

Tecr Cas9-CKO Strategy

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Overview

Target Gene Name

- Tecr

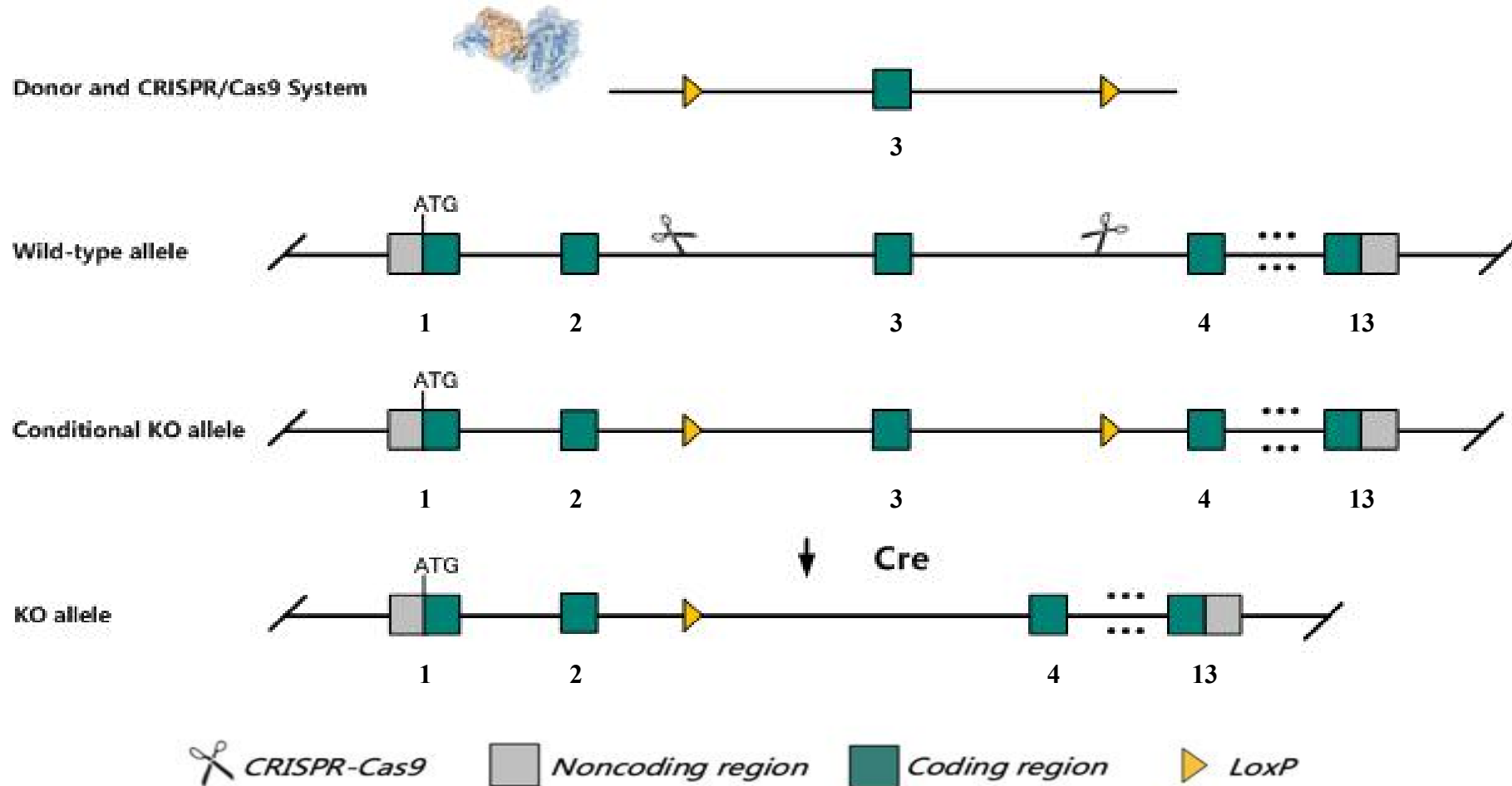
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



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

Technical Information

- The *Tecr* gene has 16 transcripts. According to the structure of *Tecr* gene, exon3 of *Tecr*-202 (ENSMUST00000163837.2) transcript is recommended as the knockout region. The region contains 214bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Tecr* 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 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.
- 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.

Gene Information

Tecr trans-2,3-enoyl-CoA reductase [Mus musculus (house mouse)]

Gene ID: 106529, updated on 29-Jan-2021

Summary

Official Symbol Tecr provided by [MGI](#)

Official Full Name trans-2,3-enoyl-CoA reductase provided by [MGI](#)

Primary source [MGI:MGI:1915408](#)

See related [Ensembl:ENSMUSG00000031708](#)

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 2410016D23Rik, A230102P12Rik, AI173355, D17Ert178, D17Ert178e, Gp, Gpsn2, SC, SC2

Expression Ubiquitous expression in adrenal adult (RPKM 340.9), mammary gland adult (RPKM 233.6) and 28 other tissues [See more](#)

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

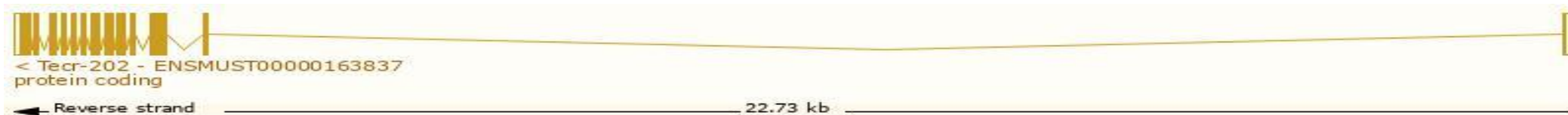
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 16 transcripts, all transcripts are shown below:

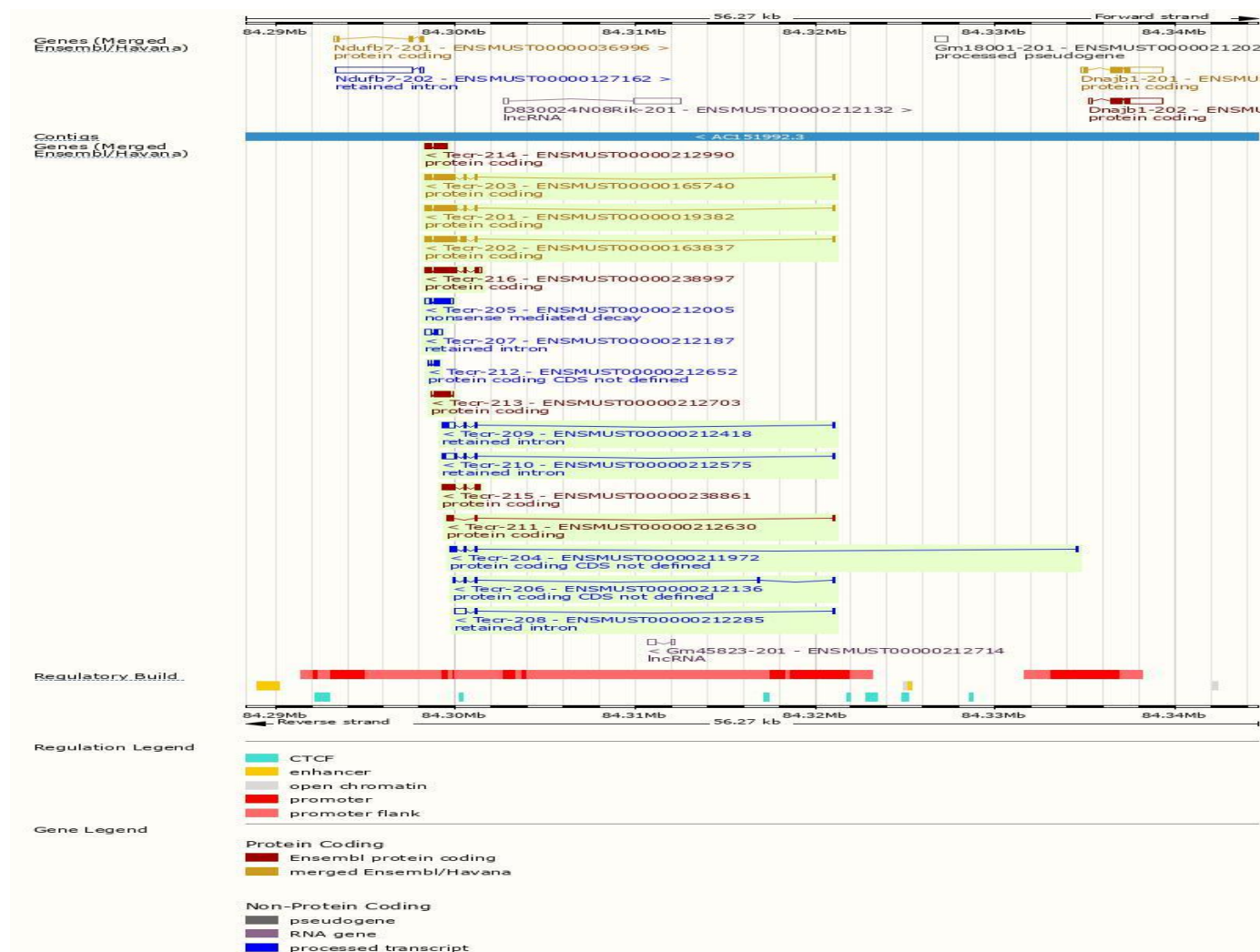
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tecr-201	ENSMUST00000019382.17	1158	308aa	Protein coding	CCDS40403		TSL:1 , GENCODE basic , APPRIS P1 ,
Tecr-203	ENSMUST00000165740.9	1120	293aa	Protein coding	CCDS52609		TSL:1 , GENCODE basic ,
Tecr-216	ENSMUST00000238997.2	1334	342aa	Protein coding	-		GENCODE basic ,
Tecr-202	ENSMUST00000163837.2	1272	362aa	Protein coding	-		TSL:1 , GENCODE basic ,
Tecr-215	ENSMUST00000238861.2	738	206aa	Protein coding	-		CDS 3' incomplete ,
Tecr-214	ENSMUST00000212990.2	648	177aa	Protein coding	-		TSL:1 , GENCODE basic ,
Tecr-213	ENSMUST00000212703.2	451	130aa	Protein coding	-		CDS 3' incomplete , TSL:1 ,
Tecr-211	ENSMUST00000212630.2	399	92aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Tecr-205	ENSMUST00000212005.2	878	107aa	Nonsense mediated decay	-		TSL:1 ,
Tecr-204	ENSMUST00000211972.2	378	No protein	Processed transcript	-		TSL:3 ,
Tecr-206	ENSMUST00000212136.2	378	No protein	Processed transcript	-		TSL:5 ,
Tecr-212	ENSMUST00000212652.2	251	No protein	Processed transcript	-		TSL:5 ,
Tecr-210	ENSMUST00000212575.2	804	No protein	Retained intron	-		TSL:3 ,
Tecr-208	ENSMUST00000212285.2	753	No protein	Retained intron	-		TSL:2 ,
Tecr-209	ENSMUST00000212418.2	734	No protein	Retained intron	-		TSL:5 ,
Tecr-207	ENSMUST00000212187.2	657	No protein	Retained intron	-		TSL:2 ,

The strategy is based on the design of *Tecr-202* transcript, the transcription is shown below:

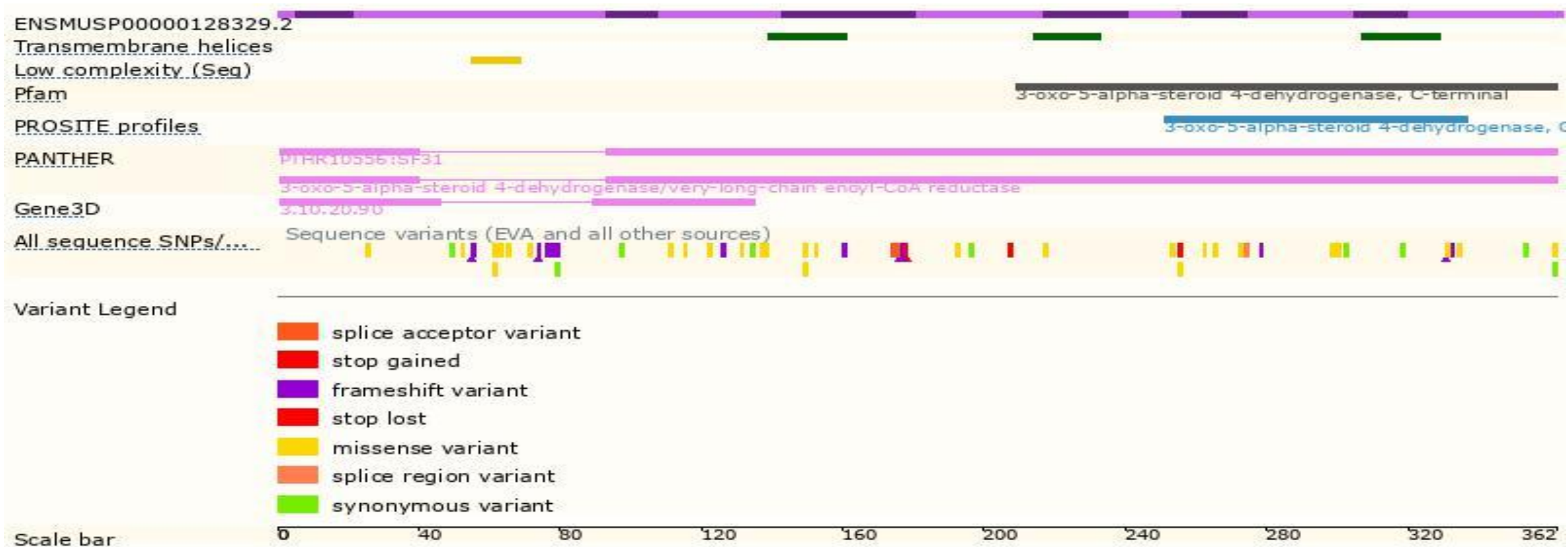


Source: <https://www.ensembl.org>

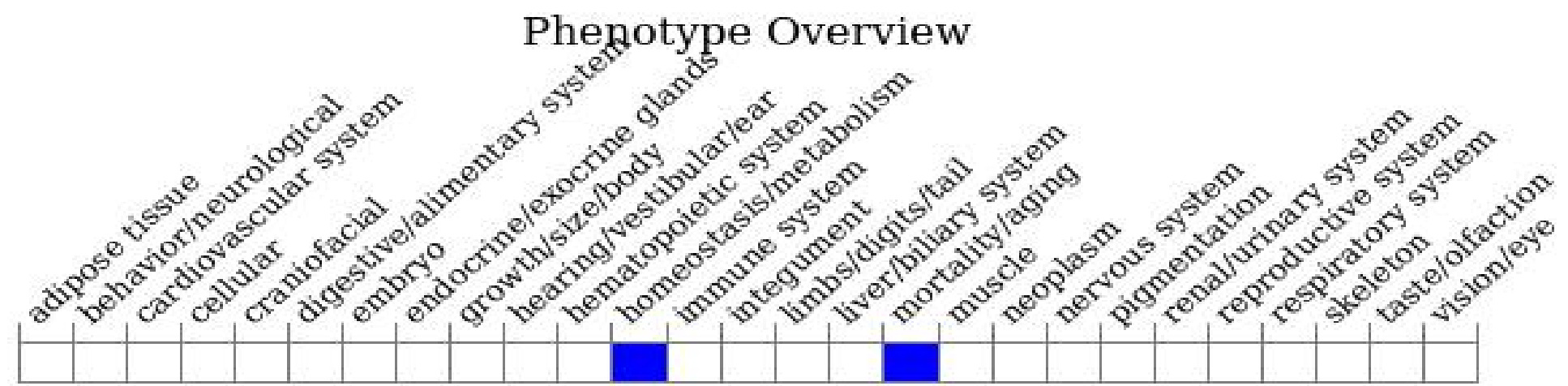
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



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Important Information

- *Tecr* is located on Chr8. 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.
- The intron2-3 is only 555bp and intron3-4 is only 253bp, loxp insertion may affect mRNA splicing.
- The KO region is about 1.9kb from *D830024N08Rik* gene. Knockout the region may affect the function of *D830024N08Rik* gene.
- Transcript *Tecr-213,214,211* may not be affected.
- 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 the existing technology level.