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Adamtsl3 Cas9-KO Strategy

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Reviewer: Xingkai Xiao

Design Date: 2023-5-29

Overview

Target Gene Name

- *Adamtsl3*

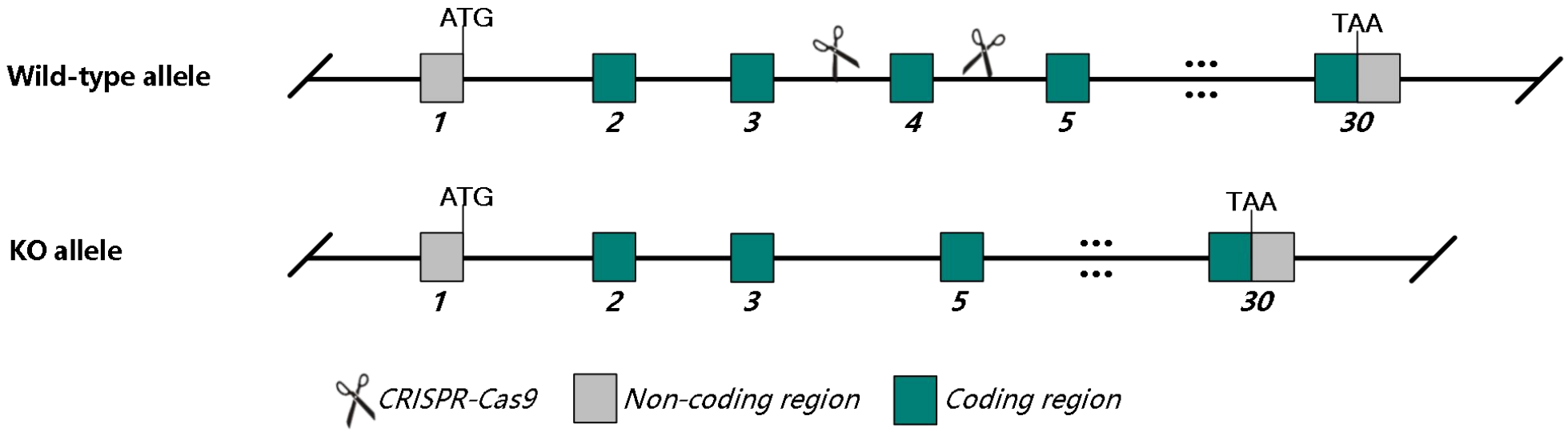
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Adamtsl3* gene.

Technical Information

- The *Adamtsl3* gene has 5 transcripts. According to the structure of *Adamtsl3* gene, exon 4 of *Adamtsl3*-203 (ENSMUST00000173287.8) is recommended as the knockout region. The region contains 128 bp of coding sequence. Knockout the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Adamtsl3* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information

Adamtsl3 ADAMTS-like 3 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 269959, updated on 12-Apr-2023

Summary

Official Symbol	Adamtsl3 provided by MGI
Official Full Name	ADAMTS-like 3 provided by MGI
Primary source	MGI:MGI:3028499
See related	Ensembl:ENSMUSG00000070469 AllianceGenome:MGI:3028499
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	mKIAA1233; C130057K09; 9230119C12Rik
Summary	Predicted to be involved in extracellular matrix organization. Predicted to be located in intracellular membrane-bounded organelle. Predicted to be active in extracellular matrix. Orthologous to human ADAMTSL3 (ADAMTS like 3). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in bladder adult (RPKM 4.3), limb E14.5 (RPKM 2.6) and 13 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**

Try the new Transcript table

Genomic context

Location: 7; 7 D3

See Adamtsl3 in Genome Data Viewer

Exon count: 31

https://www.ncbi.nlm.nih.gov/gene/269959

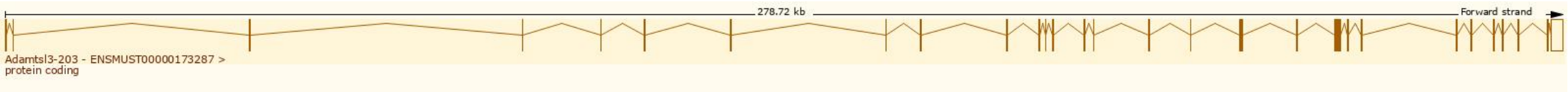
Transcript Information

The gene has 5 transcripts, all transcripts are shown below:

Show/hide columns (1 hidden) Filter

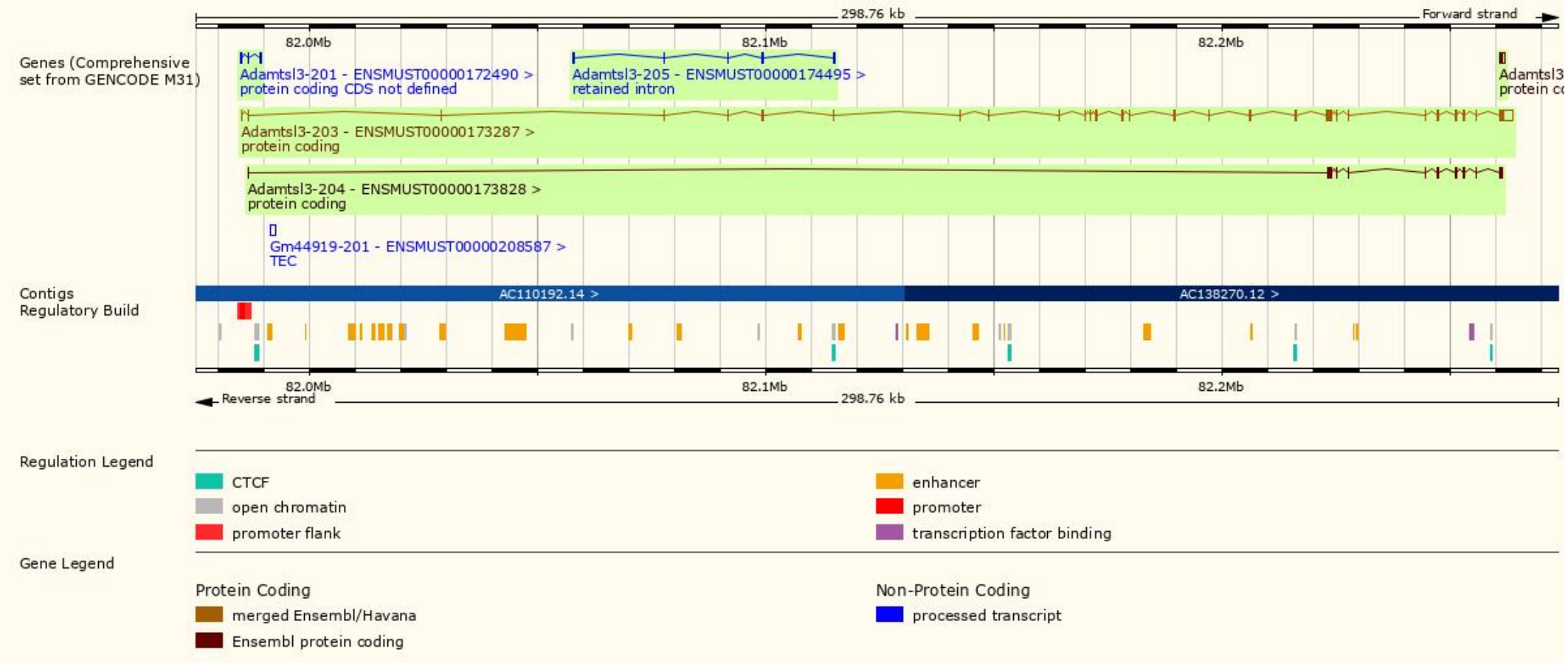
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000173287.8	Adamtsl3-203	7249	1706aa	Protein coding	CCDS57559	G3UXC7	Ensembl Canonical GENCODE basic APPRIS P1 TSL:5
ENSMUST00000173828.3	Adamtsl3-204	2292	763aa	Protein coding		G3UWL5	GENCODE basic TSL:5
ENSMUST00000172784.2	Adamtsl3-202	497	50aa	Protein coding		G3UYN1	TSL:2 CDS 5' incomplete
ENSMUST00000172490.2	Adamtsl3-201	440	No protein	Protein coding CDS not defined		-	TSL:2
ENSMUST00000174495.2	Adamtsl3-205	845	No protein	Retained intron		-	TSL:1

The strategy is based on the design of *Adamtsl3*-203 transcript, the transcription is shown below:



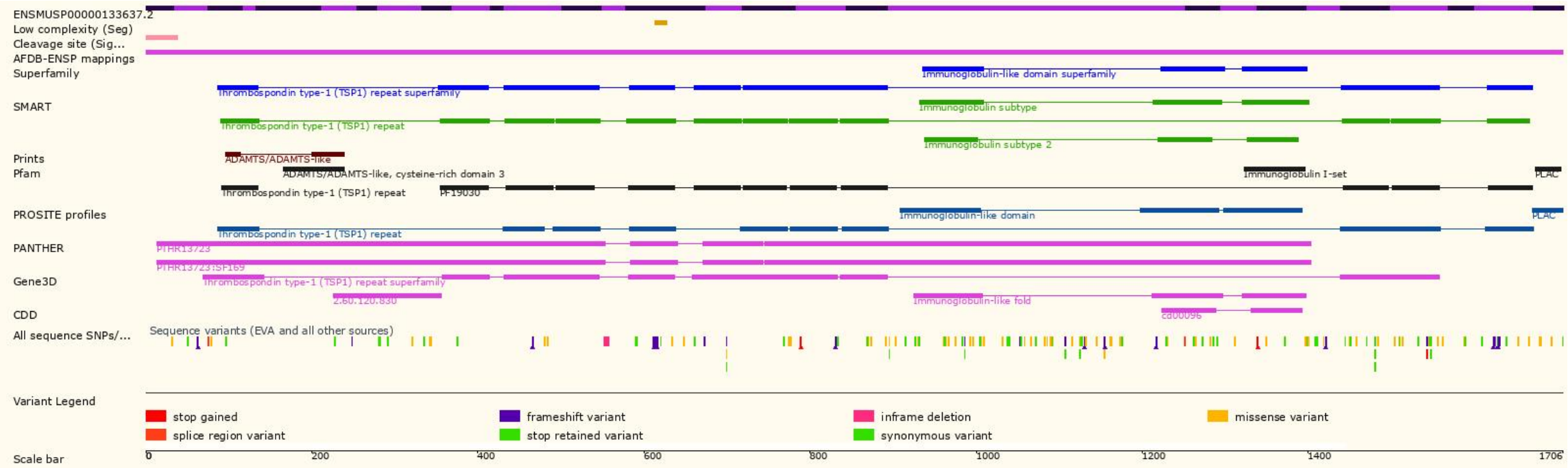
Source: http://asia.ensembl.org/

Genomic Information



Source:http://asia.ensembl.org/

Protein Information



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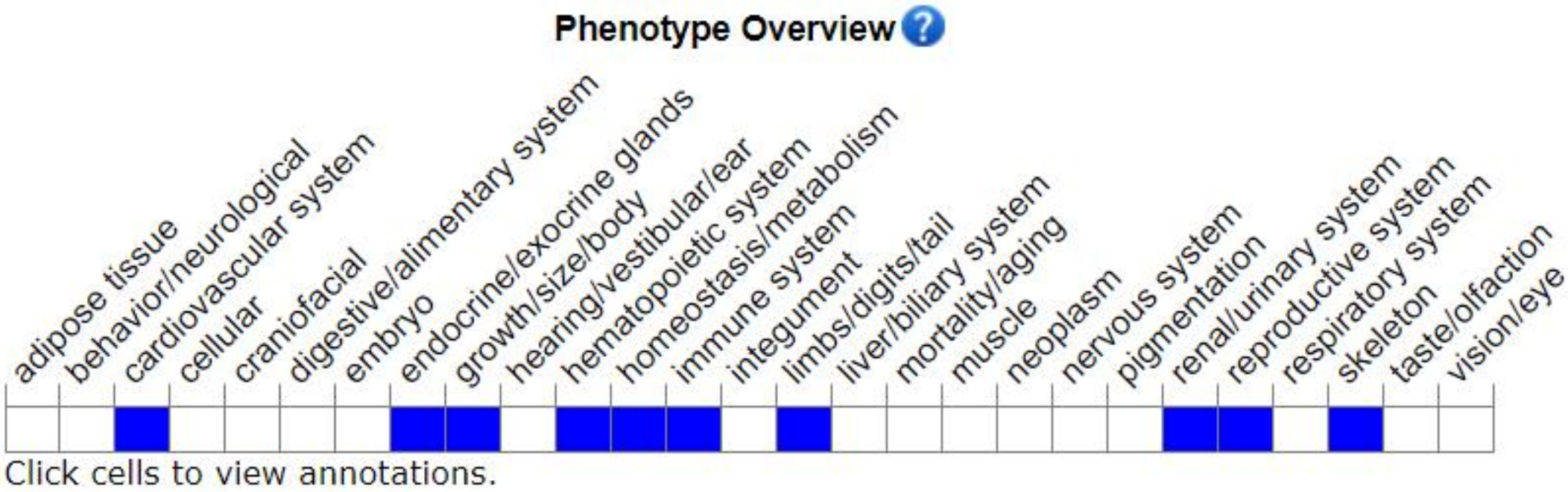
Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



Mice homozygous for a null allele exhibit increased heart weight, longer tibia bones, and exacerbated cardiac dilatation and contractile dysfunction as well as higher mortality in response to pressure overload.

Source: https://www.informatics.jax.org

Important Information

- According to the existing MGI data, mice homozygous for a null allele exhibit increased heart weight, longer tibia bones, and exacerbated cardiac dilatation and contractile dysfunction as well as higher mortality in response to pressure overload.
- This strategy may have no effect on the *Adamtsl3*-201, *Adamtsl3*-202 and *Adamtsl3*-204 transcript.
- *Adamtsl3* is located on Chr 7. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.