

Sgta Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Sgta

Project type

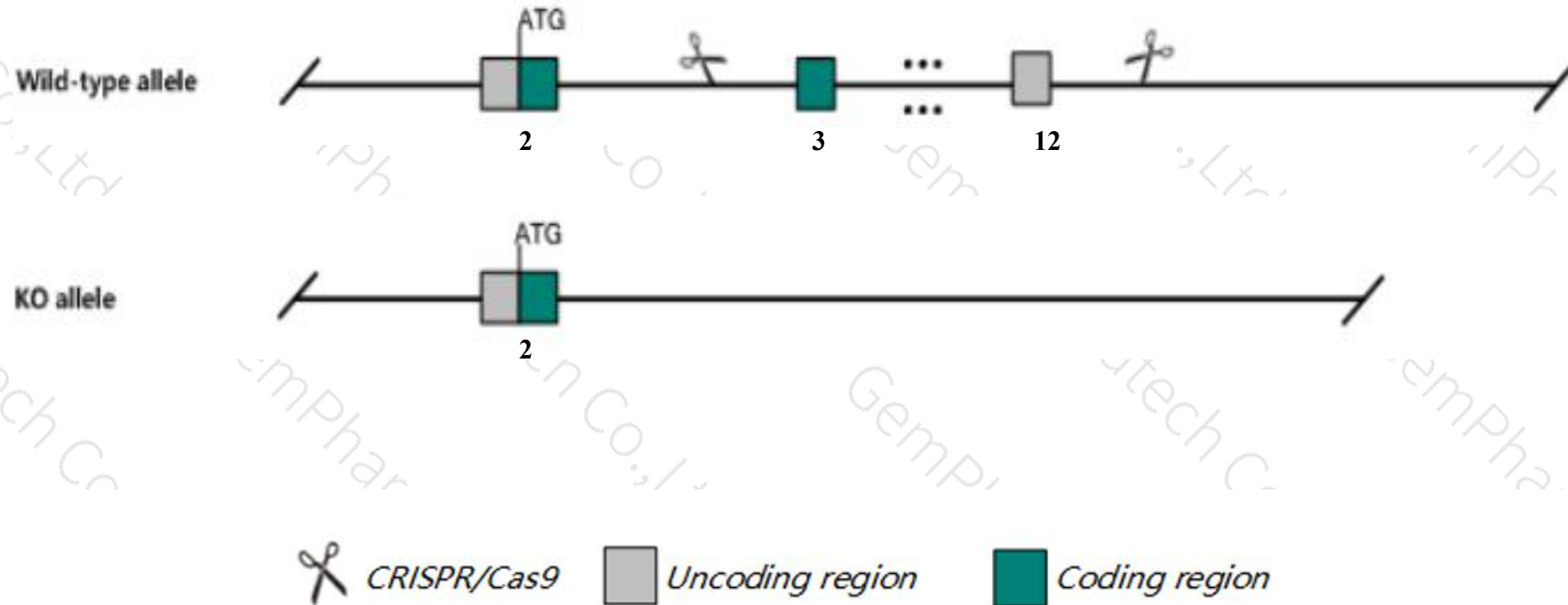
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Sgta* gene has 7 transcripts. According to the structure of *Sgta* gene, exon3-exon12 of *Sgta-201* (ENSMUST00000005067.5) transcript is recommended as the knockout region. The region contains most 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 *Sgta* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit increased neonatal death, subfertility, decreased body size, increased brain, intestine and heart weight, decreased serum insulin-like growth factor i level, large penis, and increased testis descent.
- The *Sgta* gene is located on the Chr10. 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)

Sgta small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha [Mus musculus (house mouse)]

Gene ID: 52551, updated on 13-Mar-2020

Summary



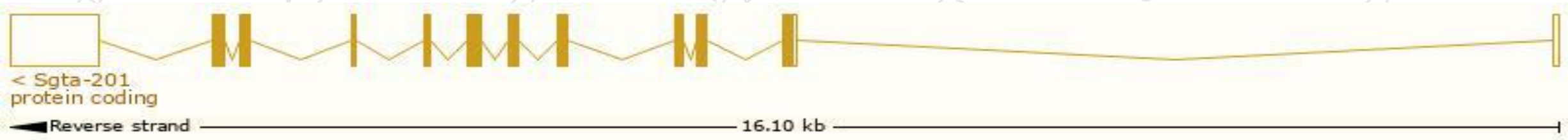
Official Symbol	Sgta provided by MGI
Official Full Name	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha provided by MGI
Primary source	MGI:MGI:1098703
See related	Ensembl:ENSMUSG000000004937
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5330427H01Rik, A1194281, D10Erd190e, Sgt, Stg
Expression	Ubiquitous expression in adrenal adult (RPKM 191.2), mammary gland adult (RPKM 106.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

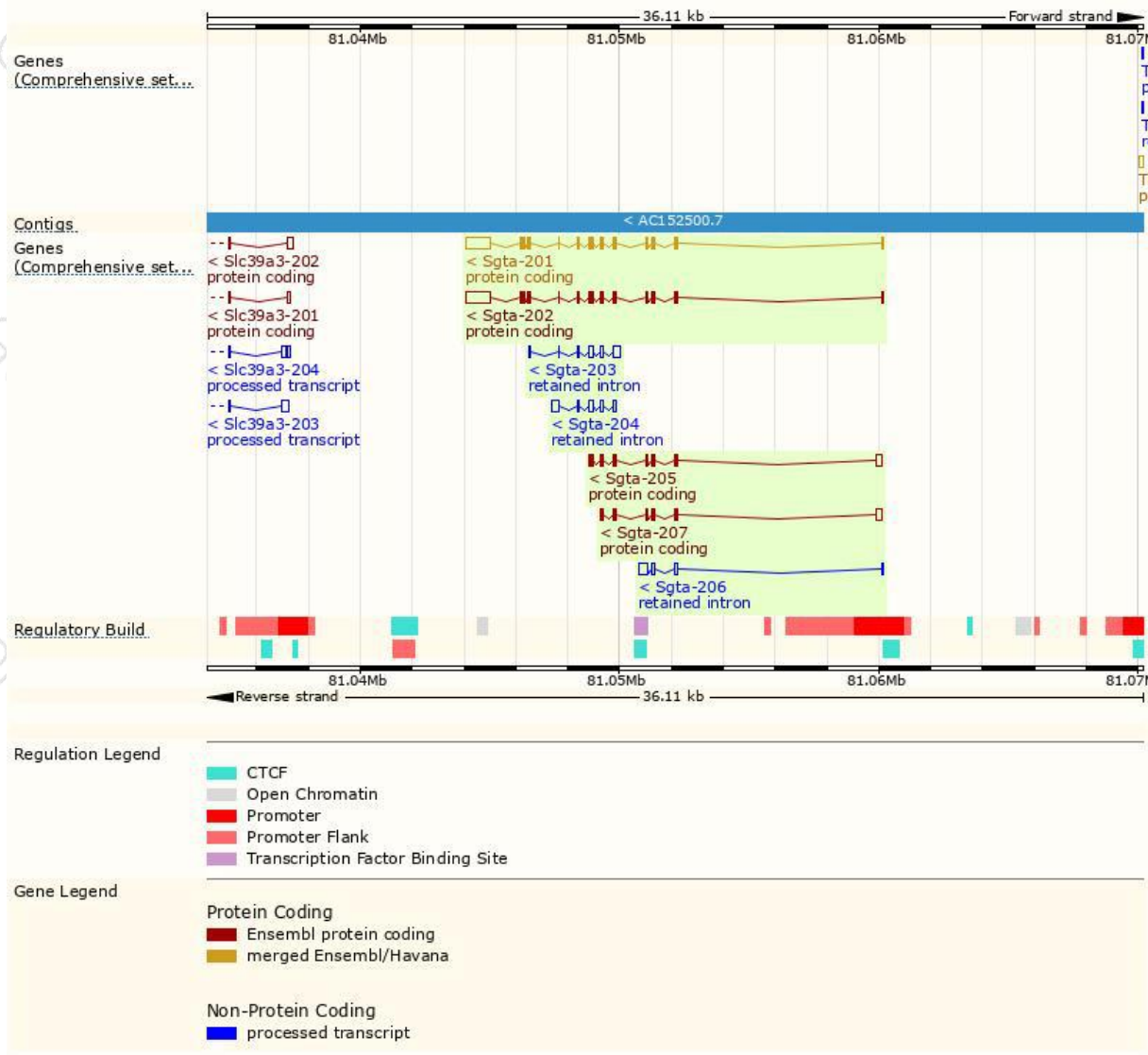
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sgta-201	ENSMUST00000005067.5	1969	315aa	Protein coding	CCDS35990	Q8BJU0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Sgta-202	ENSMUST00000218208.1	1964	314aa	Protein coding	-	Q3TN35 Q8BJU0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Sgta-205	ENSMUST00000219401.1	869	211aa	Protein coding	-	A0A1W2P6P1	CDS 3' incomplete TSL:2
Sgta-207	ENSMUST00000220317.1	775	166aa	Protein coding	-	A0A1W2P7I5	CDS 3' incomplete TSL:3
Sgta-203	ENSMUST00000219126.1	698	No protein	Retained intron	-	-	TSL:5
Sgta-204	ENSMUST00000219297.1	693	No protein	Retained intron	-	-	TSL:3
Sgta-206	ENSMUST00000220202.1	642	No protein	Retained intron	-	-	TSL:2

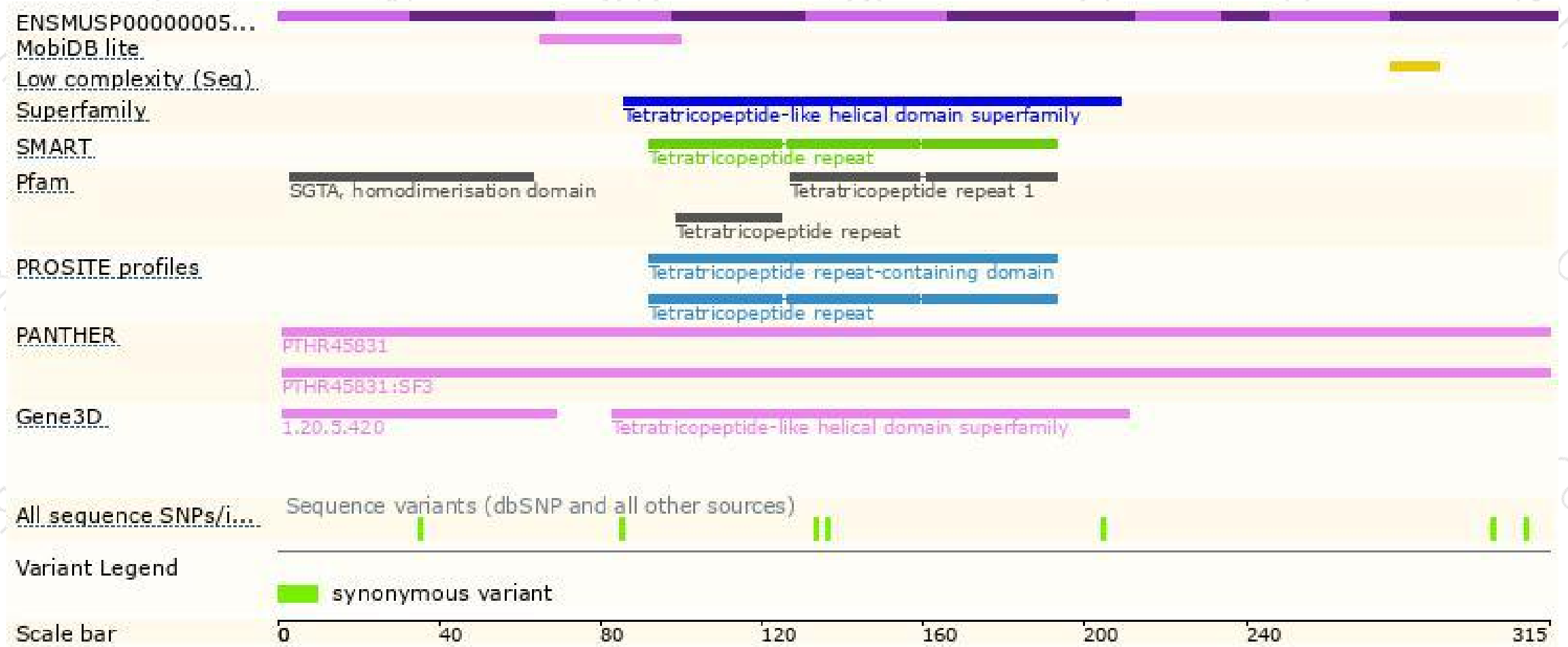
The strategy is based on the design of *Sgta-201* transcript,the transcription is shown below:



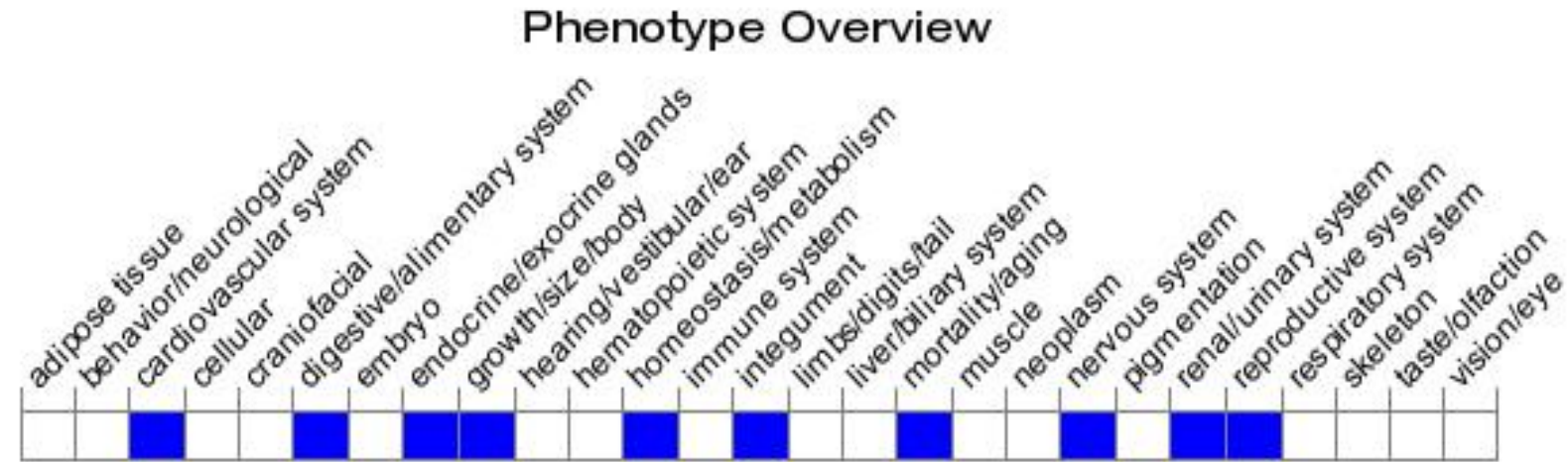
Genomic location distribution



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 knock-out allele exhibit increased neonatal death, subfertility, decreased body size, increased brain, intestine and heart weight, decreased serum insulin-like growth factor I level, large penis, and increased testis descent.

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

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