

Krt19 Cas9-CKO Strategy

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Reviewer:

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Design Date:

2020-01-23

Project Overview

Project Name

Krt19

Project type

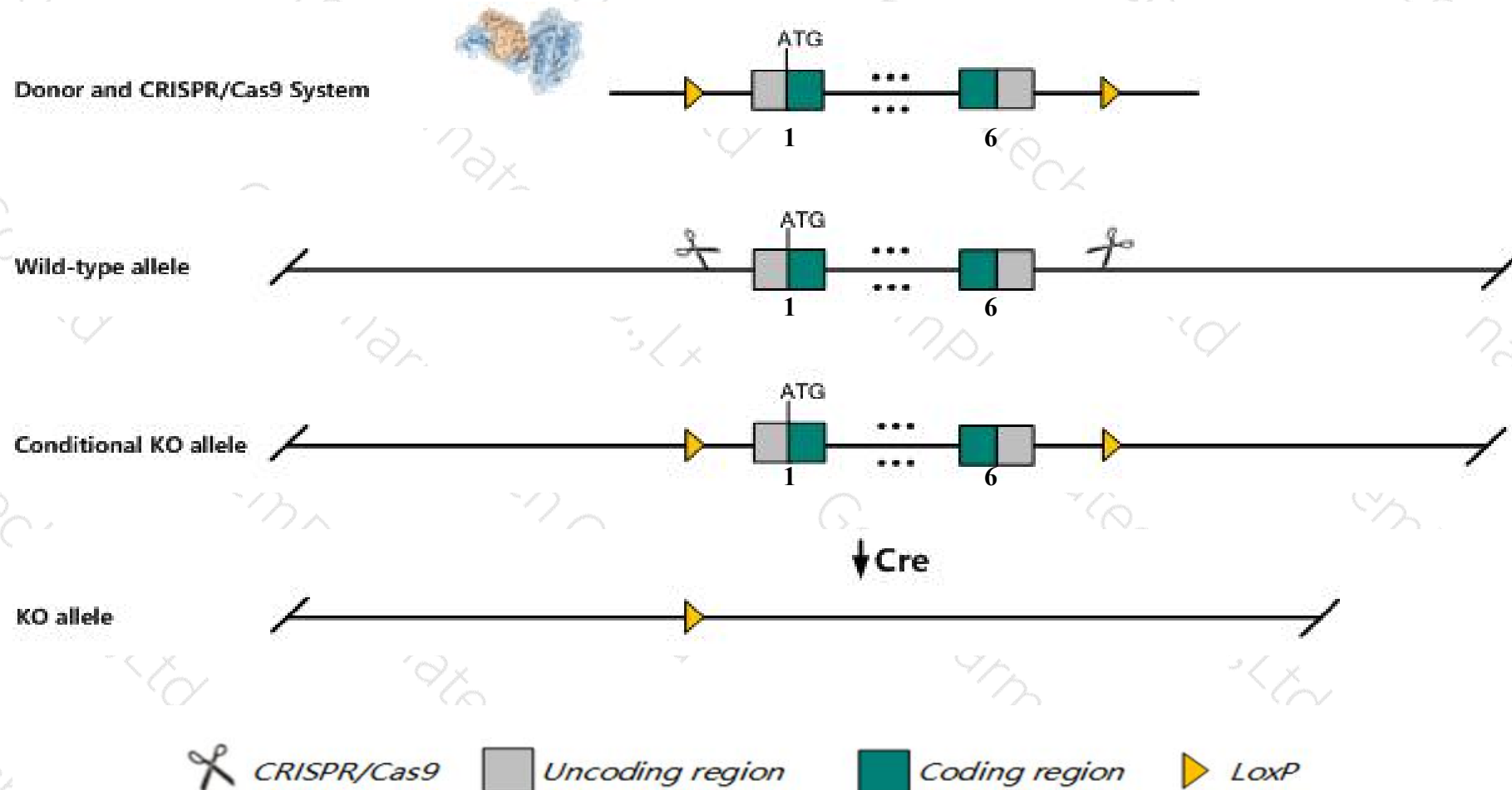
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Krt19* gene. The schematic diagram is as follows:



- The *Krt19* gene has 3 transcripts. According to the structure of *Krt19* gene, exon1-exon6 of *Krt19-201* (ENSMUST00000007317.7) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Krt19* 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- 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.

- According to the existing MGI data, Mice homozygous for a knock-in allele are viable. Mice homozygous for a reporter allele show partial and strain-dependent preweaning lethality but no anatomical or behavioral defects. Mice that are either homozygous or heterozygous for a targeted insertion into intron 6 exhibit sperm tail defects.
- The *Krt19* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Krt19 keratin 19 [*Mus musculus* (house mouse)]

Gene ID: 16669, updated on 14-Jan-2020

Summary

Official Symbol	Krt19 provided by MGI
Official Full Name	keratin 19 provided by MGI
Primary source	MGI:MGI:96693
See related	Ensembl:ENSMUSG00000020911
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	K19; CK-19; EndoC; Krt1-19; AI663979; Krt-1.19
Summary	The protein encoded by this gene is a member of the keratin family. The keratins are intermediate filament proteins responsible for the structural integrity of epithelial cells and are subdivided into cytokeratins and hair keratins. The type I cytokeratins consist of acidic proteins which are arranged in pairs of heterotypic keratin chains. Unlike its related family members, this smallest known acidic cytokeratin is not paired with a basic cytokeratin in epithelial cells. It is specifically expressed in the periderm, the transiently superficial layer that envelopes the developing epidermis. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Sep 2015]
Expression	Biased expression in colon adult (RPKM 2054.0), stomach adult (RPKM 1224.1) and 8 other tissues See more
Orthologs	human all

Genomic context

Location: 11 D; 11 63.42 cM

Exon count: 7

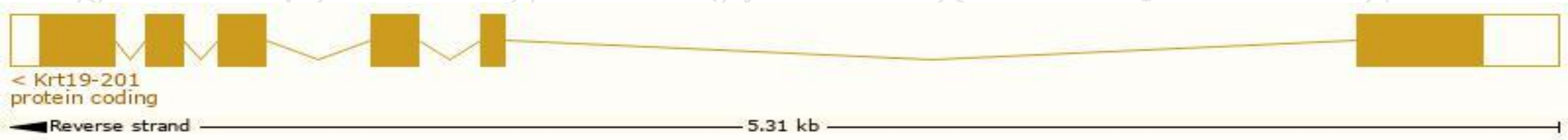
See Krt19 in [Genome Data Viewer](#)

Transcript information (Ensembl)

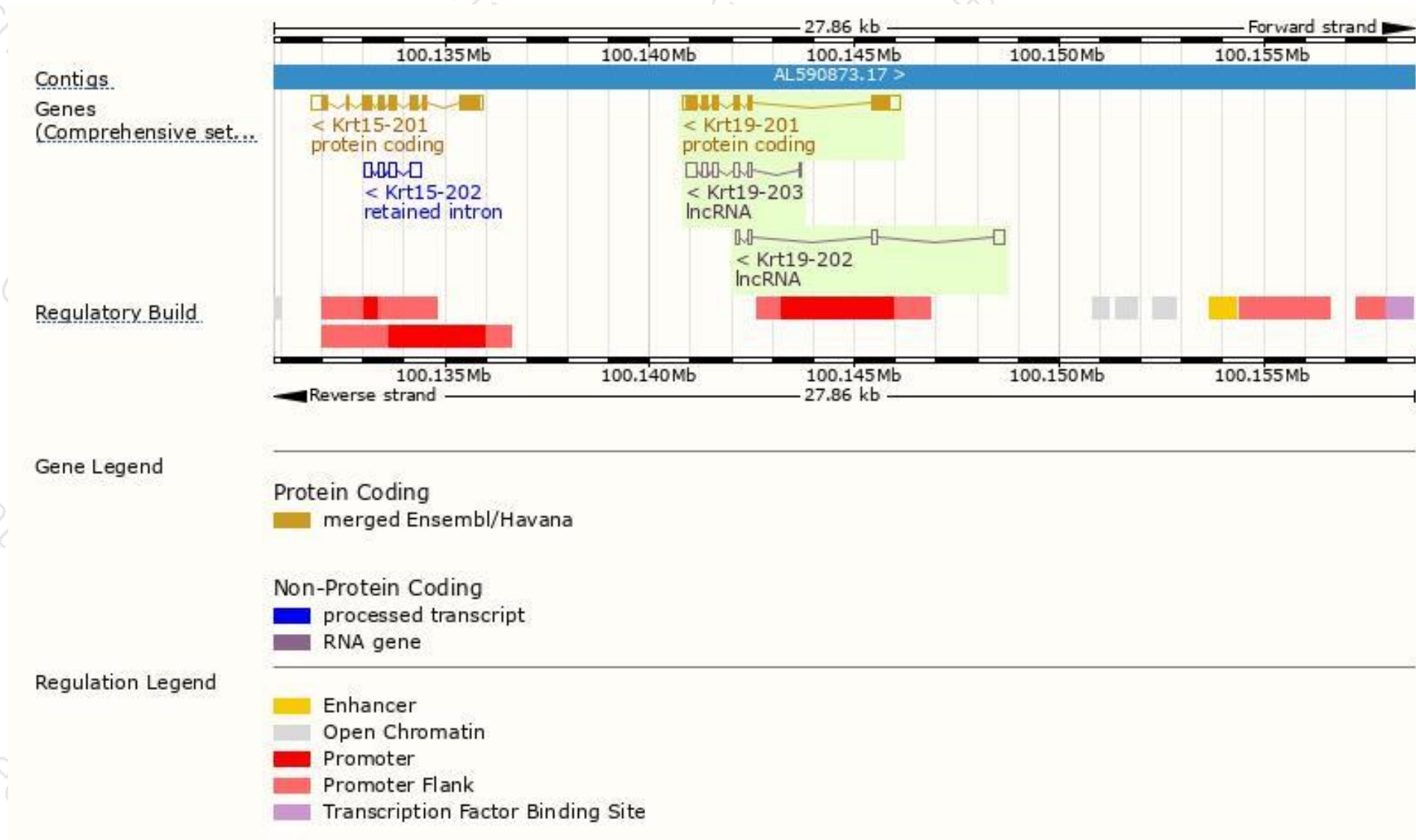
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Krt19-201	ENSMUST00000007317.7	1576	403aa	Protein coding	CCDS25411	B1AQ78 P19001	TSL:1 GENCODE basic APPRIS P1
Krt19-203	ENSMUST00000126460.7	823	No protein	lncRNA	-	-	TSL:3
Krt19-202	ENSMUST00000125888.1	546	No protein	lncRNA	-	-	TSL:5

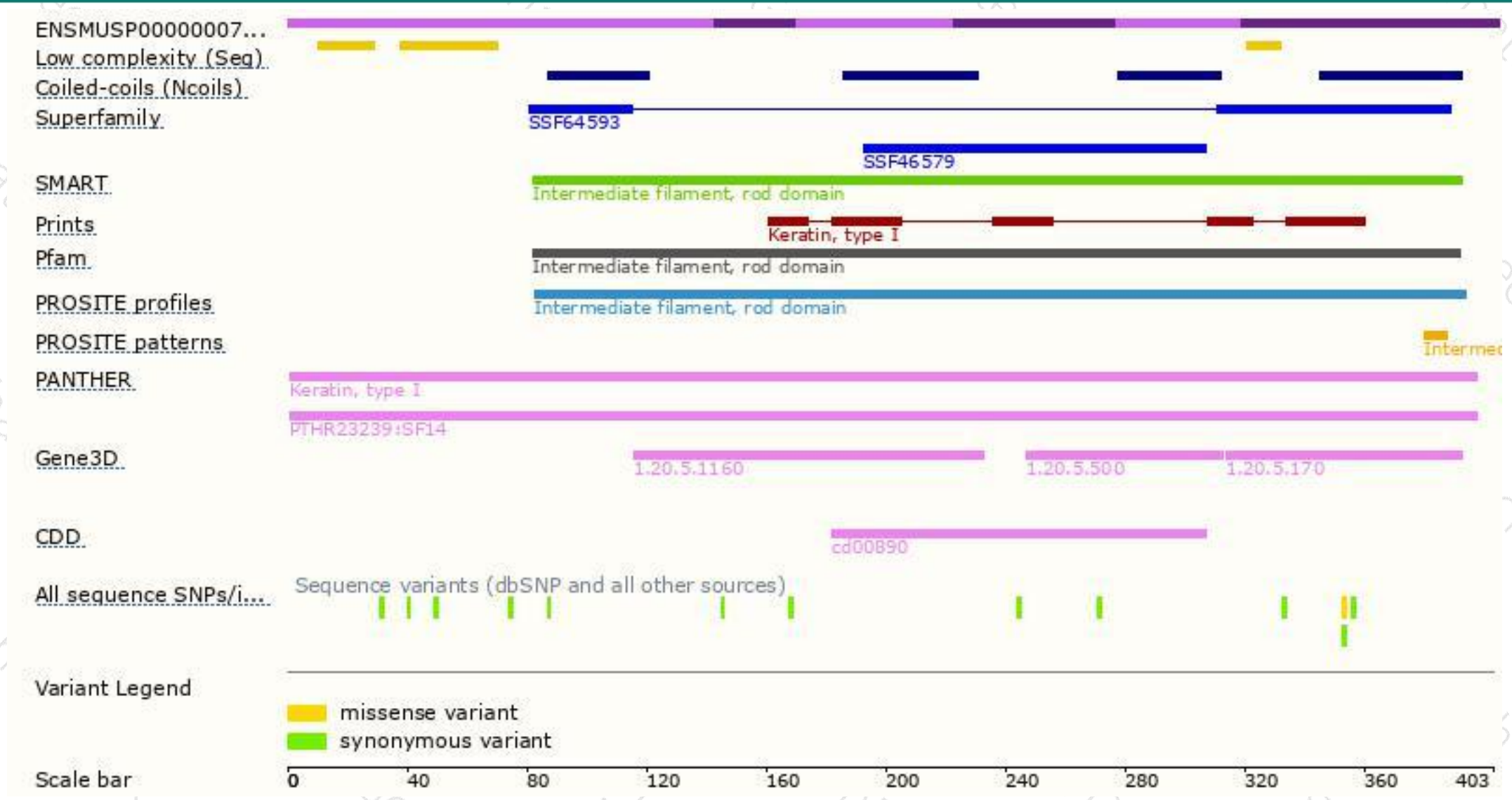
The strategy is based on the design of *Krt19-201* transcript,The transcription is shown below



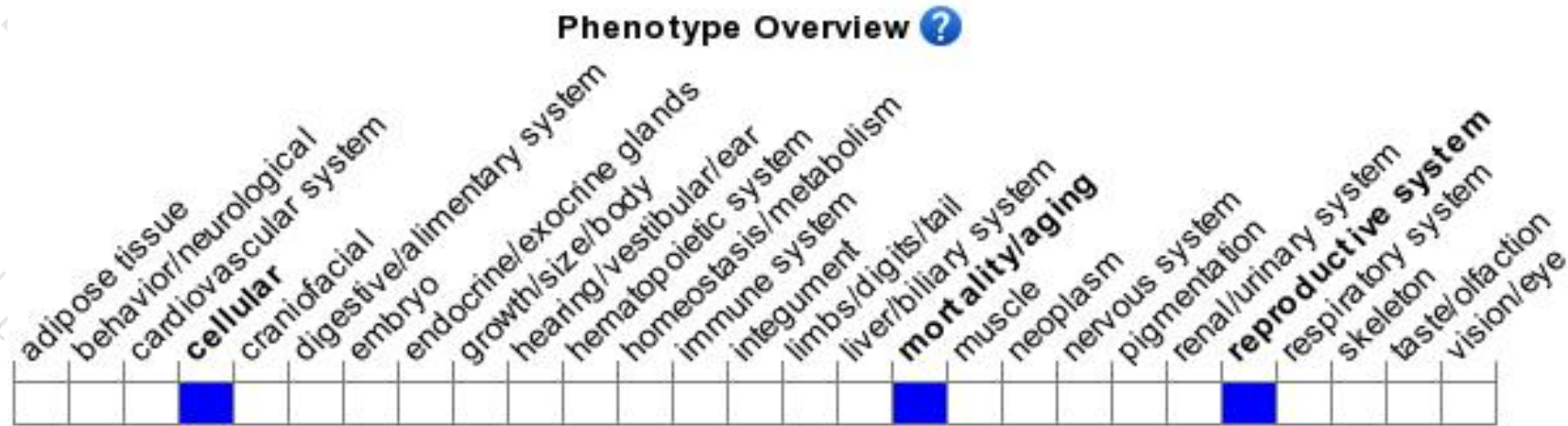
Genomic location distribution



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-in allele are viable. Mice homozygous for a reporter allele show partial and strain-dependent preweaning lethality but no anatomical or behavioral defects. Mice that are either homozygous or heterozygous for a targeted insertion into intron 6 exhibit sperm tail defects.

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

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