

***Ints13* Cas9-KO Strategy**

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Project Overview

Project Name

Ints13

Project type

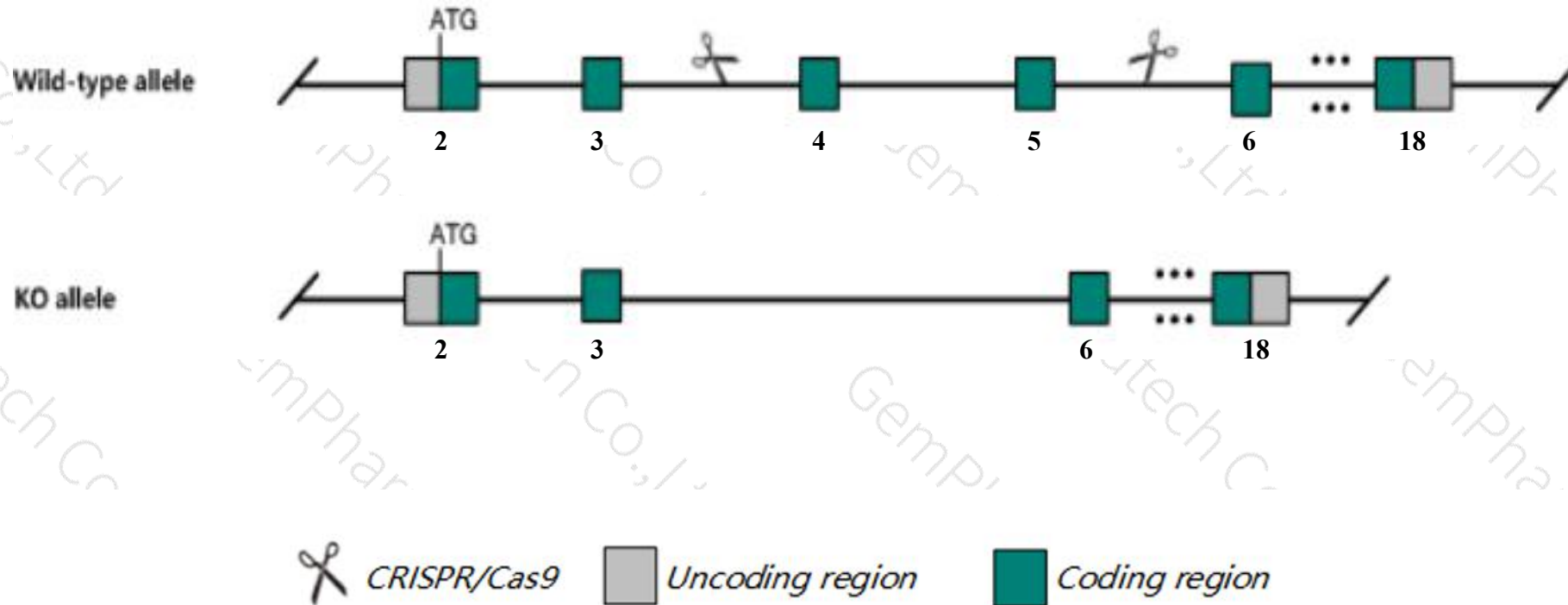
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ints13* gene. The schematic diagram is as follows:



- The *Ints13* gene has 11 transcripts. According to the structure of *Ints13* gene, exon4-exon5 of *Ints13-201* (ENSMUST00000032427.14) transcript is recommended as the knockout region. The region contains 284bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ints13* gene. The brief process is as follows: CRISPR/Cas9 system we

- The *Ints13* 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.
- Transcripts *Ints13-207* and *Ints13-209* are incomplete, so the effect on them are unknown.
- 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)

Ints13 integrator complex subunit 13 [*Mus musculus* (house mouse)]

Gene ID: 71177, updated on 13-Mar-2020

Summary

Official Symbol Ints13 provided by [MGI](#)

Official Full Name integrator complex subunit 13 provided by [MGI](#)

Primary source [MGI:MGI:1918427](#)

See related [Ensembl:ENSMUSG00000040250](#)

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 Asun; Spata30; 4933424B01Rik

Expression Ubiquitous expression in CNS E11.5 (RPKM 16.0), testis adult (RPKM 14.4) and 28 other tissues [See more](#)

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

Transcript information (Ensembl)

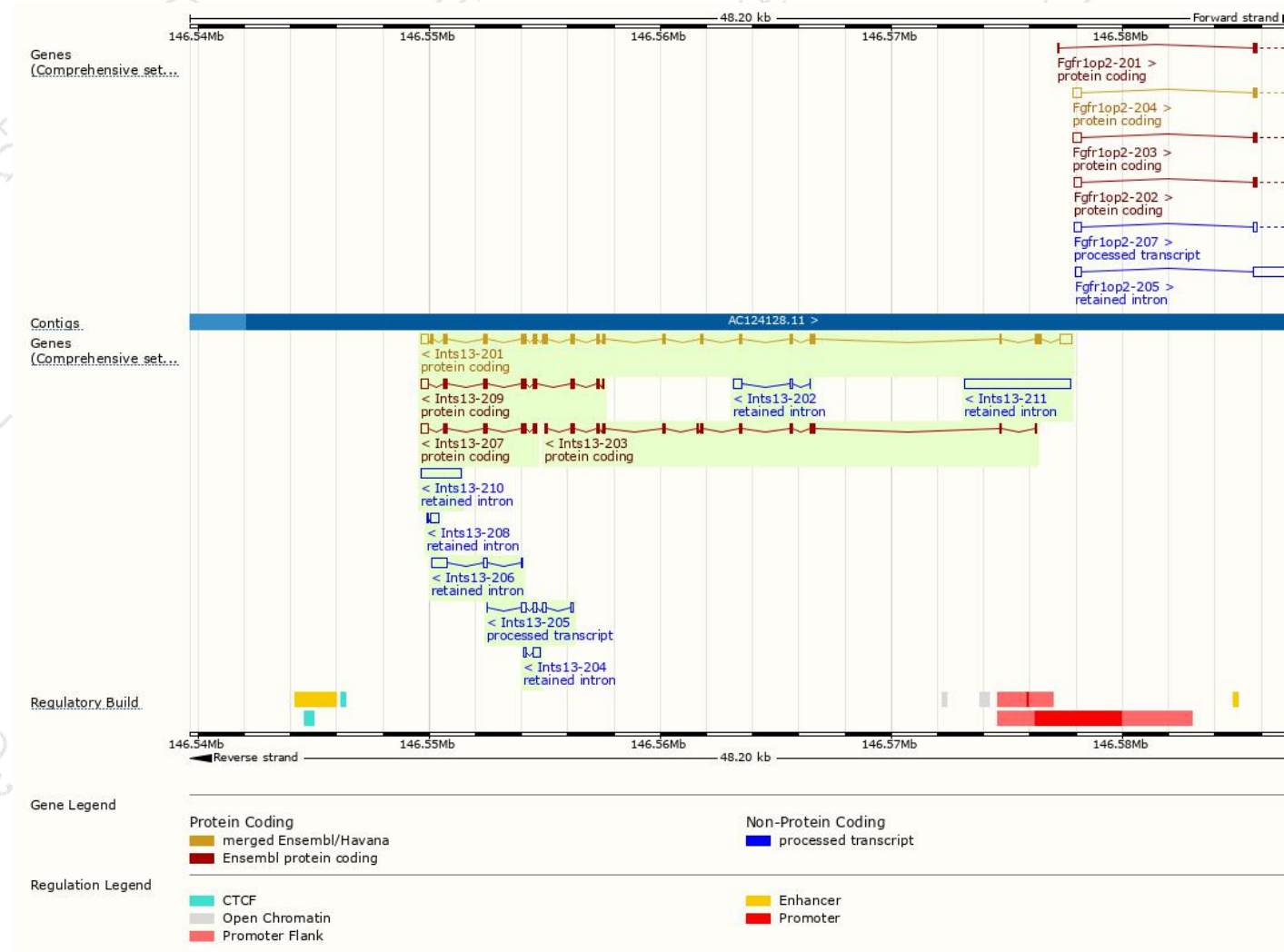
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ints13-201	ENSMUST00000032427.14	3059	732aa	Protein coding	CCDS39710	Q8QZV7	TSL:1 GENCODE basic APPRIS P1
Ints13-209	ENSMUST000000203545.2	1298	327aa	Protein coding	-	A0A0N4SVS8	CDS 5' incomplete TSL:5
Ints13-203	ENSMUST000000131662.1	1185	395aa	Protein coding	-	F6W761	CDS 5' and 3' incomplete TSL:5
Ints13-207	ENSMUST000000139979.7	1005	230aa	Protein coding	-	F7BP94	CDS 5' incomplete TSL:2
Ints13-205	ENSMUST000000135277.1	640	No protein	Processed transcript	-	-	TSL:5
Ints13-211	ENSMUST000000205078.1	4601	No protein	Retained intron	-	-	TSL:NA
Ints13-210	ENSMUST000000204234.1	1740	No protein	Retained intron	-	-	TSL:NA
Ints13-206	ENSMUST000000139546.1	873	No protein	Retained intron	-	-	TSL:2
Ints13-204	ENSMUST000000132963.1	454	No protein	Retained intron	-	-	TSL:3
Ints13-202	ENSMUST000000126996.1	426	No protein	Retained intron	-	-	TSL:5
Ints13-208	ENSMUST000000152994.1	370	No protein	Retained intron	-	-	TSL:2

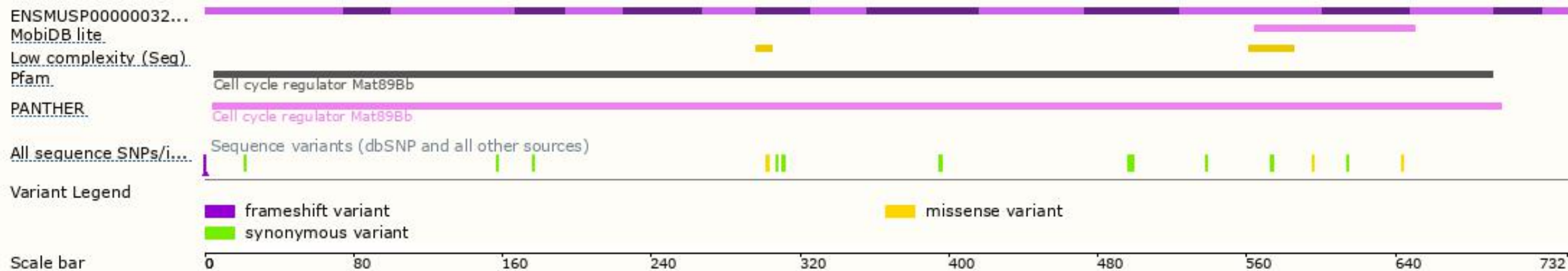
The strategy is based on the design of *Ints13-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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