Zbtb5 Cas9-CKO Strategy

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Project Overview

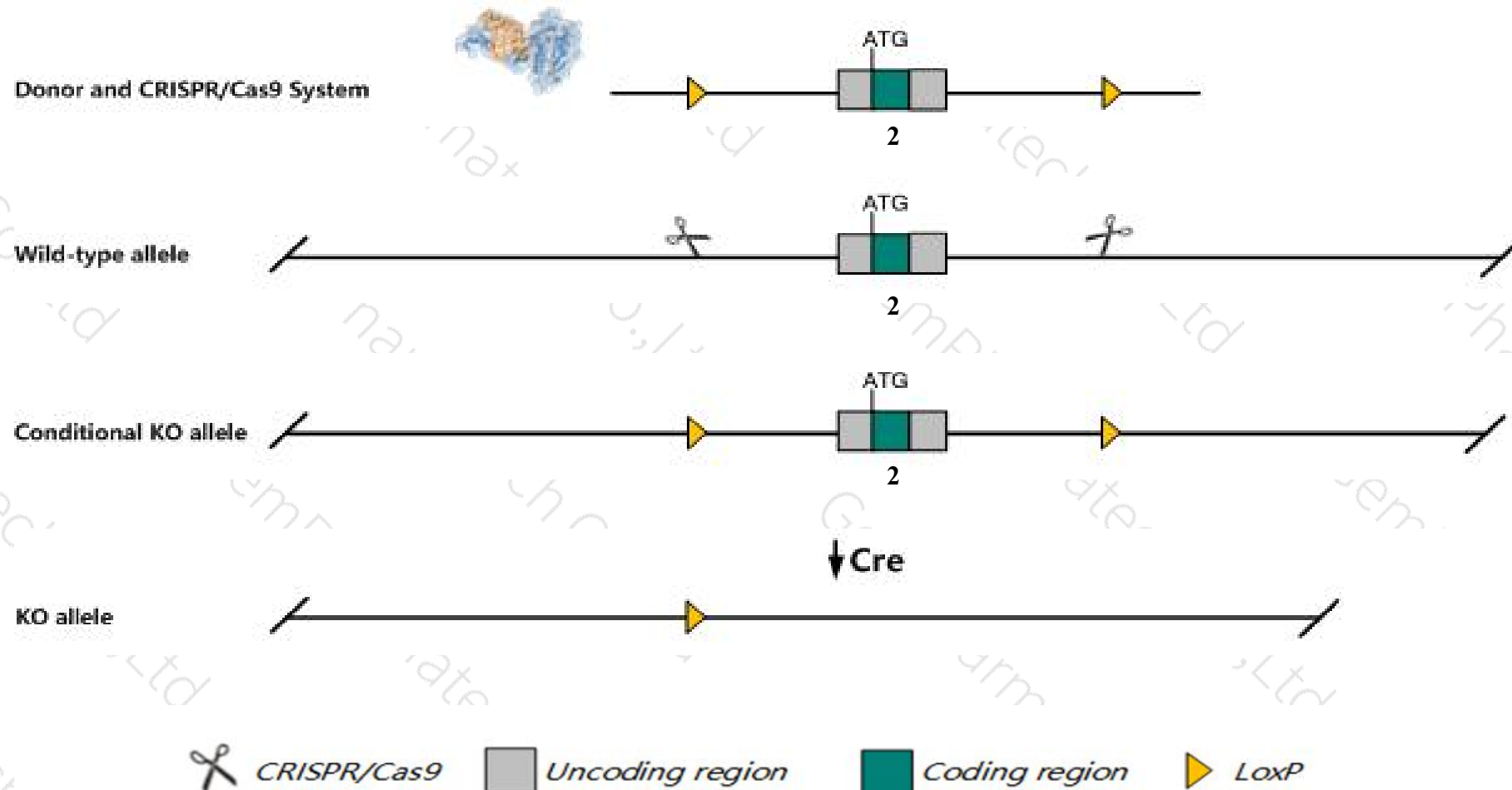|	
Project Name	*Zbtb5*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zbtb5* gene. The schematic diagram is as follows:

Technical routes

➤ The *Zbtb5* gene has 4 transcripts. According to the structure of *Zbtb5* gene, exon2 of *Zbtb5-204* (ENSMUST00000180217.1) 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 *Zbtb5* 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.

➢ The *Zbtb5* gene is located on the Chr4. 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）

Zbtb5 zinc finger and BTB domain containing 5 [Mus musculus (house mouse)]

Gene ID: 230119, updated on 13-Mar-2020

▲ Summary

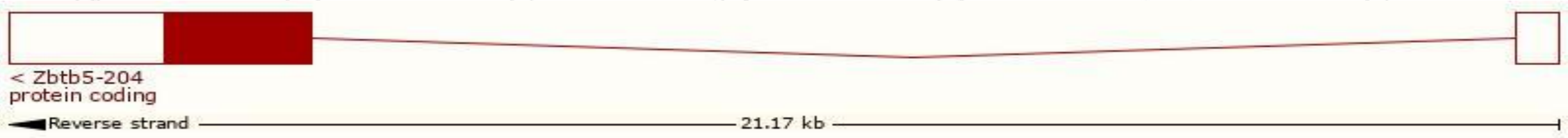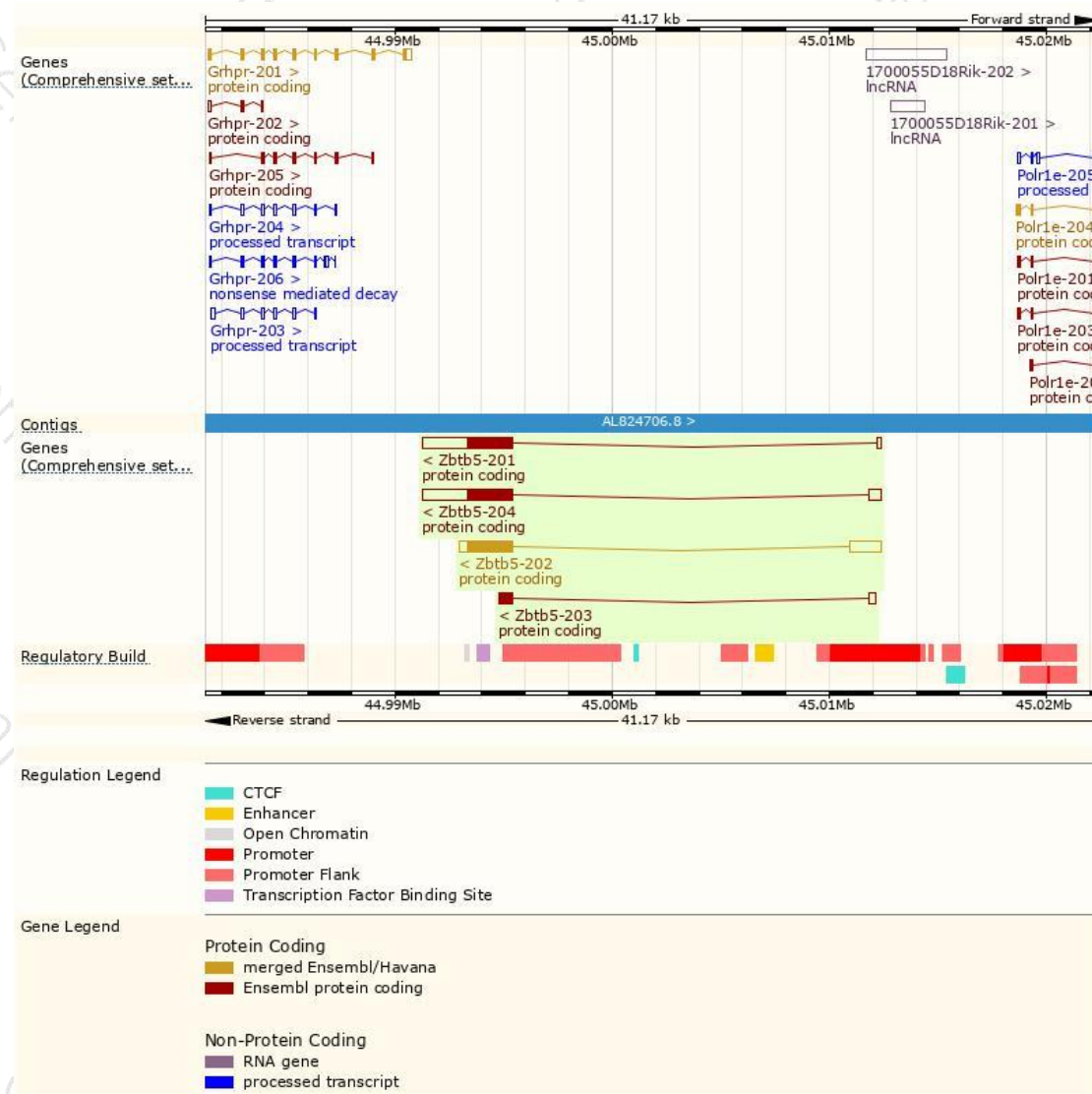|	
Official Symbol	Zbtb5 provided by MGI
Official Full Name	zinc finger and BTB domain containing 5 provided by MGI
Primary source	MGI:MGI:1924601
See related	Ensembl:ENSMUSG00000049657
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5930421I10, 9430083K24Rik, AI646847, mKIAA0354
Expression	Ubiquitous expression in testis adult (RPKM 8.9), whole brain E14.5 (RPKM 8.8) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 4 transcripts,all transcripts are shown below:

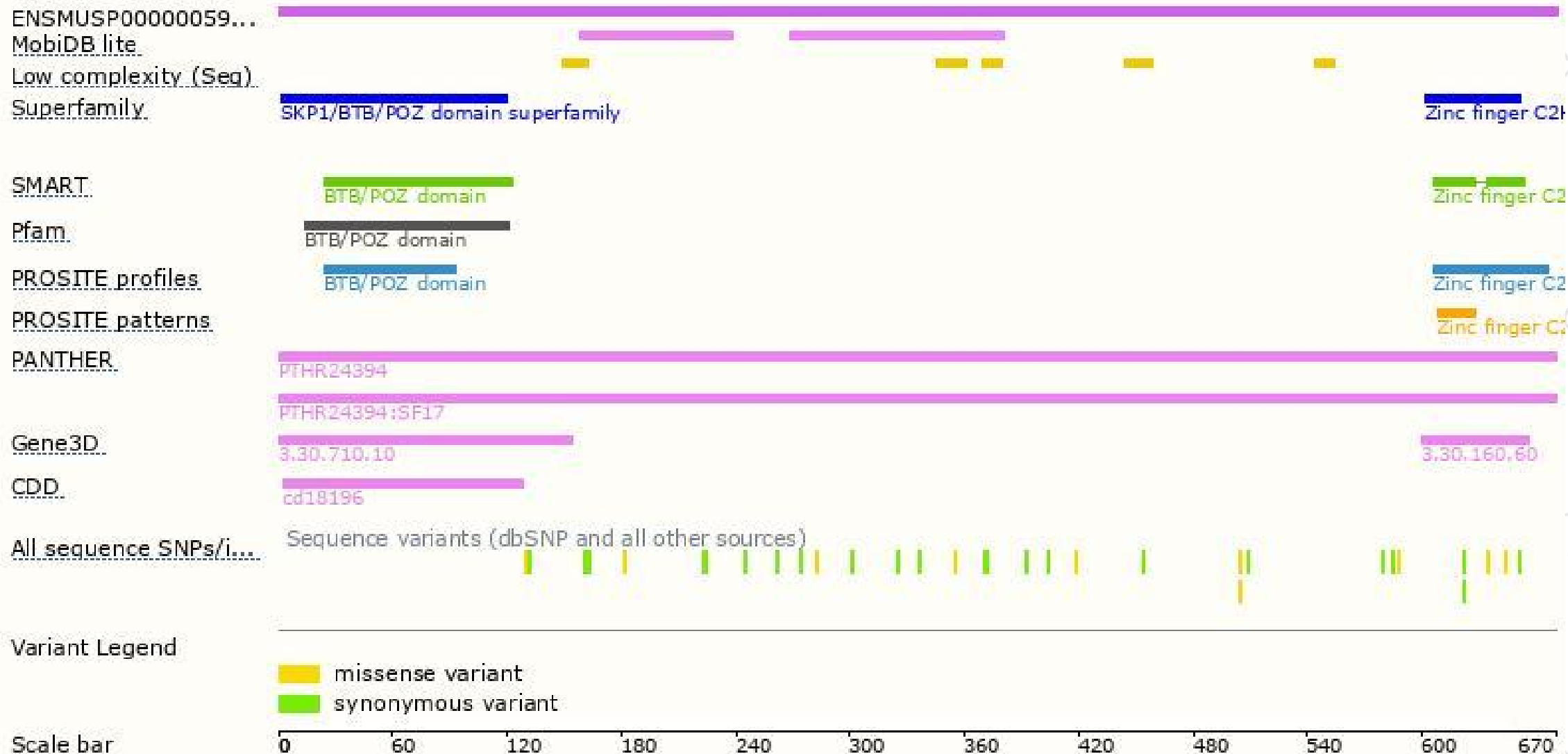| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zbtb5-204	ENSMUST00000180217.1	4708	670aa	Protein coding	CCDS18129	Q7TQG0	TSL:2 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Zbtb5-201	ENSMUST00000055028.8	4316	670aa	Protein coding	CCDS18129	Q7TQG0	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 P1
Zbtb5-202	ENSMUST00000107817.2	3867	670aa	Protein coding	CCDS18129	Q7TQG0	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 P1
Zbtb5-203	ENSMUST00000131991.1	872	189aa	Protein coding	-	B1AXQ4	CDS 3' incomplete TSL:2

The strategy is based on the design of *Zbtb5-204* transcript,The transcription is shown below
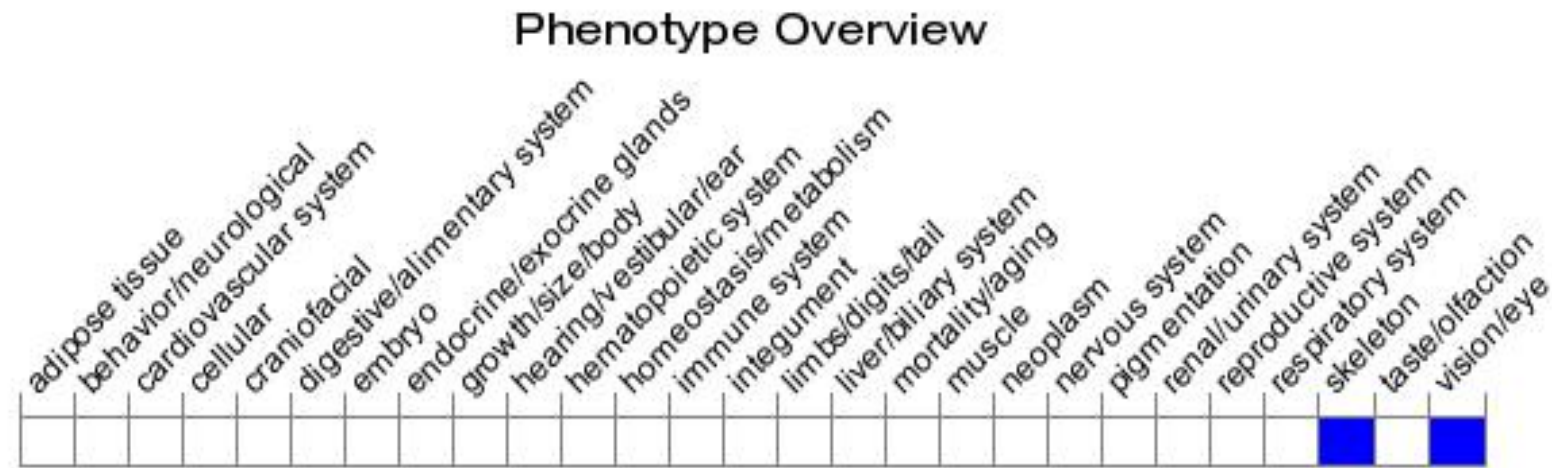

< Zbtb5-204
protein coding

◄ Reverse strand

21.17 kb

Genomic location distribution

Protein domain

ENSMUSP00000059...		
MobiDB lite		
Low complexity (Seg)		
Superfamily	SKP1/BTB/POZ domain superfamily	Zinc finger C2H
SMART	BTB/POZ domain	Zinc finger C2
Pfam	BTB/POZ domain	
PROSITE profiles	BTB/POZ domain	Zinc finger C2
PROSITE patterns		Zinc finger C2
PANTHER	PTHR24394	
	PTHR24394:SF17	
Gene3D	3.30.710.10	3.30.160.60
CDD	cd18196	
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)	

Variant Legend

▮ missense variant
▮ synonymous variant

Scale bar

0   60   120   180   240   300   360   420   480   540   600   670

Mouse phenotype description(MGI)

Phenotype Overview

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

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