Samd14 Cas9-KO Strategy

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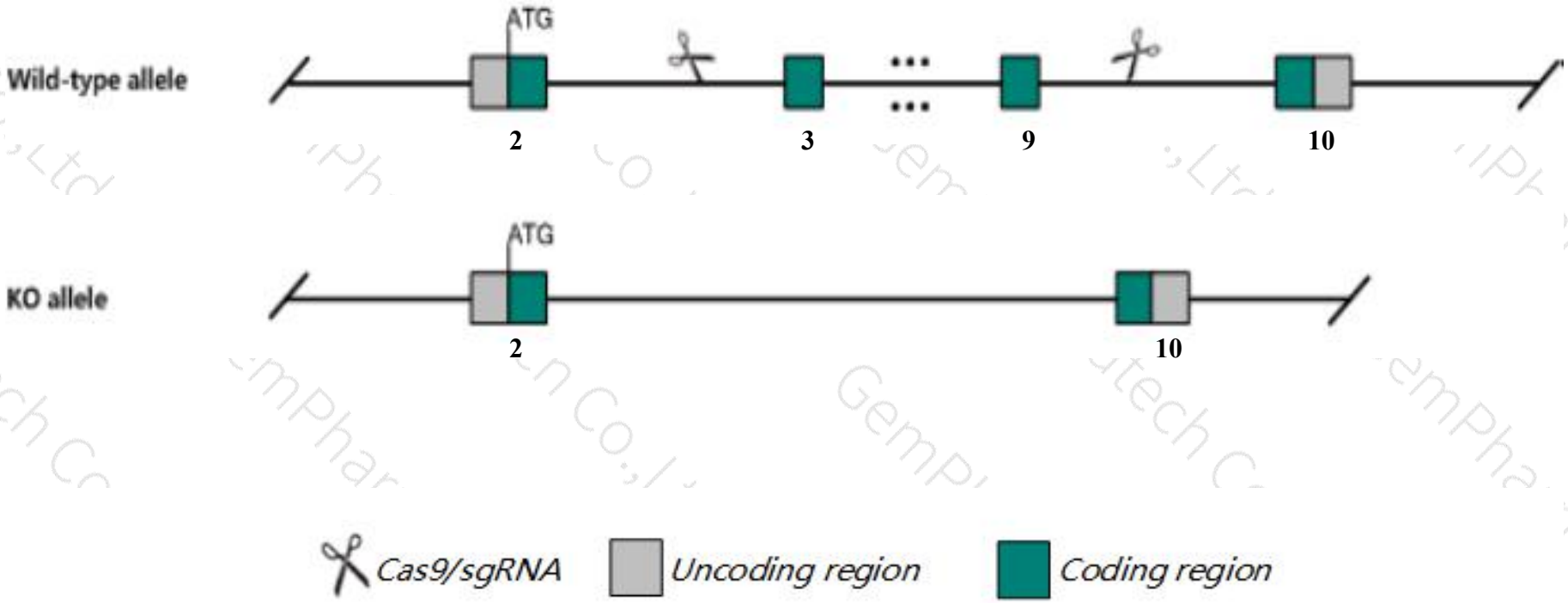
Design Date: 2020-8-17

Project Overview

Project Name	***Samd14***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Samd14* gene. The schematic diagram is as follows:



Technical routes

➢ The *Samd14* gene has 3 transcripts. According to the structure of *Samd14* gene, exon3-exon9 of *Samd14-201*(ENSMUST00000055947.9) transcript is recommended as the knockout region.The region contains 1055bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Samd14* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.

Notice

➢ According to the existing MGI data,mice homozygous for a hypomorphic allele affecting an intronic enhancer exhibit increased susceptibility to PTZ-induced anemia due to increased hematopoietic stem cell apoptosis.

➢ The *Samd14* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

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Samd14 sterile alpha motif domain containing 14 [Mus musculus (house mouse)]

Gene ID: 217125, updated on 13-Mar-2020

Summary

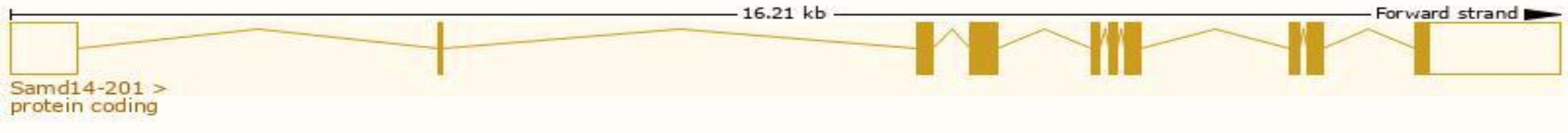
Official Symbol	Samd14 provided by MGI
Official Full Name	sterile alpha motif domain containing 14 provided byMGI
Primary source	MGI:MGI:2384945
See related	Ensembl:ENSMUSG00000047181
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI839049, AI854782, BC034054
Expression	Broad expression in whole brain E14.5 (RPKM 45.4), CNS E14 (RPKM 40.9) and 21 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

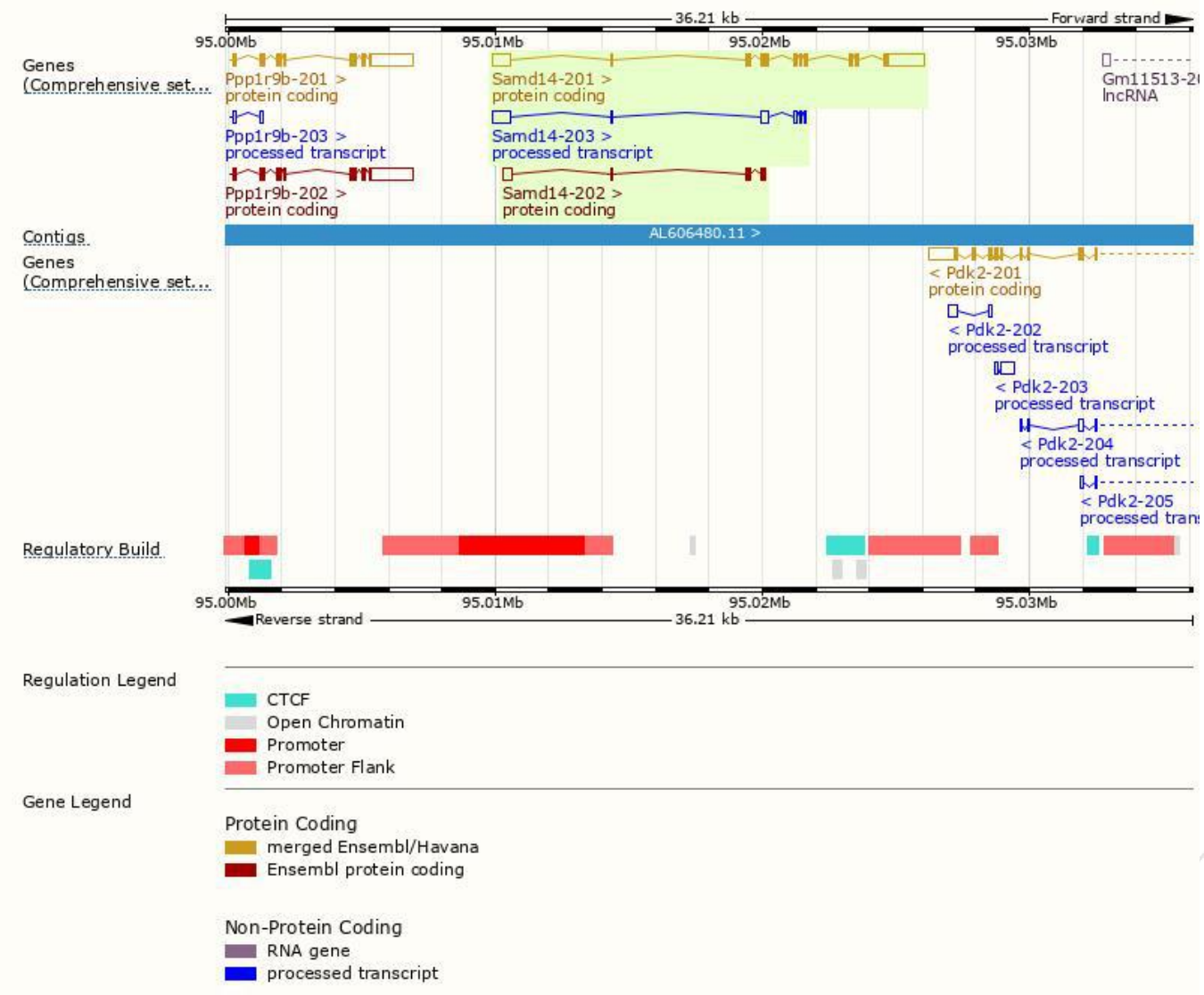
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Samd14-201	ENSMUST00000055947.9	3318	417aa	Protein coding	CCDS25269	Q8K070	TSL:1 GENCODE basic APPRIS P1
Samd14-202	ENSMUST00000124735.1	766	132aa	Protein coding	-	B7ZC59	CDS 3' incomplete TSL:3
Samd14-203	ENSMUST00000128512.1	1294	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Samd14-201* transcript,the transcription is shown below:

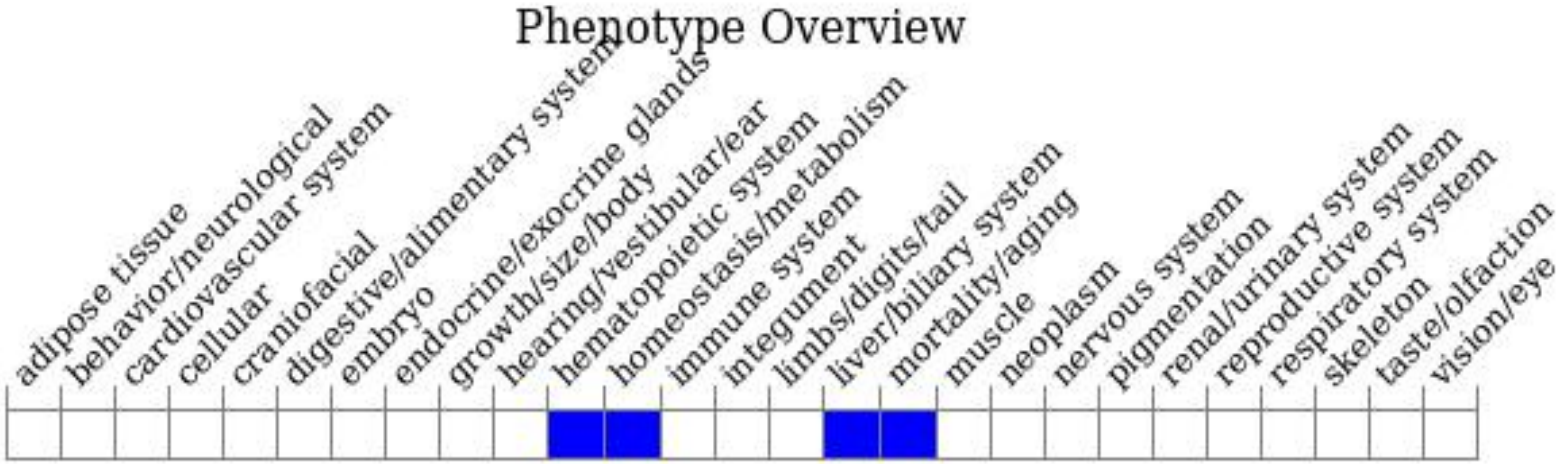


Genomic location distribution



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 hypomorphic allele affecting an intronic enhancer exhibit increased susceptibility to PTZ-induced anemia due to increased hematopoietic stem cell apoptosis.

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

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