Slc39a14 Cas9-CKO Strategy

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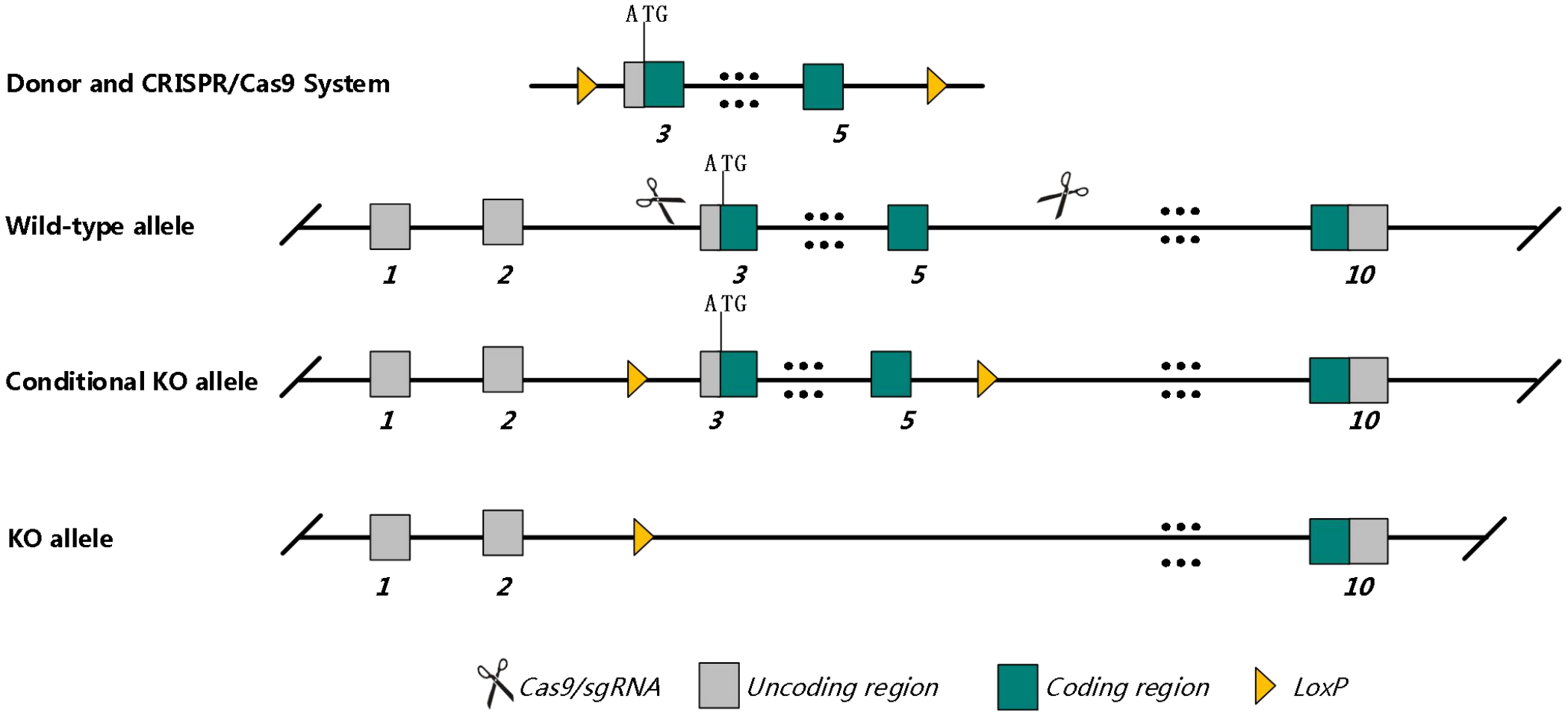
Project Overview

Project Name	***Slc39a14***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc39a14* gene. The schematic diagram is as follows:



Technical routes

- The *Slc39a14* gene has 13 transcripts. According to the structure of *Slc39a14* gene, exon3-exon5 of *Slc39a14-202* (ENSMUST00000068044.13) 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 *Slc39a14* 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.

Notice

- According to the existing MGI data,Homozygotes for a null allele show dwarfism, scoliosis, osteopenia, short long bones, altered gluconeogenesis and chondrocyte differentiation, low plasma IGF-I and liver zinc levels. Homozygotes for another null allele show reduced liver zinc levels and hepatocyte proliferation after hepatectomy.

- The *Slc39a14* gene is located on the Chr14. 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）

集萃药康 GemPharmatech

Slc39a14 solute carrier family 39 (zinc transporter), member 14 [Mus musculus (house mouse)]

Gene ID: 213053, updated on 31-Jan-2019

Summary

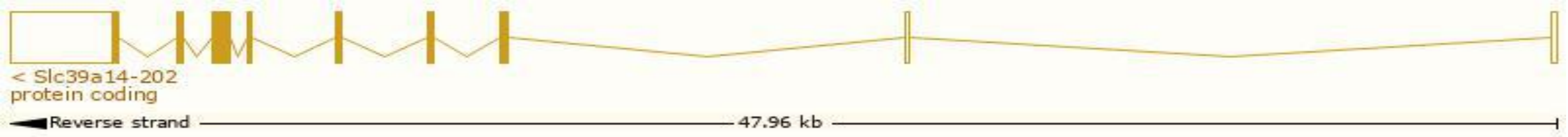
Official Symbol	Slc39a14 provided by MGI
Official Full Name	solute carrier family 39 (zinc transporter), member 14 provided byMGI
Primary source	MGI:MGI:2384851
See related	Ensembl:ENSMUSG00000022094
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	FAD-123, ZIP-14, Zip14, fad123
Expression	Ubiquitous expression in liver adult (RPKM 12.6), liver E18 (RPKM 11.1) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

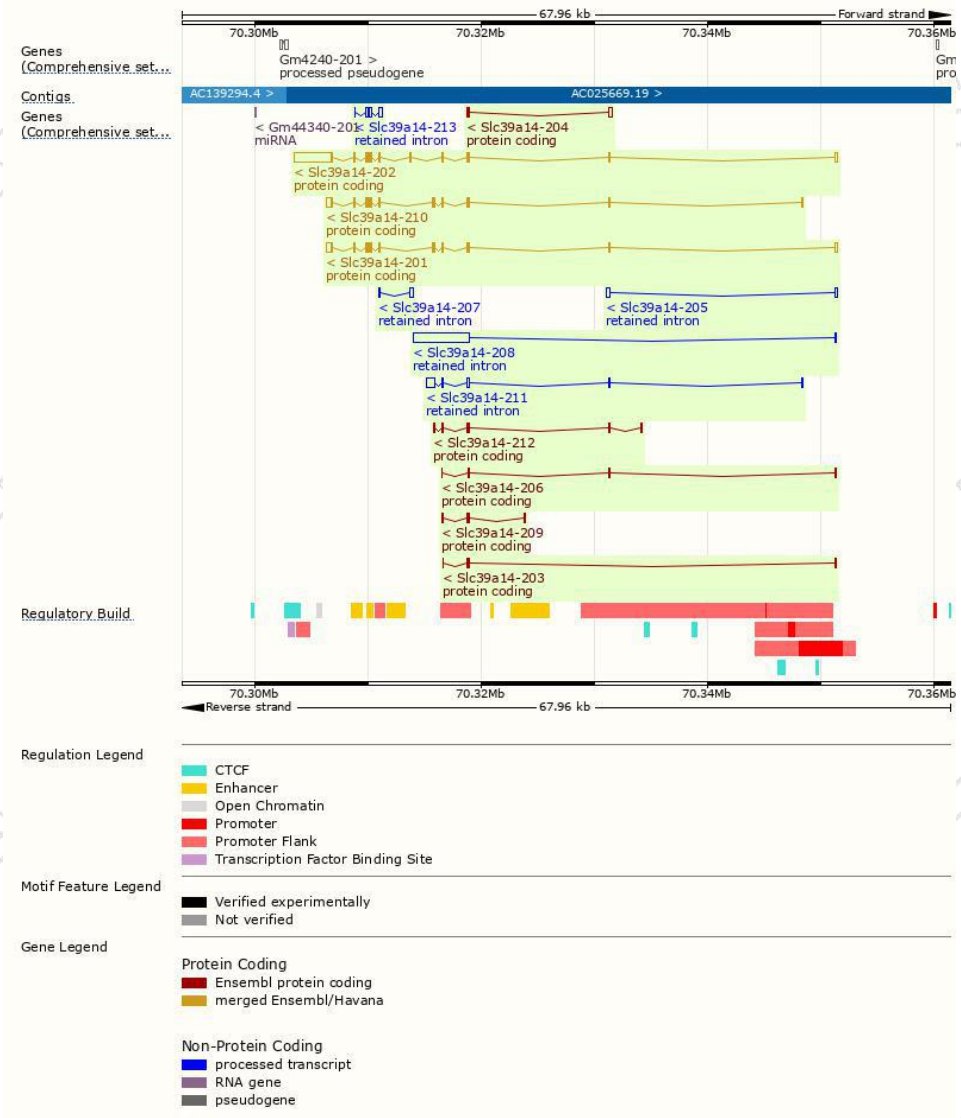
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc39a14-202	ENSMUST00000068044.13	4926	489aa	Protein coding	CCDS36969	Q75N73	TSL:5 GENCODE basic APPRIS P3
Slc39a14-201	ENSMUST00000022688.9	2098	489aa	Protein coding	CCDS49536	A0A0R4J1V1	TSL:1 GENCODE basic APPRIS ALT2
Slc39a14-210	ENSMUST00000152067.7	2075	489aa	Protein coding	CCDS49536	A0A0R4J1V1	TSL:1 GENCODE basic APPRIS ALT2
Slc39a14-212	ENSMUST00000152442.7	734	164aa	Protein coding	-	D3Z6P5	CDS 3' incomplete TSL:5
Slc39a14-209	ENSMUST00000151011.7	508	129aa	Protein coding	-	D3YXD7	CDS 3' incomplete TSL:2
Slc39a14-203	ENSMUST00000127000.1	479	109aa	Protein coding	-	D3Z354	CDS 3' incomplete TSL:5
Slc39a14-204	ENSMUST00000139284.1	458	64aa	Protein coding	-	D3Z4Q7	CDS 3' incomplete TSL:2
Slc39a14-206	ENSMUST00000143153.1	374	48aa	Protein coding	-	D3Z3C5	CDS 3' incomplete TSL:5
Slc39a14-208	ENSMUST00000146453.1	5117	No protein	Retained intron	-	-	TSL:2
Slc39a14-211	ENSMUST00000152202.7	1398	No protein	Retained intron	-	-	TSL:2
Slc39a14-213	ENSMUST00000155825.1	845	No protein	Retained intron	-	-	TSL:3
Slc39a14-205	ENSMUST00000142598.1	436	No protein	Retained intron	-	-	TSL:2
Slc39a14-207	ENSMUST00000145040.1	364	No protein	Retained intron	-	-	TSL:5

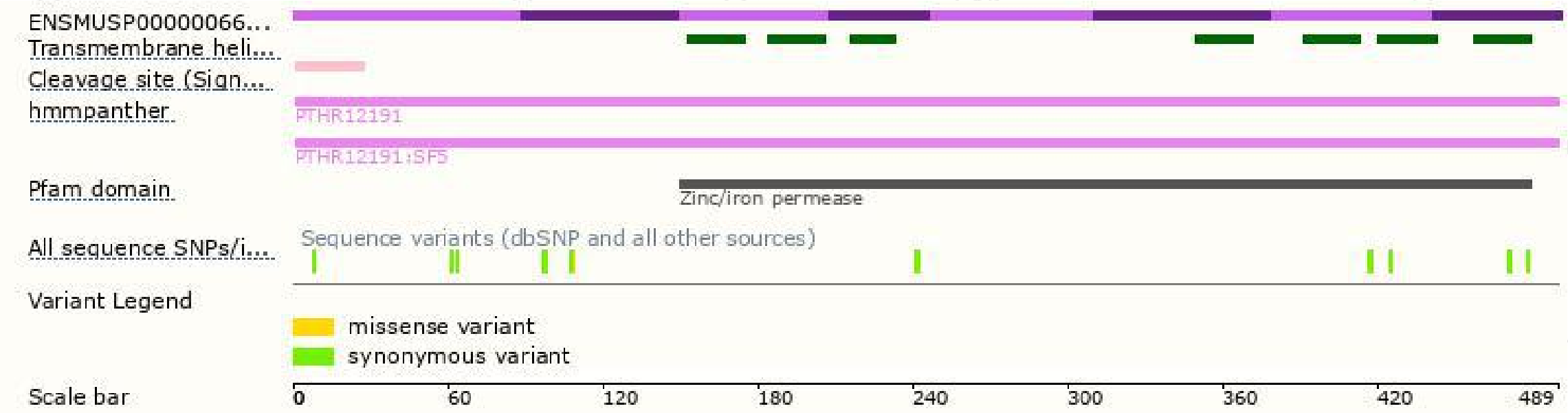
The strategy is based on the design of *Slc39a14-202* transcript,The transcription is shown below



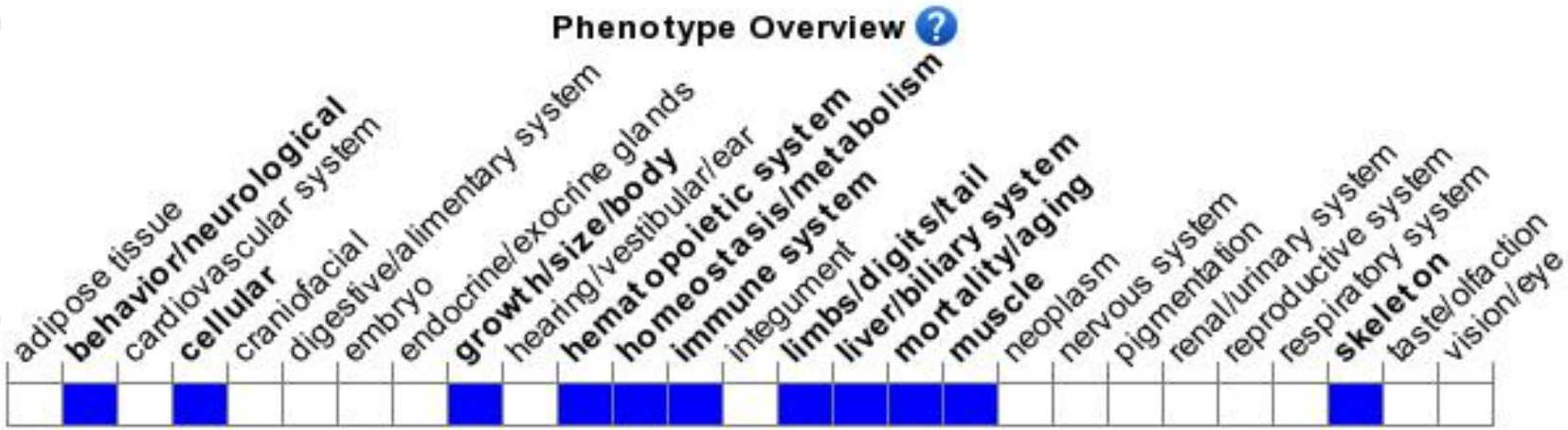
Genomic location distribution



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,Homozygotes for a null allele show dwarfism, scoliosis, osteopenia, short long bones, altered gluconeogenesis and chondrocyte differentiation, low plasma IGF-I and liver zinc levels. Homozygotes for another null allele show reduced liver zinc levels and hepatocyte proliferation after hepatectomy.

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

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