Ints11 Cas9-CKO Strategy

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Project Overview

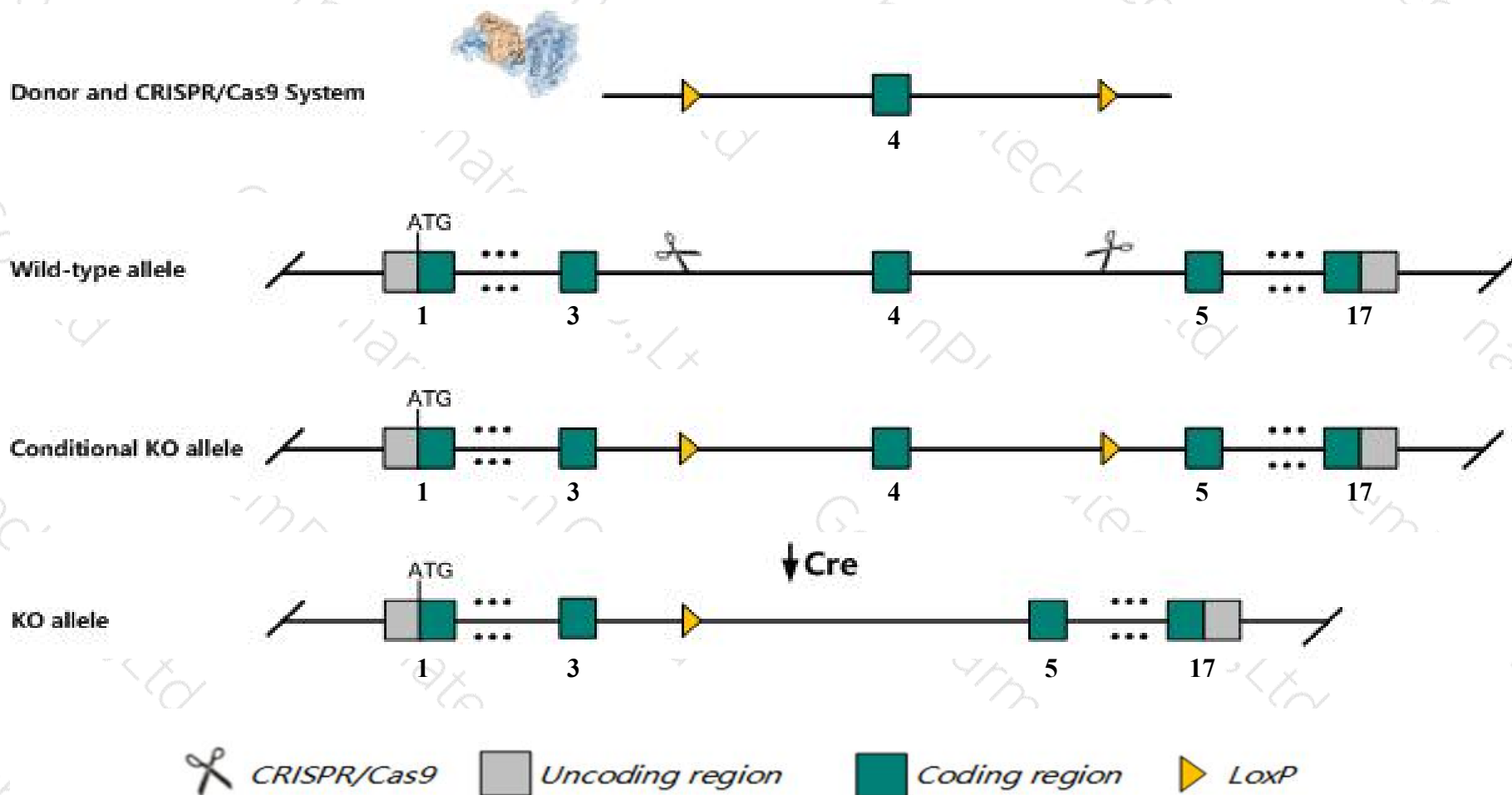|	
Project Name	*Ints11*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ints11* gene. The schematic diagram is as follows:

Technical routes

➤ The *Ints11* gene has 7 transcripts. According to the structure of *Ints11* gene, exon4 of *Ints11-201* (ENSMUST00000030901.8) transcript is recommended as the knockout region.The region contains Ens 229bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Ints11* 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 *Ints11* gene is located on the Chr4. 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）

Ints11 integrator complex subunit 11 [Mus musculus (house mouse)]

Gene ID: 71957, updated on 31-Jan-2019

Summary

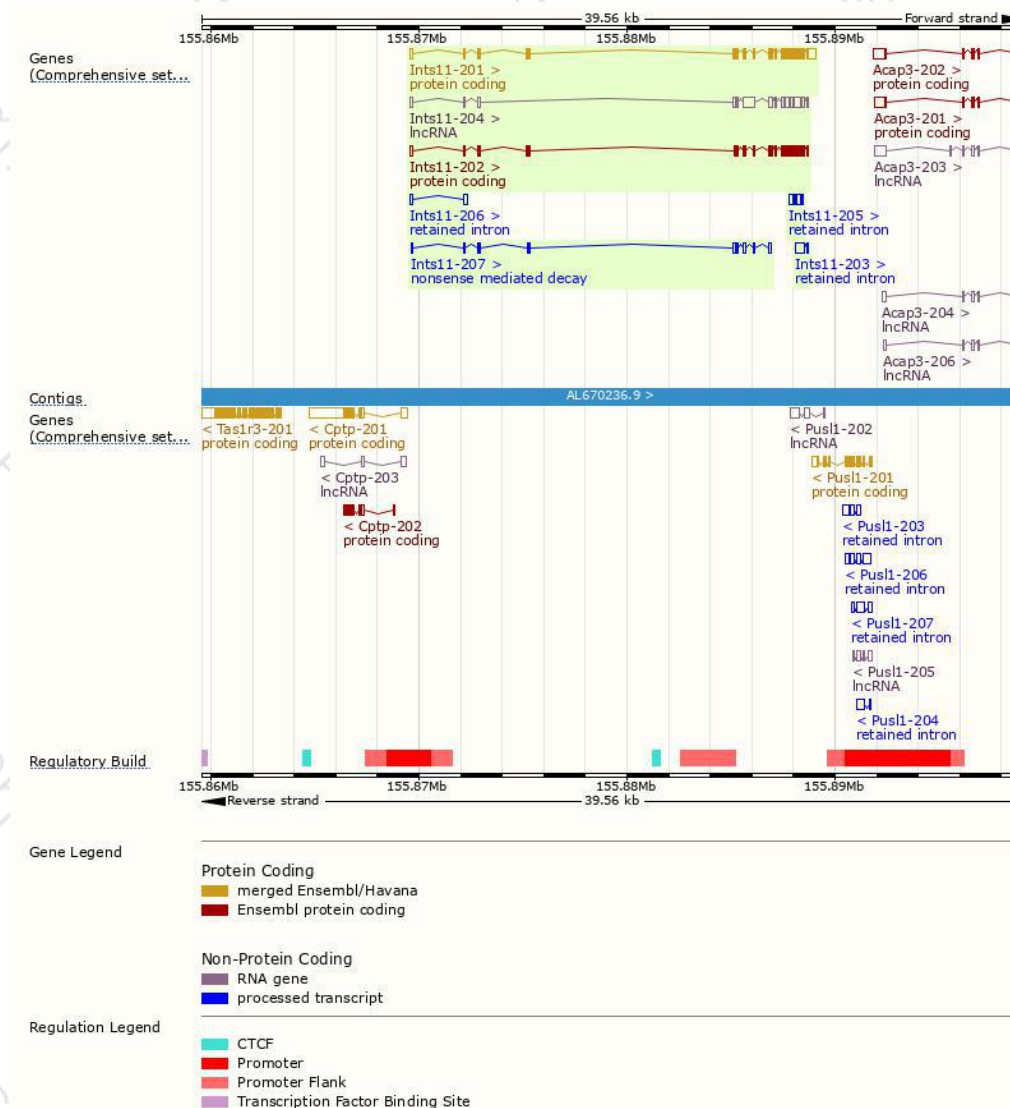|	
Official Symbol	Ints11 provided by MGI
Official Full Name	integrator complex subunit 11 provided by MGI
Primary source	MGI:MGI:1919207
See related	Ensembl:ENSMUSG00000029034
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410006F12Rik, AU044035, Cpsf3l
Expression	Ubiquitous expression in thymus adult (RPKM 20.9), CNS E14 (RPKM 18.1) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ints11-201	ENSMUST00000030901.8	2368	600aa	Protein coding	CCDS19048	Q9CWS4	TSL:1 GENCODE basic APPRIS P1
Ints11-202	ENSMUST00000120794.7	1884	578aa	Protein coding	-	A8Y5J3	TSL:5 GENCODE basic
Ints11-207	ENSMUST00000156460.1	880	94aa	Nonsense mediated decay	-	D6RH69	TSL:5
Ints11-203	ENSMUST00000132632.1	517	No protein	Retained intron	-	-	TSL:1
Ints11-205	ENSMUST00000135844.1	481	No protein	Retained intron	-	-	TSL:2
Ints11-206	ENSMUST00000149458.1	340	No protein	Retained intron	-	-	TSL:2
Ints11-204	ENSMUST00000134678.7	2197	No protein	lncRNA	-	-	TSL:5

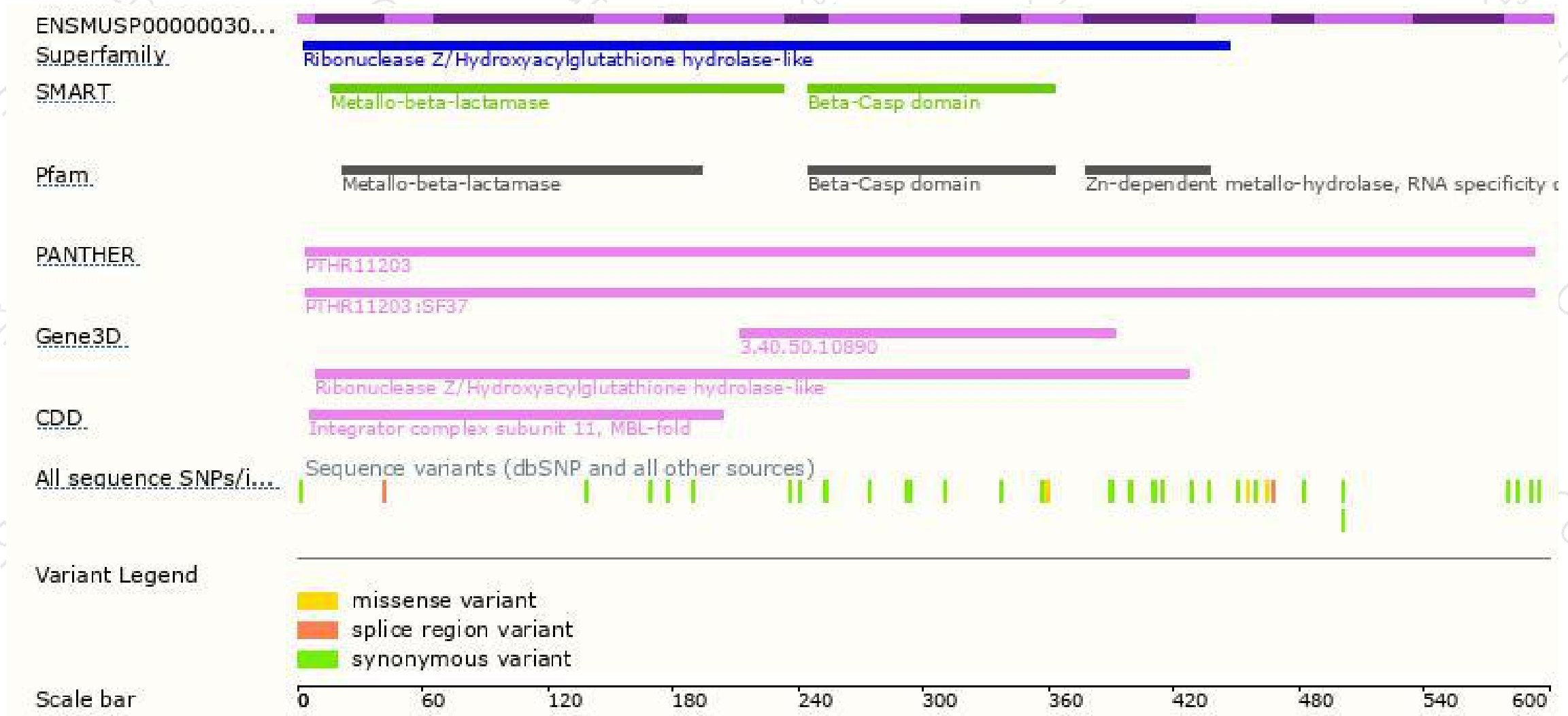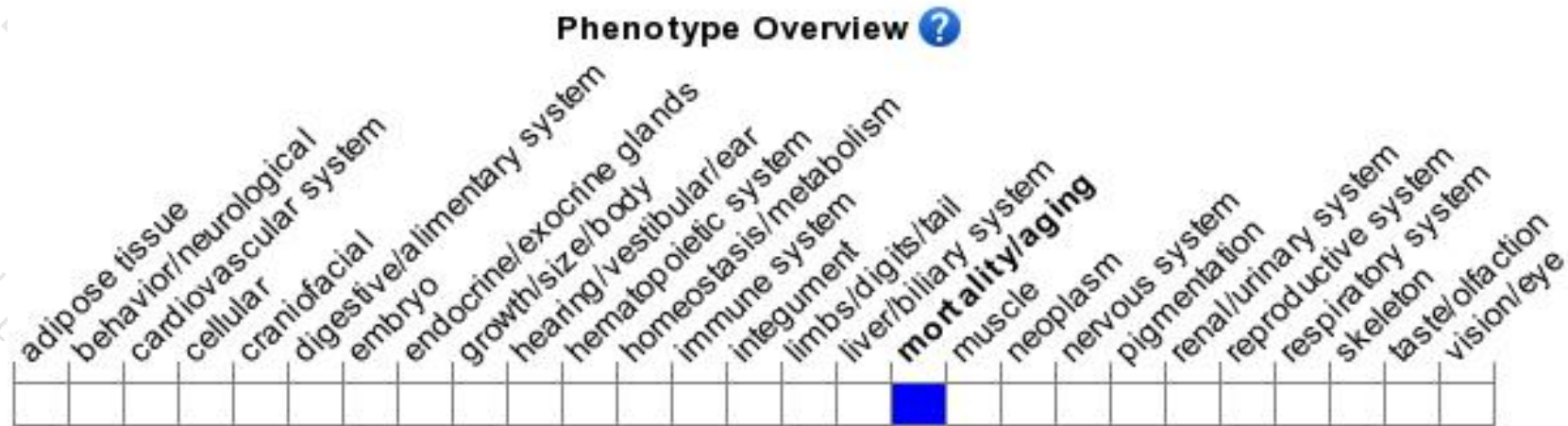The strategy is based on the design of *Ints11-201* transcript,The transcription is shown below

Genomic location distribution

Protein domain

ENSMUSP00000030...		
Superfamily	Ribonuclease Z/Hydroxyacylglutathione hydrolase-like	
SMART	Metallo-beta-lactamase	Beta-Casp domain
Pfam	Metallo-beta-lactamase	Beta-Casp domain · Zn-dependent metallo-hydrolase, RNA specificity
PANTHER	PTHR11203	
	PTHR11203:SF37	
Gene3D	3.40.50.10890	
	Ribonuclease Z/Hydroxyacylglutathione hydrolase-like	
CDD	Integrator complex subunit 11, MBL-fold	
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)	

Variant Legend

- missense variant
- splice region variant
- synonymous variant

Scale bar: 0 60 120 180 240 300 360 420 480 540 600

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.
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