

Ebf3 Cas9-KO Strategy

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Project Overview



Project Name

Ebf3

Project type

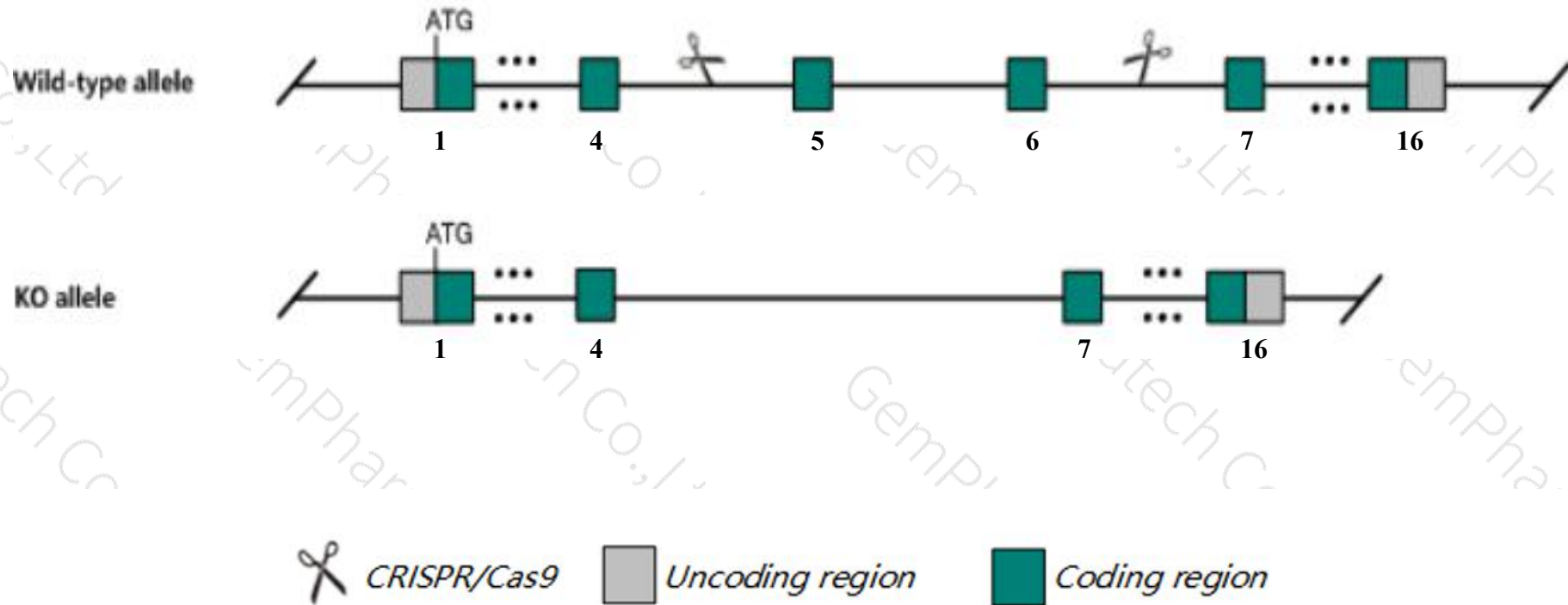
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ebf3* gene. The schematic diagram is as follows:



- The *Ebf3* gene has 8 transcripts. According to the structure of *Ebf3* gene, exon5-exon6 of *Ebf3-201*(ENSMUST00000033378.12) transcript is recommended as the knockout region. The region contains 143bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ebf3* 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, homozygous mutant mice die perinatally and exhibit impaired olfactory neuron projection.
- The *Ebf3* 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)

Ebf3 early B cell factor 3 [Mus musculus (house mouse)]

Gene ID: 13593, updated on 13-Mar-2020

Summary

Official Symbol Ebf3 provided by [MGI](#)

Official Full Name early B cell factor 3 provided by [MGI](#)

Primary source [MGI:MGI:894289](#)

See related [Ensembl:ENSMUSG00000010476](#)

Gene type protein coding

RefSeq status VALIDATED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as 3110018A08Rik, O/E-2, mKIAA4201

Expression Biased expression in CNS E14 (RPKM 24.6), limb E14.5 (RPKM 23.6) and 9 other tissues [See more](#)

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

Transcript information (Ensembl)

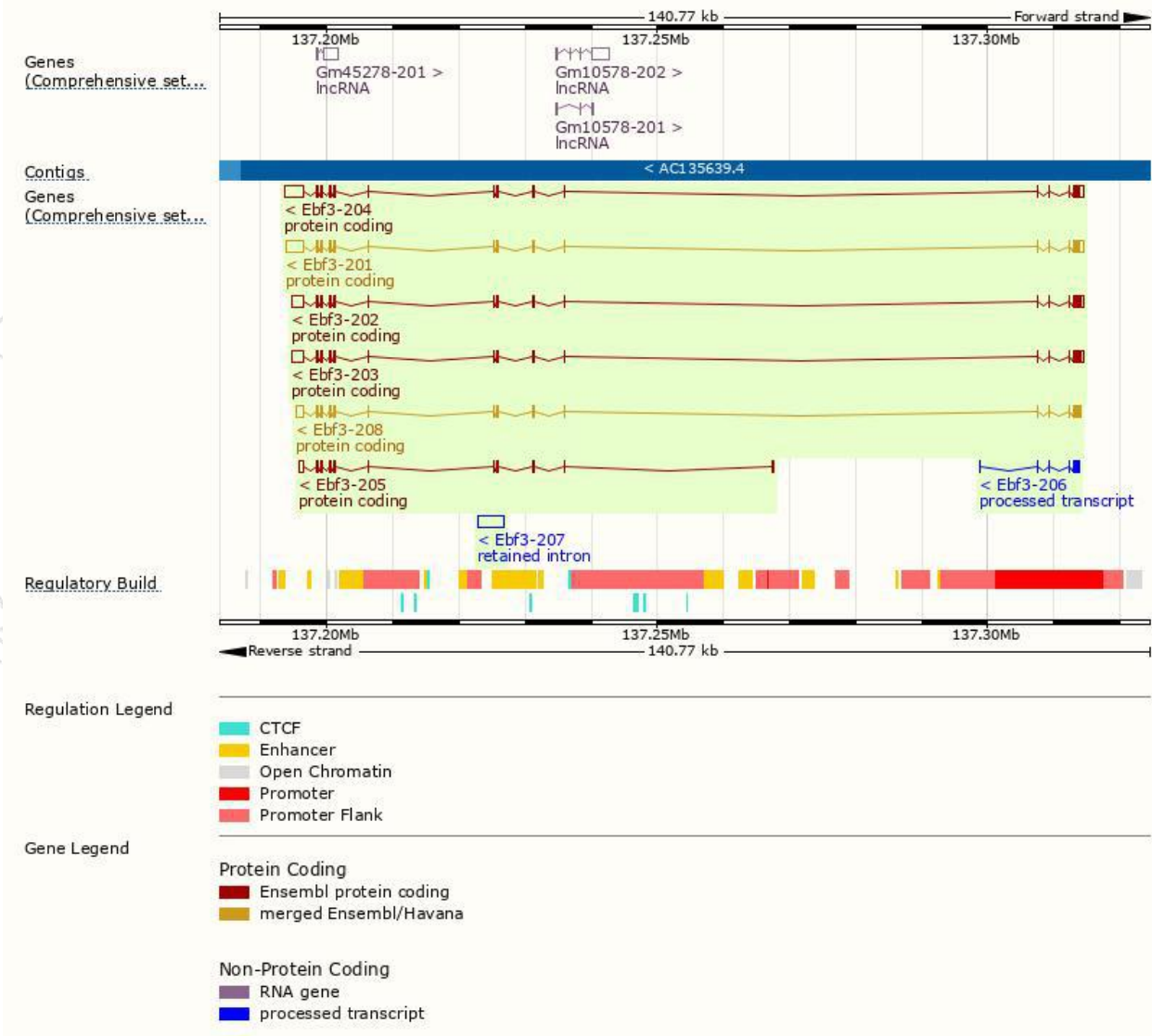
The gene has 8 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ebf3-204	ENSMUST00000169486.8	4994	587aa	Protein coding	CCDS52423	Q6NXL3	TSL:5 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 ALT1
Ebf3-201	ENSMUST00000333378.12	4838	551aa	Protein coding	CCDS21946	Q08791	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 P3
Ebf3-202	ENSMUST00000106118.9	3736	587aa	Protein coding	CCDS52423	Q6NXL3	TSL:5 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 ALT1
Ebf3-203	ENSMUST00000168203.1	3724	587aa	Protein coding	CCDS52423	Q6NXL3	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 ALT1
Ebf3-208	ENSMUST00000210774.1	2994	596aa	Protein coding	CCDS52422	Q08791	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 ALT1
Ebf3-205	ENSMUST00000209578.1	1863	344aa	Protein coding	-	Q3UUB6	TSL:1 GENCODE basic
Ebf3-206	ENSMUST00000209864.1	739	No protein	Processed transcript	-	-	TSL:3
Ebf3-207	ENSMUST00000209905.1	4008	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *Ebf3-201* transcript, the transcription is shown below:



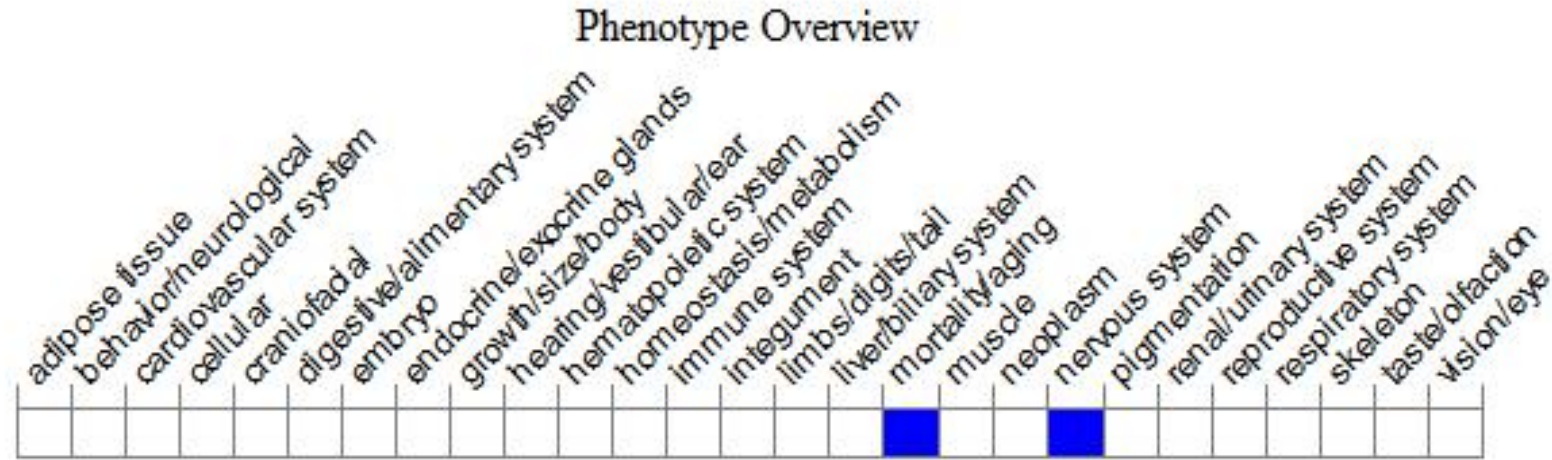
Genomic location distribution



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 mutant mice die perinatally and exhibit impaired olfactory neuron projection.

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

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