

Aspn Cas9-KO Strategy

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Reviewer :

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Project Overview

Project Name

Aspn

Project type

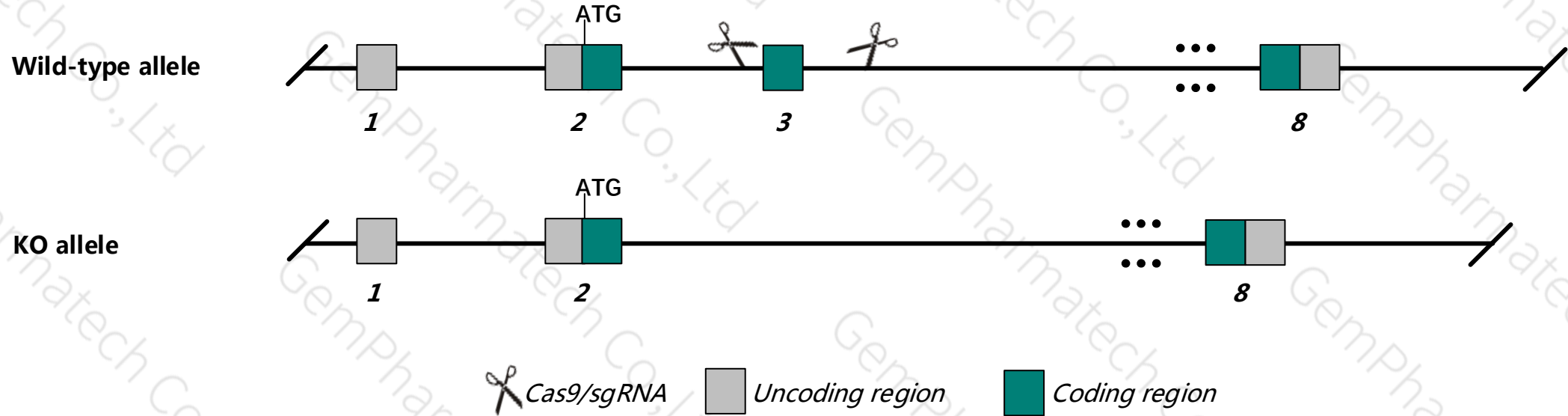
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



Technical routes

- The *Aspn* gene has 2 transcripts. According to the structure of *Aspn* gene, exon3 of *Aspn*-201 (ENSMUST00000021820.13) transcript is recommended as the knockout region. The region contains 113bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Aspn* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9, sgRNA 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 KO region contains partial intron of the *Cenpp* gene. Knockout the region may affect the function of *Cenpp* gene.
- The *Aspn* gene is located on the Chr13. 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)

Aspn asporin [*Mus musculus* (house mouse)]

Gene ID: 66695, updated on 14-Jan-2020

Summary

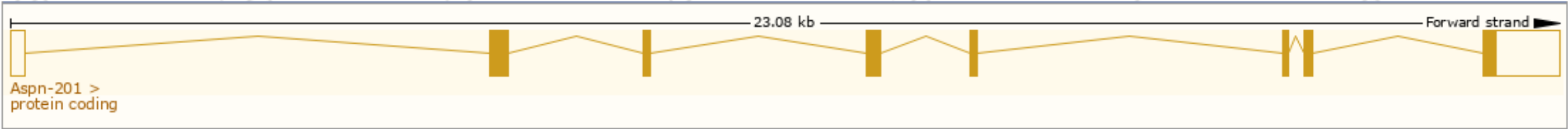
Official Symbol	Aspn provided by MGI
Official Full Name	asporin provided by MGI
Primary source	MGI:MGI:1913945
See related	Ensembl:ENSMUSG000000021388
Gene type	protein coding
RefSeq status	REVIEWED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Plap1; Slrr1c; AA986886; 4631401G09Rik
Summary	This gene encodes a member of the small leucine-rich proteoglycan family. The encoded protein is an extracellular matrix protein that modulates the transforming growth factor-beta signaling pathway, regulating cartilage matrix gene expression and cartilage formation. The protein plays a role in the pathology of osteoarthritis. Alternative splicing results in multiple transcript variants.[provided by RefSeq, Feb 2010]
Expression	Biased expression in limb E14.5 (RPKM 23.1), CNS E14 (RPKM 4.5) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

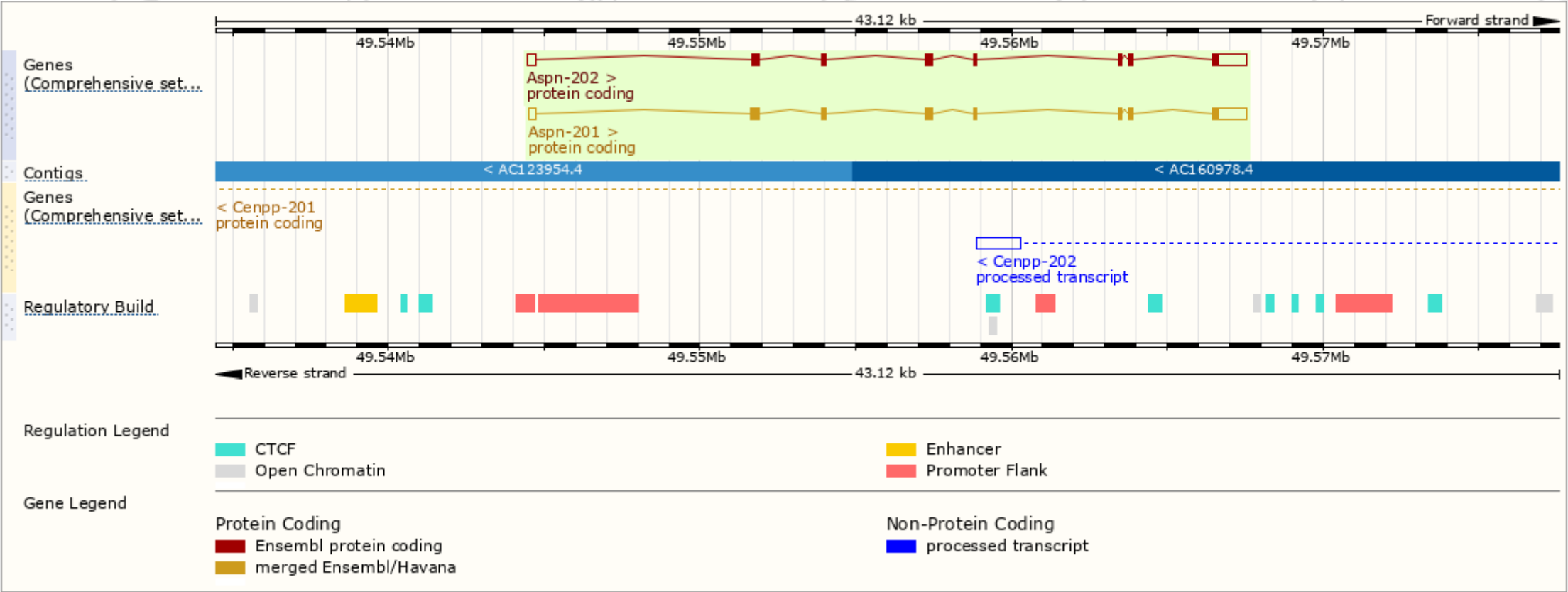
The gene has 2 transcripts, and all transcripts are shown below:

Name ▴	Transcript ID ▴	bp ▴	Protein ▴	Biotype ▴	CCDS ▴	UniProt ▴	Flags ▴
Aspn-202	ENSMUST00000177948.1	2329	373aa	 Protein coding	CCDS26503 	A6H6K1  Q99MQ4 	TSL:1 GENCODE basic APPRIS P1
Aspn-201	ENSMUST00000021820.13	2310	373aa	 Protein coding	CCDS26503 	A6H6K1  Q99MQ4 	TSL:1 GENCODE basic APPRIS P1

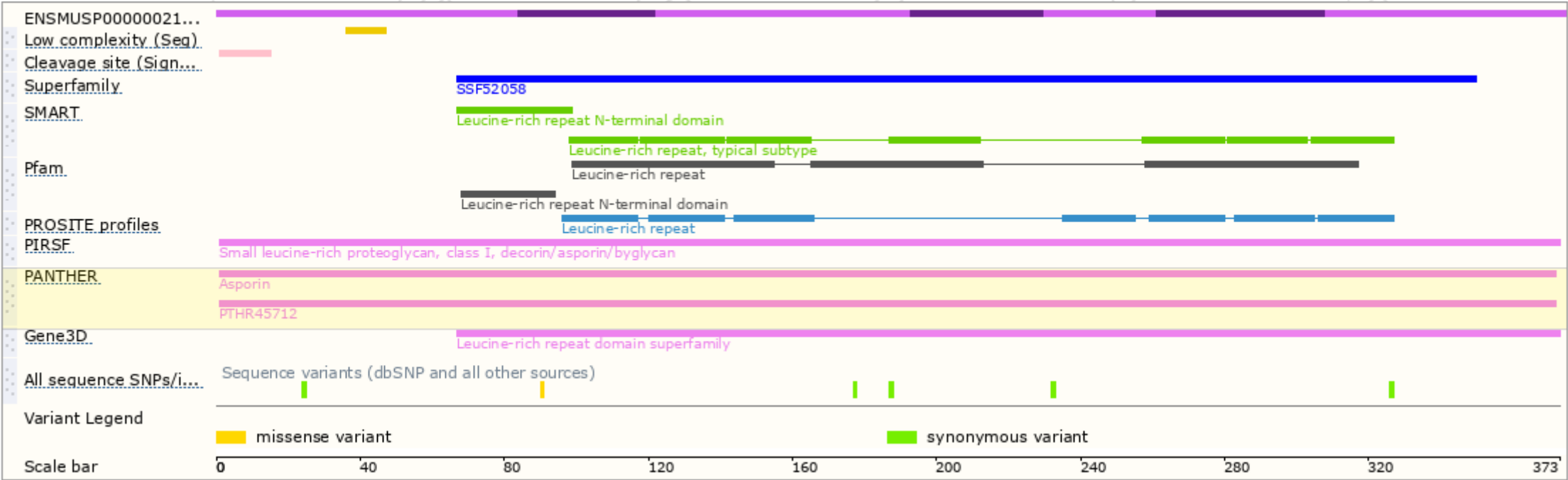
The strategy is based on the design of *Aspn-201* transcript, The transcription is shown below



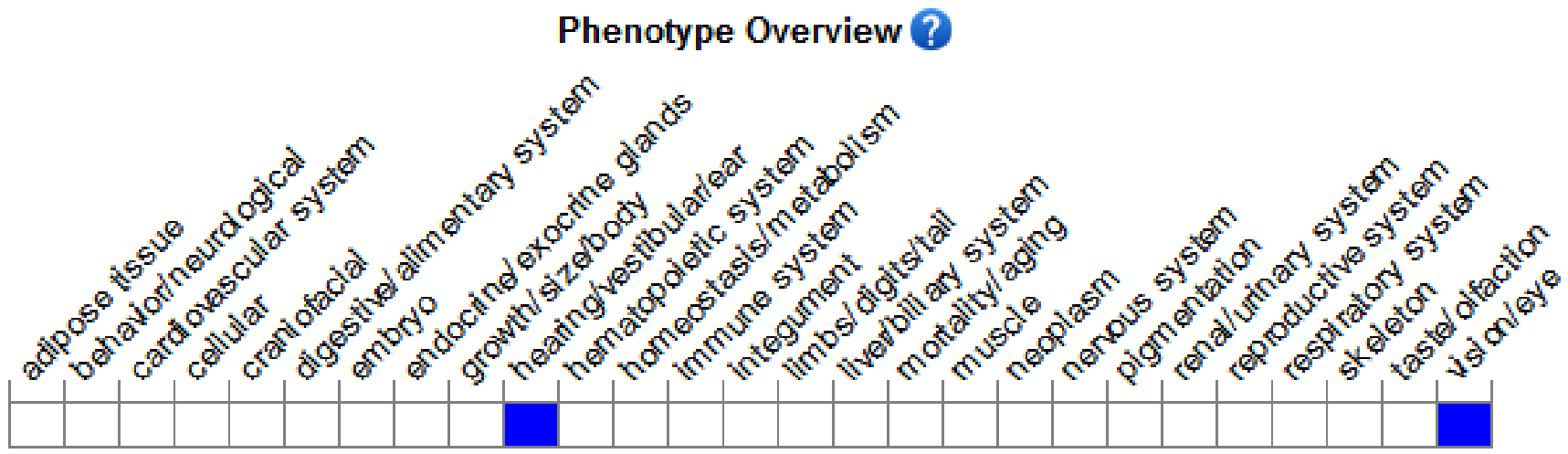
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Click cells to view annotations.

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(<http://www.informatics.jax.org/>) .

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