Hmg20a Cas9-KO Strategy

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Project Overview

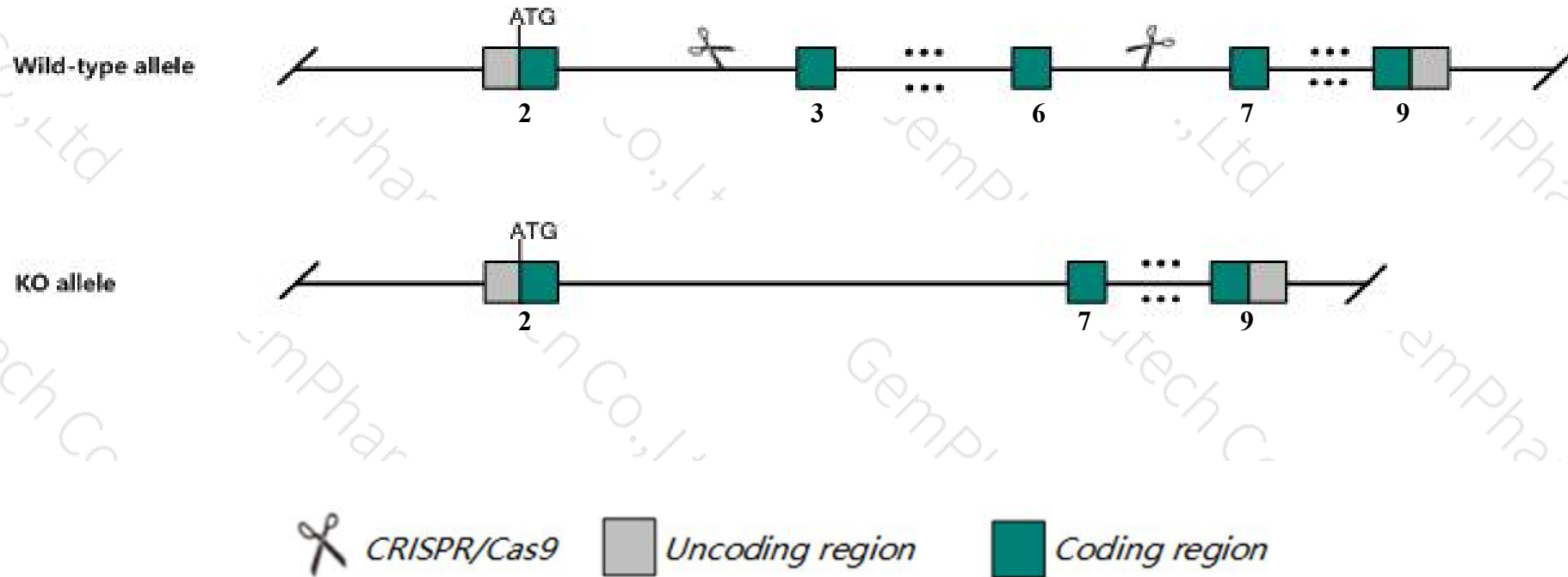|	
Project Name	*Hmg20a*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hmg20a* gene. The schematic diagram is as follows:

Technical routes

➤ The *Hmg20a* gene has 6 transcripts. According to the structure of *Hmg20a* gene, exon3-exon6 of *Hmg20a-201* (ENSMUST00000034879.4) transcript is recommended as the knockout region.The region contains 523bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Hmg20a* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

➢ The effect on transcript *Hmg20a*-202 is unknown.

➢ The *Hmg20a* gene is located on the Chr9. 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）

Hmg20a   high mobility group 20A [*Mus musculus* (house mouse)]

Gene ID: 66867, updated on 18-Feb-2020

Summary

Official Symbol	Hmg20a provided by MGI
Official Full Name	high mobility group 20A provided by MGI
Primary source	MGI:MGI:1914117
See related	Ensembl:ENSMUSG00000032329
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	Ibraf; Hmgxb1; 1200004E06Rik; 5730490E10Rik
Expression	Ubiquitous expression in CNS E18 (RPKM 21.5), whole brain E14.5 (RPKM 21.1) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 9; 9 B

Exon count: 10

See Hmg20a in Genome Data Viewer

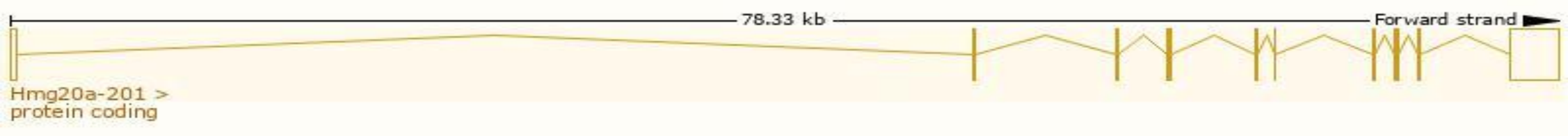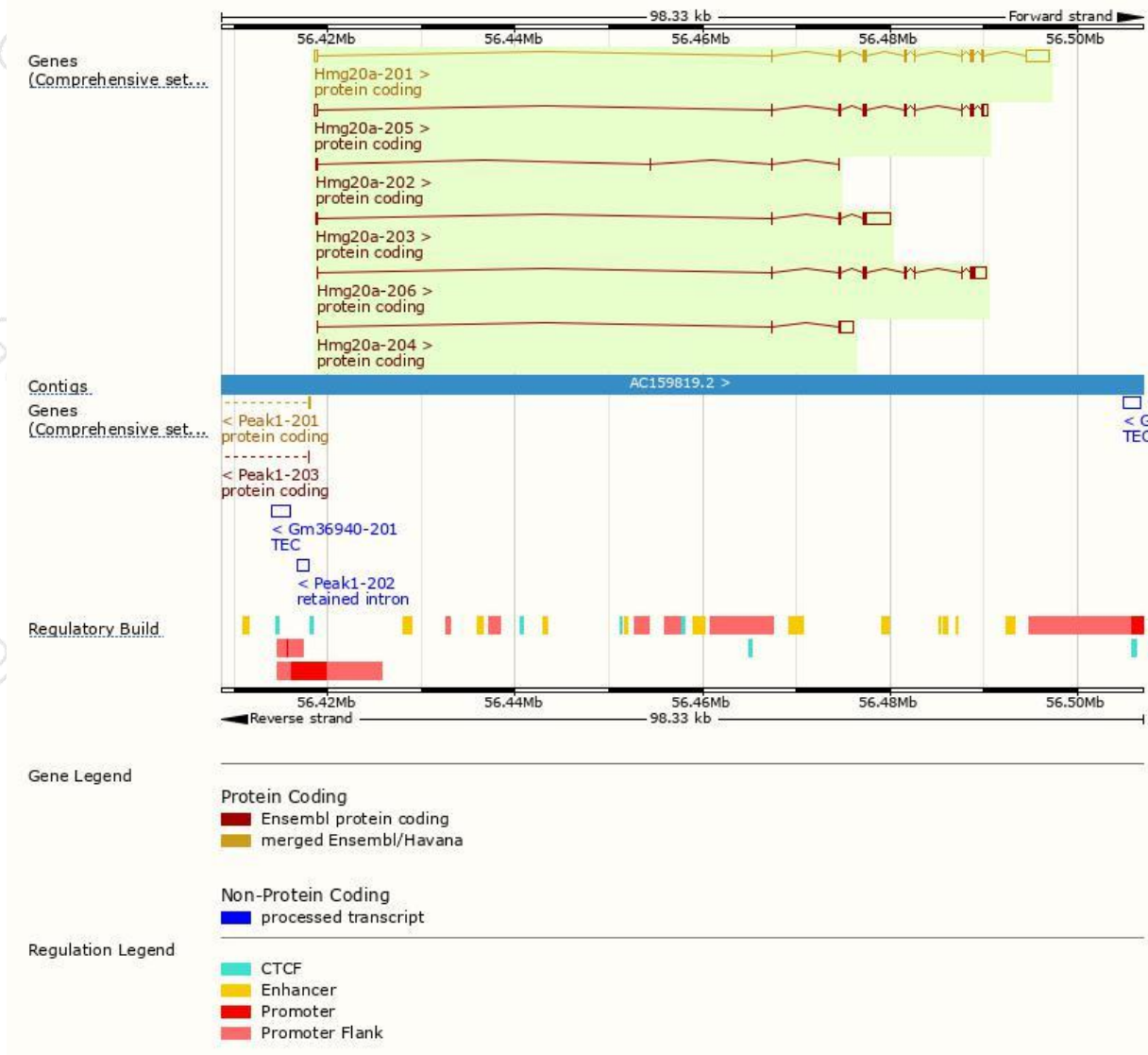| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	9	NC_000075.6 (56418619..56496936)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	9	NC_000075.5 (56266653..56344743)

Transcript information（Ensembl）

The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hmg20a-201	ENSMUST00000034879.4	3778	346aa	Protein coding	CCDS23208	Q9DC33	TSL:1 GENCODE basic APPRIS P1
Hmg20a-205	ENSMUST00000215269.1	1700	346aa	Protein coding	CCDS23208	Q9DC33	TSL:1 GENCODE basic APPRIS P1
Hmg20a-203	ENSMUST00000214771.1	3191	180aa	Protein coding	-	A0A1L1SRA5	TSL:1 GENCODE basic
Hmg20a-206	ENSMUST00000217518.1	2468	379aa	Protein coding	-	Q9DC33	TSL:1 GENCODE basic
Hmg20a-204	ENSMUST00000214869.1	1782	101aa	Protein coding	-	Q9DC33	TSL:1 GENCODE basic
Hmg20a-202	ENSMUST00000213242.1	335	33aa	Protein coding	-	A0A1L1SSI9	CDS 3' incomplete TSL:5

The strategy is based on the design of *Hmg20a-201* transcript,The transcription is shown below
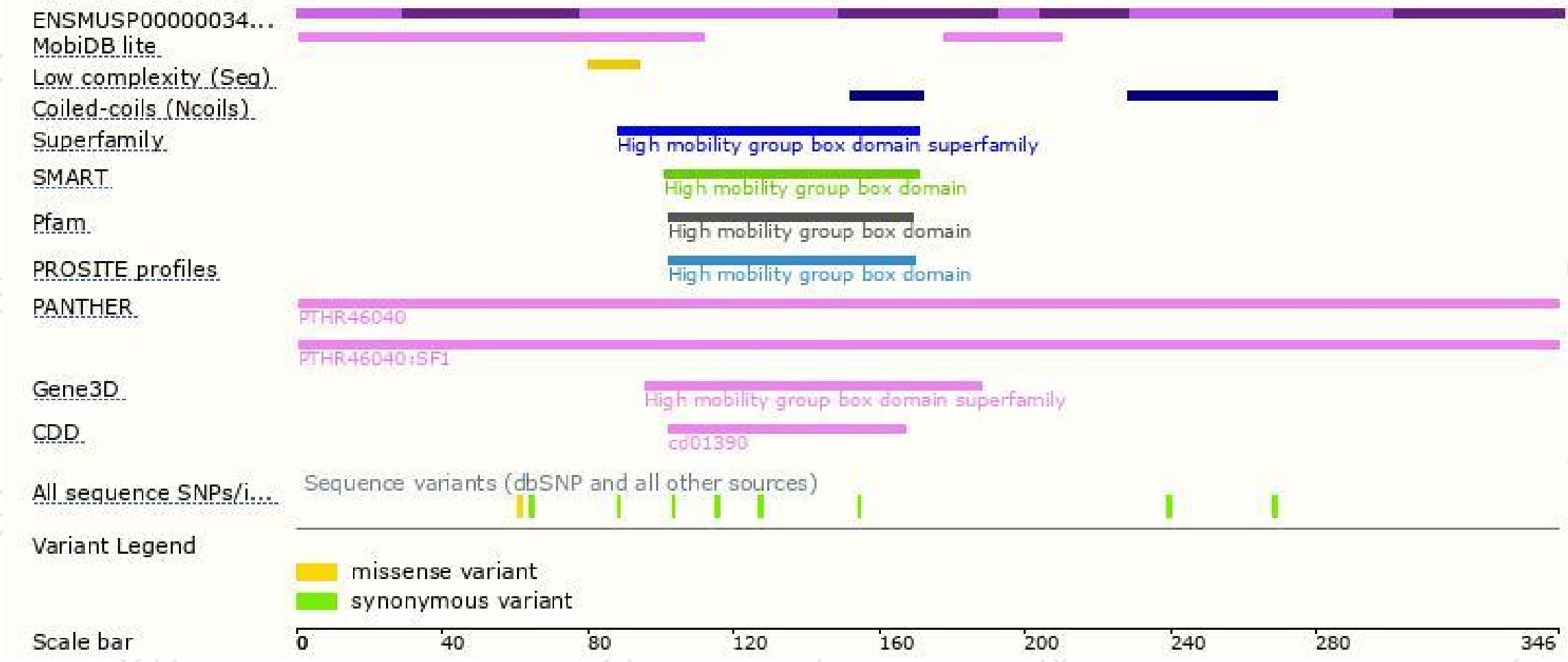

78.33 kb — Forward strand

Hmg20a-201 >
protein coding

Genomic location distribution

Protein domain

ENSMUSP00000034...	
MobiDB lite	
Low complexity (Seg)	
Coiled-coils (Ncoils)	
Superfamily	High mobility group box domain superfamily
SMART	High mobility group box domain
Pfam	High mobility group box domain
PROSITE profiles	High mobility group box domain
PANTHER	PTHR46040
	PTHR46040:SF1
Gene3D	High mobility group box domain superfamily
CDD	cd01390
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)
Variant Legend	

Variant Legend
- 🟨 missense variant
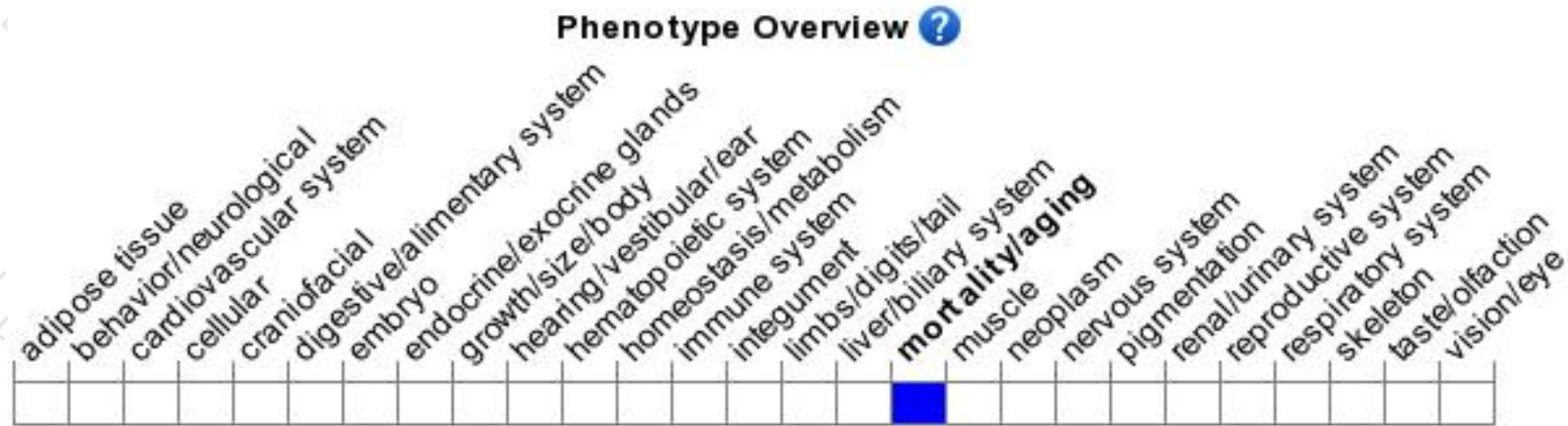- 🟩 synonymous variant

Scale bar: 0   40   80   120   160   200   240   280   346

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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