Mmp13 Cas9-KO Strategy

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Reviewer: Ruirui Zhang

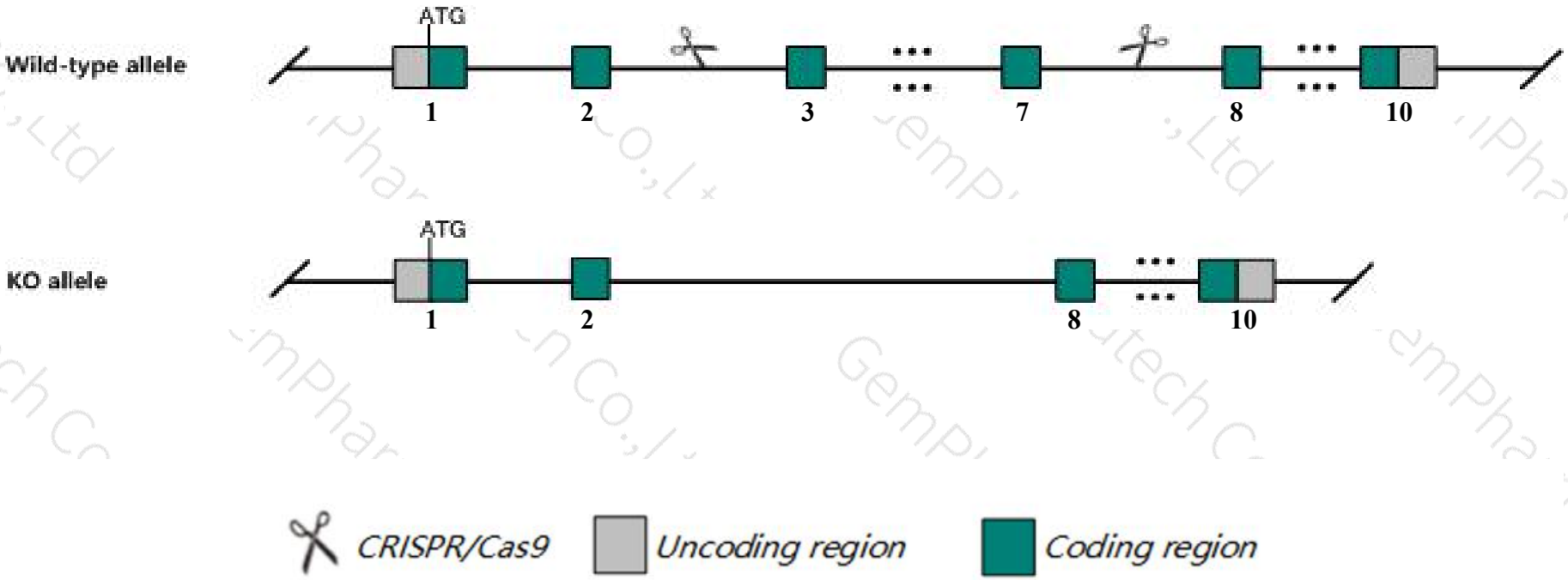
Design Date: 2019/10/21

Project Overview

Project Name	***Mmp13***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mmp13* gene. The schematic diagram is as follows:



Technical routes

➢ The *Mmp13* gene has 1 transcript. According to the structure of *Mmp13* gene, exon3-exon7 of *Mmp13-201* (ENSMUST00000015394.9) transcript is recommended as the knockout region.The region contains 689bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mmp13* gene. The brief process is as follows: CRISPR/Cas9 syster

Notice

➢ According to the existing MGI data,Homozygous null mice display increased width of hypertrophic chondrocyte zone and increased trabecular bone.

➢ The *Mmp13* gene is located on the Chr9. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

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Mmp13 matrix metallopeptidase 13 [*Mus musculus* (house mouse)]

Gene ID: 17386, updated on 10-Oct-2019

Summary

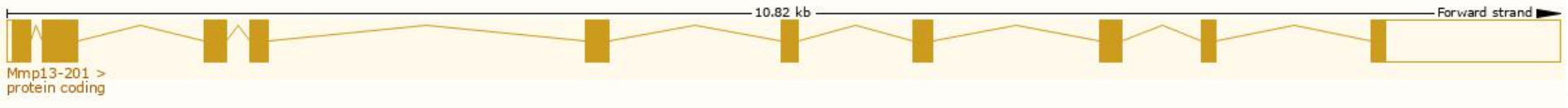
Official Symbol	Mmp13 provided by MGI
Official Full Name	matrix metallopeptidase 13 provided by MGI
Primary source	MGI:MGI:1340026
See related	Ensembl:ENSMUSG00000050578
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Clg; Mmp1; MMP-13
Summary	This gene encodes a member of the matrix metalloproteinase family that plays a role in wound healing, skeletal development and bone remodeling. The encoded protein is activated by the removal of an N-terminal activation peptide to generate a zinc-dependent endopeptidase enzyme that can cleave various native collagens, including types I - IV, X and XIV. Mice lacking the encoded protein display profound defects in growth plate cartilage as well as a delay in the endochondral bone development. Lack of the encoded protein also impairs the wound healing process due to reduced keratinocyte migration and vascular density at the wound site. This gene is located in a cluster of other matrix metalloproteinase genes on chromosome 9. [provided by RefSeq, Jun 2015]
Expression	Biased expression in CNS E18 (RPKM 1.3), limb E14.5 (RPKM 0.9) and 13 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

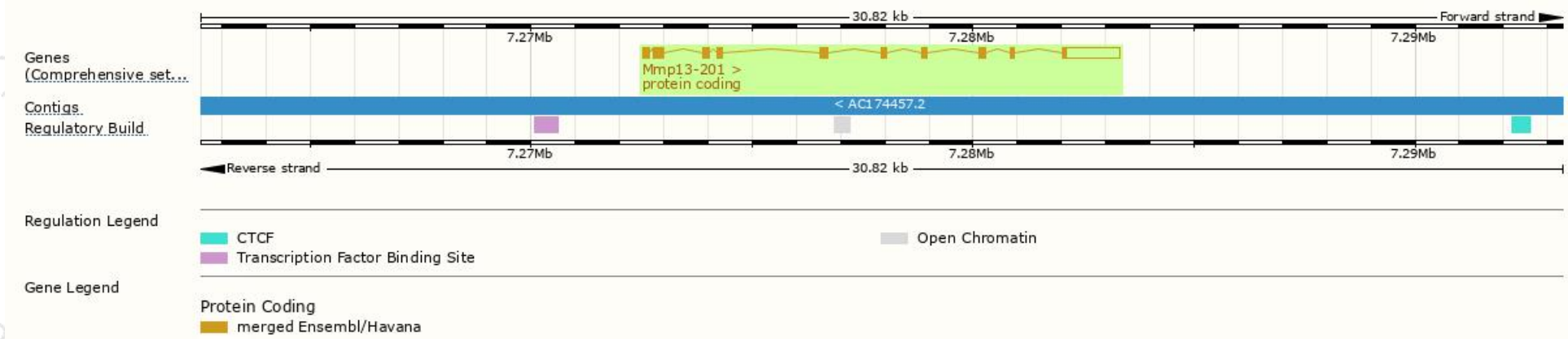
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mmp13-201	ENSMUST00000015394.9	2673	472aa	Protein coding	CCDS22803	P33435 Q3U9V5	TSL:1 GENCODE basic APPRIS P1

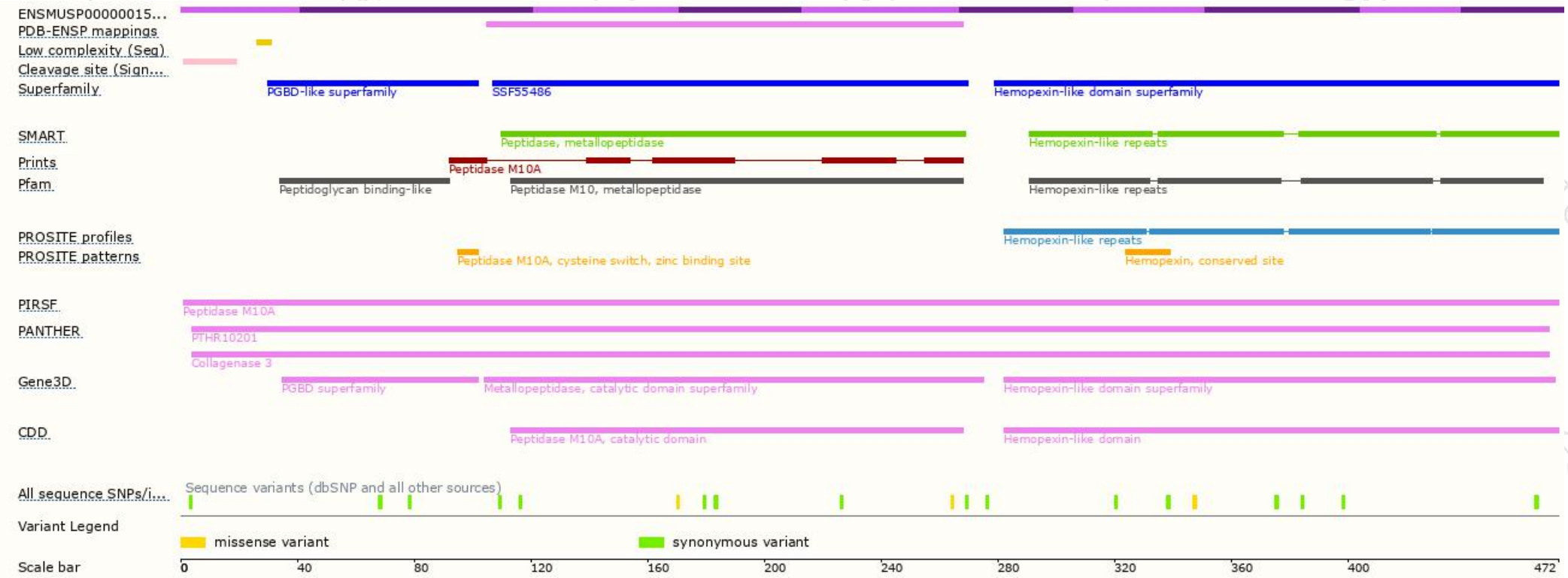
The strategy is based on the design of *Mmp13-201* transcript,The transcription is shown below



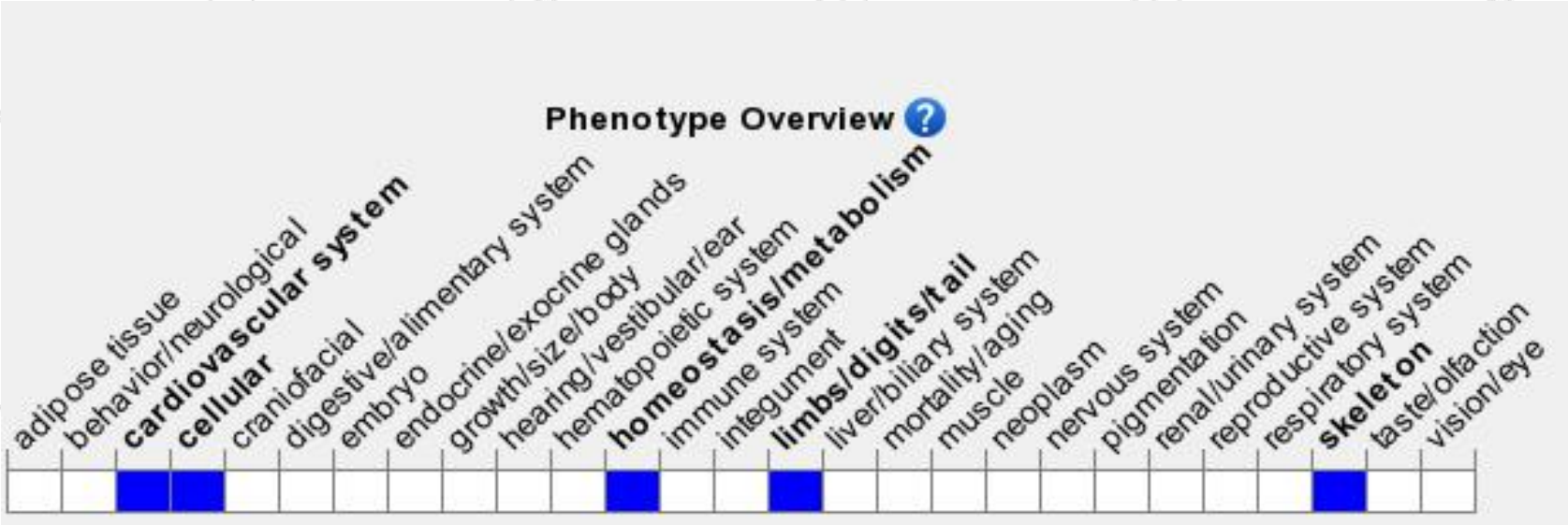
Genomic location distribution



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,Homozygous null mice display increased width of hypertrophic chondrocyte zone and increased trabecular bone.

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

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