

Mgrn1 Cas9-KO Strategy

Designer:

Daohua Xu

Reviewer :

Huimin Su

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Project Overview

Project Name

Mgrn1

Project type

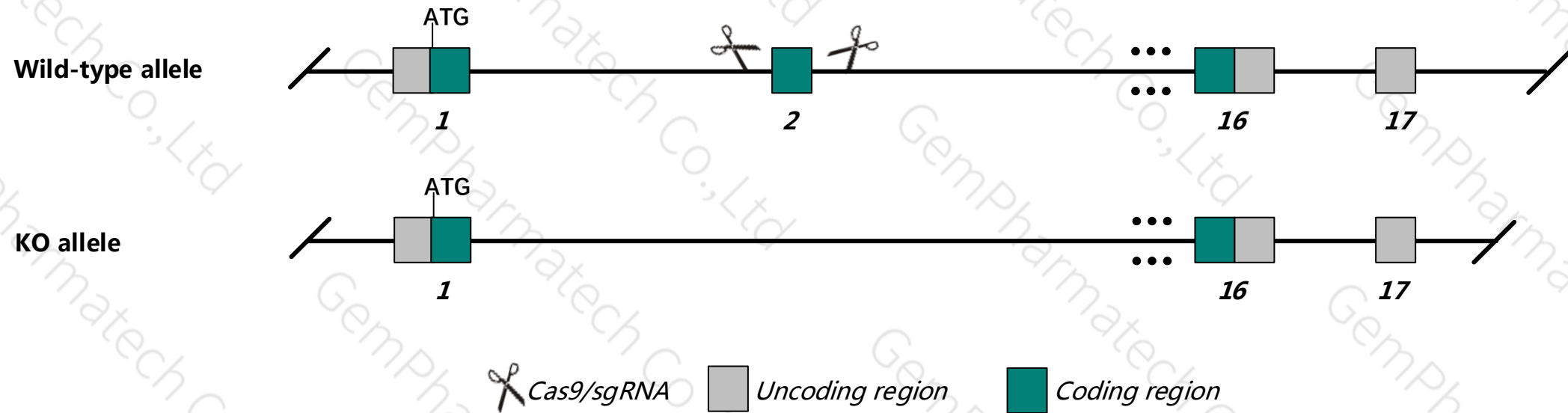
Cas9-KO

Animal background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mgrn1* gene. The schematic diagram is as follows:



Technical routes

- The *Mgrn1* gene has 8 transcripts, According to the structure of *Mgrn1* gene, exon2 of *Mgrn1*-203 transcript is recommended as the knockout region. The region contains the 122bp coding sequence. Knock out the region, result in destruction of protein.
- This project uses CRISPR/Cas9 technology to modify *Mgrn1* gene. The brief process is as follows: sgRNA was transcribed in vitro, Cas9, sgRNA were microinjected into fertilized eggs of C57BL/6JGpt mice and homologous recombination was carried out to obtain F0 mice. A stable and hereditary F1 generation mouse model was obtained by mating F0 generation mice with C57BL/6JGpt mice which were confirmed positive by PCR-sequencing.

- According to the existing MGI data , Homozygotes for mutant alleles exhibit darkening of agouti hair and suppression of the obesity associated with certain agouti mutations. Homozygotes for an induced null mutation also have curly whiskers and develop a progressive spongiform neuropathology.
- The *Mgrn1* gene is located in the Chr16. If the knockout mice are mixed with other mice, two target genes are avoided on the same chromosome as possible, otherwise the offspring of mice with double gene positive and homozygous gene knockout can not be obtained.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)

Mgrn1 mahogunin, ring finger 1 [*Mus musculus* (house mouse)]

Gene ID: 17237, updated on 3-Jan-2019

Summary

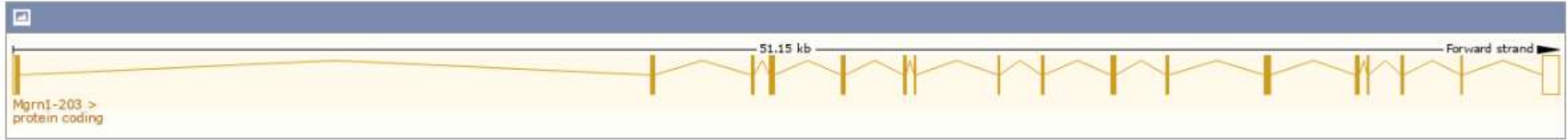
Official Symbol	Mgrn1 provided by MGI
Official Full Name	mahogunin, ring finger 1 provided by MGI
Primary source	MGI:MGI:2447670
See related	Ensembl:ENSMUSG00000022517
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	md; nc; mKIAA0544; 2610042J20Rik
Expression	Ubiquitous expression in heart adult (RPKM 66.4), ovary adult (RPKM 57.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

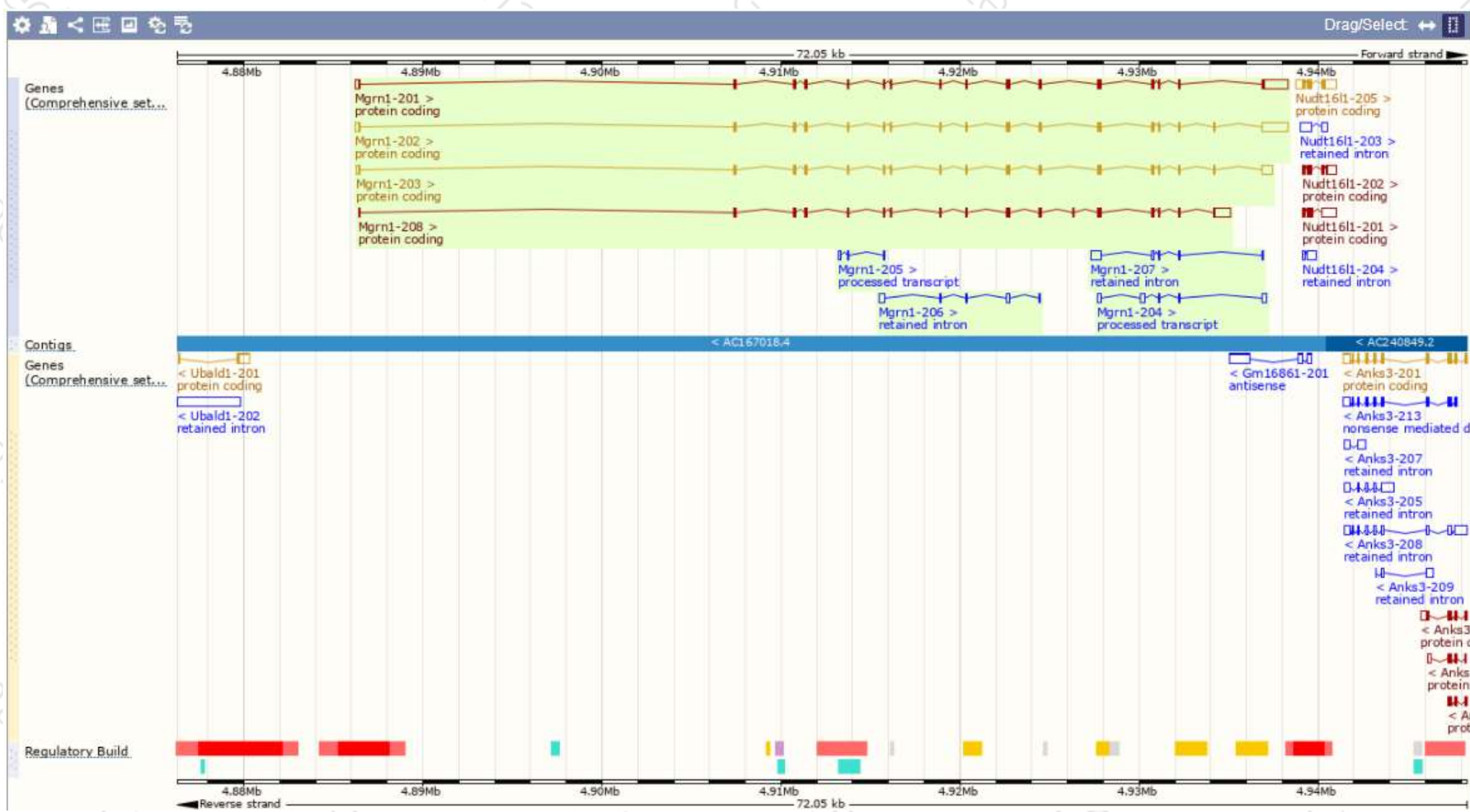
The gene has 8 transcripts, and all transcripts are shown below :

Show/hide columns (1 hidden)								Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags	
Mgrn1-202	ENSMUST00000070658.15	3138	532aa	Protein coding	CCDS49751	Q9D074	NM_029657 NP_083933	TSL:1	GENCODE basic APPRIS P3
Mgrn1-203	ENSMUST00000229038.1	2250	533aa	Protein coding	CCDS57016	Q9D074	NM_001252437 NP_001239366		GENCODE basic APPRIS ALT2
Mgrn1-201	ENSMUST00000023159.9	3095	556aa	Protein coding	-	Q9D074	NM_001357061 NP_001343990	TSL:1	GENCODE basic APPRIS ALT2
Mgrn1-208	ENSMUST00000230990.1	2519	554aa	Protein coding	-	Q9D074	NP_001343991		GENCODE basic APPRIS ALT2
Mgrn1-204	ENSMUST00000230108.1	844	No protein	Processed transcript	-	-	-		
Mgrn1-205	ENSMUST00000230220.1	323	No protein	Processed transcript	-	-	-		
Mgrn1-207	ENSMUST00000230738.1	931	No protein	Retained intron	-	-	-		
Mgrn1-206	ENSMUST00000230653.1	670	No protein	Retained intron	-	-	-		

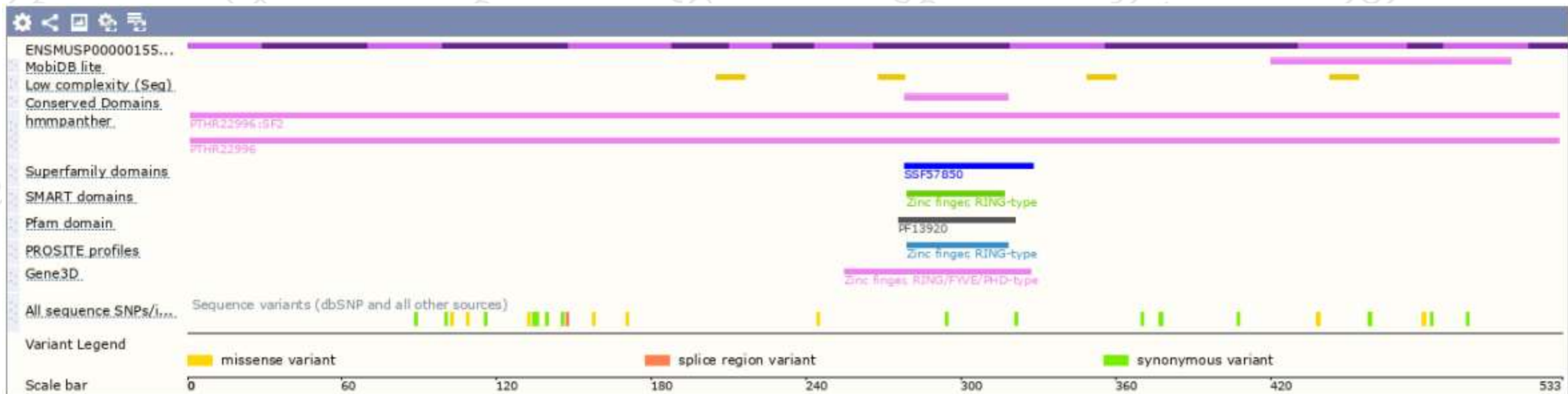
The strategy is based on the design of *Mgrn1-203* transcript,The transcription is shown below :



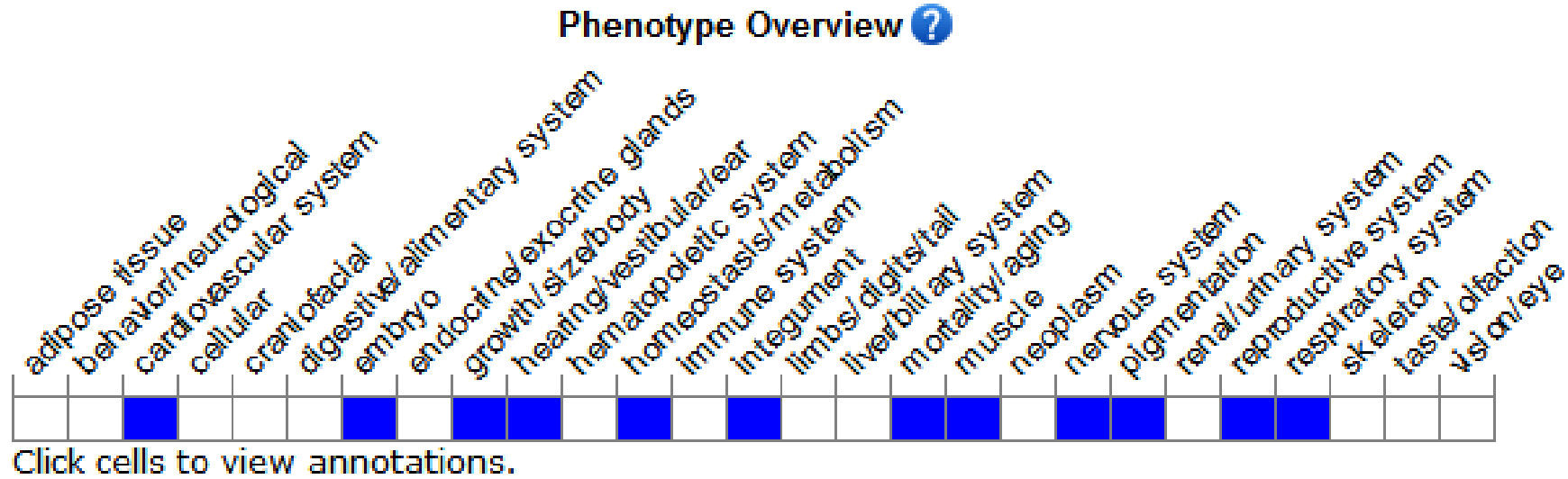
Genomic location distribution



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/>).

According to the existing MGI data, Homozygotes for mutant alleles exhibit darkening of agouti hair and suppression of the obesity associated with certain agouti mutations. Homozygotes for an induced null mutation also have curly whiskers and develop a progressive spongiform neuropathology.

If you have any questions, you are welcome to inquire.
Tel: 025-5864 1534

