

# *Sash1* Cas9-KO Strategy

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Design Date: 2019-7-22

# Project Overview

**Project Name**

***Sash1***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sash1* gene. The schematic diagram is as follows:



- The *Sash1* gene has 4 transcripts. According to the structure of *Sash1* gene, exon5-exon6 of *Sash1-201* (ENSMUST00000015449.5) transcript is recommended as the knockout region. The region contains 128bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sash1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Sash1* 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.
- The N-terminal of *Sash1* gene will remain 102aa, it may remain the partial function of *Sash1* gene.
- Transcript *Sash1*-204 may not be affected. And the effect on transcript *Sash1*-202&203 is unknown.
- 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)

## Sash1 SAM and SH3 domain containing 1 [Mus musculus (house mouse)]

Gene ID: 70097, updated on 19-Mar-2019

### Summary



<b>Official Symbol</b>	Sash1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	SAM and SH3 domain containing 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1917347</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000015305</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	1100001C18Rik, 2500002E12Rik, A330076K04Rik, mKIAA0790
<b>Expression</b>	Ubiquitous expression in lung adult (RPKM 10.4), subcutaneous fat pad adult (RPKM 8.3) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

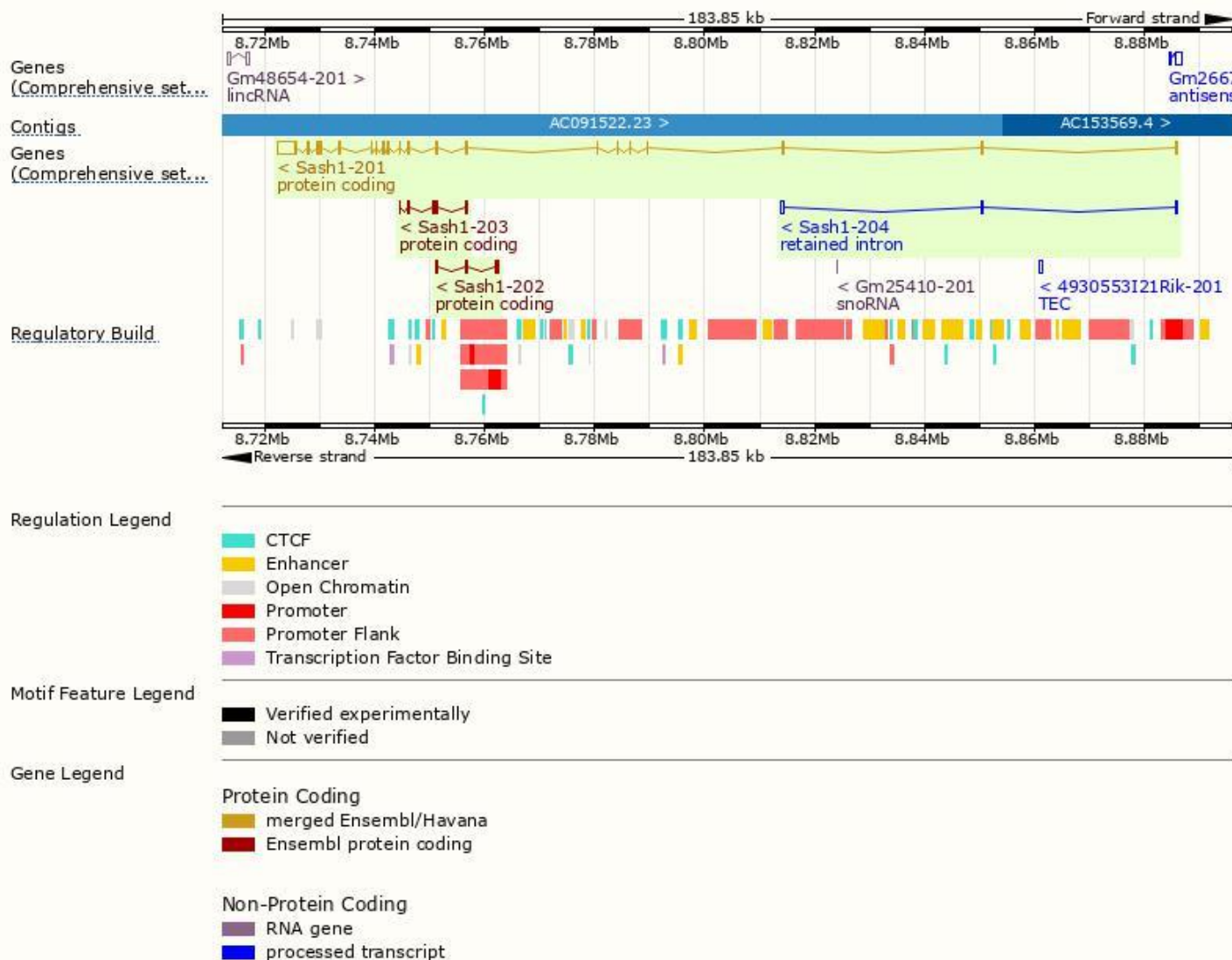
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sash1-201	<a href="#">ENSMUST00000015449.5</a>	7183	<a href="#">1230aa</a>	Protein coding	<a href="#">CCDS23692</a>	<a href="#">F8VQK5</a>	TSL:1 GENCODE basic APPRIS P1
Sash1-203	<a href="#">ENSMUST00000212869.1</a>	1074	<a href="#">358aa</a>	Protein coding	-	<a href="#">A0A1D5RMH4</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Sash1-202	<a href="#">ENSMUST00000212553.1</a>	840	<a href="#">157aa</a>	Protein coding	-	<a href="#">A0A1D5RM71</a>	CDS 3' incomplete TSL:2
Sash1-204	<a href="#">ENSMUST00000213032.1</a>	1078	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Sash1-201* transcript,The transcription is shown below

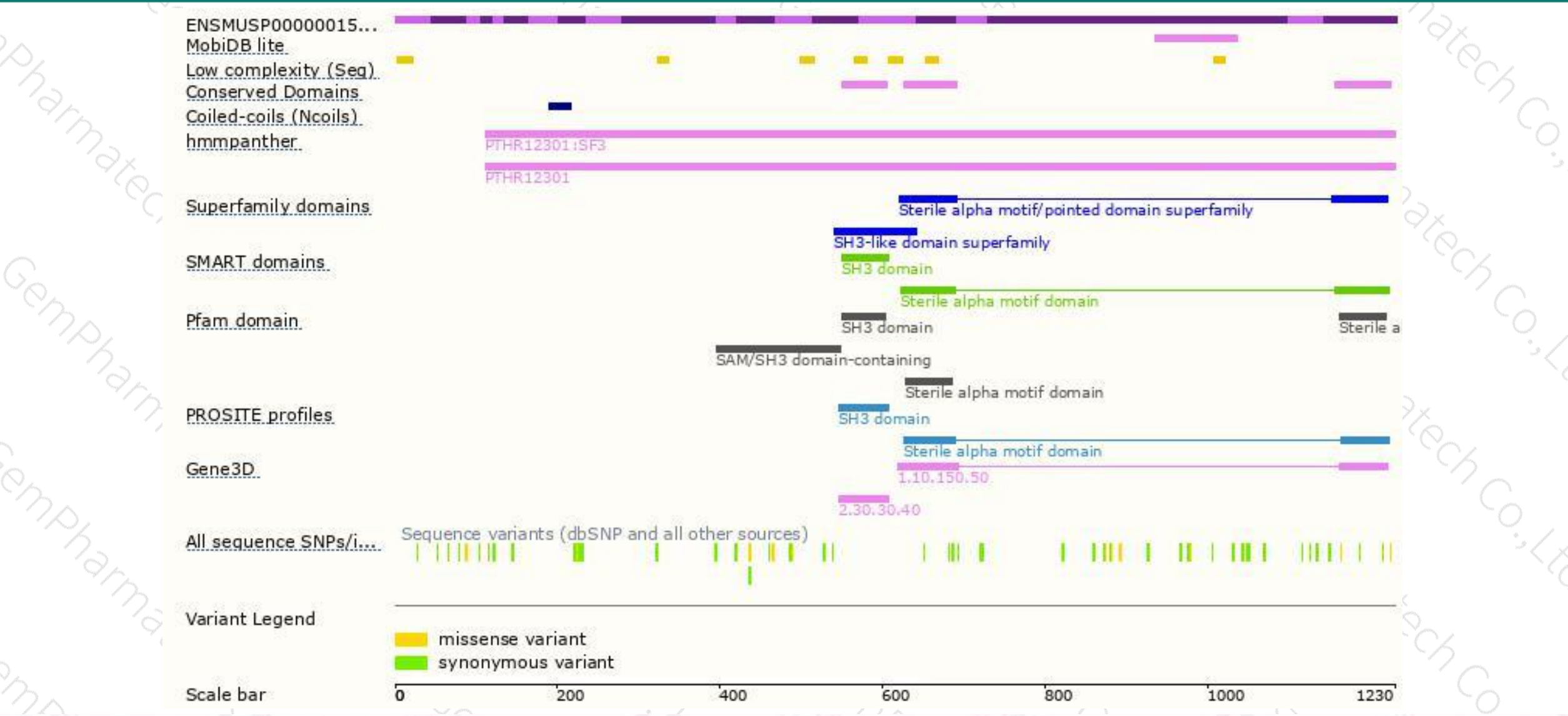


# Genomic location distribution





# Protein domain



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

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