

# *Bmp8b* Cas9-KO Strategy

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**Reviewer: Huan wang**

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# Project Overview

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**Project Name**

*Bmp8b*

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**Project type**

**Cas9-KO**

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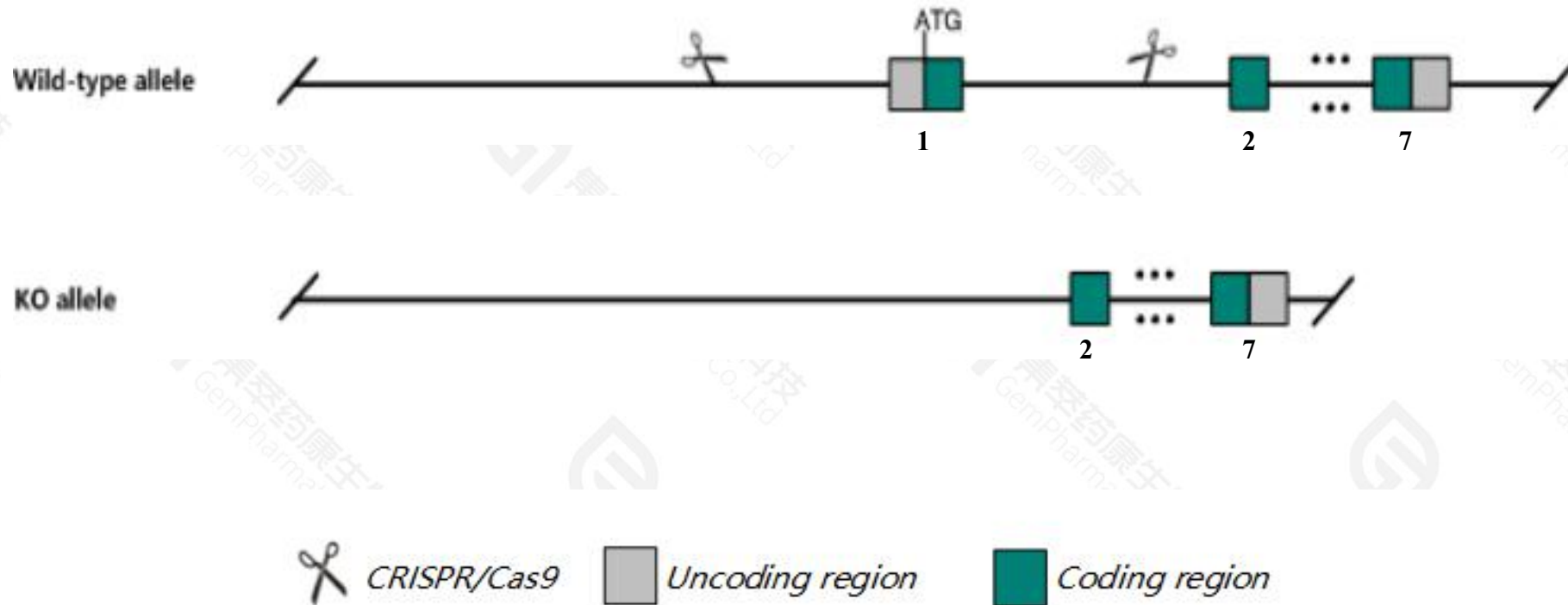
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bmp8b* gene. The schematic diagram is as follows:



- The *Bmp8b* gene has 2 transcripts. According to the structure of *Bmp8b* gene, exon1 of *Bmp8b*-201(ENSMUST00000002457.2) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bmp8b* gene. The brief process is as follows: CRISPR/Cas9 system 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.



- According to the existing MGI data, incidence of lethality among homozygous null mutants is variable depending on genetic background and due to allantoic and embryonic abnormalities. Heterozygous and surviving homozygous males exhibit varying degrees of germ cell deficiency and infertility, also background dependent.
- The *Bmp8b* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information (NCBI)

## Bmp8b bone morphogenetic protein 8b [Mus musculus (house mouse)]

Gene ID: 12164, updated on 13-Mar-2020

### Summary

**Official Symbol** Bmp8b provided by [MGI](#)

**Official Full Name** bone morphogenetic protein 8b provided by [MGI](#)

**Primary source** [MGI:MGI:107335](#)

**See related** [Ensembl:ENSMUSG00000002384](#)

**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** Op3

**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. The encoded protein may play a role in the generation of primordial germ cells, and has been shown to stimulate thermogenesis in brown adipose tissue. Male mice lacking a functional copy of this gene exhibit variable degrees of germ-cell deficiency. Homozygous knockout mice of both sexes exhibit impaired thermogenesis and reduced metabolic rate, resulting in weight gain. This gene may have arose from a gene duplication event and its gene duplicate is also present on chromosome 4. [provided by RefSeq, Jul 2016]

**Expression** Biased expression in small intestine adult (RPKM 3.9), large intestine adult (RPKM 1.9) and 8 other tissues [See more](#)

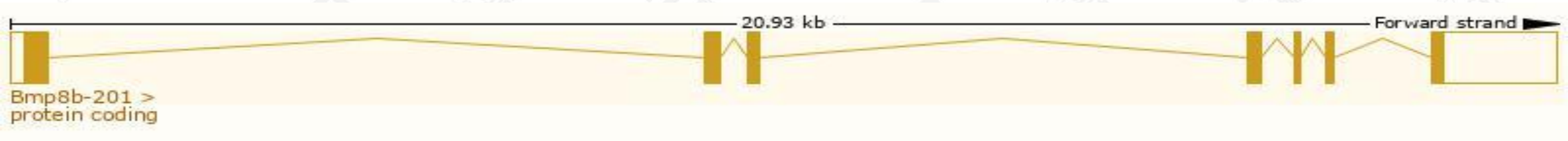
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

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

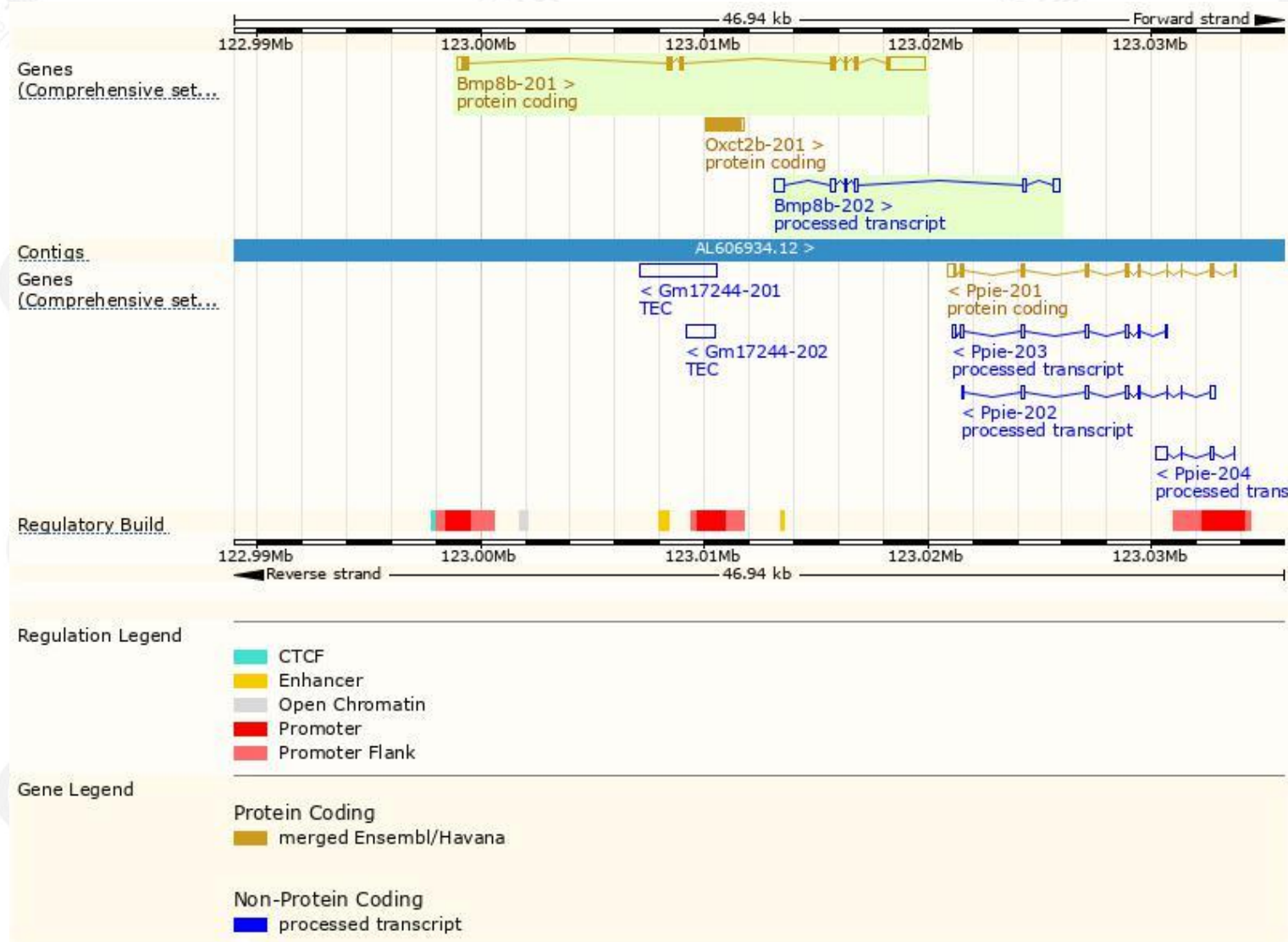
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bmp8b-201	<a href="#">ENSMUST00000002457.1</a>	2940	<a href="#">399aa</a>	Protein coding	<a href="#">CCDS18608</a>	<a href="#">P55105</a>	TSL:1 GENCODE basic APPRIS P1
Bmp8b-202	<a href="#">ENSMUST00000151850.1</a>	1326	No protein	Processed transcript	-	-	TSL:1

The strategy is based on the design of *Bmp8b-201* transcript,the transcription is shown below:





# Genomic location distribution

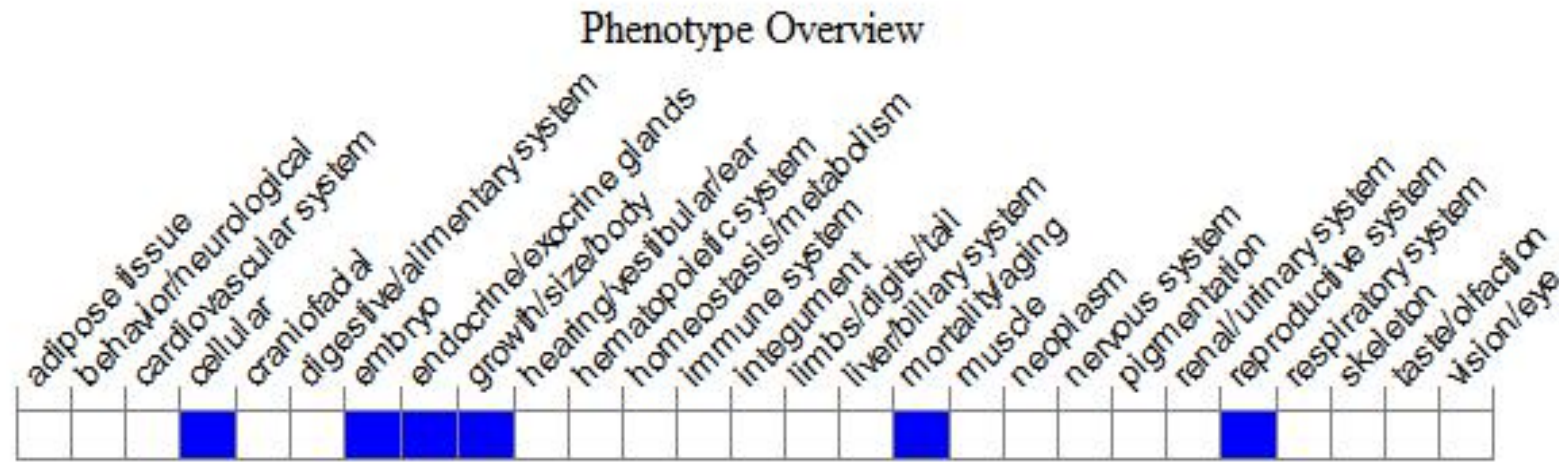




# Protein domain



# 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, incidence of lethality among homozygous null mutants is variable depending on genetic background and due to allantoic and embryonic abnormalities. Heterozygous and surviving homozygous males exhibit varying degrees of germ cell deficiency and infertility, also background dependent.

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