

# *Col1a2* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Col1a2***

**Project type**

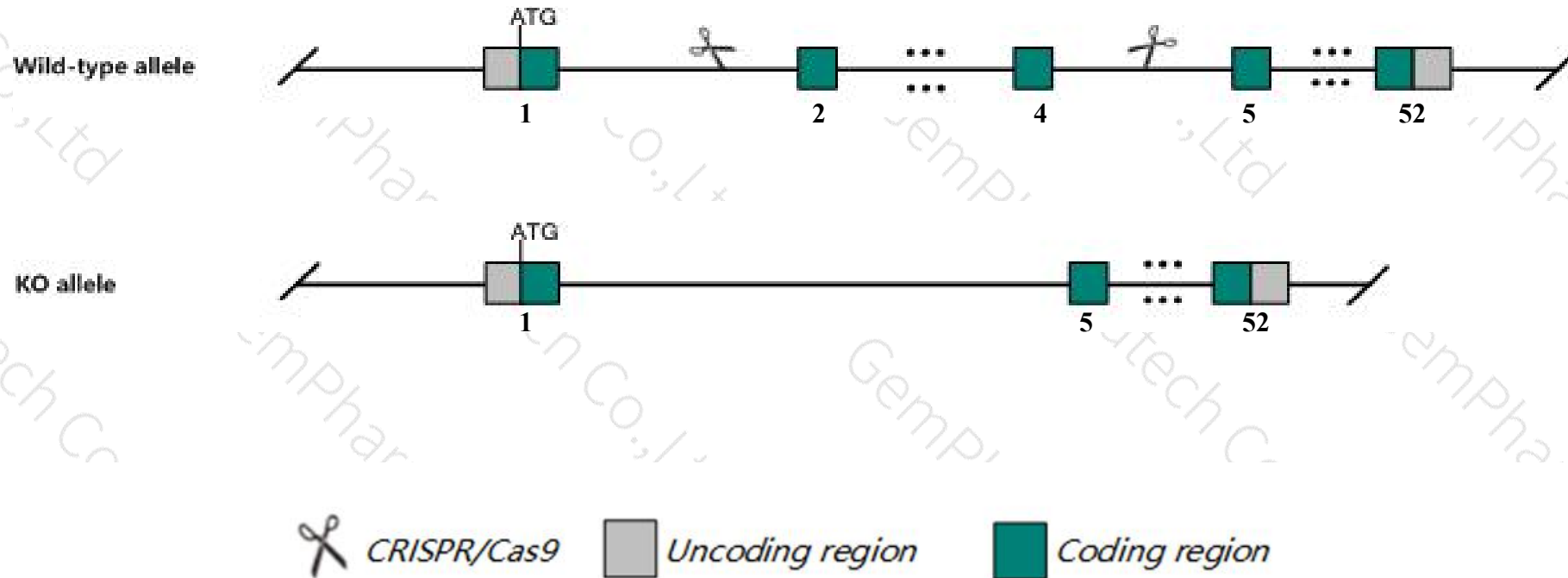
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Colla2* gene. The schematic diagram is as follows:



- The *Colla2* gene has 8 transcripts. According to the structure of *Colla2* gene, exon2-exon4 of *Colla2-201* (ENSMUST00000031668.9) transcript is recommended as the knockout region. The region contains 62bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Colla2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, The tails of mice heterozygous for an ENU-induced mutation at this locus are flexible or rubbery.
- The *Colla2* gene is located on the Chr6. 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)

## Col1a2 collagen, type I, alpha 2 [Mus musculus (house mouse)]

Gene ID: 12843, updated on 26-Feb-2019

### Summary



**Official Symbol** Col1a2 provided by [MGI](#)

**Official Full Name** collagen, type I, alpha 2 provided by [MGI](#)

**Primary source** [MGI:MGI:88468](#)

**See related** [Ensembl:ENSMUSG00000029661](#)

**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** AA960264, AI325291, Col1a-2, Cola-2, Cola2, oim

**Summary** This gene encodes the alpha-2 subunit of the fibril-forming type I collagen, the most abundant protein of bone, skin and tendon extracellular matrices. The encoded protein, in association with alpha-1 subunit, forms heterotrimeric type I procollagen that undergoes proteolytic processing during fibril formation. Mice harboring certain mutations in the encoded gene exhibit symptoms of moderate to severe forms of osteogenesis imperfecta. [provided by RefSeq, Dec 2015]

**Expression** Biased expression in bladder adult (RPKM 443.5), limb E14.5 (RPKM 423.9) and 13 other tissues [See more](#)

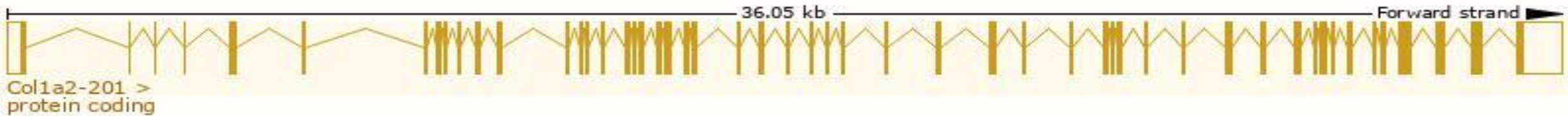
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

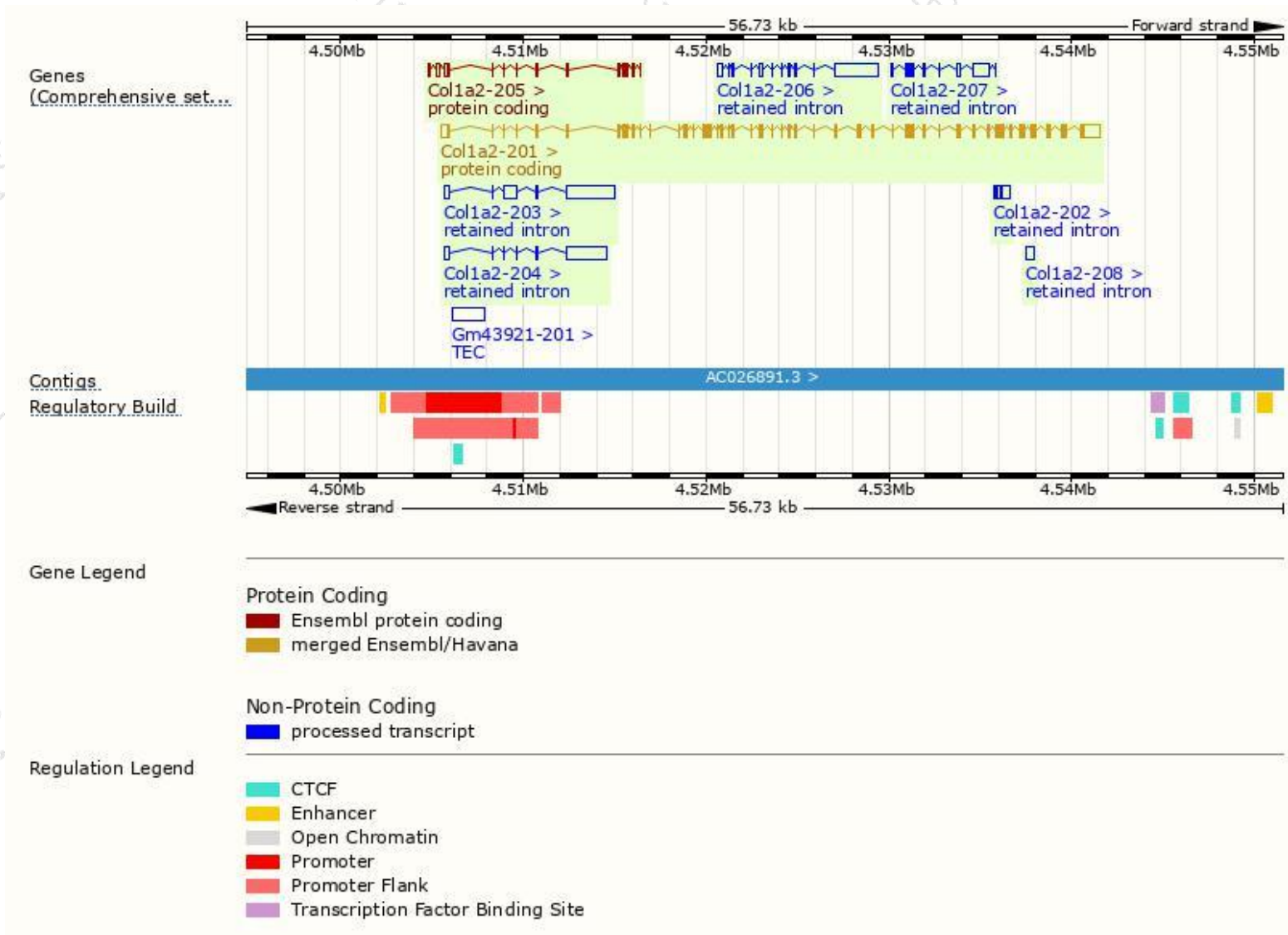
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Col1a2-201	<a href="#">ENSMUST00000031668.9</a>	5348	<a href="#">1372aa</a>	Protein coding	<a href="#">CCDS39420</a>	<a href="#">Q01149 Q3TX57</a>	TSL:1 GENCODE basic APPRIS P1
Col1a2-205	<a href="#">ENSMUST00000141483.7</a>	850	<a href="#">177aa</a>	Protein coding	-	<a href="#">E0CXI2</a>	CDS 3' incomplete TSL:5
Col1a2-203	<a href="#">ENSMUST00000132029.1</a>	3689	No protein	Retained intron	-	-	TSL:2
Col1a2-206	<a href="#">ENSMUST00000148864.1</a>	3221	No protein	Retained intron	-	-	TSL:1
Col1a2-204	<a href="#">ENSMUST00000138511.7</a>	2550	No protein	Retained intron	-	-	TSL:1
Col1a2-207	<a href="#">ENSMUST00000155687.2</a>	1519	No protein	Retained intron	-	-	TSL:5
Col1a2-202	<a href="#">ENSMUST00000124686.1</a>	628	No protein	Retained intron	-	-	TSL:3
Col1a2-208	<a href="#">ENSMUST00000203346.1</a>	502	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *Col1a2-201* transcript,The transcription is shown below

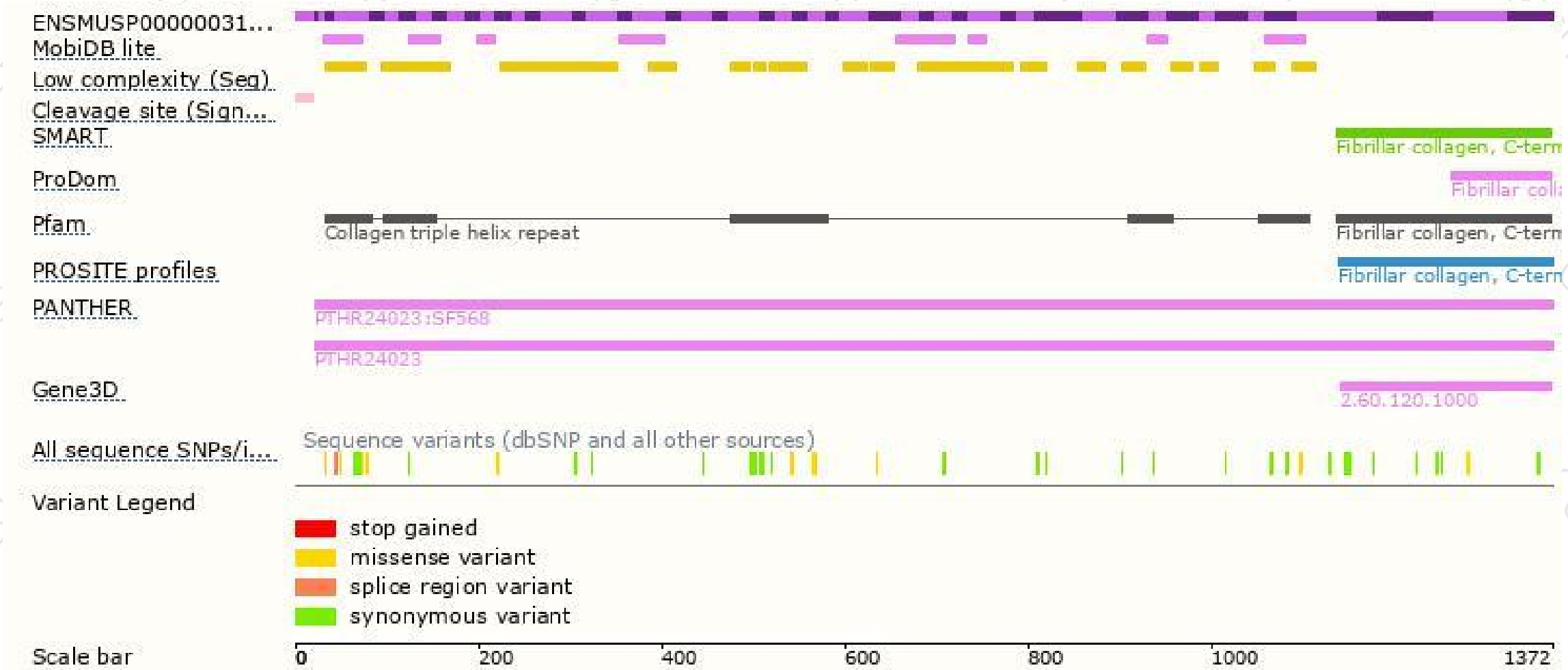


# Genomic location distribution





# Protein domain



Fibrillar collagen, C-term

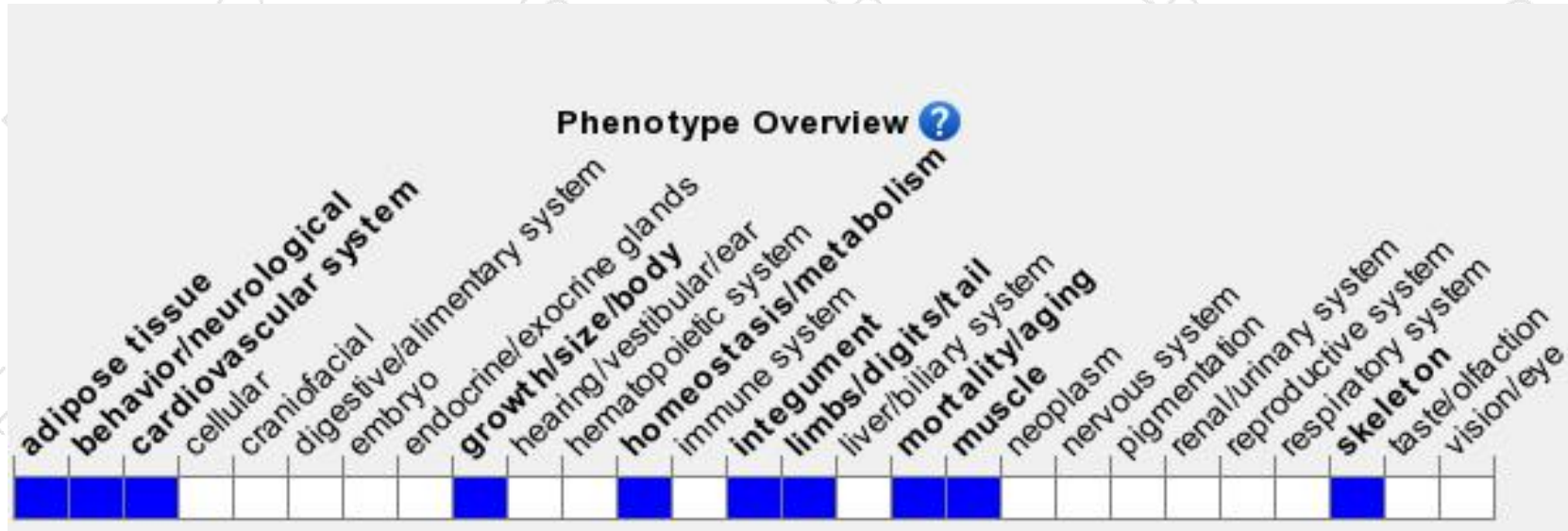
Fibrillar collagen

Fibrillar collagen, C-term

Fibrillar collagen, C-term

2.60.120.1000

# 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, The tails of mice heterozygous for an ENU-induced mutation at this locus are flexible or rubbery.

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

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