Virma Cas9-CKO *Strategy*

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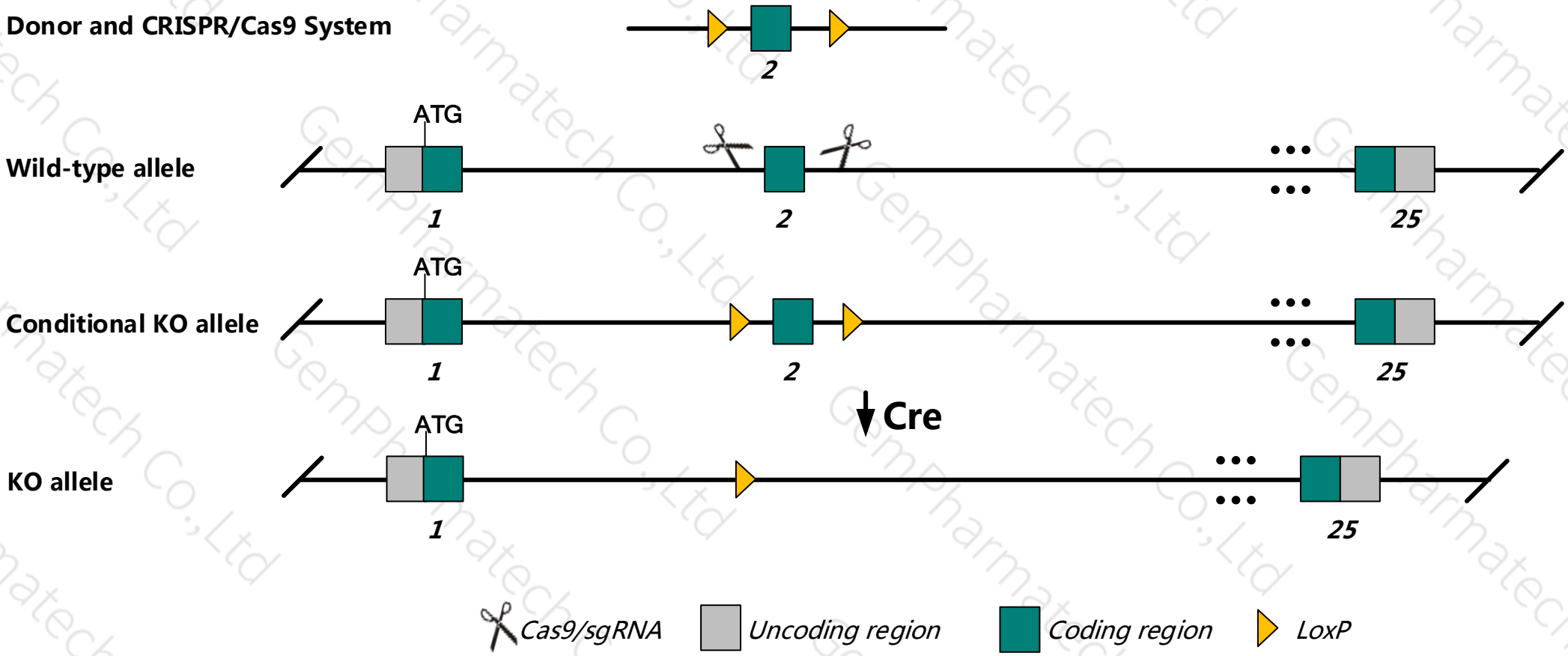
Project Overview

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

Conditional Knockout strategy

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



Technical routes

- The *Virma* gene has 3 transcripts.According to the structure of *Virma* gene, exon2 of *Virma*-203 (ENSMUST00000108307.2) transcript is recommended as the knockout region.The region contains 116bp coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Virma* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA 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 was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

Notice

- The *Virma* 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 the loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

Virma vir like m6A methyltransferase associated [*Mus musculus* (house mouse)]

Gene ID: 66185, updated on 12-Aug-2018

Summary

Official Symbol	Virma provided by MGI
Official Full Name	vir like m6A methyltransferase associated provided by MGI
Primary source	MGI:MGI:1913435
See related	Ensembl:ENSMUSG00000040720 Vega:OTTMUSG00000004468
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	Kiaa1429; mKIAA1429; 1110037F02Rik; 4930422M05Rik
Expression	Ubiquitous expression in limb E14.5 (RPKM 9.4), CNS E11.5 (RPKM 9.3) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 3 transcripts, and all transcripts are shown below:

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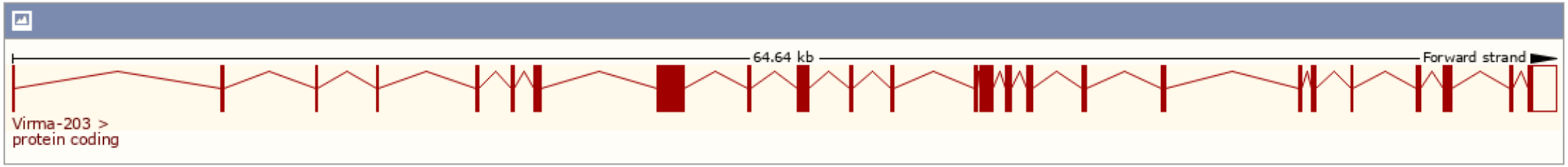
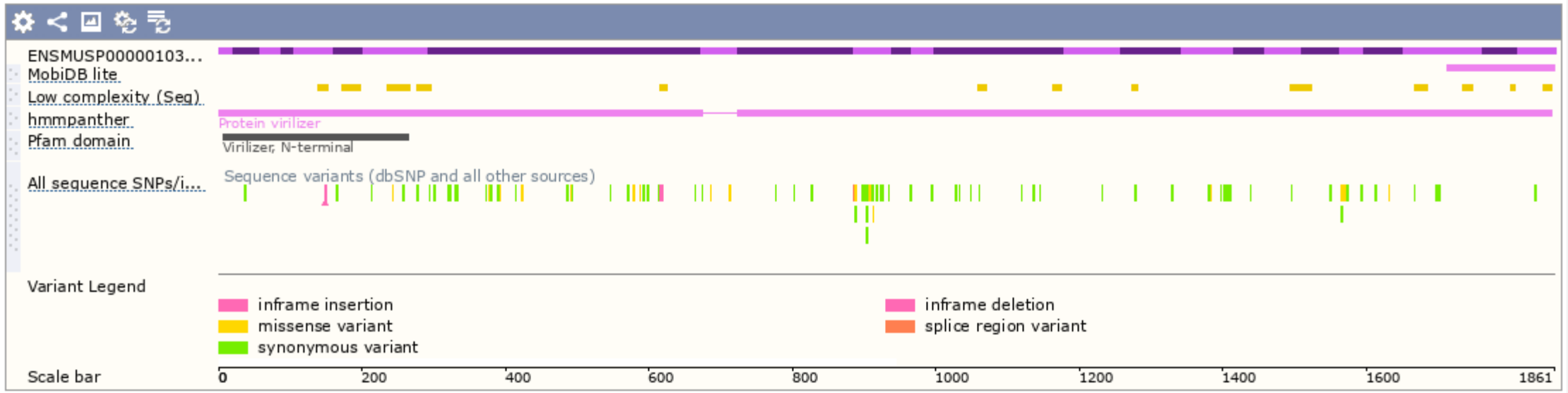
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
Virma-203	ENSMUST00000108307.2	6571	1861aa	Protein coding	CCDS38693	E9PZY8	NM_001081183 NP_001074652	TSL:5 GENCODE basic
Virma-202	ENSMUST00000059914.12	6506	1811aa	Protein coding	CCDS84705	A2AIV2	NM_001347055 NP_001333984	TSL:1 GENCODE basic APPRIS P1
Virma-201	ENSMUST00000055372.13	3954	1139aa	Protein coding	-	A2AIV2	-	TSL:1 GENCODE basic

The strategy is based on the design of *Virma*-203 transcript,The transcription is shown below

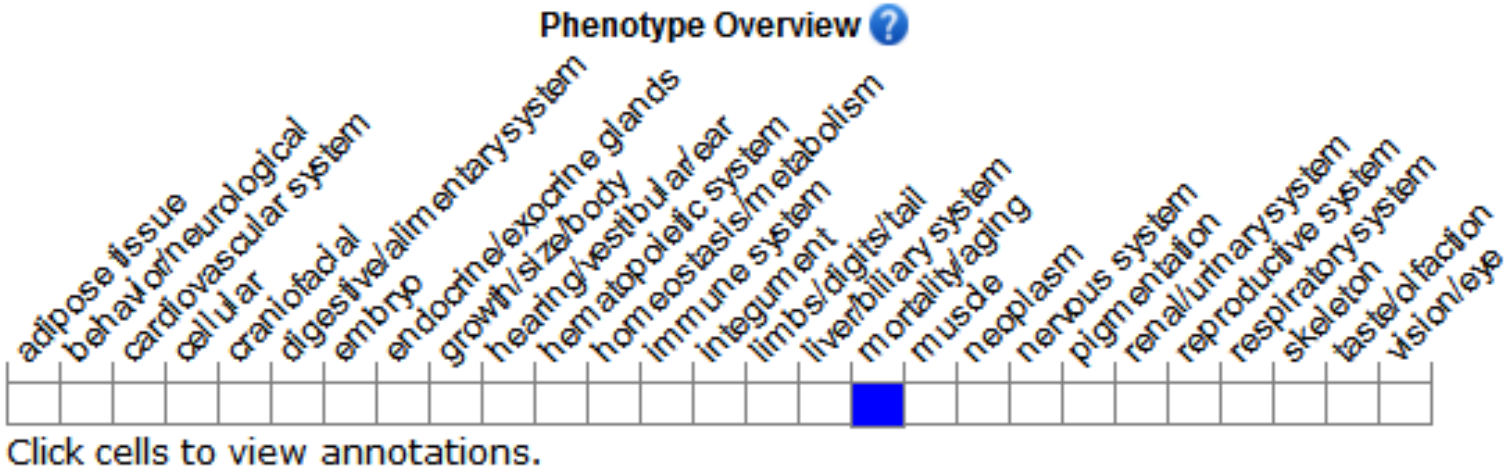


Genomic location distribution

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/) .

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

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