

Itga10 Cas9-KO Strategy

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Design Date: 2018-11-12

Project Overview



Project Name

Itga10

Project type

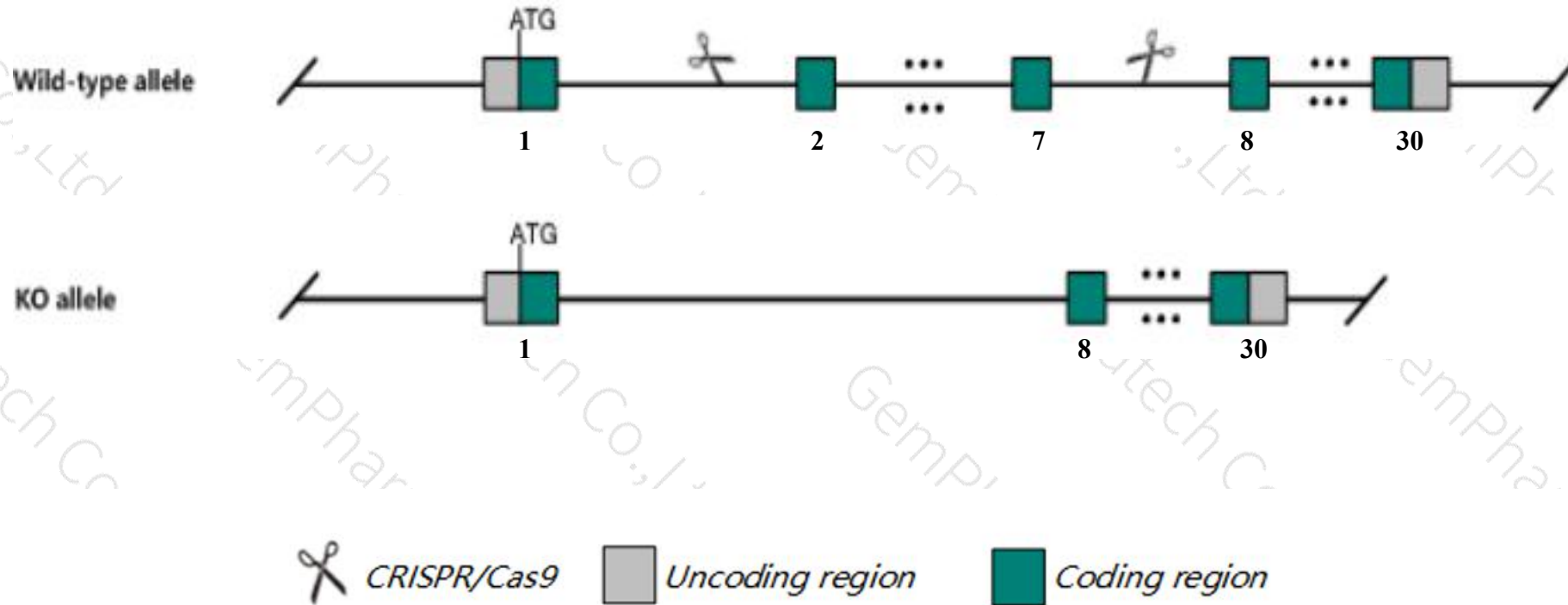
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Itga10* gene. The schematic diagram is as follows:



- The *Itga10* gene has 3 transcripts. According to the structure of *Itga10* gene, exon2-exon7 of *Itga10*-202(ENSMUST00000119365.7) transcript is recommended as the knockout region. The region contains 706bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Itga10* gene. The brief process is as follows: CRISPR/Cas9 system 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

- Gm42957-201 will be destroyed.
- According to the existing MGI data, homozygous null mice display slightly shortened long bones and mild abnormalities in epiphyseal plate morphology.
- The *Itga10* gene is located on the Chr3. 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)

Itga10 integrin, alpha 10 [Mus musculus (house mouse)]

Gene ID: 213119, updated on 13-Mar-2020

Summary



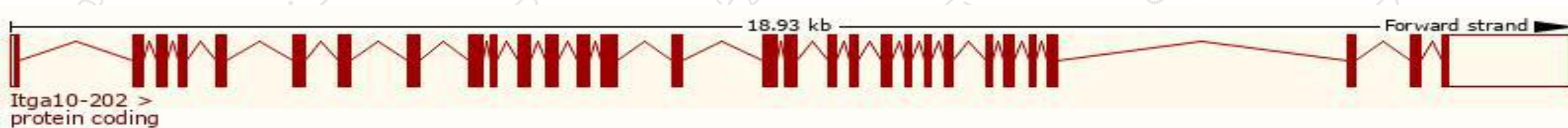
Official Symbol	Itga10 provided by MGI
Official Full Name	integrin, alpha 10 provided by MGI
Primary source	MGI:MGI:2153482
See related	Ensembl:ENSMUSG00000090210
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A630048L14
Expression	Broad expression in limb E14.5 (RPKM 8.9), CNS E14 (RPKM 2.3) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

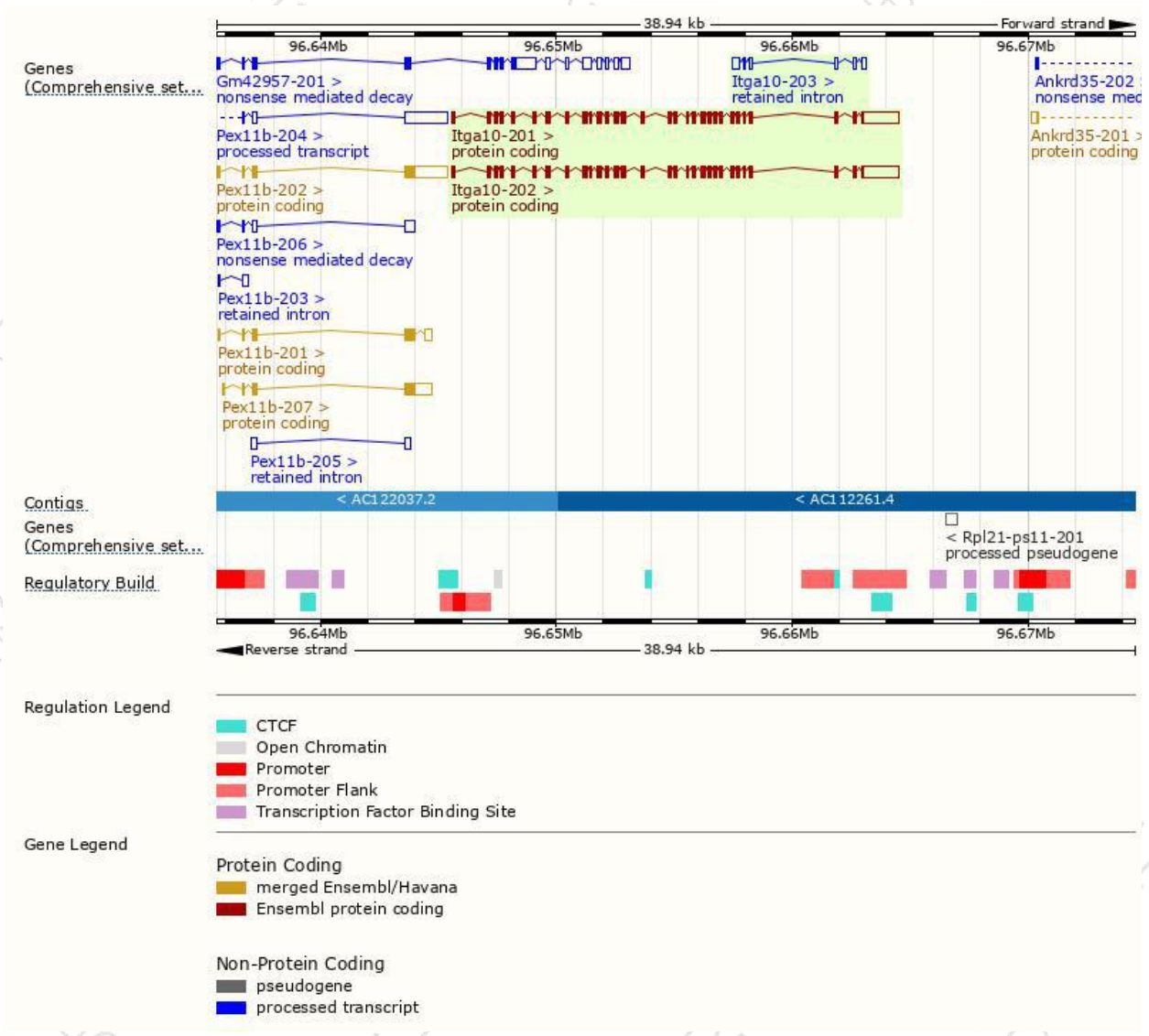
The gene has 3 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Itga10-202	ENSMUST00000119365.7	5035	1166aa	Protein coding	CCDS38557	E9PXZ3	TSL:1 GENCODE basic APPRIS P2
Itga10-201	ENSMUST00000029744.5	5044	1167aa	Protein coding	-	E9Q6R1	TSL:5 GENCODE basic APPRIS ALT2
Itga10-203	ENSMUST00000127607.1	902	No protein	Retained intron	-	-	TSL:5

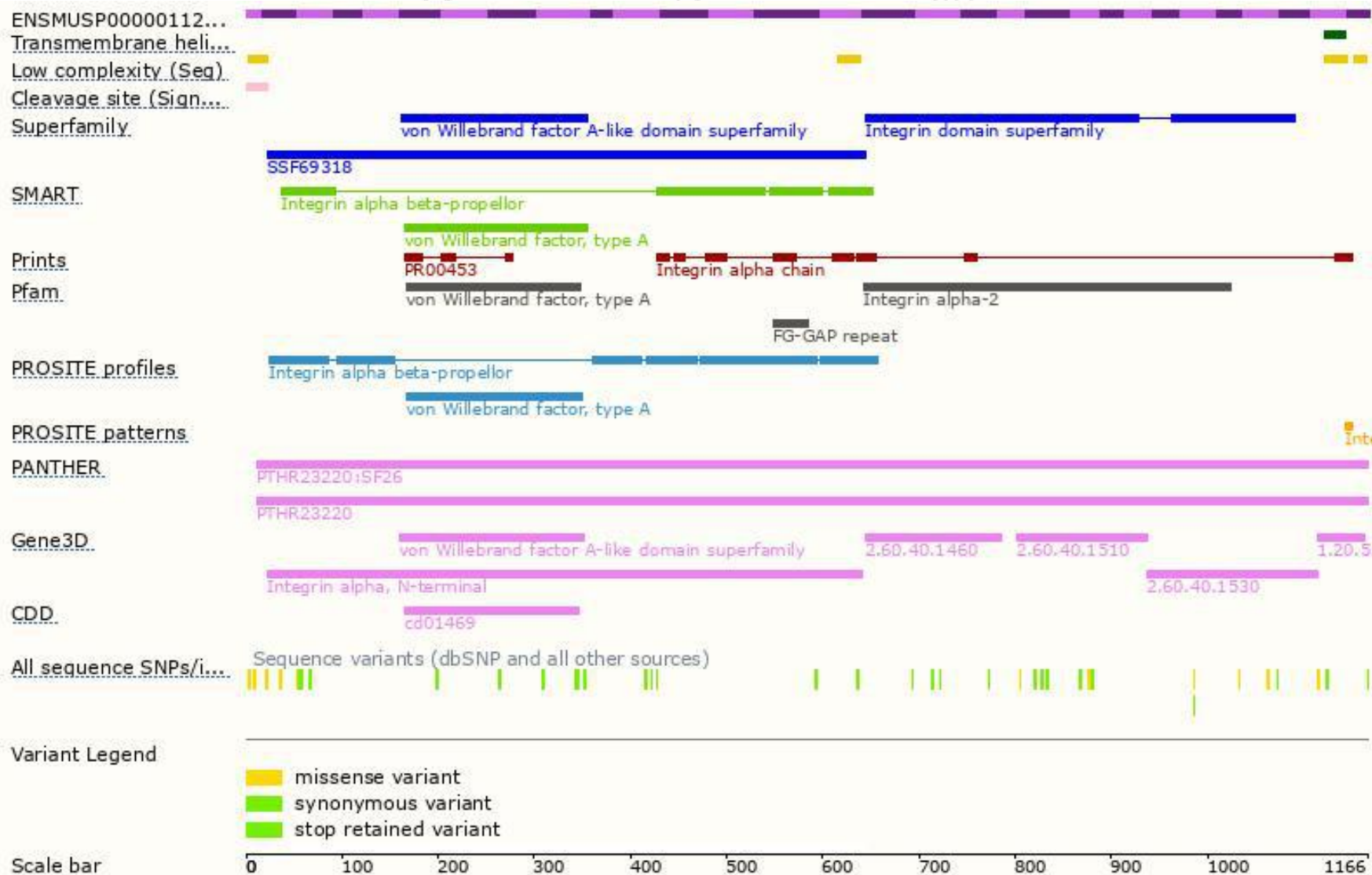
The strategy is based on the design of *Itga10-202* transcript, the transcription is shown below:



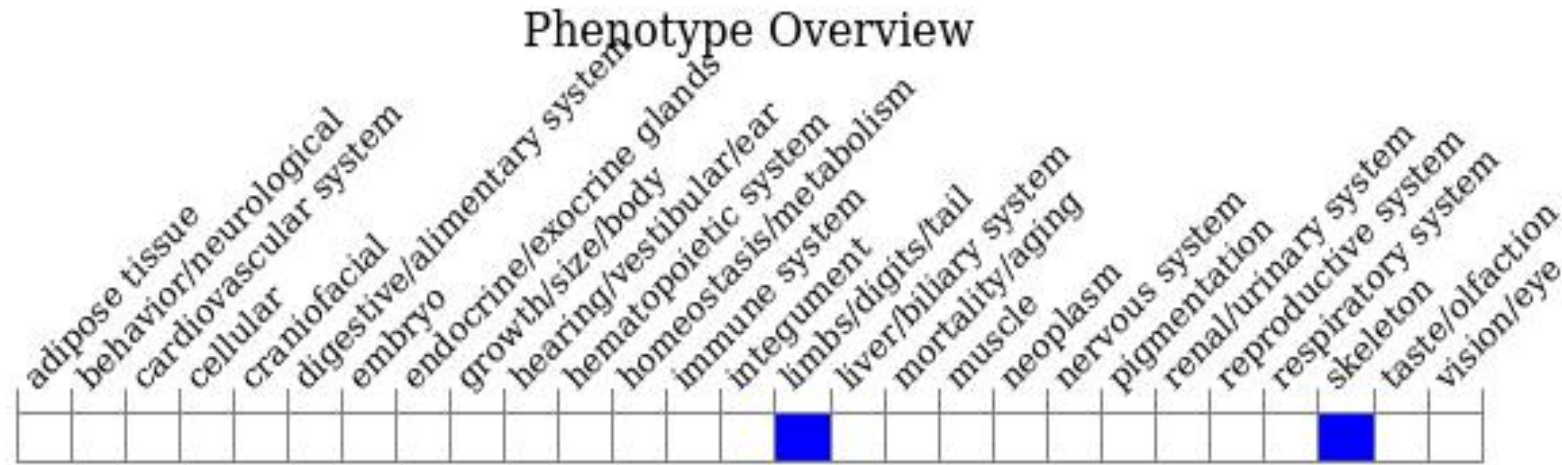
Genomic location distribution



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, homozygous null mice display slightly shortened long bones and mild abnormalities in epiphyseal plate morphology.

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

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