Scin Cas9-CKO Strategy

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Project Overview

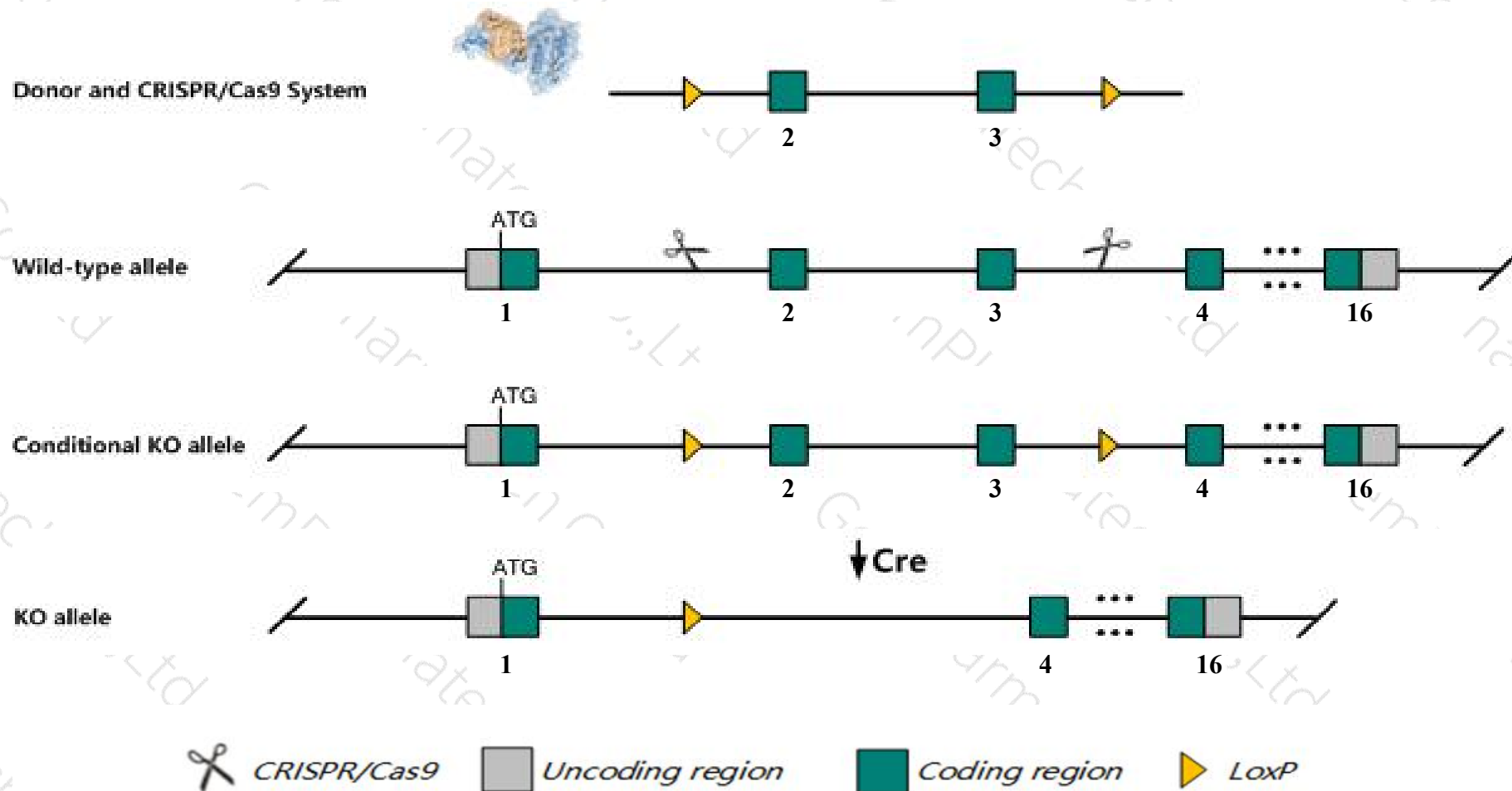|	
Project Name	*Scin*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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

Technical routes

➤ The *Scin* gene has 2 transcripts. According to the structure of *Scin* gene, exon2-exon3 of *Scin-201* (ENSMUST00000002640.5) transcript is recommended as the knockout region.The region contains Ens 317bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Scin* 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.

Notice

➢ According to the existing MGI data,Mice homozygous for a conditional allele knocked-out in osteoclasts exhibit impaired osteoclast differentiation and reduced peridontal disease-mediated bone loss.

➢ The *Scin* gene is located on the Chr12. 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）

Scin scinderin [Mus musculus (house mouse)]

Gene ID: 20259, updated on 31-Jan-2019

▲Summary

|	
Official Symbol	Scin provided by MGI
Official Full Name	scinderin provided byMGI
Primary source	MGI:MGI:1306794
See related	Ensembl:ENSMUSG00000002565
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	AW545522, adseverin
Expression	Biased expression in colon adult (RPKM 56.3), large intestine adult (RPKM 22.6) and 4 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

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

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Scin-201	ENSMUST00000002640.5	2995	715aa	Protein coding	CCDS49055	Q60604	TSL:1 GENCODE basic APPRIS P1
Scin-202	ENSMUST00000078481.13	2654	615aa	Protein coding	CCDS25891	Q60604	TSL:1 GENCODE basic

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

< Scin-201
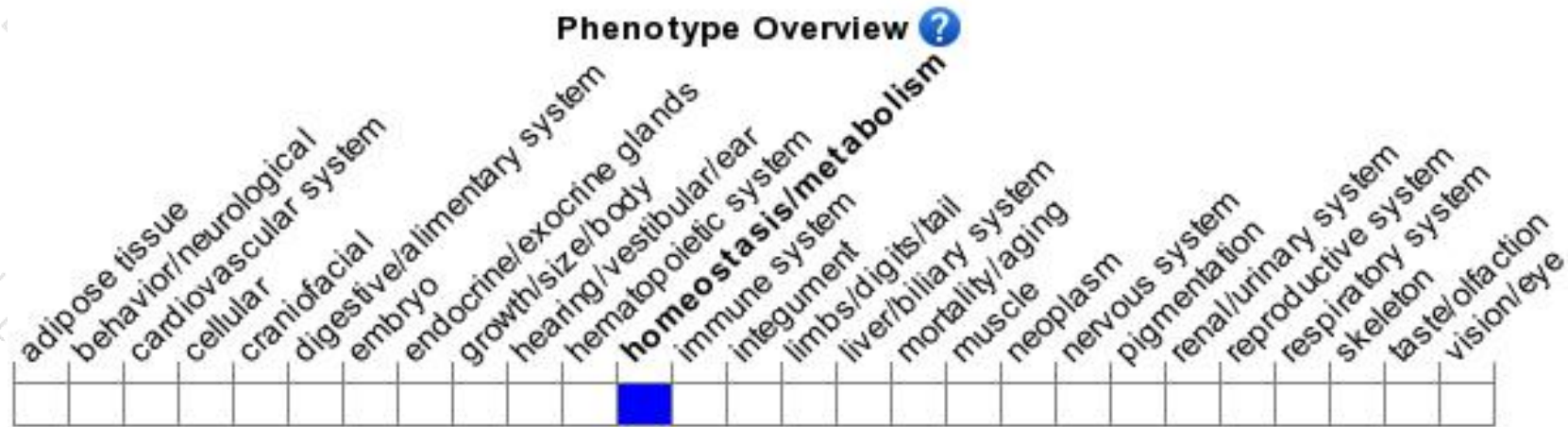protein coding

◄— Reverse strand

74.46 kb
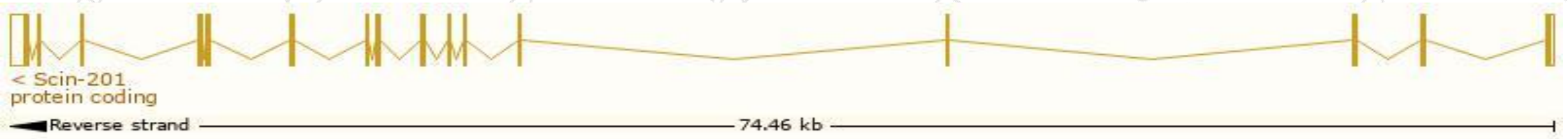
Genomic location distribution
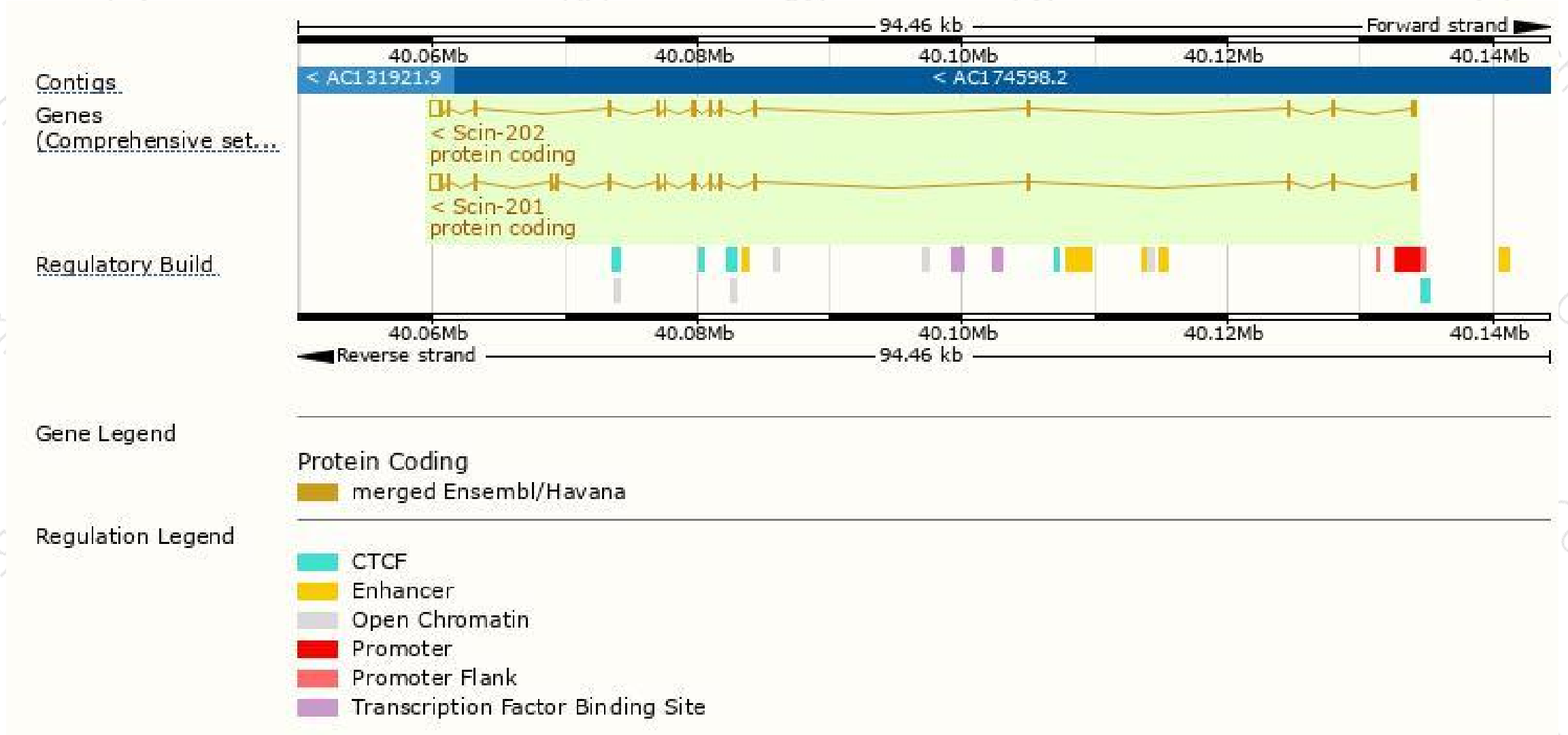
Protein domain
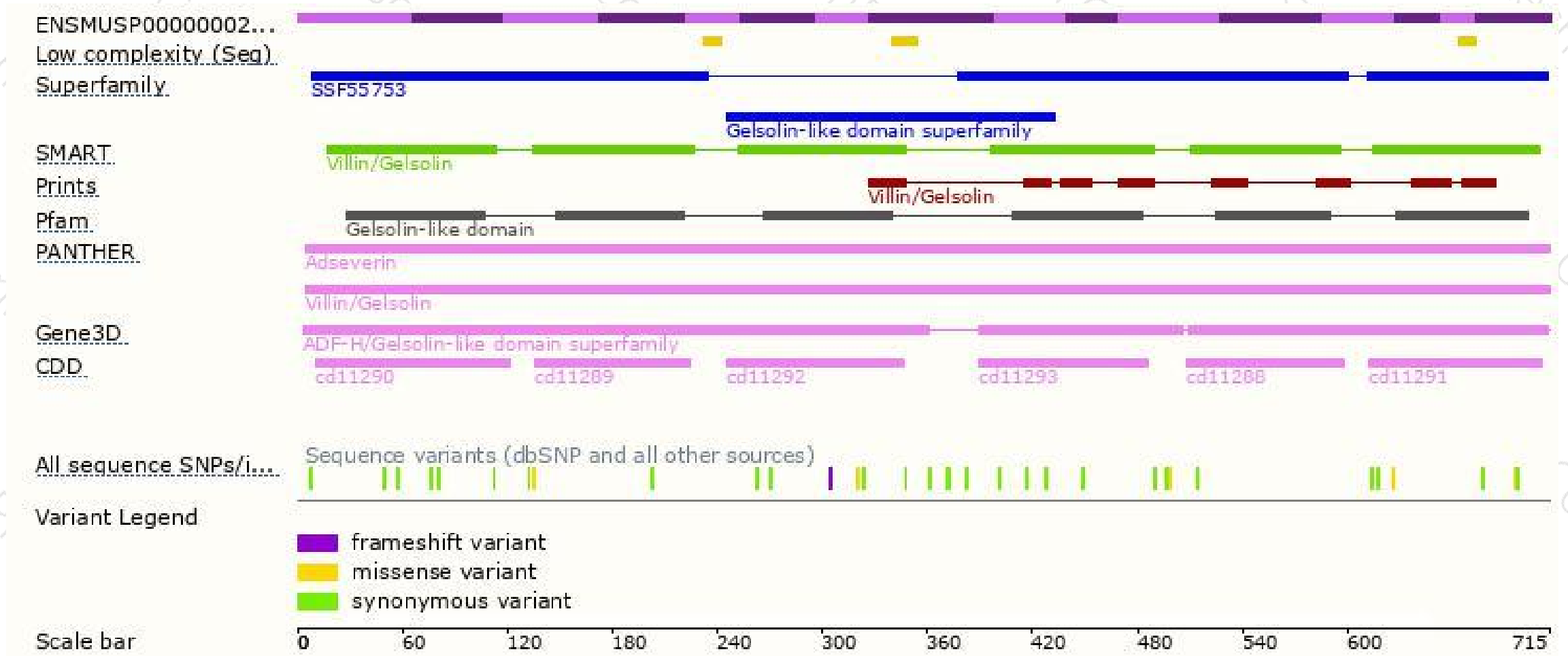
Mouse phenotype description(MGI)

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 conditional allele knocked-out in osteoclasts exhibit impaired osteoclast differentiation and reduced peridontal disease-mediated bone loss.

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