

***Zic3* Cas9-KO Strategy**

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Project Overview

Project Name

Zic3

Project type

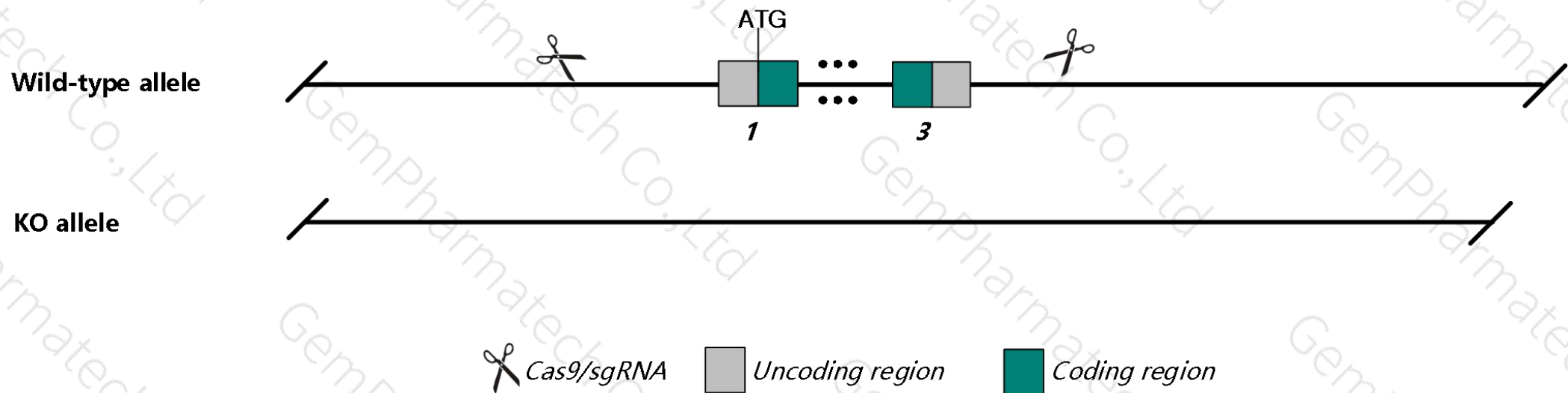
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zic3* gene. The schematic diagram is as follows:



Technical routes

- The *Zic3* gene has 4 transcripts. According to the structure of *Zic3* gene, exon1-exon3 of *Zic3-201* (ENSMUST00000088627.10) 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 *Zic3* gene. The brief process is as follows: CRISPR/Cas9 system transfects 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.

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- According to the existing MGI data, Mutants show incomplete penetrance varying by genetic background and allele. Phenotypes range from bent tail/skeletal abnormalities to severe defects in embryo turning, cardiac development and neural tube closure resulting in death at embryonic day 18.5
- The *Zic3* gene is located on the ChrX. 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)

Zic3 zinc finger protein of the cerebellum 3 [*Mus musculus* (house mouse)]

Gene ID: 22773, updated on 12-Mar-2019

Summary

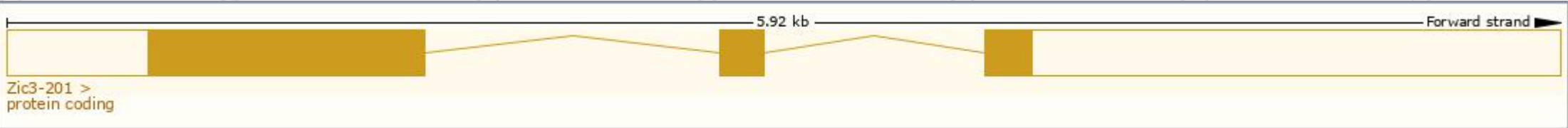
Official Symbol	Zic3 provided by MGI
Official Full Name	zinc finger protein of the cerebellum 3 provided by MGI
Primary source	MGI:MGI:106676
See related	Ensembl:ENSMUSG00000067860
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Bn; Ka
Expression	Biased expression in CNS E11.5 (RPKM 5.2), whole brain E14.5 (RPKM 4.7) and 7 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

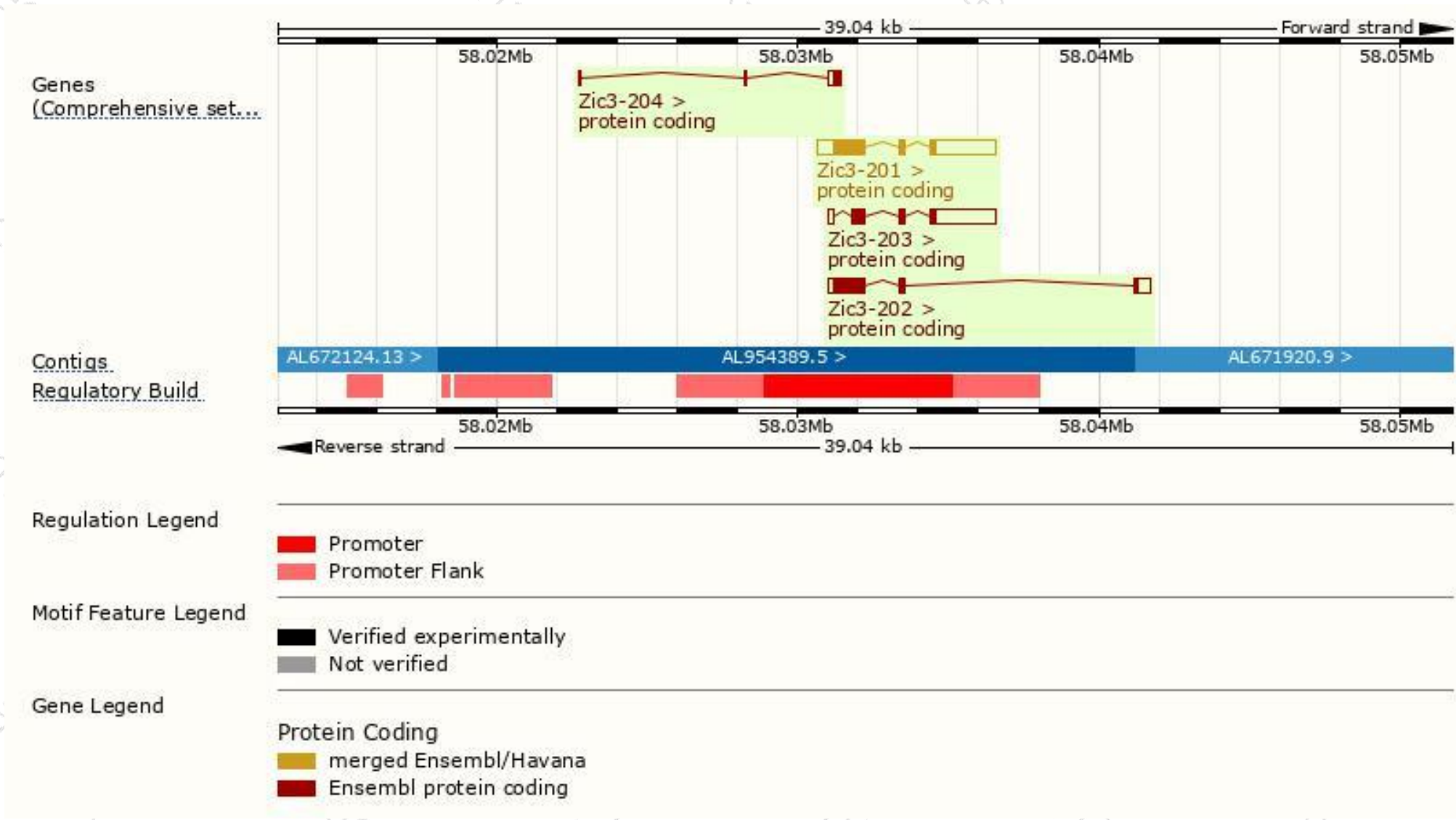
The gene has 4 transcripts,all transcripts are shown below:

Show/hide columns (1 hidden)							Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Zic3-201	ENSMUST00000088627.10	3949	466aa	Protein coding	CCDS30155	Q62521	TSL:1	GENCODE basic APPRIS P2
Zic3-203	ENSMUST00000088631.10	2980	246aa	Protein coding	-	A2AWK6	TSL:5	GENCODE basic
Zic3-202	ENSMUST00000088629.3	1951	456aa	Protein coding	-	Q62521	TSL:1	GENCODE basic APPRIS ALT1
Zic3-204	ENSMUST00000137687.1	566	89aa	Protein coding	-	A2AWK4	CDS 3' incomplete	TSL:3

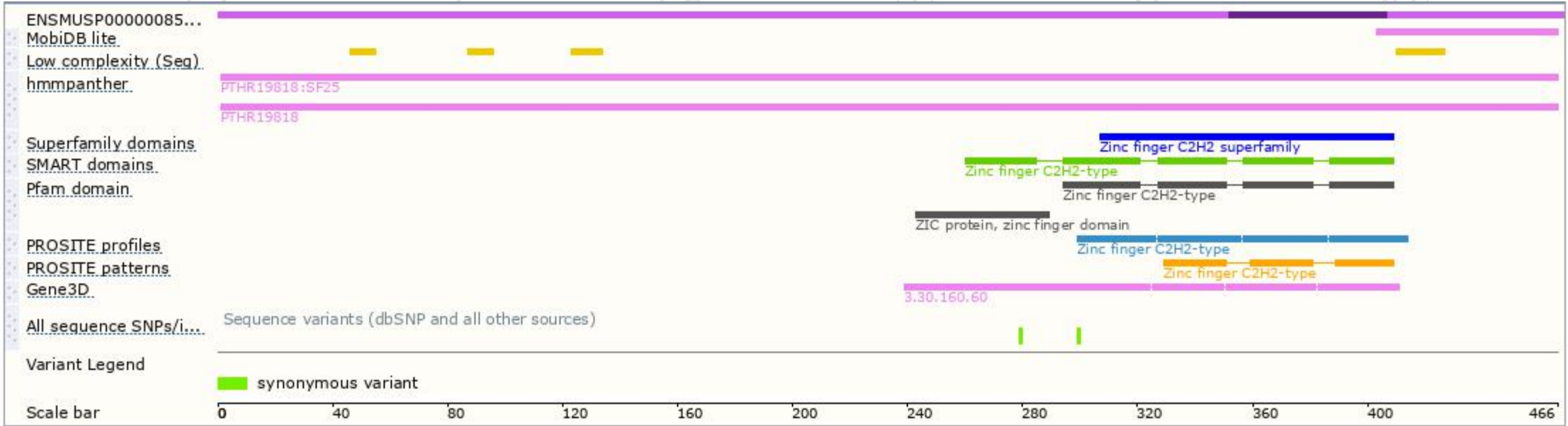
The strategy is based on the design of *Zic3-201* transcript,The transcription is shown below



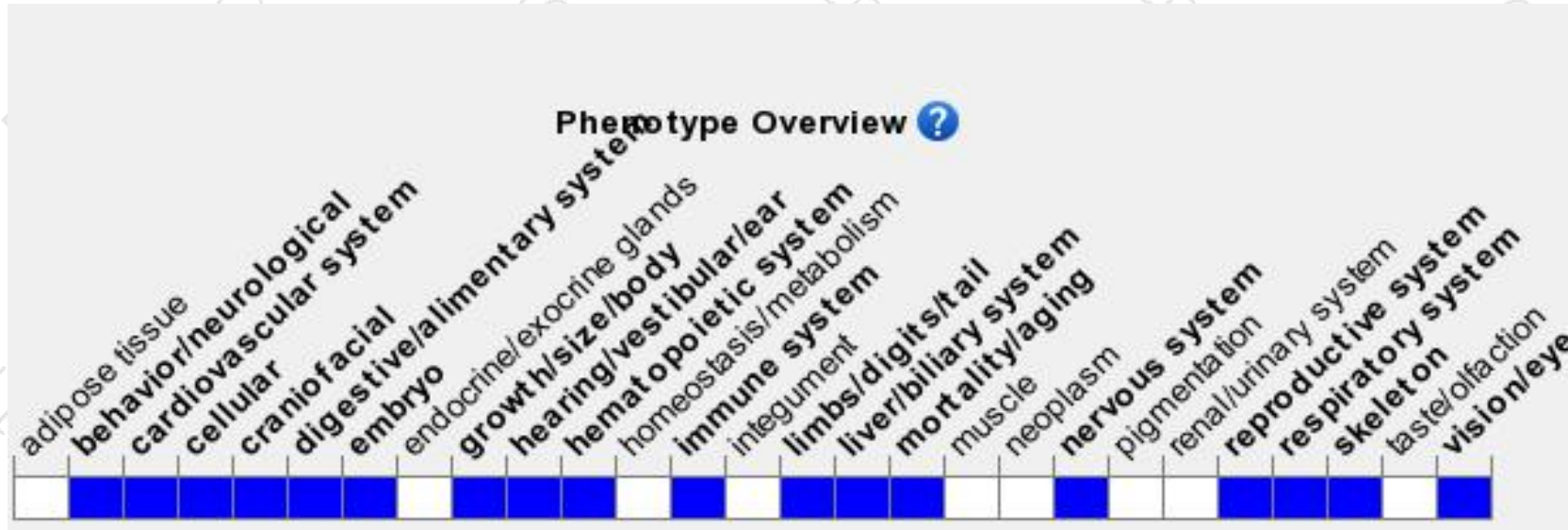
Genomic location distribution



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, Mutants show incomplete penetrance varying by genetic background and allele.

Phenotypes range from bent tail/skeletal abnormalities to severe defects in embryo turning, cardiac development and neural tube closure resulting in death at embryonic day 18.5

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

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