

# ***Mlst8*** Cas9-CKO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Mlst8***

**Project type**

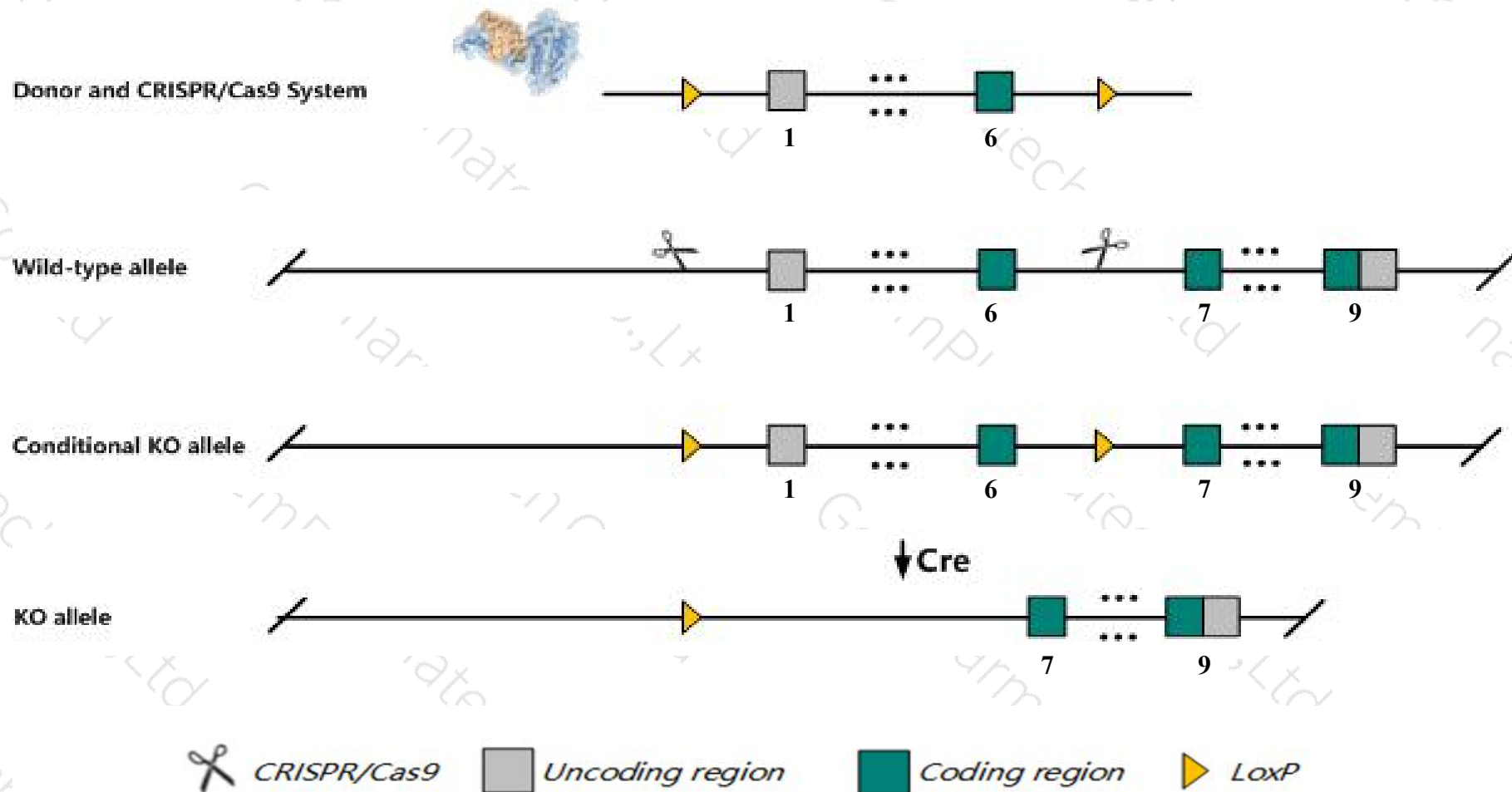
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mlst8* gene. The schematic diagram is as follows:



# Technical routes

- The *Mlst8* gene has 10 transcripts. According to the structure of *Mlst8* gene, exon1-exon6 of *Mlst8-201* (ENSMUST00000070888.13) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mlst8* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a null mutation exhibit lethality around E10.5 and abnormal yolk sac vasculature, brain development and heart development.
- This strategy may affect the 5-terminal regulation of the gene of interest and *Gm50062*.
- The *Mlst8* gene is located on the Chr17. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



# Gene information (NCBI)

## Mlst8 MTOR associated protein, LST8 homolog (S. cerevisiae) [Mus musculus (house mouse)]

Gene ID: 56716, updated on 19-Feb-2019

### Summary



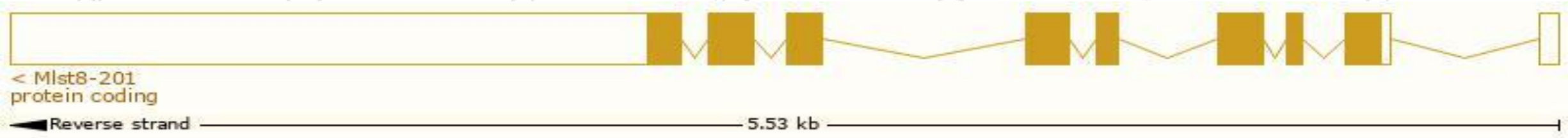
<b>Official Symbol</b>	Mlst8 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	MTOR associated protein, LST8 homolog (S. cerevisiae) provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1929514</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000024142</a>
<b>Gene type</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>	0610033N12Rik, AA409454, AI505104, AI851821, Gbl
<b>Expression</b>	Ubiquitous expression in thymus adult (RPKM 14.9), large intestine adult (RPKM 14.2) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

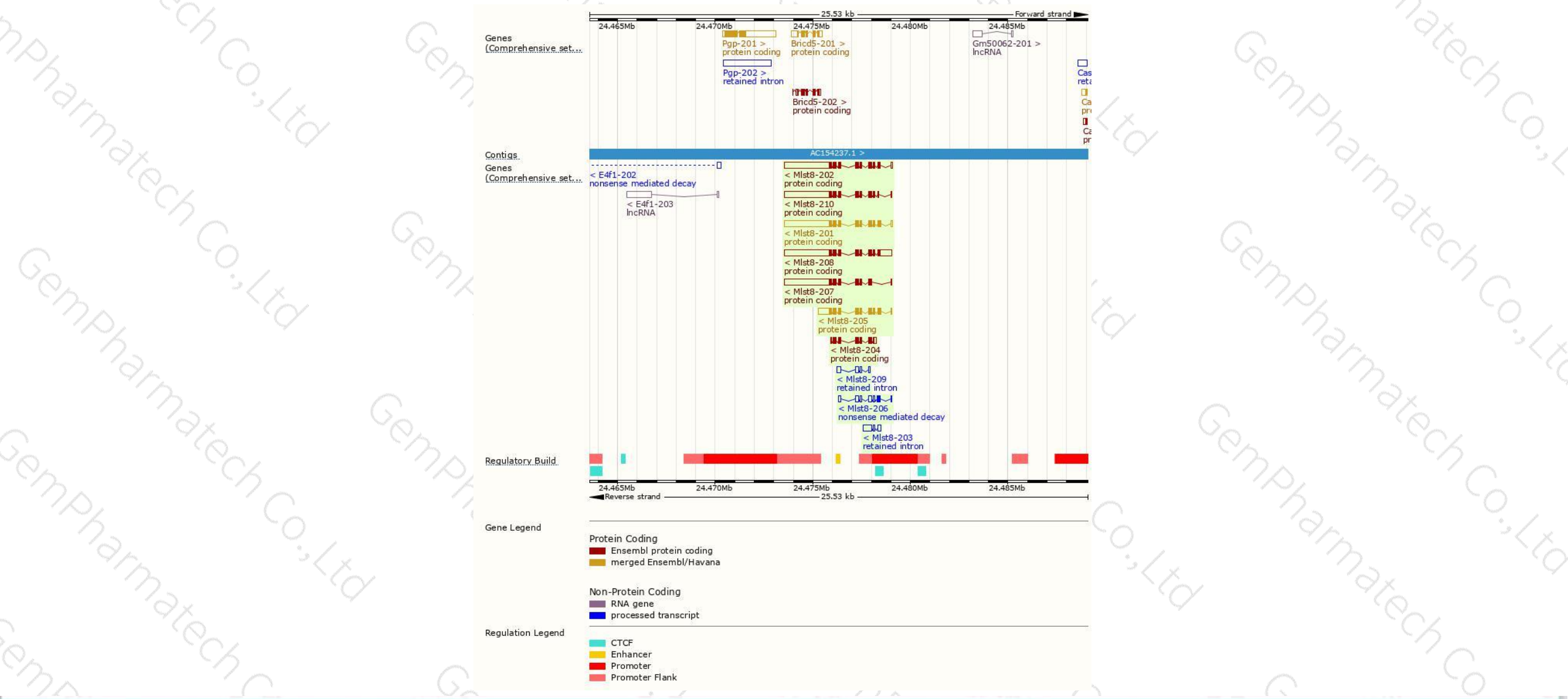
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mlst8-208	<a href="#">ENSMUST00000234686.1</a>	3855	<a href="#">326aa</a>	Protein coding	<a href="#">CCDS28484</a>	-	GENCODE basic APPRIS P1
Mlst8-201	<a href="#">ENSMUST00000070888.13</a>	3358	<a href="#">326aa</a>	Protein coding	<a href="#">CCDS28484</a>	<a href="#">Q9DCJ1</a>	TSL:1 GENCODE basic APPRIS P1
Mlst8-202	<a href="#">ENSMUST00000179163.2</a>	3340	<a href="#">326aa</a>	Protein coding	<a href="#">CCDS28484</a>	<a href="#">Q9DCJ1</a>	TSL:1 GENCODE basic APPRIS P1
Mlst8-205	<a href="#">ENSMUST00000234335.1</a>	1574	<a href="#">326aa</a>	Protein coding	<a href="#">CCDS28484</a>	-	GENCODE basic APPRIS P1
Mlst8-210	<a href="#">ENSMUST00000234941.1</a>	3223	<a href="#">271aa</a>	Protein coding	-	-	GENCODE basic
Mlst8-207	<a href="#">ENSMUST00000234543.1</a>	3127	<a href="#">260aa</a>	Protein coding	-	-	GENCODE basic
Mlst8-204	<a href="#">ENSMUST00000234147.1</a>	850	<a href="#">238aa</a>	Protein coding	-	-	CDS 3' incomplete
Mlst8-206	<a href="#">ENSMUST00000234516.1</a>	786	<a href="#">56aa</a>	Nonsense mediated decay	-	-	
Mlst8-203	<a href="#">ENSMUST00000234032.1</a>	668	No protein	Retained intron	-	-	
Mlst8-209	<a href="#">ENSMUST00000234892.1</a>	519	No protein	Retained intron	-	-	

The strategy is based on the design of *Mlst8-201* transcript,The transcription is shown below



# Genomic location distribution





# Protein domain

ENSMUSP00000065...

[Superfamily](#)

[SMART](#)

[Prints](#)

[Pfam](#)

[PROSITE profiles](#)

[PROSITE patterns](#)

[PANTHER](#)

[Gene3D](#)

[CDD](#)

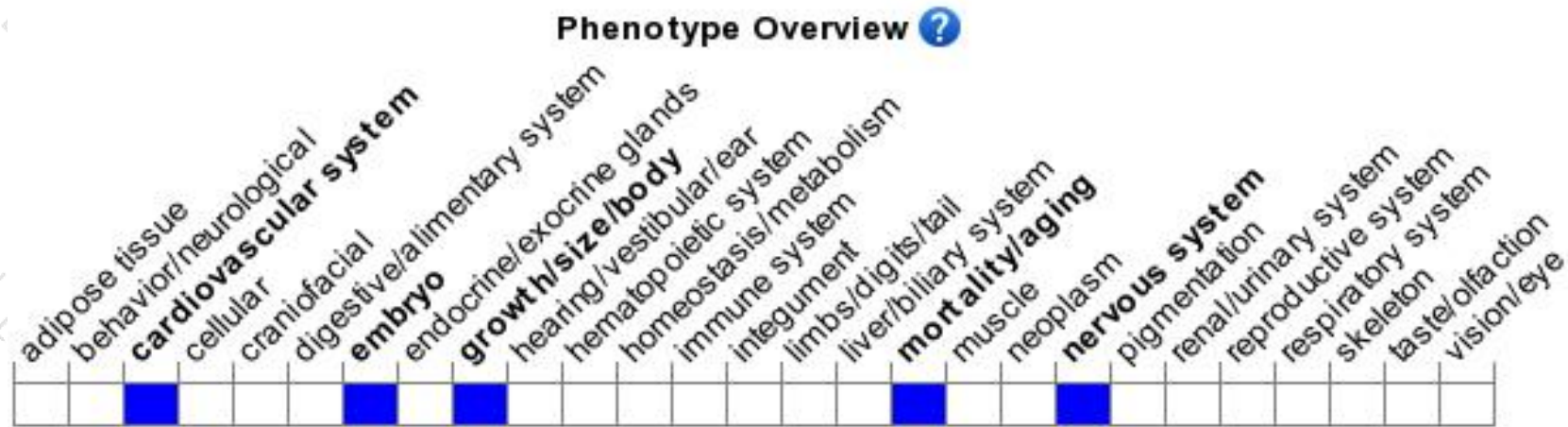
[All sequence SNPs/i....](#)

Variant Legend

Scale bar



# 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 null mutation exhibit lethality around E10.5 and abnormal yolk sac vasculature, brain development and heart development.

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

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