

Ahcyl1 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Ahcyll

Project type

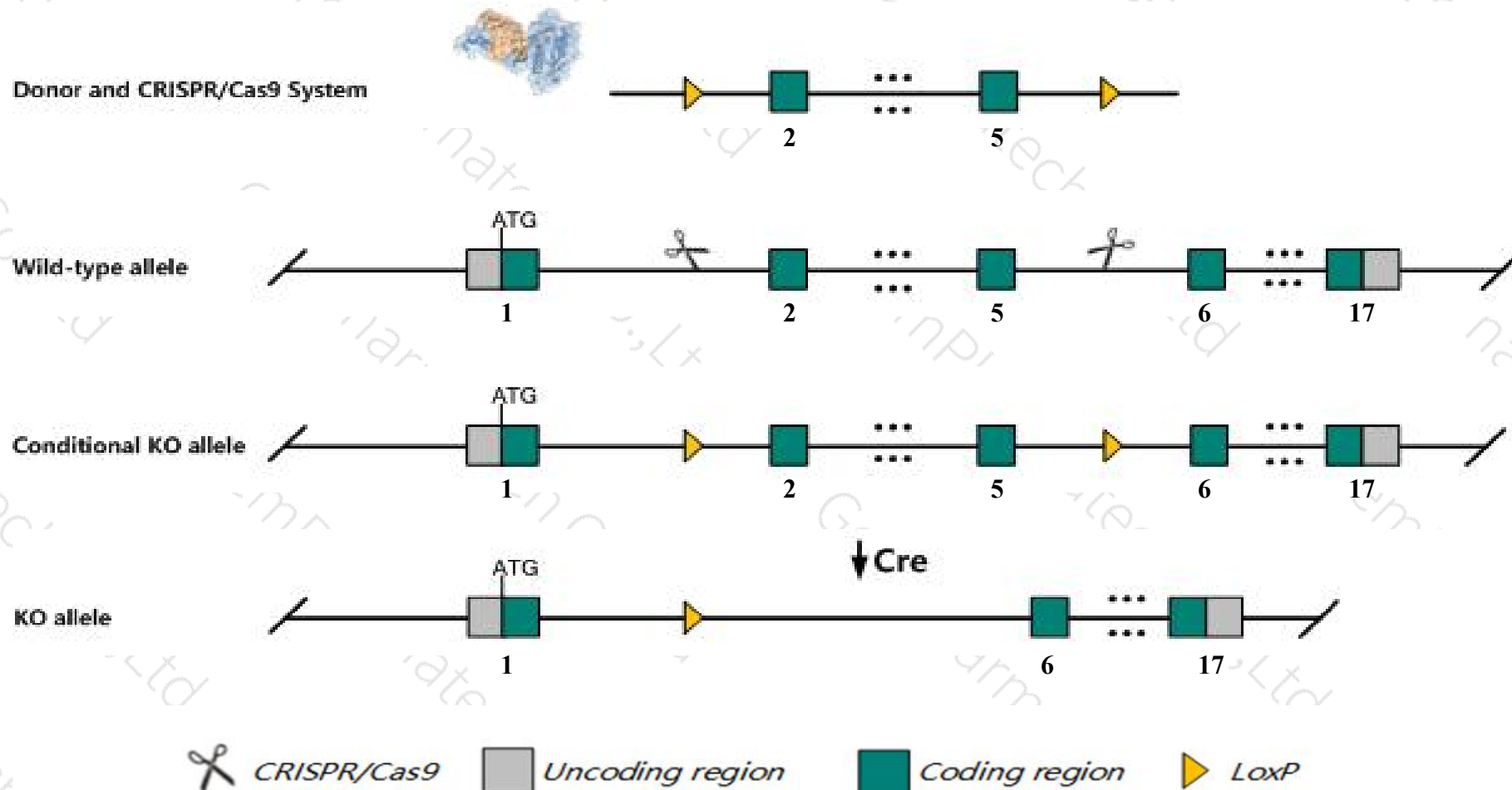
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Ahcyll* gene has 8 transcripts. According to the structure of *Ahcyll* gene, exon2-exon5 of *Ahcyll*-201 (ENSMUST00000029490.14) transcript is recommended as the knockout region. The region contains 460bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ahcyll* 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 knock-out allele display abnormal exocrine pancreas physiology.
- The *Ahcyll* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Ahcy1 S-adenosylhomocysteine hydrolase-like 1 [Mus musculus (house mouse)]

Gene ID: 229709, updated on 7-Apr-2019

Summary



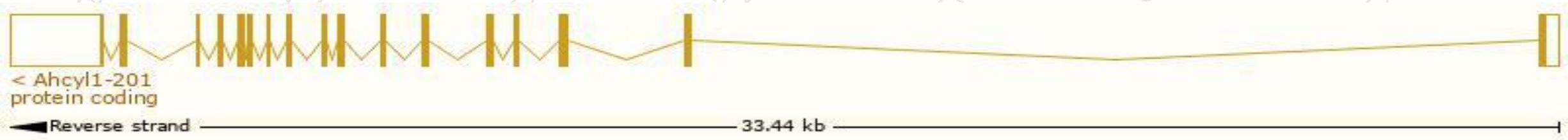
Official Symbol	Ahcy1 provided by MGI
Official Full Name	S-adenosylhomocysteine hydrolase-like 1 provided by MGI
Primary source	MGI:MGI:2385184
See related	Ensembl:ENSMUSG000000027893
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110034F20Rik, AA409031, AA414901, Ahcy-rs3, DCAL, Irbit
Expression	Ubiquitous expression in cerebellum adult (RPKM 80.6), cortex adult (RPKM 64.9) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

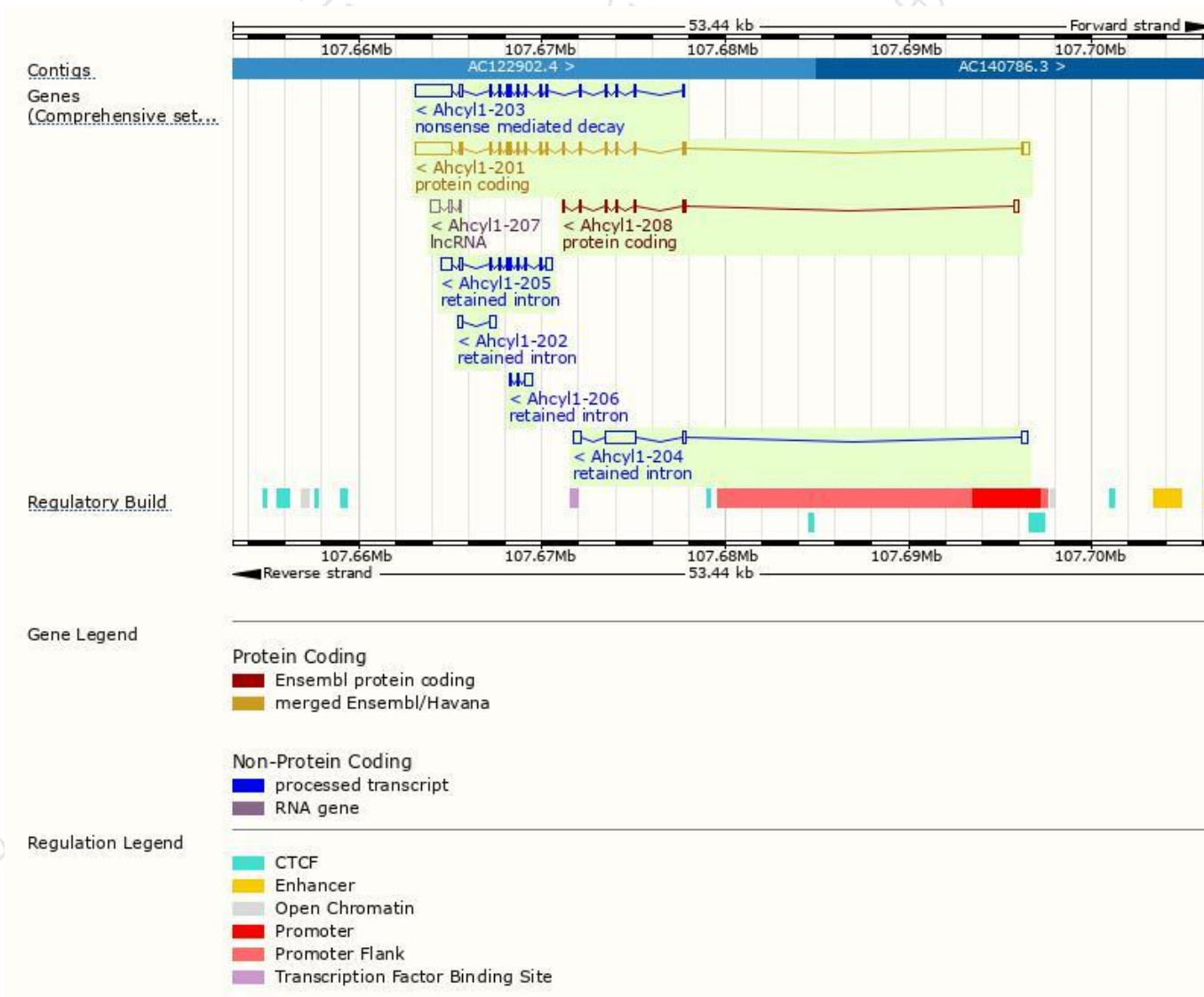
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ahcy11-201	ENSMUST00000029490.14	3863	530aa	Protein coding	CCDS38593	Q80SW1	TSL:1 GENCODE basic APPRIS P1
Ahcy11-208	ENSMUST00000153623.1	831	210aa	Protein coding	-	D3Z2Q0	CDS 3' incomplete TSL:3
Ahcy11-203	ENSMUST00000138091.7	3291	182aa	Nonsense mediated decay	-	F7ATQ6	CDS 5' incomplete TSL:5
Ahcy11-204	ENSMUST00000138116.1	2580	No protein	Retained intron	-	-	TSL:2
Ahcy11-205	ENSMUST00000144864.7	1689	No protein	Retained intron	-	-	TSL:2
Ahcy11-202	ENSMUST00000137583.1	587	No protein	Retained intron	-	-	TSL:3
Ahcy11-206	ENSMUST00000151935.1	583	No protein	Retained intron	-	-	TSL:2
Ahcy11-207	ENSMUST00000153530.1	737	No protein	lncRNA	-	-	TSL:3

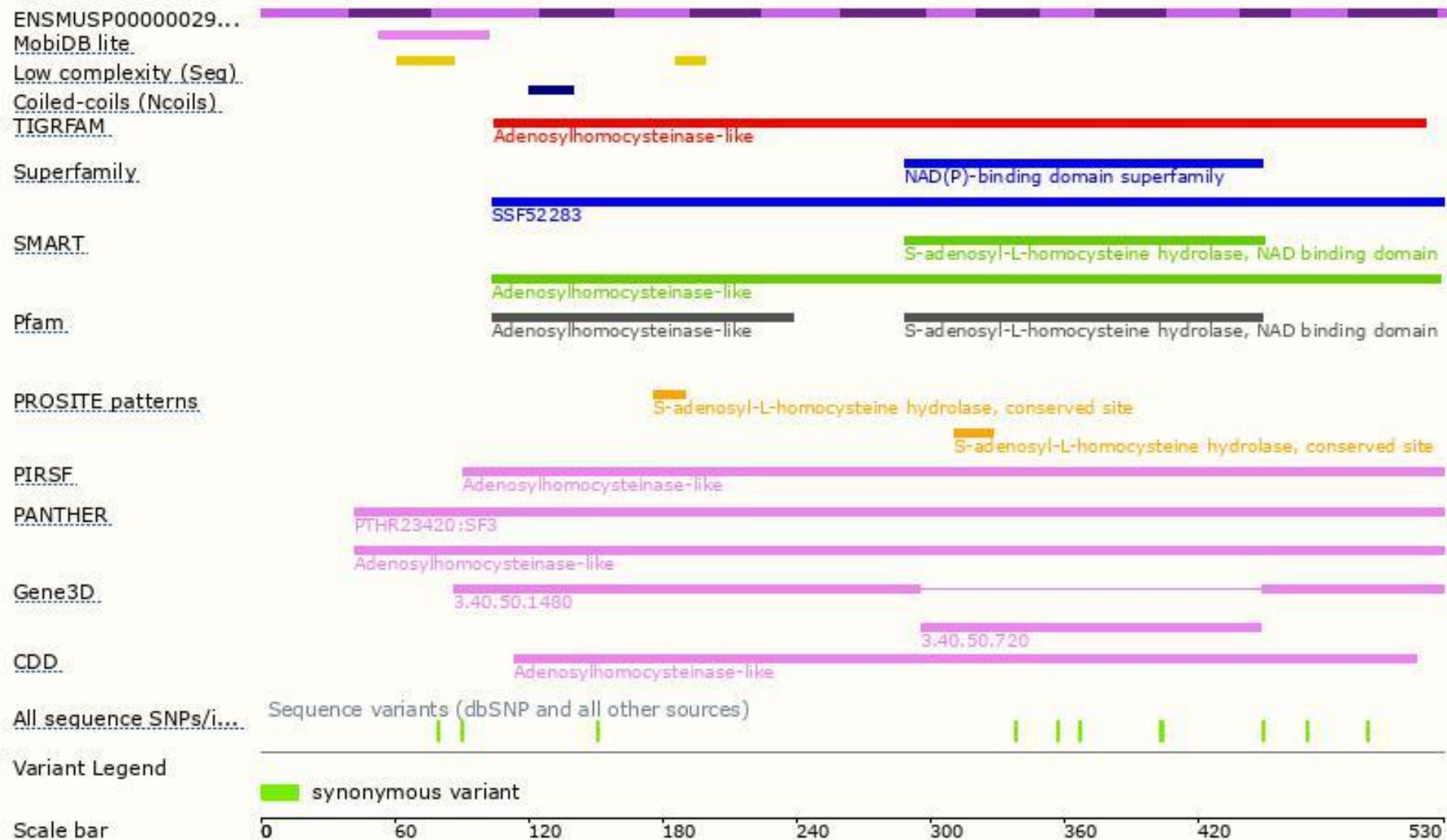
The strategy is based on the design of *Ahcy11-201* transcript,The transcription is shown below



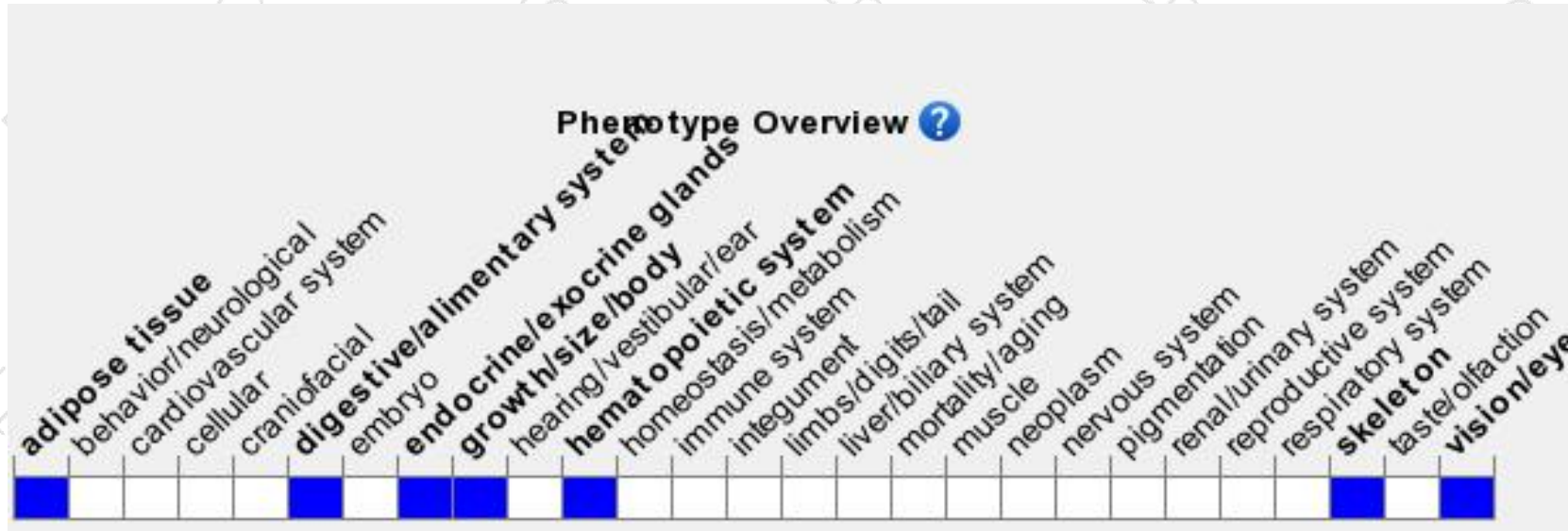
Genomic location distribution



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, Mice homozygous for a knock-out allele display abnormal exocrine pancreas physiology.

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

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