

# ***Bmp5 Cas9-CKO Strategy***

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# Project Overview

**Project Name**

***Bmp5***

**Project type**

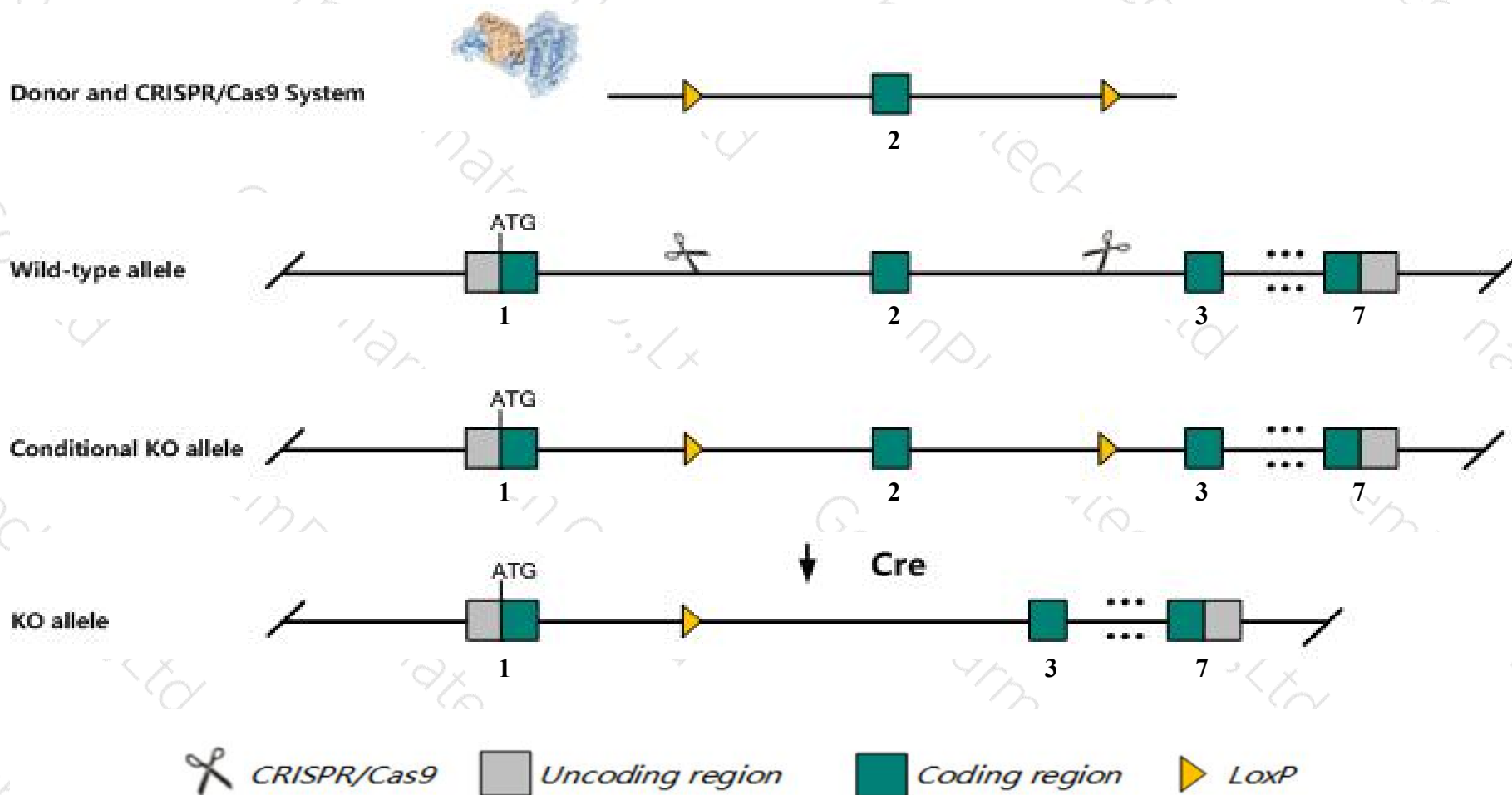
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bmp5* gene. The schematic diagram is as follows:



# Technical routes

- The *Bmp5* gene has 2 transcripts. According to the structure of *Bmp5* gene, exon2 of *Bmp5-201* (ENSMUST00000012281.7) transcript is recommended as the knockout region. The region contains 193bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bmp5* 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.

- According to the existing MGI data, Homozygous recessive mutants have shortened, slightly ruffled external ears due to a defective cartilage framework affecting the whole skeleton; a series of genomic deletions of the region cause embryonic lethality.
- The *Bmp5* 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)

## Bmp5 bone morphogenetic protein 5 [Mus musculus (house mouse)]

Gene ID: 12160, updated on 31-Jan-2019

### Summary



**Official Symbol** Bmp5 provided by [MGI](#)

**Official Full Name** bone morphogenetic protein 5 provided by [MGI](#)

**Primary source** [MGI:MGI:88181](#)

**See related** [Ensembl:ENSMUSG000000032179](#)

**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** AU023399, se

**Summary** This gene encodes a secreted ligand of the TGF-beta (transforming growth factor-beta) superfamily of proteins. Ligands of this family bind various TGF-beta receptors leading to recruitment and activation of SMAD family transcription factors that regulate gene expression. The encoded preproprotein is proteolytically processed to generate each subunit of the disulfide-linked homodimer, which plays a role in bone and cartilage development. Mice with null mutations in this gene exhibit a short ear phenotype, which is characterized by reduced size of the external ear, altered size and shape of the sternum, and other skeletal and soft-tissue abnormalities. [provided by RefSeq, Jul 2016]

**Expression** Biased expression in bladder adult (RPKM 8.5), lung adult (RPKM 3.4) and 10 other tissues [See more](#)

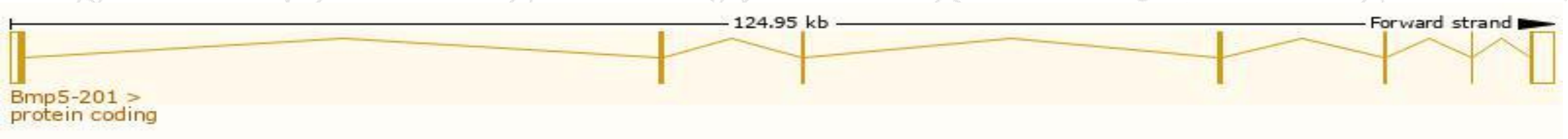
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

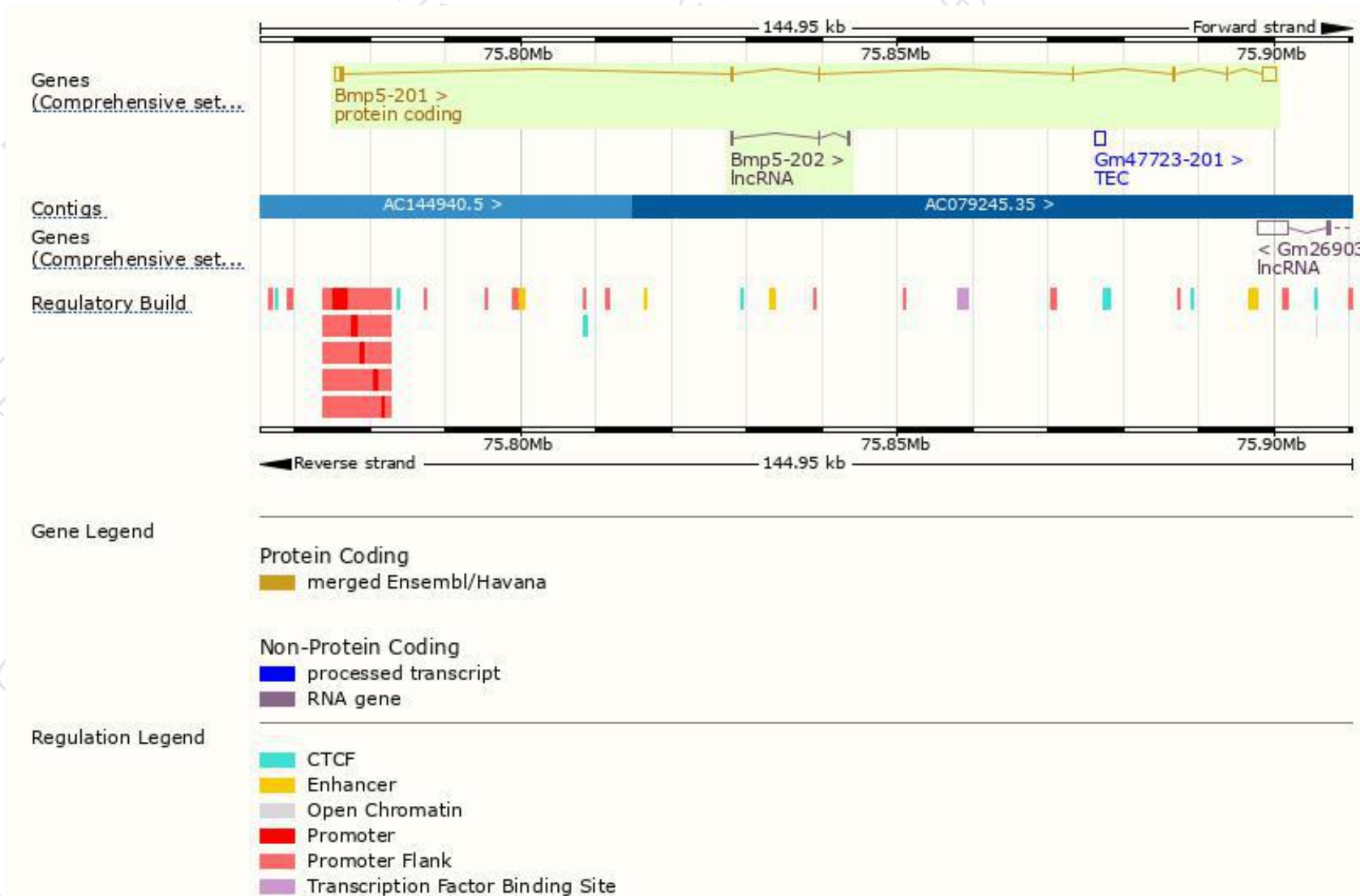
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bmp5-201	<a href="#">ENSMUST00000012281.7</a>	3822	<a href="#">454aa</a>	Protein coding	<a href="#">CCDS23348</a>	<a href="#">P49003</a>	TSL:1 GENCODE basic APPRIS P1
Bmp5-202	<a href="#">ENSMUST00000137213.1</a>	541	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Bmp5-201* transcript,The transcription is shown below



# Genomic location distribution

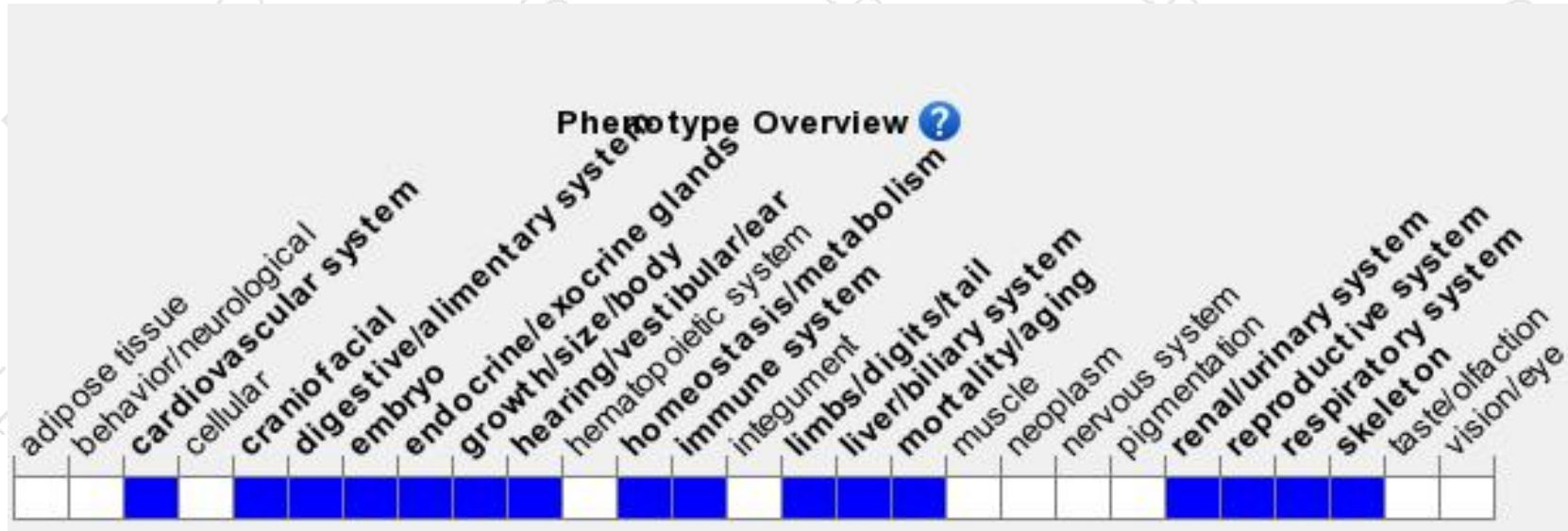




# Protein domain



# 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 recessive mutants have shortened, slightly ruffled external ears due to a defective cartilage framework affecting the whole skeleton; a series of genomic deletions of the region cause embryonic lethality.

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

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