

# *St18* Cas9-KO Strategy

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**Reviewer:**

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**Design Date:**

**2020-2-20**

# Project Overview

**Project Name**

***St18***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *St18* gene. The schematic diagram is as follows:



- The *St18* gene has 13 transcripts. According to the structure of *St18* gene, exon6 of *St18-208* (ENSMUST00000140079.7) transcript is recommended as the knockout region. The region contains 31bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *St18* gene. The brief process is as follows: CRISPR/Cas9 system w

- The *St18* gene is located on the Chr1. 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)

## St18 suppression of tumorigenicity 18 [Mus musculus (house mouse)]

Gene ID: 240690, updated on 3-Feb-2019

### Summary



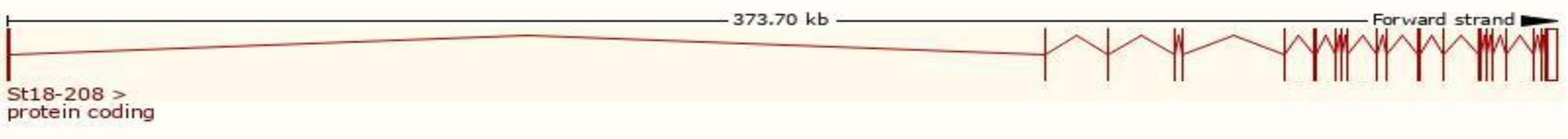
<b>Official Symbol</b>	St18 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	suppression of tumorigenicity 18 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2446700</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000033740</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	AV348974, Myt3, NZF-3, Nzf3, mKIAA0535
<b>Expression</b>	Biased expression in cerebellum adult (RPKM 6.1), CNS E11.5 (RPKM 3.2) and 5 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

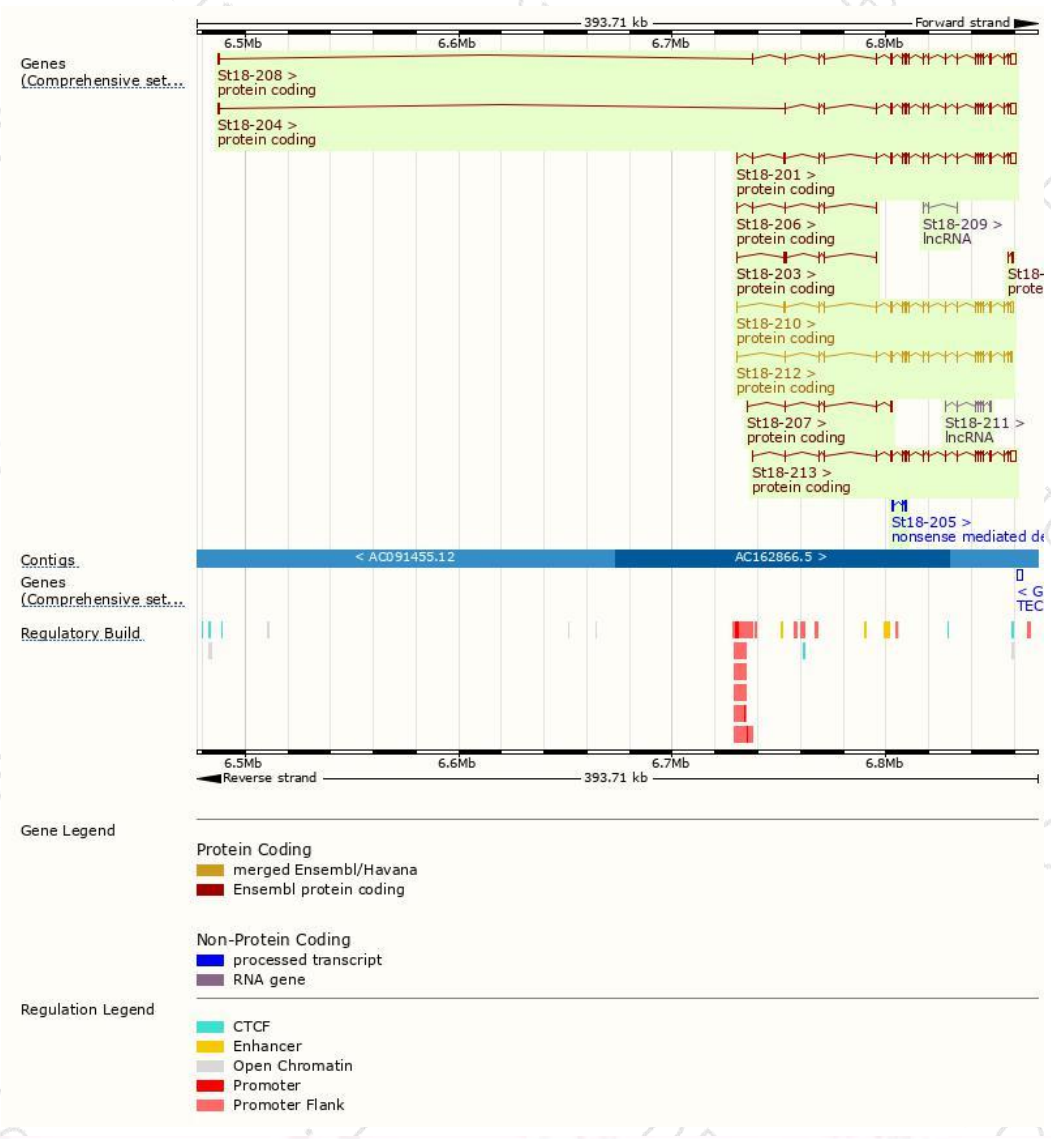
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
St18-208	<a href="#">ENSMUST00000140079.7</a>	5892	<a href="#">1045aa</a>	Protein coding	<a href="#">CCDS14810</a>	<a href="#">Q148A0</a> <a href="#">Q80TY4</a>	TSL:1 GENCODE basic APPRIS P1
St18-201	<a href="#">ENSMUST00000043578.12</a>	5862	<a href="#">1045aa</a>	Protein coding	<a href="#">CCDS14810</a>	<a href="#">Q148A0</a> <a href="#">Q80TY4</a>	TSL:1 GENCODE basic APPRIS P1
St18-204	<a href="#">ENSMUST00000131494.7</a>	5720	<a href="#">1045aa</a>	Protein coding	<a href="#">CCDS14810</a>	<a href="#">Q148A0</a> <a href="#">Q80TY4</a>	TSL:1 GENCODE basic APPRIS P1
St18-213	<a href="#">ENSMUST00000163727.3</a>	5604	<a href="#">1045aa</a>	Protein coding	<a href="#">CCDS14810</a>	<a href="#">Q148A0</a> <a href="#">Q80TY4</a>	TSL:5 GENCODE basic APPRIS P1
St18-210	<a href="#">ENSMUST00000150761.7</a>	4264	<a href="#">1045aa</a>	Protein coding	<a href="#">CCDS14810</a>	<a href="#">Q148A0</a> <a href="#">Q80TY4</a>	TSL:1 GENCODE basic APPRIS P1
St18-212	<a href="#">ENSMUST00000151281.7</a>	3533	<a href="#">1045aa</a>	Protein coding	<a href="#">CCDS14810</a>	<a href="#">Q148A0</a> <a href="#">Q80TY4</a>	TSL:1 GENCODE basic APPRIS P1
St18-207	<a href="#">ENSMUST00000139838.7</a>	792	<a href="#">215aa</a>	Protein coding	-	<a href="#">D3YZ65</a>	CDS 3' incomplete TSL:3
St18-202	<a href="#">ENSMUST00000130338.1</a>	720	<a href="#">95aa</a>	Protein coding	-	<a href="#">A0A0A6YVU2</a>	CDS 5' incomplete TSL:3
St18-203	<a href="#">ENSMUST00000131467.7</a>	585	<a href="#">83aa</a>	Protein coding	-	<a href="#">D3YUH3</a>	CDS 3' incomplete TSL:3
St18-206	<a href="#">ENSMUST00000139756.7</a>	435	<a href="#">42aa</a>	Protein coding	-	<a href="#">A0A0A6YXN3</a>	CDS 3' incomplete TSL:3
St18-205	<a href="#">ENSMUST00000132207.1</a>	684	<a href="#">108aa</a>	Nonsense mediated decay	-	<a href="#">A0A0A6YY81</a>	CDS 5' incomplete TSL:3
St18-211	<a href="#">ENSMUST00000151015.1</a>	817	No protein	Processed transcript	-	-	TSL:5
St18-209	<a href="#">ENSMUST00000142304.1</a>	445	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *St18-208* transcript,The transcription is shown below

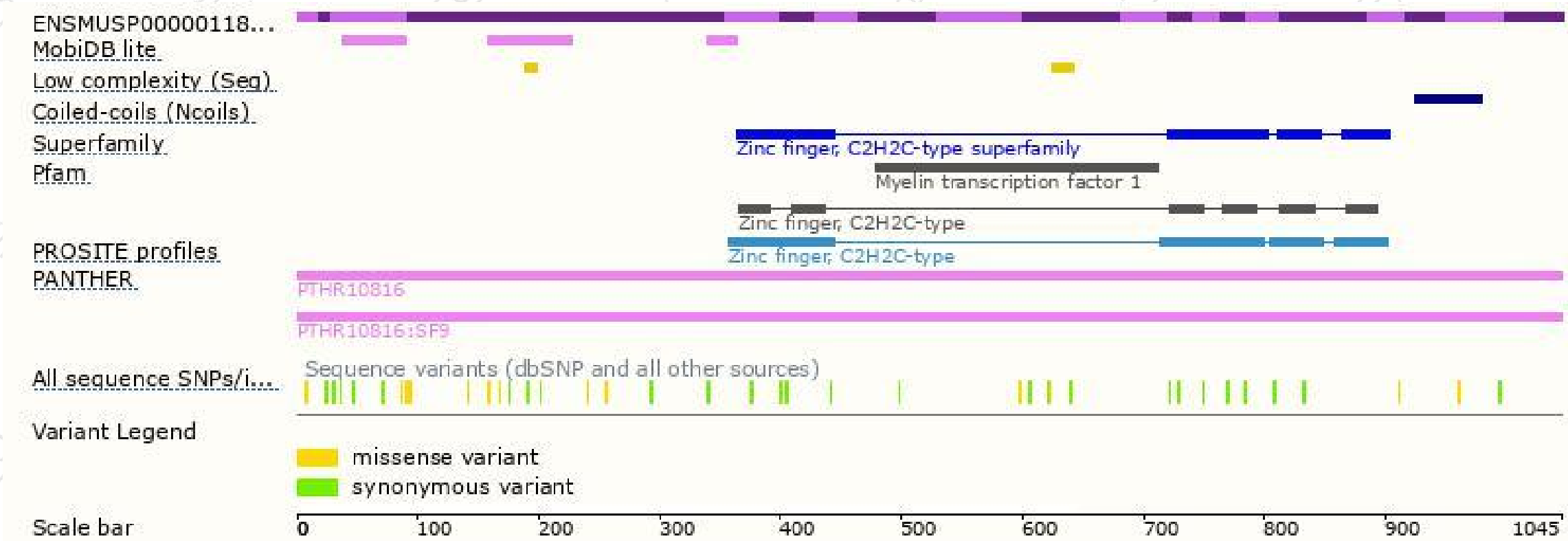


# Genomic location distribution



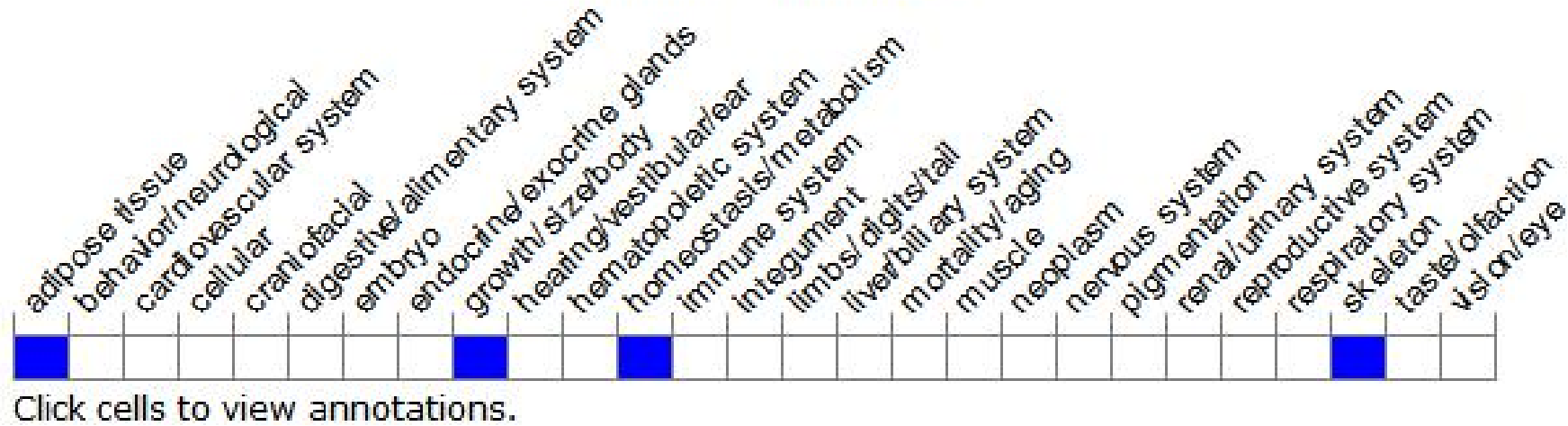


# Protein domain



# Mouse phenotype description(MGI )

## Phenotype Overview ?



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

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

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