

Ddx58 Cas9-KO Strategy

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Project Overview

Project Name

Ddx58

Project type

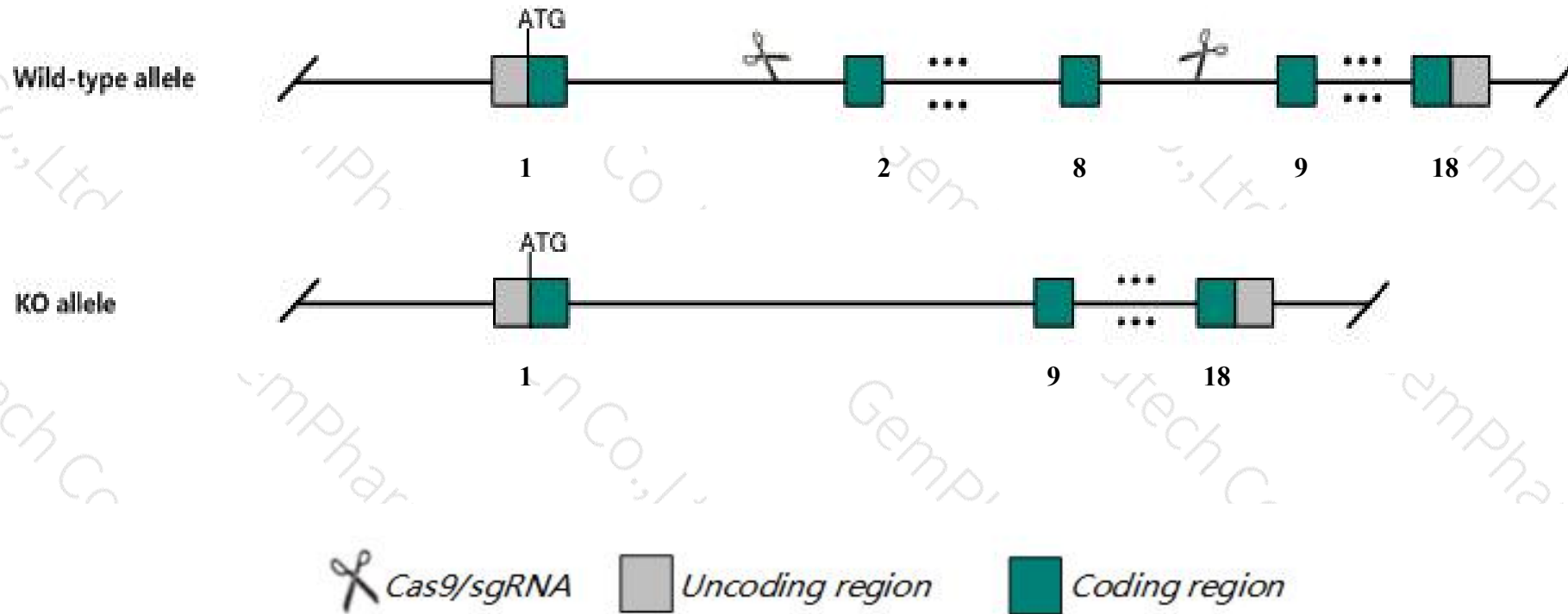
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ddx58* gene. The schematic diagram is as follows:



- The *Ddx58* gene has 10 transcripts. According to the structure of *Ddx58* gene, exon2-exon8 of *Ddx58-201* (ENSMUST00000037907.12) transcript is recommended as the knockout region. The region contains 1109bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ddx58* 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, Most homozygotes for a null allele die in utero with liver apoptosis while survivors show impaired IFN induction and succumb to infection with certain RNA viruses. Homozygotes for another null allele are viable but develop colitis and progressive granulocytosis leading to chronic myeloid leukemia.
- The *Ddx58* gene is located on the Chr4. 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)

Ddx58 DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 [Mus musculus (house mouse)]

Gene ID: 230073, updated on 25-Mar-2019

Summary

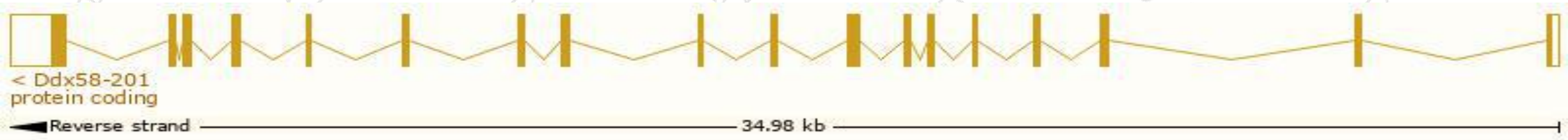
Official Symbol	Ddx58 provided by MGI
Official Full Name	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 provided by MGI
Primary source	MGI:MGI:2442858
See related	Ensembl:ENSMUSG00000040296
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	6430573D20Rik, C330021E21, RIG-I, RLR-1
Expression	Ubiquitous expression in placenta adult (RPKM 6.5), spleen adult (RPKM 6.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

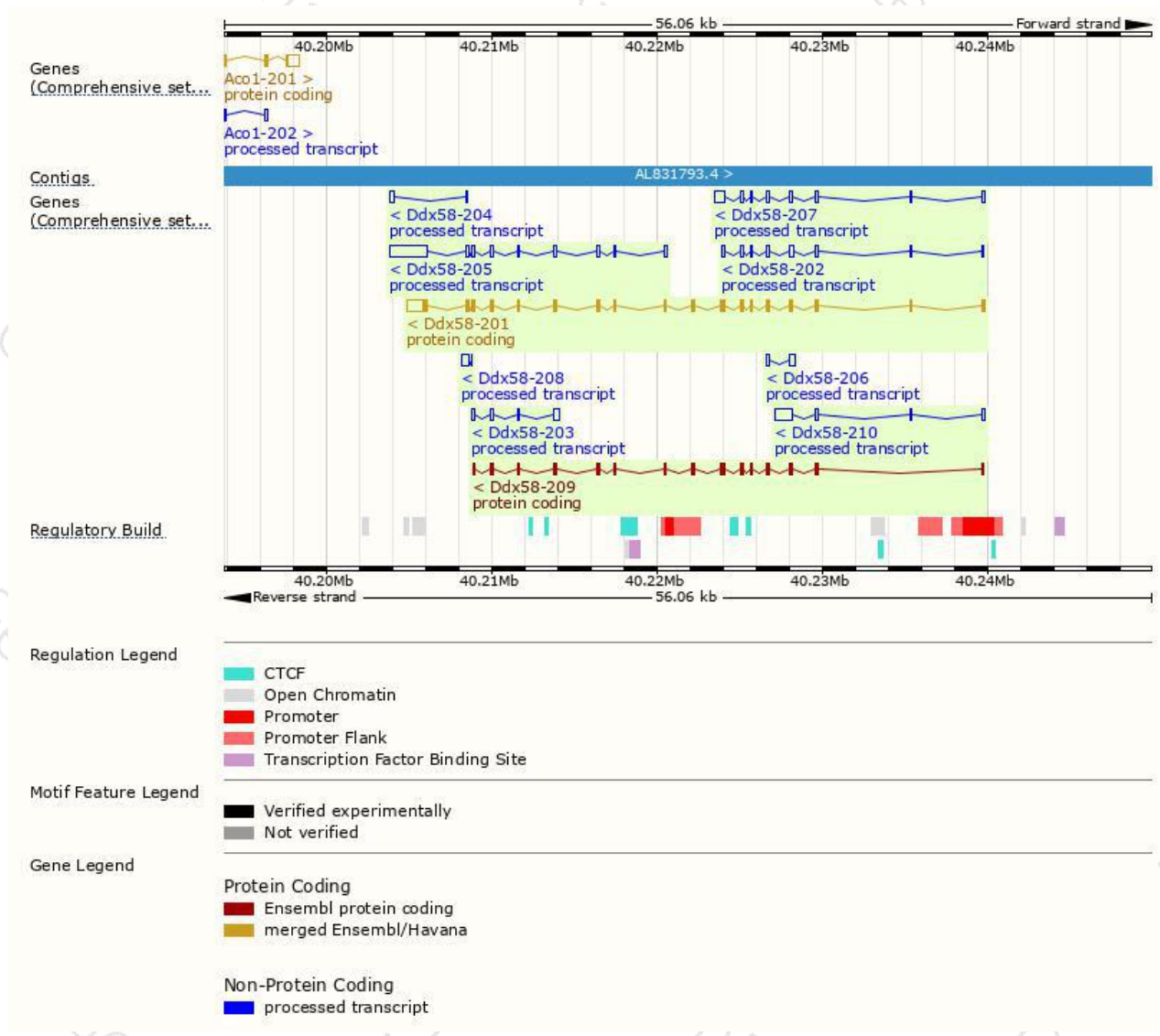
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ddx58-201	ENSMUST00000037907.12	3874	926aa	Protein coding	CCDS18043	Q6Q899	TSL:1 GENCODE basic APPRIS P1
Ddx58-202	ENSMUST00000127026.7	1250	No protein	Processed transcript	-	-	TSL:1
Ddx58-203	ENSMUST00000135966.1	756	No protein	Processed transcript	-	-	TSL:3
Ddx58-204	ENSMUST00000136435.1	386	No protein	Processed transcript	-	-	TSL:3
Ddx58-205	ENSMUST00000137903.7	3533	No protein	Processed transcript	-	-	TSL:1
Ddx58-206	ENSMUST00000139110.1	541	No protein	Processed transcript	-	-	TSL:2
Ddx58-207	ENSMUST00000139583.7	1641	No protein	Processed transcript	-	-	TSL:1
Ddx58-208	ENSMUST00000140616.1	435	No protein	Processed transcript	-	-	TSL:3
Ddx58-209	ENSMUST00000142055.1	2127	707aa	Protein coding	-	A2AP29	CDS 3' incomplete TSL:5
Ddx58-210	ENSMUST00000149539.1	1607	No protein	Processed transcript	-	-	TSL:1

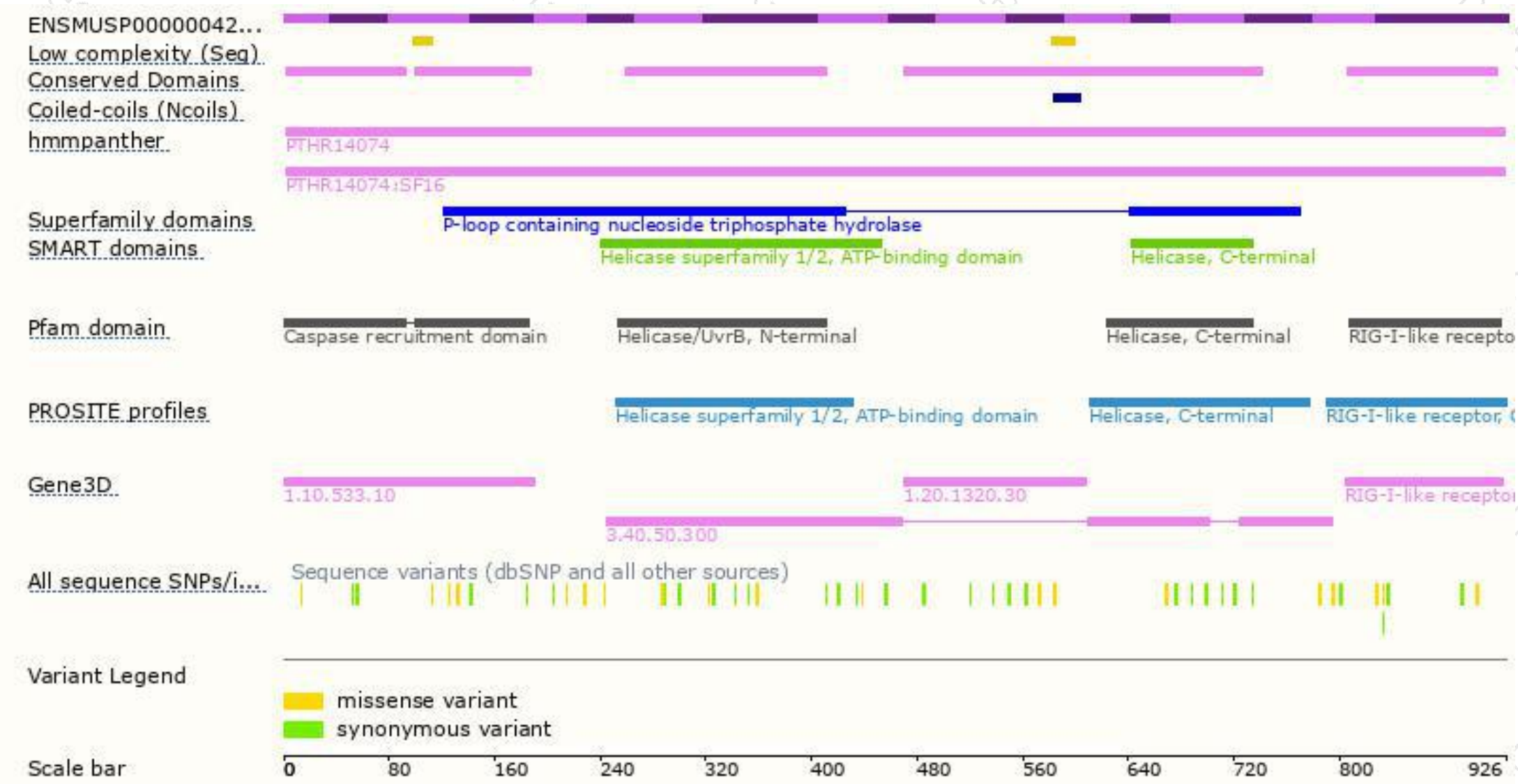
The strategy is based on the design of *Ddx58-201* transcript,The transcription is shown below



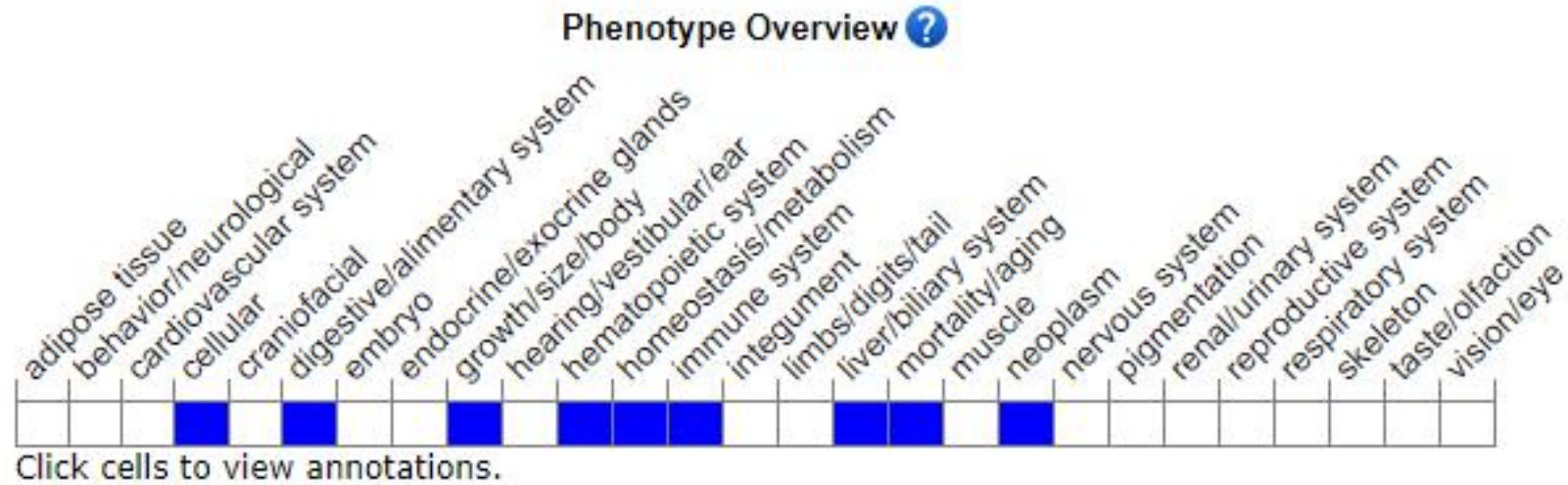
Genomic location distribution



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, Most homozygotes for a null allele die in utero with liver apoptosis while survivors show impaired IFN induction and succumb to infection with certain RNA viruses. Homozygotes for another null allele are viable but develop colitis and progressive granulocytosis leading to chronic myeloid leukemia.

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

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