

Zic1 Cas9-KO Strategy

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Overview

Target Gene Name

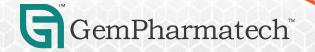
• Zic1

Project Type

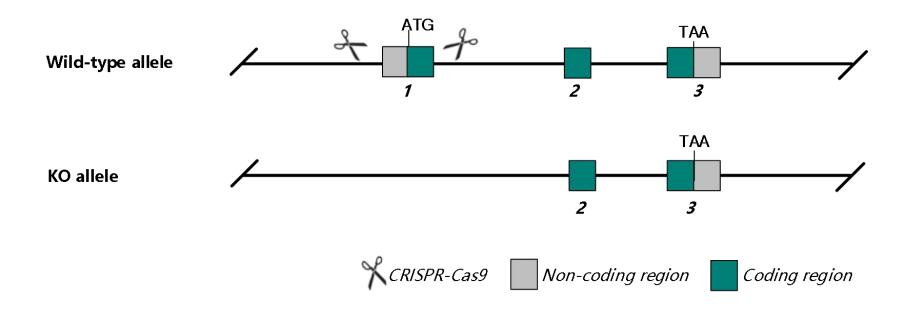
• Cas9-KO

Genetic Background

• C57BL/6JGpt



Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Zic1 gene.



Technical Information

- The Zic1 gene has 3 transcripts. According to the structure of Zic1 gene, exon 1 of Zic1-201 (ENSMUST00000034927.13) transcript is recommended as the knockout region. The region contains 982 bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Zic1* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.



Gene Information

Zic1 zinc finger protein of the cerebellum 1 [Mus musculus (house mouse)]

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Gene ID: 22771, updated on 17-Jan-2023



Official Symbol Zic1 provided by MGI

Official Full Name zinc finger protein of the cerebellum 1 provided by MGI

Primary source MGI:MGI:106683

See related Ensembl:ENSMUSG00000032368 AllianceGenome:MGI:106683

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 ZIC; ZNF201

Summary Enables DNA-binding transcription activator activity, RNA polymerase II-specific and RNA polymerase II cis-regulatory region sequence-specific DNA

binding activity. Involved in several processes, including central nervous system development; positive regulation of protein import into nucleus; and regulation of smoothened signaling pathway. Acts upstream of or within adult walking behavior and central nervous system development. Located in cytoplasm and nucleus. Is expressed in several structures, including central nervous system; embryo mesenchyme; future brain; metanephros; and visual system. Used to study Dandy-Walker syndrome and Joubert syndrome. Human ortholog(s) of this gene implicated in Dandy-Walker syndrome and

craniosynostosis. Orthologous to human ZIC1 (Zic family member 1). [provided by Alliance of Genome Resources, Apr 2022]

Expression Biased expression in cerebellum adult (RPKM 92.7), whole brain E14.5 (RPKM 45.5) and 4 other tissues See more

Orthologs human all

Try the new Gene table

Try the new Transcript table



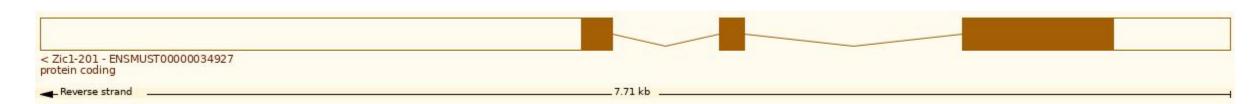


Transcript Information

The gene has 3 transcripts, all transcripts are shown below:

Transcript ID	Name	bp 🌲	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000034927.13	Zic1-201	5606	447aa	Protein coding	CCDS23403 €	P46684©	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000065360.5	Zic1-202	2811	447aa	Protein coding	CCDS23403 ₽	P46684@	GENCODE basic APPRIS P1 TSL:1
ENSMUST00000173121.2	Zic1-203	395	No protein	Protein coding CDS not defined		·-	TSL:5

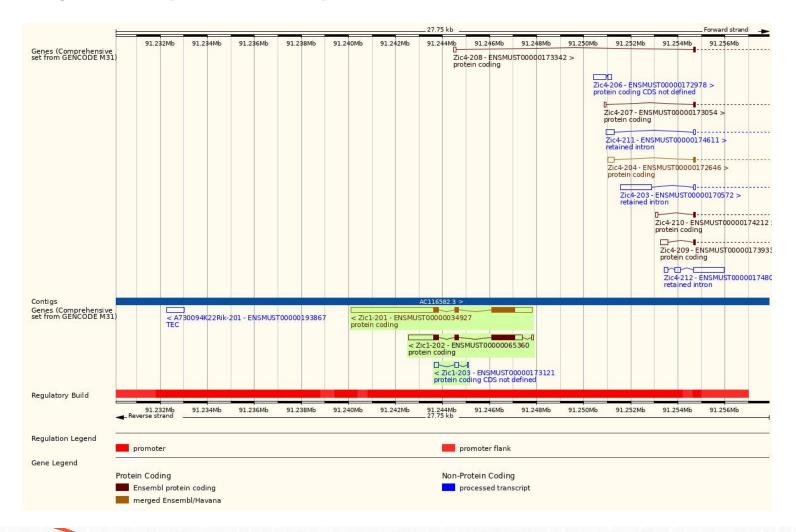
The strategy is based on the design of *Zic1*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org



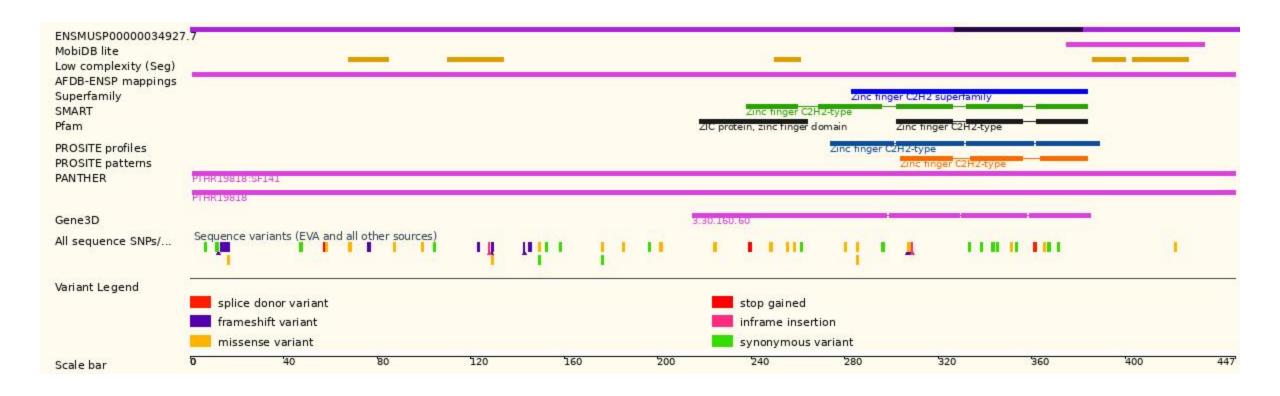
Genomic Information





Source: : https://www.ensembl.org

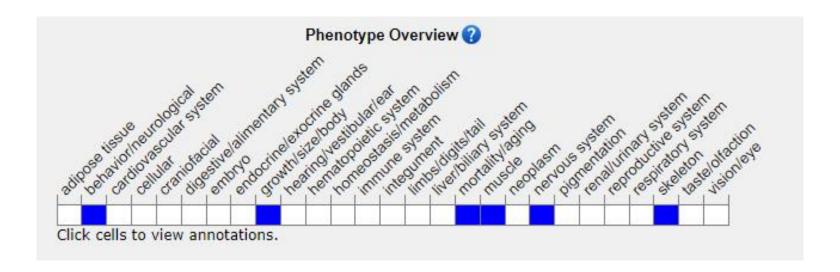
Protein Information





Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



• Homozygous mutants show cerebellar hypoplasia with a missing lobule of the anterior lobe. Newborn pups suckle poorly. 50% die within one day of birth and almost all die within 3 weeks; longer survivors show marked ataxia and exhibit tonic convulsions.



Important Information

- This strategy may affect the regulatory expression of the side gene Zic4.
- Zic1 is located on Chr 9. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

