

# *Cebpa* Cas9-KO Strategy

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# Project Overview

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**Project Name**

*Cebpa*

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**Project type**

**Cas9-KO**

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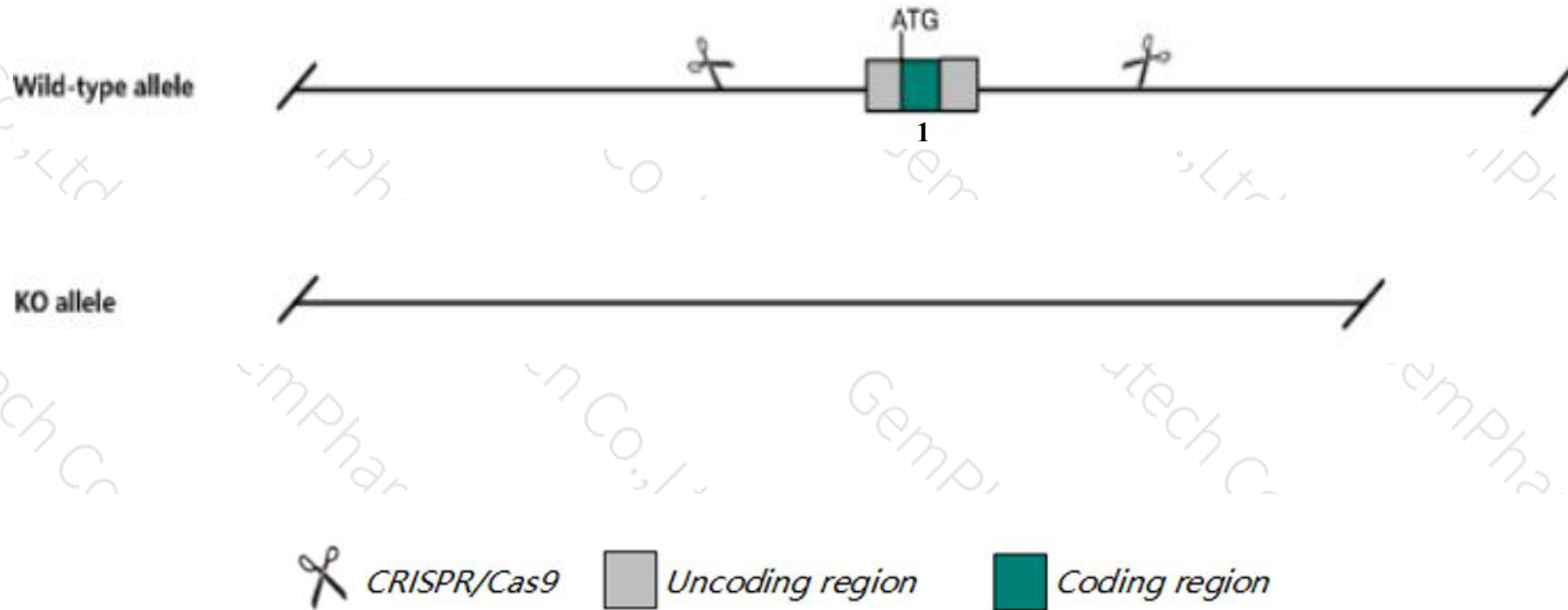
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

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



- The *Cebpa* gene has 2 transcripts. According to the structure of *Cebpa* gene, exon1 of *Cebpa-201* (ENSMUST00000042985.10) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cebpa* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygotes for targeted null mutations exhibit defects of the liver, neutrophils, lung, and brown fat, resulting in impaired glycogen storage and lipid accumulation, hypoglycemia, reduced uncoupling protein, and neonatal lethality.
- The *Cebpa* gene is located on the Chr7. 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)

## Cebpa CCAAT/enhancer binding protein (C/EBP), alpha [Mus musculus (house mouse)]

Gene ID: 12606, updated on 22-Mar-2020

### Summary

**Official Symbol** Cebpa provided by MGI

**Official Full Name** CCAAT/enhancer binding protein (C/EBP), alpha provided by MGI

**Primary source** [MGI:MGI:99480](#)

**See related** [Ensembl:ENSMUSG00000034957](#)

**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** C/ebpalpha, CBF-A, Cebp

**Summary** This intronless gene encodes a transcription factor that contains a basic leucine zipper (bZIP) domain and recognizes the CCAAT motif in the promoters of target genes. The encoded protein functions in homodimers and also heterodimers with CCAAT/enhancer-binding proteins beta and gamma. Activity of this protein can modulate the expression of genes involved in cell cycle regulation as well as in body weight homeostasis. The use of alternative in-frame non-AUG (CUG) and AUG start codons results in several protein isoforms with different lengths. Differential translation initiation is mediated by an out-of-frame, upstream open reading frame which is located between the CUG and the first AUG start codons. [provided by RefSeq, Sep 2014]

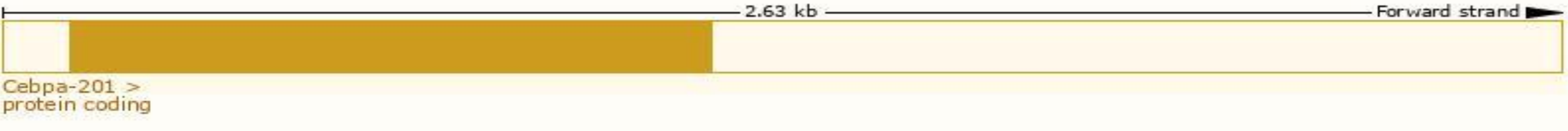
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

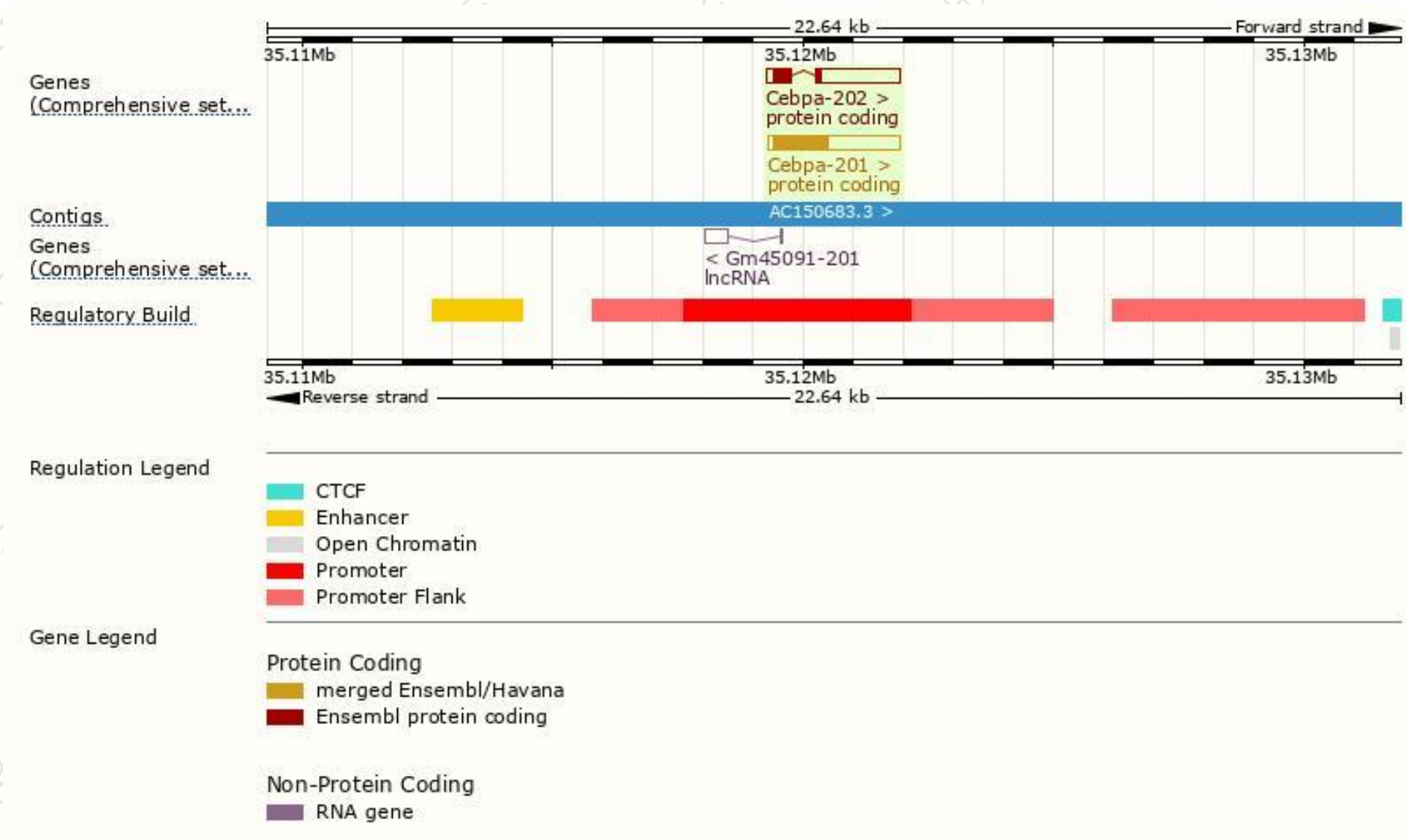
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cebpa-201	<a href="#">ENSMUST00000042985.10</a>	2626	<a href="#">359aa</a>	Protein coding	<a href="#">CCDS21145</a>	<a href="#">P53566</a>	TSL:NA 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
Cebpa-202	<a href="#">ENSMUST000000205391.1</a>	2161	<a href="#">159aa</a>	Protein coding	-	<a href="#">A0A0U1RPE0</a>	TSL:5 GENCODE basic

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



# Genomic location distribution

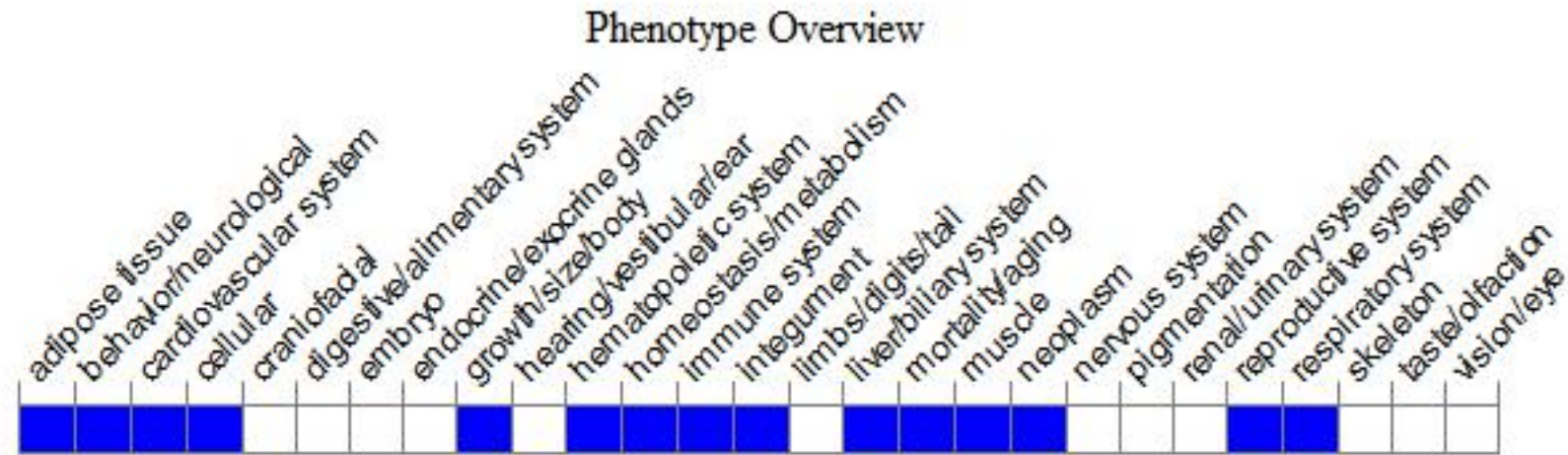




# Protein domain



# 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, homozygotes for targeted null mutations exhibit defects of the liver, neutrophils, lung, and brown fat, resulting in impaired glycogen storage and lipid accumulation, hypoglycemia, reduced uncoupling protein, and neonatal lethality.

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

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