

Ints12 Cas9-CKO Strategy

Designer:

Huan Fan

Design Date:

2019-10-18

Project Overview

Project Name

Ints12

Project type

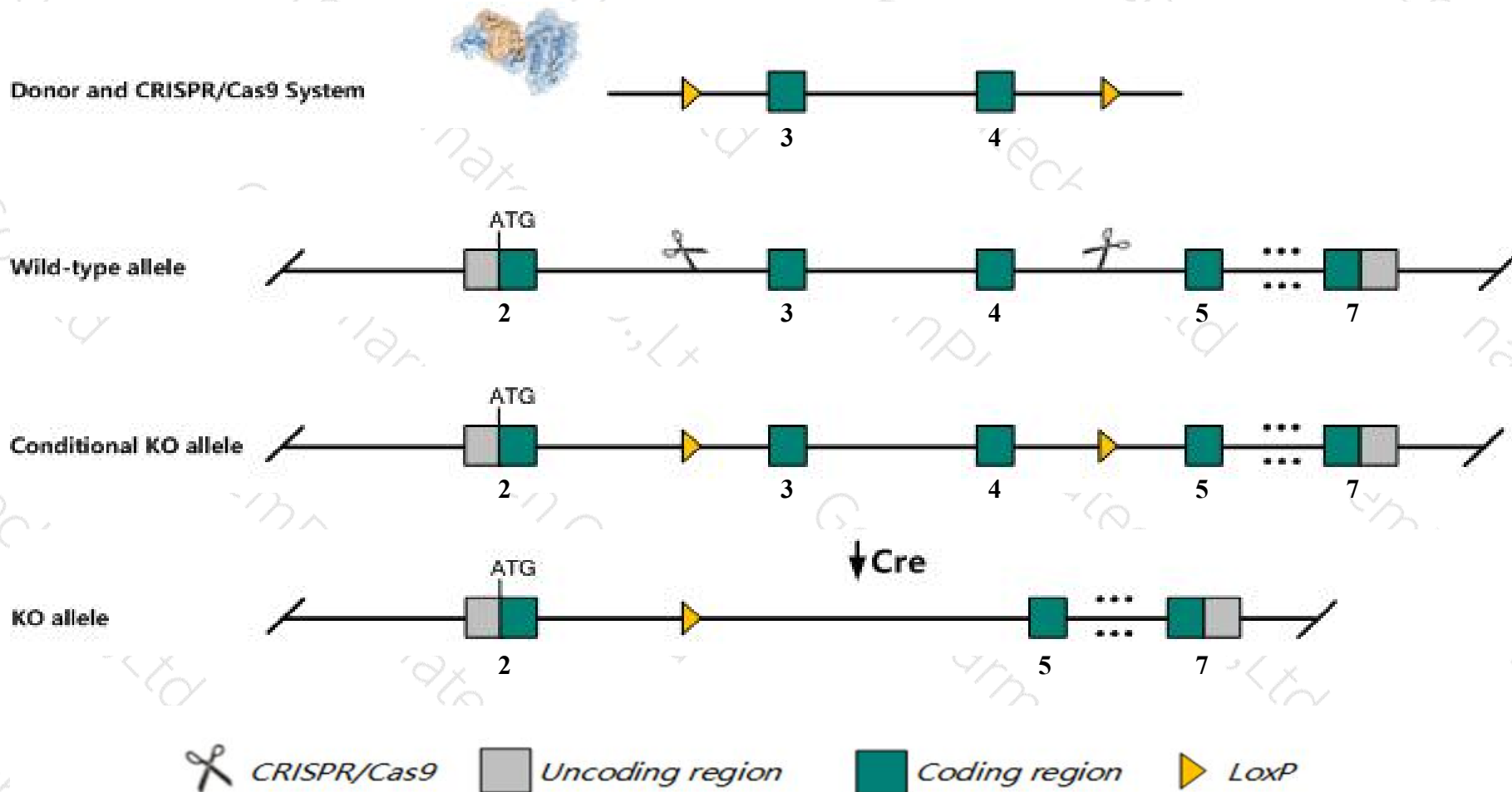
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ints12* gene. The schematic diagram is as follows:



Technical routes

- The *Ints12* gene has 3 transcripts. According to the structure of *Ints12* gene, exon3-exon4 of *Ints12-201* (ENSMUST00000029650.8) transcript is recommended as the knockout region. The region contains 338bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ints12* gene. The brief process is as follows: CRISPR/Cas9 system 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

- The *Ints12* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Ints12 integrator complex subunit 12 [Mus musculus (house mouse)]

Gene ID: 71793, updated on 9-Apr-2019

Summary



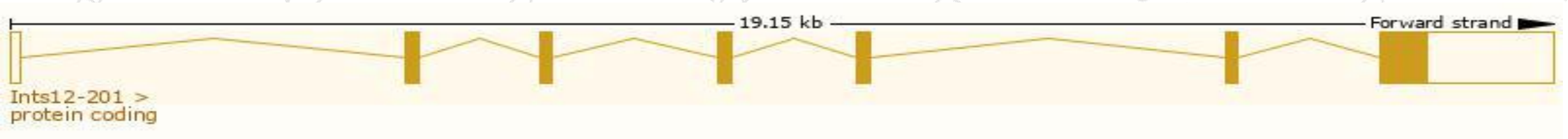
Official Symbol	Ints12 provided by MGI
Official Full Name	integrator complex subunit 12 provided by MGI
Primary source	MGI:MGI:1919043
See related	Ensembl:ENSMUSG00000028016
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110020M19Rik, 2810027J24Rik, 4930529N21Rik, A230056J18Rik, AI666778, Phf22, int12
Expression	Ubiquitous expression in CNS E11.5 (RPKM 6.0), placenta adult (RPKM 4.7) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

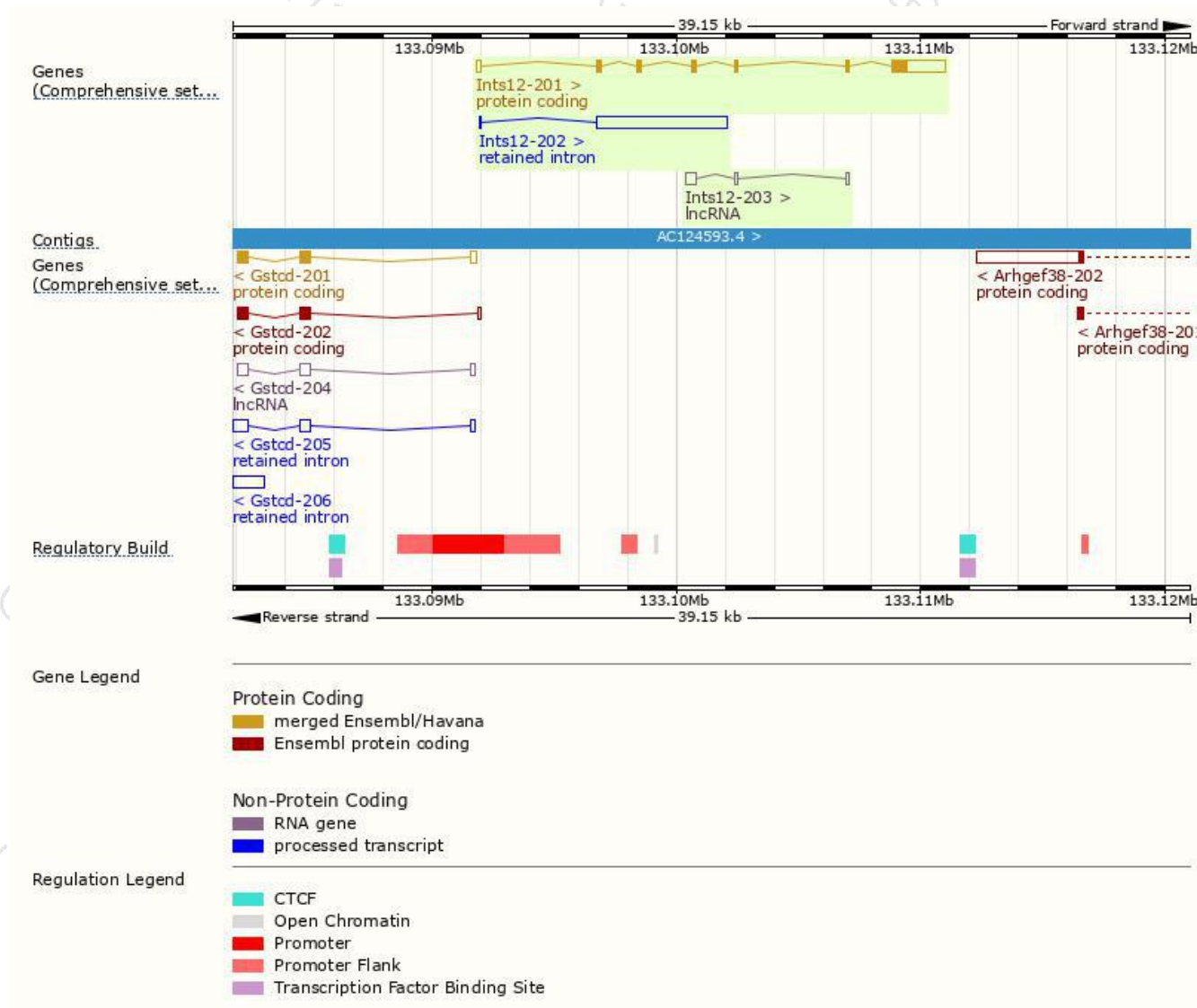
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ints12-201	ENSMUST00000029650.8	3101	461aa	Protein coding	CCDS17848	Q9D168	TSL:1 GENCODE basic APPRIS P1
Ints12-202	ENSMUST00000160036.2	5386	No protein	Retained intron	-	-	TSL:1
Ints12-203	ENSMUST00000160669.1	728	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Ints12-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP00000029...

[SIFTS import](#)

[MobiDB lite](#)

[Low complexity \(Seq\)](#)

[Superfamily](#)

[SMART](#)

[Pfam](#)

[PROSITE profiles](#)

[PROSITE patterns](#)

[PANTHER](#)

[Gene3D](#)

[CDD](#)

[All sequence SNPs/i....](#)

Variant Legend

-  missense variant
-  splice region variant
-  synonymous variant

Scale bar

0 40 80 120 160 200 240 280 320 360 400 461

Zinc finger, FYVE/PHD-type

Zinc finger, PHD-type

Zinc finger, PHD-finger

Zinc finger, PHD-finger

Zinc finger, PHD-type, conserved site

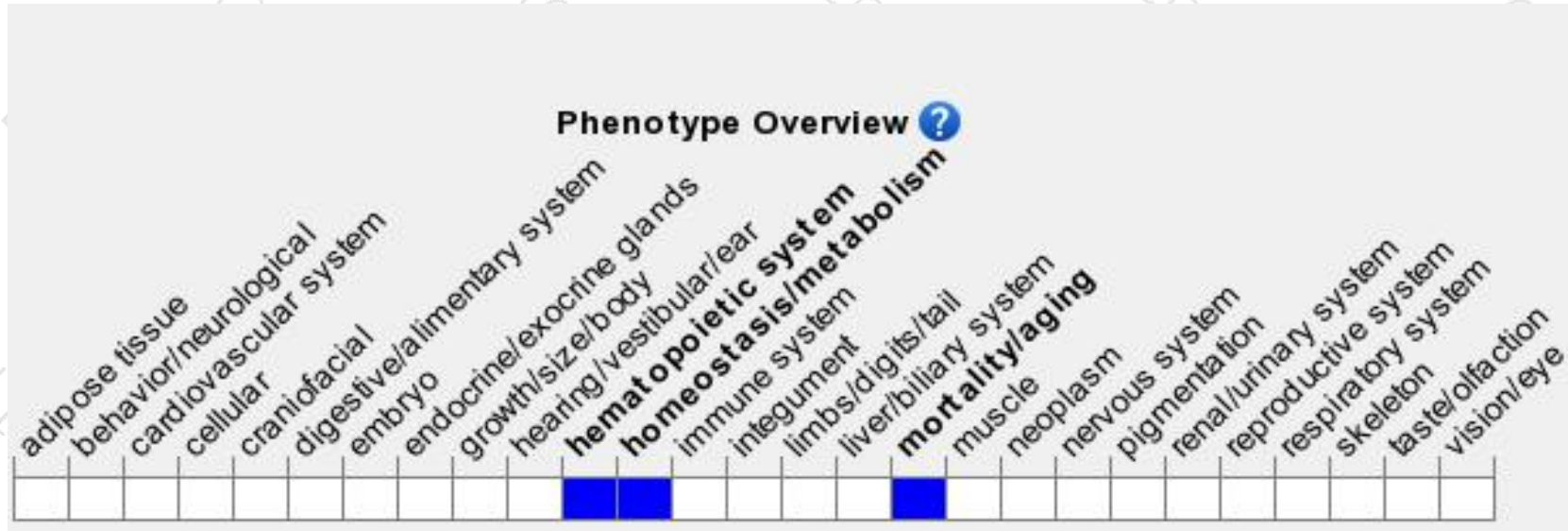
Integrator complex subunit 12

Zinc finger, RING/FYVE/PHD-type

Int12, PHD finger

Sequence variants (dbSNP and all other sources)

Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

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

Tel: 400-9660890

