

# Tbcd Cas9-CKO Strategy

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# Overview

## Target Gene Name

- Tbcd

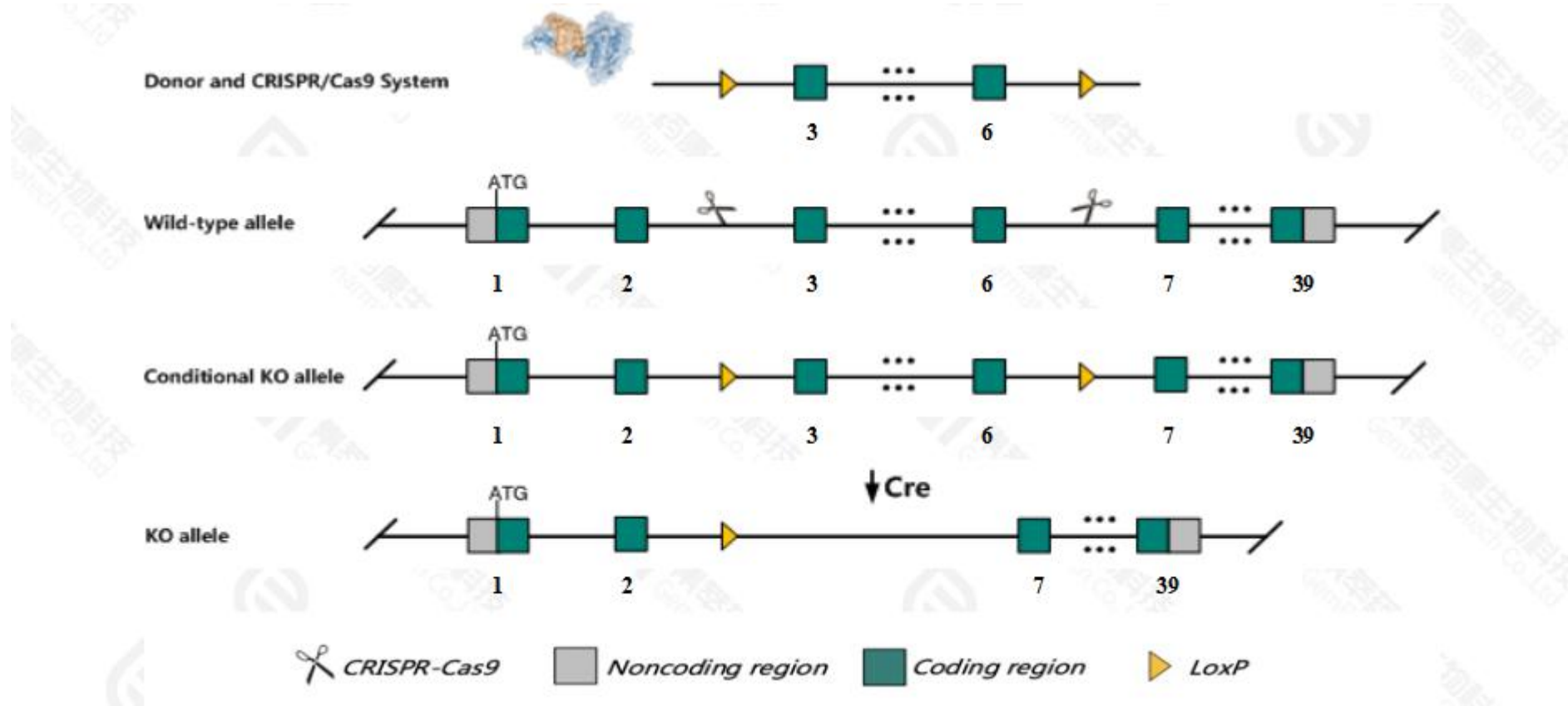
## Project Type

- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Tbcd* gene.

# Technical Information

- The *Tbcd* gene has 8 transcripts. According to the structure of *Tbcd* gene, exon3-exon6 of *Tbcd-201*(ENSMUST00000103013.10) transcript is recommended as the knockout region. The region contains 403bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Tbcd* 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 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.
- 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.

# Gene Information

## Tbcd tubulin-specific chaperone d [Mus musculus (house mouse)]

Gene ID: 108903, updated on 24-Apr-2022

### Summary



<b>Official Symbol</b>	Tbcd provided by <a href="#">MGI</a>
<b>Official Full Name</b>	tubulin-specific chaperone d provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1919686</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000039230</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	2310057L06Rik, A030005L14Rik, mKIAA0988
<b>Expression</b>	Ubiquitous expression in CNS E18 (RPKM 8.3), whole brain E14.5 (RPKM 7.8) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

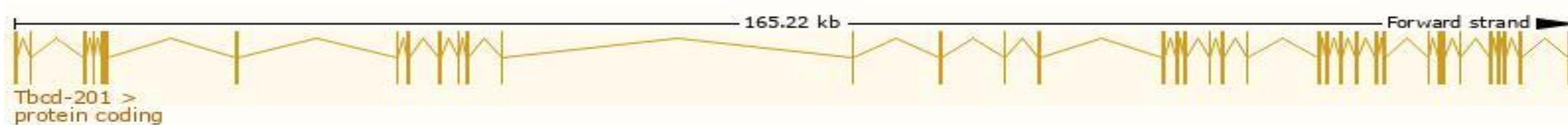
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tbcd-201	<a href="#">ENSMUST00000103013.10</a>	3906	<a href="#">1196aa</a>	Protein coding	<a href="#">CCDS25778</a>		TSL:1 , GENCODE basic , APPRIS P1 ,
Tbcd-202	<a href="#">ENSMUST00000106093.2</a>	368	<a href="#">84aa</a>	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Tbcd-203	<a href="#">ENSMUST00000125167.8</a>	944	<a href="#">72aa</a>	Nonsense mediated decay	-		CDS 5' incomplete , TSL:5 ,
Tbcd-207	<a href="#">ENSMUST00000151666.2</a>	1324	No protein	Processed transcript	-		TSL:1 ,
Tbcd-204	<a href="#">ENSMUST00000139414.8</a>	1292	No protein	Processed transcript	-		TSL:1 ,
Tbcd-206	<a href="#">ENSMUST00000147560.8</a>	699	No protein	Processed transcript	-		TSL:5 ,
Tbcd-208	<a href="#">ENSMUST00000155666.8</a>	4832	No protein	Retained intron	-		TSL:1 ,
Tbcd-205	<a href="#">ENSMUST00000147470.2</a>	716	No protein	Retained intron	-		TSL:5 ,

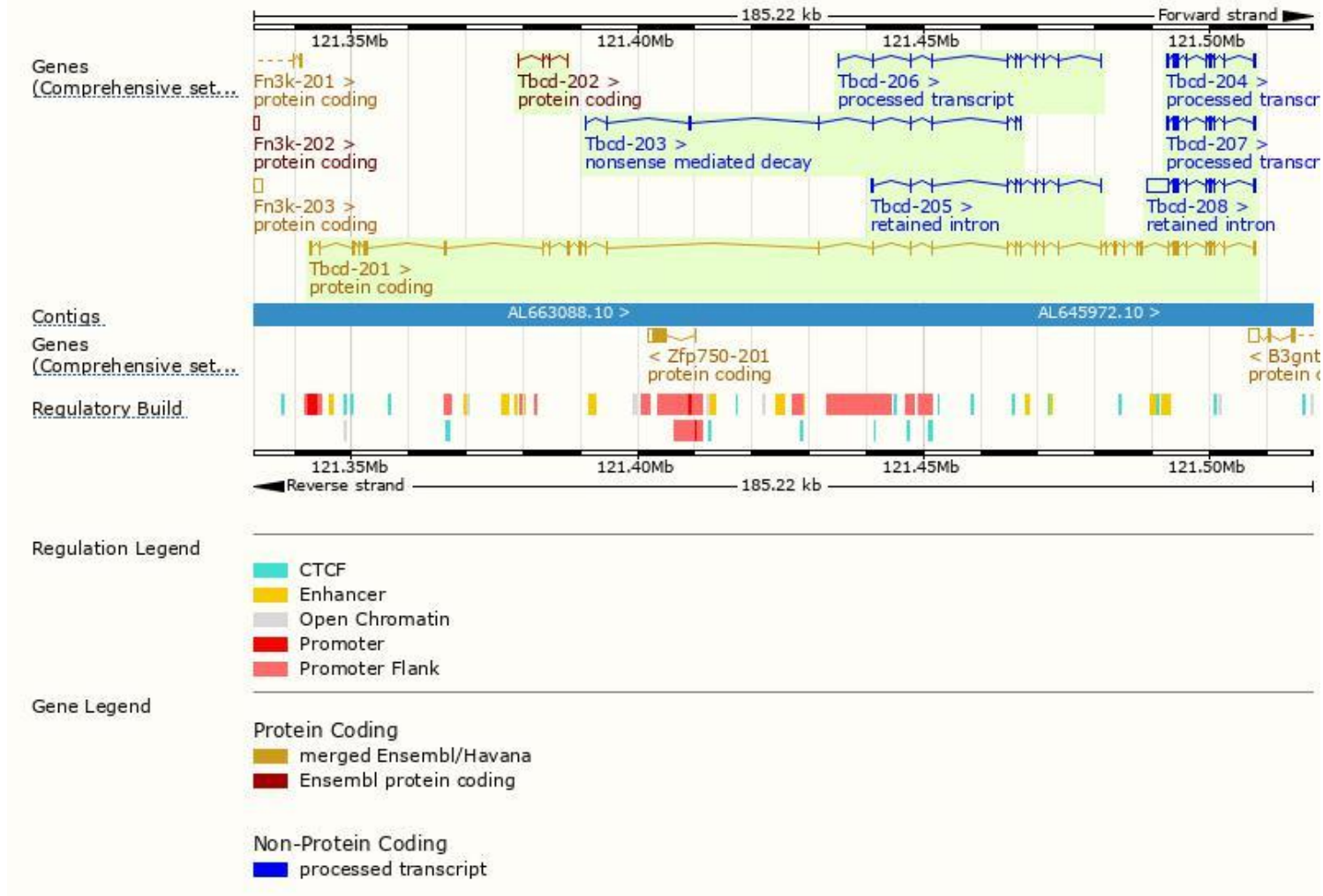
The strategy is based on the design of Tbcd-201 transcript, the transcription is shown below:



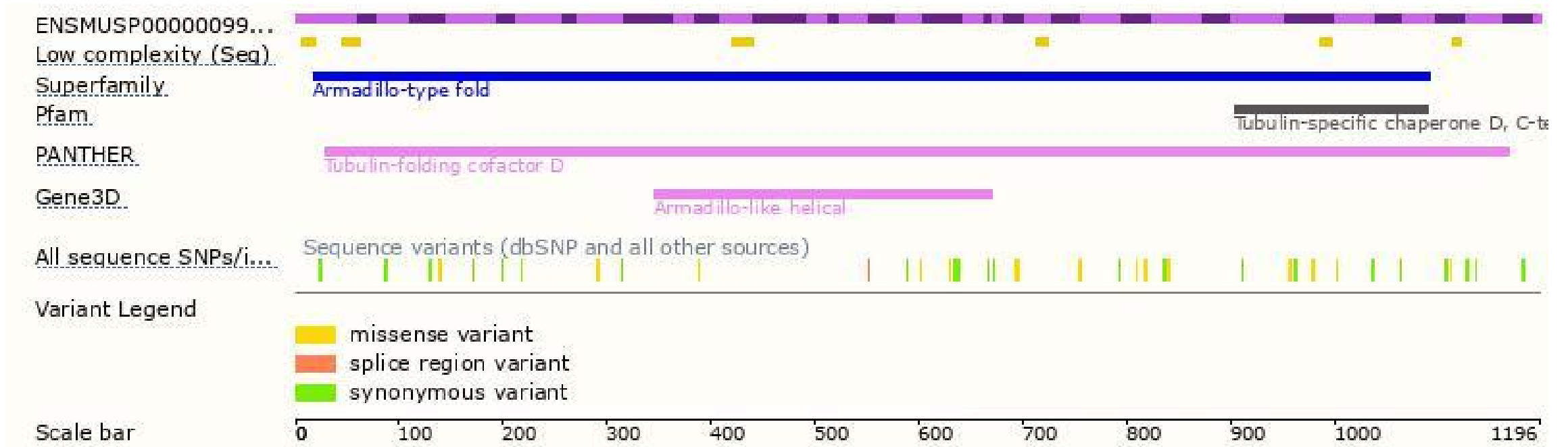
Source: <https://www.ensembl.org>



# Genomic Information

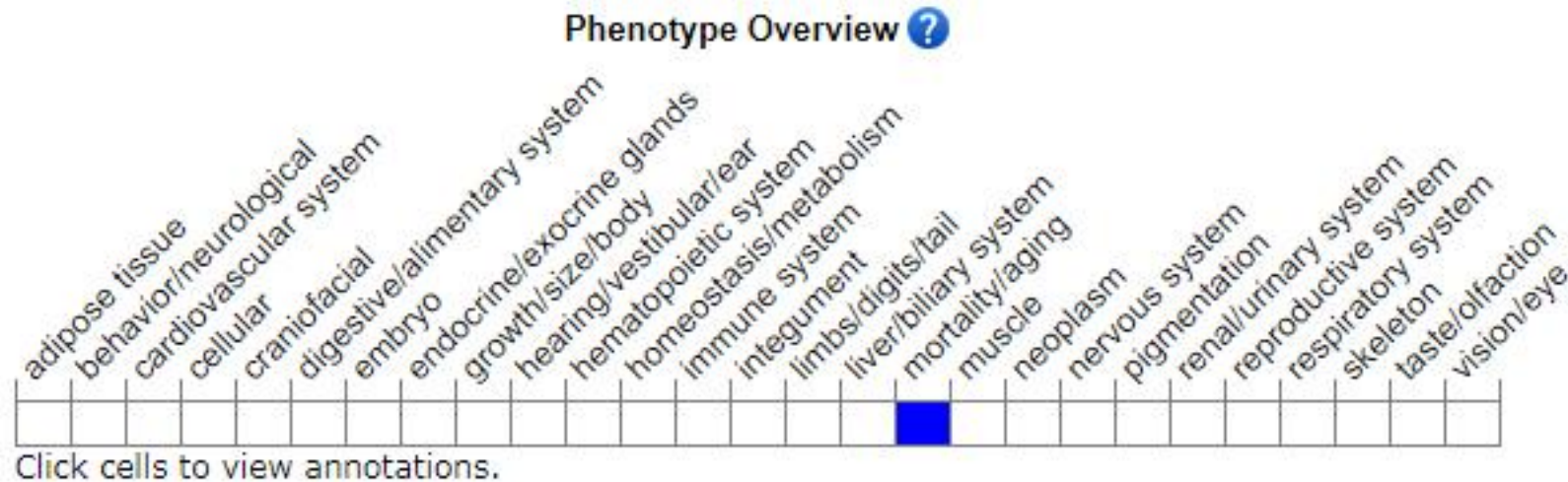


# Protein Information





# Mouse Phenotype Information (MGI)



- Phenotypes affected by the mutations of Tbcd gene are marked in blue.

# Important Information

- Transcript Tbcd-202 may not be affected.
- The *Tbcd* gene is located on the Chr11. 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.