

Flna Cas9-KO Strategy

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Project Overview

Project Name

Flna

Project type

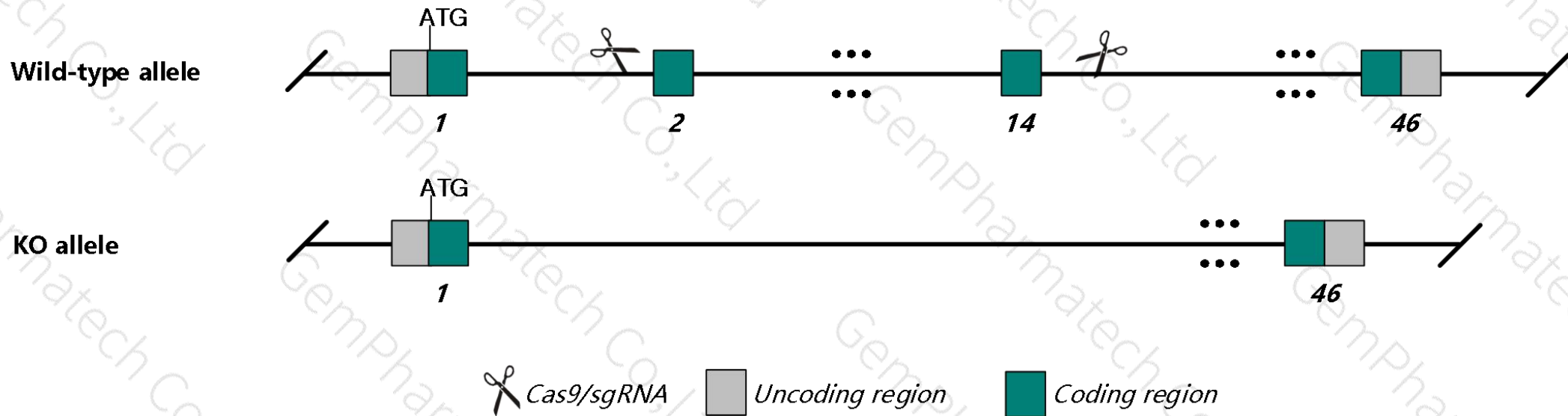
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Flna* gene has 15 transcripts. According to the structure of *Flna* gene, exon2-exon14 of *Flna*-202 (ENSMUST00000101454.8) transcript is recommended as the knockout region. The region contains 1907bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Flna* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Females heterozygous for an X-linked, ENU-induced mutation exhibit dilated pupils and milder cardiac, sternum, and palate defects than males. Hemizygous males are inviable and exhibit incomplete septation of the outflow tract, septal defects, cleft palate and incomplete fusion of the sternum.
- The *Flna* gene is located on the ChrX. 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)

Flna filamin, alpha [Mus musculus (house mouse)]

Gene ID: 192176, updated on 5-Feb-2019

Summary



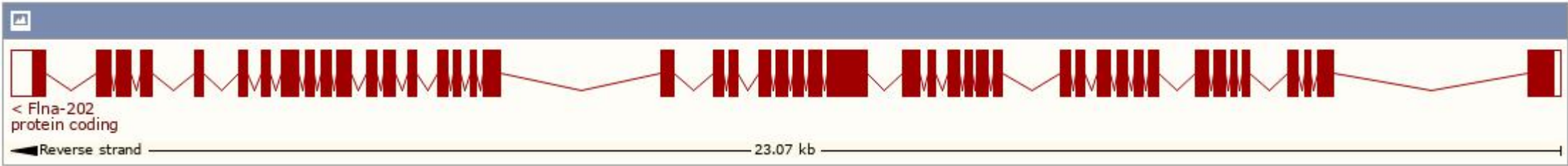
Official Symbol	Flna provided by MGI
Official Full Name	filamin, alpha provided by MGI
Primary source	MGI:MGI:95556
See related	Ensembl:ENSMUSG00000031328
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ABP-280, Dilp2, F730004A14Rik, Fln1, GENA 379, filamin-1
Expression	Broad expression in bladder adult (RPKM 809.2), ovary adult (RPKM 279.4) and 17 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

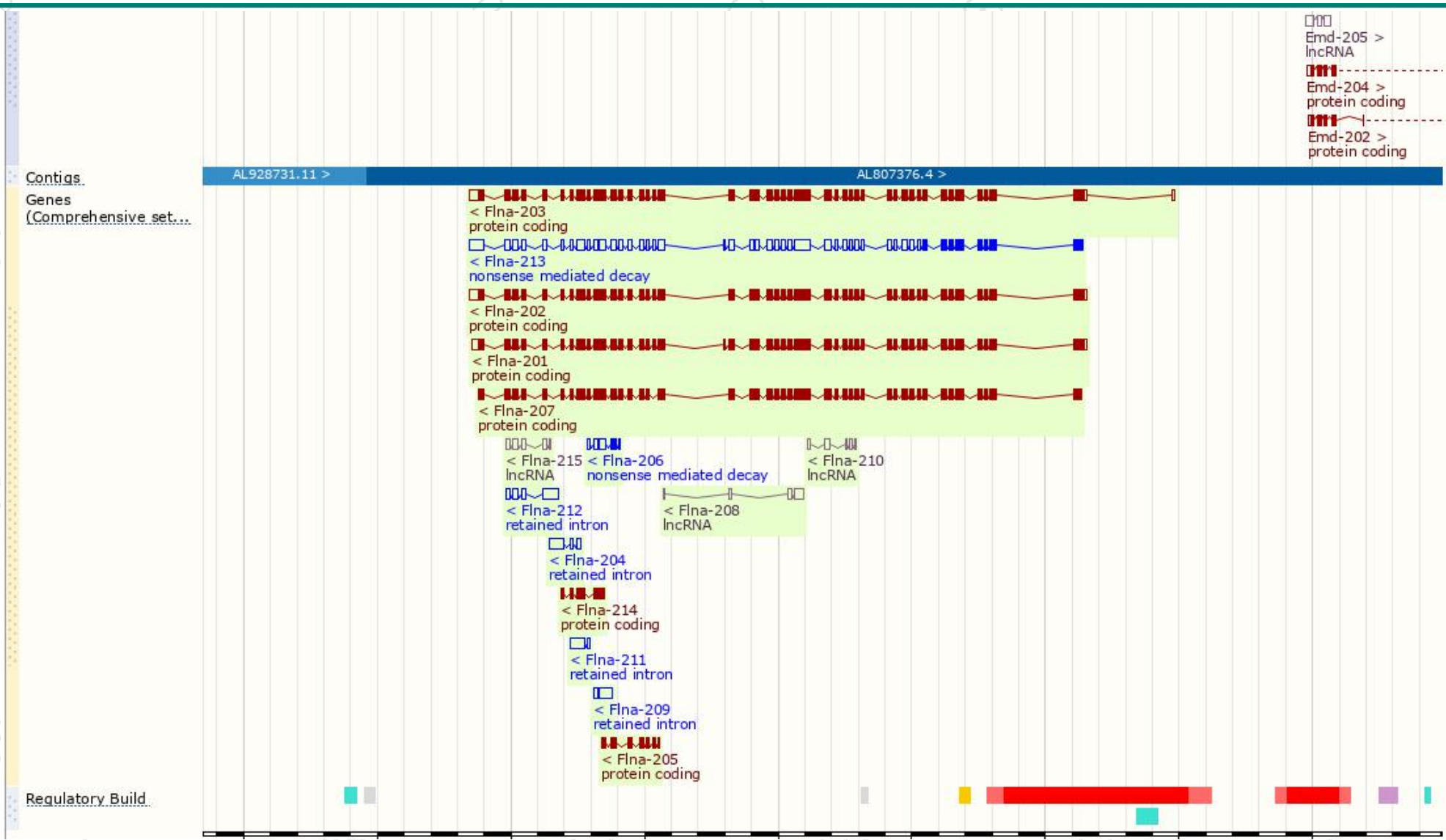
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Flna-203	ENSMUST00000114299.7	8456	2639aa	Protein coding	CCDS41018	B7FAU9	TSL:5 GENCODE basic APPRIS P2
Flna-202	ENSMUST00000101454.8	8345	2639aa	Protein coding	CCDS41018	B7FAU9	TSL:1 GENCODE basic APPRIS P2
Flna-201	ENSMUST00000033699.12	8312	2647aa	Protein coding	-	Q8BTM8	TSL:5 GENCODE basic APPRIS ALT1
Flna-207	ENSMUST00000130007.7	7753	2583aa	Protein coding	-	B7FAV1	CDS 5' incomplete TSL:5
Flna-205	ENSMUST00000127463.1	841	280aa	Protein coding	-	F6Z2C0	CDS 5' and 3' incomplete TSL:5
Flna-214	ENSMUST00000150554.1	832	277aa	Protein coding	-	J3JS91	CDS 5' and 3' incomplete TSL:5
Flna-213	ENSMUST00000144429.7	8233	511aa	Nonsense mediated decay	-	F6XC15	CDS 5' incomplete TSL:1
Flna-206	ENSMUST00000127924.7	704	74aa	Nonsense mediated decay	-	F7AVL7	CDS 5' incomplete TSL:3
Flna-212	ENSMUST00000141528.1	1106	No protein	Retained intron	-	-	TSL:2
Flna-204	ENSMUST00000124950.1	797	No protein	Retained intron	-	-	TSL:2
Flna-211	ENSMUST00000133609.1	638	No protein	Retained intron	-	-	TSL:2
Flna-209	ENSMUST00000133174.1	632	No protein	Retained intron	-	-	TSL:2
Flna-215	ENSMUST00000156766.7	738	No protein	lncRNA	-	-	TSL:5
Flna-208	ENSMUST00000130203.1	689	No protein	lncRNA	-	-	TSL:5
Flna-210	ENSMUST00000133288.1	558	No protein	lncRNA	-	-	TSL:2

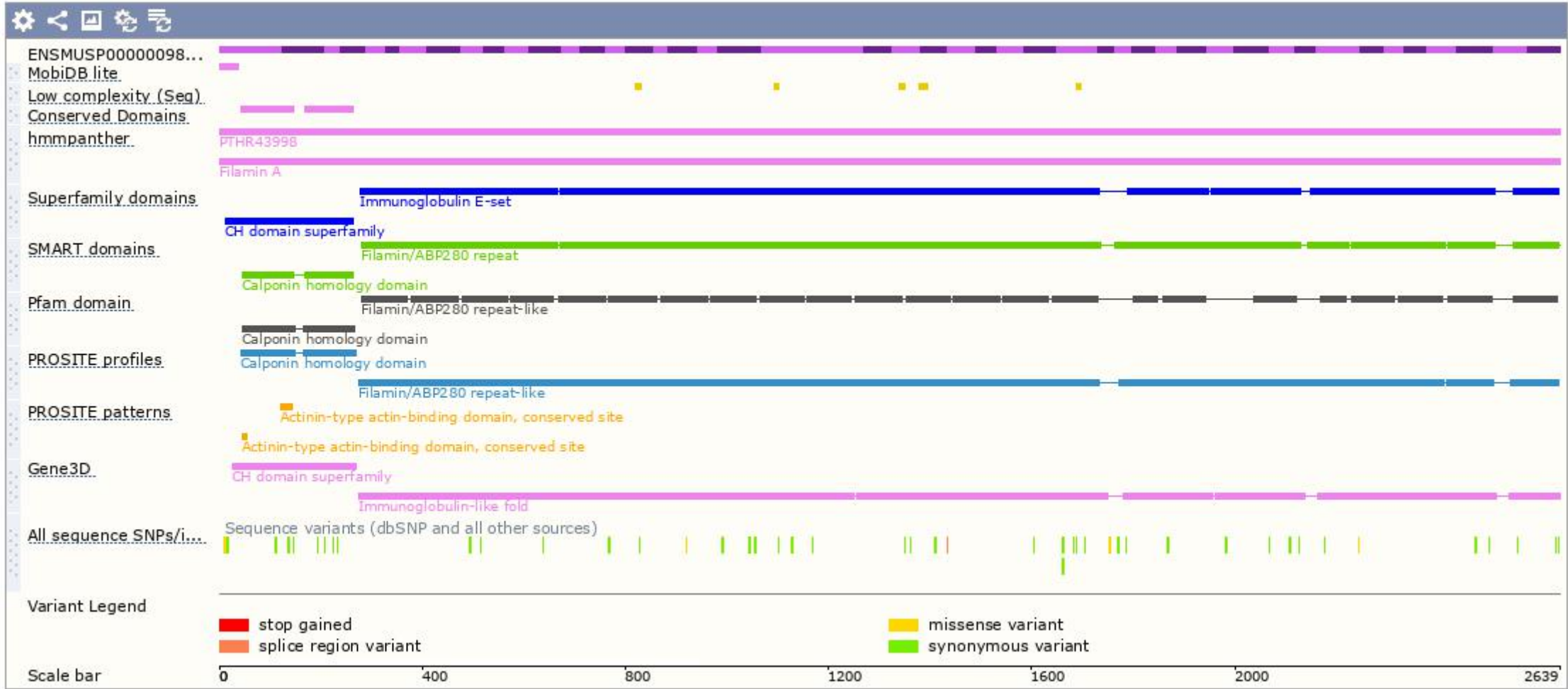
The strategy is based on the design of *Flna-202* transcript,The transcription is shown below



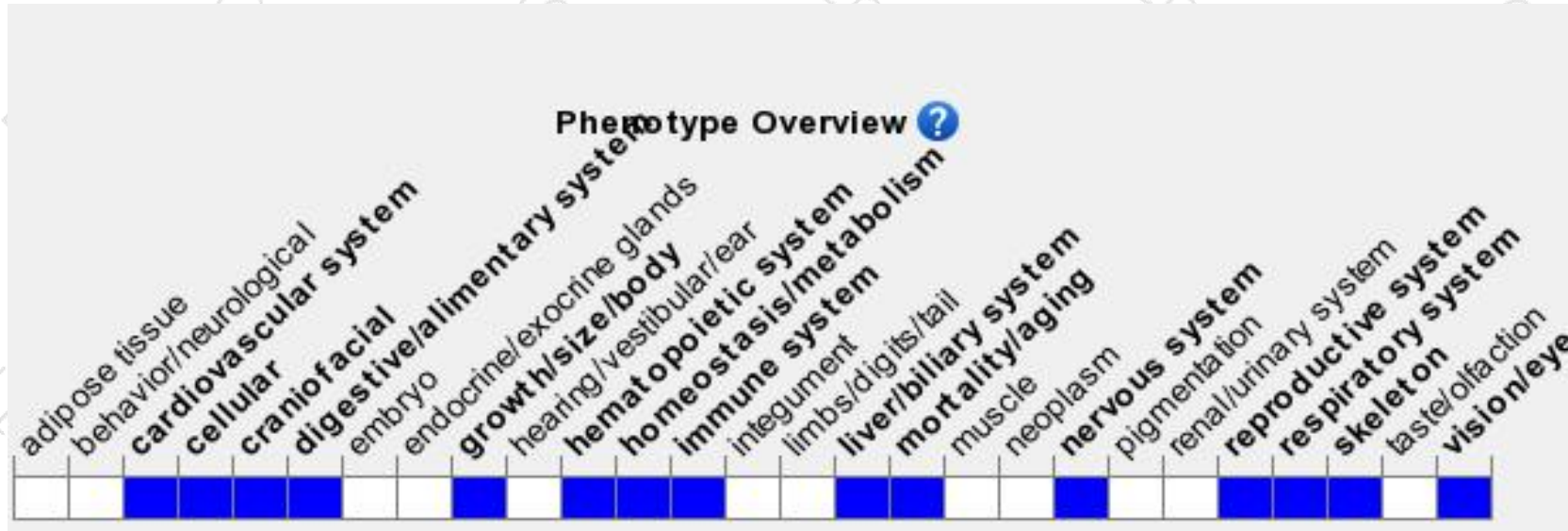
Genomic location distribution



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, Females heterozygous for an X-linked, ENU-induced mutation exhibit dilated pupils and milder cardiac, sternum, and palate defects than males. Hemizygous males are inviable and exhibit incomplete septation of the outflow tract, septal defects, cleft palate and incomplete fusion of the sternum.

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

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