

Krt15 Cas9-KO Strategy

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Design Date: 2020/2/11

Project Overview



Project Name

Krt15

Project type

Cas9-KO

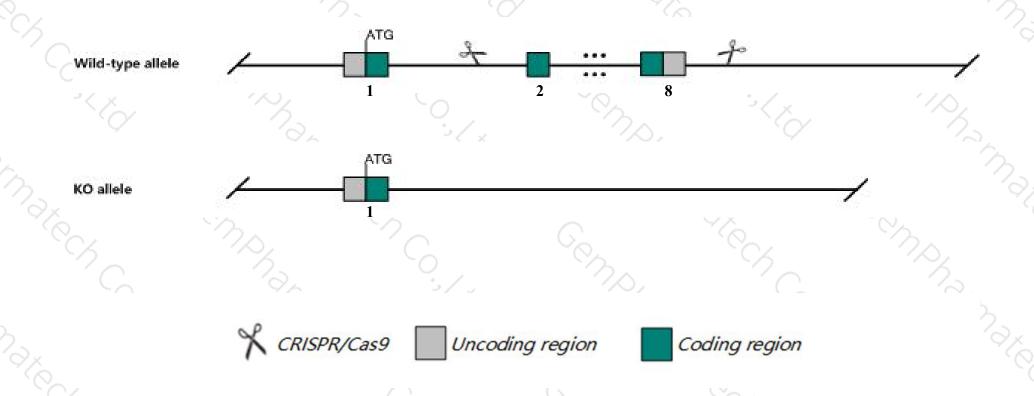
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Krt15 gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Krt15* gene has 2 transcripts. According to the structure of *Krt15* gene, exon2-exon8 of *Krt15-201* (ENSMUST00000107411.2) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify Krt15 gene. The brief process is as follows: CRISPR/Cas9 system we

Notice



- > According to the existing MGI data, Mice homozygous for a knock-out allele exhibit impaired esophageal epithelial regeneration with thicker epithelia due to enhanced basal cell proliferation.
- The *Krt15* gene is located on the Chr11. 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)



Krt15 keratin 15 [Mus musculus (house mouse)]

Gene ID: 16665, updated on 5-Jan-2020

Summary

☆ ?

Official Symbol Krt15 provided by MGI
Official Full Name keratin 15 provided by MGI

Primary source MGI:MGI:96689

See related Ensembl: ENSMUSG00000054146

Gene type protein coding
RefSeq status VALIDATED
Organism <u>Mus musculus</u>

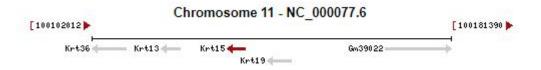
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;

Muroidea; Muridae; Murinae; Mus; Mus

Also known as K15; Krt1-15; Al528832

Expression Biased expression in bladder adult (RPKM 231.5), limb E14.5 (RPKM 52.7) and 1 other tissue See more

Orthologs human all



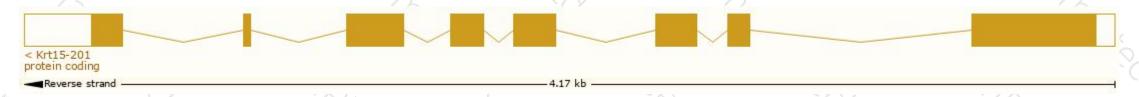
Transcript information (Ensembl)



The gene has 2 transcripts, all transcripts are shown below:

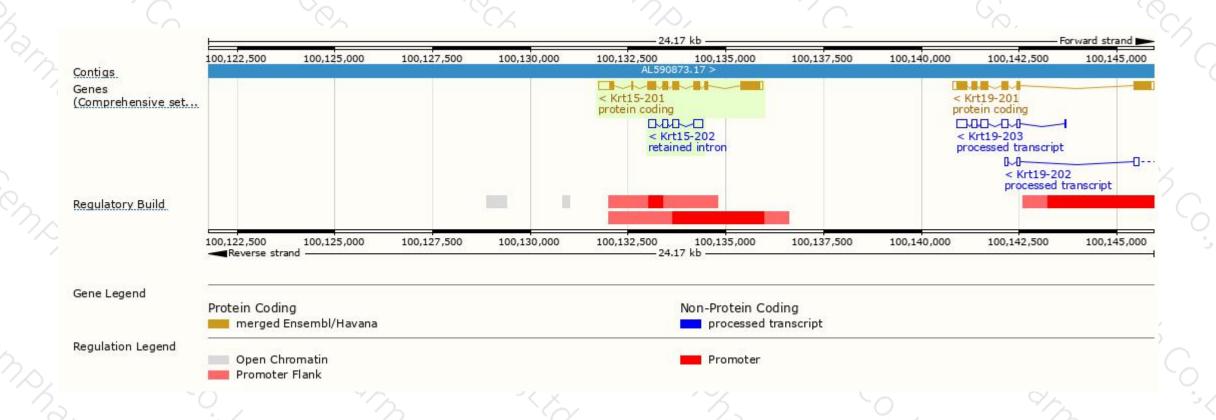
Name	Transcript ID ENSMUST00000107411.2	1			CCDS CCDS25410 ₽	UniProt ♦ B1AQ77 &	Flags		
							TSL:1	GENCODE basic	APPRIS P1
Krt15-202	ENSMUST00000148502.1	689	No protein	Retained intron	~	150		TSL:2	

The strategy is based on the design of *Krt15-201* transcript, The transcription is shown below



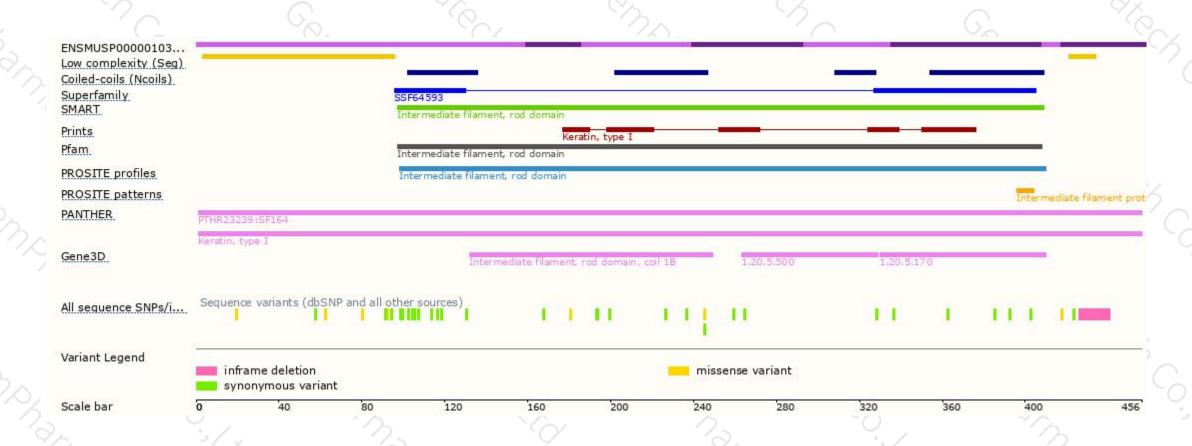
Genomic location distribution





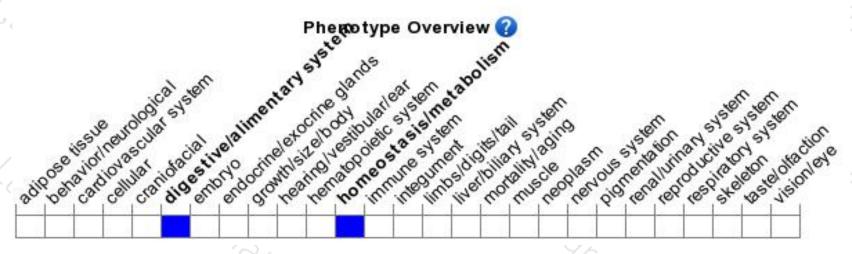
Protein domain





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 impaired esophageal epithelial regeneration with thicker epithelia due to enhanced basal cell proliferation.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





