

Ints7 Cas9-KO Strategy

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Project Overview

Project Name

Ints7

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ints7* gene. The schematic diagram is as follows:



- The *Ints7* gene has 6 transcripts. According to the structure of *Ints7* gene, exon2-exon3 of *Ints7-201* (ENSMUST00000045450.6) transcript is recommended as the knockout region. The region contains 277bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ints7* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Ints7* gene is located on the Chr1. 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)

Ints7 integrator complex subunit 7 [*Mus musculus* (house mouse)]

Gene ID: 77065, updated on 12-Aug-2019

Summary

Official Symbol	Ints7 provided by MGI
Official Full Name	integrator complex subunit 7 provided by MGI
Primary source	MGI:MGI:1924315
See related	Ensembl:ENSMUSG00000037461
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	int7; 5930412E23Rik
Expression	Ubiquitous expression in limb E14.5 (RPKM 15.5), thymus adult (RPKM 13.6) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 1; 1 H6

Exon count: 20

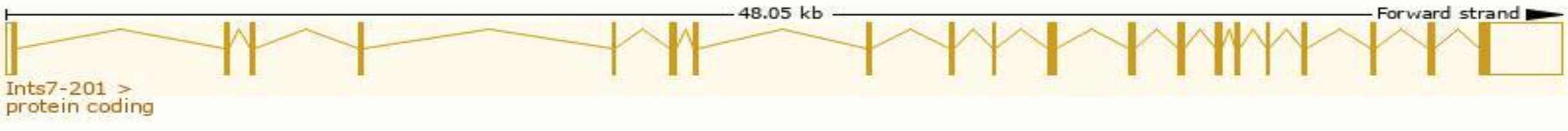
See Ints7 in [Genome Data Viewer](#)

Transcript information (Ensembl)

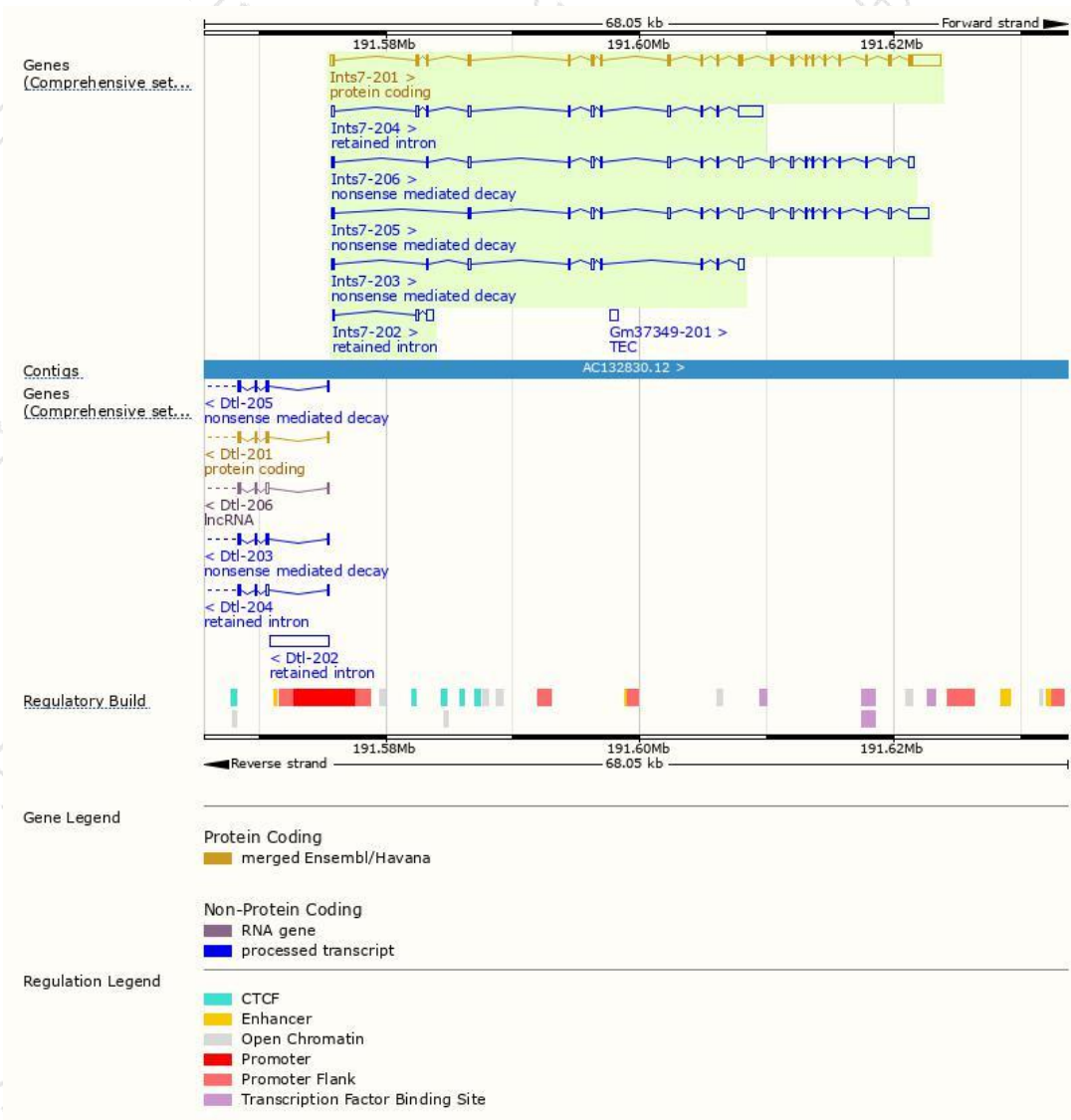
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ints7-201	ENSMUST00000045450.6	5347	966aa	Protein coding	CCDS35825	A0A0R4J0E4	TSL:1 GENCODE basic APPRIS P1
Ints7-205	ENSMUST00000194785.1	4002	60aa	Nonsense mediated decay	-	A0A0A6YX34	TSL:1
Ints7-206	ENSMUST00000194877.5	3069	42aa	Nonsense mediated decay	-	A0A0A6YWX4	TSL:1
Ints7-203	ENSMUST00000193569.5	1510	42aa	Nonsense mediated decay	-	A0A0A6YWX4	TSL:2
Ints7-204	ENSMUST00000193961.5	3177	No protein	Retained intron	-	-	TSL:2
Ints7-202	ENSMUST00000192681.1	849	No protein	Retained intron	-	-	TSL:2

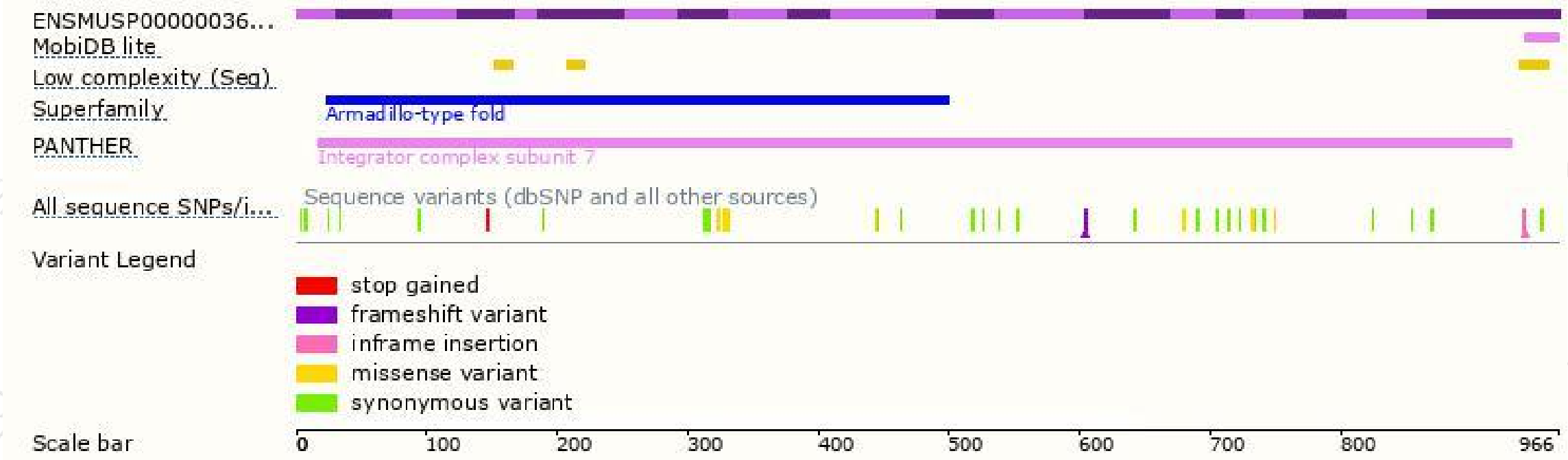
The strategy is based on the design of *Ints7-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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