

Ldlr-p.D622N Mouse Model Strategy

-CRISPR/Cas9 technology

Designer Ruirui Zhang
Reviewer Xiaojing Li
Date 2021-9-9



集萃药康
GemPharmatech

Project Overview

Project Name

Ldlr-p.D622N

Project Type

Cas9-KI(PM)

Background

C57BL/6JGpt

Project Cycle

5-8 months

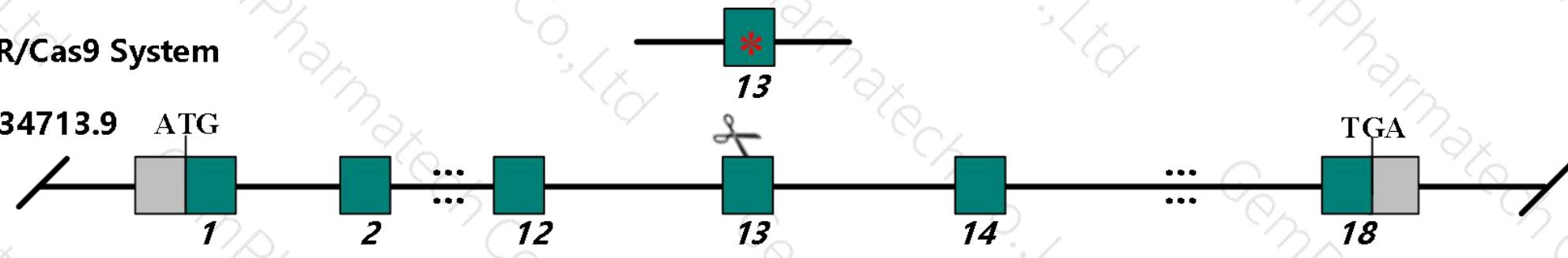
Strategy

This model uses CRISPR/Cas9 technology to edit the *Ldlr* gene and the schematic diagram is as follow:

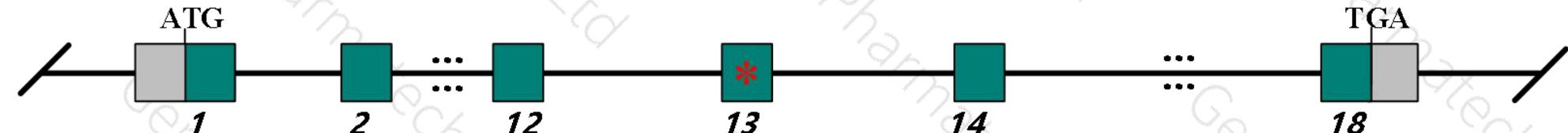
Donor and CRISPR/Cas9 System

ENSMUST00000034713.9

Wild-type allele



Targeted allele



CRISPR/Cas9 System



Uncoding region



Coding region

* Mutant sites: *Ldlr-p.D622N*

Technical Description

- According to the data of Ensembl, mouse *Ldlr* gene has 7 transcripts.
- The mouse model will introduce *p.D622N* point mutation in exon13 of *Ldlr*-201 (ENSMUST00000034713.9), the 622th amino acid of *Ldlr* is mutated from D(Asp) to N(Asn).
- *Ldlr*-201 has 18 exons, the translation start codon ATG is located in exon1, and the translation stop codon TGA is located in exon18, which encodes 862 amino acids.
- In this project, *Ldlr* gene will be modified by CRISPR/Cas9 technology. The brief process is as follows: the donor vector and gRNA were constructed in vitro, Cas9, donor and gRNA were microinjected into the fertilized eggs of C57BL/6JGpt mice, and obtained positive F0 generation mice. The F0 positive mice were mated with C57BL/6JGpt mice, the pups will be genotyped by PCR, followed by sequence analysis.

Notice

- According to the data of MGI, homozygous targeted mutants exhibit 2X higher total plasma cholesterol and 7-9X higher IDL and LDL levels on a normal diet compared to controls. On a high cholesterol diet, mutant effects dramatically increase and mice develop xanthomatosis and atherosclerosis.
- In addition to the target mutation of p.D622N, it may be necessary to introduce 1~2 amino acid synonymous mutations on exon13.
- Mouse *Ldlr* gene is located on Chr9. Please take the loci in consideration when breeding this mutation mice with other gene modified strains, if the other gene is also on Chr9, it may be extremely hard to get double gene positive homozygotes.
- The scheme is designed according to the genetic information in the existing database. Due to the complex process of gene transcription and translation, it cannot be predicted completely at the present technology level.

Sequence homology Analysis



Human *LDLR* gene has 5 protein coding transcripts

Human LDLR Transcripts	Amino Acids
NM_000527.5 → NP_000518.1	860aa
NM_001195798.2 → NP_001182727.1	858aa
NM_001195799.2 → NP_001182728.1	819aa
NM_001195800.2 → NP_001182729.1	692aa
NM_001195803.2 → NP_001182732.1	682aa

Mouse *Ldlr* gene has 3 protein coding transcript.

Mouse Ldlr Transcripts	Amino Acids
NM_001252658.1 → NP_001239587.1	810aa
NM_001252659.1 → NP_001239588.1	861aa
NM_010700.3 → NP_034830.2	862aa

Based on the data of NCBI, there are 5 transcripts of human *LDLR* gene, which encode amino acids of different lengths, and the mouse *Ldlr* gene has 3 transcripts. The homology of human NP 000518.1 and mouse NP 034830.2 is about 78.0%.

Mutation Site

Before mutation

	D	K	V	Y	W	T	D	V	I	N	E	A	I	F	S	A	N	R	L	T	G					
AACACGCTCG	GTCCTCTTCC	GTACATACCA	CCTGTGTAGG	ACAAAGTGT	TTGGACA	GAT	GTCATAAACG	AAGCCATT	TTT	CAGTGCCAAT	CGACTCACGG															
TTGTGCGAGC	CAGGAGAAGG	CATGTATGGT	GGACACATCC	TGTTTCACAT	AACCTGT	CTA	CAGTATTG	GC	TTCGGTAAAAA	GTCACGGTTA	GCTGAGTGCC															
?G	S	D	V	N	L	V	A	E	N	L	L	S	P	E	D	I	V	L	F	H	K	V	T	Q	P	R
GTTCAGATGT	GAATTGGTG	GCTGAAAACC	TCTTGTCCCC	GGAGGACATT	GTCCTGTTCC	ACAAGGTCAC	ACAGCCTAGA	GGTAAGCTCG	GCCCTGTCCC																	
CAAAGTCTACA	CTTAAACCAC	CGACTTTGG	AGAACAGGGG	CCTCCTGTAA	CAGGACAAGG	TGTTCCAGTG	TGTCGGATCT	CCATTGAGC	CGGGACAGGG																	

After mutation

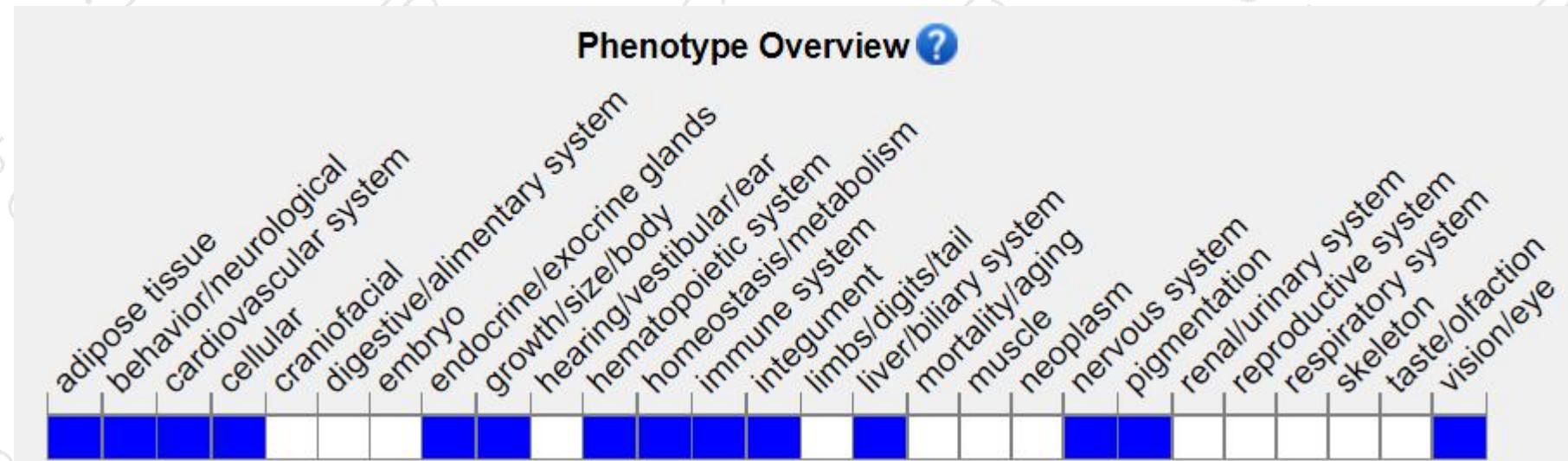
	D	K	V	Y	W	T	N	V	I	N	E	A	I	F	S	A	N	R	L	T	G					
AACACGCTCG	GTCCTCTTCC	GTACATACCA	CCTGTGTAGG	ACAAAGTGT	TTGGACA	AAT	GTCATAAACG	AAGCCATT	TTT	CAGTGCCAAT	CGACTCACGG															
TTGTGCGAGC	CAGGAGAAGG	CATGTATGGT	GGACACATCC	TGTTTCACAT	AACCTGT	TTA	CAGTATTG	GC	TTCGGTAAAAA	GTCACGGTTA	GCTGAGTGCC															
?G	S	D	V	N	L	V	A	E	N	L	L	S	P	E	D	I	V	L	F	H	K	V	T	Q	P	R
GTTCAGATGT	GAATTGGTG	GCTGAAAACC	TCTTGTCCCC	GGAGGACATT	GTCCTGTTCC	ACAAGGTCAC	ACAGCCTAGA	GGTAAGCTCG	GCCCTGTCCC																	
CAAAGTCTACA	CTTAAACCAC	CGACTTTGG	AGAACAGGGG	CCTCCTGTAA	CAGGACAAGG	TGTTCCAGTG	TGTCGGATCT	CCATTGAGC	CGGGACAGGG																	

The yellow region is exon13 of *Ldlr-201*, and the red region represents the p.D622N mutation site.

Mouse phenotype description(MGI)



<http://www.informatics.jax.org/marker/MGI:96765>



Homozygous targeted mutants exhibit 2X higher total plasma cholesterol and 7-9X higher IDL and LDL levels on a normal diet compared to controls. On a high cholesterol diet, mutant effects dramatically increase and mice develop xanthomatosis and atherosclerosis.

Gene name and location (NCBI)

Ldlr low density lipoprotein receptor [*Mus musculus* (house mouse)]

Gene ID: 16835, updated on 6-Sep-2021

 Download Datasets

Summary



Official Symbol Ldlr provided by [MGI](#)

Official Full Name low density lipoprotein receptor provided by [MGI](#)

Primary source [MGI](#):[MGI](#):96765

See related [Ensembl](#):[ENSMUSG00000032193](#)

Gene type protein coding

RefSeq status VALIDATED

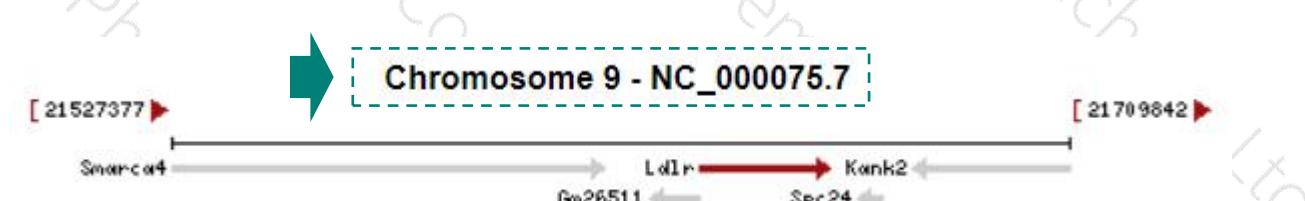
Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as Hlb301

Expression Ubiquitous expression in colon adult (RPKM 56.3), adrenal adult (RPKM 52.3) and 27 other tissues [See more](#)

Orthologs [human](#) [all](#)

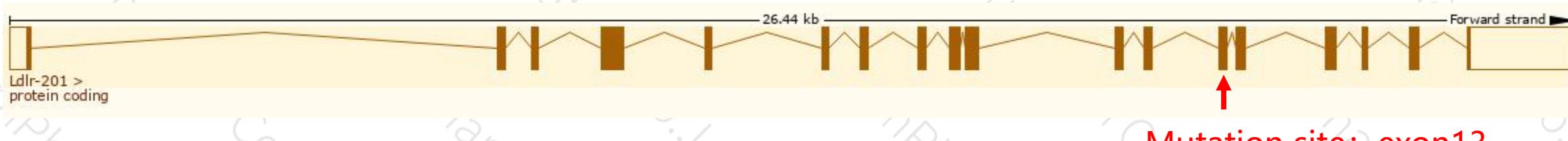


Transcript information (Ensembl)

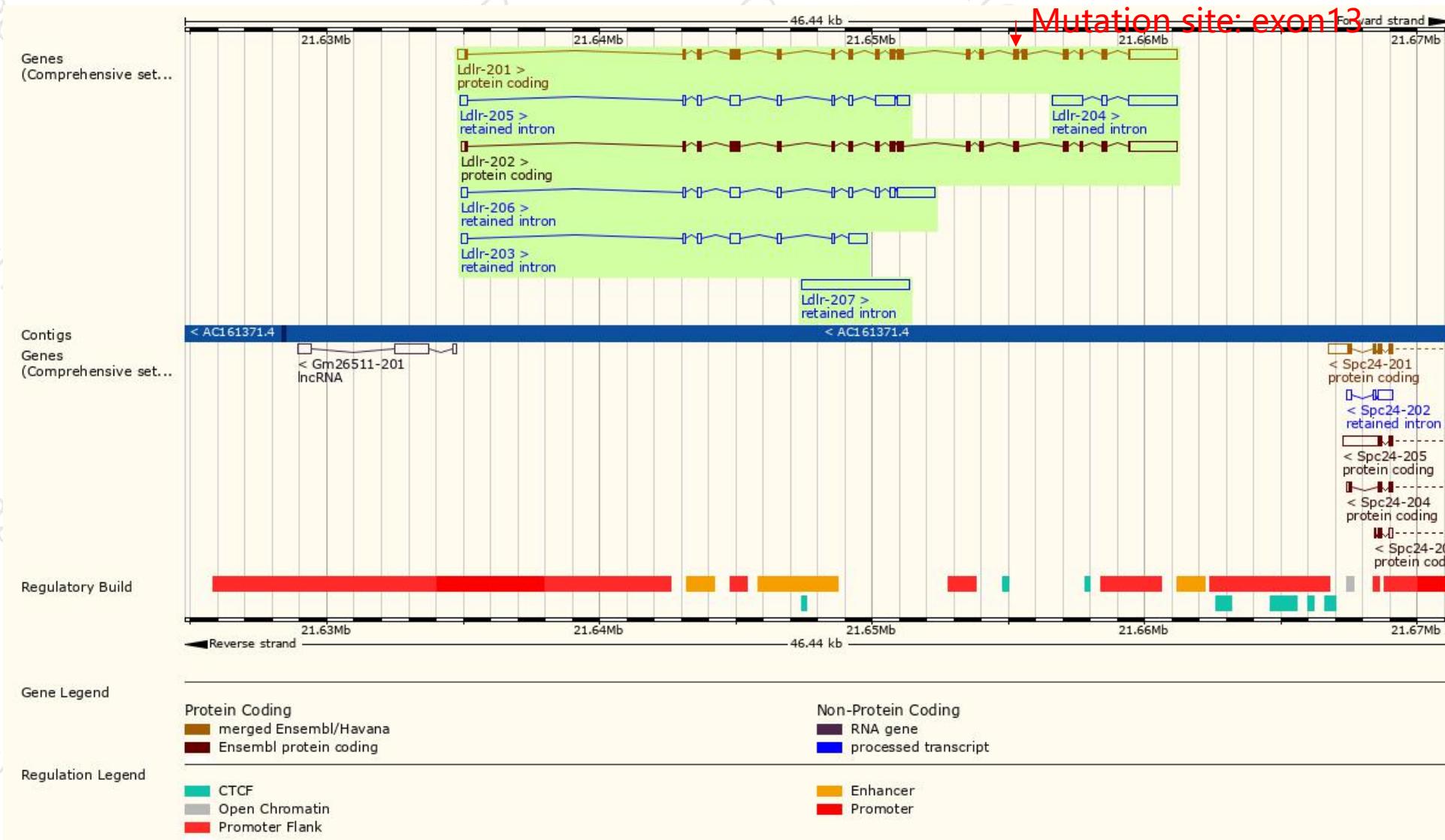
The gene has 7 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt Match	Flags
Ldlr-202	ENSMUST00000213114.2	4318	810aa	Protein coding	-	A0A1L1SRE8	GENCODE basic TSL:1
Ldlr-201	ENSMUST0000034713.9	4627	862aa	Protein coding	CCDS22910	P35951	GENCODE basic APPRIS P1 TSL:1
Ldlr-207	ENSMUST00000217613.2	3980	No protein	Retained intron	-	-	TSL:NA
Ldlr-204	ENSMUST00000214549.2	3049	No protein	Retained intron	-	-	TSL:1
Ldlr-206	ENSMUST00000217111.2	2854	No protein	Retained intron	-	-	TSL:1
Ldlr-205	ENSMUST00000215917.2	2383	No protein	Retained intron	-	-	TSL:1
Ldlr-203	ENSMUST00000214359.2	1739	No protein	Retained intron	-	-	TSL:1

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

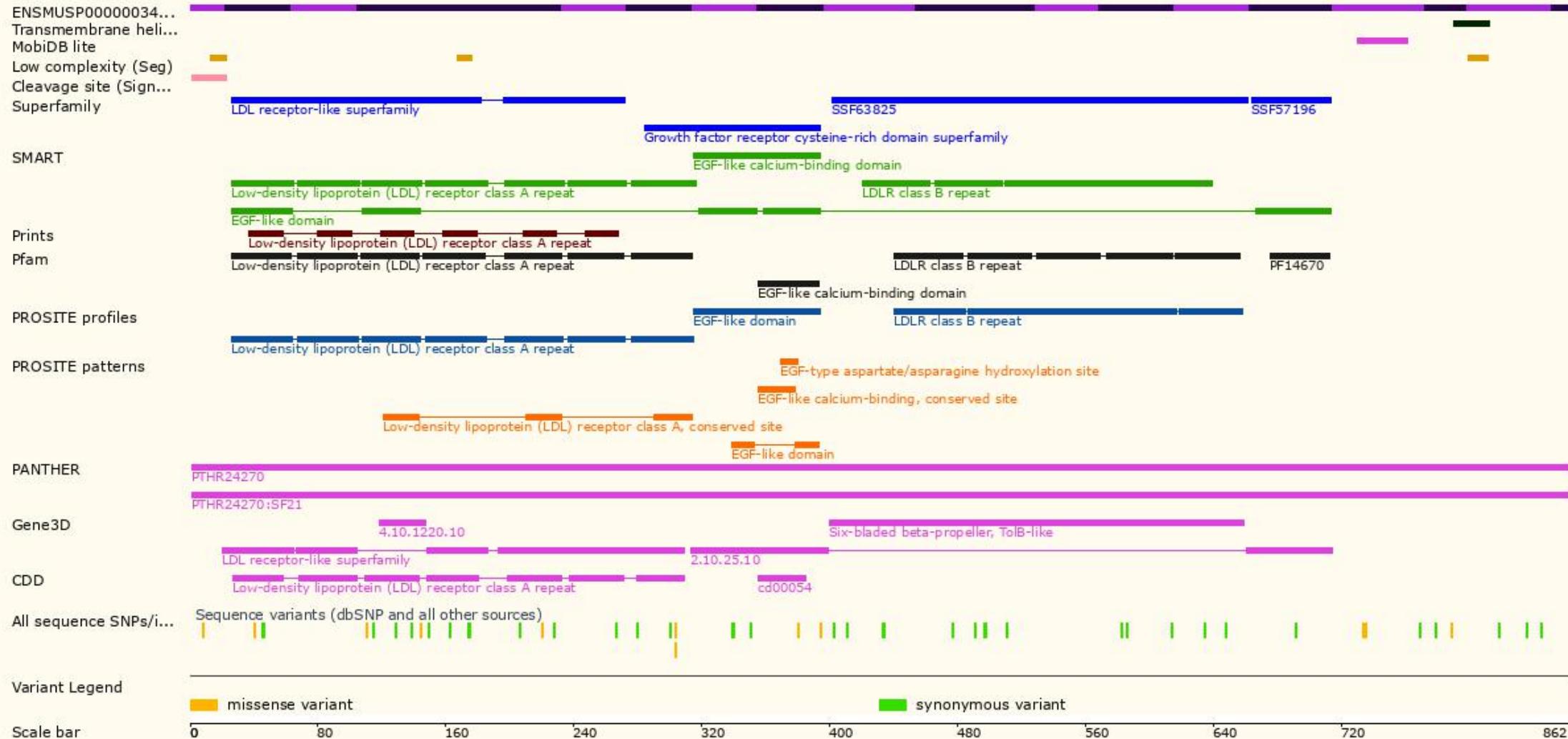


Genomic location distribution



Protein domain

Protein domains for ENSMUSP00000034713.8



If you have any questions, please feel free to contact us.
Tel: 025-5864 1534



集萃药康生物科技
GemPharmatech Co.,Ltd



服务号



订阅号