Mmp8 Cas9-CKO Strategy

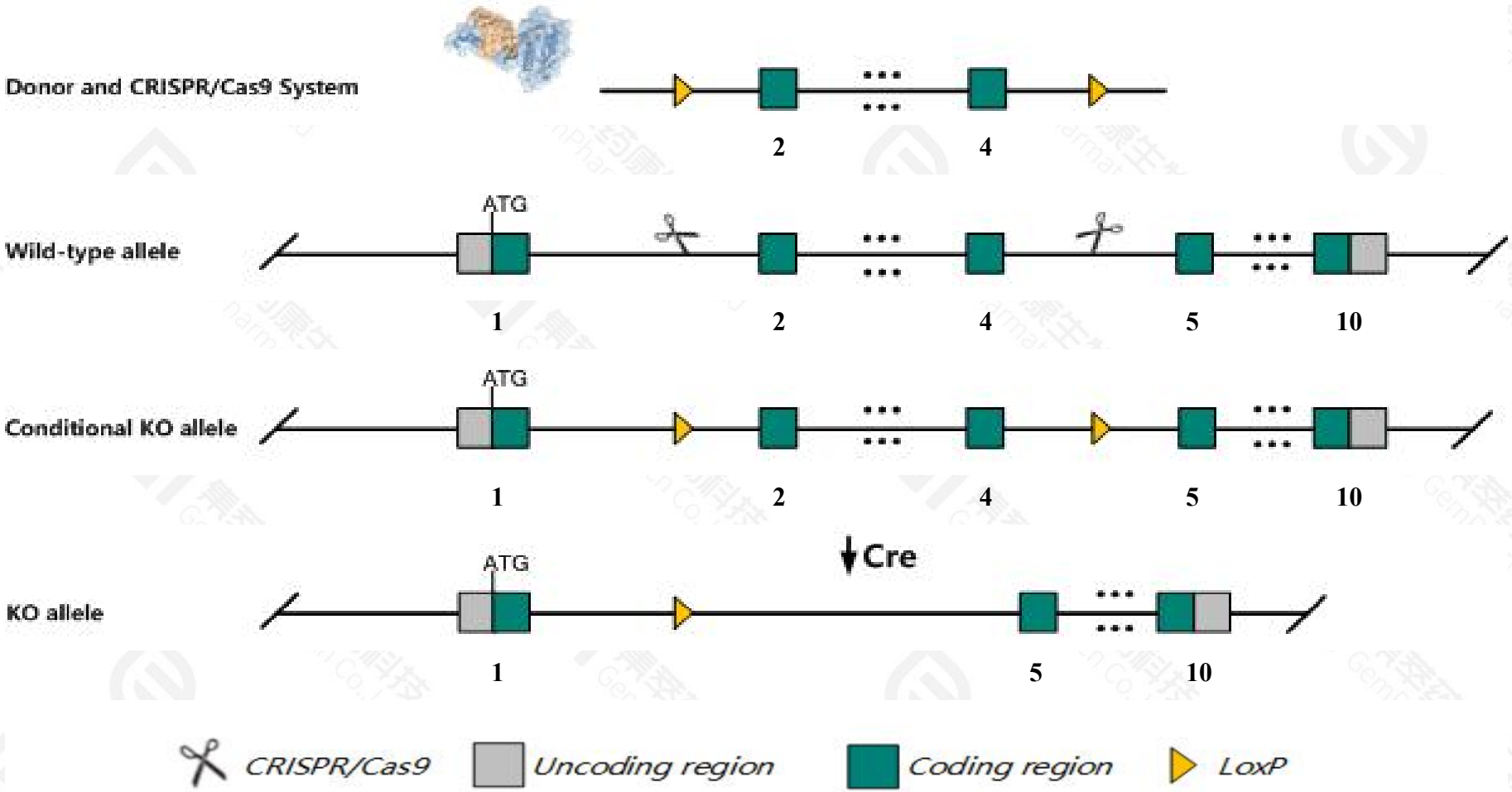
Designer: Daohua Xu

Project Overview

Project Name	***Mmp8***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mmp8* gene. The schematic diagram is as follows:



Technical routes

➢ The *Mmp8* gene has 1 transcript. According to the structure of *Mmp8* gene, exon2-exon4 of *Mmp8-201*(ENSMUST00000018765.4) transcript is recommended as the knockout region.The region contains 514bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mmp8* 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,homozygous null males, and to a lesser extent ovariectomized or tamoxifen-treated null females, show increased susceptibility to chemically-induced skin tumors, a sustained inflammatory response to carcinogens, and increased PMN burden in the alveolar space during LPS-mediated acute lung injury.

➢ The *Mmp8* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information（NCBI）

集萃药康 GemPharmatech

Mmp8 matrix metallopeptidase 8 [Mus musculus (house mouse)]

Gene ID: 17394, updated on 13-Mar-2020

Summary

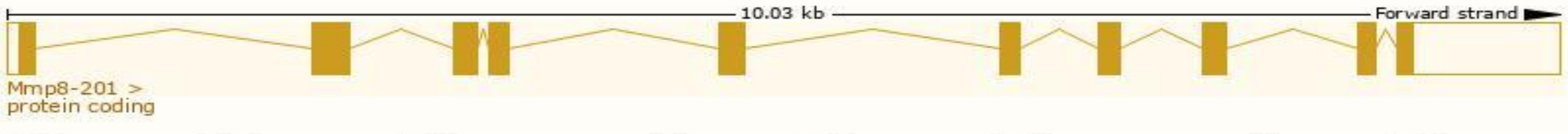
Official Symbol	Mmp8 provided by MGI
Official Full Name	matrix metallopeptidase 8 provided byMGI
Primary source	MGI:MGI:1202395
See related	Ensembl:ENSMUSG00000005800
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BB138268
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 that degrades types I, II and III collagens. Mice lacking the encoded protein exhibit abnormalities in the inflammatory responses to various agents. This gene is located in a cluster of other matrix metalloproteinase genes on chromosome 9. [provided by RefSeq, Feb 2016]
Expression	Biased expression in liver E18 (RPKM 19.0) and liver E14.5 (RPKM 0.8)See more
Orthologs	human all

Transcript information（Ensembl）

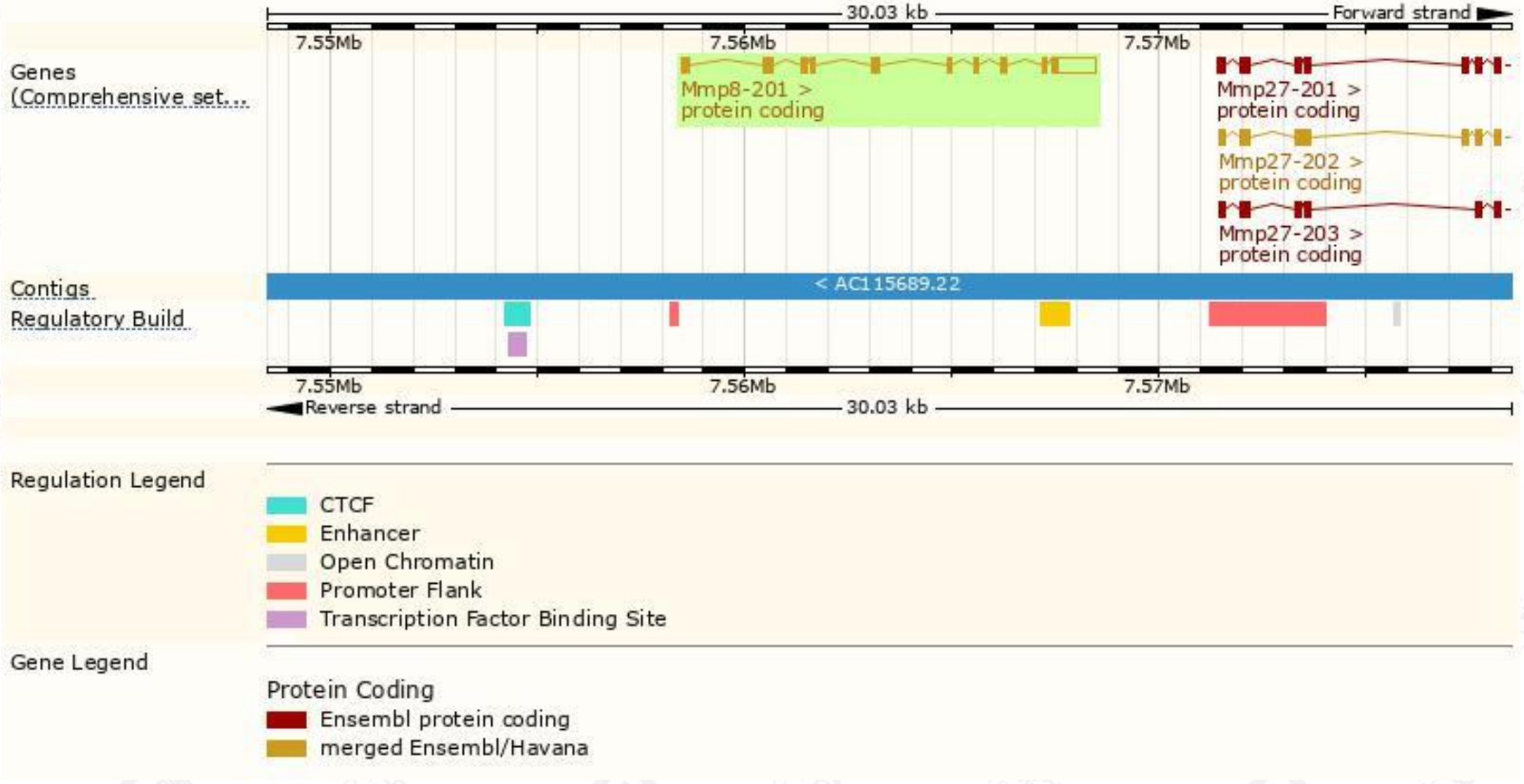
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mmp8-201	ENSMUST00000018765.3	2425	465aa	Protein coding	CCDS22808	O70138	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

The strategy is based on the design of *Mmp8-201* transcript,the transcription is shown below:

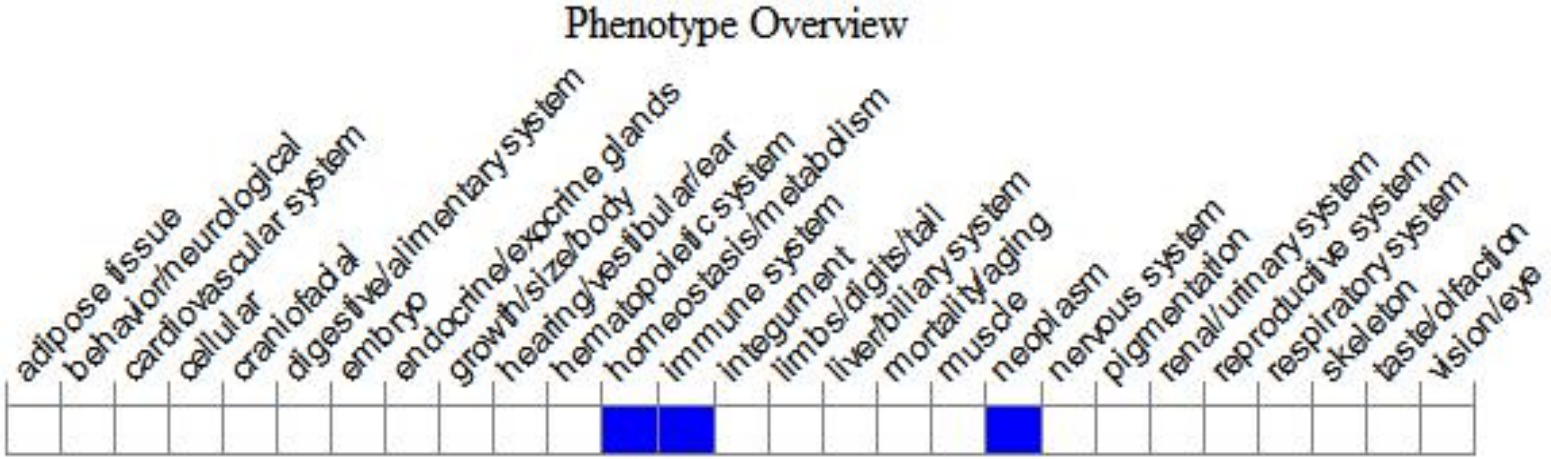


Genomic location distribution



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 males, and to a lesser extent ovariectomized or tamoxifen-treated null females, show increased susceptibility to chemically-induced skin tumors, a sustained inflammatory response to carcinogens, and increased PMN burden in the alveolar space during LPS-mediated acute lung injury.

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