Itga7 Cas9-CKO Strategy

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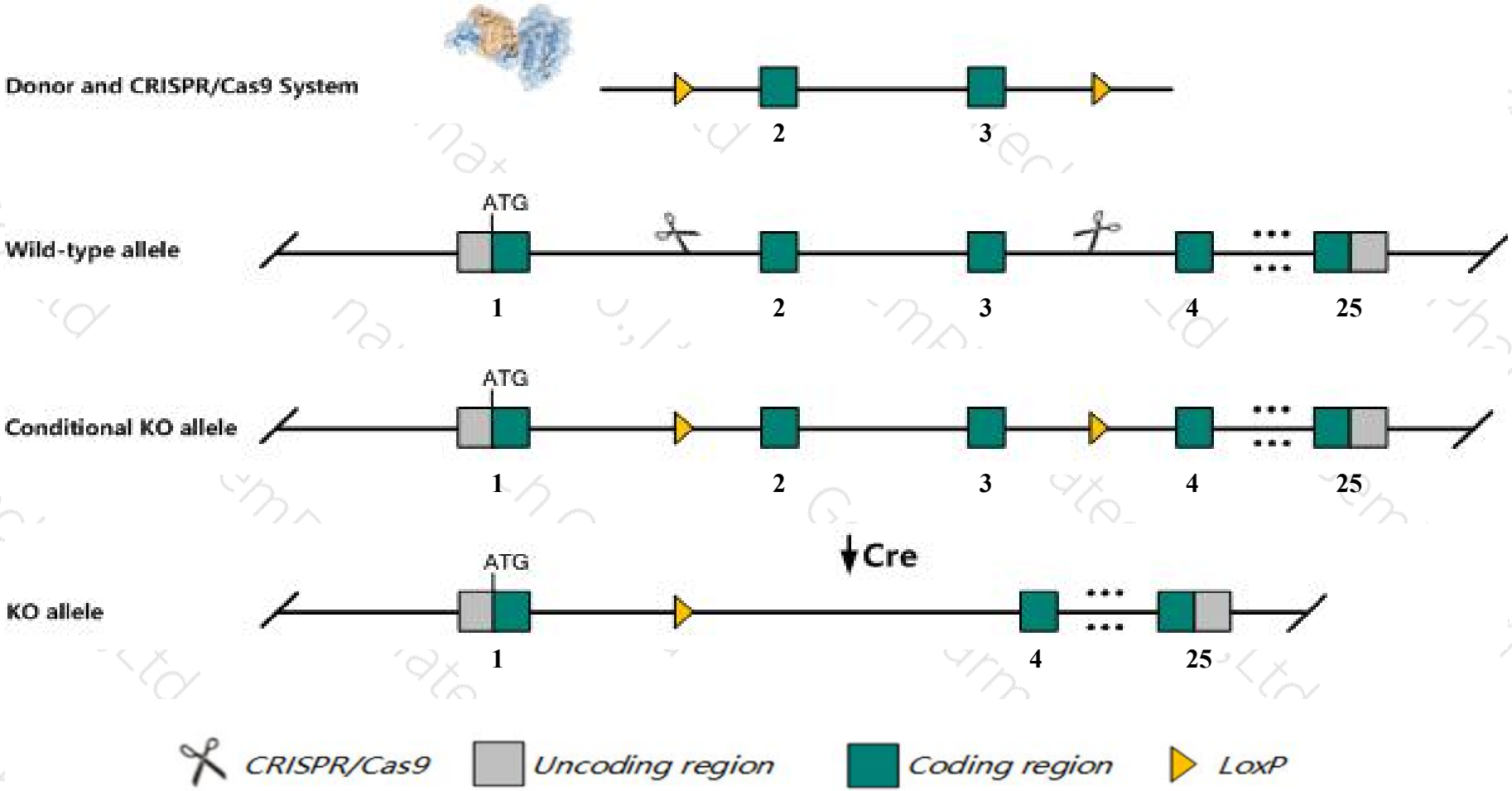
Project Overview

Project Name	***Itga7***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Itga7* gene. The schematic diagram is as follows:



Technical routes

- The *Itga7* gene has 5 transcripts. According to the structure of *Itga7* gene, exon2-exon3 of *Itga7-201* (ENSMUST00000099112.3) transcript is recommended as the knockout region.The region contains 208bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Itga7* gene. The brief process is as follows:gRNA was transcribed in vitro, donor was constructed.Cas9, gRNA 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 disruptions of this gene display characteristics of muscular dystrophy.
- Transcript *Itga7 -204* may not be affected.
- The *Itga7* gene is located on the Chr10. 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）

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Itga7 integrin alpha 7 [Mus musculus (house mouse)]

Gene ID: 16404, updated on 13-Mar-2020

Summary

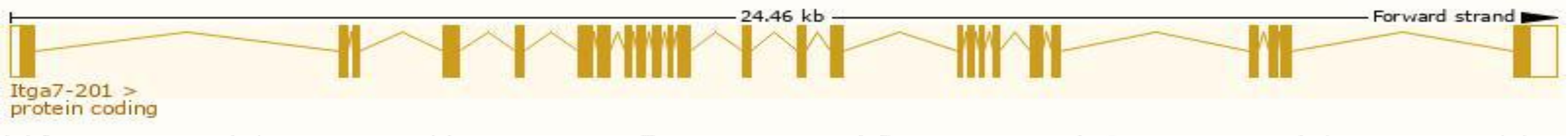
Official Symbol	Itga7 provided by MGI
Official Full Name	integrin alpha 7 provided by MGI
Primary source	MGI:MGI:102700
See related	Ensembl:ENSMUSG00000025348
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	[a]7, alpha7
Summary	This gene encodes a member of the integrin family of cell surface proteins that mediate cellular interactions with the extracellular matrix and other cells. The encoded transmembrane protein is the alpha subunit that forms a noncovalent heterodimer with the beta subunit to form the functional integrin receptor that binds to laminin. Mice lacking the encoded protein exhibit symptoms of progressive muscular dystrophy, impaired axonal regeneration and cerebral vascular defects. [provided by RefSeq, Aug 2016]
Expression	Broad expression in subcutaneous fat pad adult (RPKM 28.3), heart adult (RPKM 26.2) and 21 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

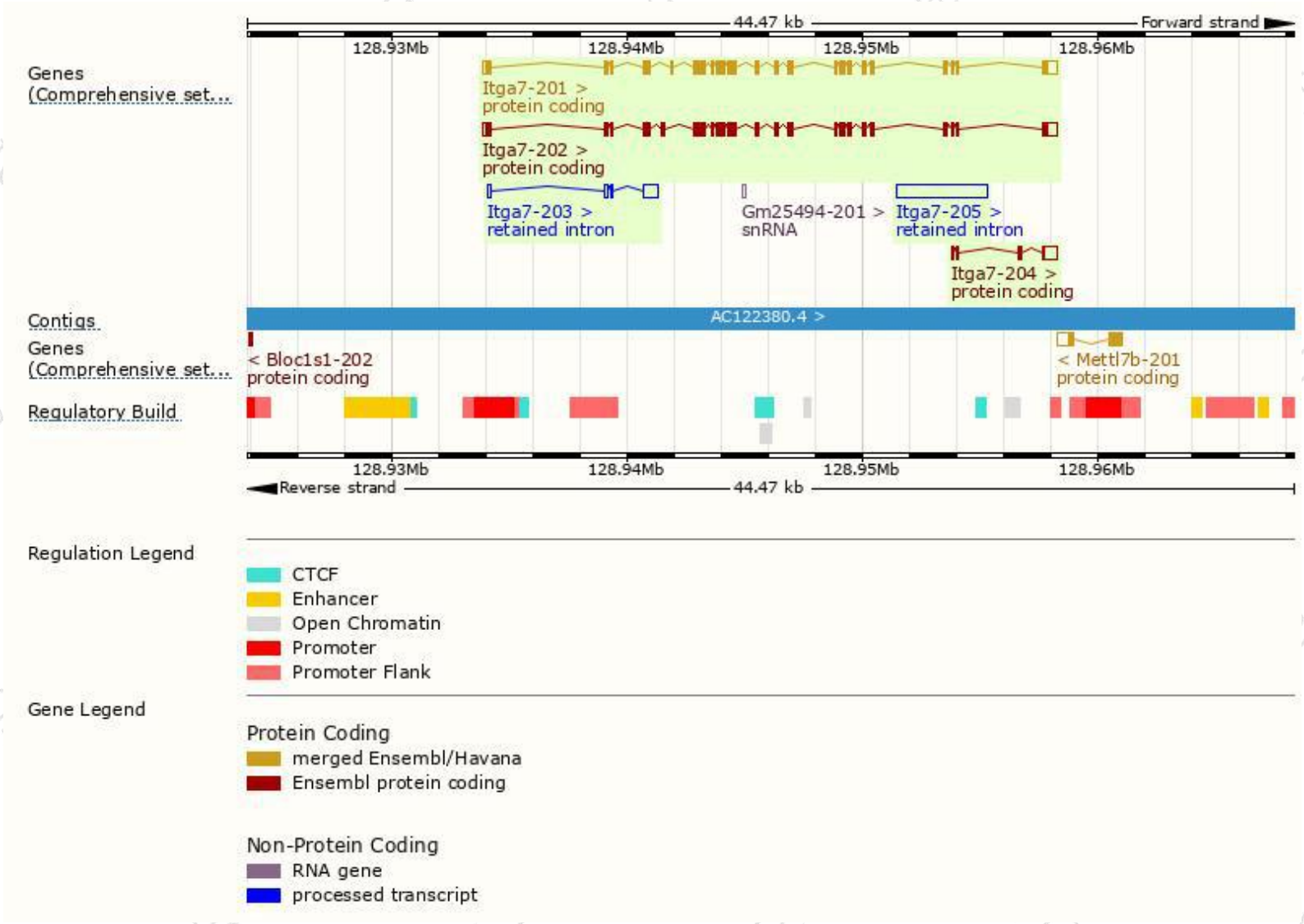
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Itga7-201	ENSMUST00000099112.3	4013	1136aa	Protein coding	CCDS24300	G3X9Q1	TSL:2 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Itga7-202	ENSMUST00000218290.1	4020	1140aa	Protein coding	-	Q3TZS3	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Itga7-204	ENSMUST00000219427.1	984	128aa	Protein coding	-	A0A1W2P7M9	CDS 5' incomplete TSL:1
Itga7-205	ENSMUST00000219897.1	3843	No protein	Retained intron	-	-	TSL:NA
Itga7-203	ENSMUST00000218387.1	933	No protein	Retained intron	-	-	TSL:3

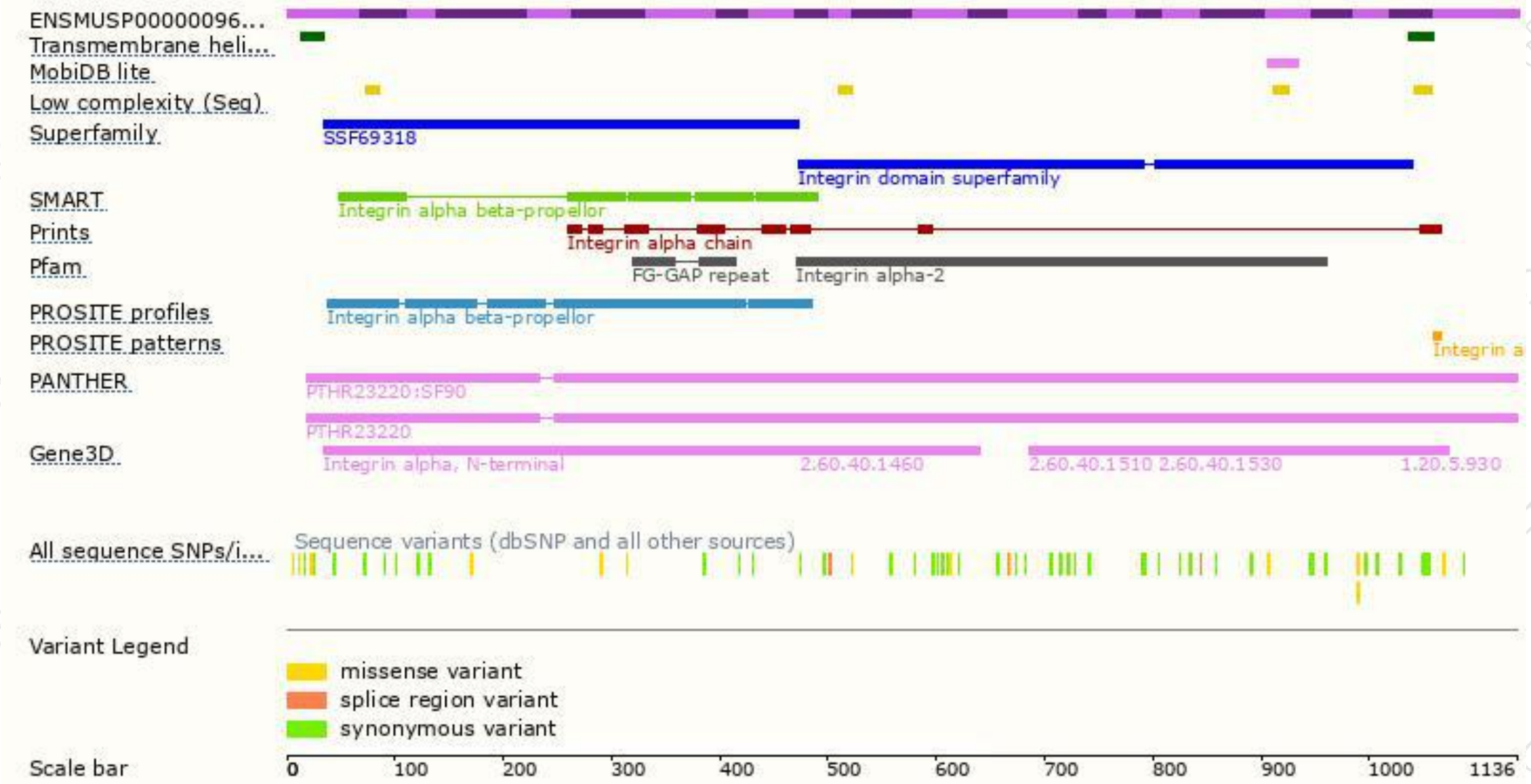
The strategy is based on the design of *Itga7-201* transcript,the transcription is shown below:



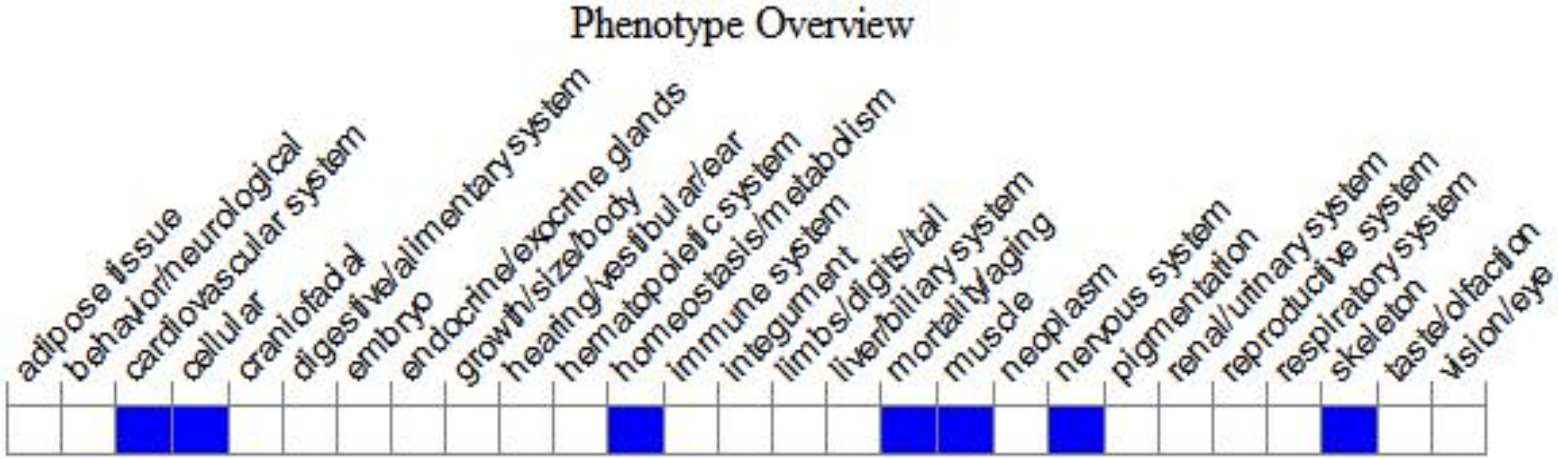
Genomic location distribution



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 disruptions of this gene display characteristics of muscular dystrophy.

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

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