

Ints2 Cas9-KO Strategy

Designer:

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Design Date:

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Project Overview

Project Name

Ints2

Project type

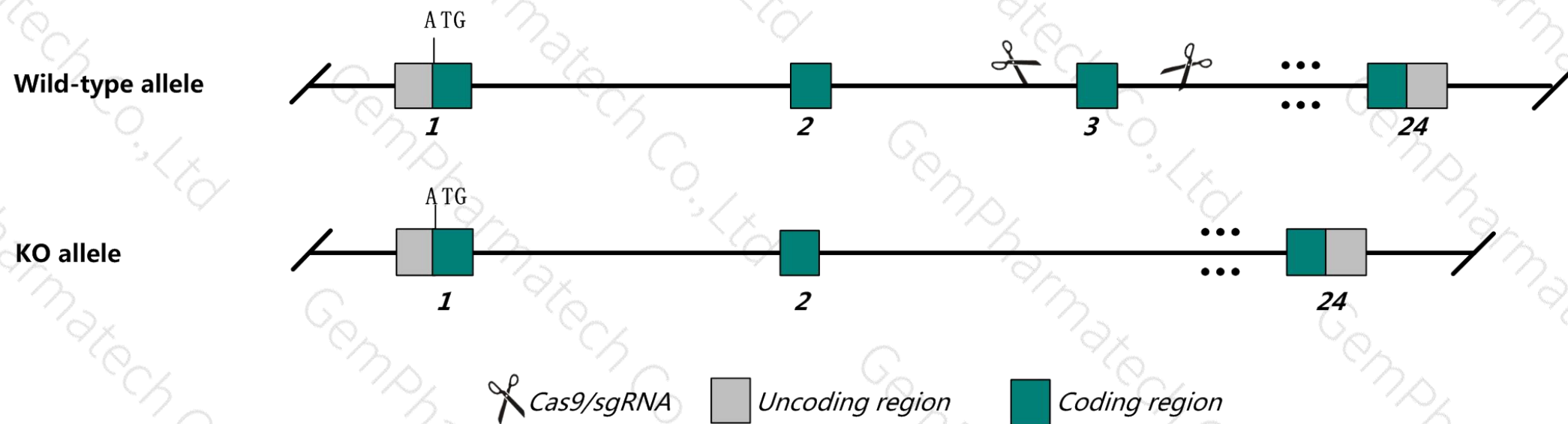
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ints2* gene. The schematic diagram is as follows:



Technical routes

- The *Ints2* gene has 11 transcripts. According to the structure of *Ints2* gene, exon3 of *Ints2*-202 transcript is recommended as the knockout region. The region contains 103bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ints2* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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.

- Transcript *Ints2-205,208* may not be affected.
- The KO region contains functional region of the *Brip1os* gene. Knockout the region may affect the function of *Brip1os* gene.
- The *Ints2* gene is located on the Chr11. 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)

Ints2 integrator complex subunit 2 [*Mus musculus* (house mouse)]

Gene ID: 70422, updated on 4-Jul-2019

Summary



Official Symbol Ints2 provided by [MGI](#)

Official Full Name integrator complex subunit 2 provided by [MGI](#)

Primary source [MGI:MGI:1917672](#)

See related [Ensembl:ENSMUSG00000018068](#)

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 AA408260; A1987735; mKIAA1287; 2810417D08Rik

Expression Ubiquitous expression in CNS E11.5 (RPKM 9.9), CNS E14 (RPKM 7.3) and 24 other tissues [See more](#)

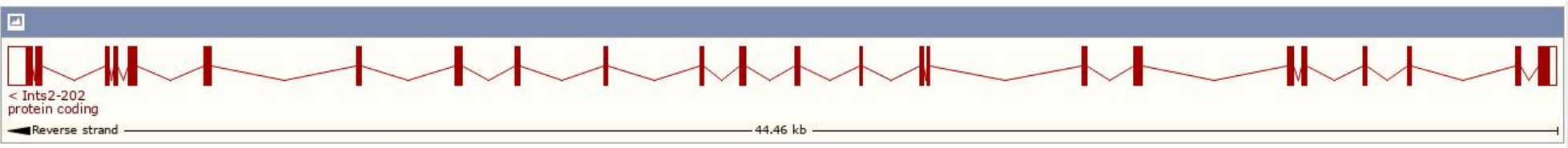
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

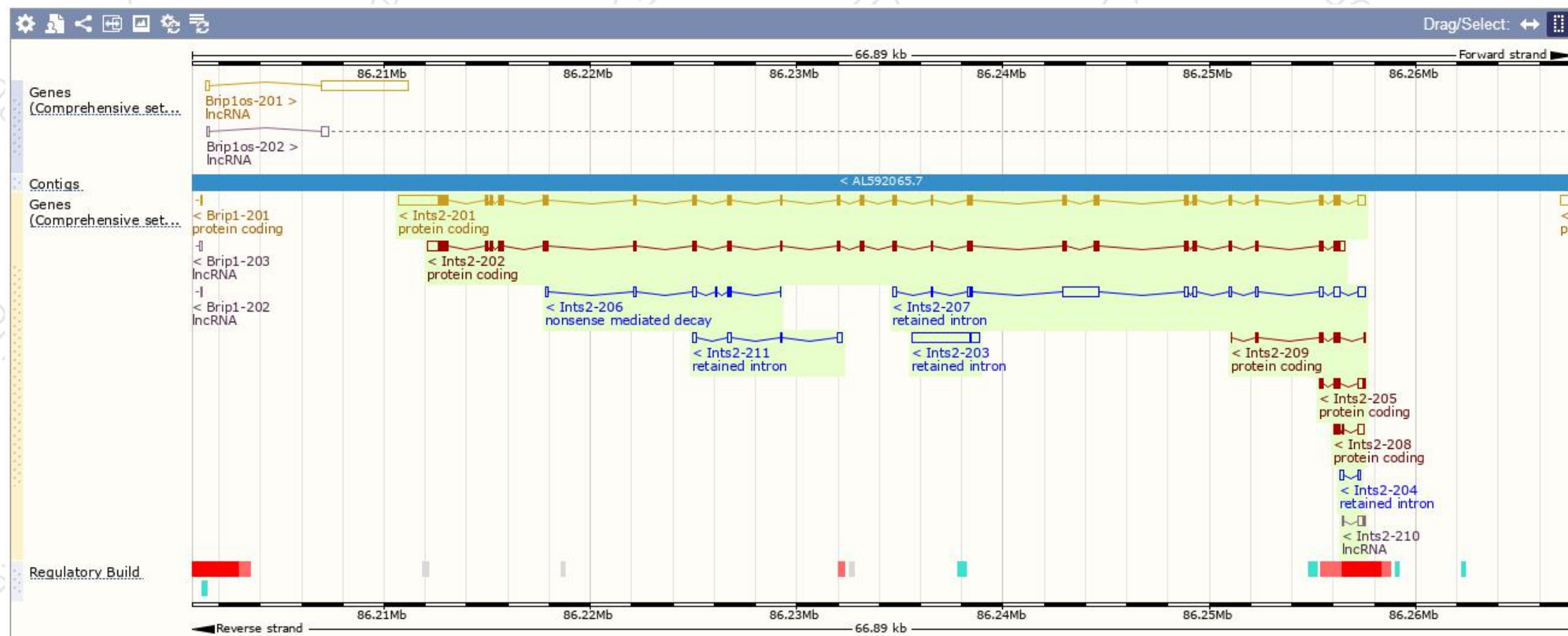
The gene has 11 transcripts, and all transcripts are shown below:

Show/hide columns (1 hidden)		Filter					
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ints2-201	ENSMUST00000018212.12	5906	1198aa	Protein coding	CCDS25198	Q80UK8	TSL:1 GENCODE basic APPRIS P1
Ints2-202	ENSMUST000000108039.7	4369	1198aa	Protein coding	CCDS25198	Q80UK8	TSL:1 GENCODE basic APPRIS P1
Ints2-208	ENSMUST000000136469.1	695	97aa	Protein coding	-	Q5SXZ7	CDS 3' incomplete TSL:2
Ints2-205	ENSMUST000000132024.7	694	140aa	Protein coding	-	A0A0A0MQG3	CDS 3' incomplete TSL:3
Ints2-209	ENSMUST000000139285.7	638	189aa	Protein coding	-	X1WI16	CDS 3' incomplete TSL:3
Ints2-206	ENSMUST000000134828.7	721	67aa	Nonsense mediated decay	-	H3BK92	CDS 5' incomplete TSL:3
Ints2-207	ENSMUST000000134883.1	3414	No protein	Retained intron	-	-	TSL:2
Ints2-203	ENSMUST000000127745.1	3181	No protein	Retained intron	-	-	TSL:1
Ints2-211	ENSMUST000000146421.1	684	No protein	Retained intron	-	-	TSL:2
Ints2-204	ENSMUST000000130614.1	282	No protein	Retained intron	-	-	TSL:3
Ints2-210	ENSMUST000000141756.1	328	No protein	lncRNA	-	-	TSL:5

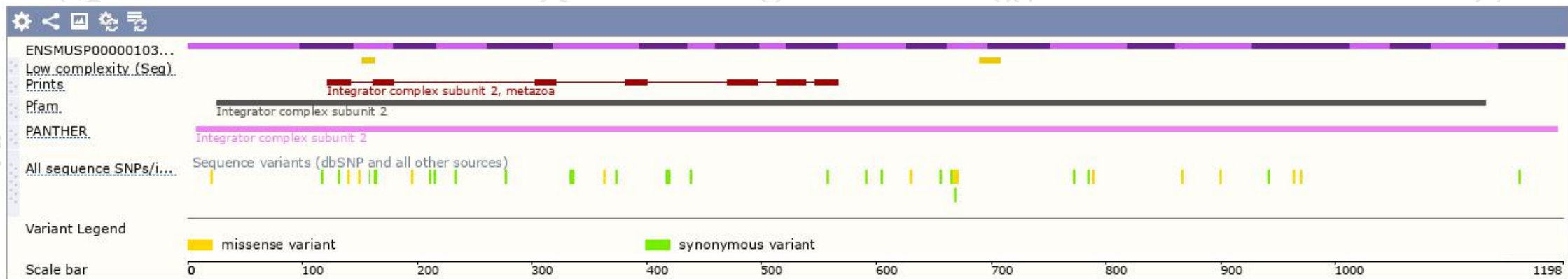
The strategy is based on the design of *Ints2-202* transcript, The transcription is shown below



Genomic location distribution

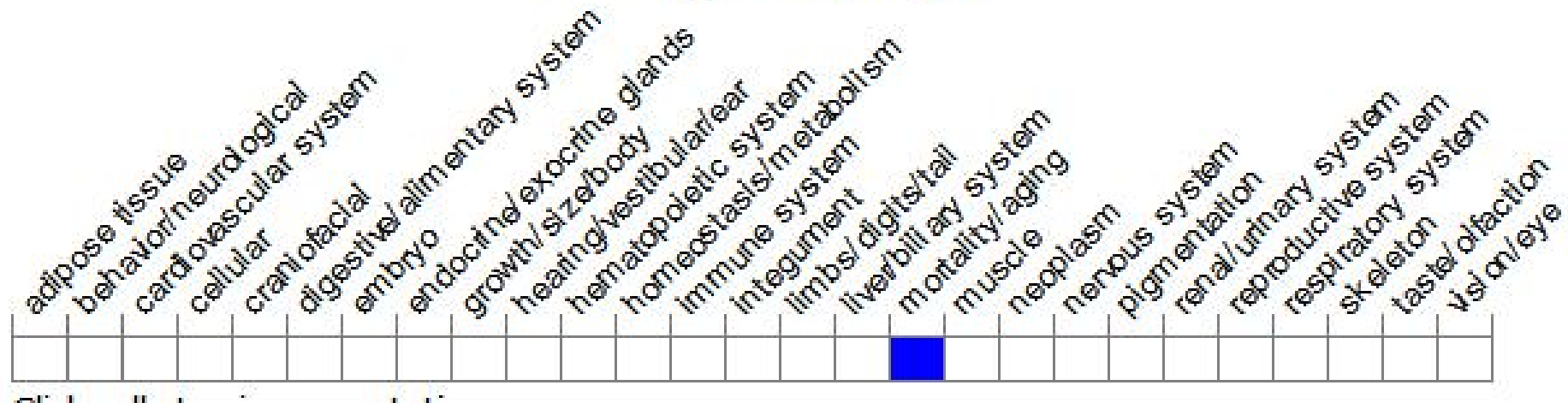


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview ?



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, Mutations in this locus affect cell-cycle regulation and apoptosis. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

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