

# ***Stag3* Cas9-KO Strategy**

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# Project Overview

**Project Name**

*Stag3*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Stag3* gene. The schematic diagram is as follows:



- The *Stag3* gene has 9 transcripts. According to the structure of *Stag3* gene, exon5-exon29 of *Stag3-201* (ENSMUST00000048028.14) transcript is recommended as the knockout region. The region contains 2899bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Stag3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a transgenic gene disruption exhibit azoospermia and lack oocytes.
- Transcript *Stag3*-202 may not be affected. And the effect on transcript *Stag3*-204&205&208 is unknown.
- The knockout region is near to the N-terminal of *Gpc2* gene, this strategy may influence the regulatory function of the N-termina of *Gpc2* gene.
- The N-terminal of *Stag3* gene will remain 127aa, it may remain the partial function of *Stag3* gene.
- The *Stag3* gene is located on the Chr5. 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)

## Stag3 stromal antigen 3 [ *Mus musculus* (house mouse) ]

Gene ID: 50878, updated on 12-Aug-2019

### Summary

Official Symbol	Stag3 provided by <a href="#">MGI</a>
Official Full Name	stromal antigen 3 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1355311</a>
See related	<a href="#">Ensembl:ENSMUSG00000036928</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	SA-2
Expression	Biased expression in testis adult (RPKM 51.9), CNS E18 (RPKM 4.9) and 3 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

### Genomic context

Location: 5 G2; 5 77.01 cM

See Stag3 in [Genome Data Viewer](#)

Exon count: 35

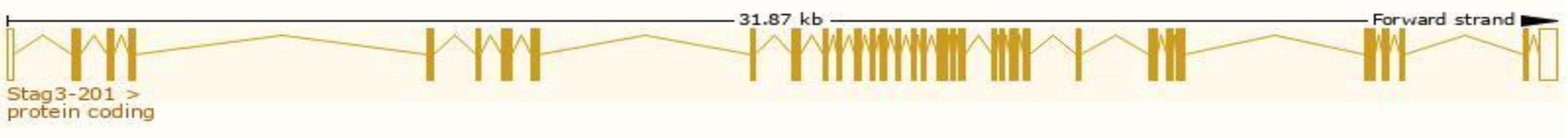
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	5	NC_000071.6 (138272514..138312397)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	5	NC_000071.5 (138721737..138753621)

# Transcript information (Ensembl)

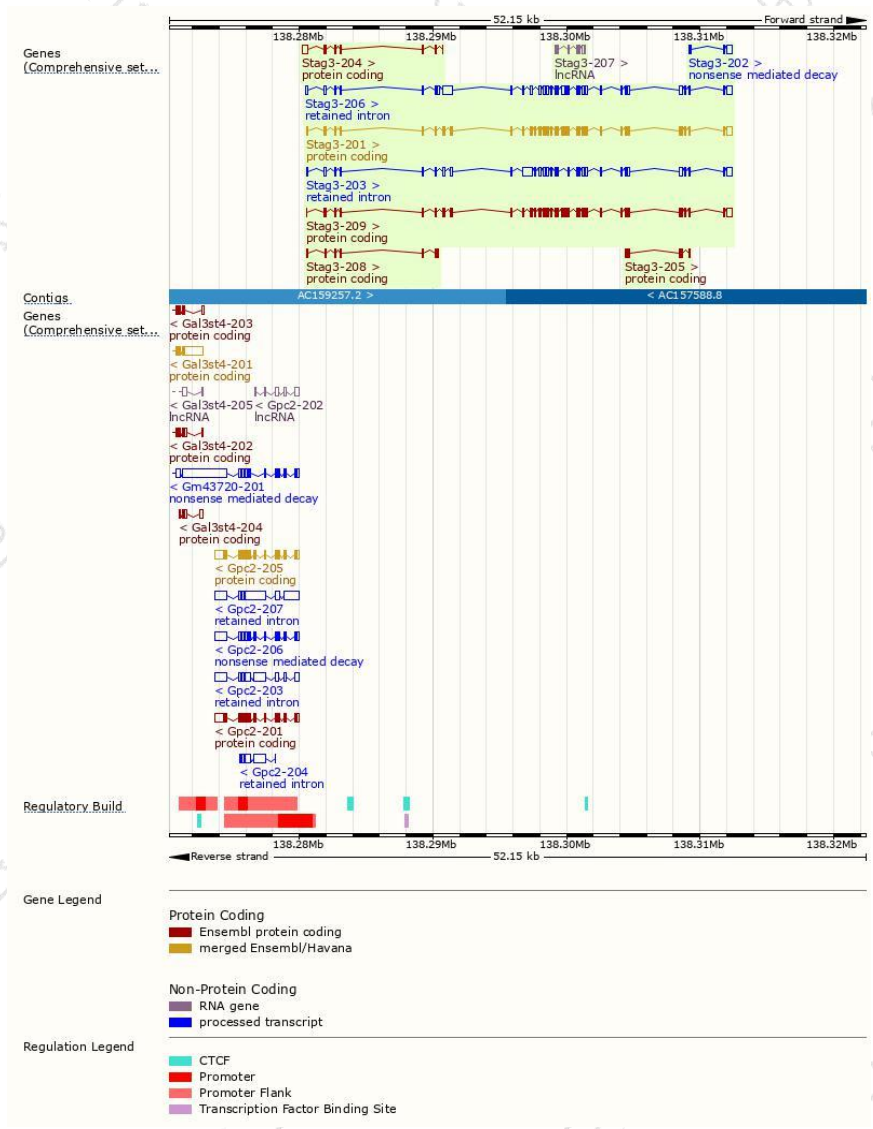
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stag3-201	<a href="#">ENSMUST00000048028.14</a>	4211	<a href="#">1240aa</a>	Protein coding	<a href="#">CCDS39344</a>	<a href="#">O70576</a>	TSL:1 GENCODE basic APPRIS P1
Stag3-209	<a href="#">ENSMUST00000162245.7</a>	4123	<a href="#">1240aa</a>	Protein coding	<a href="#">CCDS39344</a>	<a href="#">O70576</a>	TSL:5 GENCODE basic APPRIS P1
Stag3-204	<a href="#">ENSMUST00000160729.7</a>	989	<a href="#">199aa</a>	Protein coding	-	<a href="#">E0CYH8</a>	CDS 3' incomplete TSL:2
Stag3-208	<a href="#">ENSMUST00000161691.1</a>	763	<a href="#">200aa</a>	Protein coding	-	<a href="#">E0CXH6</a>	CDS 3' incomplete TSL:3
Stag3-205	<a href="#">ENSMUST00000160849.1</a>	458	<a href="#">152aa</a>	Protein coding	-	<a href="#">F7CBN2</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:3
Stag3-202	<a href="#">ENSMUST00000159189.1</a>	591	<a href="#">45aa</a>	Nonsense mediated decay	-	<a href="#">F6TV98</a>	CDS 5' incomplete TSL:2
Stag3-206	<a href="#">ENSMUST00000161113.7</a>	4669	No protein	Retained intron	-	-	TSL:2
Stag3-203	<a href="#">ENSMUST00000159483.7</a>	4456	No protein	Retained intron	-	-	TSL:2
Stag3-207	<a href="#">ENSMUST00000161615.1</a>	574	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Stag3-201* transcript,The transcription is shown below

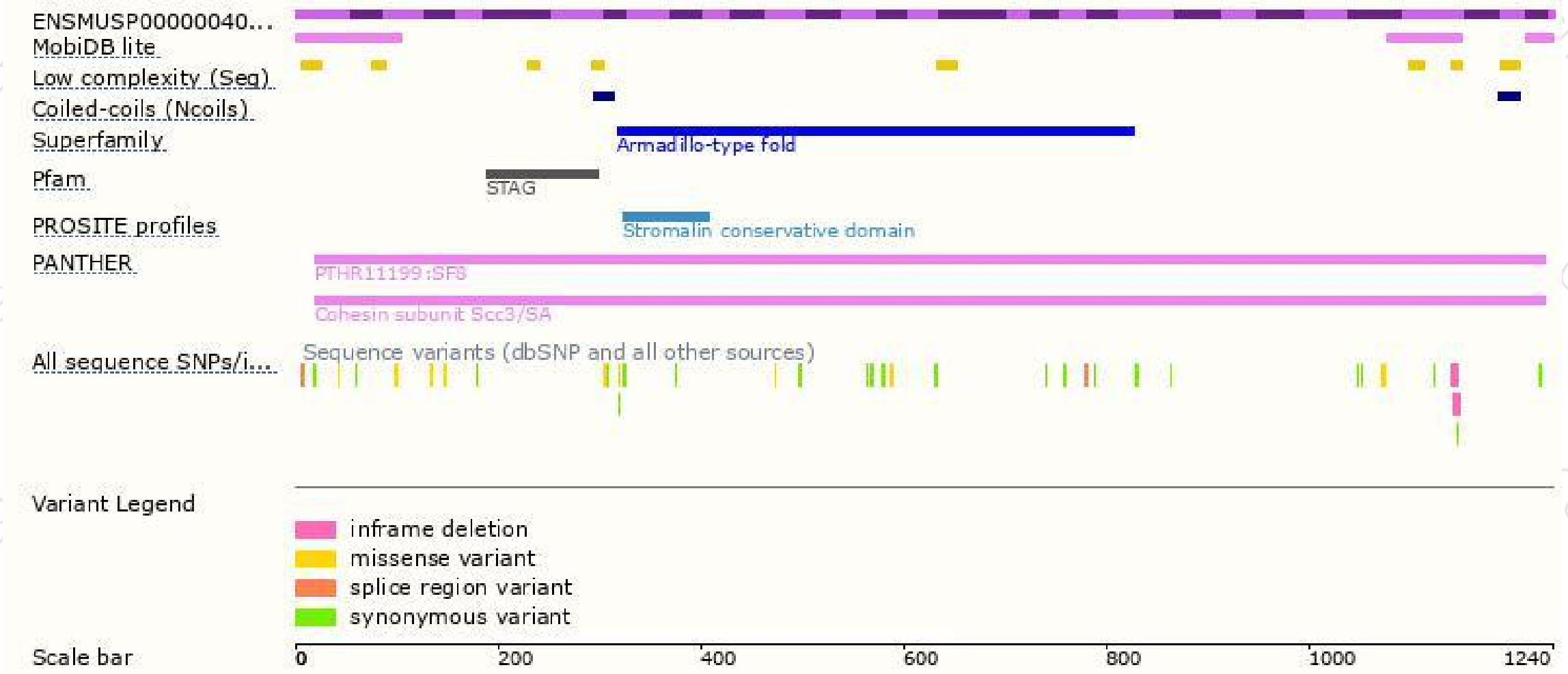


# Genomic location distribution

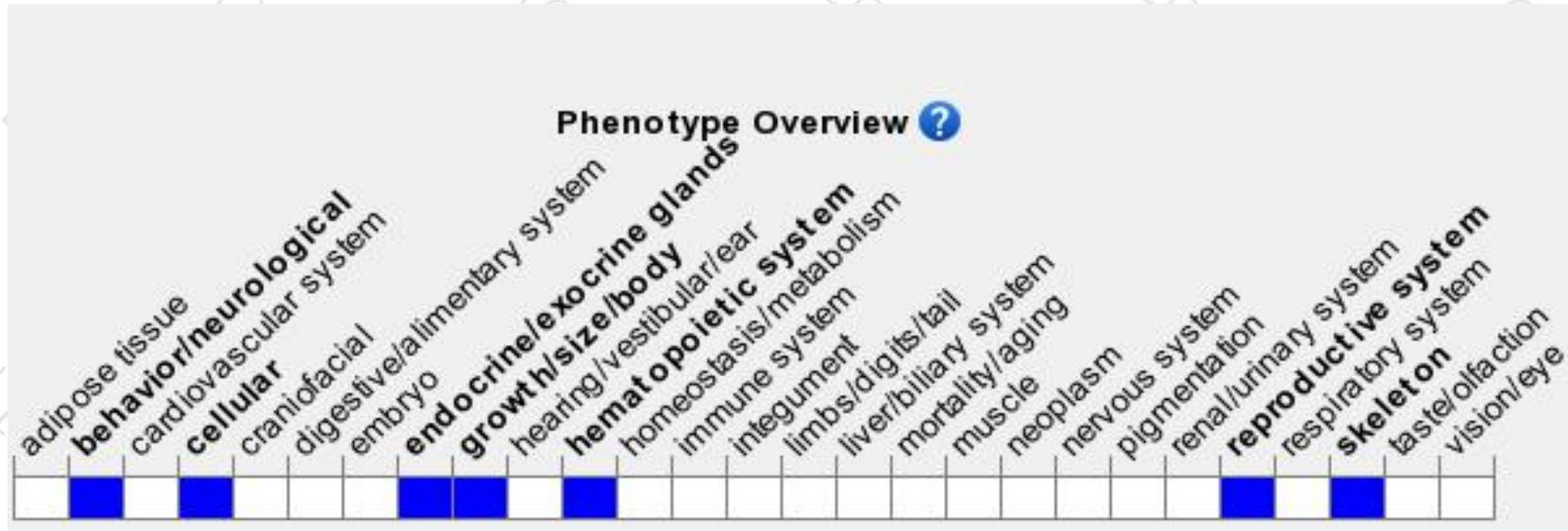




# Protein domain



# 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 transgenic gene disruption exhibit azoospermia and lack oocytes.

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

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