

Ehmt1 Cas9-CKO Strategy

Designer: Jinlong Zhao

Reviewer: Shilei Zhu

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Project Overview

Project Name

Ehmt1

Project type

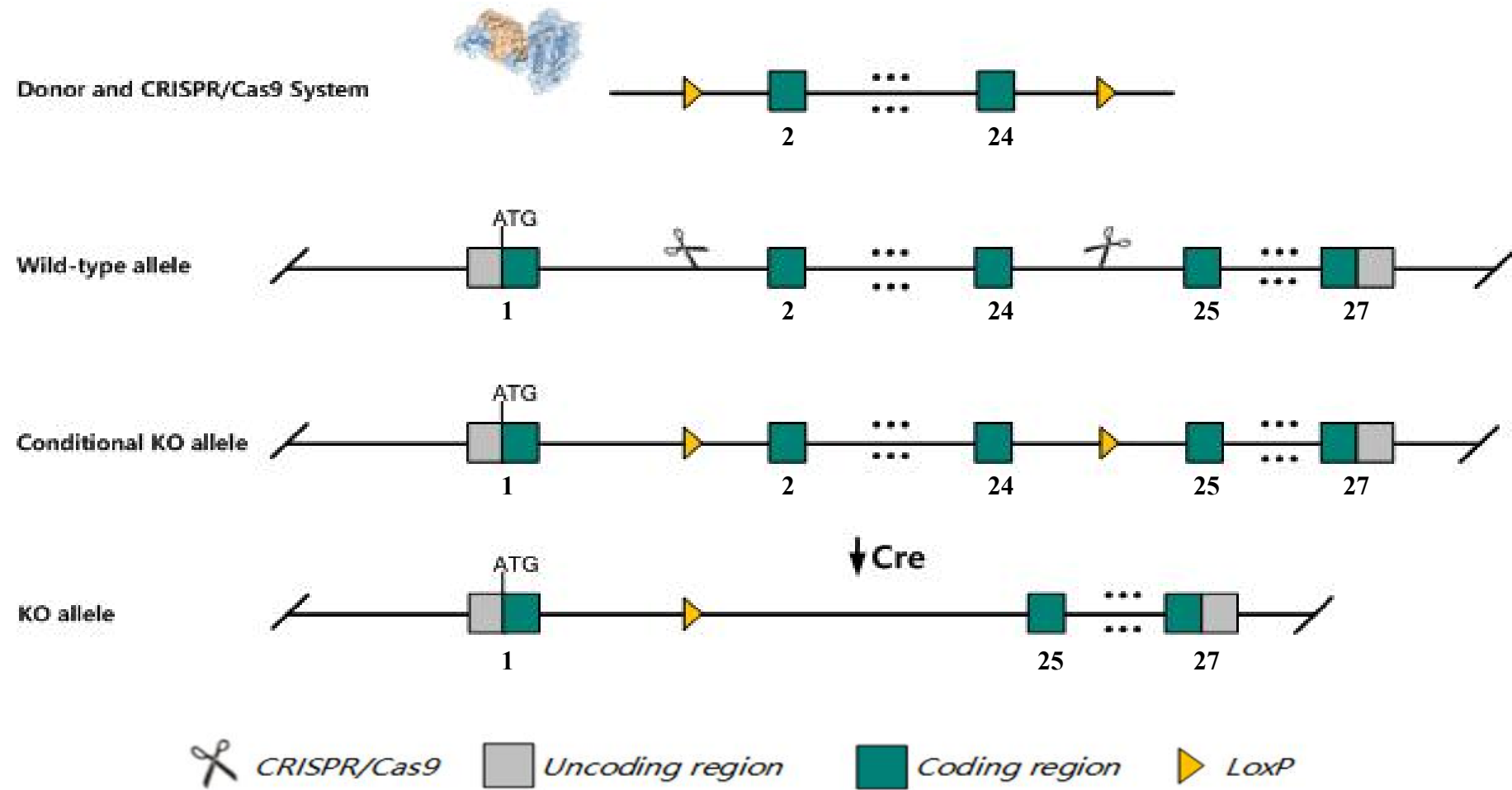
Cas9-CKO

Strain background

C57BL/6J

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ehmt1* gene. The schematic diagram is as follows:



The *Ehmt1* gene has 18 transcripts. According to the structure of *Ehmt1* gene, exon2-exon24 of *Ehmt1*-210 (ENSMUST00000147147.7) transcript is recommended as the knockout region. The region contains 3434bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Ehmt1* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.

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, Nullizygous embryos die circa E9.5 showing delayed growth and incomplete somite formation and neural groove closure. Heterozygotes show behavioral deficits and synaptic dysfunction. Homozygotes with a H3K9me1-binding mutant form show delayed prenatal growth and bone ossification and postnatal death.

The *Ehmt1* gene is located on the Chr2. 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.

Ehmt1 euchromatic histone methyltransferase 1 [Mus musculus (house mouse)]

Gene ID: 77683, updated on 31-Jan-2019

Summary

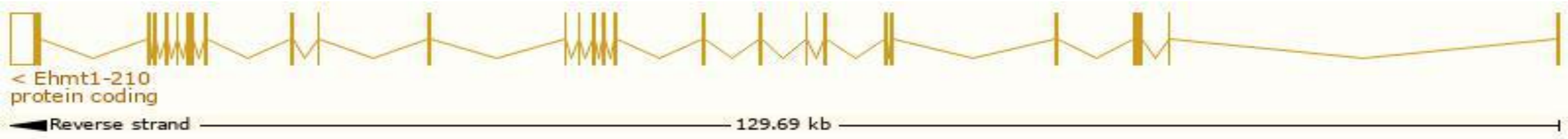
Official Symbol	Ehmt1 provided by MGI
Official Full Name	euchromatic histone methyltransferase 1 provided by MGI
Primary source	MGI:MGI:1924933
See related	Ensembl:ENSMUSG00000036893
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9230102N17Rik, D330003E03, Eu-HMTase1, GLP, GLP1, KMT1D, mKIAA1876
Expression	Ubiquitous expression in CNS E11.5 (RPKM 26.6), whole brain E14.5 (RPKM 23.0) and 28 other tissues See more
Orthologs	human all

Transcript information Ensembl

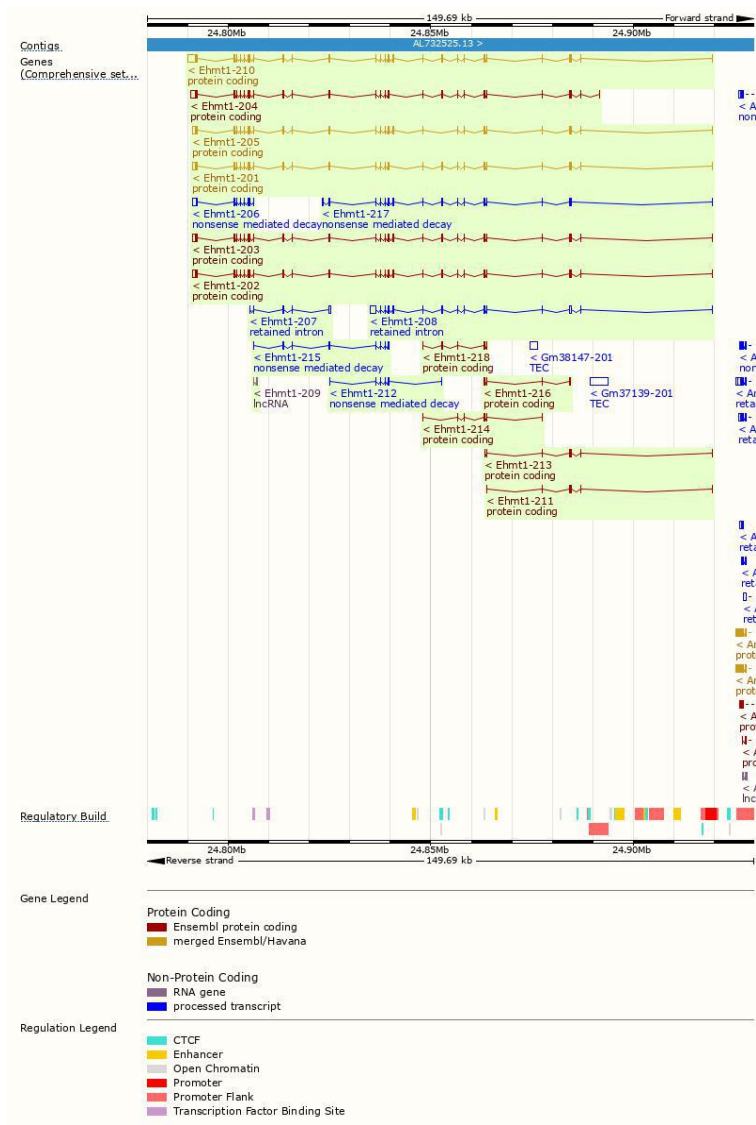
The gene has 18 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ehmt1-210	ENSMUST00000147147.7	5953	1296aa	Protein coding	CCDS15740	Q5DW34	TSL:1 GENCODE basic APPRIS P3
Ehmt1-203	ENSMUST00000102938.9	4680	1289aa	Protein coding	CCDS59635	A0A0H2UH19	TSL:1 GENCODE basic APPRIS ALT2
Ehmt1-201	ENSMUST00000046227.11	4554	1248aa	Protein coding	CCDS59636	Q5DW34	TSL:5 GENCODE basic APPRIS ALT2
Ehmt1-205	ENSMUST00000114432.8	4539	1243aa	Protein coding	CCDS59634	Q5DW34	TSL:5 GENCODE basic APPRIS ALT2
Ehmt1-204	ENSMUST00000114418.9	4902	1248aa	Protein coding	-	E9Q5A3	TSL:5 GENCODE basic APPRIS ALT2
Ehmt1-202	ENSMUST00000091348.10	4615	1288aa	Protein coding	-	Z4YJZ7	TSL:5 GENCODE basic APPRIS ALT2
Ehmt1-213	ENSMUST00000152161.7	1121	362aa	Protein coding	-	A2AIS5	CDS 3' incomplete TSL:5
Ehmt1-211	ENSMUST00000150379.1	884	286aa	Protein coding	-	A0A1B0GXE2	CDS 3' incomplete TSL:1
Ehmt1-216	ENSMUST00000198923.4	764	254aa	Protein coding	-	A0A0G2JF19	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
Ehmt1-218	ENSMUST00000207383.1	695	232aa	Protein coding	-	A0A140LI14	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Ehmt1-214	ENSMUST00000152325.7	671	224aa	Protein coding	-	F6WWY8	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
Ehmt1-217	ENSMUST00000200655.4	2582	45aa	Nonsense mediated decay	-	A0A0G2JFQ4	TSL:5
Ehmt1-206	ENSMUST00000134775.2	1971	107aa	Nonsense mediated decay	-	A0A0A6YXD1	CDS 5' incomplete TSL:1
Ehmt1-215	ENSMUST00000152636.3	865	203aa	Nonsense mediated decay	-	A0A0A6YWA0	CDS 5' incomplete TSL:3
Ehmt1-212	ENSMUST00000150836.7	756	24aa	Nonsense mediated decay	-	A0A0A6YXA8	CDS 5' incomplete TSL:3
Ehmt1-208	ENSMUST00000139000.3	3651	No protein	Retained intron	-	-	TSL:2
Ehmt1-207	ENSMUST00000138805.7	811	No protein	Retained intron	-	-	TSL:3
Ehmt1-209	ENSMUST00000144672.1	416	No protein	lncRNA	-	-	TSL:2

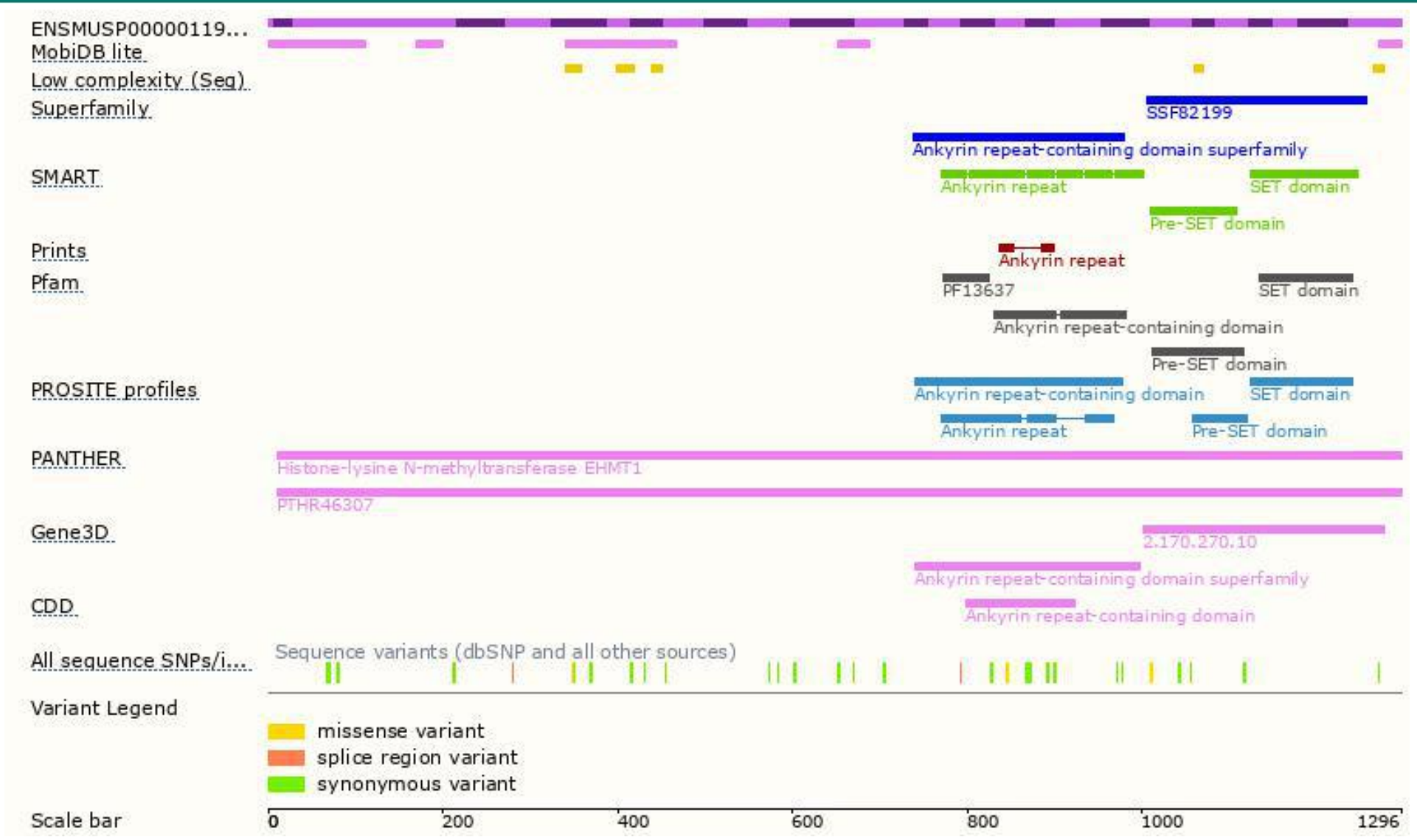
The strategy is based on the design of *Ehmt1-210* transcript,The transcription is shown below



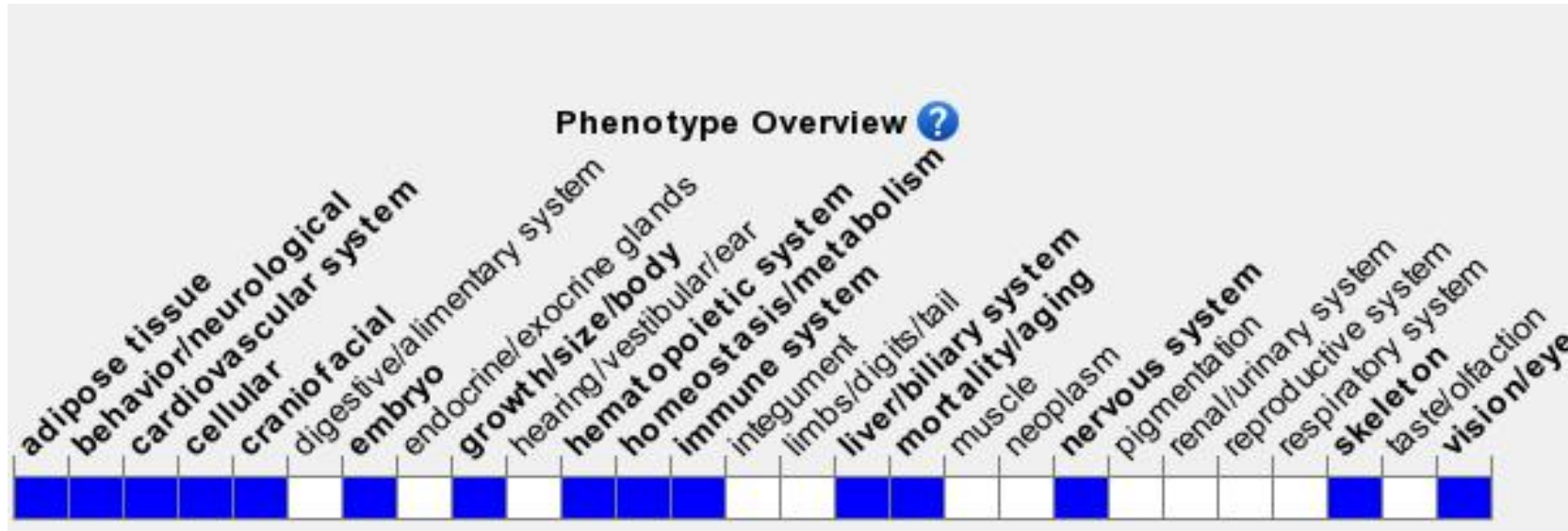
Genomic location distribution



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.
Tel: 400-9660890

