

Patz1 Cas9-CKO Strategy

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Design Date: 2019-8-9

Project Overview

Project Name

Patz1

Project type

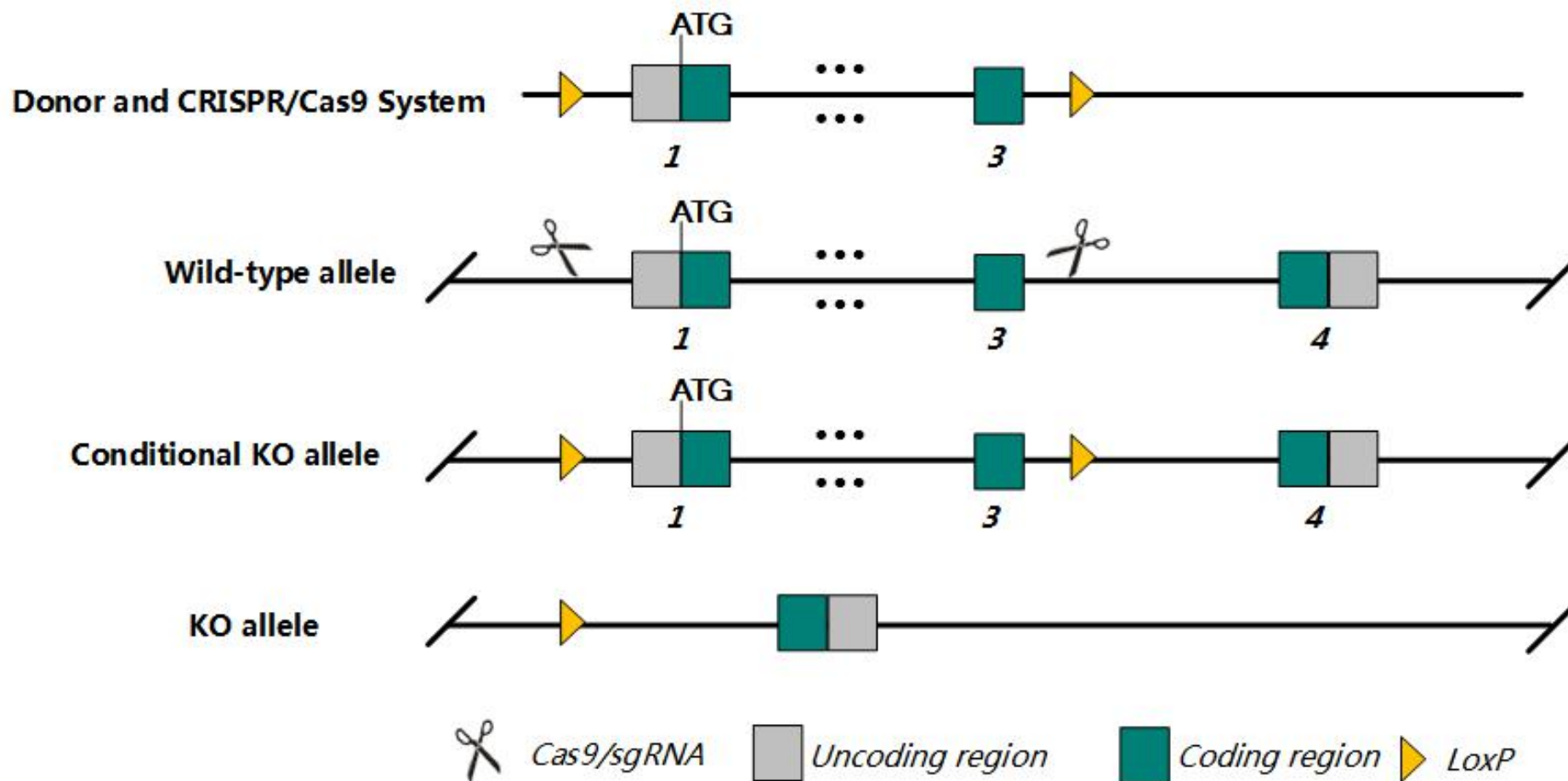
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Patz1* gene. The schematic diagram is as follows:



- The *Patz1* gene has 12 transcripts. According to the structure of *Patz1* gene, exon1-exon3 of *Patz1-201* (ENSMUST00000057089.12) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Patz1* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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, Mice homozygous for a null allele exhibit some embryonic and fetal lethality, exencephaly, nervous system defects, outflow defects, transposition of great arteries, postnatal growth retardation and male and female infertility.
- The floxed region is near to the N-terminal of *Gm11944* gene, this strategy may influence the regulatory function of the N-terminal of *Gm11944* gene.
- The *Patz1* gene is located on the Chr11. 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)

Patz1 POZ (BTB) and AT hook containing zinc finger 1 [Mus musculus (house mouse)]

Gene ID: 56218, updated on 31-Jan-2019

Summary



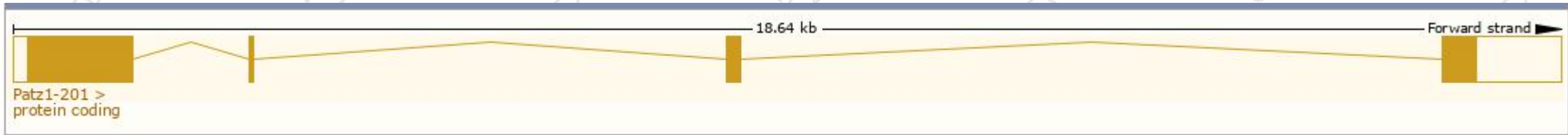
Official Symbol	Patz1 provided by MGI
Official Full Name	POZ (BTB) and AT hook containing zinc finger 1 provided by MGI
Primary source	MGI:MGI:1891832
See related	Ensembl:ENSMUSG00000020453
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	8430401L15Rik, A1447519, Mazr, Patz, Zfp278
Expression	Ubiquitous expression in thymus adult (RPKM 44.7), ovary adult (RPKM 21.8) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

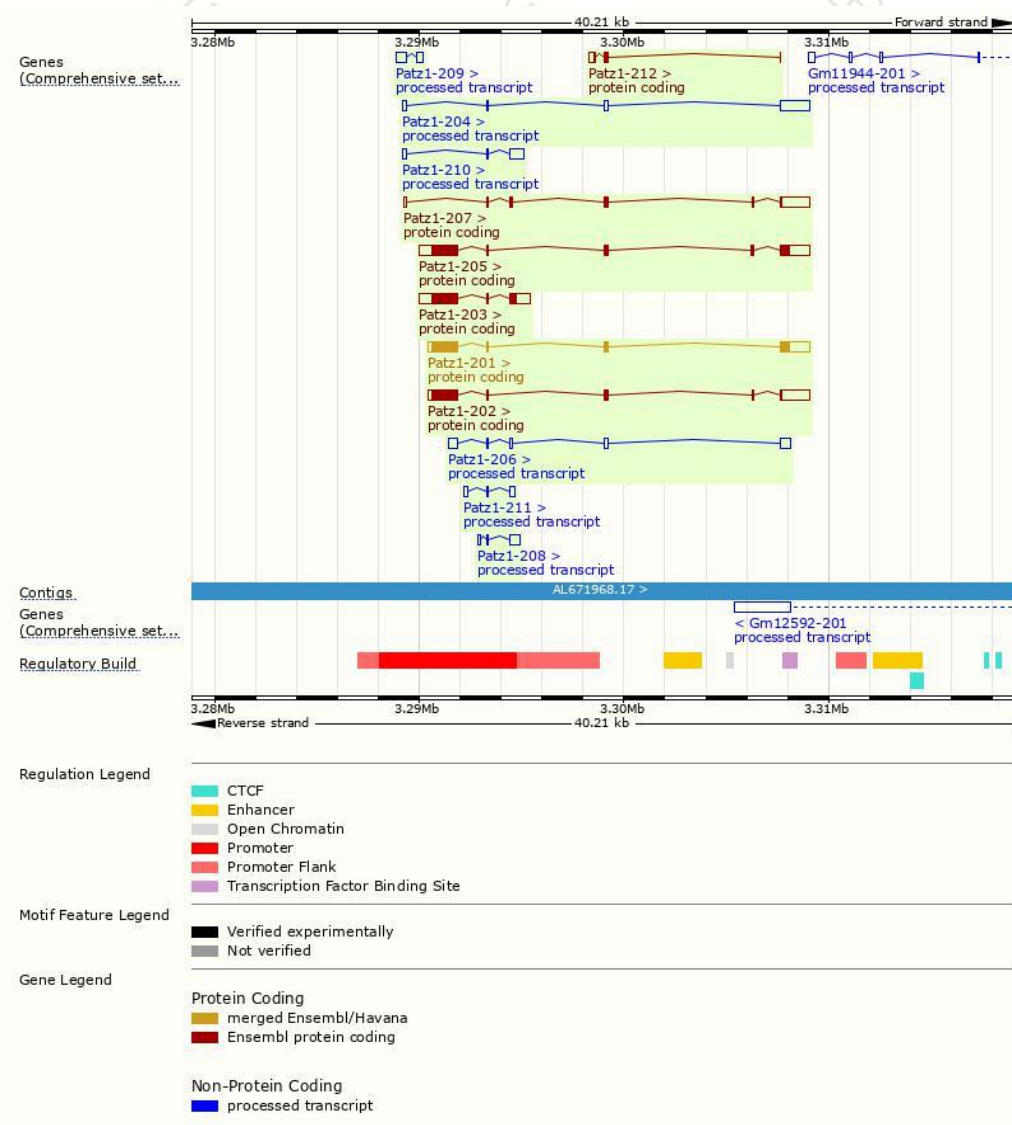
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Patz1-202	ENSMUST00000093402.11	3173	537aa	Protein coding	CCDS56754	Q5NBZ1	TSL:2 GENCODE basic
Patz1-201	ENSMUST00000057089.12	3118	641aa	Protein coding	CCDS24356	Q9JMG9	TSL:1 GENCODE basic
Patz1-205	ENSMUST00000110043.7	3702	687aa	Protein coding	-	Q5NBY9	TSL:5 GENCODE basic APPRIS P1
Patz1-203	ENSMUST00000094471.9	2930	537aa	Protein coding	-	Q5NBZ2	TSL:1 GENCODE basic
Patz1-207	ENSMUST00000134089.7	1904	102aa	Protein coding	-	Q7TNQ3	TSL:1 GENCODE basic
Patz1-212	ENSMUST00000154319.1	495	70aa	Protein coding	-	Q5NBY8	CDS 3' incomplete TSL:5
Patz1-204	ENSMUST00000101644.9	1853	No protein	Processed transcript	-	-	TSL:1
Patz1-206	ENSMUST00000123983.7	1249	No protein	Processed transcript	-	-	TSL:3
Patz1-210	ENSMUST00000144396.7	844	No protein	Processed transcript	-	-	TSL:3
Patz1-209	ENSMUST00000142561.1	798	No protein	Processed transcript	-	-	TSL:2
Patz1-208	ENSMUST00000136285.1	652	No protein	Processed transcript	-	-	TSL:2
Patz1-211	ENSMUST00000153603.7	456	No protein	Processed transcript	-	-	TSL:2

The strategy is based on the design of *Patz1-201* transcript,The transcription is shown below



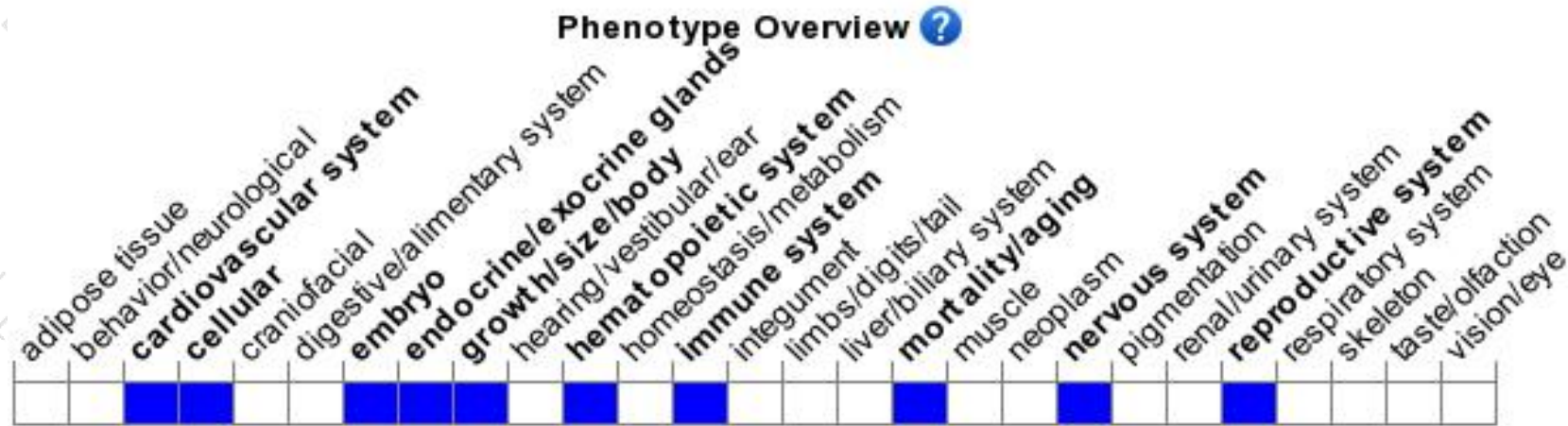
Genomic location distribution



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, Mice homozygous for a null allele exhibit some embryonic and fetal lethality, exencephaly, nervous system defects, outflow defects, transposition of great arteries, postnatal growth retardation and male and female infertility.

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

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