Sgms1 Cas9-KO Strategy

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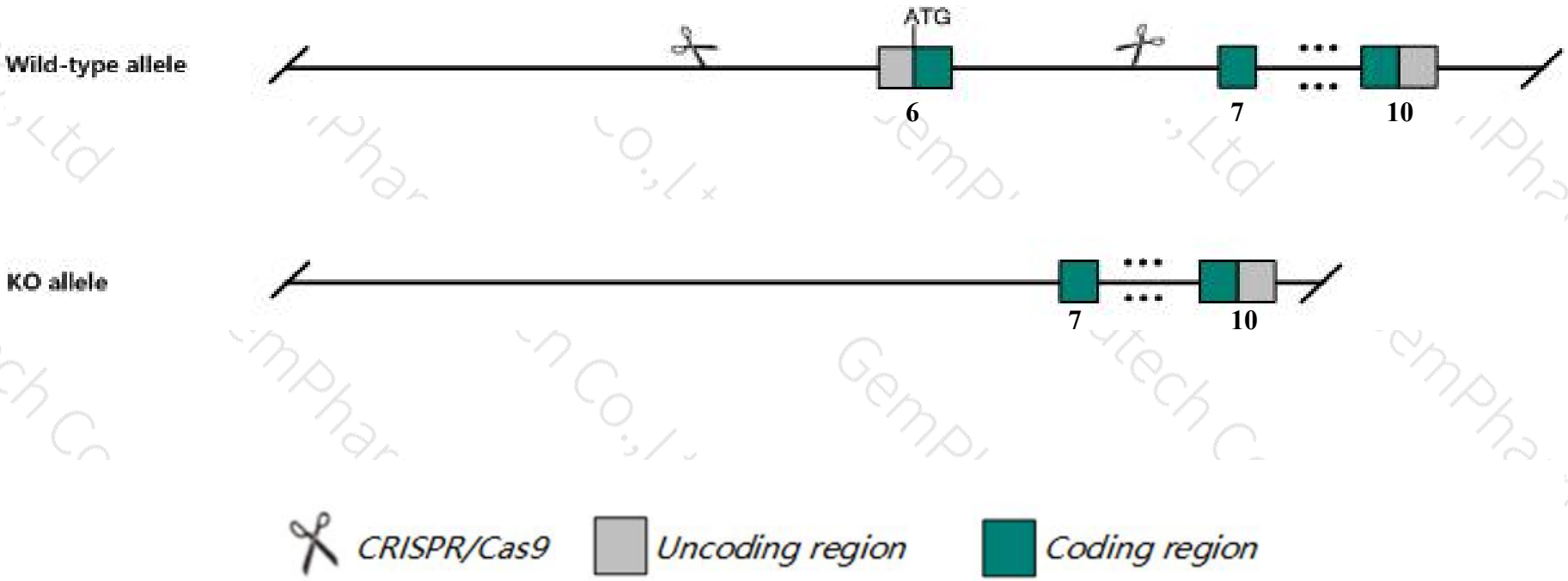
Project Overview

Project Name	***Sgms1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sgms1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Sgms1* gene has 15 transcripts. According to the structure of *Sgms1* gene, exon6 of *Sgms1-209* (ENSMUST00000142618.7) 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 *Sgms1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,Mice homozygous for a knock-out allele exhibit premature death, impaired insulin tolerance, increased insulin sensitivity, decreased insulin secretion, and abnormal pancreatic islet cell mitochondria morphology.

➢ The *Sgms1* gene is located on the Chr19. 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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Sgms1 sphingomyelin synthase 1 [Mus musculus (house mouse)]

Gene ID: 208449, updated on 31-Jan-2019

Summary

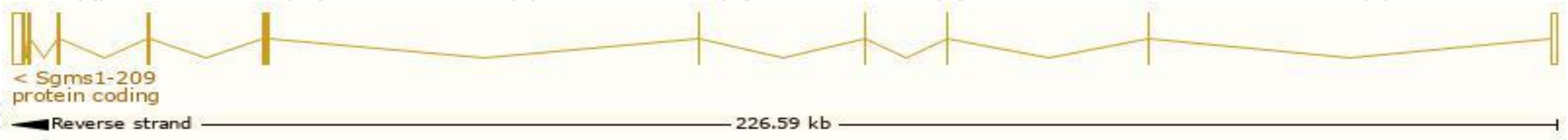
Official Symbol	Sgms1 provided by MGI
Official Full Name	sphingomyelin synthase 1 provided by MGI
Primary source	MGI:MGI:2444110
See related	Ensembl:ENSMUSG00000040451
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9530058O11Rik, AI841905, C80702, Mob, Sms1, Sor1, Tmem23
Expression	Broad expression in testis adult (RPKM 37.1), genital fat pad adult (RPKM 8.2) and 20 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

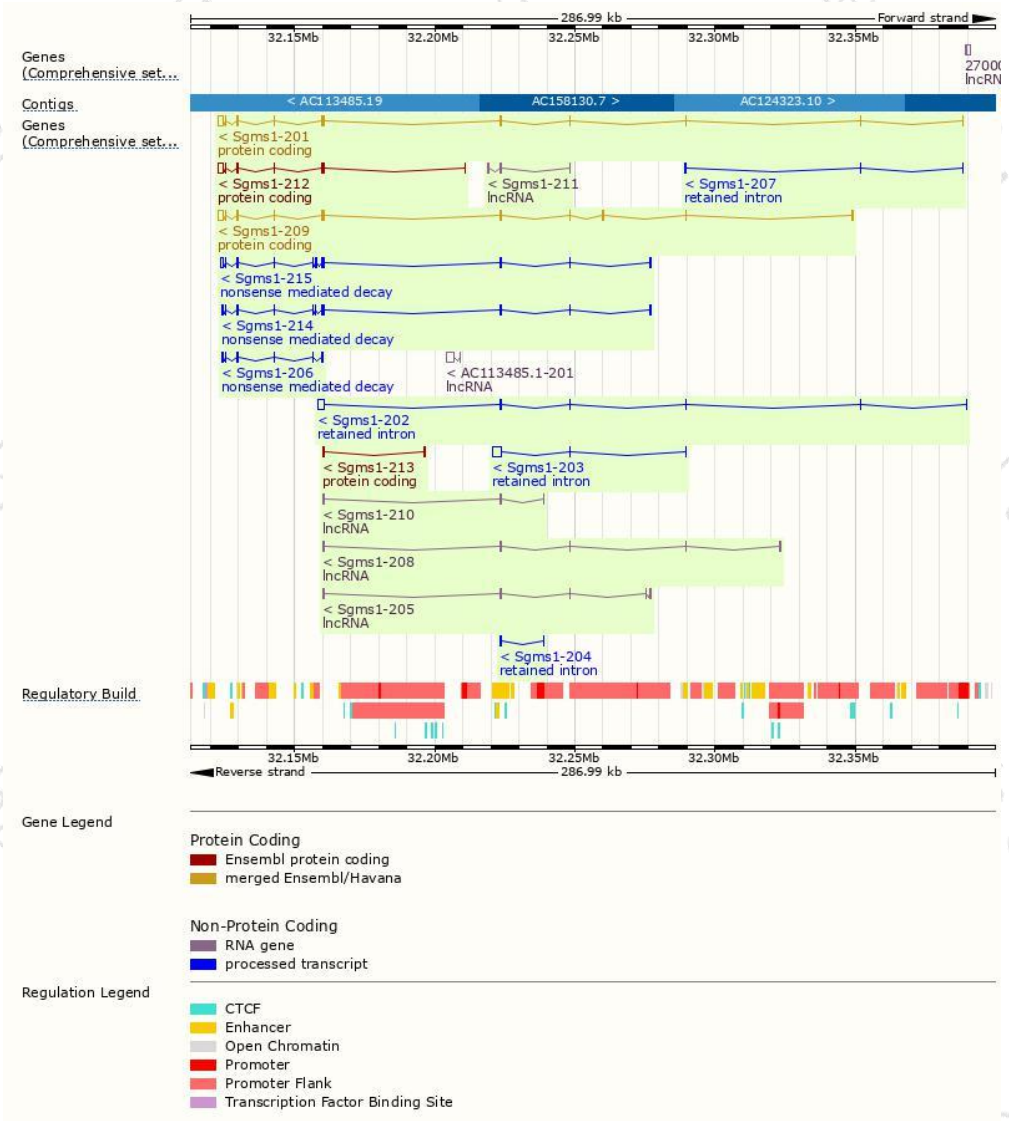
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sgms1-209	ENSMUST00000142618.7	4036	419aa	Protein coding	CCDS29750	Q8VCQ6	TSL:1 GENCODE basic APPRIS P1
Sgms1-201	ENSMUST00000099514.9	3665	419aa	Protein coding	CCDS29750	Q8VCQ6	TSL:1 GENCODE basic APPRIS P1
Sgms1-212	ENSMUST00000151289.8	3262	419aa	Protein coding	CCDS29750	Q8VCQ6	TSL:1 GENCODE basic APPRIS P1
Sgms1-213	ENSMUST00000151822.1	427	34aa	Protein coding	-	D3YV54	CDS 3' incomplete TSL:3
Sgms1-215	ENSMUST00000236410.1	2593	293aa	Nonsense mediated decay	-	-	
Sgms1-214	ENSMUST00000152340.7	1986	217aa	Nonsense mediated decay	-	Q8VCQ6	TSL:2
Sgms1-206	ENSMUST00000134415.1	1595	220aa	Nonsense mediated decay	-	E3W996	TSL:5
Sgms1-203	ENSMUST00000124483.1	3086	No protein	Retained intron	-	-	TSL:2
Sgms1-202	ENSMUST00000124012.7	2566	No protein	Retained intron	-	-	TSL:2
Sgms1-207	ENSMUST00000141252.1	676	No protein	Retained intron	-	-	TSL:2
Sgms1-204	ENSMUST00000126332.1	357	No protein	Retained intron	-	-	TSL:2
Sgms1-208	ENSMUST00000141655.7	603	No protein	lncRNA	-	-	TSL:2
Sgms1-211	ENSMUST00000149934.1	483	No protein	lncRNA	-	-	TSL:5
Sgms1-210	ENSMUST00000149107.7	358	No protein	lncRNA	-	-	TSL:2
Sgms1-205	ENSMUST00000131768.7	353	No protein	lncRNA	-	-	TSL:2

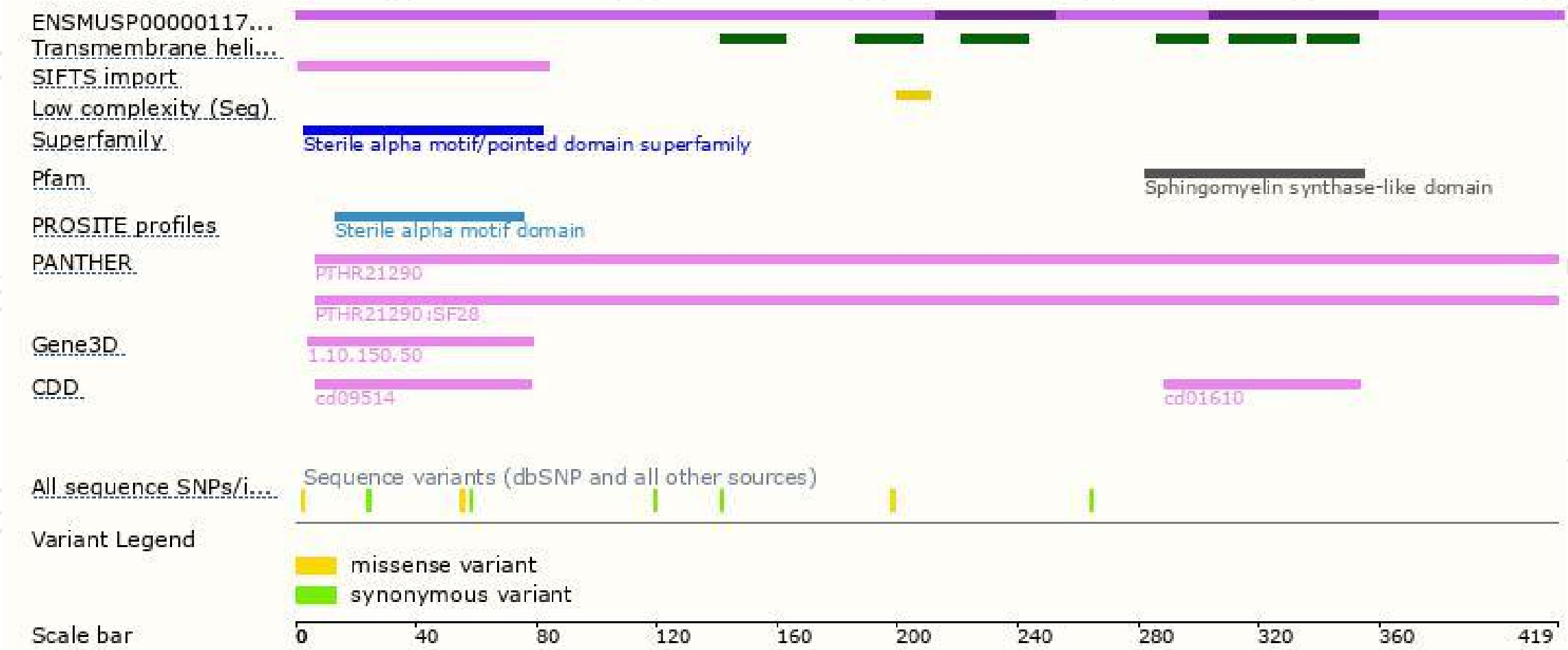
The strategy is based on the design of *Sgms1-209* transcript,The transcription is shown below



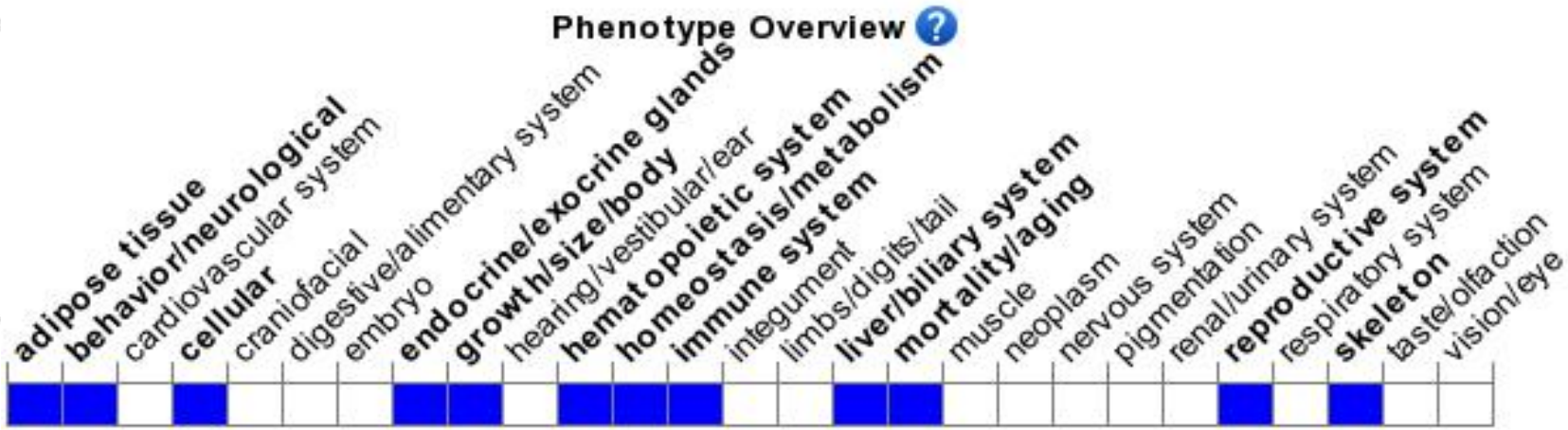
Genomic location distribution



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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