GemPharmatech™

Cpe Cas9-KO Strategy

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Overview

Target Gene Name

- Cpe

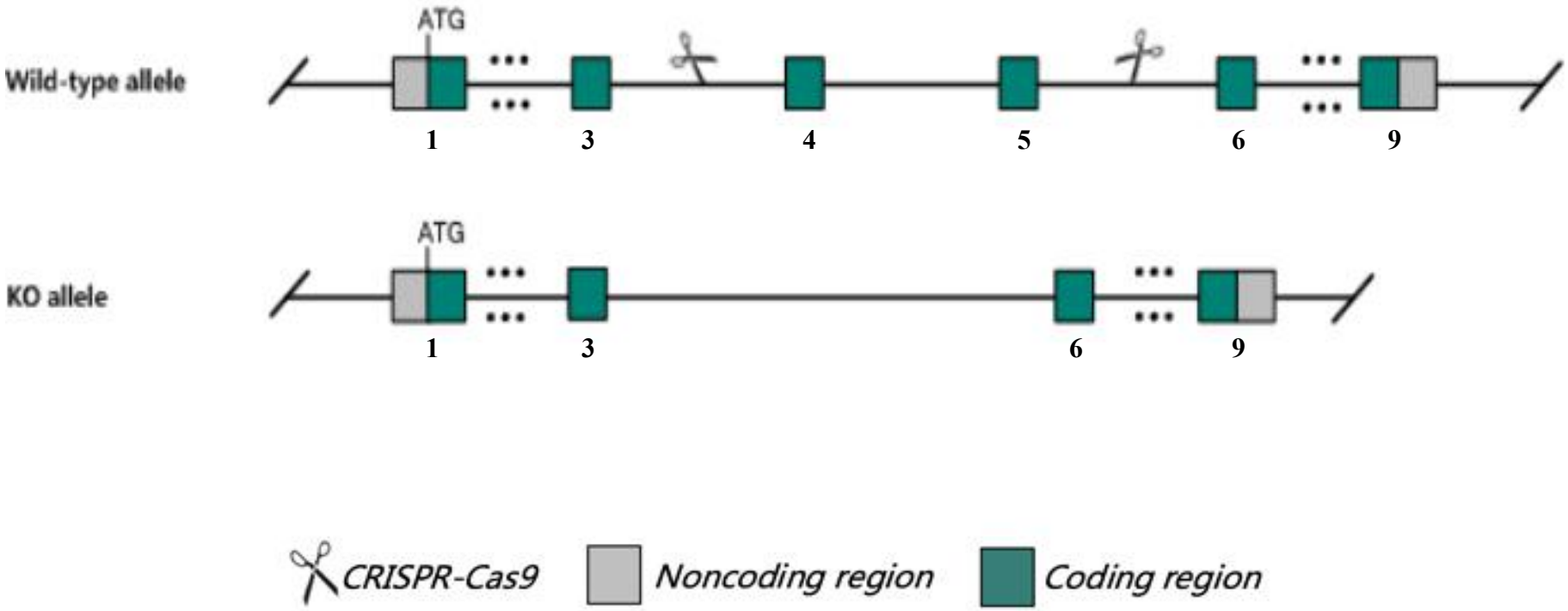
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Technical Information

- The *Cpe* gene has 4 transcripts. According to the structure of *Cpe* gene, exon4-exon5 of *Cpe*-201 (ENSMUST00000048967.9) transcript is recommended as the knockout region. The region contains 301bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Cpe* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information

Cpe carboxypeptidase E [Mus musculus (house mouse)]

Gene ID: 12876, updated on 13-Mar-2020

Summary

Official Symbol	Cpe provided by MGI
Official Full Name	carboxypeptidase E provided by MGI
Primary source	MGI:MGI:101932
See related	Ensembl:ENSMUSG00000037852
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	CPH, Cph-1, Cph1, NF-alpha1, R74677, fat
Summary	This gene encodes carboxypeptidase E, a prohormone-processing exopeptidase found in secretory granules of endocrine and neuroendocrine cells. The encoded preproprotein undergoes proteolytic processing to generate a mature, functional enzyme that cleaves the C-terminal basic residues of protein substrates. A missense mutation in this gene is responsible for the obesity phenotype in a mouse model known as the "fat mouse." Mice lacking the functional product of this gene exhibit impaired processing of multiple peptide hormones such as proinsulin, prodynorphin, proneurotensin, promelanin-concentrating hormone and pro-opiomelanocortin. [provided by RefSeq, Jan 2016]
Expression	Biased expression in frontal lobe adult (RPKM 416.8), cortex adult (RPKM 400.4) and 14 other tissues See more
Orthologs	human all

Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

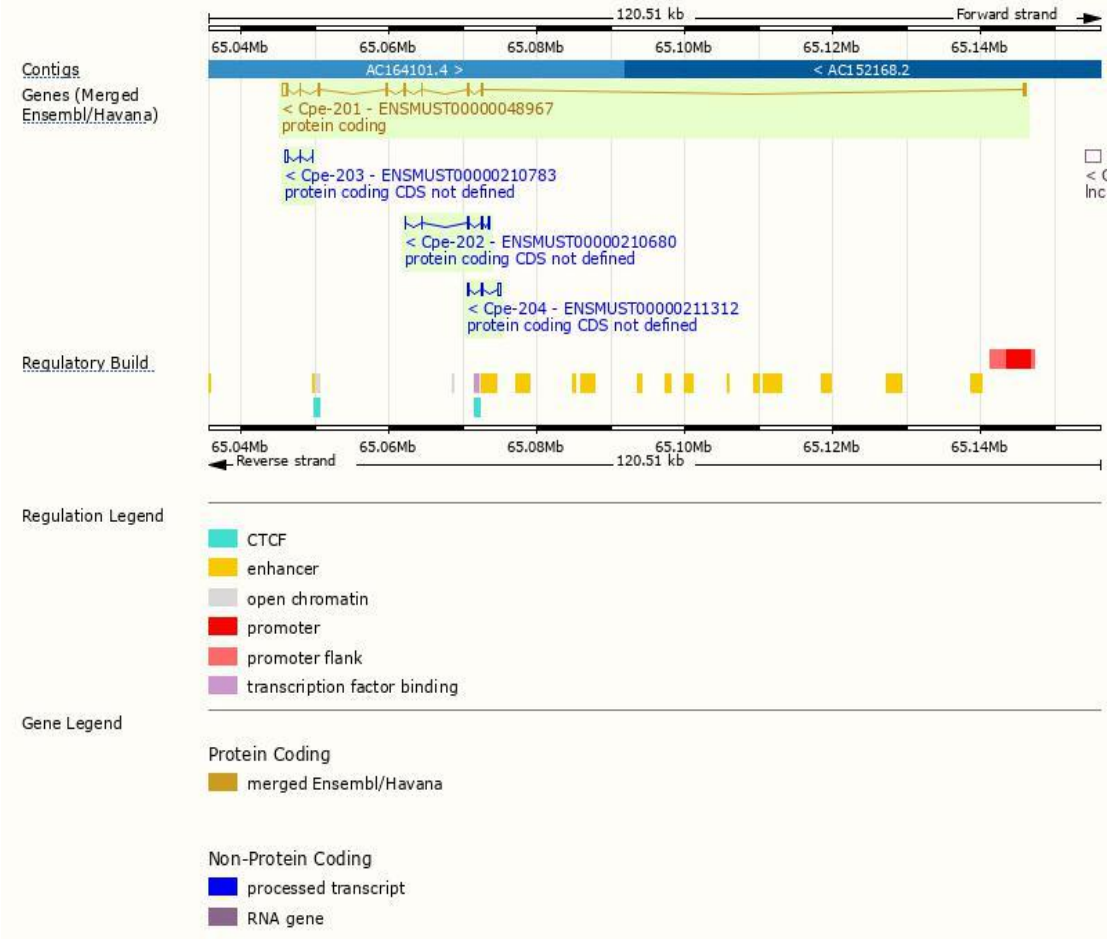
The gene has 4 transcripts,all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000048967.9	Cpe-201	2117	476aa	Protein coding	CCDS22327	Q00493 Q543R4	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000211312.2	Cpe-204	688	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000210680.2	Cpe-202	590	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000210783.2	Cpe-203	550	No protein	Protein coding CDS not defined		-	TSL:3

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

Source: https://www.ensembl.org

Genomic Information



Source: : https://www.ensembl.org

Protein Information

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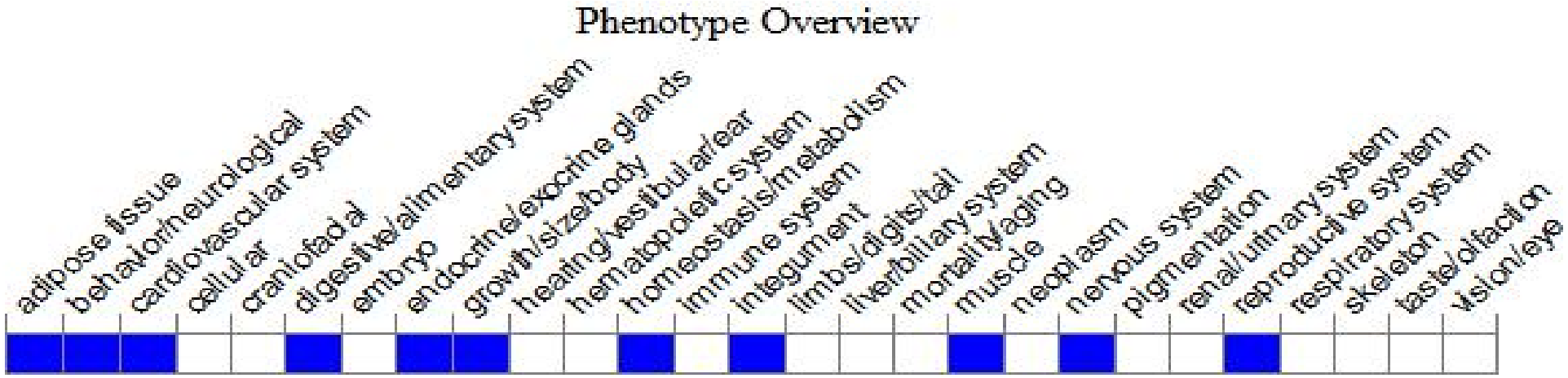
Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



- Mice homozygous for a spontaneous or a targeted null mutation display progressive obesity, abnormal blood glucose and lipid regulation, and have reduced fertility. Aberrant prohormone processing and secretion appears to be the cause of these phenotypes.

Source: https://www.informatics.jax.org

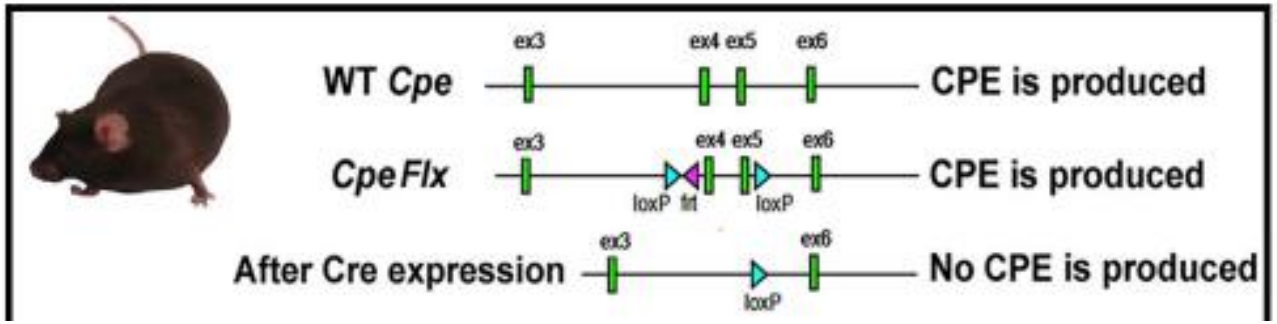
References

Resource

Cell Chemical Biology

Neuropeptidomic Analysis of a Genetically Defined Cell Type in Mouse Brain and Pituitary

Graphical Abstract



Authors

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Correspondence

Important Information

- *Cpe* is located on Chr8. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.