

Lrba Cas9-CKO Strategy

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Design Date:

2020-2-25

Project Overview

Project Name

Lrba

Project type

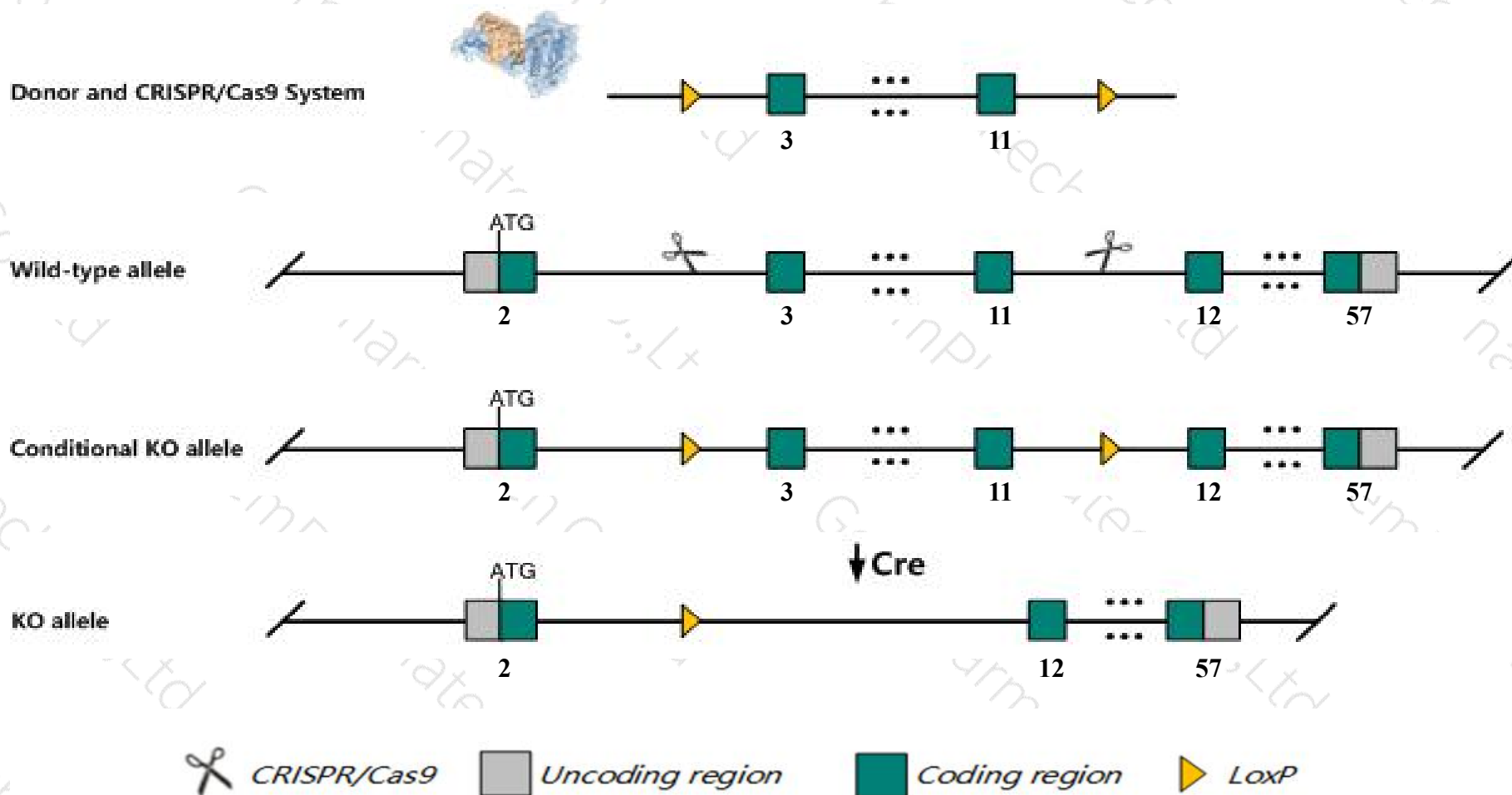
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Lrba* gene has 8 transcripts. According to the structure of *Lrba* gene, exon3-exon11 of *Lrba*-201 (ENSMUST00000107635.6) transcript is recommended as the knockout region. The region contains 1277bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lrba* 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.

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit increased numbers of myeloid-derived suppressor cells and regulatory T cells, abnormal NK cell physiology, impaired rejection of allogeneic, xenogeneic and missing self bone-marrow grafts, and resistance to acute graft vs host disease.
- Transcript *Lrba-206* may not be affected.
- The *Lrba* 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)

Lrba LPS-responsive beige-like anchor [Mus musculus (house mouse)]

Gene ID: 80877, updated on 16-Mar-2019

Summary



Official Symbol	Lrba provided by MGI
Official Full Name	LPS-responsive beige-like anchor provided by MGI
Primary source	MGI:MGI:1933162
See related	Ensembl:ENSMUSG00000028080
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	C80285, D3Erd775e, Lab300, Lba
Expression	Ubiquitous expression in kidney adult (RPKM 5.1), large intestine adult (RPKM 4.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

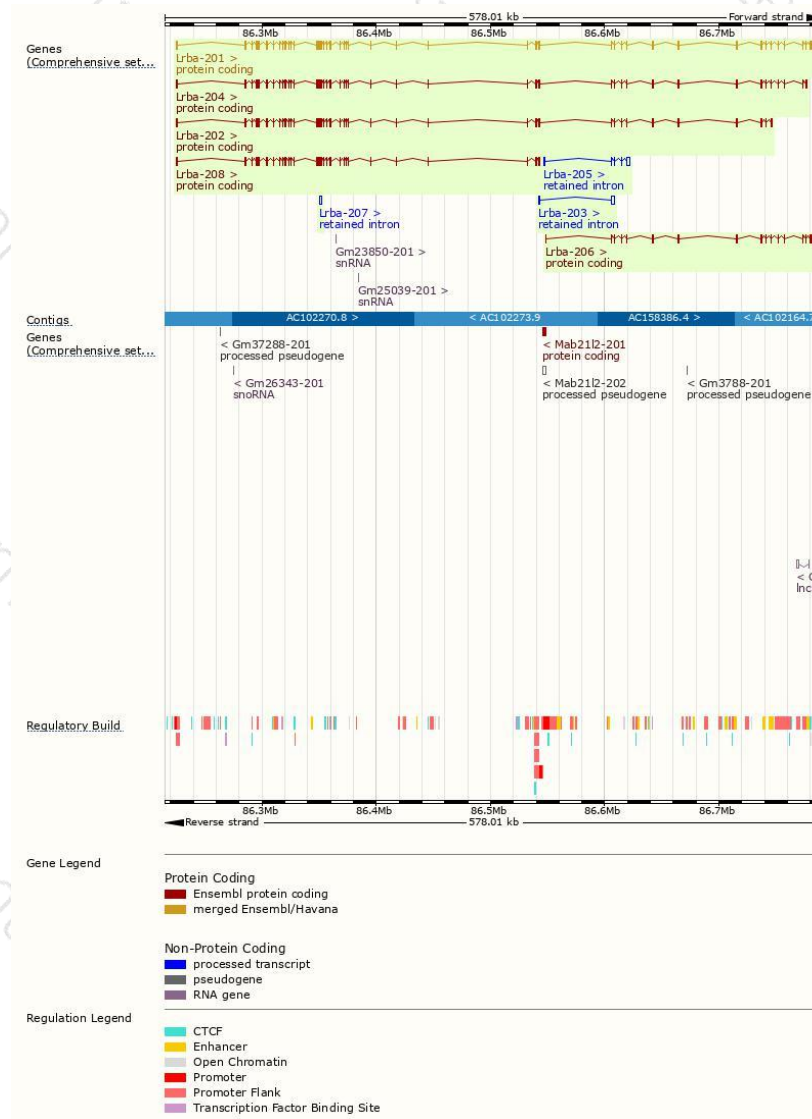
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lrba-201	ENSMUST00000107635.6	9888	2854aa	Protein coding	CCDS38470	E9Q3Y4	TSL:1 GENCODE basic APPRIS P3
Lrba-204	ENSMUST00000194759.5	9379	2790aa	Protein coding	CCDS79933	A0A0A6YXL6	TSL:1 GENCODE basic APPRIS ALT2
Lrba-202	ENSMUST00000192145.5	8843	2577aa	Protein coding	CCDS79934	A0A0A6YXX3	TSL:1 GENCODE basic APPRIS ALT2
Lrba-208	ENSMUST00000212390.1	6372	2124aa	Protein coding	-	A0A1D5RM41	CDS 3' incomplete TSL:5
Lrba-206	ENSMUST00000195524.1	3322	758aa	Protein coding	-	Q8BSM6	TSL:1 GENCODE basic
Lrba-205	ENSMUST00000195398.1	4283	No protein	Retained intron	-	-	TSL:1
Lrba-203	ENSMUST00000194674.1	3231	No protein	Retained intron	-	-	TSL:1
Lrba-207	ENSMUST00000195966.1	1338	No protein	Retained intron	-	-	TSL:NA

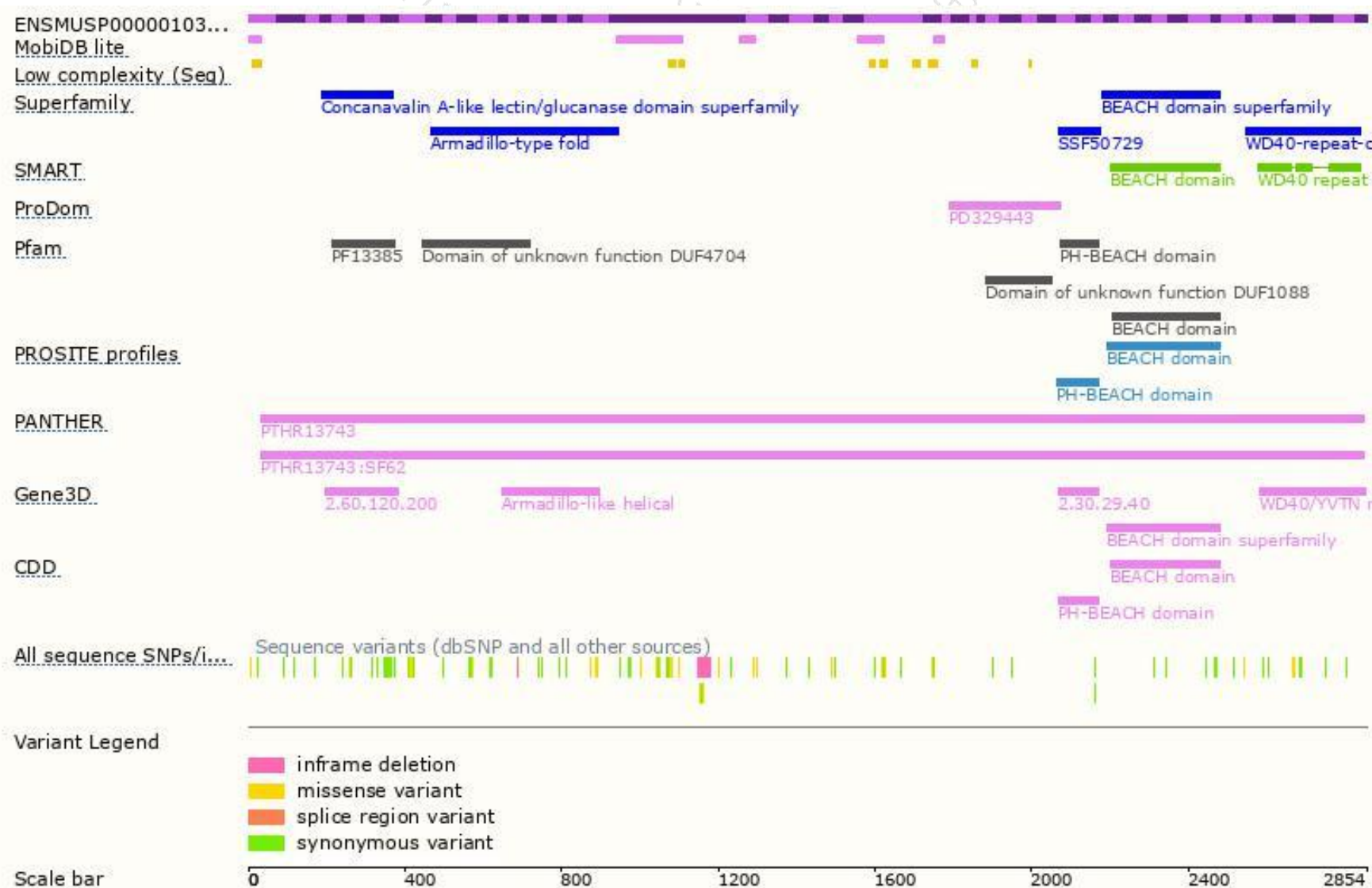
The strategy is based on the design of *Lrba-201* transcript,The transcription is shown below



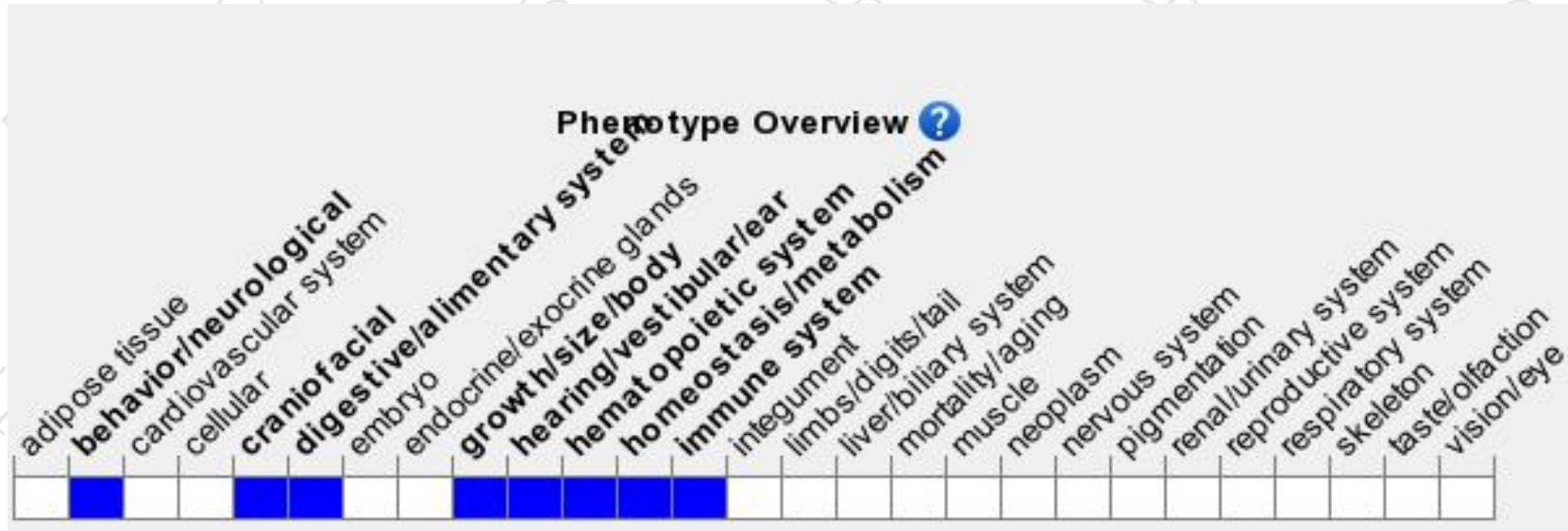
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



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, Mice homozygous for a knock-out allele exhibit increased numbers of myeloid-derived suppressor cells and regulatory T cells, abnormal NK cell physiology, impaired rejection of allogeneic, xenografts, and missing self bone-marrow grafts, and resistance to acute graft vs host disease.

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

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