

***Zdhhc17* Cas9-CKO Strategy**

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Reviewer:

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Design Date:

2020-2-14

Project Overview

Project Name

Zdhhc17

Project type

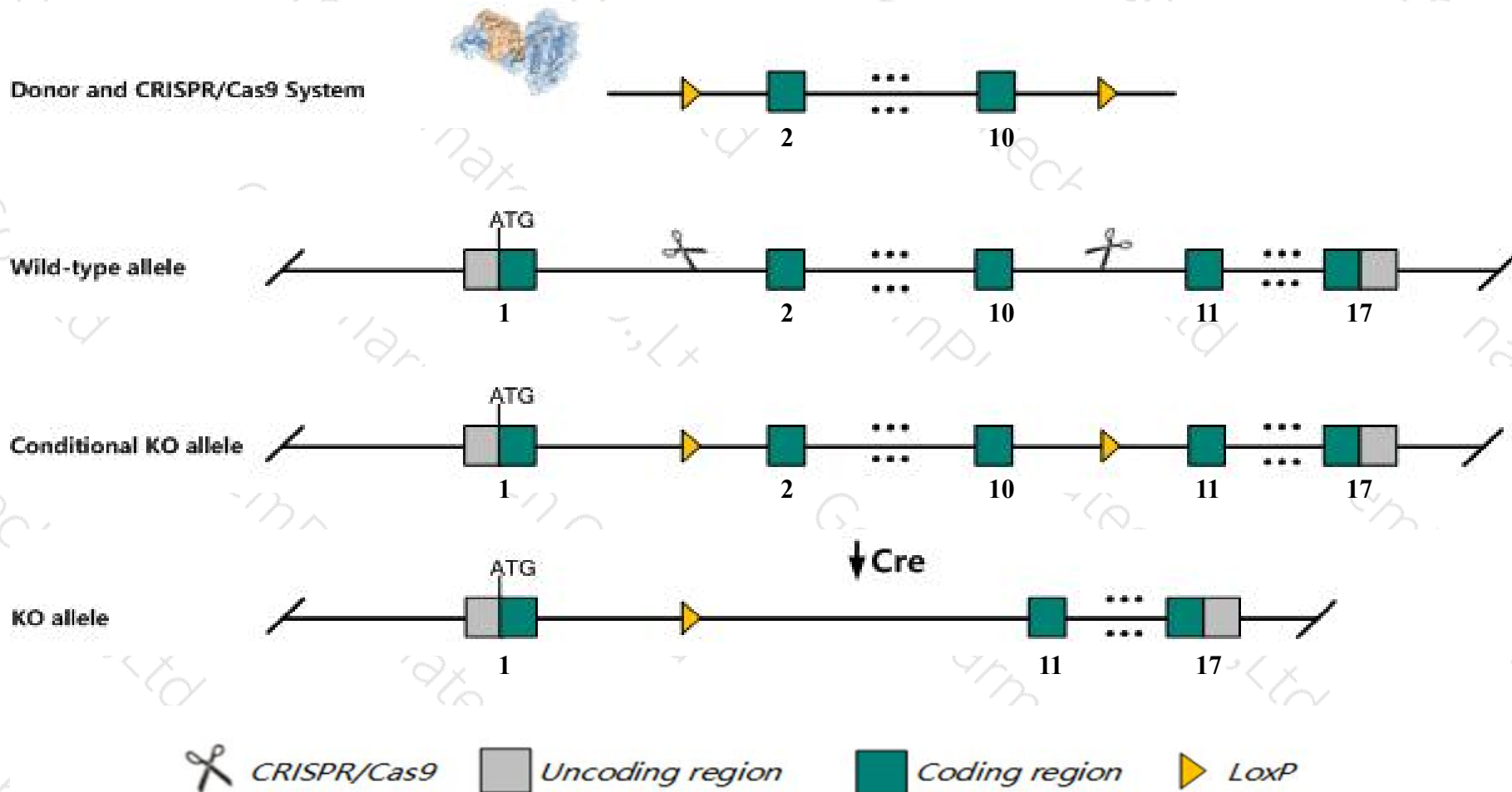
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zdhhc17* gene. The schematic diagram is as follows:



Technical routes

- The *Zdhhc17* gene has 10 transcripts. According to the structure of *Zdhhc17* gene, exon2-exon10 of *Zdhhc17-201* (ENSMUST00000041723.14) transcript is recommended as the knockout region. The region contains 1048bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zdhhc17* 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 exhibit reminiscent of Huntington disease (decreased body weight, impaired coordination, hyperactivity, increased rearing, decreased prepulse inhibition, increased stereotypic behavior, reduced striatum, and decreased brain weight).
- The *Zdhhc17* gene is located on the Chr10. 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)

Zdhhc17 zinc finger, DHHC domain containing 17 [Mus musculus (house mouse)]

Gene ID: 320150, updated on 31-Jan-2019

Summary



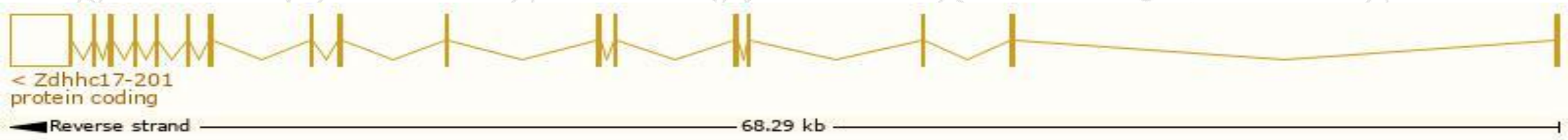
Official Symbol	Zdhhc17 provided by MGI
Official Full Name	zinc finger, DHHC domain containing 17 provided by MGI
Primary source	MGI:MGI:2445110
See related	Ensembl:ENSMUSG000000035798
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A230053P19Rik, BB187739, D130071N24Rik, DHHC-17, Hip14
Expression	Broad expression in cerebellum adult (RPKM 24.0), CNS E18 (RPKM 21.9) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

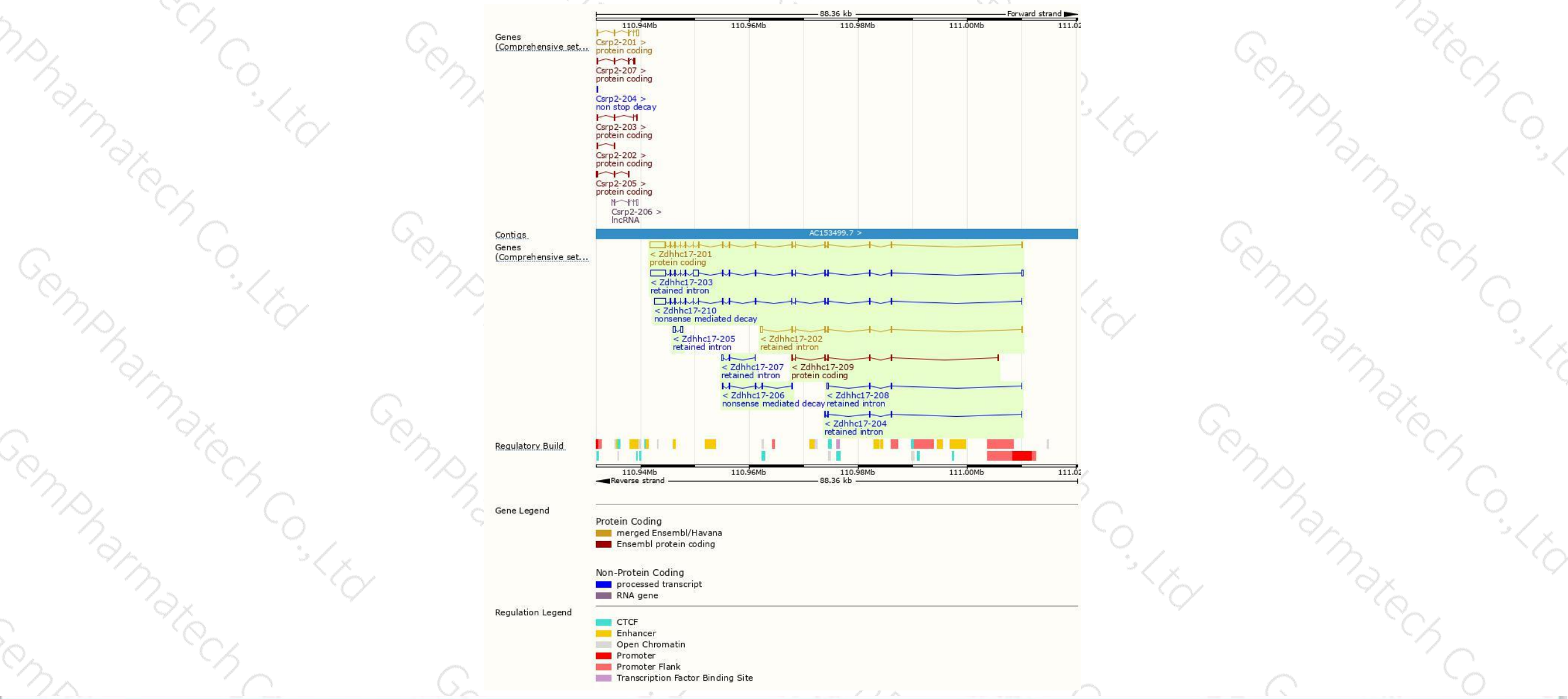
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zdhhc17-201	ENSMUST00000041723.14	4548	632aa	Protein coding	CCDS56748	Q80TN5	TSL:1 GENCODE basic APPRIS P1
Zdhhc17-209	ENSMUST00000219307.1	740	82aa	Protein coding	-	A0A1W2P6S3	CDS 3' incomplete TSL:3
Zdhhc17-210	ENSMUST00000220247.1	3635	192aa	Nonsense mediated decay	-	A0A1W2P7M2	CDS 5' incomplete TSL:1
Zdhhc17-206	ENSMUST00000218895.1	643	64aa	Nonsense mediated decay	-	A0A1W2P760	CDS 5' incomplete TSL:3
Zdhhc17-203	ENSMUST00000217698.1	5497	No protein	Retained intron	-	-	TSL:2
Zdhhc17-202	ENSMUST00000099285.3	1146	No protein	Retained intron	-	-	TSL:2
Zdhhc17-205	ENSMUST00000217982.1	714	No protein	Retained intron	-	-	TSL:3
Zdhhc17-208	ENSMUST00000218981.1	564	No protein	Retained intron	-	-	TSL:2
Zdhhc17-204	ENSMUST00000217793.1	557	No protein	Retained intron	-	-	TSL:2
Zdhhc17-207	ENSMUST00000218972.1	555	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Zdhhc17-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP00000043...

Transmembrane heli...

Low complexity (Seq)

Superfamily

SMART

Prints

Pfam

PROSITE profiles

PANTHER

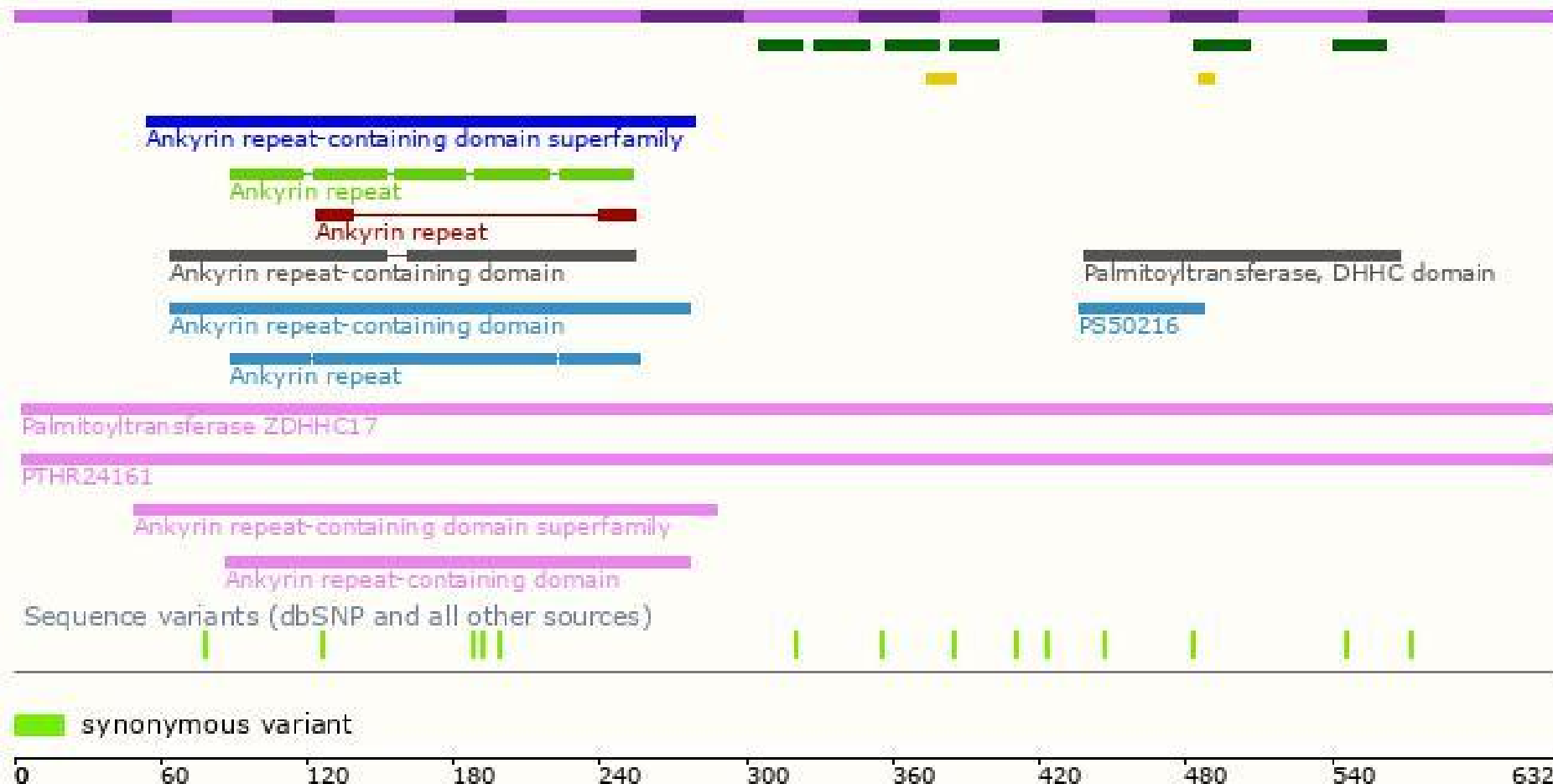
Gene3D

CDD

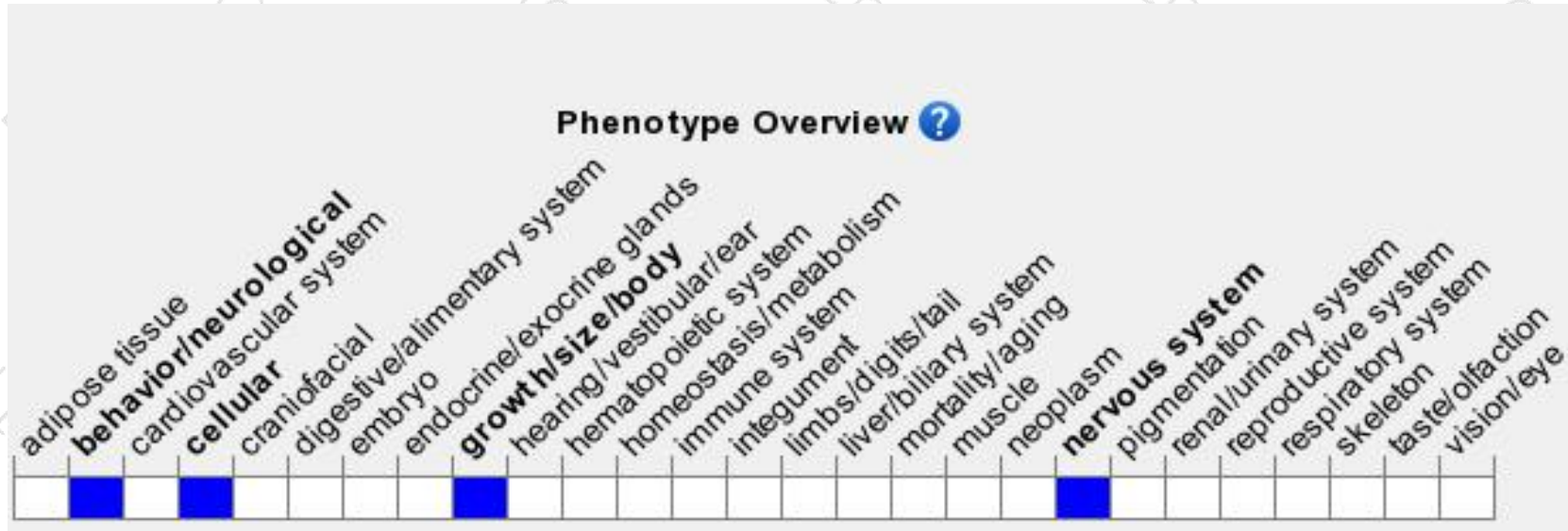
All sequence SNPs/i...

Variant Legend

Scale bar



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 exhibit reminiscent of Huntington disease (decreased body weight, impaired coordination, hyperactivity, increased rearing, decreased prepulse inhibition, increased stereotypic behavior, reduced striatum, and decreased brain weight).

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

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