Mpg Cas9-CKO Strategy

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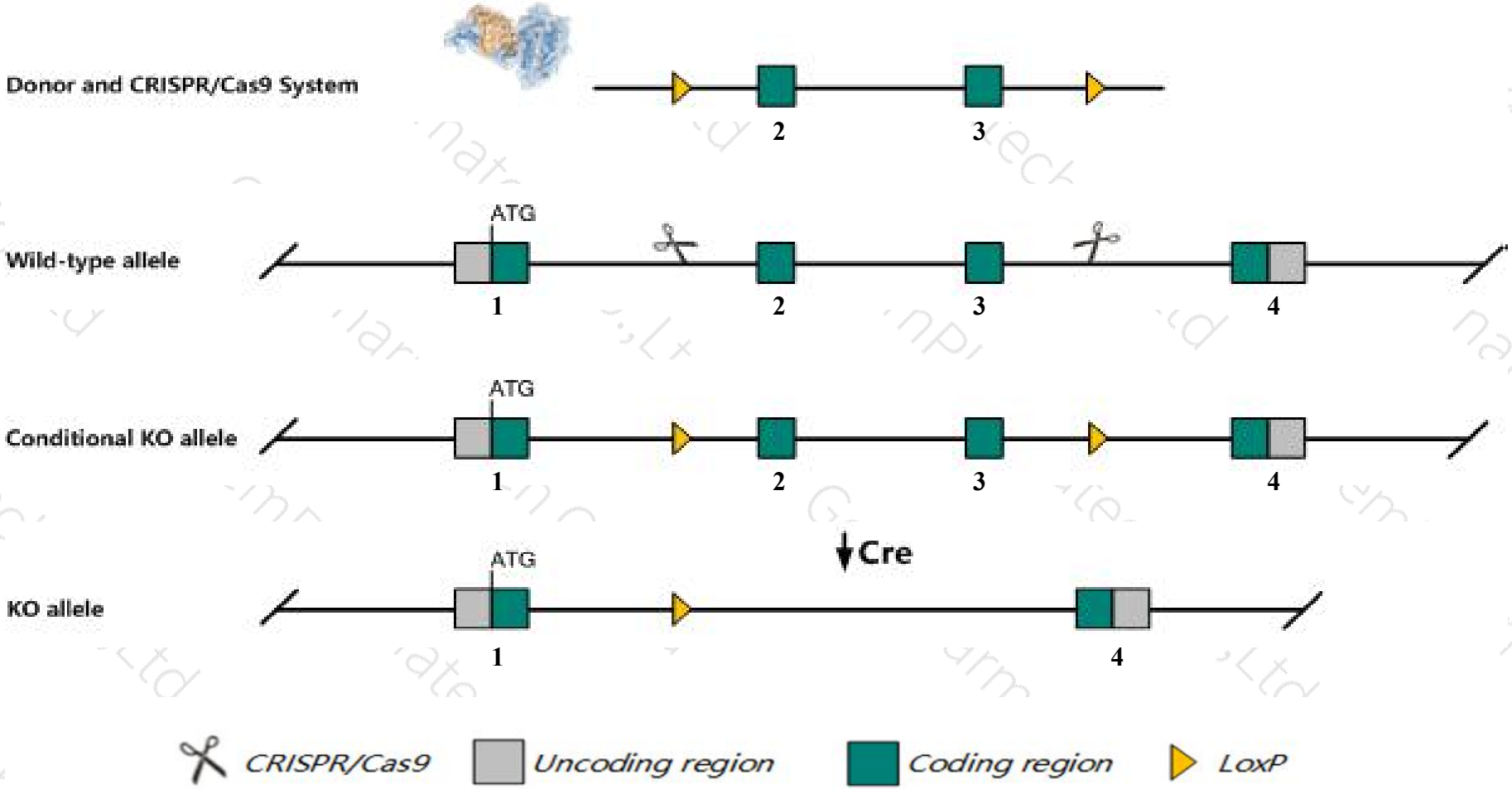
Project Overview

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

Conditional Knockout strategy

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



Technical routes

- The *Mpg* gene has 4 transcripts. According to the structure of *Mpg* gene, exon2-exon3 of *Mpg-201* (ENSMUST00000020528.13) transcript is recommended as the knockout region.The region contains 403bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Mpg* gene. The brief process is as follows:CRISPR/Cas9 system 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 will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

- According to the existing MGI data,Homozygotes for a targeted null mutation exhibit impaired base excision repair of alkylation-induced DNA damage, and increased sensitivity to methyl methanesulfonate and streptozoticin-induced diabetes. Mutants are fertile and long-lived.
- Transcript *Mpg*-202 may directly destroy.
- *Mpg* gene is located in intron of *Nprl3* gene,the partial sequence of intron of *Nprl3* gene will be deleted together in this strategy.
- The floxed region is near to the N-terminal of *Rhbdf1* gene C-terminal of and *Nprl3* gene,this strategy may influence the regulatory function of the N-terminal of *Rhbdf1* gene C-terminal of and *Nprl3* gene.
- The *Mpg* gene is located on the Chr11. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Mpg N-methylpurine-DNA glycosylase [*Mus musculus* (house mouse)]

Gene ID: 268395, updated on 12-Aug-2019

Summary

Official Symbol	Mpg provided by MGI
Official Full Name	N-methylpurine-DNA glycosylase provided by MGI
Primary source	MGI:MGI:97073
See related	Ensembl:ENSMUSG00000020287
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	Aag; APNG; Mid1; AI326268; 9830006D05
Expression	Ubiquitous expression in adrenal adult (RPKM 8.1), genital fat pad adult (RPKM 7.4) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 11 A4; 11 18.83 cM

See Mpg in Genome Data Viewer

Exon count: 4

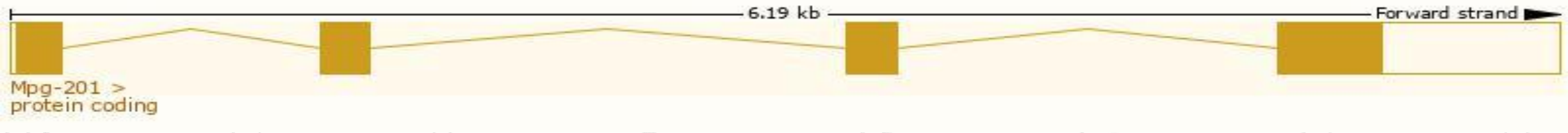
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (32226505..32232702)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (32126505..32132702)

Transcript information（Ensembl）

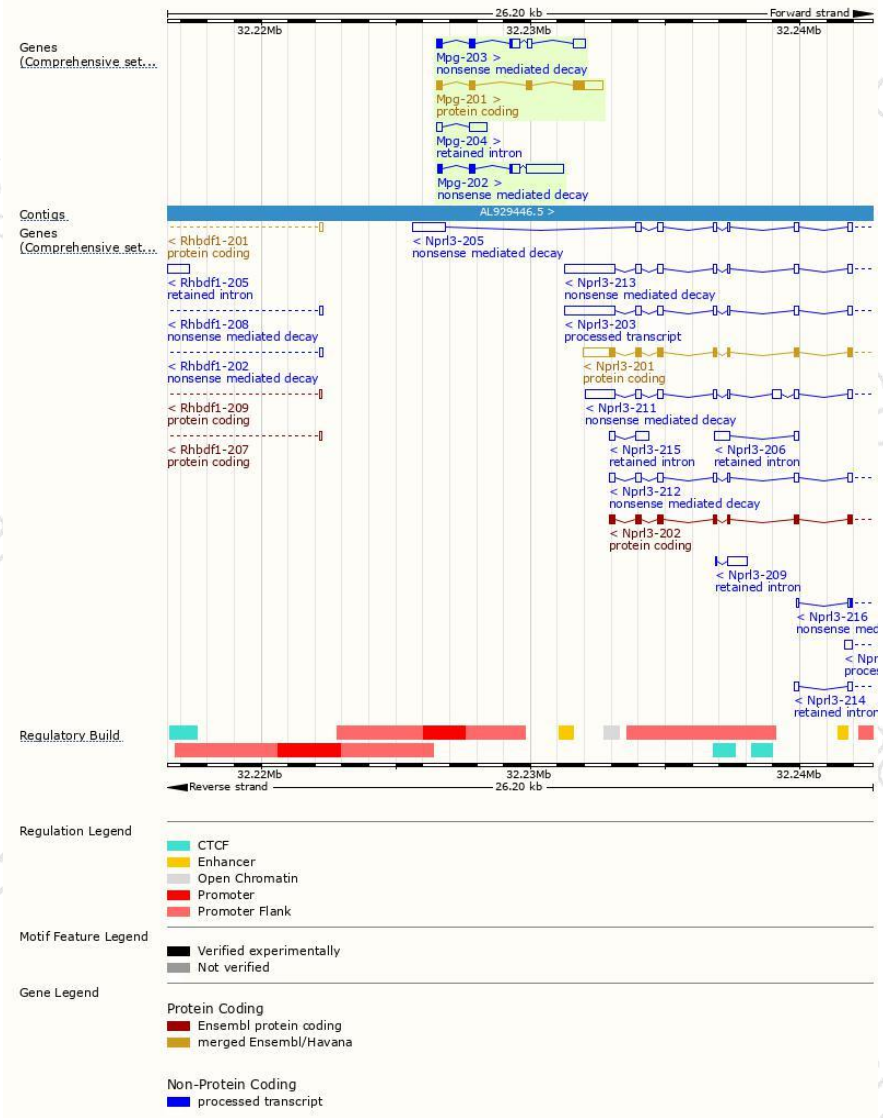
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mpg-201	ENSMUST00000020528.13	1737	333aa	Protein coding	CCDS24520	Q04841	TSL:1 GENCODE basic APPRIS P1
Mpg-202	ENSMUST00000138050.1	2143	146aa	Nonsense mediated decay	-	F2Z3Y1	TSL:1
Mpg-203	ENSMUST00000142964.7	1404	146aa	Nonsense mediated decay	-	F2Z3Y1	TSL:1
Mpg-204	ENSMUST00000144903.1	834	No protein	Retained intron	-	-	TSL:2

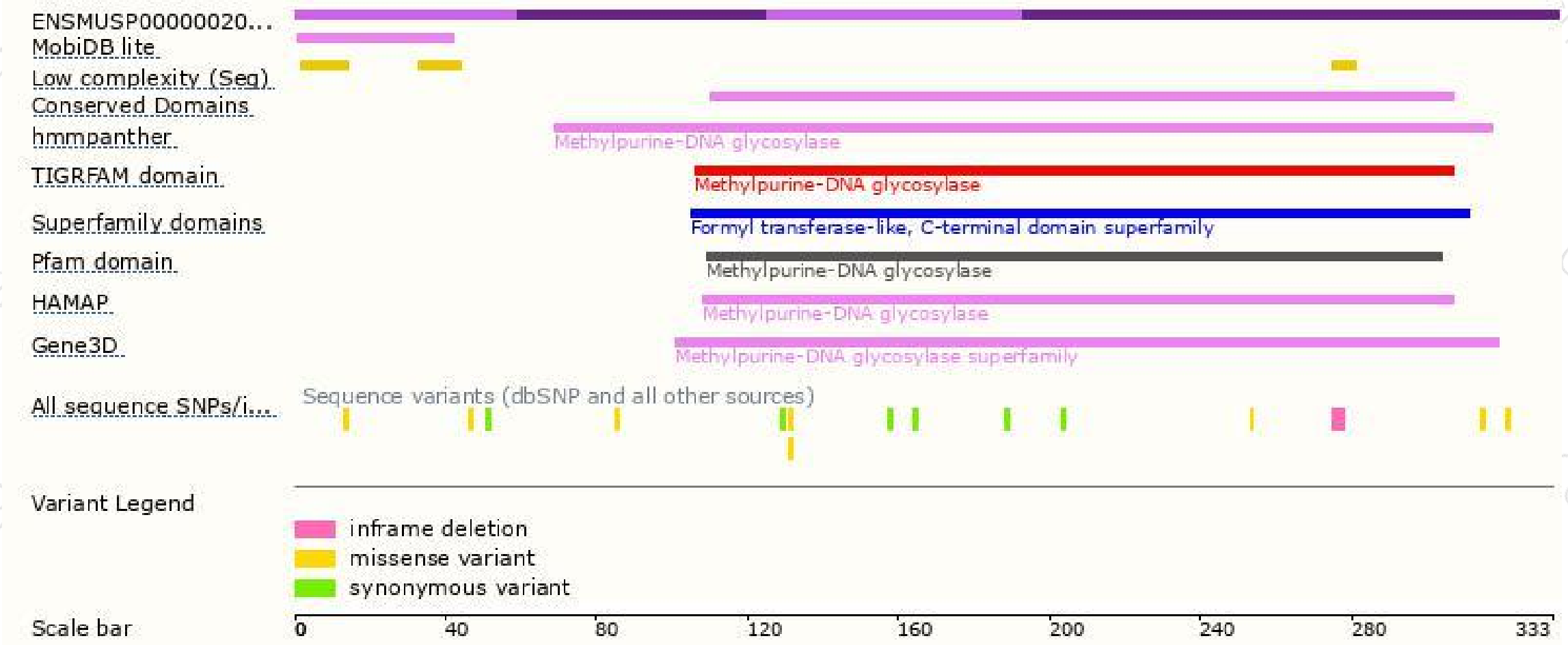
The strategy is based on the design of *Mpg-201* transcript,The transcription is shown below



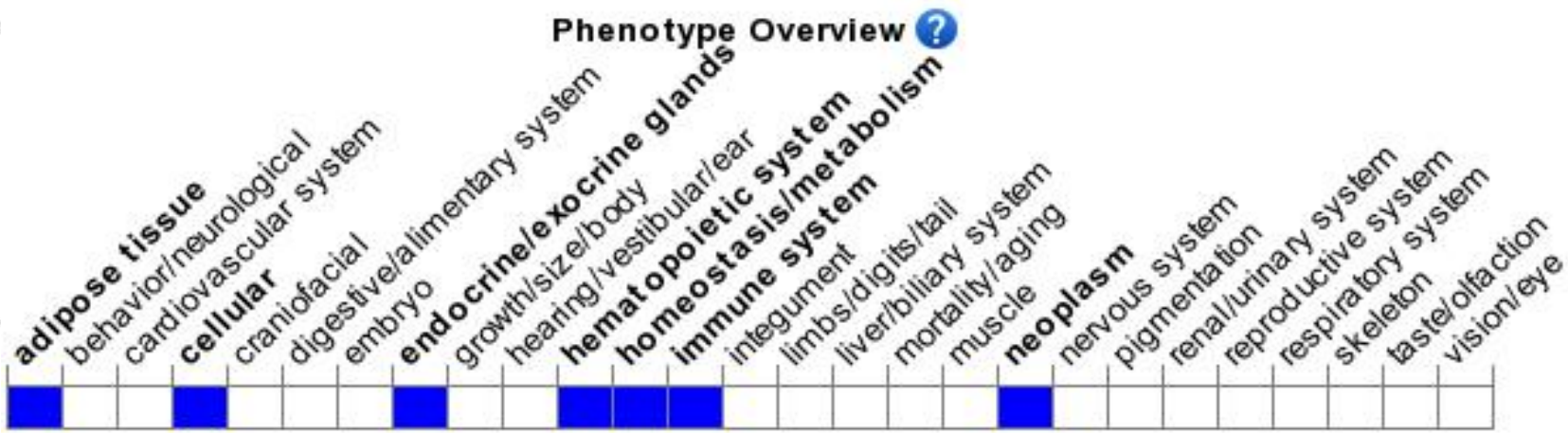
Genomic location distribution



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/).

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

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