded growth of the skeleton, especially in the cranium and long bones. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Feb 2016]
Expression	Biased expression in CNS E18 (RPKM 3.8), limb E14.5 (RPKM 3.0) and 8 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

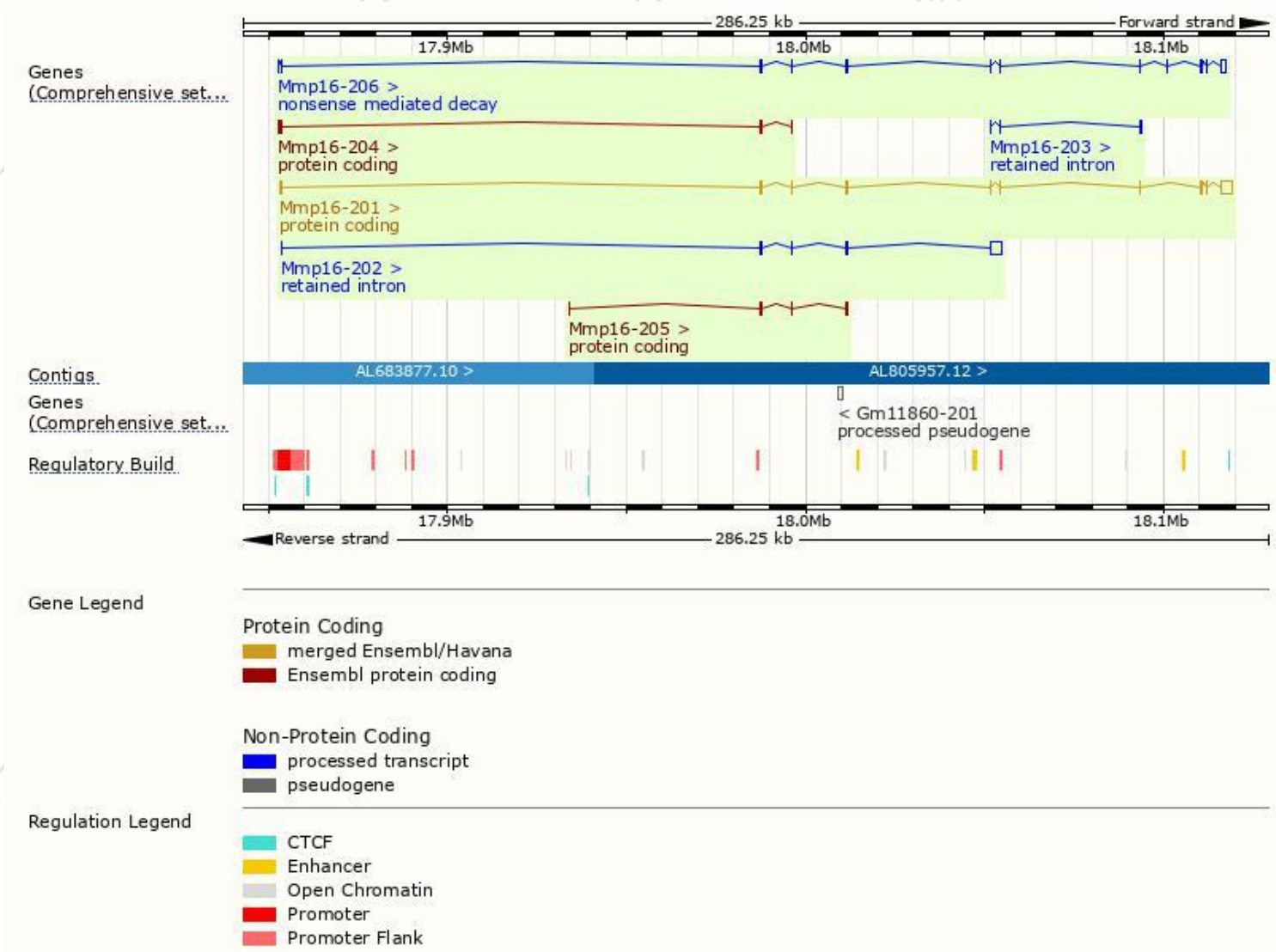
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mmp16-201	ENSMUST00000029881.9	5011	607aa	Protein coding	CCDS17989	Q9WTR0	TSL:1 GENCODE basic APPRIS P1
Mmp16-204	ENSMUST00000142434.7	853	127aa	Protein coding	-	B1AVG8	CDS 3' incomplete TSL:2
Mmp16-205	ENSMUST00000149353.1	601	174aa	Protein coding	-	B1AVH0	CDS 3' incomplete TSL:3
Mmp16-206	ENSMUST00000183662.7	3470	415aa	Nonsense mediated decay	-	V9GXD8	TSL:1
Mmp16-202	ENSMUST00000133416.1	3797	No protein	Retained intron	-	-	TSL:2
Mmp16-203	ENSMUST00000139418.1	729	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Mmp16-201* transcript,The transcription is shown below

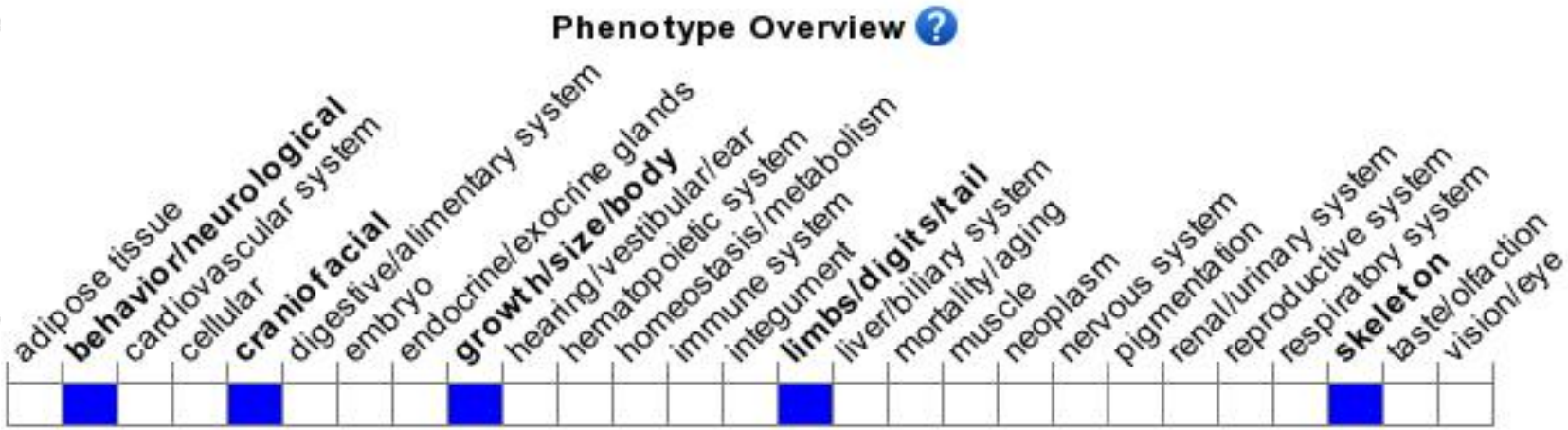


Genomic location distribution



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/).

According to the existing MGI data,Mice homozygous for a gene disruption display normal morphology, clinical chemistry, hematology, and behavior. Mice homozygous for a null allele exhibit reduced skeletal growth.

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

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