

Tac2 Cas9-KO Strategy

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Reviewer:

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Project Overview



Project Name

Tac2

Project type

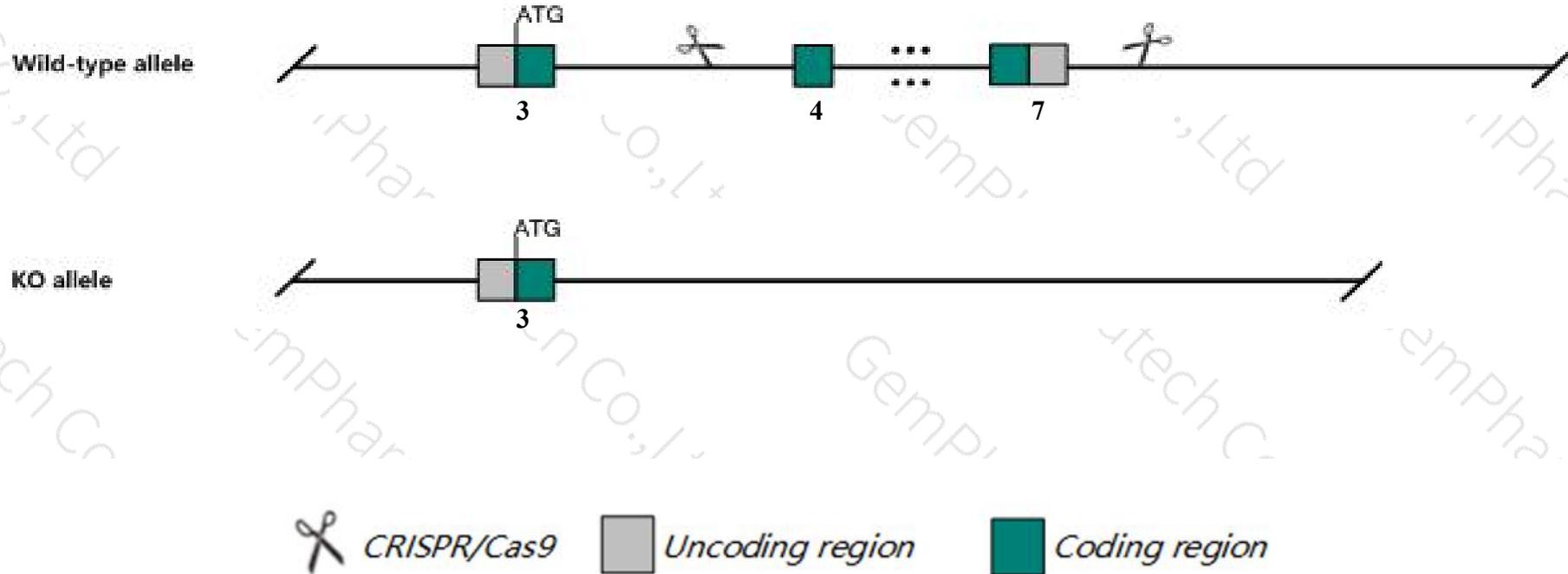
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tac2* gene. The schematic diagram is as follows:



- The *Tac2* gene has 4 transcripts. According to the structure of *Tac2* gene, exon4-exon7 of *Tac2-202* (ENSMUST00000179960.7) transcript is recommended as the knockout region. The region contains 247bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tac2* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit delayed female sexual maturation and fertility.
- The *Tac2* gene is located on the Chr10. 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)

Tac2 tachykinin 2 [Mus musculus (house mouse)]

Gene ID: 21334, updated on 31-Jan-2019

Summary



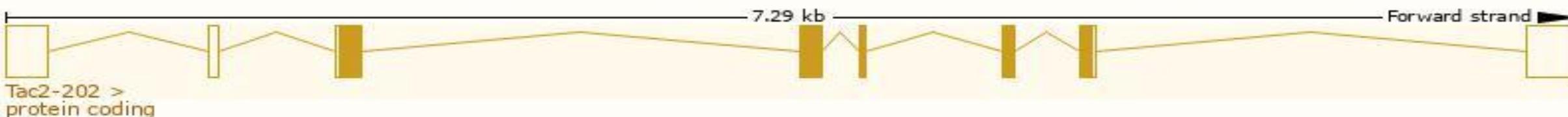
Official Symbol	Tac2 provided by MGI
Official Full Name	tachykinin 2 provided by MGI
Primary source	MGI:MGI:98476
See related	Ensembl:ENSMUSG00000025400
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	PPT-B, Tac3
Summary	This gene encodes a member of the tachykinin family of signaling peptides that is widely expressed in the central nervous system and plays a role in diverse processes such as water homeostasis, pulmonary inflammation, cognition, fear memory consolidation and preeclampsia. The encoded protein is enzymatically processed to generate the mature neuropeptide. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jul 2015]
Expression	Biased expression in liver E14.5 (RPKM 9.9), liver E14 (RPKM 8.0) and 9 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

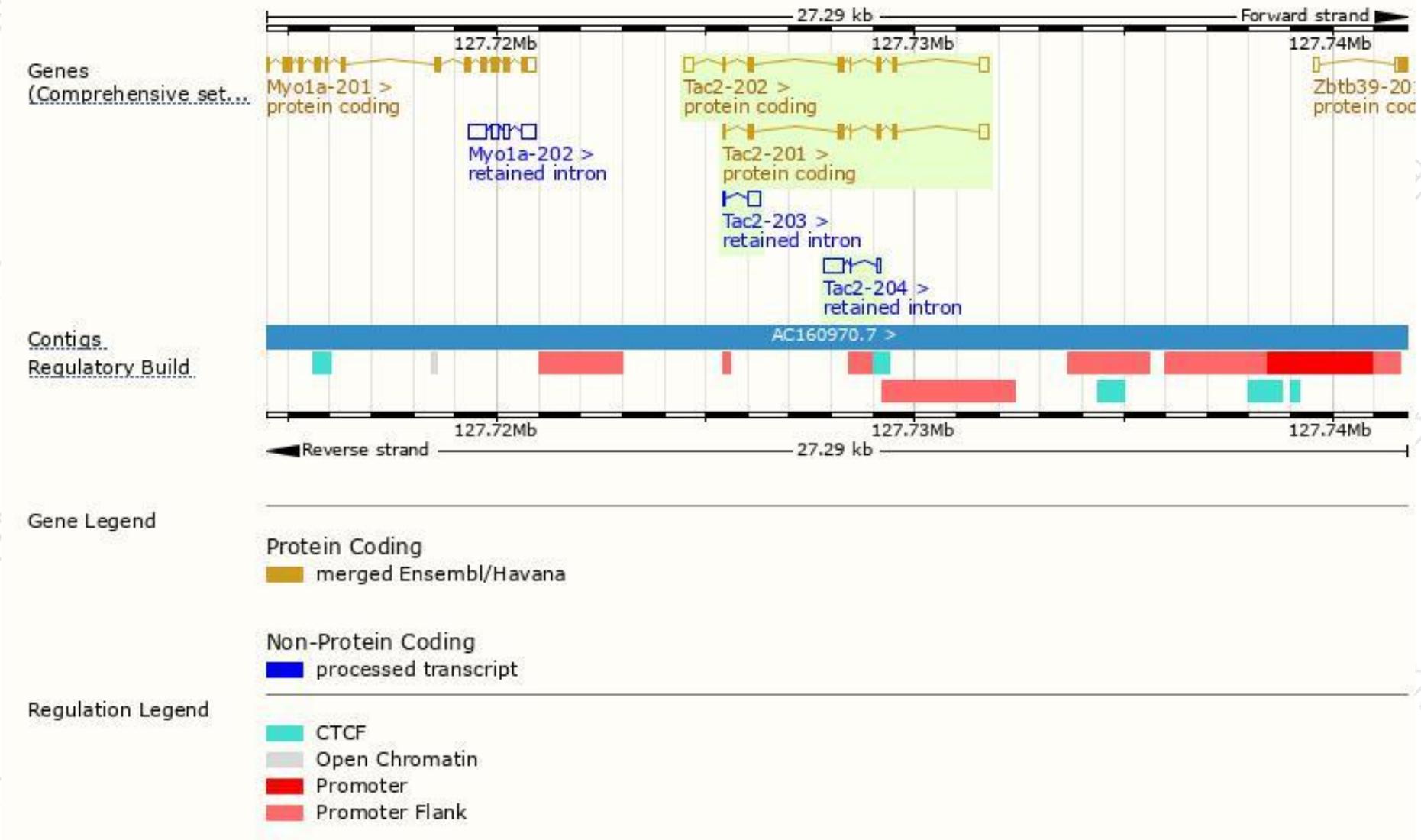
The gene has 4 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tac2-202	ENSMUST00000179960.7	852	116aa	Protein coding	CCDS24248	P55099	TSL:1 GENCODE basic APPRIS P1
Tac2-201	ENSMUST00000026466.4	678	116aa	Protein coding	CCDS24248	P55099	TSL:1 GENCODE basic APPRIS P1
Tac2-204	ENSMUST00000218048.1	514	No protein	Retained intron	-	-	TSL:5
Tac2-203	ENSMUST00000217729.1	358	No protein	Retained intron	-	-	TSL:3

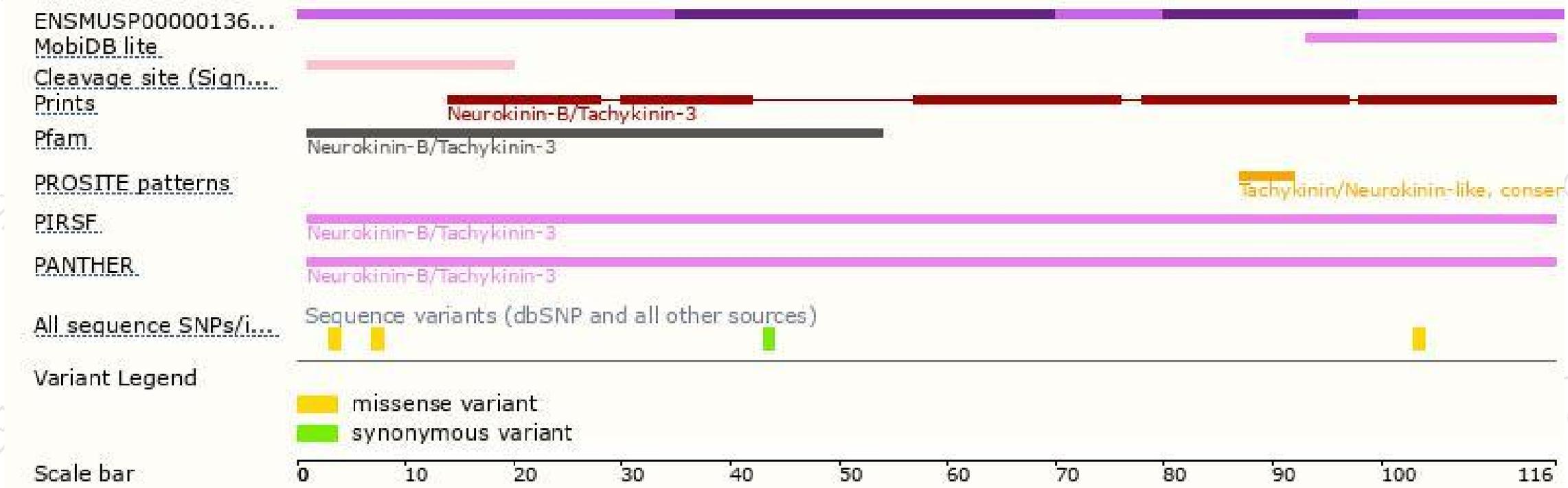
The strategy is based on the design of *Tac2-202* transcript, The transcription is shown below



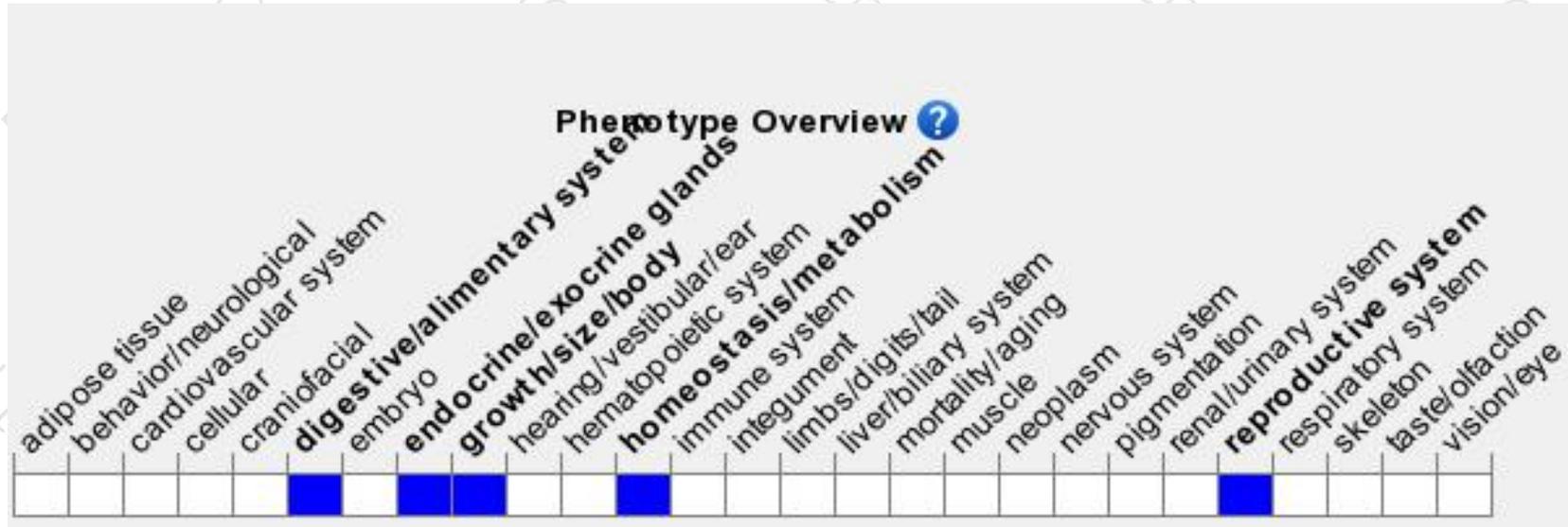
Genomic location distribution



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 delayed female sexual maturation and fertility.

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

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