

Hif1a Cas9-KO Strategy

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Project Overview

Project Name

Hif1a

Project type

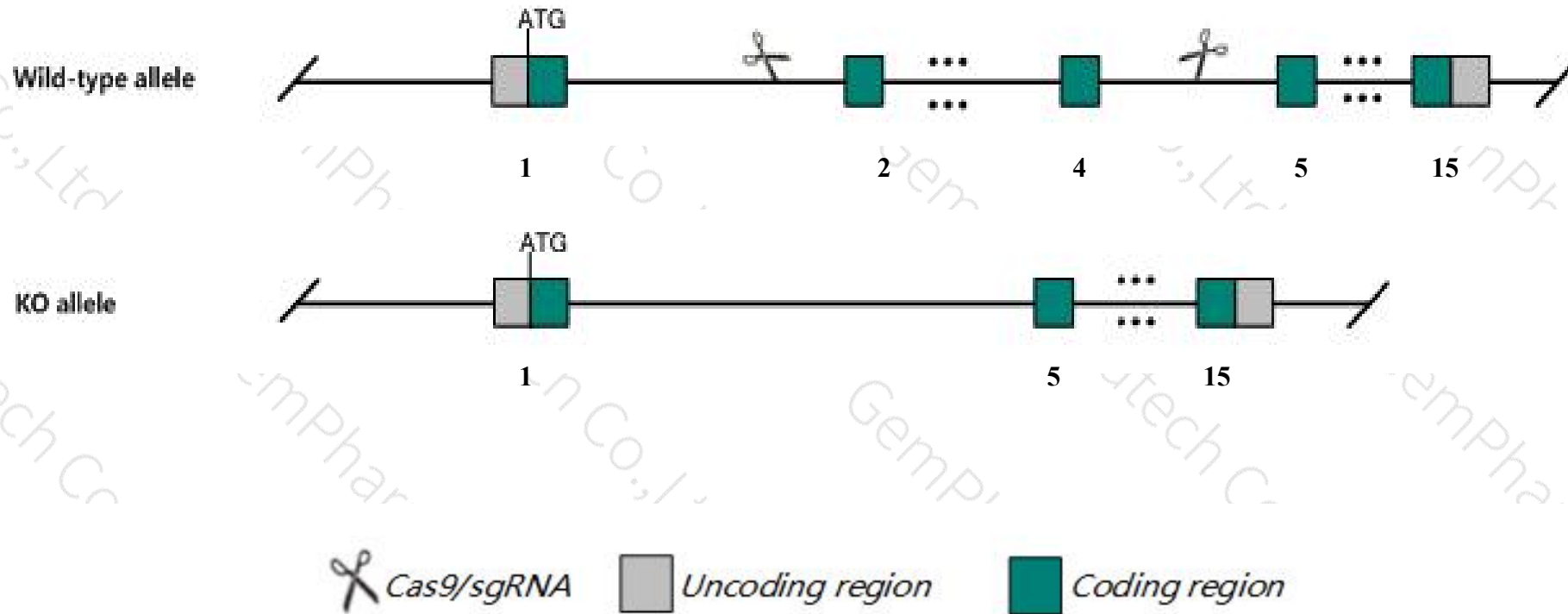
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hif1a* gene. The schematic diagram is as follows:



- The *Hif1a* gene has 5 transcripts. According to the structure of *Hif1a* gene, exon2-exon4 of *Hif1a-201* (ENSMUST00000021530.7) transcript is recommended as the knockout region. The region contains 422bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hif1a* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Homozygous null mutants die during embryonic development with severe cardiovascular malformations, neural tube defects, cephalic defects, reduced somite number and increased hypoxia.
- The *Hif1a* gene is located on the Chr12. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)

Hif1a hypoxia inducible factor 1, alpha subunit [Mus musculus (house mouse)]

Gene ID: 15251, updated on 9-Apr-2019

Summary



Official Symbol Hif1a provided by [MGI](#)

Official Full Name hypoxia inducible factor 1, alpha subunit provided by [MGI](#)

Primary source [MGI:MGI:106918](#)

See related [Ensembl:ENSMUSG000000021109](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as AA959795, HIF-1-alpha, HIF1-alpha, HIF1alpha, MOP1, bHLHe78

Summary This gene encodes the alpha subunit which, along with the beta subunit, forms a heterodimeric transcription factor that regulates the cellular and developmental response to reduced oxygen tension. The transcription factor has been shown to regulate genes involved in several biological processes, including erythropoiesis and angiogenesis which aid in increased delivery of oxygen to hypoxic regions. The transcription factor also plays a role in the induction of genes involved in cell proliferation and survival, energy metabolism, apoptosis, and glucose and iron metabolism. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Sep 2015]

Expression Ubiquitous expression in placenta adult (RPKM 31.3), limb E14.5 (RPKM 21.7) and 28 other tissues [See more](#)

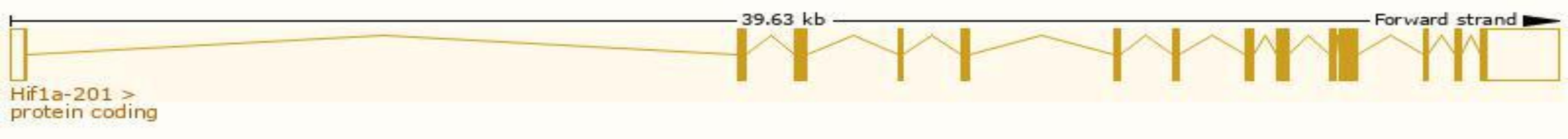
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

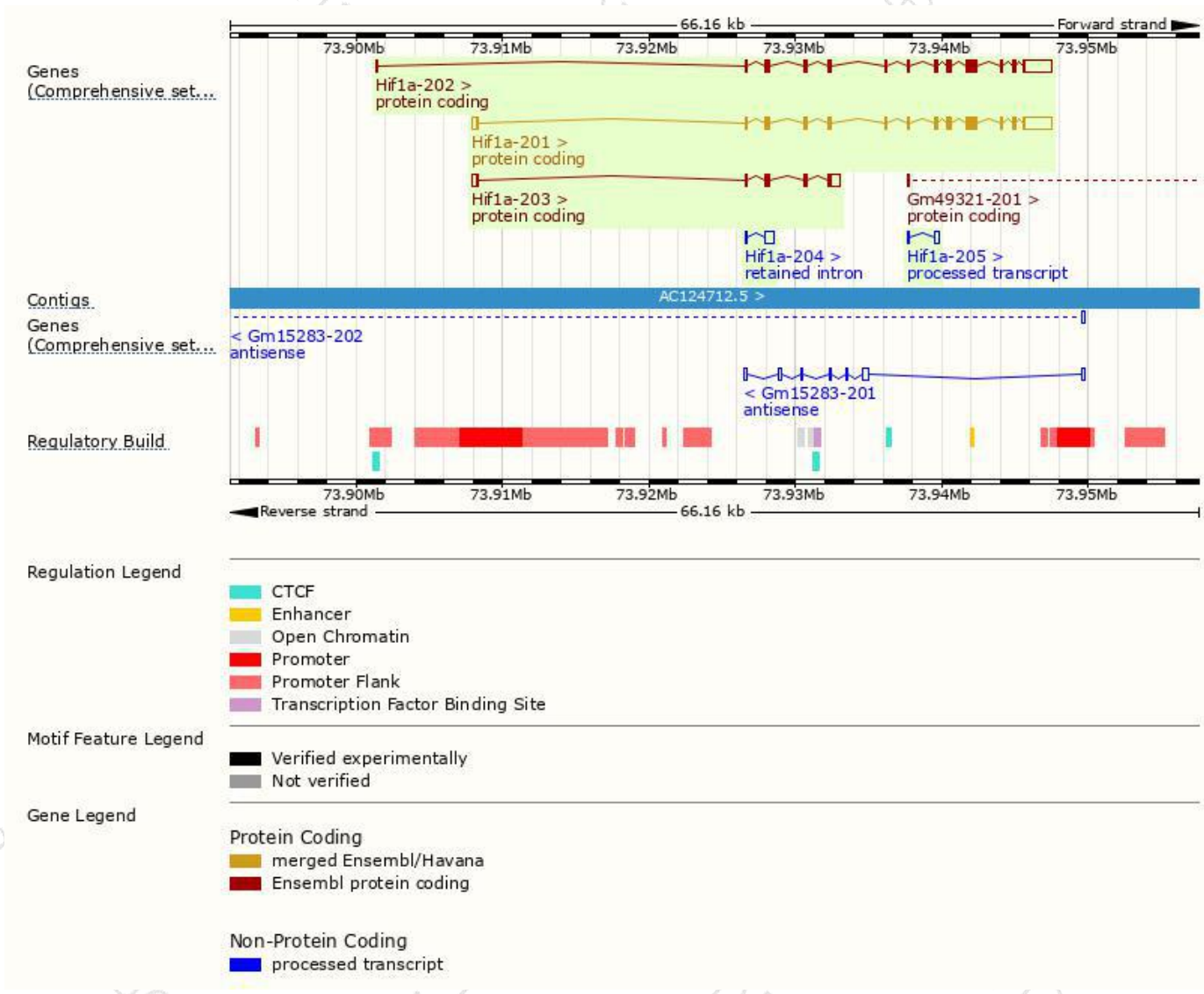
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hif1a-201	ENSMUST00000021530.7	4724	836aa	Protein coding	CCDS25977	Q61221	TSL:1 GENCODE basic APPRIS P3
Hif1a-202	ENSMUST00000110461.7	4385	810aa	Protein coding	CCDS83968	A0A0R4J1E9	TSL:1 GENCODE basic APPRIS ALT 2
Hif1a-203	ENSMUST00000110464.7	1759	258aa	Protein coding	-	A0A0R4J1F0	TSL:1 GENCODE basic
Hif1a-205	ENSMUST00000157041.1	484	No protein	Processed transcript	-	-	TSL:3
Hif1a-204	ENSMUST00000149740.1	693	No protein	Retained intron	-	-	TSL:1

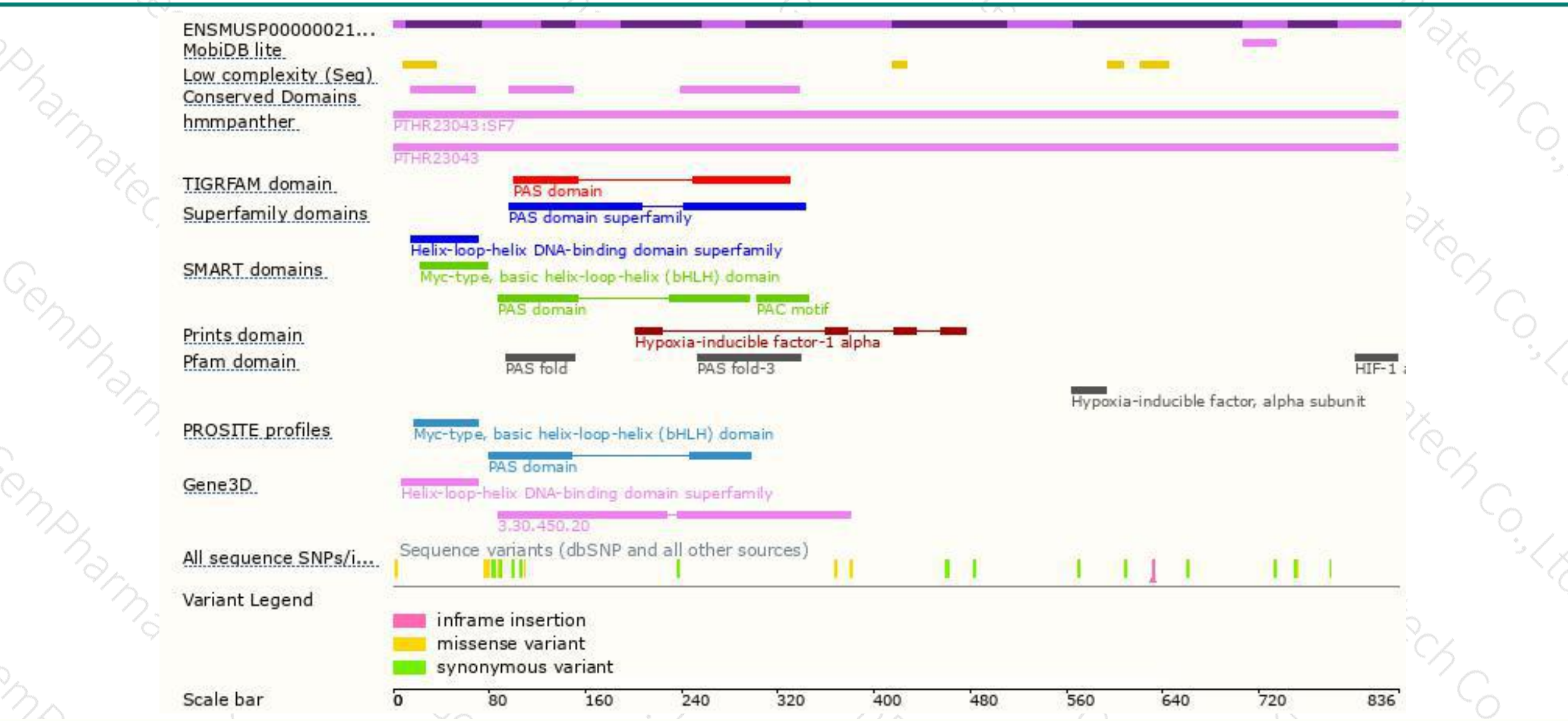
The strategy is based on the design of *Hif1a-201* transcript,The transcription is shown below



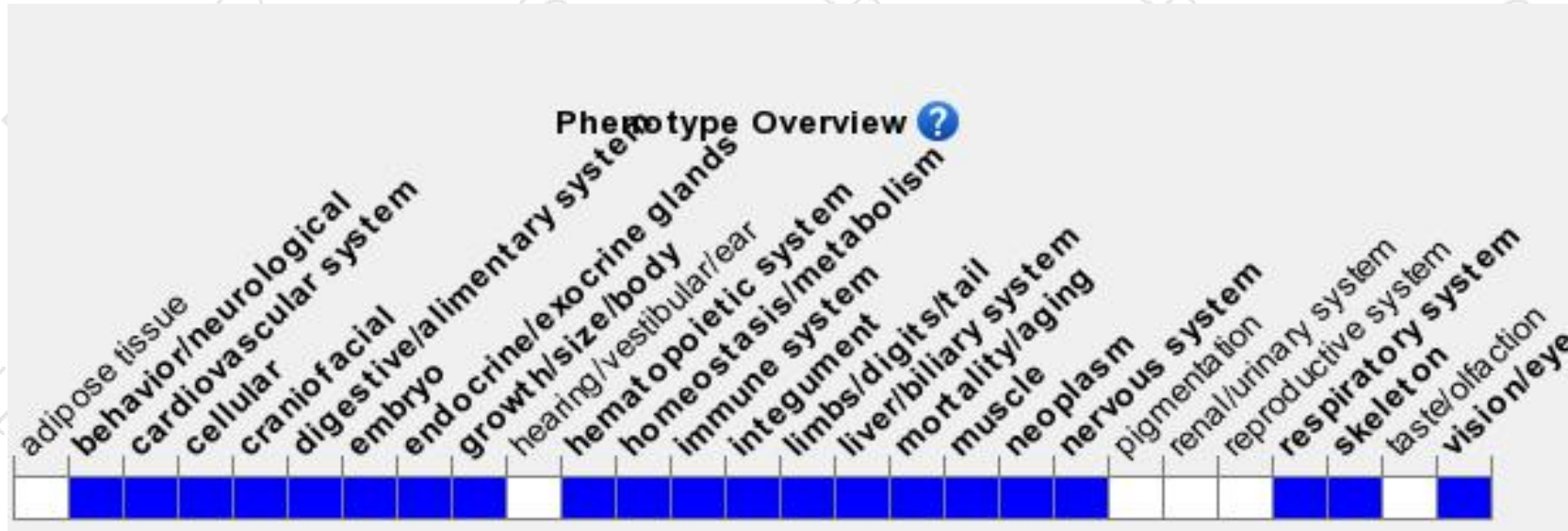
Genomic location distribution



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, Homozygous null mutants die during embryonic development with severe cardiovascular malformations, neural tube defects, cephalic defects, reduced somite number and increased hypoxia.

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

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