Rbbp7 Cas9-CKO Strategy

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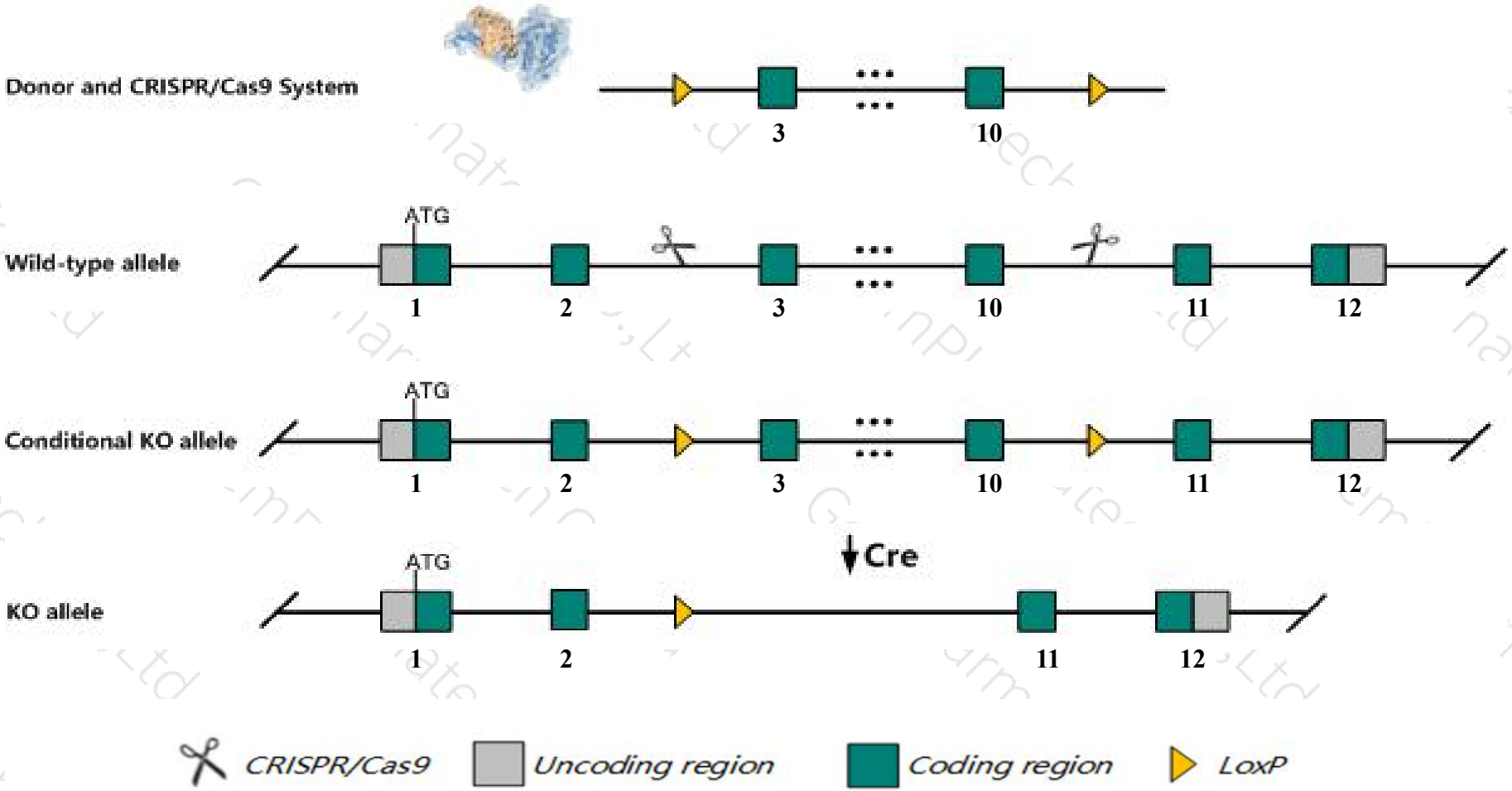
Project Overview

Project Name	***Rbbp7***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rbbp7* gene. The schematic diagram is as follows:



Technical routes

- The *Rbbp7* gene has 5 transcripts. According to the structure of *Rbbp7* gene, exon3-exon10 of *Rbbp7-201* (ENSMUST00000033720.11) transcript is recommended as the knockout region.The region contains 937bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Rbbp7* 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.

Notice

➢ According to the existing MGI data,Male chimeras hemizygous for a gene trapped allele exhibit posterior patterning and embryo turning defects.

➢The N-terminal of *Rbbp7* gene will remain 53aa,it may remain the partial function of *Rbbp7* gene.

➢ The *Rbbp7* gene is located on the ChrX. 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）

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Rbbp7 retinoblastoma binding protein 7, chromatin remodeling factor [*Mus musculus* (house mouse)]

Gene ID: 245688, updated on 12-Aug-2019

Summary

Official Symbol	Rbbp7 provided by MGI
Official Full Name	retinoblastoma binding protein 7, chromatin remodeling factor provided by MGI
Primary source	MGI:MGI:1194910
See related	Ensembl:ENSMUSG00000031353
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	mRbAp46; AA409861; AI173248; AU019541; BB114024
Expression	Broad expression in placenta adult (RPKM 217.3), liver E18 (RPKM 180.1) and 21 other tissues See more
Orthologs	human all

Genomic context

Location: X; X F4

See Rbbp7 in Genome Data Viewer

Exon count: 13

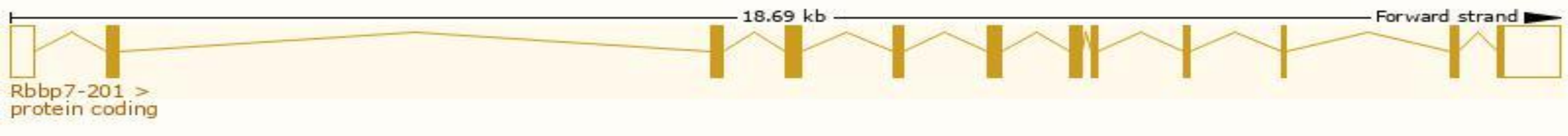
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	X	NC_000086.7 (162760372..162779090)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	X	NC_000086.6 (159198304..159217022)

Transcript information（Ensembl）

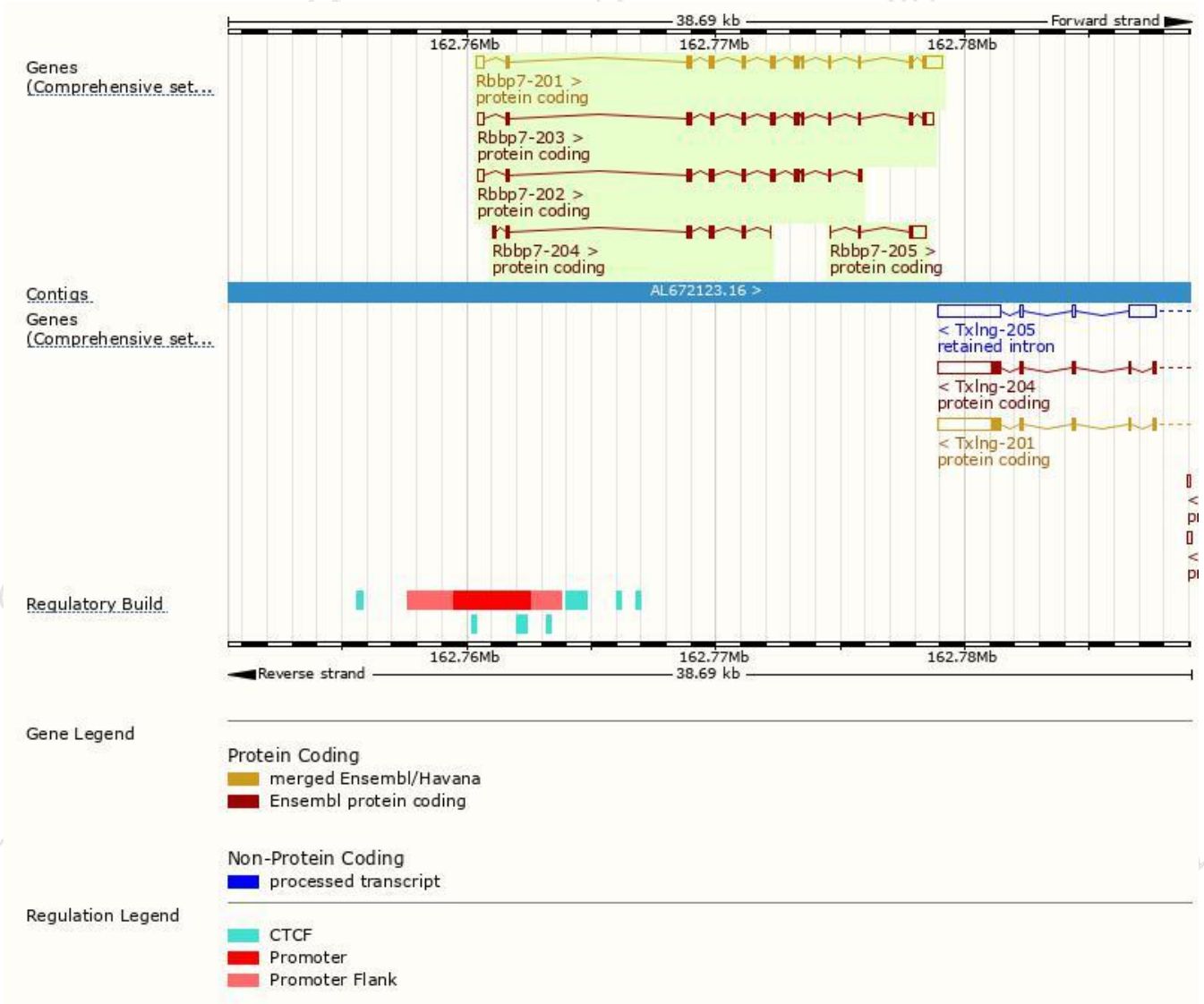
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rbbp7-201	ENSMUST00000033720.11	2244	425aa	Protein coding	CCDS30509	Q60973	TSL:1 GENCODE basic APPRIS P1
Rbbp7-203	ENSMUST00000112327.7	1862	416aa	Protein coding	-	A2AFJ1	TSL:5 GENCODE basic
Rbbp7-202	ENSMUST00000112326.7	1430	386aa	Protein coding	-	A2AFI9	TSL:1 GENCODE basic
Rbbp7-205	ENSMUST00000143681.1	784	76aa	Protein coding	-	F6U539	CDS 5' incomplete TSL:1
Rbbp7-204	ENSMUST00000138791.1	705	235aa	Protein coding	-	F6ZLC6	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

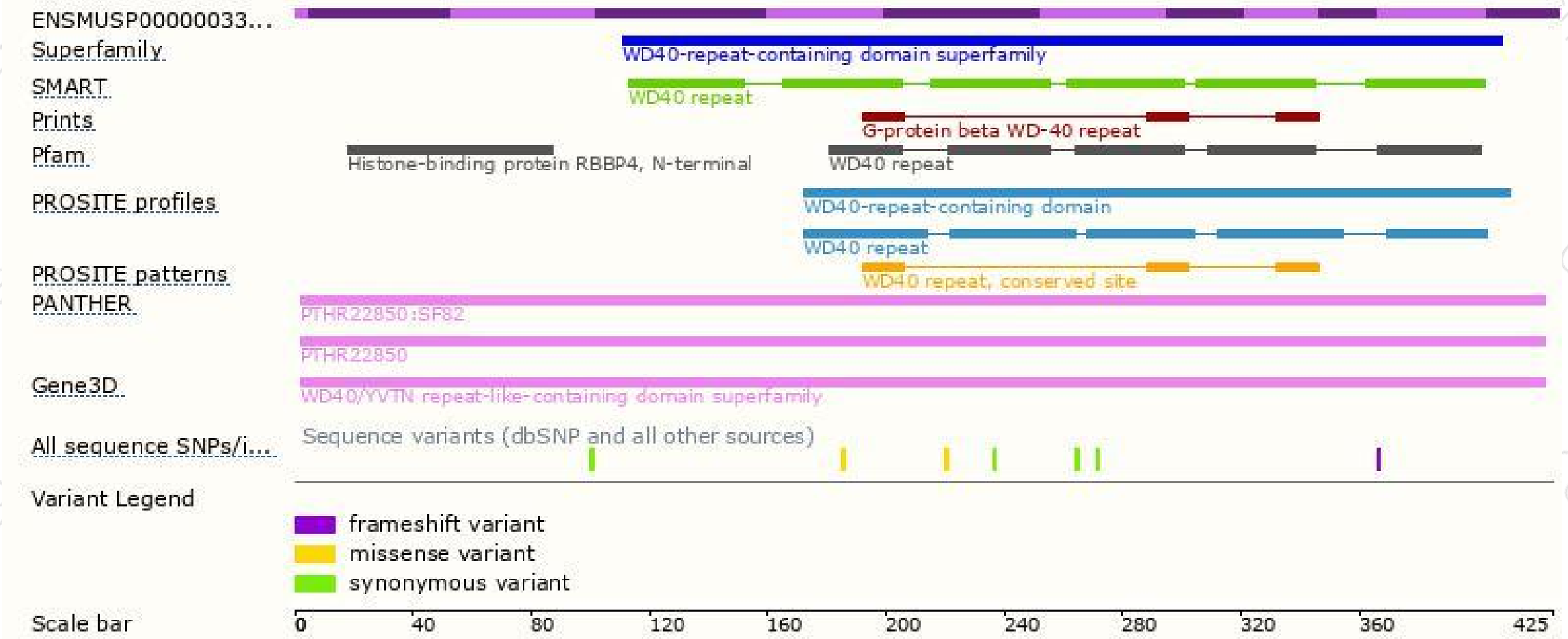
The strategy is based on the design of *Rbbp7-201* transcript,The transcription is shown below



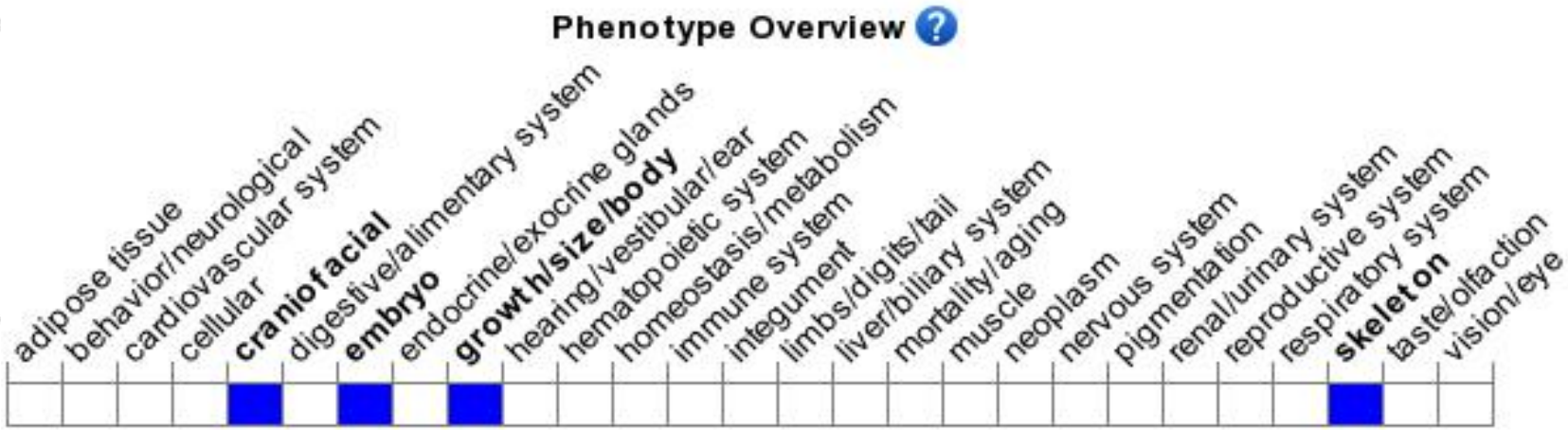
Genomic location distribution



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,Male chimeras hemizygous for a gene trapped allele exhibit posterior patterning and embryo turning defects.

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

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