

# *Cflar* Cas9-KO Strategy

**Designer:**

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**Design Date:**

**2019-8-8**

# Project Overview

**Project Name**

*Cflar*

**Project type**

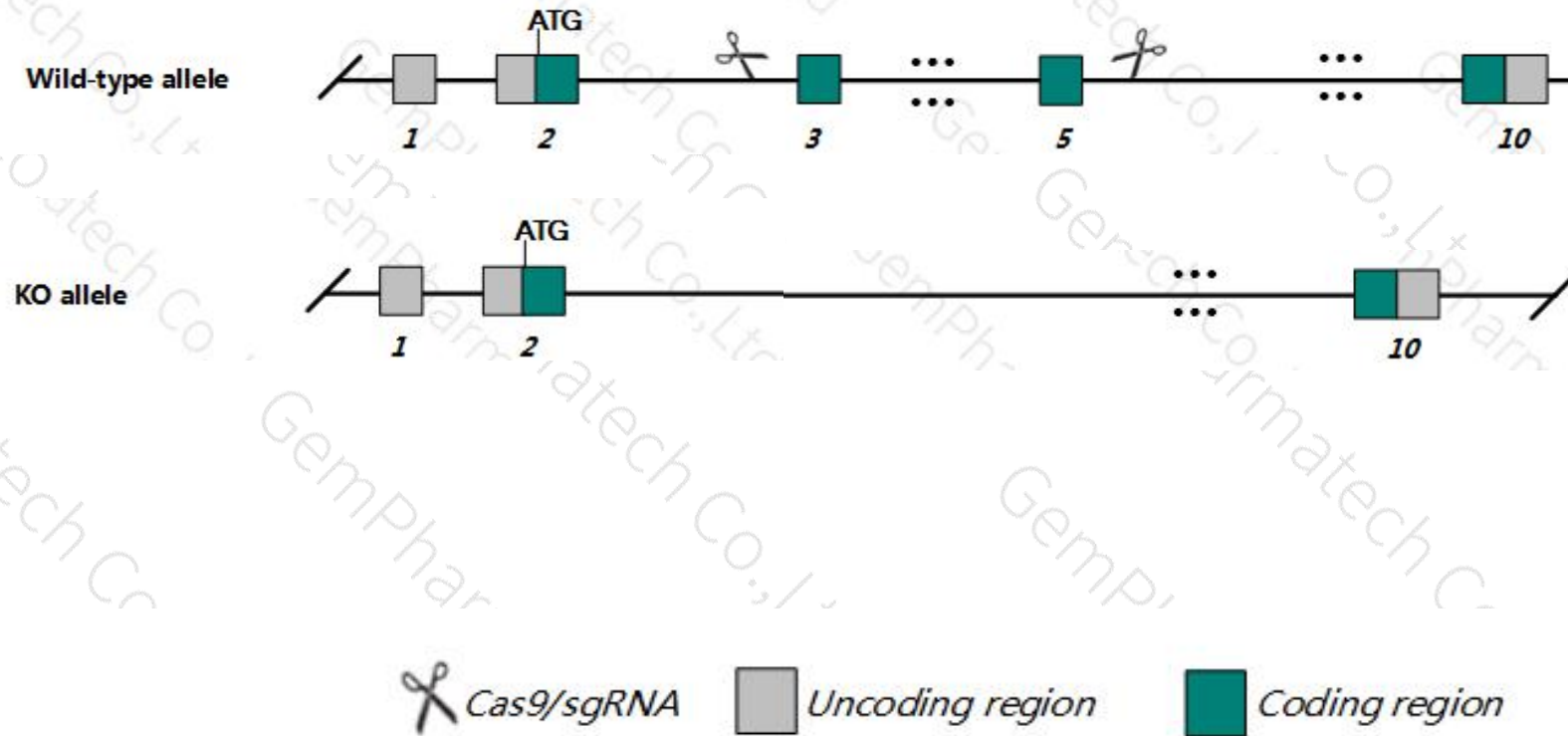
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Cflargene* has 13 transcripts. According to the structure of *Cflar* gene, exon3-5 of *Cdkn2a-205* (ENSMUST00000114313.7) transcript is recommended as the knockout region. The region contains 316bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cflargene*. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygous mutation of this gene results in embryonic lethality by E10.5. Mutant embryos exhibit cardiac developmental abnormalities and pooling of blood in the head and abdominal regions.
- The *Cflargene* is located on the Chr4. 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)

## Cflar CASP8 and FADD-like apoptosis regulator [ *Mus musculus* (house mouse) ]

Gene ID: 12633, updated on 12-Aug-2018

### Summary

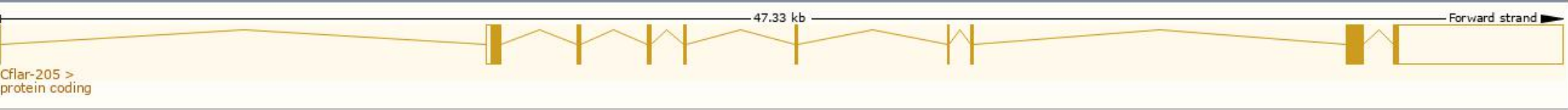
Official Symbol	Cflar provided by <a href="#">MGI</a>
Official Full Name	CASP8 and FADD-like apoptosis regulator provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1336166</a>
See related	<a href="#">Ensembl:ENSMUSG00000026031</a> <a href="#">Vega:OTTMUSG00000019581</a>
Gene type	protein 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	Cash; Flip; MRIT; CLARP; FLAME; Casper; Gm9845; c-Flip; FLAME-1; I-FLICE; 2310024N18Rik; A430105C05Rik
Expression	Ubiquitous expression in lung adult (RPKM 9.2), kidney adult (RPKM 7.4) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

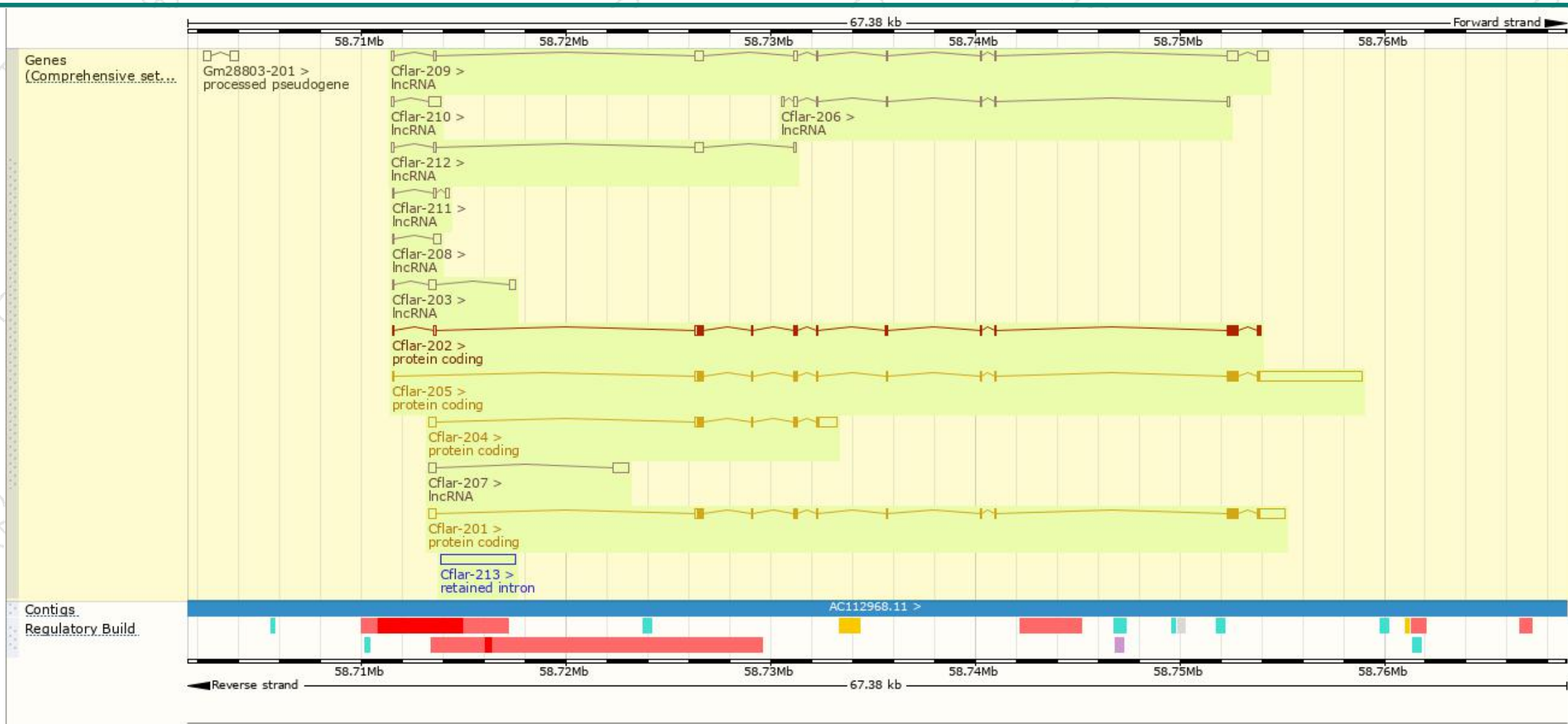
The gene has 13 transcripts,all transcripts are shown below:

Show/hide columns (1 hidden)		Filter						
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
Cflar-205	<a href="#">ENSMUST00000114313.7</a>	6572	<a href="#">481aa</a>	Protein coding	<a href="#">CCDS14978</a>	<a href="#">Q35732</a> <a href="#">Q812G4</a>	<a href="#">NM_001289704</a> <a href="#">NM_001293804</a> <a href="#">NM_001293805</a> <a href="#">NP_001276633</a> <a href="#">NP_001280733</a> <a href="#">NP_001280734</a>	TSL:1 GENCODE basic APPRIS P2
Cflar-201	<a href="#">ENSMUST00000069333.7</a>	3163	<a href="#">481aa</a>	Protein coding	<a href="#">CCDS14978</a>	<a href="#">Q35732</a> <a href="#">Q812G4</a>	<a href="#">NM_207653</a> <a href="#">NP_997536</a>	TSL:1 GENCODE basic APPRIS P2
Cflar-204	<a href="#">ENSMUST00000114309.7</a>	2010	<a href="#">215aa</a>	Protein coding	<a href="#">CCDS35582</a>	<a href="#">Q35732</a> <a href="#">Q5U4G3</a>	<a href="#">NM_009805</a> <a href="#">NP_033935</a>	TSL:1 GENCODE basic
Cflar-202	<a href="#">ENSMUST00000097722.8</a>	1771	<a href="#">484aa</a>	Protein coding	-	<a href="#">A0A2C9F2D9</a>	-	TSL:5 GENCODE basic APPRIS ALT2
Cflar-209	<a href="#">ENSMUST00000140940.7</a>	2064	No protein	Processed transcript	-	-	-	TSL:1
Cflar-207	<a href="#">ENSMUST00000123553.1</a>	1100	No protein	Processed transcript	-	-	-	TSL:2
Cflar-203	<a href="#">ENSMUST00000097723.2</a>	708	No protein	Processed transcript	-	-	-	TSL:3
Cflar-212	<a href="#">ENSMUST00000164900.7</a>	694	No protein	Processed transcript	-	-	-	TSL:3
Cflar-210	<a href="#">ENSMUST00000149874.7</a>	676	No protein	Processed transcript	-	-	<a href="#">NR_149258</a>	TSL:1
Cflar-206	<a href="#">ENSMUST00000123032.1</a>	623	No protein	Processed transcript	-	-	-	TSL:5
Cflar-208	<a href="#">ENSMUST00000124567.1</a>	378	No protein	Processed transcript	-	-	-	TSL:2
Cflar-211	<a href="#">ENSMUST00000156870.1</a>	351	No protein	Processed transcript	-	-	<a href="#">NR_149256</a>	TSL:3
Cflar-213	<a href="#">ENSMUST00000189858.1</a>	3677	No protein	Retained intron	-	-	-	TSL:NA

The strategy is based on the design of *Cflar-205* transcript,The transcription is shown below

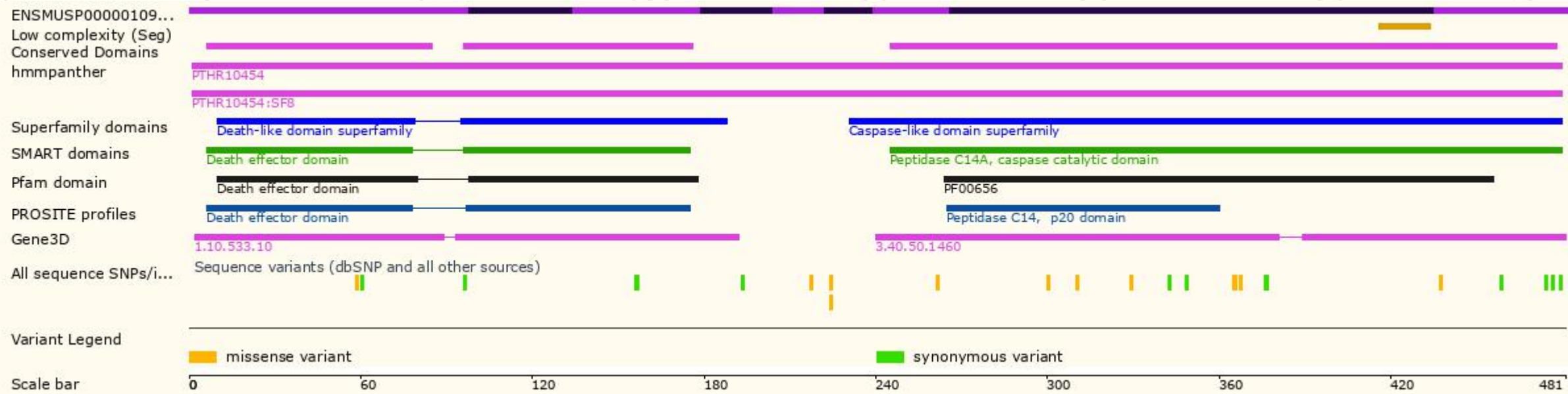


# Genomic location distribution

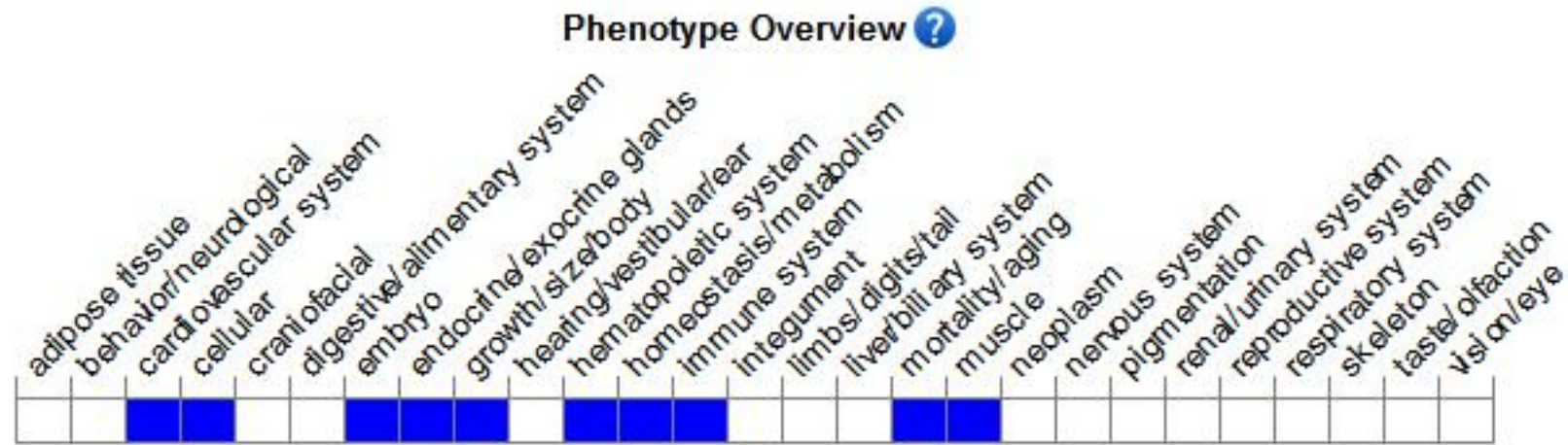




# Protein domain



# 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, Homozygous mutation of this gene results in embryonic lethality by E10.5.

Mutant embryos exhibit cardiac developmental abnormalities and pooling of blood in the head and abdominal regions.

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

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