Cenpe Cas9-KO Strategy

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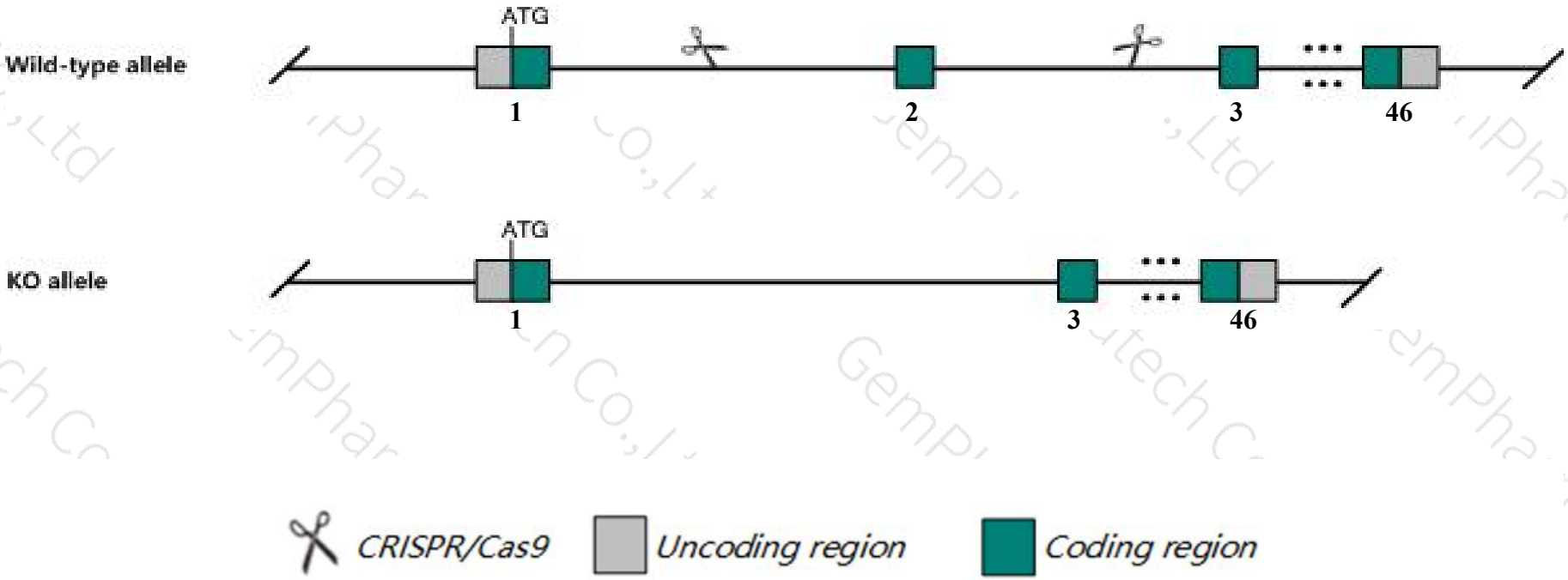
Design Date: 2019-7-24

Project Overview

Project Name	***Cenpe***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ The *Cenpe* gene has 5 transcripts. According to the structure of *Cenpe* gene, exon2 of *Cenpe-201* (ENSMUST00000062893.11) transcript is recommended as the knockout region.The region contains 92bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cenpe* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele display early embryonic lethality. Mutant embryos grown in culture exhibit inner cell mass growth defects and mitotic chromosome misalignment.

- The *Cenpe* gene is located on the Chr3. 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）

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Cenpe centromere protein E [Mus musculus (house mouse)]

Gene ID: 229841, updated on 5-Feb-2019

Summary

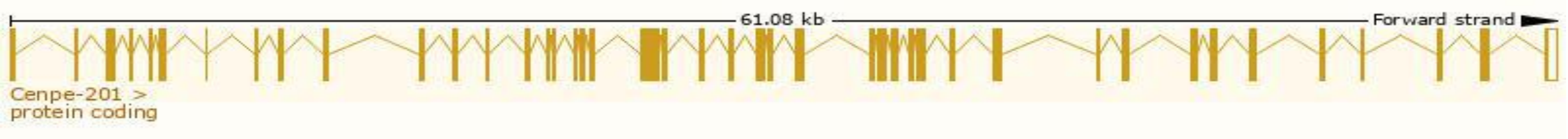
Official Symbol	Cenpe provided by MGI
Official Full Name	centromere protein E provided by MGI
Primary source	MGI:MGI:1098230
See related	Ensembl:ENSMUSG00000045328
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	312kDa, AU019344, BC049989, C530022J18, CENP-E, Kif10
Expression	Biased expression in CNS E11.5 (RPKM 11.9), liver E14 (RPKM 8.2) and 9 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

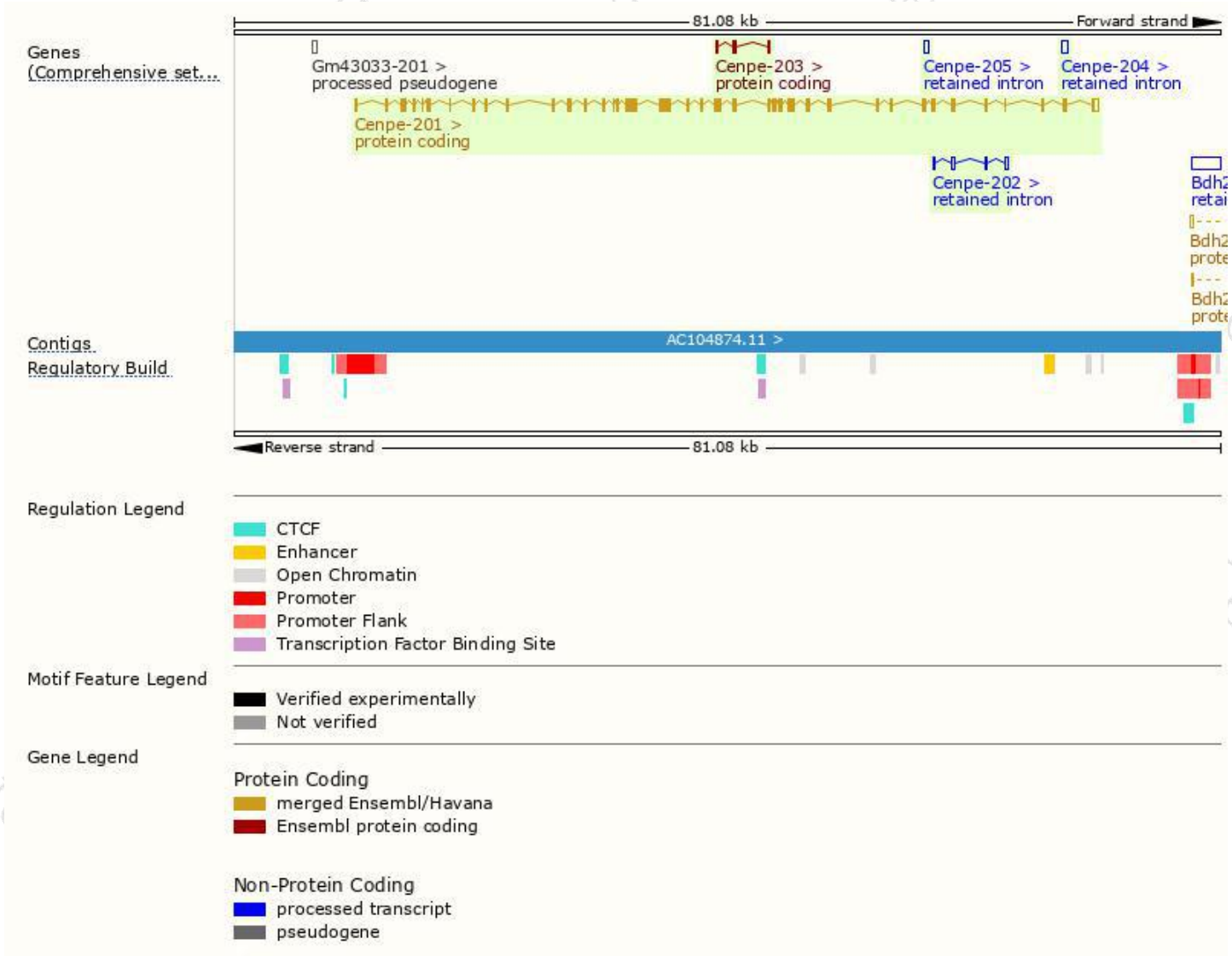
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cenpe-201	ENSMUST00000062893.11	7910	2471aa	Protein coding	CCDS51072	E9QKK1	TSL:5 GENCODE basic APPRIS P1
Cenpe-203	ENSMUST00000197369.2	582	194aa	Protein coding	-	A0A0G2JG58	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Cenpe-202	ENSMUST00000197273.1	747	No protein	Retained intron	-	-	TSL:3
Cenpe-204	ENSMUST00000199497.1	532	No protein	Retained intron	-	-	TSL:NA
Cenpe-205	ENSMUST00000200616.1	440	No protein	Retained intron	-	-	TSL:NA

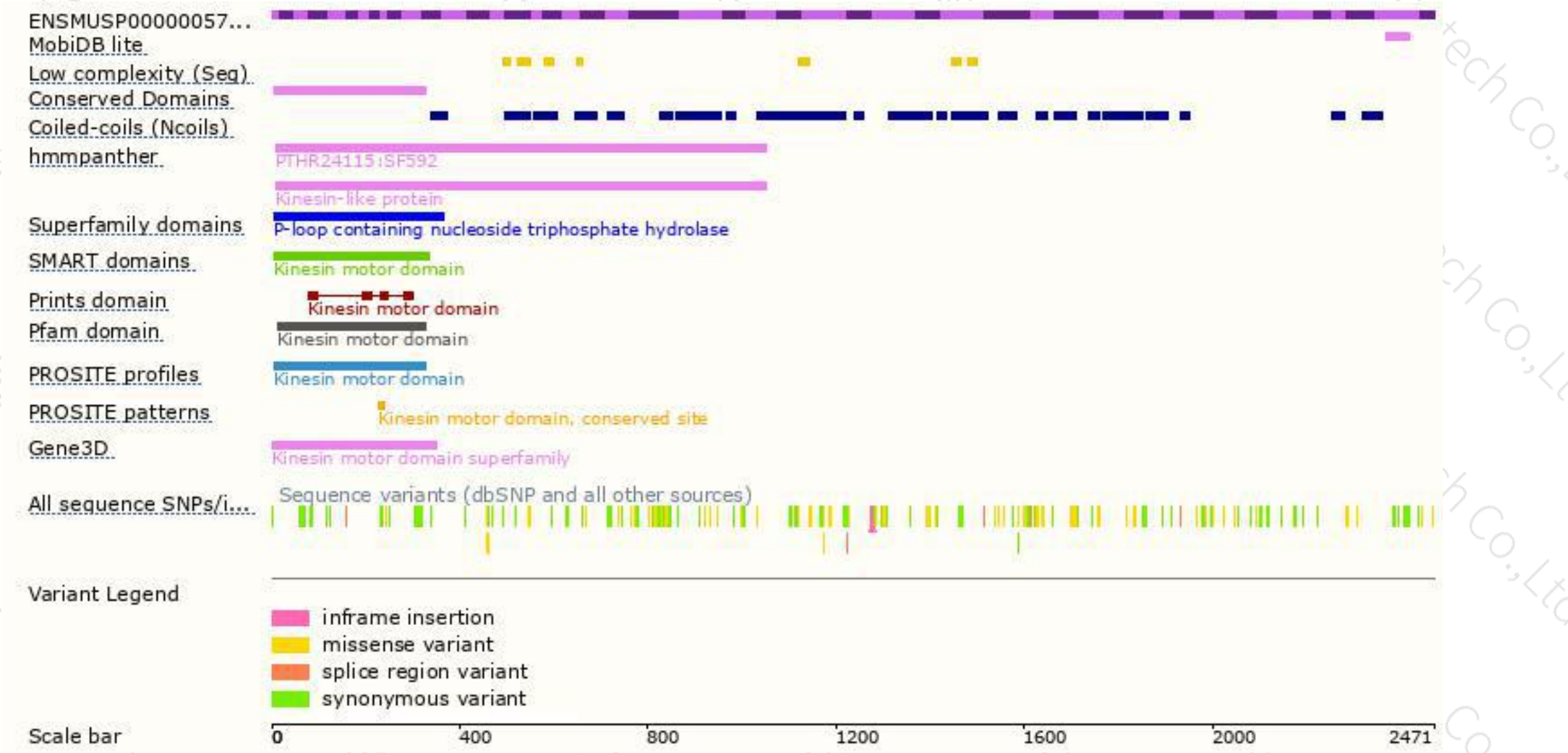
The strategy is based on the design of *Cenpe-201* transcript,The transcription is shown below



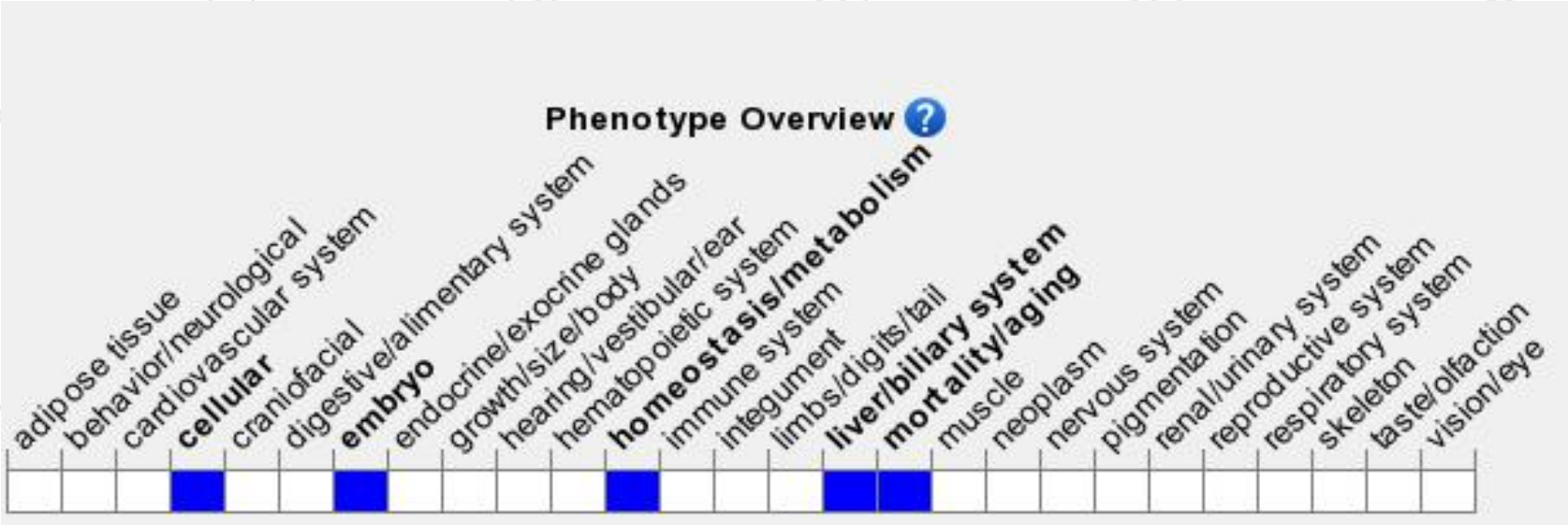
Genomic location distribution



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/).

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

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