

Bcat2 Cas9-CKO Strategy

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Project Overview



Project Name Bcat2

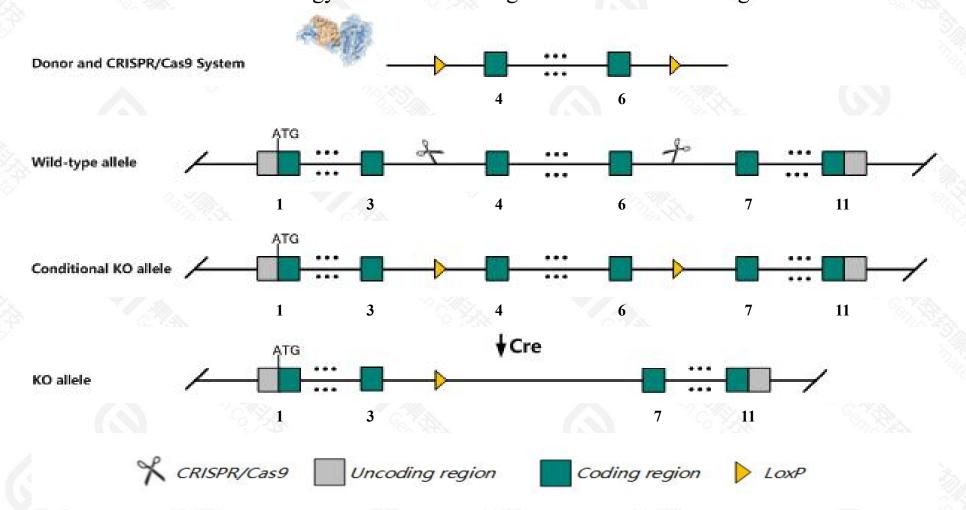
Project type Cas9-CKO

Strain background C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Bcat2* gene. The schematic diagram is as follows:



Technical routes



- > The *Bcat2* gene has 8 transcripts. According to the structure of *Bcat2* gene, exon4-exon6 of *Bcat2*201(ENSMUST00000033098.16) transcript is recommended as the knockout region. The region contains 395bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Bcat2* 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.

Notice



- > According to the existing MGI data, the metabolism of branched chain amino acid is impaired in homozygous null mice, resulting in a phenotype similar to human maple syrup urine disease. Mutants exhibit a failure to thrive and die prematurely, though the severity of the symptoms can be ameliorated with a restricted diet.
- > The *Bcat2* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



Bcat2 branched chain aminotransferase 2, mitochondrial [Mus musculus (house mouse)]

Gene ID: 12036, updated on 13-Mar-2020

Summary



Official Symbol Bcat2 provided by MGI

Official Full Name branched chain aminotransferase 2, mitochondrial provided by MGI

Primary source MGI:MGI:1276534

See related Ensembl: ENSMUSG00000030826

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 Bcat(m), Bcat-2, Eca40

Expression Ubiquitous expression in adrenal adult (RPKM 36.2), subcutaneous fat pad adult (RPKM 34.2) and 28 other tissuesSee more

Orthologs <u>human</u> all

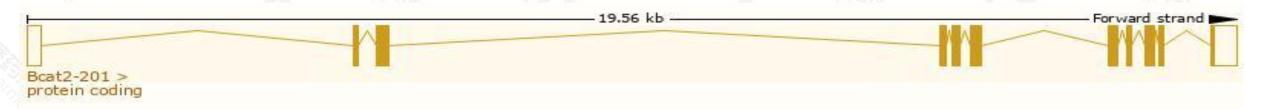
Transcript information (Ensembl)



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

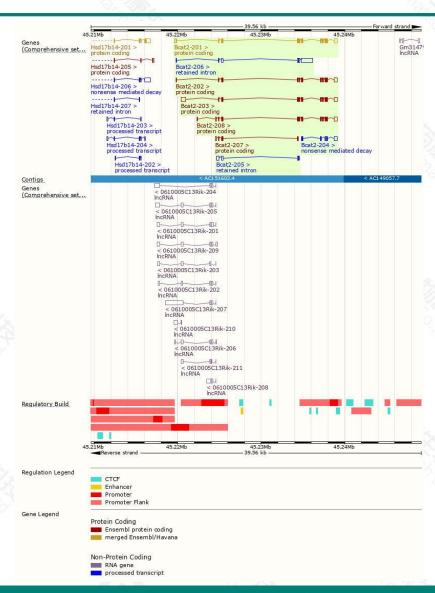
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bcat2-203	ENSMUST00000209204.1	2081	353aa	Protein coding	CCDS57549	<u>088374</u>	TSL:1 GENCODE basic
Bcat2-201	ENSMUST00000033098.15	1772	<u>393aa</u>	Protein coding	CCDS21252	O35855 Q3ULU3	TSL:1 GENCODE basic APPRIS P1
Bcat2-208	ENSMUST00000211173.1	1684	<u>353aa</u>	Protein coding	CCDS57549	<u>088374</u>	TSL:1 GENCODE basic
Bcat2-202	ENSMUST00000120864.9	1536	388aa	Protein coding	-	A0A1B0GX27	TSL:5 GENCODE basic
Bcat2-207	ENSMUST00000210811.1	486	<u>97aa</u>	Protein coding	-	A0A1B0GST1	CDS 3' incomplete TSL:3
Bcat2-204	ENSMUST00000209410.1	917	<u>101aa</u>	Nonsense mediated decay	-	A0A1B0GQY4	CDS 5' incomplete TSL:5
Bcat2-206	ENSMUST00000209569.1	1905	No protein	Retained intron	12		TSL:1
Bcat2-205	ENSMUST00000209543.1	632	No protein	Retained intron	- 2	120	TSL:2
	TV 2	300		07.178	. VO. 77.75	to a	WWW.

The strategy is based on the design of *Bcat2-201* transcript, the transcription is shown below:



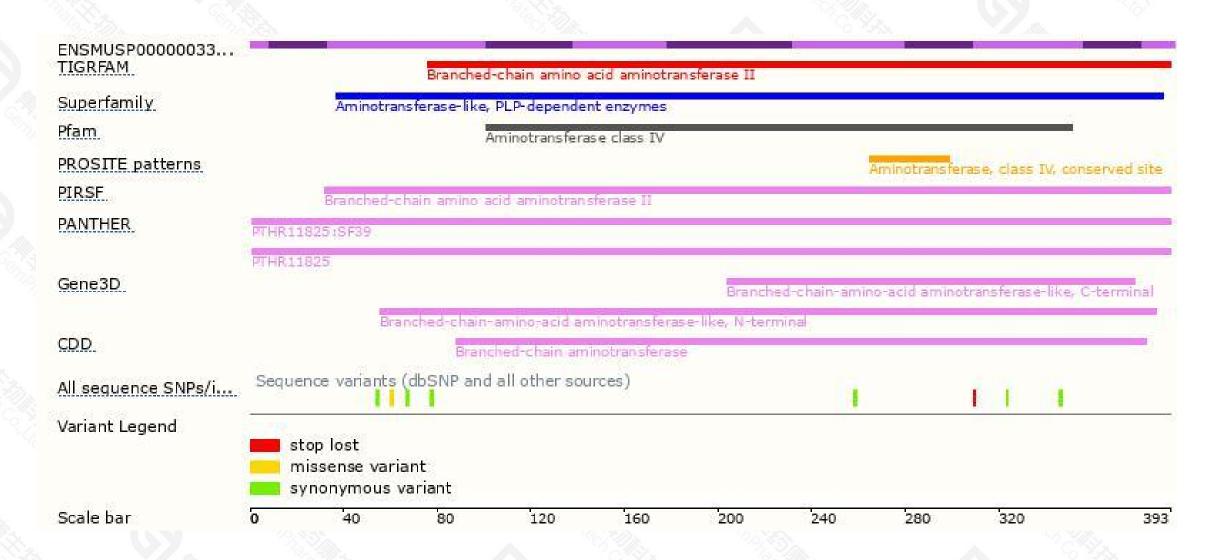
Genomic location distribution





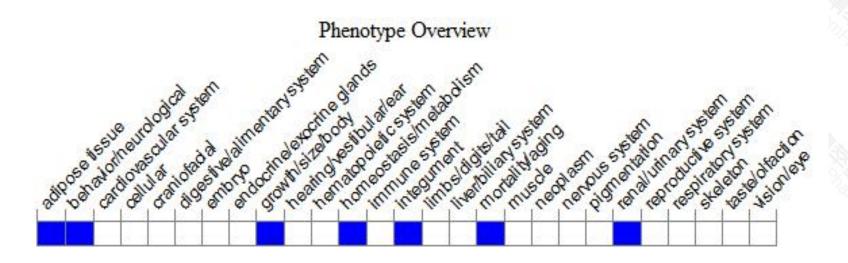
Protein domain





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, the metabolism of branched chain amino acid is impaired in homozygous null mice, resulting in a phenotype similar to human maple syrup urine disease. Mutants exhibit a failure to thrive and die prematurely, though the severity of the symptoms can be ameliorated with a restricted diet.



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

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