

Liph Cas9-KO Strategy

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Project Overview

Project Name

Liph

Project type

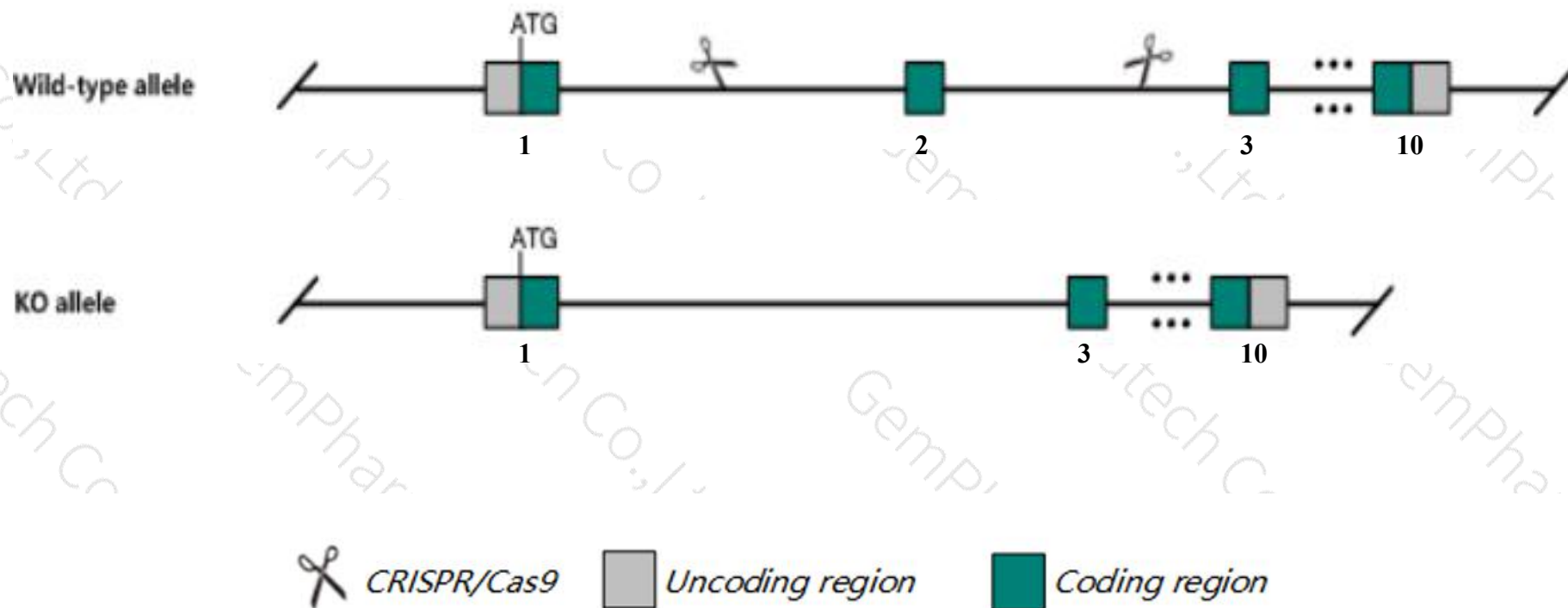
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Liph* gene has 6 transcripts. According to the structure of *Liph* gene, exon2 of *Liph*-201 (ENSMUST00000060673.7) transcript is recommended as the knockout region. The region contains 368bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Liph* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit wavy vibrissae and wavy and matted coats associated with impaired inner rooth sheath formation.
- The *Liph* gene is located on the Chr16. 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)

Liph lipase, member H [*Mus musculus* (house mouse)]

Gene ID: 239759, updated on 13-Mar-2020

Summary

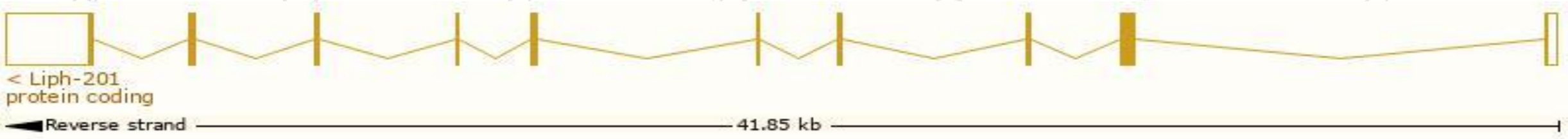
Official Symbol	Liph provided by MGI
Official Full Name	lipase, member H provided by MGI
Primary source	MGI:MGI:2388029
See related	Ensembl:ENSMUSG00000044626
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	P3; H06; Lpd1; Lpd2; Lpd1r; PLA1B; mPA-PLA1; D16Wsu119e; C130037N08Rik
Expression	Biased expression in placenta adult (RPKM 8.8), large intestine adult (RPKM 8.0) and 7 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

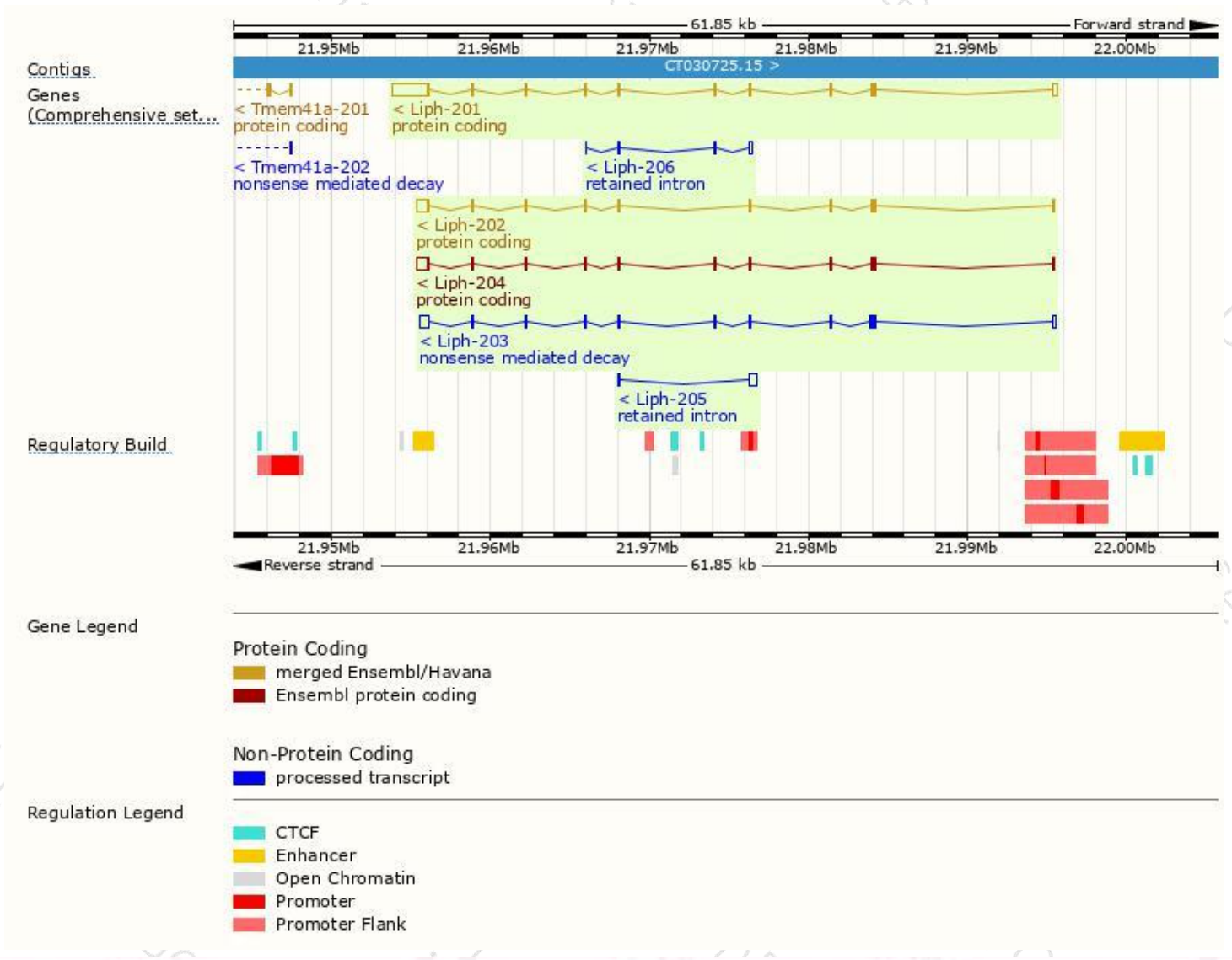
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Liph-201	ENSMUST00000060673.7	3923	451aa	Protein coding	CCDS37296	Q8CIV3	TSL:1 GENCODE basic APPRIS P2
Liph-202	ENSMUST00000074230.11	2051	421aa	Protein coding	CCDS37295	Q8CIV3	TSL:1 GENCODE basic
Liph-204	ENSMUST00000231766.1	2118	449aa	Protein coding	-	Q8CIV3	GENCODE basic APPRIS ALT1
Liph-203	ENSMUST00000231682.1	2065	146aa	Nonsense mediated decay	-	A0A338P6M6	-
Liph-205	ENSMUST00000232120.1	690	No protein	Retained intron	-	-	-
Liph-206	ENSMUST00000232673.1	535	No protein	Retained intron	-	-	-

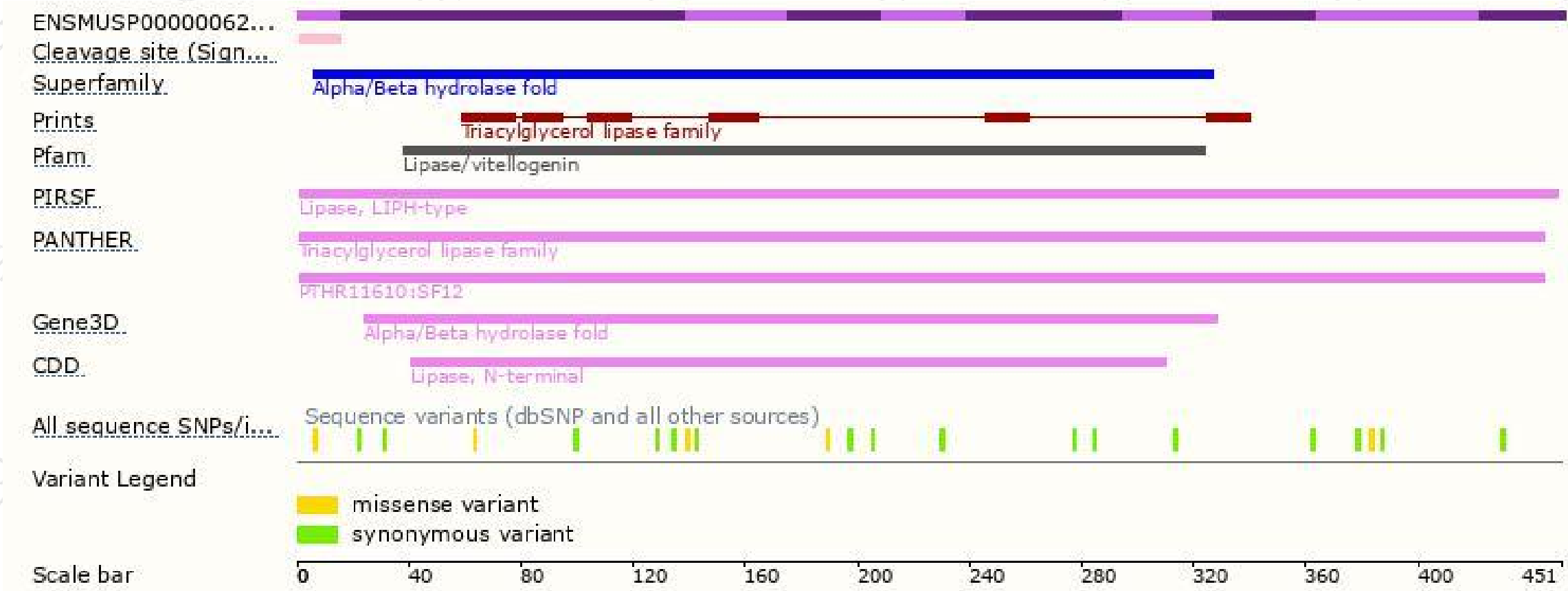
The strategy is based on the design of *Liph-201* transcript,The transcription is shown below



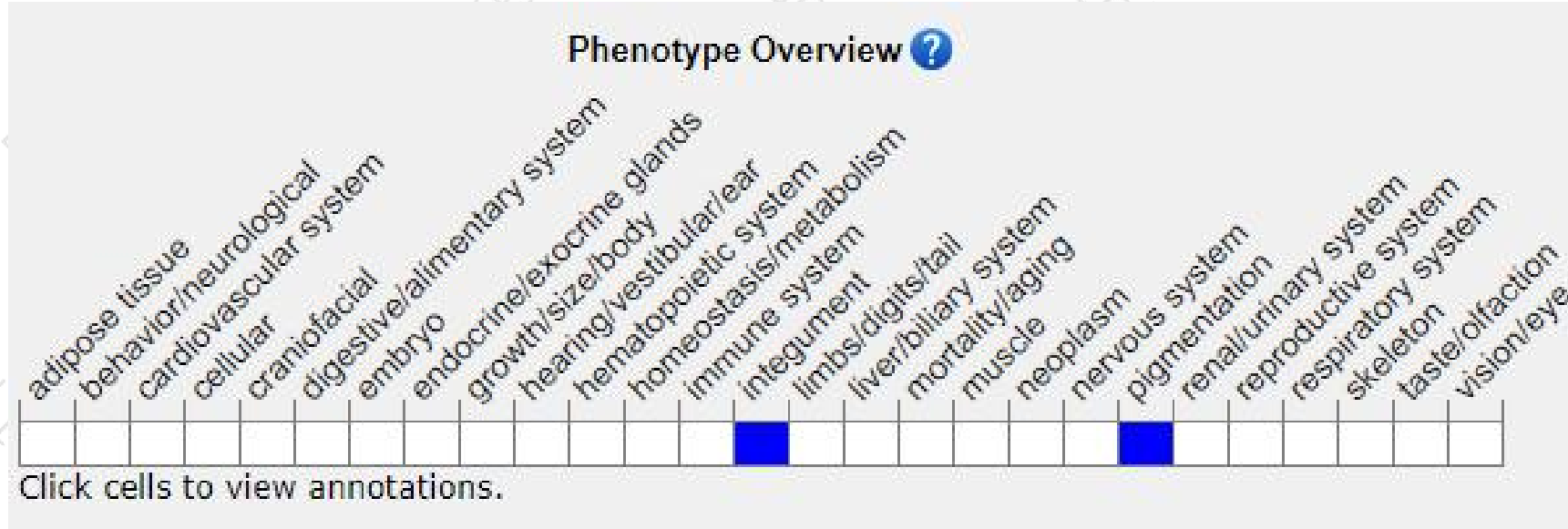
Genomic location distribution



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, Mice homozygous for a knock-out allele exhibit wavy vibrissae and wavy and matted coats associated with impaired inner rooth sheath formation.

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

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