

# *Uvr*ag Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Uvr<sup>a</sup>*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Uvrac* gene has 8 transcripts. According to the structure of *Uvrac* gene, exon2 of *Uvrac-201* (ENSMUST00000037968.9) transcript is recommended as the knockout region. The region contains 118bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Uvrac* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a transposon induced knock-out allele are viable and fertile but exhibit impaired autophagic flux, autophagosome accumulation in the heart, and age-related cardiomyopathy associated with compromised cardiac function and heart inflammation.
- The *Uvr* gene is located on the Chr7. 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)

## Uvrage UV radiation resistance associated gene [Mus musculus (house mouse)]

Gene ID: 78610, updated on 31-Jan-2019

### Summary



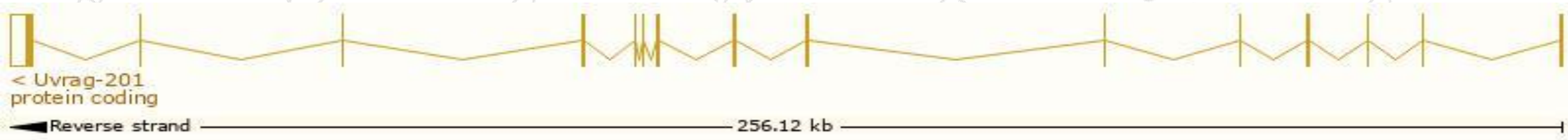
<b>Official Symbol</b>	Uvrage provided by <a href="#">MGI</a>
<b>Official Full Name</b>	UV radiation resistance associated gene provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1925860</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000035354</a>
<b>Gene type</b>	protein 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>	9530039D02Rik, A1648770, BB124205, Uvrage1, Uvrage
<b>Expression</b>	Ubiquitous expression in spleen adult (RPKM 13.8), thymus adult (RPKM 12.8) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

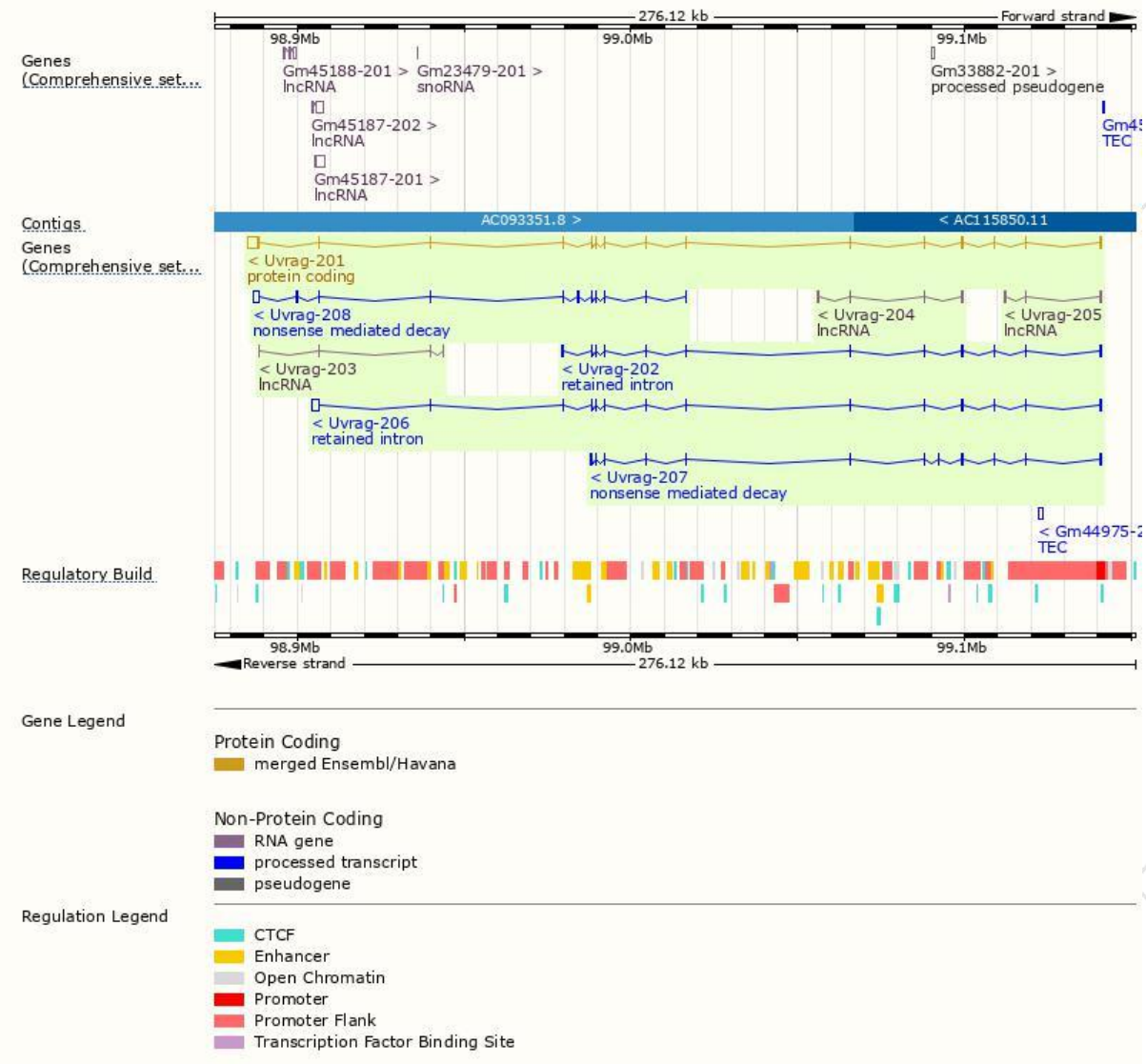
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Uvrage-201	<a href="#">ENSMUST00000037968.9</a>	5157	<a href="#">698aa</a>	Protein coding	<a href="#">CCDS21476</a>	<a href="#">Q8K245</a>	TSL:1 GENCODE basic APPRIS P1
Uvrage-208	<a href="#">ENSMUST00000209123.1</a>	3147	<a href="#">162aa</a>	Nonsense mediated decay	-	<a href="#">A0A140LHA4</a>	CDS 5' incomplete TSL:1
Uvrage-207	<a href="#">ENSMUST00000208992.1</a>	1577	<a href="#">150aa</a>	Nonsense mediated decay	-	<a href="#">A0A140LI21</a>	TSL:1
Uvrage-206	<a href="#">ENSMUST00000208609.1</a>	3725	No protein	Retained intron	-	-	TSL:1
Uvrage-202	<a href="#">ENSMUST00000207032.1</a>	1792	No protein	Retained intron	-	-	TSL:1
Uvrage-205	<a href="#">ENSMUST00000208502.1</a>	654	No protein	lncRNA	-	-	TSL:1
Uvrage-203	<a href="#">ENSMUST00000207919.1</a>	376	No protein	lncRNA	-	-	TSL:3
Uvrage-204	<a href="#">ENSMUST00000208012.1</a>	366	No protein	lncRNA	-	-	TSL:3

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

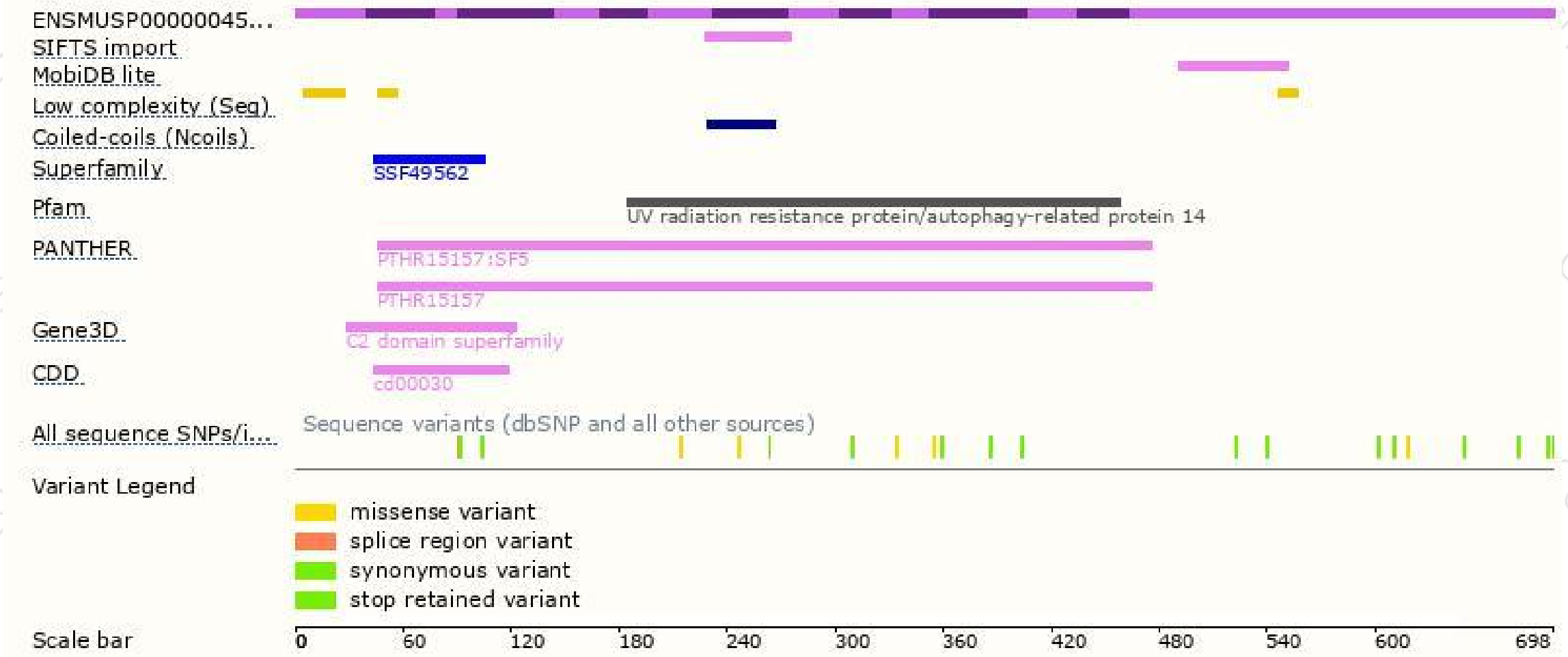


# Genomic location distribution

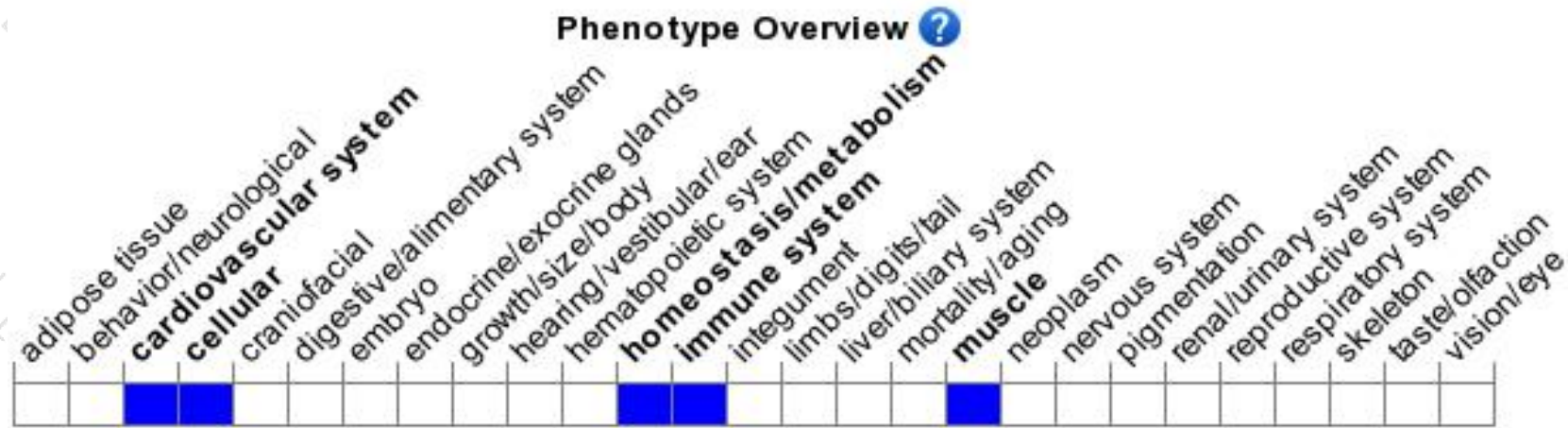




# Protein domain



# 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 transposon induced knock-out allele are viable and fertile but exhibit impaired autophagic flux, autophagosome accumulation in the heart, and age-related cardiomyopathy associated with compromised cardiac function and heart inflammation.

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

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