Lmo2 Cas9-KO Strategy

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Design Date: 2020-7-20

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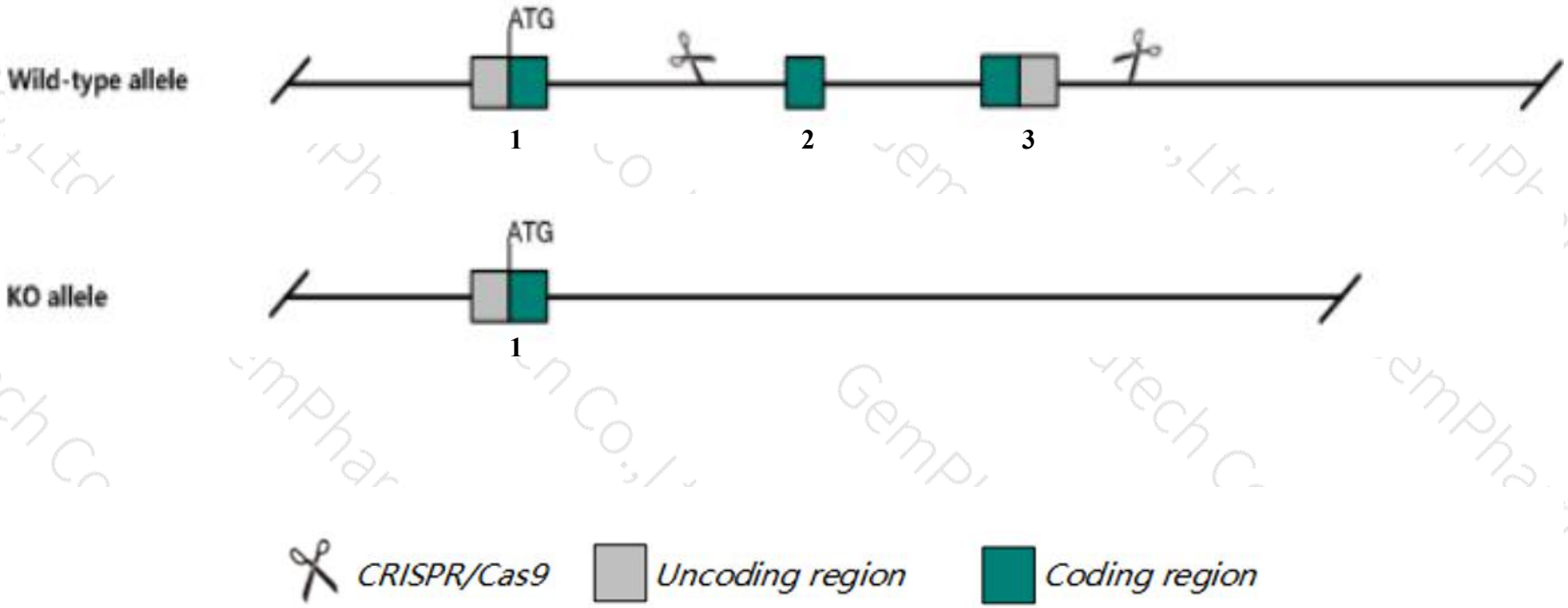
Project Overview

Project Name	***Lmo2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lmo2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Lmo2* gene has 8 transcripts. According to the structure of *Lmo2* gene, exon2-exon3 of *Lmo2-202*(ENSMUST00000111140.2) transcript is recommended as the knockout region.The region contains most 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 *Lmo2* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➢ According to the existing MGI data,homozygotes for a targeted null mutation exhibit lack of yolk sac erythropoiesis and die around embryonic day 10.5.

➢ *4931422A03Rik* gene will be deleted.

➢ The *Lmo2* gene is located on the Chr2. 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）

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Lmo2 LIM domain only 2 [Mus musculus (house mouse)]

Gene ID: 16909, updated on 13-Mar-2020

Summary

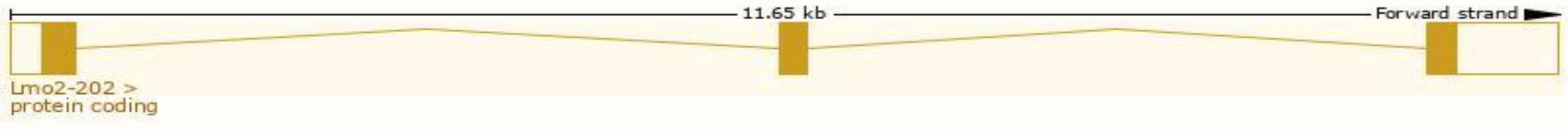
Official Symbol	Lmo2 provided by MGI
Official Full Name	LIM domain only 2 provided by MGI
Primary source	MGI:MGI:102811
See related	Ensembl:ENSMUSG00000032698
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Rbtn-2, Rbtn2, Rhom-2, Ttg2
Expression	Broad expression in liver E14 (RPKM 70.3), liver E14.5 (RPKM 65.0) and 18 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

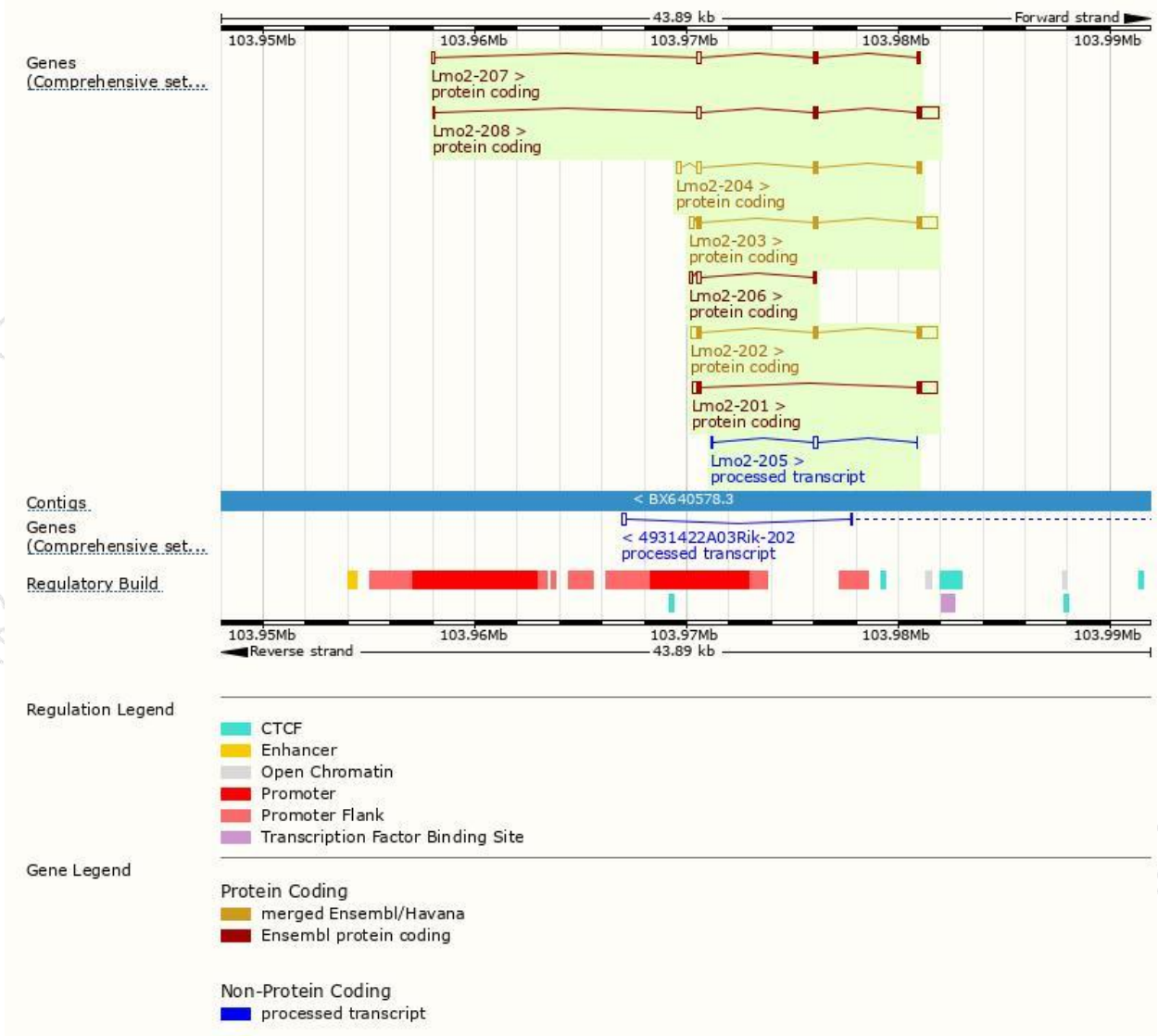
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lmo2-202	ENSMUST00000111140.2	1706	228aa	Protein coding	CCDS16482	A2BHP3	TSL:1 GENCODE basic
Lmo2-203	ENSMUST00000111143.7	1654	220aa	Protein coding	CCDS50651	A2BHP5	TSL:1 GENCODE basic
Lmo2-208	ENSMUST00000170926.7	1529	158aa	Protein coding	CCDS50652	P25801 Q544Z2	TSL:2 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Lmo2-201	ENSMUST00000111139.2	1434	156aa	Protein coding	-	A2BHP1	TSL:5 GENCODE basic
Lmo2-204	ENSMUST00000123437.7	848	158aa	Protein coding	-	P25801 Q544Z2	CDS 3' incomplete TSL:2
Lmo2-207	ENSMUST00000156813.7	710	144aa	Protein coding	-	A2BHP2	CDS 3' incomplete TSL:2
Lmo2-206	ENSMUST00000138815.1	478	59aa	Protein coding	-	A2BHP4	CDS 3' incomplete TSL:3
Lmo2-205	ENSMUST00000133210.1	328	No protein	Processed transcript	-	-	TSL:1

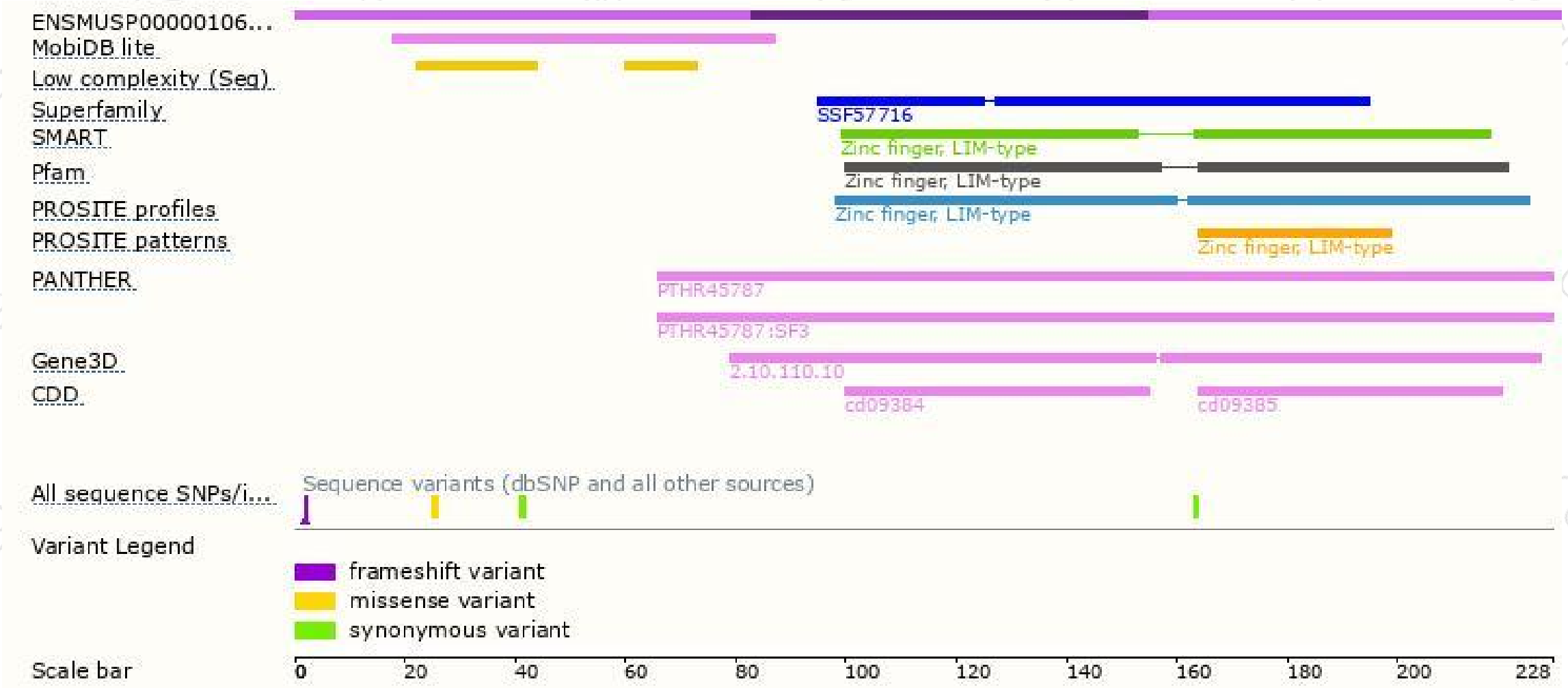
The strategy is based on the design of *Lmo2-202* transcript,the transcription is shown below:



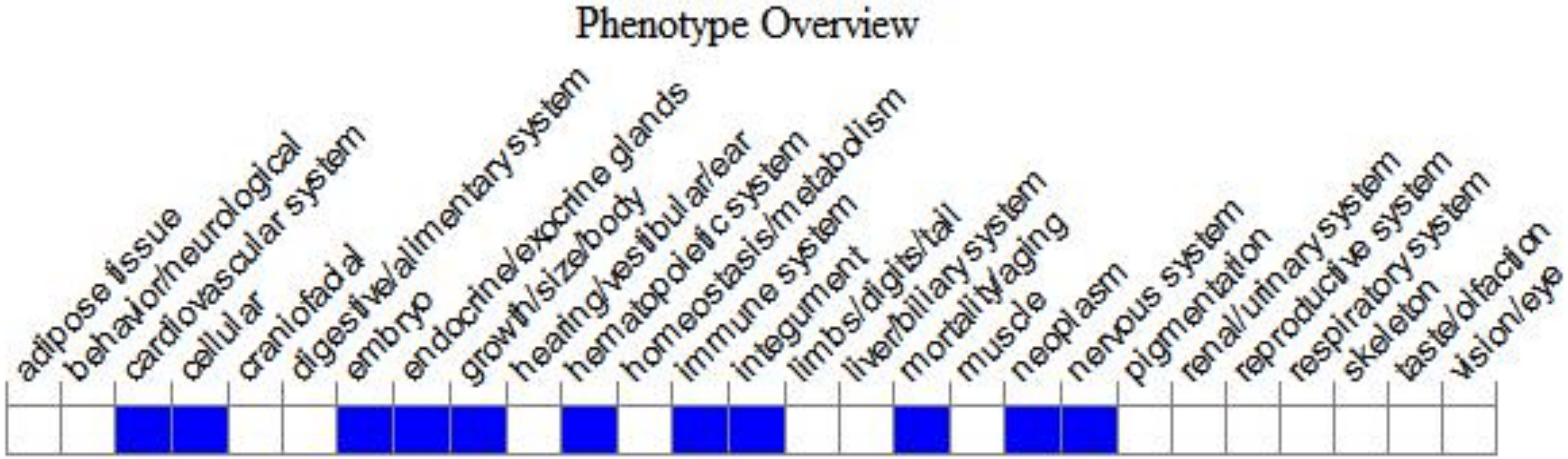
Genomic location distribution



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,homozygotes for a targeted null mutation exhibit lack of yolk sac erythropoiesis and die around embryonic day 10.5.

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

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