

Zfp423 Cas9-CKO Strategy

Designer:

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Project Overview

Project Name

Zfp423

Project type

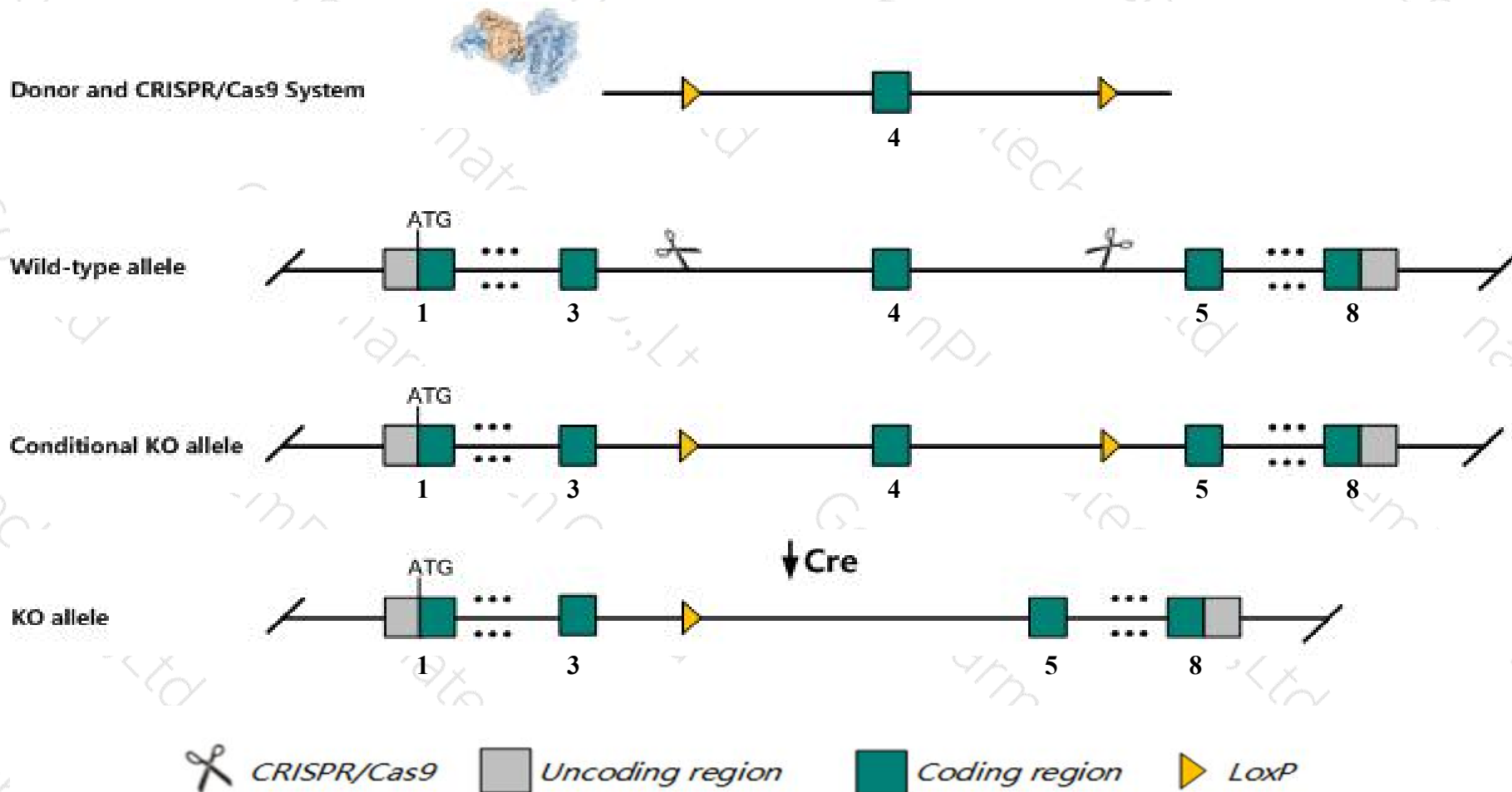
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp423* gene. The schematic diagram is as follows:



Technical routes

- The *Zfp423* gene has 7 transcripts. According to the structure of *Zfp423* gene, exon4 of *Zfp423-202* (ENSMUST00000109655.8) transcript is recommended as the knockout region. The region contains 3215bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp423* 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.

- According to the existing MGI data, Mutations in this gene lead to postnatal lethality, abnormal gait, ataxia, reduced body size, loss of the corpus callosum, reduction of the hippocampus, olfactory bulb defects, and variable malformation of the cerebellum, including vermis agenesis, due to reduced proliferation of neural precursors.
- The *Zfp423* gene is located on the Chr8. 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)

Zfp423 zinc finger protein 423 [Mus musculus (house mouse)]

Gene ID: 94187, updated on 12-Mar-2019

Summary



Official Symbol	Zfp423 provided by MGI
Official Full Name	zinc finger protein 423 provided by MGI
Primary source	MGI:MGI:1891217
See related	Ensembl:ENSMUSG00000045333
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	Ebfaz, Roaz, Zfp104, Znf423, ataxia1, mKIAA0760, nur12
Expression	Broad expression in whole brain E14.5 (RPKM 14.4), subcutaneous fat pad adult (RPKM 12.1) and 20 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp423-202	ENSMUST00000109655.8	4907	1292aa	Protein coding	CCDS52627	Q80TS5	TSL:1 GENCODE basic APPRIS P3
Zfp423-203	ENSMUST00000165770.8	4334	1167aa	Protein coding	CCDS80911	G3UW89	TSL:1 GENCODE basic APPRIS ALT1
Zfp423-201	ENSMUST00000052250.14	4510	1271aa	Protein coding	-	Q80TS5	TSL:1 GENCODE basic
Zfp423-207	ENSMUST00000174764.1	746	244aa	Protein coding	-	G3UZP1	CDS 3' incomplete TSL:3
Zfp423-206	ENSMUST00000174249.1	371	121aa	Protein coding	-	G3UYI9	CDS 3' incomplete TSL:2
Zfp423-205	ENSMUST00000173725.7	696	No protein	lncRNA	-	-	TSL:3
Zfp423-204	ENSMUST00000173092.1	386	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Zfp423-202* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP00000105...

MobiDB lite

Low complexity (Seq)

Superfamily

SMART

Pfam

PROSITE profiles

PROSITE patterns

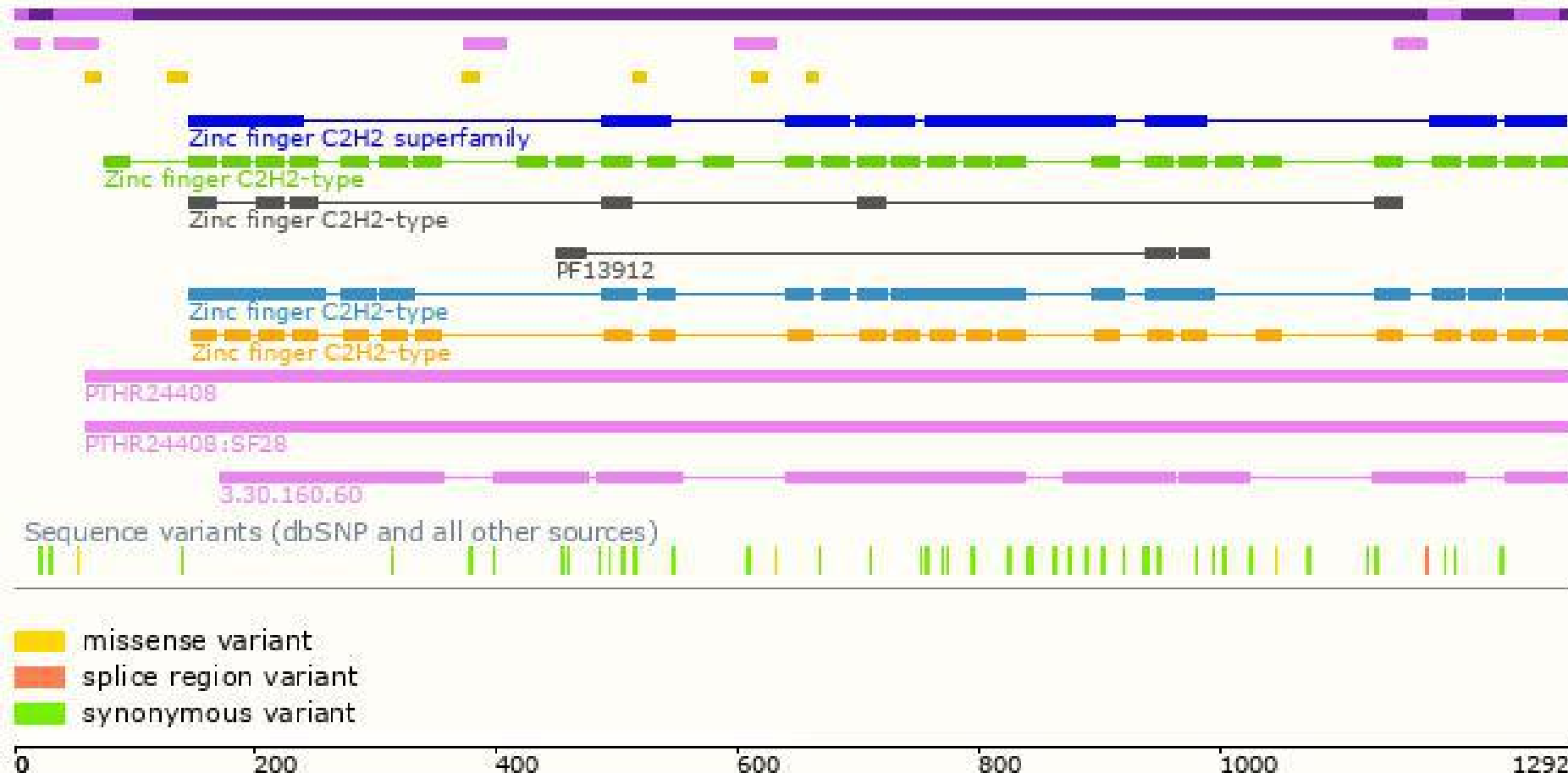
PANTHER

Gene3D

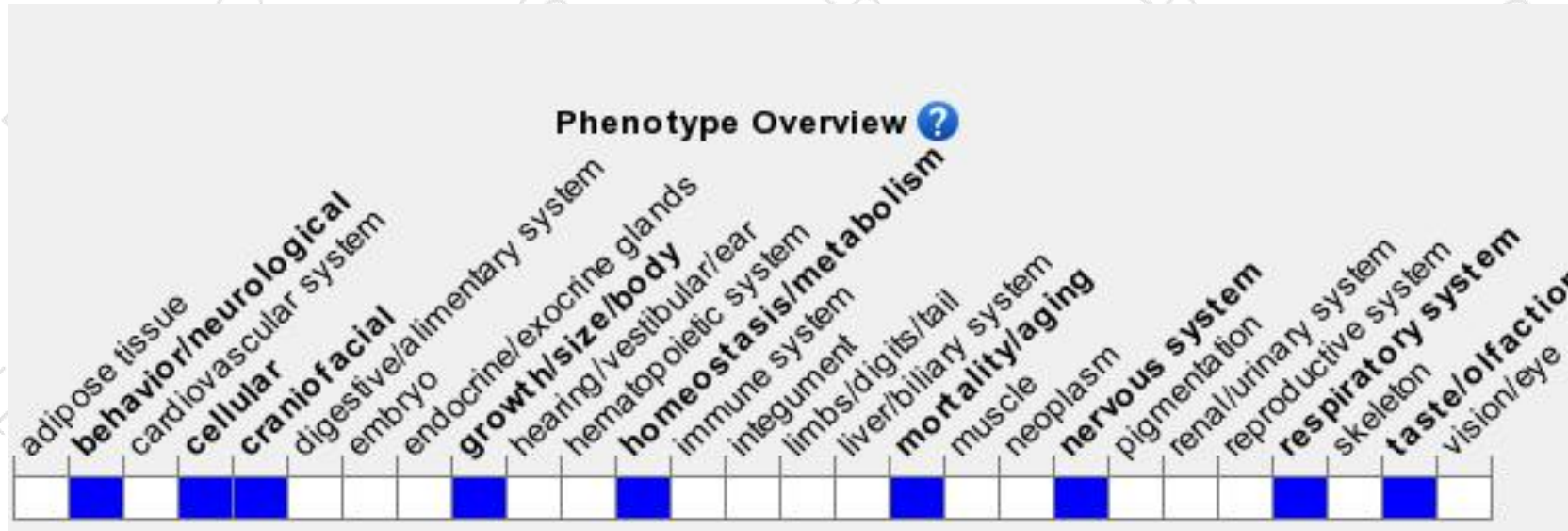
All sequence SNPs/i...

Variant Legend

Scale bar



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, Mutations in this gene lead to postnatal lethality, abnormal gait, ataxia, reduced body size, loss of the corpus callosum, reduction of the hippocampus, olfactory bulb defects, and variable malformation of the cerebellum, including vermis agenesis, due to reduced proliferation of neural precursors.

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

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