Hhatl Cas9-KO *Strategy*

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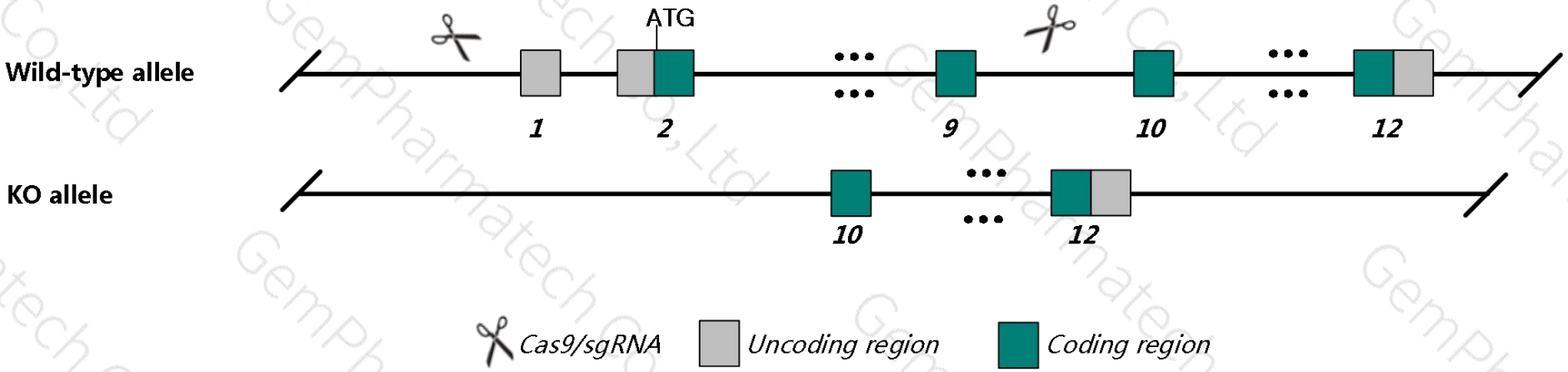
Project Overview

Project Name	***Hhatl***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

- The *Hhatl* gene has 6 transcripts.According to the structure of *Hhatl* gene, exon1-9 of *Hhatl*-201 (ENSMUST00000035110.10) transcript is recommended as the knockout region.The region contains start codon ATG of coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Hhatl* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA 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.

Notice

- The *Hhatl* gene is located on the Chr9. 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）

集萃药康 GemPharmatech

Hhatl hedgehog acyltransferase-like [*Mus musculus* (house mouse)]

Gene ID: 74770, updated on 12-Aug-2019

Summary

Official Symbol	Hhatl provided by MGI
Official Full Name	hedgehog acyltransferase-like provided by MGI
Primary source	MGI:MGI:1922020
See related	Ensembl:ENSMUSG00000032523
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	Gup1; Mg56; 1110011D13Rik
Expression	Biased expression in heart adult (RPKM 20.6), mammary gland adult (RPKM 4.7) and 6 other tissues See more
Orthologs	human all

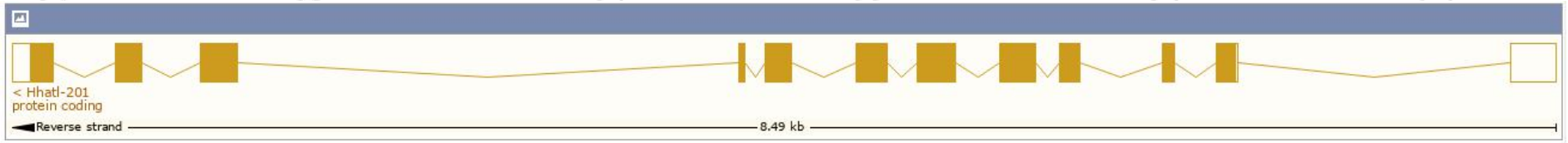
Transcript information（Ensembl）

The gene has 6 transcripts, and all transcripts are shown below:

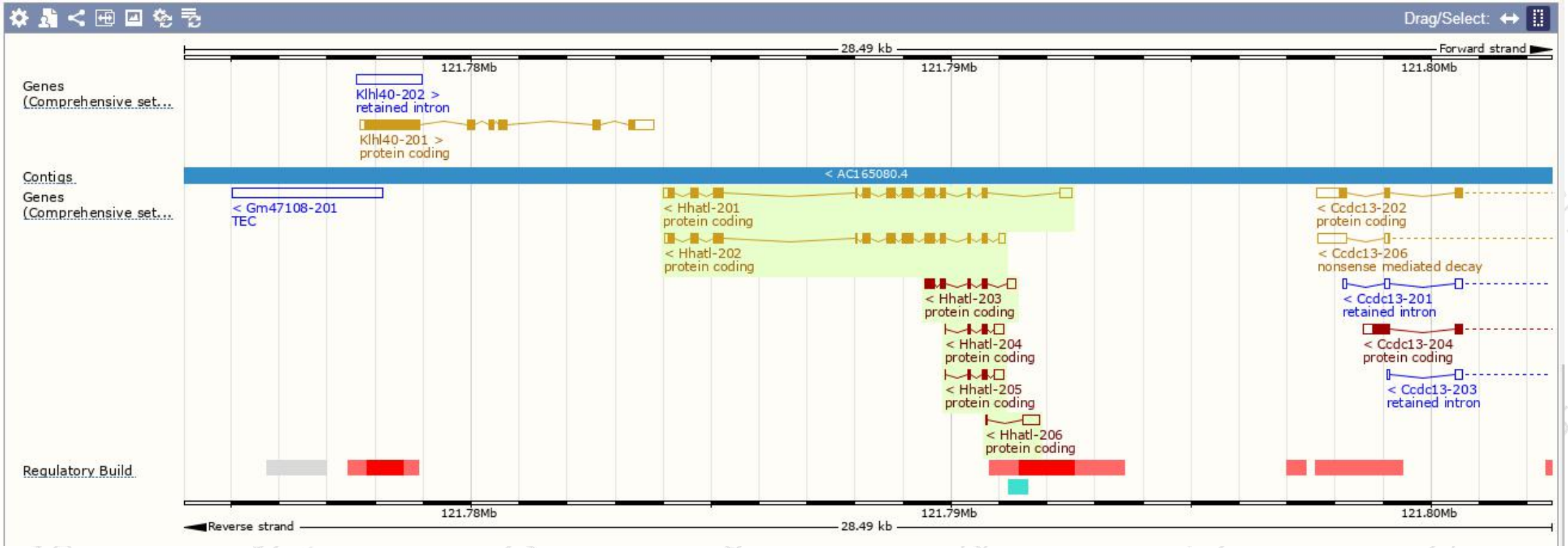
Show/hide columns (1 hidden) Filter

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hhatl-201	ENSMUST00000035110.10	1870	503aa	Protein coding	CCDS23638	Q9D1G3	TSL:1 GENCODE basic APPRIS P1
Hhatl-202	ENSMUST00000163981.2	1744	503aa	Protein coding	CCDS23638	Q9D1G3	TSL:1 GENCODE basic APPRIS P1
Hhatl-203	ENSMUST00000214768.1	652	157aa	Protein coding	-	A0A1L1SRJ1	CDS 3' incomplete TSL:3
Hhatl-206	ENSMUST00000217652.1	409	11aa	Protein coding	-	A0A1L1SUF7	CDS 3' incomplete TSL:3
Hhatl-205	ENSMUST00000215910.1	398	64aa	Protein coding	-	A0A1L1SR86	CDS 3' incomplete TSL:5
Hhatl-204	ENSMUST00000215477.1	391	64aa	Protein coding	-	A0A1L1SR86	CDS 3' incomplete TSL:5

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

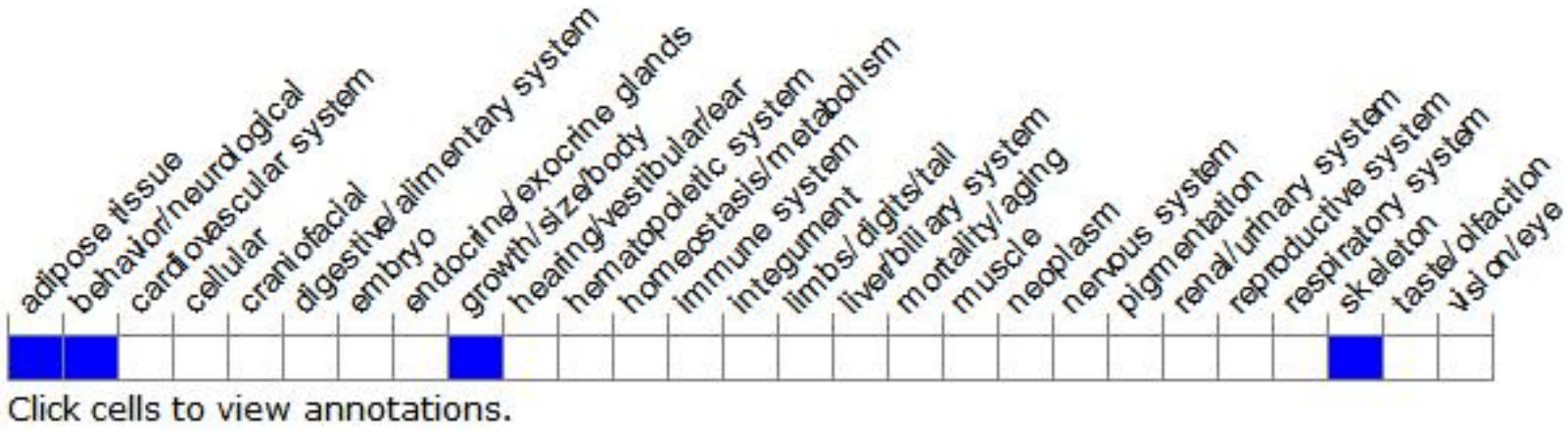


Genomic location distribution



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,Mutations in this locus affect cell-cycle regulation and apoptos is. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

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