

Herc3 Cas9-CKO Strategy

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Project Overview

Project Name

Herc3

Project type

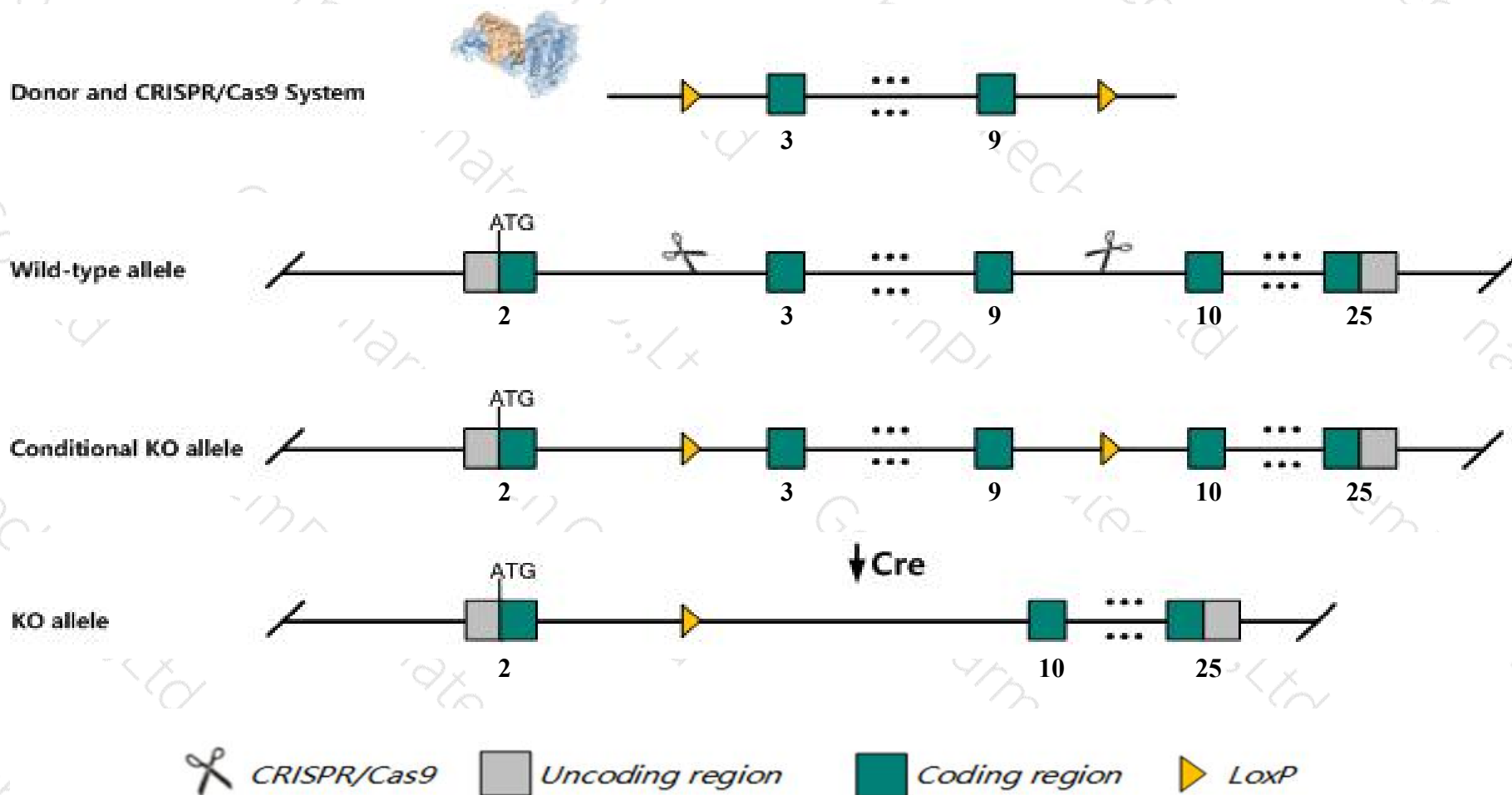
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Herc3* gene. The schematic diagram is as follows:



- The *Herc3* gene has 12 transcripts. According to the structure of *Herc3* gene, exon3-exon9 of *Herc3-202* (ENSMUST00000041401.10) transcript is recommended as the knockout region. The region contains 920bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Herc3* 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 null allele exhibit abnormal hair follicle bulge morphology.
- The *Herc3* gene is located on the Chr6. 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)

Herc3 hect domain and RLD 3 [Mus musculus (house mouse)]

Gene ID: 73998, updated on 31-Jan-2019

Summary



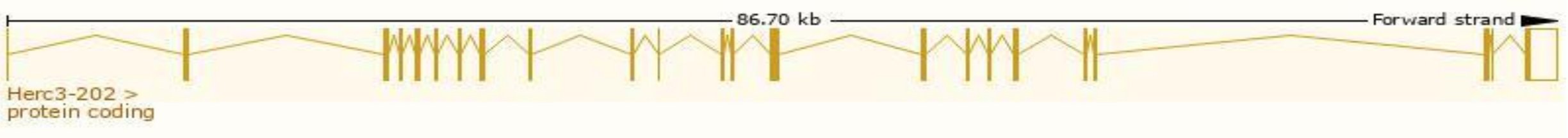
Official Symbol	Herc3 provided by MGI
Official Full Name	hect domain and RLD 3 provided by MGI
Primary source	MGI:MGI:1921248
See related	Ensembl:ENSMUSG00000029804
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5730409F18Rik, A1646603, mKIAA0032
Expression	Broad expression in cortex adult (RPKM 14.6), frontal lobe adult (RPKM 10.7) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

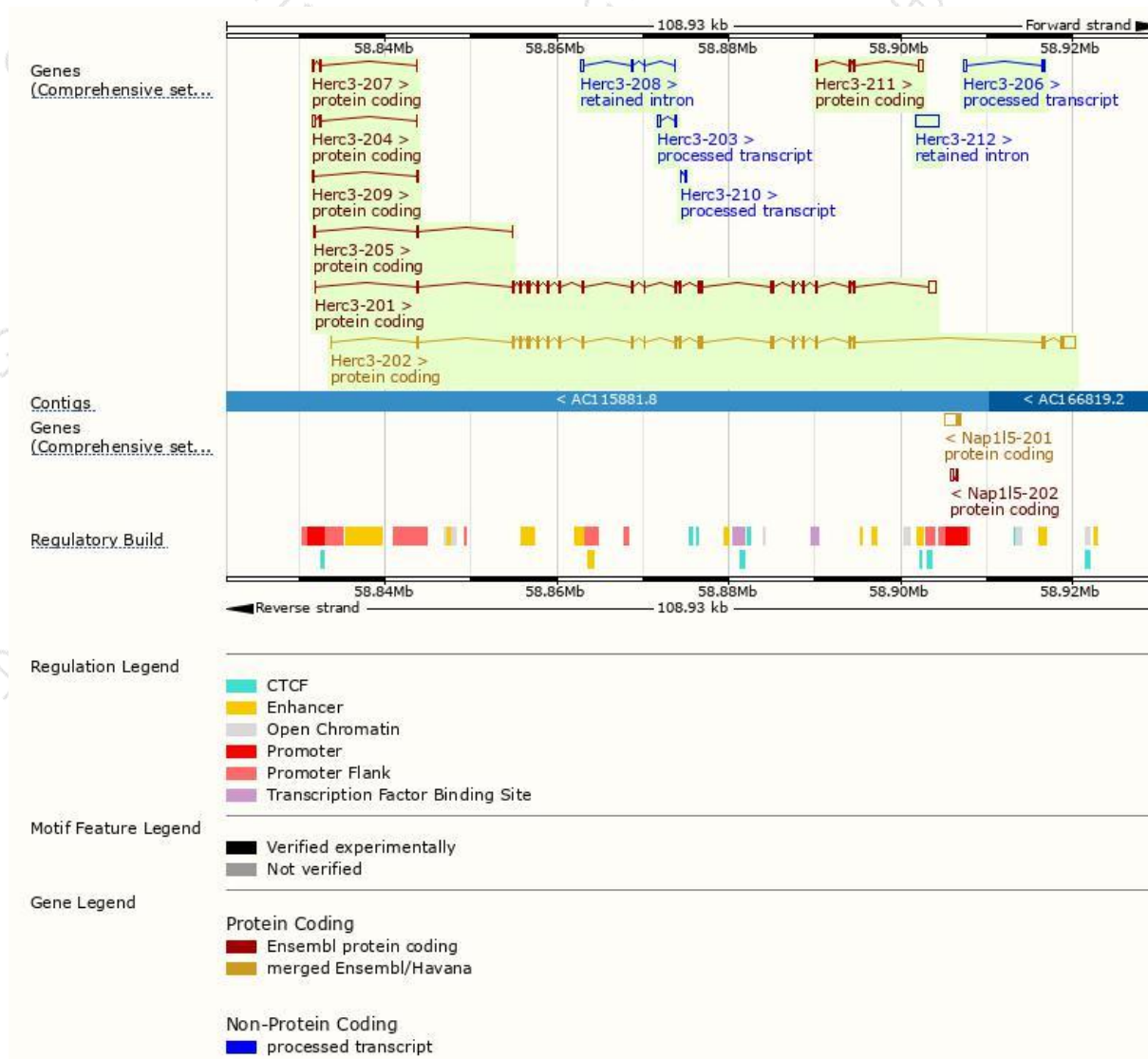
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Herc3-202	ENSMUST00000041401.10	4731	1050aa	Protein coding	CCDS20196	A6H6S0	TSL:1 GENCODE basic APPRIS P1
Herc3-201	ENSMUST00000031823.11	3596	913aa	Protein coding	-	G5E876	TSL:1 GENCODE basic
Herc3-211	ENSMUST00000204629.1	722	97aa	Protein coding	-	A0A0N4SW02	CDS 5' incomplete TSL:5
Herc3-204	ENSMUST00000122981.1	676	27aa	Protein coding	-	D3Z2S3	CDS 3' incomplete TSL:2
Herc3-205	ENSMUST00000126292.7	446	77aa	Protein coding	-	D3Z6D4	CDS 3' incomplete TSL:3
Herc3-207	ENSMUST00000141600.7	438	32aa	Protein coding	-	D3Z3U0	CDS 3' incomplete TSL:2
Herc3-209	ENSMUST00000203714.3	374	75aa	Protein coding	-	A0A0N4SVW7	CDS 3' incomplete TSL:5
Herc3-206	ENSMUST00000131132.1	636	No protein	Processed transcript	-	-	TSL:2
Herc3-203	ENSMUST00000122908.1	410	No protein	Processed transcript	-	-	TSL:3
Herc3-210	ENSMUST00000204196.1	234	No protein	Processed transcript	-	-	TSL:3
Herc3-212	ENSMUST00000205139.1	2762	No protein	Retained intron	-	-	TSL:NA
Herc3-208	ENSMUST00000154290.1	418	No protein	Retained intron	-	-	TSL:3

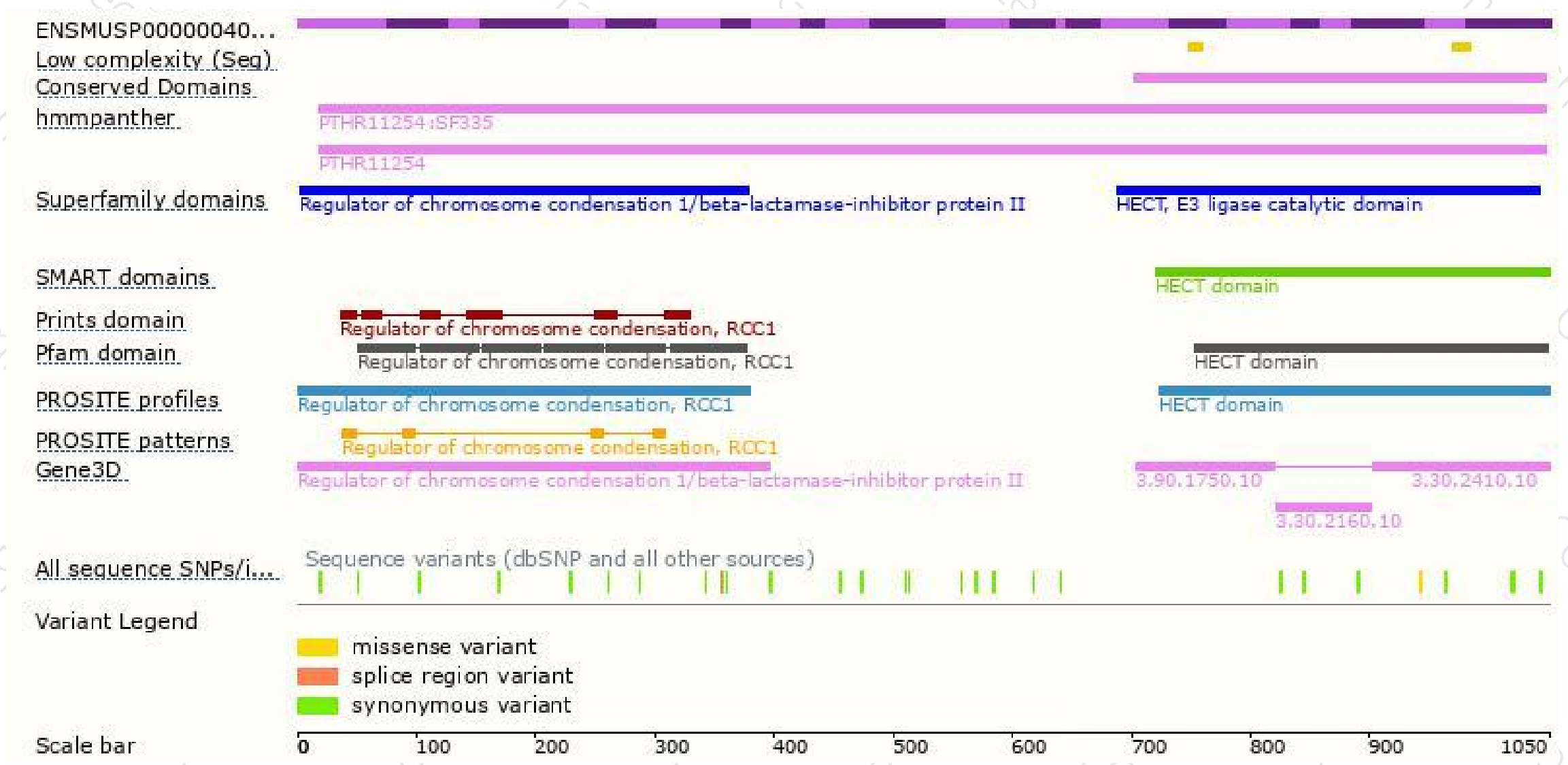
The strategy is based on the design of *Herc3-202* transcript,The transcription is shown below



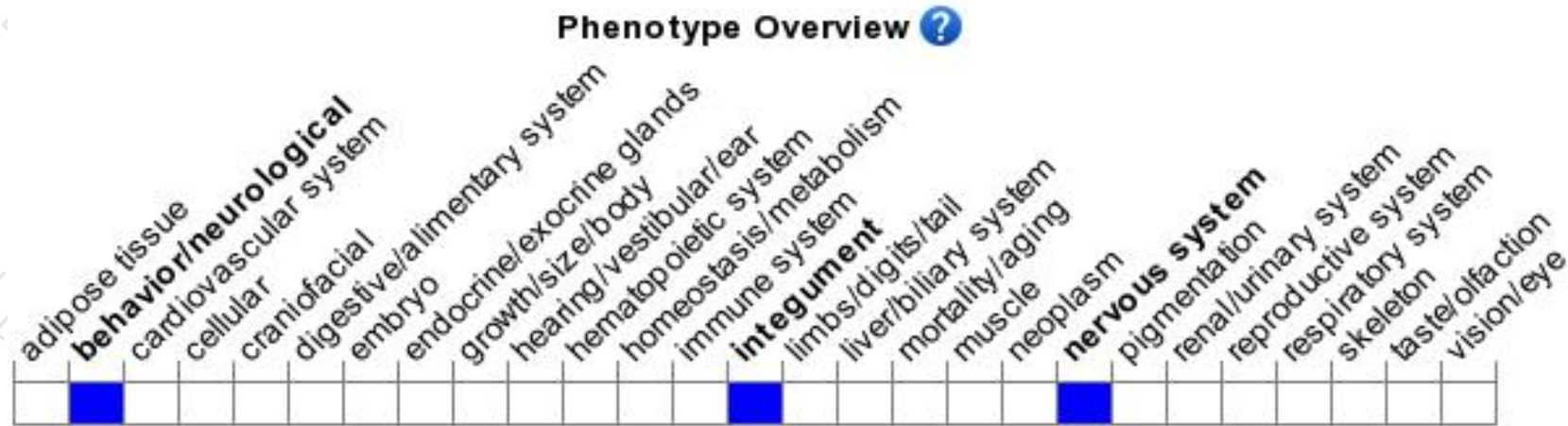
Genomic location distribution



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 null allele exhibit abnormal hair follicle bulge morphology.

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

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