

# Kbtbd13 Cas9-KO Strategy

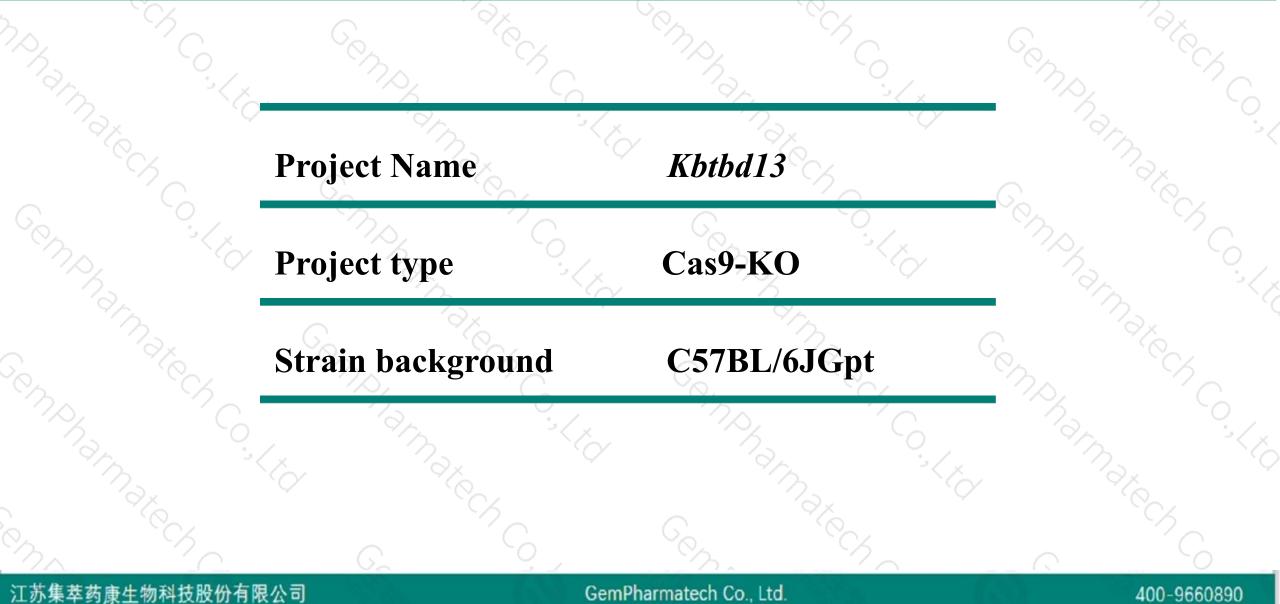
Designer: Zihe Cui

**Reviewer: Ruirui Zhang** 

Design Date: 2021-3-8

### **Project Overview**





## **Knockout** strategy



This model will use CRISPR/Cas9 technology to edit the *Kbtbd13* gene. The schematic diagram is as follows:

Wild-type allele

KO allele CRISPR/Cas9 Uncoding region Coding region

ATG

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400-9660890



The Kbtbd13 gene has 1 transcript. According to the structure of Kbtbd13 gene, exon1 of Kbtbd13-201(ENSMUST0000068307.3) 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 *Kbtbd13* 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.

- > The *Kbtbd13* gene is located on the Chr9. 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.

Notice

## **Gene information (NCBI)**



#### Kbtbd13 kelch repeat and BTB (POZ) domain containing 13 [ Mus musculus (house mouse) ]

Gene ID: 74492, updated on 22-Nov-2020

#### Summary

Official Symbol	Kbtbd13 provided by MGI
Official Full Name	kelch repeat and BTB (POZ) domain containing 13 provided by MGI
Primary source	MGI:MGI:1921742
See related	Ensembl:ENSMUSG0000054978
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
	Myomorpha; Muroidea; Murinae; Mus; Mus
Also known as	5430433E21Rik
Orthologs	human all

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# **Transcript information (Ensembl)**



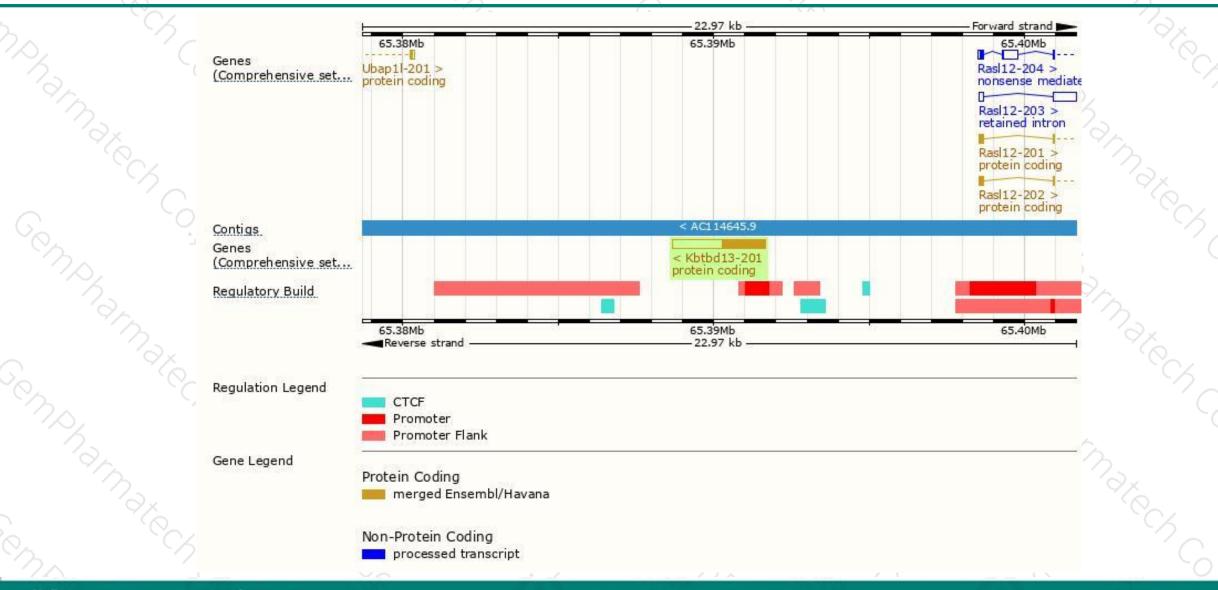
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kbtbd13-201	ENSMUST0000068307.3	2969	<u>458aa</u>	Protein coding	CCDS57682	<u>Q8C828</u>	TSL:NA GENCODE basic APPRIS P1

The strategy is based on the design of *Kbtbd13-201* transcript, the transcription is shown below:

< Kbtbd13-201 protein coding						
Reverse strand			2.9	7 kb		
DB Harr		narma,	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	ND Harr	harma.	.<
	No.			- Con		X

### **Genomic location distribution**



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### **Protein domain**



		5 °C2	<u></u>		6	- CO/
ENSMUSP00000136 Superfamily	SKP1/BTB/POZ do	main superfamily	Kelch-type beta prope	ller		- <sup>2</sup> 6
SMART			CONTRACTOR OF A DESCRIPTION OF A DESCRIP	eat type 1		• 
Pfam PROSITE profiles	BTB/POZ domain		Kelch repeat	type 1		
PANTHER	PTHR46375					- C
	PTHR46375:SF3					
Gene3D	3.30,710,10		pe beta propeller			
CDD	cd18320	cd18486				
All sequence SNPs/i	Sequence variants	(dbSNP and all other	sources)	1	Ϋ́.	2
Variant Legend	missense var					~
Scale bar	<b>o</b> 40	80 120	160 200 2	40 280 320	360 400	458
						~? C
	G_	9.2				<u> </u>

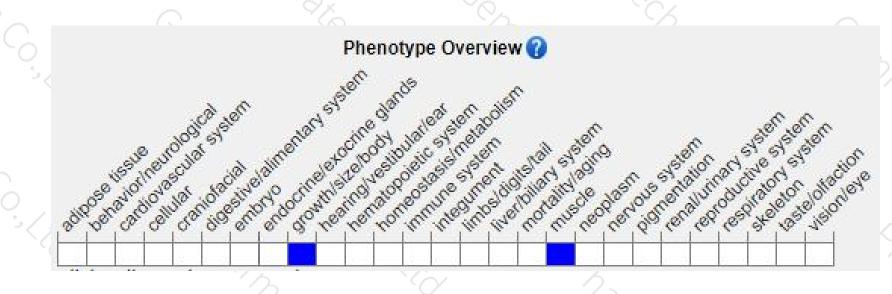
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# Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

Homozygosity for a specific point mutation increases muscle weight and slows muscle relaxation kinetics.



If you have any questions, you are welcome to inquire. Tel: 400-9660890



