Rbm15 Cas9-KO Strategy

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Project Overview

Project Name	***Rbm15***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rbm15* gene. The schematic diagram is as follows:

Technical routes

➢ The *Rbm15* gene has 2 transcripts. According to the structure of *Rbm15* gene, exon1 of *Rbm15-201* (ENSMUST00000061772.10) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rbm15* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,Mice homozygous for a knock-out allele exhibit embryonic lethality around E9.5. Mice homozygous for a floxed allele activate in hematopoietic cells exhibit increased megakaryocyte cell number, long-term hematopoietic stem cells, and red pulp as well as decreased B cells and leukocytes.

➢ The *Rbm15* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

Rbm15   RNA binding motif protein 15 [*Mus musculus* (house mouse)]

Gene ID: 229700, updated on 12-Aug-2019

▲ Summary

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Official Symbol	Rbm15 provided by MGI
Official Full Name	RNA binding motif protein 15 provided by MGI
Primary source	MGI:MGI:2443205
See related	Ensembl:ENSMUSG00000048109
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	mKIAA1438; C230088J01Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 2.5), limb E14.5 (RPKM 1.9) and 28 other tissues See more
Orthologs	human all

The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags		
Rbm15-201	ENSMUST00000061772.10	4343	962aa	Protein coding	CCDS38590	Q0VBL3	TSL:1	GENCODE basic	APPRIS P1
Rbm15-202	ENSMUST00000197769.1	5967	No protein	Retained intron	-	-		TSL:NA	

The strategy is based on the design of *Rbm15-201* transcript,The transcription is shown below

< Rbm15-201
protein coding

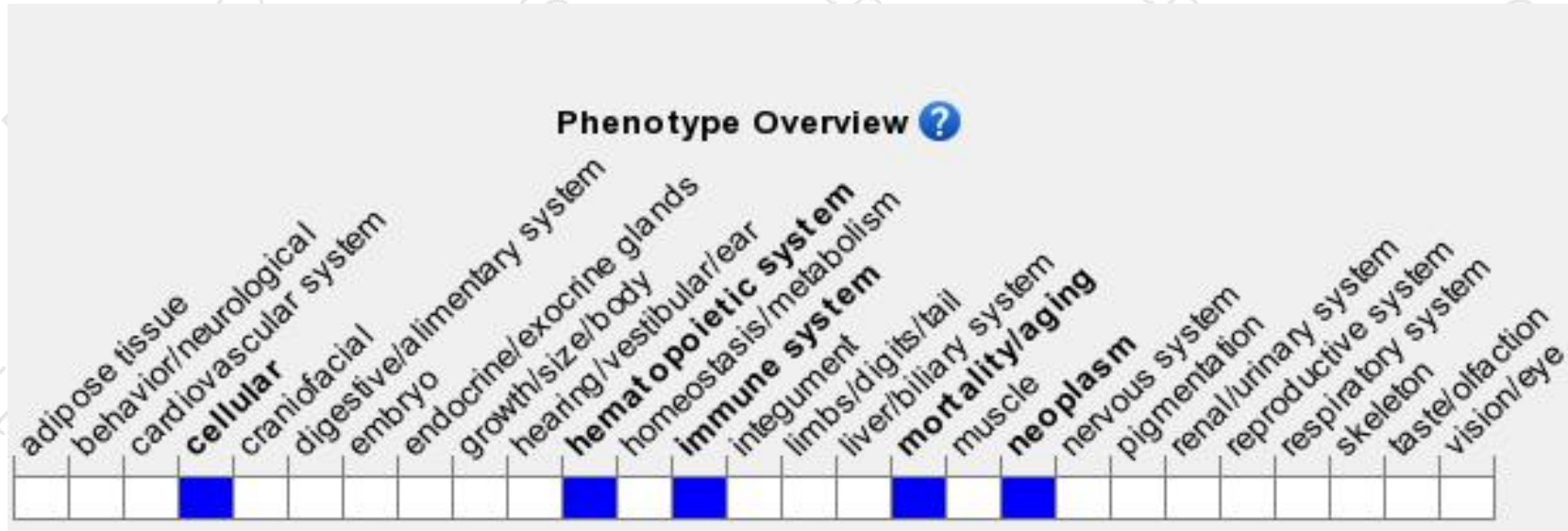◄— Reverse strand ——————————— 8.25 kb ———————————
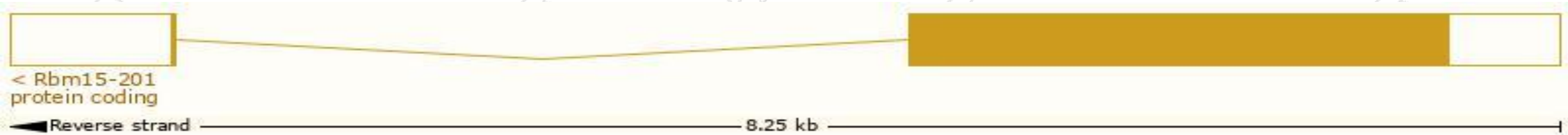
Genomic location distribution
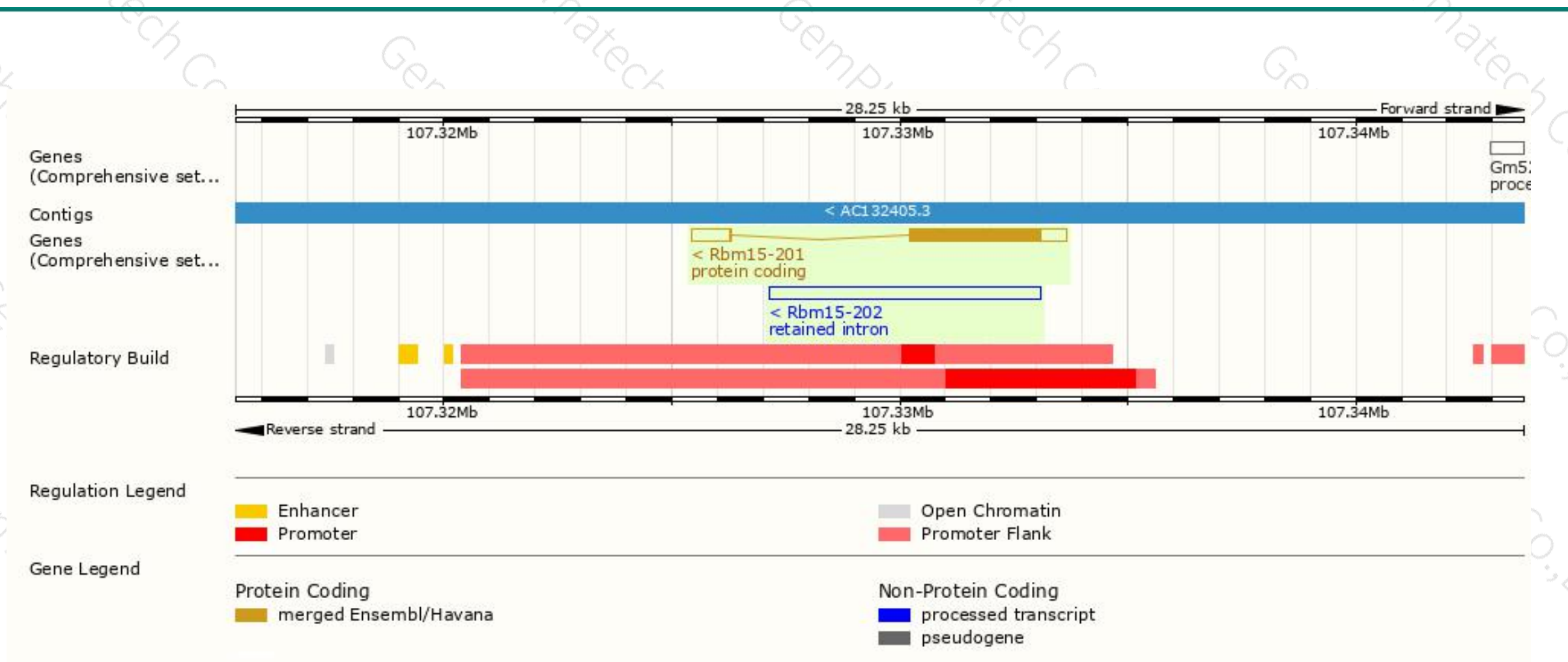
Protein domain
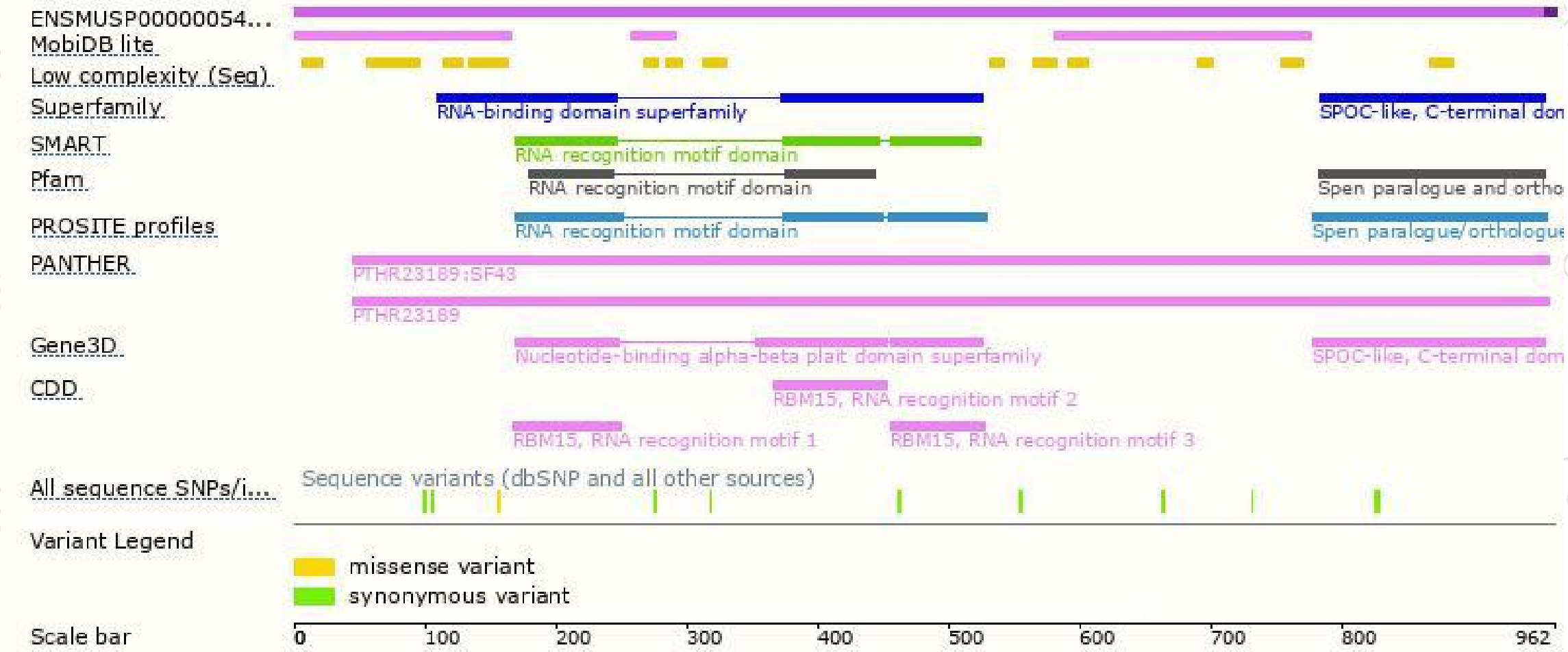
Mouse phenotype description(MGI)

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 embryonic lethality around E9.5. Mice homozygous for a floxed allele activate in hematopoietic cells exhibit increased megakaryocyte cell number, long-term hematopoietic stem cells, and red pulp as well as decreased B cells and leukocytes.

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