

# ***Zbtb18* Cas9-KO Strategy**

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**Reviewer: Yumeng Wang**

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# Project Overview

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**Project Name**

***Zbtb18***

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**Project type**

**Cas9-KO**

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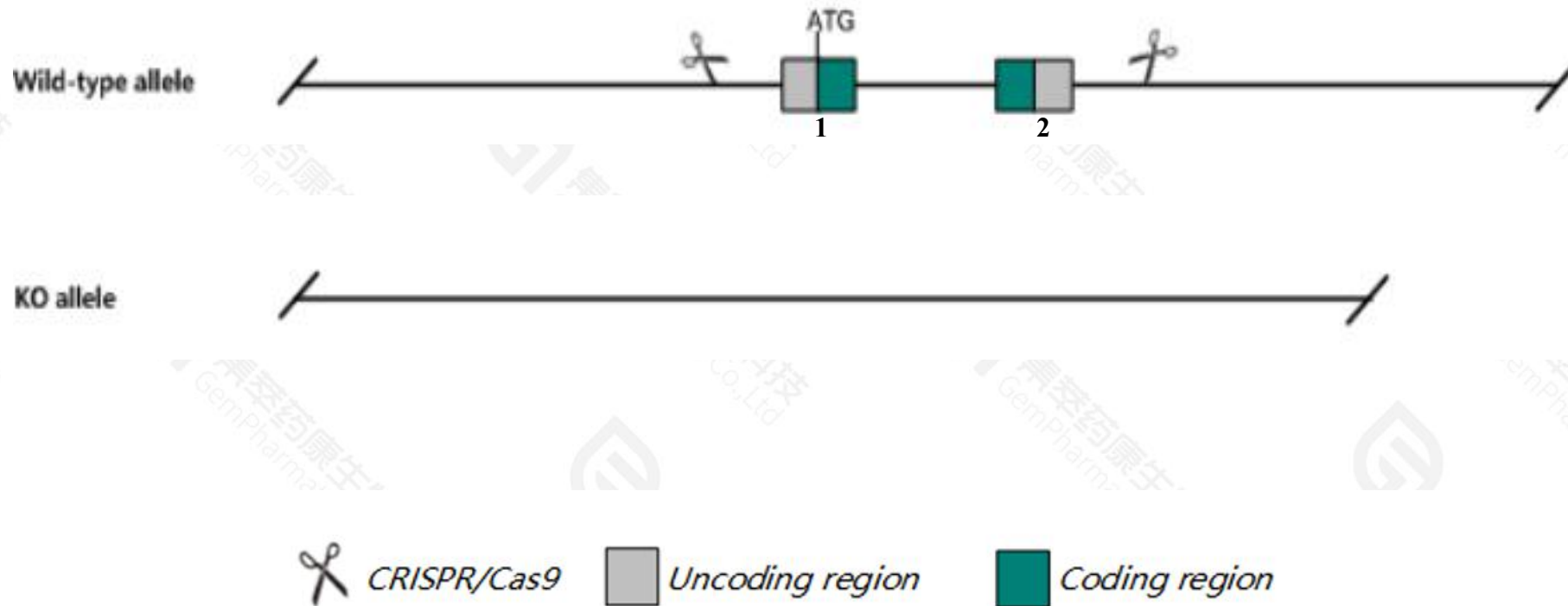
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zbtb18* gene. The schematic diagram is as follows:



- The *Zbtb18* gene has 12 transcripts. According to the structure of *Zbtb18* gene, exon1-exon2 of *Zbtb18*-202(ENSMUST00000094276.4) 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 *Zbtb18* 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, mice homozygous for a knock-out allele exhibit neonatal lethality, cortical and hippocampal hypoplasia and laminar disorganization, and abnormal neuron apoptosis and cell cycling.
- The KO region contains functional region of the *Gm26801-201*. Knockout the region may affect the function of *Gm26801-201* gene .
- The *Zbtb18* gene is located on the Chr1. 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)

## Zbtb18 zinc finger and BTB domain containing 18 [Mus musculus (house mouse)]

Gene ID: 30928, updated on 13-Mar-2020

### Summary



**Official Symbol** Zbtb18 provided by [MGI](#)

**Official Full Name** zinc finger and BTB domain containing 18 provided by [MGI](#)

**Primary source** [MGI:MGI:1353609](#)

**See related** [Ensembl:ENSMUSG00000063659](#)

**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** RP58, Zfp238, Znf238., zfp-238

**Expression** Broad expression in cerebellum adult (RPKM 43.4), CNS E18 (RPKM 26.5) and 23 other tissues [See more](#)

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

# Transcript information (Ensembl)

The gene has 12 transcripts,all transcripts are shown below:

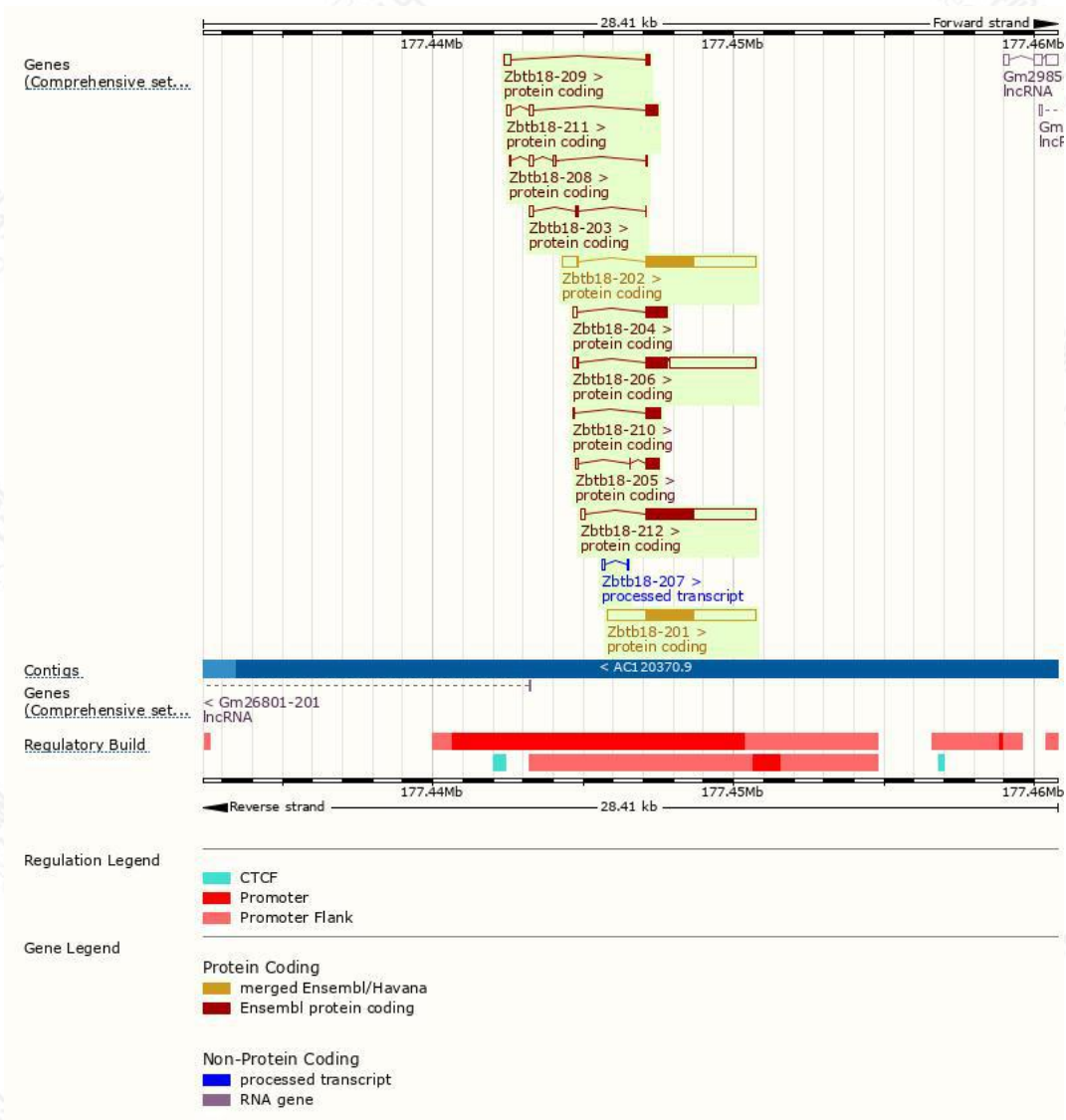
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zbtb18-201	<a href="#">ENSMUST00000077225.7</a>	4944	<a href="#">522aa</a>	Protein coding	<a href="#">CCDS15553</a>	<a href="#">Q9WUK6</a>	TSL:NA GENCODE basic APPRIS P3
Zbtb18-202	<a href="#">ENSMUST00000094276.4</a>	4204	<a href="#">531aa</a>	Protein coding	<a href="#">CCDS35800</a>	<a href="#">H7BX69</a>	TSL:2 GENCODE basic APPRIS ALT1
Zbtb18-212	<a href="#">ENSMUST00000195612.1</a>	3790	<a href="#">522aa</a>	Protein coding	<a href="#">CCDS15553</a>	<a href="#">Q9WUK6</a>	TSL:1 GENCODE basic APPRIS P3
Zbtb18-206	<a href="#">ENSMUST00000193480.1</a>	3734	<a href="#">236aa</a>	Protein coding	-	<a href="#">A0A0A6YWR6</a>	TSL:1 GENCODE basic
Zbtb18-204	<a href="#">ENSMUST00000192851.1</a>	857	<a href="#">228aa</a>	Protein coding	-	<a href="#">A0A0A6YY33</a>	CDS 3' incomplete TSL:5
Zbtb18-211	<a href="#">ENSMUST00000195549.5</a>	646	<a href="#">128aa</a>	Protein coding	-	<a href="#">A0A0A6YXP2</a>	CDS 3' incomplete TSL:3
Zbtb18-205	<a href="#">ENSMUST00000193440.1</a>	549	<a href="#">138aa</a>	Protein coding	-	<a href="#">A0A0A6YW03</a>	CDS 3' incomplete TSL:5
Zbtb18-210	<a href="#">ENSMUST00000195388.1</a>	525	<a href="#">161aa</a>	Protein coding	-	<a href="#">A0A0A6YWT8</a>	CDS 3' incomplete TSL:5
Zbtb18-209	<a href="#">ENSMUST00000195002.1</a>	394	<a href="#">45aa</a>	Protein coding	-	<a href="#">A0A0A6YXT0</a>	CDS 3' incomplete TSL:1
Zbtb18-208	<a href="#">ENSMUST00000194319.1</a>	335	<a href="#">14aa</a>	Protein coding	-	<a href="#">A0A0A6YX98</a>	CDS 3' incomplete TSL:5
Zbtb18-203	<a href="#">ENSMUST00000192699.1</a>	218	<a href="#">7aa</a>	Protein coding	-	<a href="#">A0A1Y7VJC4</a>	CDS 3' incomplete TSL:5
Zbtb18-207	<a href="#">ENSMUST00000194269.1</a>	100	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Zbtb18-202* transcript,the transcription is shown below:



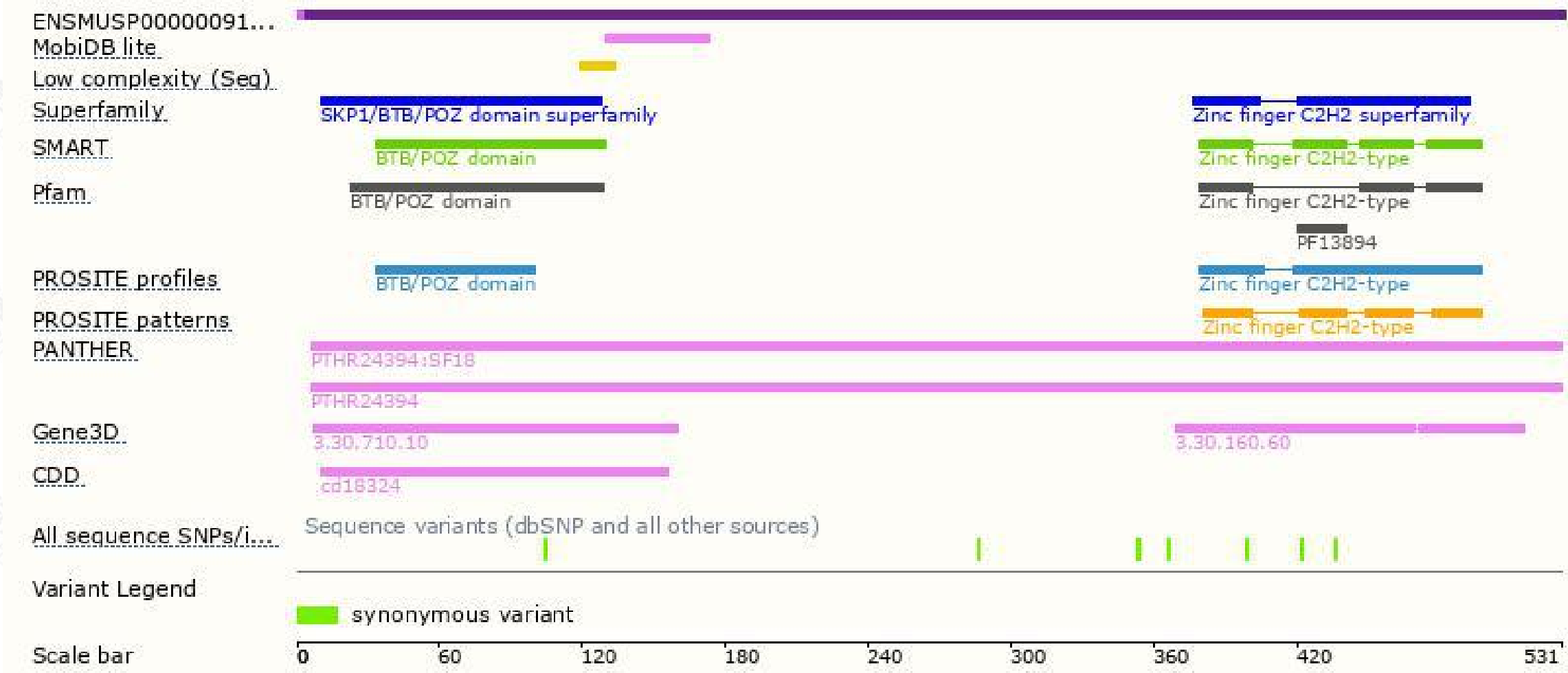


# Genomic location distribution

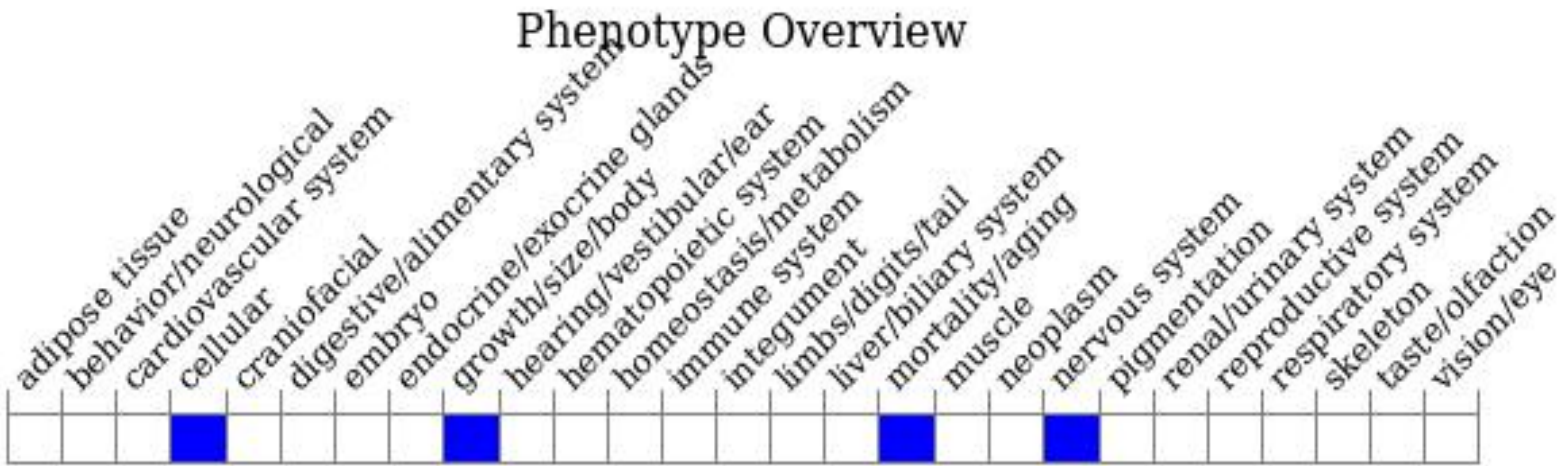




# Protein domain



# 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,mice homozygous for a knock-out allele exhibit neonatal lethality, cortical and hippocampal hypoplasia and laminar disorganization, and abnormal neuron apoptosis and cell cycling.

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