Lyl1 Cas9-CKO Strategy

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Project Overview

Project Name	***Lyl1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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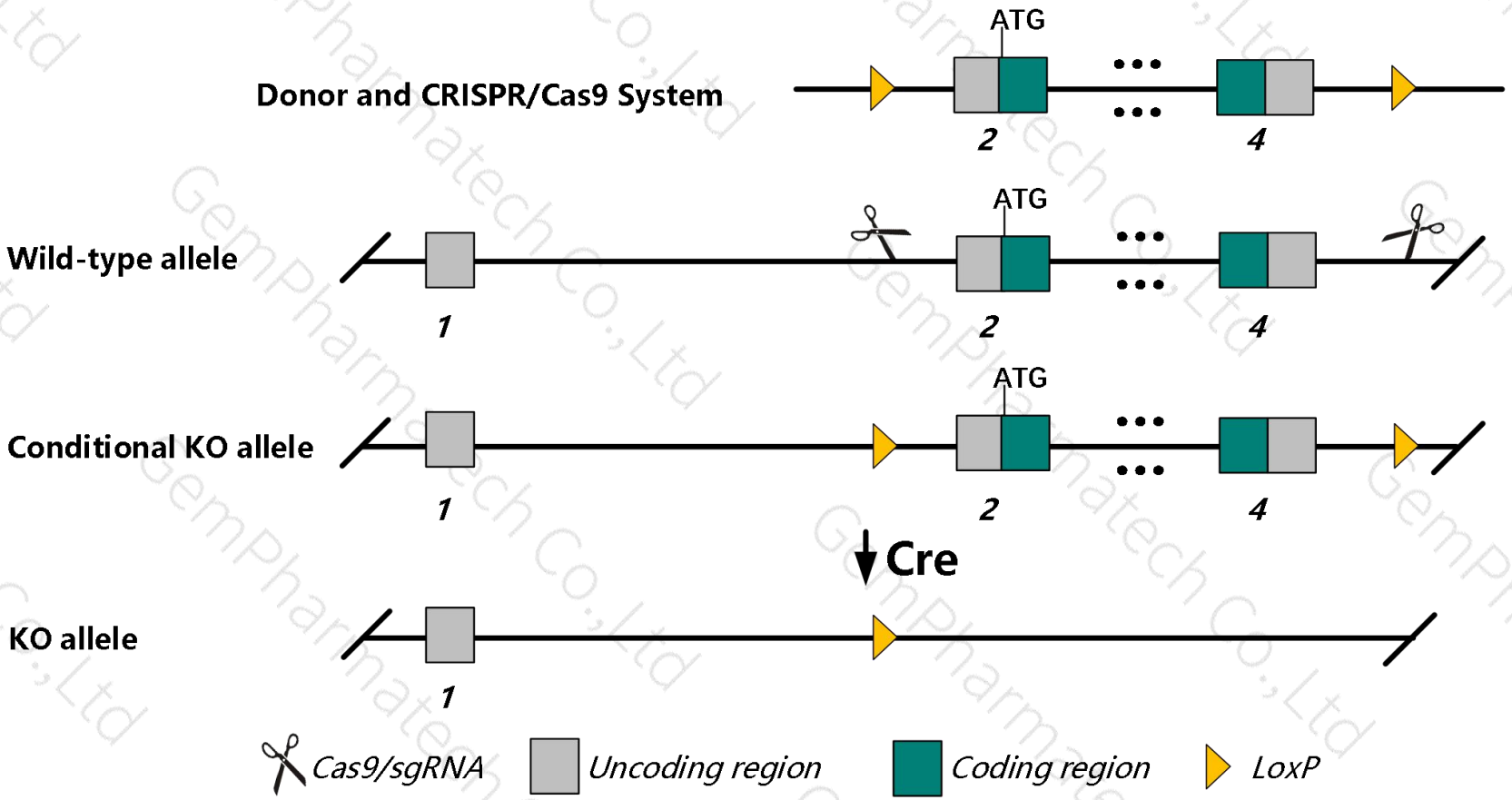
This model will use CRISPR/Cas9 technology to edit the *Lyl1* gene. The schematic diagram is as follows:



Technical routes

- The *Lyl1* gene has 4 transcripts. According to the structure of *Lyl1* gene, exon2-exon4 of *Lyl1-201* (ENSMUST00000037165.5) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Lyl1* 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

- According to the existing MGI data,Mice with mutation of this gene are vaible and fertile. Defects in production and differentiation of progenitor cells are observed, along with impaired ability of fetal liver or bone marrow cells in reconstituting B and T lineages after transplant.
- *Nfix* gene will be deleted in this strategy.
- The *Lyl1* gene is located on the Chr8. 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）

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Lyl1 lymphoblastomic leukemia 1 [*Mus musculus* (house mouse)]

Gene ID: 17095, updated on 2-Nov-2019

Summary

Official Symbol	Lyl1 provided by MGI
Official Full Name	lymphoblastomic leukemia 1 provided by MGI
Primary source	MGI:MGI:96891
See related	Ensembl:ENSMUSG00000034041
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	Lyl-1; bHLHa18
Expression	Broad expression in spleen adult (RPKM 50.2), liver E14.5 (RPKM 33.8) and 18 other tissues See more
Orthologs	human all

Genomic context

Location: 8 C2; 8 41.02 cM

See Lyl1 in Genome Data Viewer

Exon count: 5

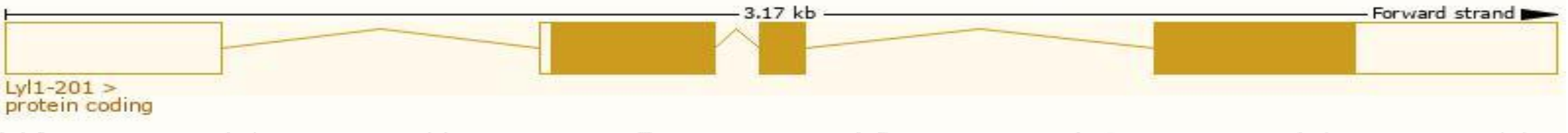
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	8	NC_000074.6 (84701423..84704716)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	8	NC_000074.5 (87225356..87228615)

Transcript information（Ensembl）

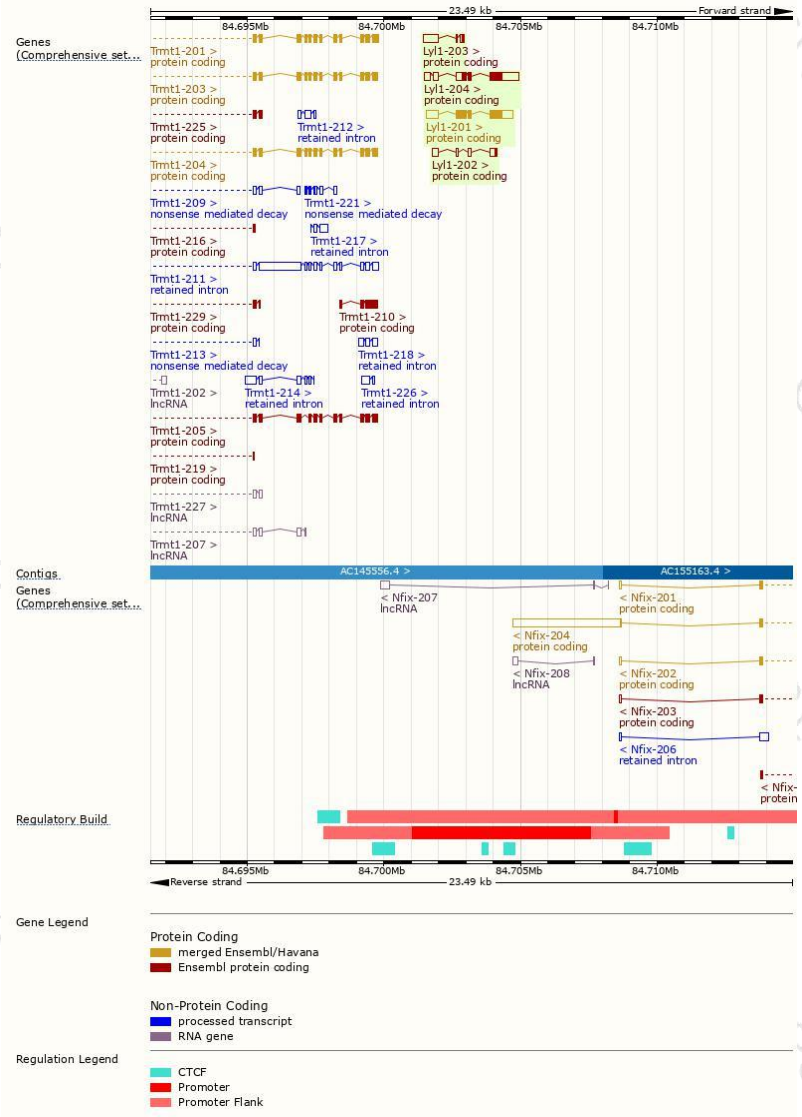
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lyl1-201	ENSMUST00000037165.5	1714	278aa	Protein coding	CCDS22476	P27792	TSL:1 GENCODE basic APPRIS P2
Lyl1-204	ENSMUST00000238562.1	1922	205aa	Protein coding	-	-	GENCODE basic APPRIS ALT2
Lyl1-203	ENSMUST00000238364.1	743	20aa	Protein coding	-	-	CDS 3' incomplete
Lyl1-202	ENSMUST00000238338.1	644	34aa	Protein coding	-	-	CDS 3' incomplete

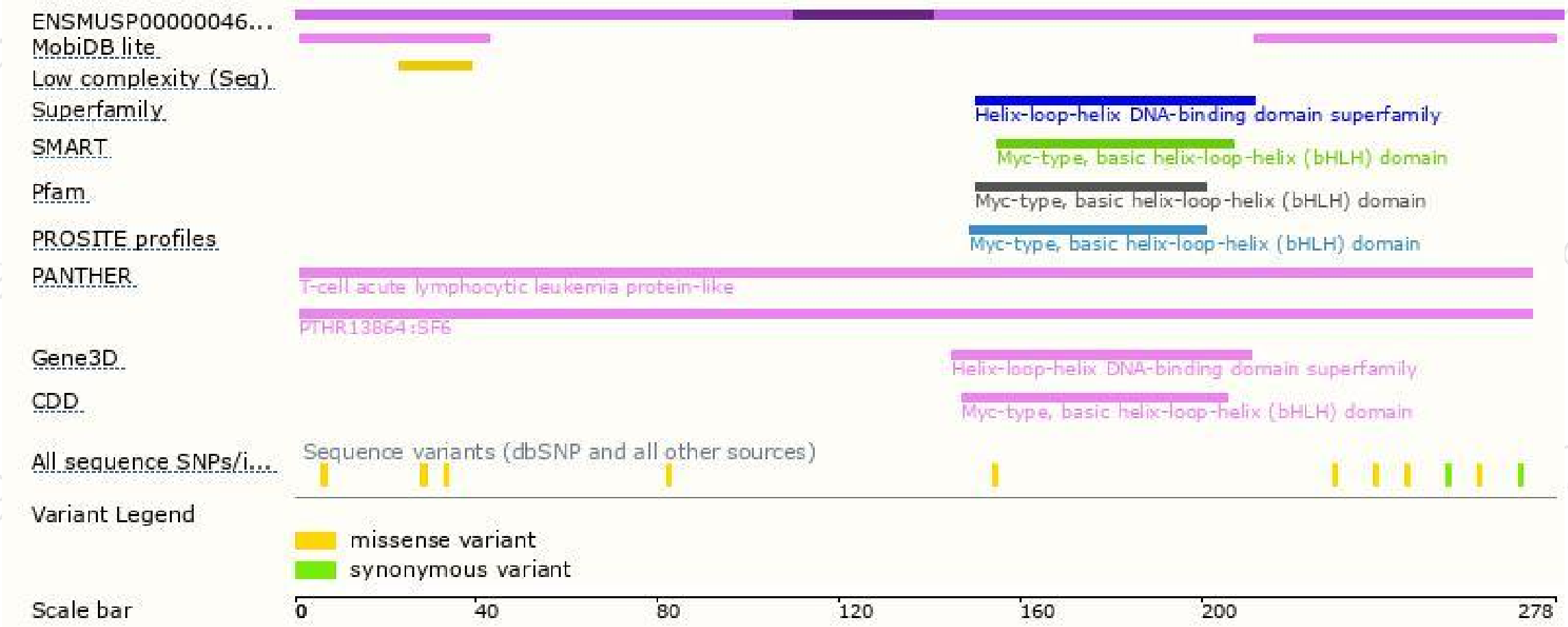
The strategy is based on the design of *Lyl1-201* transcript,The transcription is shown below



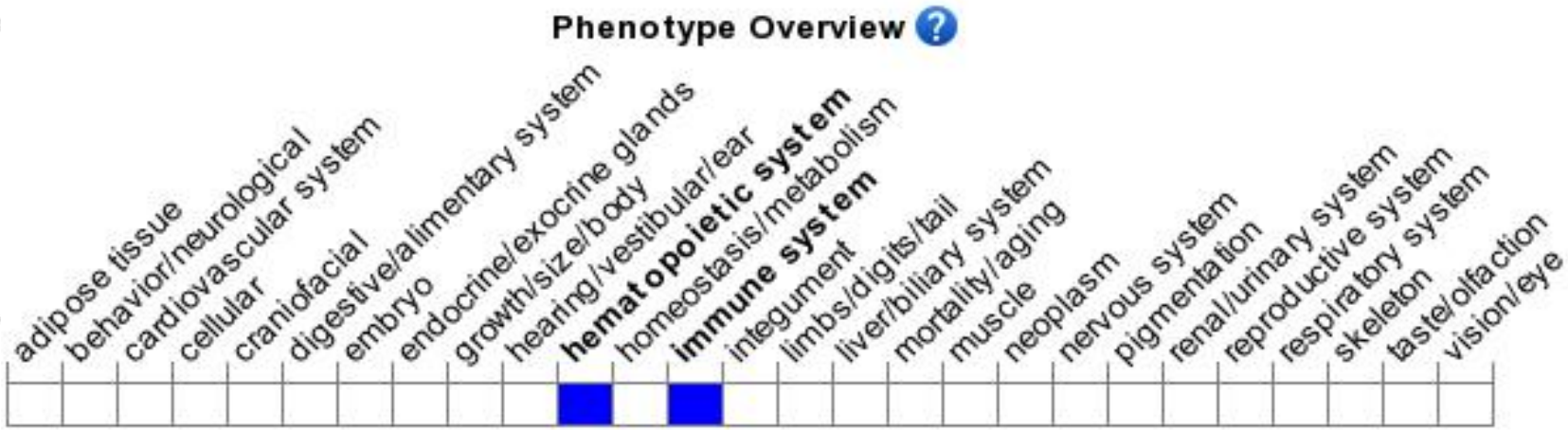
Genomic location distribution



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/).

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

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