Gdf15 Cas9-KO *Strategy*

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Project Overview

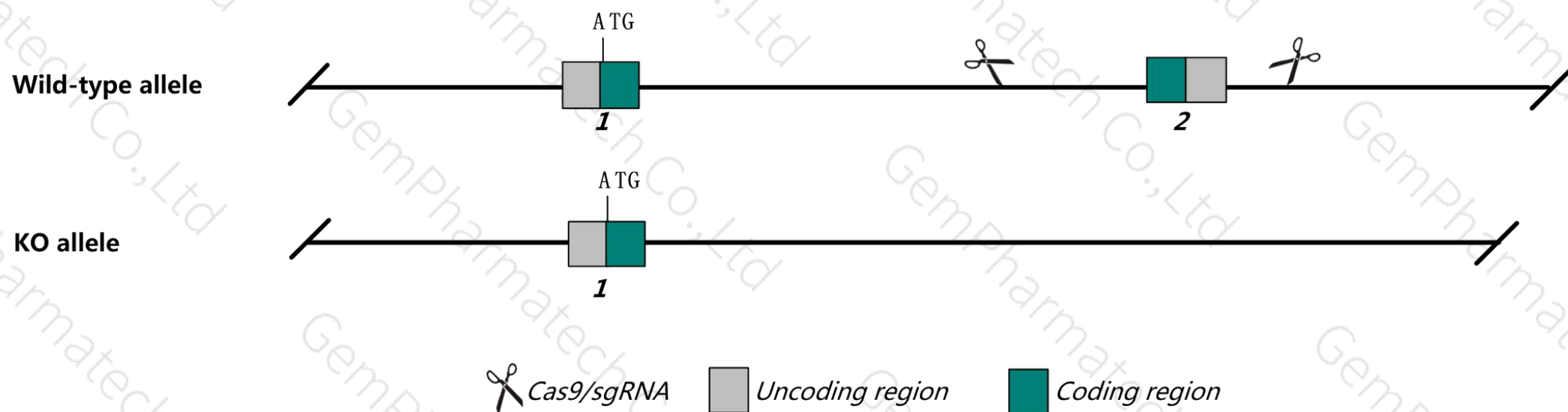|	
Project Name	*Gdf15*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gdf15* gene. The schematic diagram is as follows:

Technical routes

➤ The *Gdf15* gene has 2 transcripts.According to the structure of *Gdf15* gene, exon2 of *Gdf15*-201 transcript is recommended as the knockout region.The region contains most 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 *Gdf15* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA 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.

Notice

➤ According to the existing MGI data，Homozygous null mice showed no obvious major abnormalities, but exhibit progressive postnatal losses of spinal, facial, and trigeminal motoneurons, accelerated thrombus formation following injury, and decreased bleeding times.

➤ The *Gdf15* gene is located on the Chr8. 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）

Gdf15 growth differentiation factor 15 [*Mus musculus* (house mouse)]

Gene ID: 23886, updated on 16-Jul-2019

▲ Summary

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Official Symbol	Gdf15 provided by MGI
Official Full Name	growth differentiation factor 15 provided by MGI
Primary source	MGI:MGI:1346047
See related	Ensembl:ENSMUSG00000038508
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	SBF; MIC-1; NAG-1
Summary	This gene encodes a secreted ligand of the TGF-beta (transforming growth factor-beta) superfamily of proteins. Ligands of this family bind various TGF-beta receptors leading to recruitment and activation of SMAD family transcription factors that regulate gene expression. The encoded preproprotein is proteolytically processed to generate each subunit of the disulfide-linked homodimer. The protein is expressed in a broad range of cell types, acts as a pleiotropic cytokine and is involved in the stress response program of cells after cellular injury. Increased protein levels are associated with disease states such as tissue hypoxia, inflammation, acute injury and oxidative stress. Mice lacking a functional copy of this gene exhibit progressive loss of motor neurons, and more rapid blood clot formation. [provided by RefSeq, Aug 2016]
Expression	Broad expression in colon adult (RPKM 10.6), liver adult (RPKM 10.3) and 19 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags		
Gdf15-201	ENSMUST00000003808.7	1545	303aa	Protein coding	CCDS22376	Q9Z0J7	TSL:1	GENCODE basic	APPRIS P1
Gdf15-202	ENSMUST00000110103.1	1380	303aa	Protein coding	CCDS22376	Q9Z0J7	TSL:1	GENCODE basic	APPRIS P1

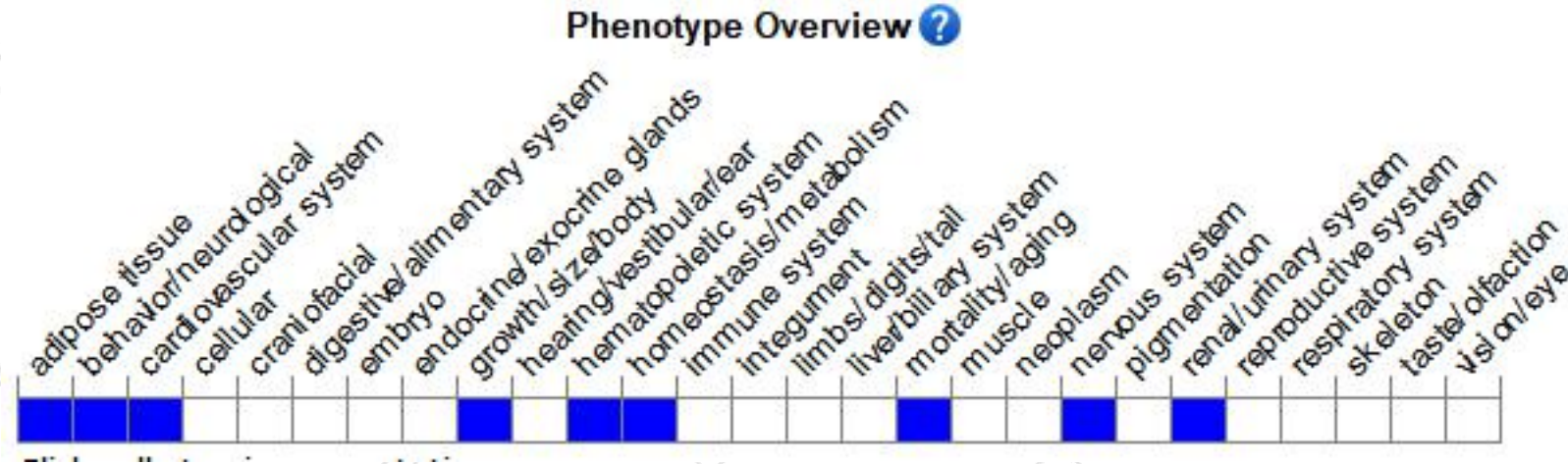The strategy is based on the design of *Gdf15*-201 transcript,The transcription is shown below

< Gdf15-201
protein coding

◄—— Reverse strand   2.70 kb
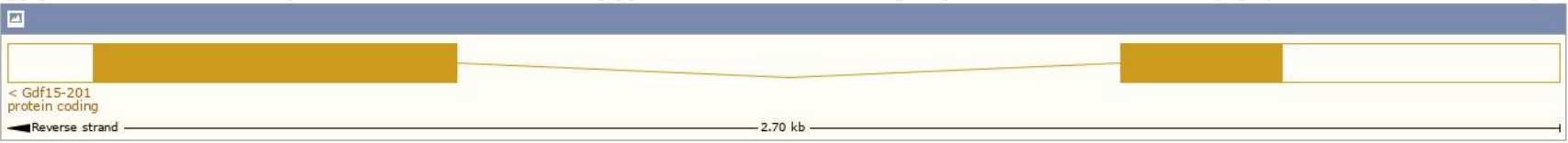
Genomic location distribution
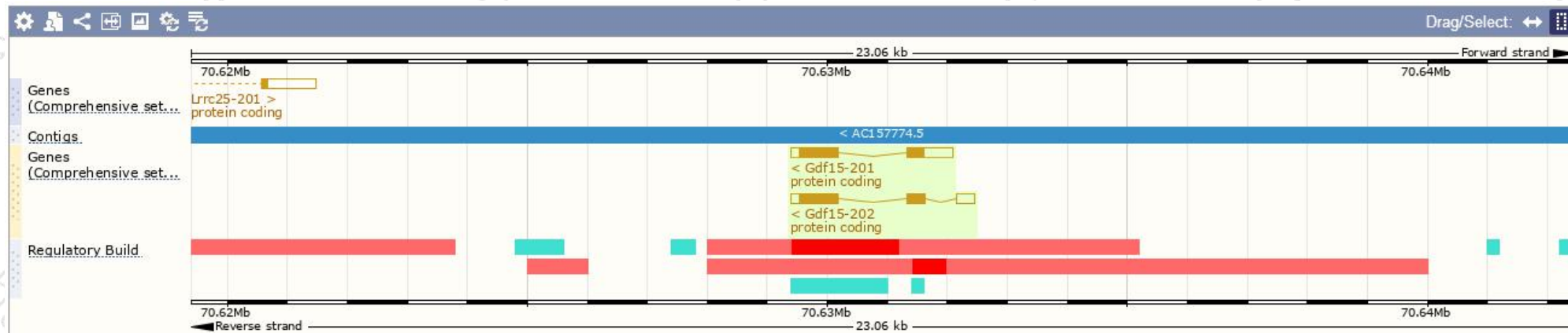
Protein domain
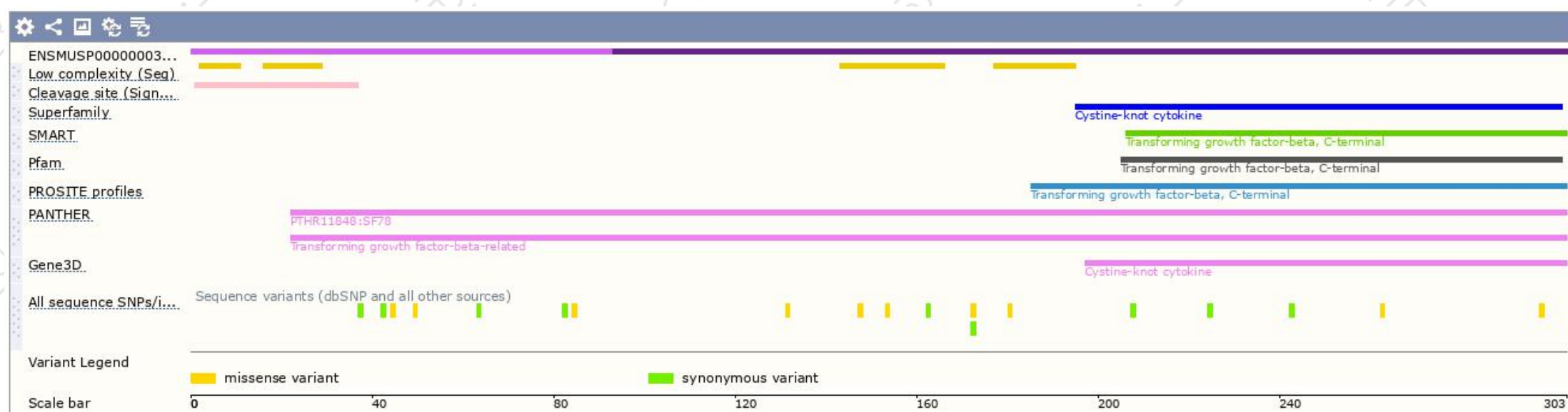
Mouse phenotype description(MGI)

Phenotype Overview

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,Mutations in this locus affect cell-cycle regulation and apoptos is. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

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