Sat1 Cas9-CKO Strategy

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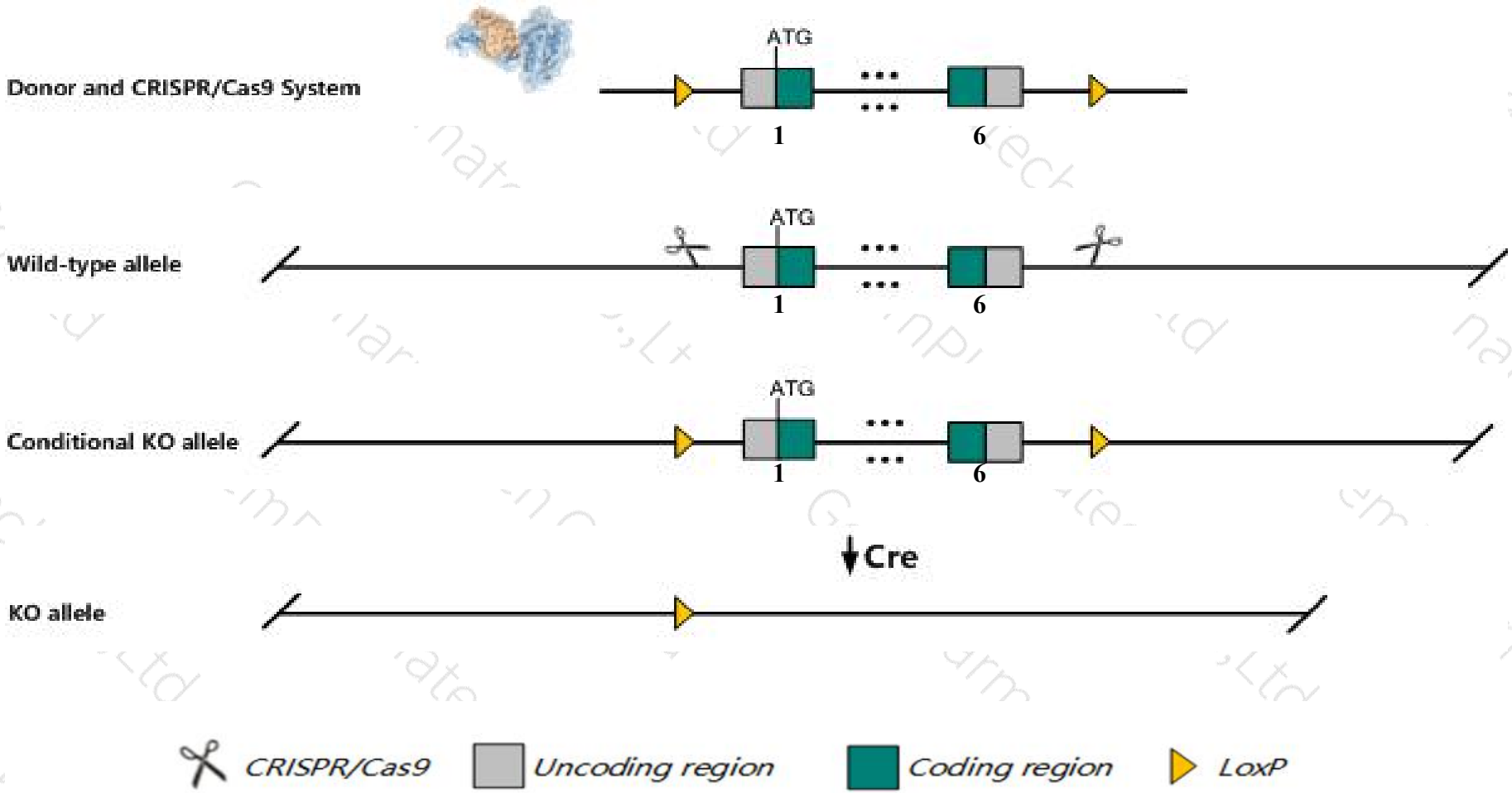
Project Overview

Project Name	***Sat1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sat1* gene. The schematic diagram is as follows:



Technical routes

- The *Sat1* gene has 7 transcripts. According to the structure of *Sat1* gene, exon1-exon6 of *Sat1-201* (ENSMUST00000026318.14) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Sat1* 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,Mice homozygous for a knock-out allele exhibit reduced female fertility, increased percent body fat and total fat pad weight, abnormal liver and white adipose tissue physiology, abnormal aerobic energy metabolism, increased serum leptin levels, and increased weight gain on a high-fat diet.

➢ The *Sat1* gene is located on the ChrX. 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）

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Sat1 spermidine/spermine N1-acetyl transferase 1 [*Mus musculus* (house mouse)]

Gene ID: 20229, updated on 12-Aug-2019

Summary

Official Symbol	Sat1 provided by MGI
Official Full Name	spermidine/spermine N1-acetyl transferase 1 provided by MGI
Primary source	MGI:MGI:98233
See related	Ensembl:ENSMUSG00000025283
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	Sat; SSAT; AA617398
Expression	Broad expression in bladder adult (RPKM 89.1), placenta adult (RPKM 43.0) and 22 other tissues See more
Orthologs	human all

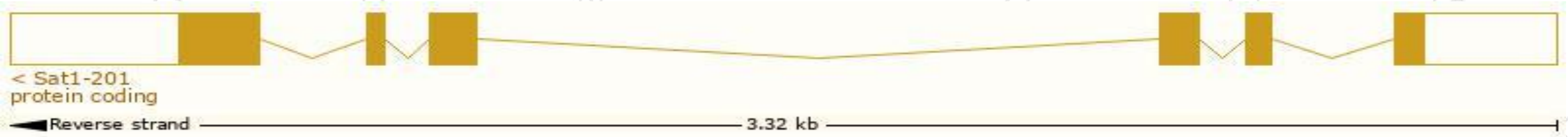
Chromosome X - NC_000086.7

Transcript information（Ensembl）

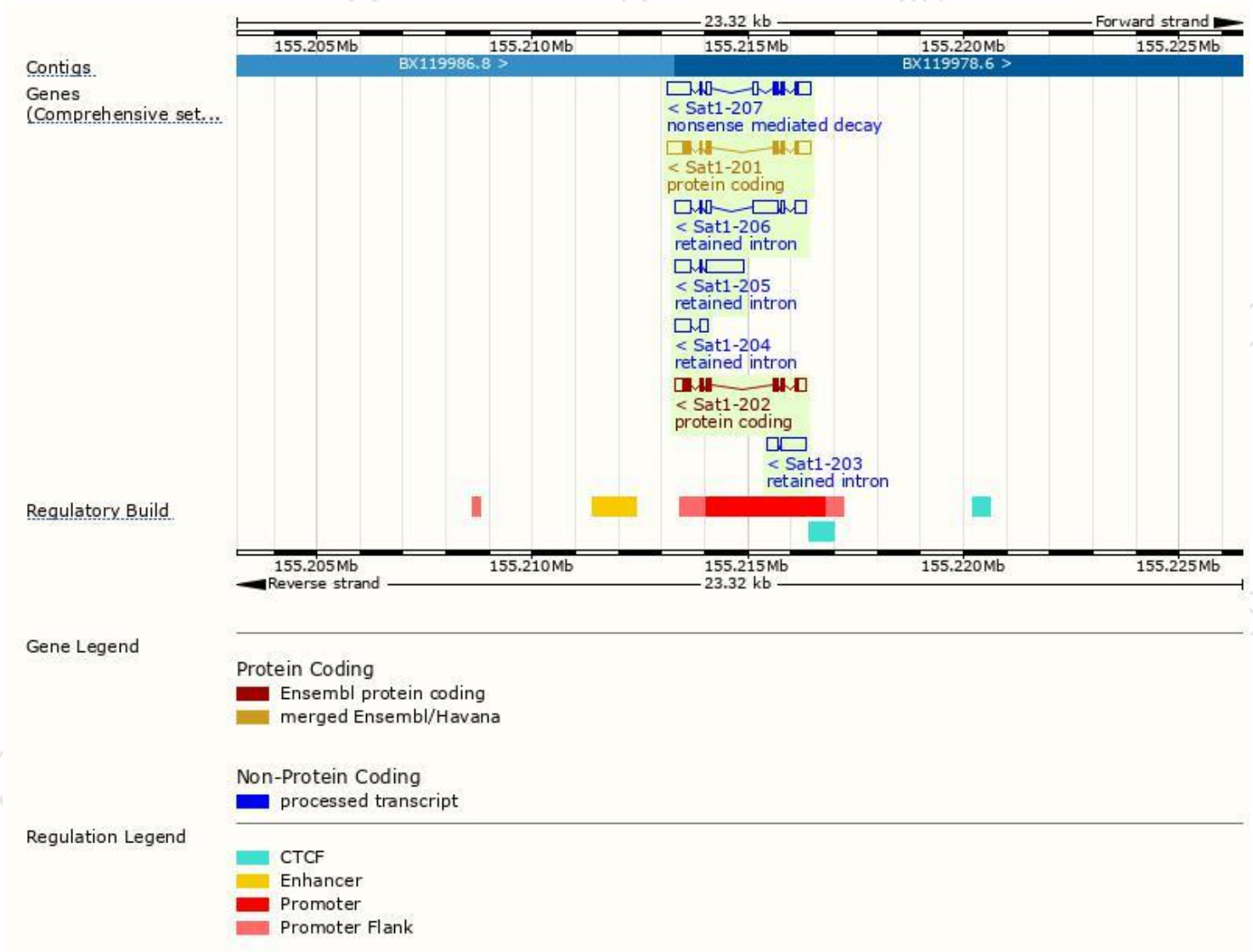
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Sat1-201	ENSMUST00000026318.14	1162	171aa	ENSMUSP00000026318.8	Protein coding	CCDS30495	P48026	TSL:1 GENCODE basic APPRIS P1
Sat1-202	ENSMUST00000112551.3	896	178aa	ENSMUSP00000108170.3	Protein coding	-	A2BES2	TSL:2 GENCODE basic
Sat1-207	ENSMUST00000152463.7	1272	71aa	ENSMUSP00000138776.1	Nonsense mediated decay	-	S4R2T2	TSL:5
Sat1-206	ENSMUST00000150046.1	1352	No protein	-	Retained intron	-	-	TSL:5
Sat1-205	ENSMUST00000138944.7	1275	No protein	-	Retained intron	-	-	TSL:1
Sat1-203	ENSMUST00000123337.1	773	No protein	-	Retained intron	-	-	TSL:3
Sat1-204	ENSMUST00000134855.7	525	No protein	-	Retained intron	-	-	TSL:2

The strategy is based on the design of *Sat1-201* transcript,The transcription is shown below

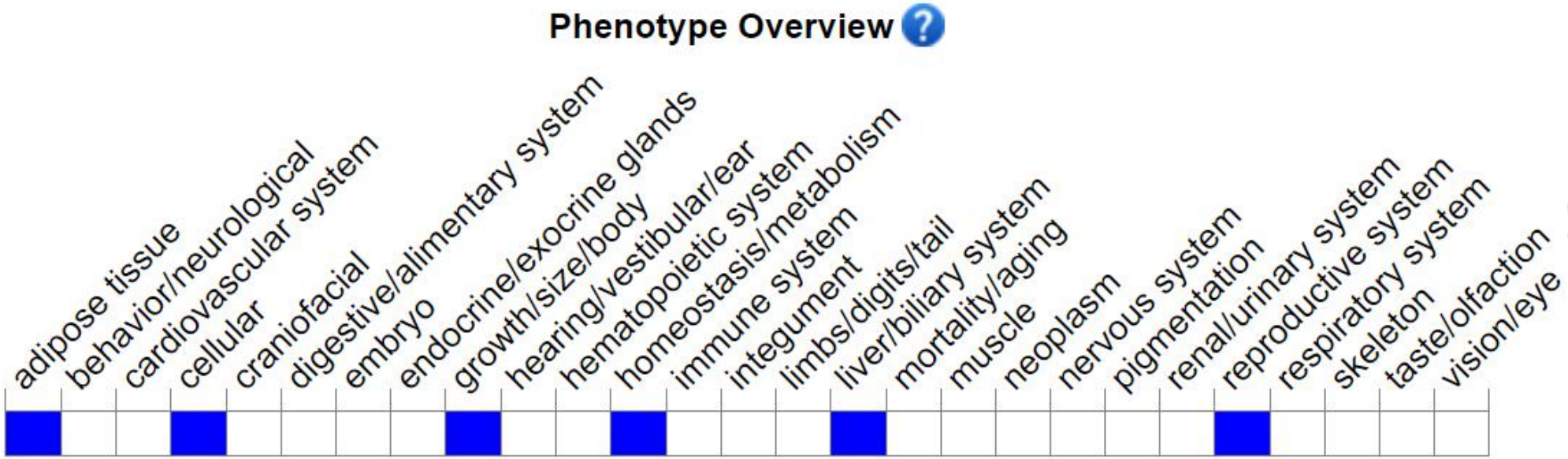


Genomic location distribution



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/).

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

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