

Magi1 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Magi1

Project type

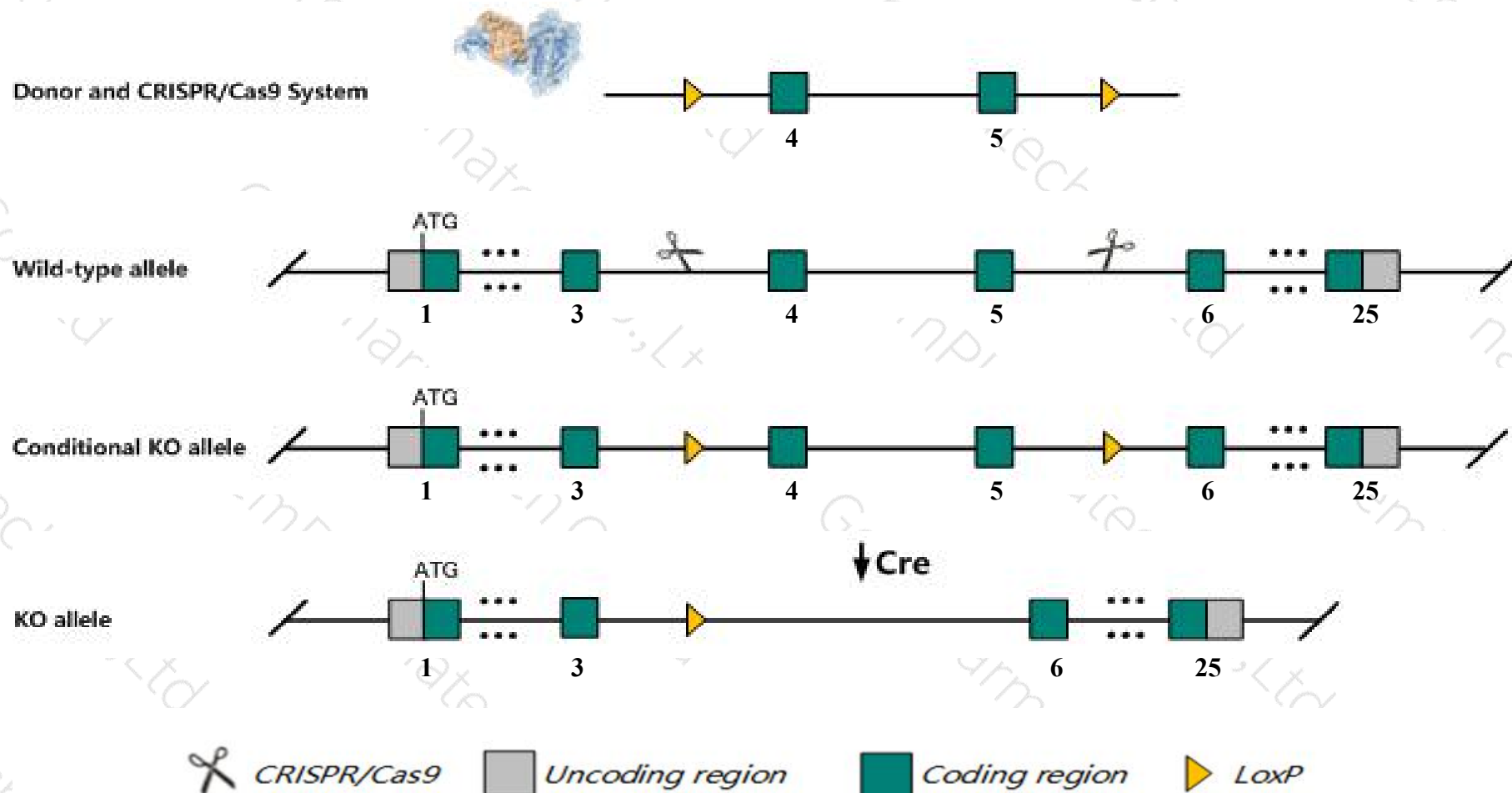
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Magi1* gene. The schematic diagram is as follows:



- The *Magil* gene has 11 transcripts. According to the structure of *Magil* gene, exon4-exon5 of *Magil*-208 (ENSMUST00000204347.2) transcript is recommended as the knockout region. The region contains 409bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Magil* 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.

- The KO region contains the *Gm23035* gene. Knockout the region will affect the function of *Gm23035* gene.
- The *Magil* gene is located on the Chr6. 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)

Magi1 membrane associated guanylate kinase, WW and PDZ domain containing 1 [Mus musculus (house mouse)]

Gene ID: 14924, updated on 19-Mar-2019

Summary



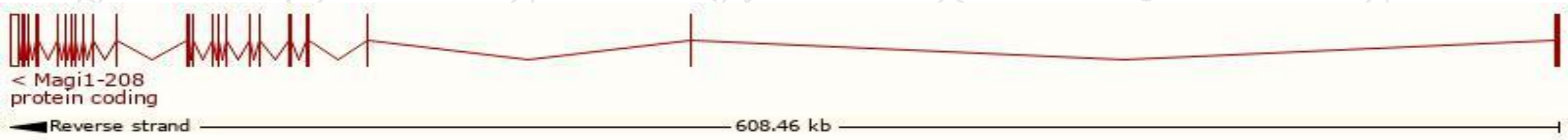
Official Symbol	Magi1 provided by MGI
Official Full Name	membrane associated guanylate kinase, WW and PDZ domain containing 1 provided by MGI
Primary source	MGI:MGI:1203522
See related	Ensembl:ENSMUSG00000045095
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AIP3, BAP1, Baiap1, Gukmi1, MAGI1c, Magi-1, TNRC19, WWP3, mKIAA4129
Expression	Broad expression in CNS E14 (RPKM 9.8), whole brain E14.5 (RPKM 9.3) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

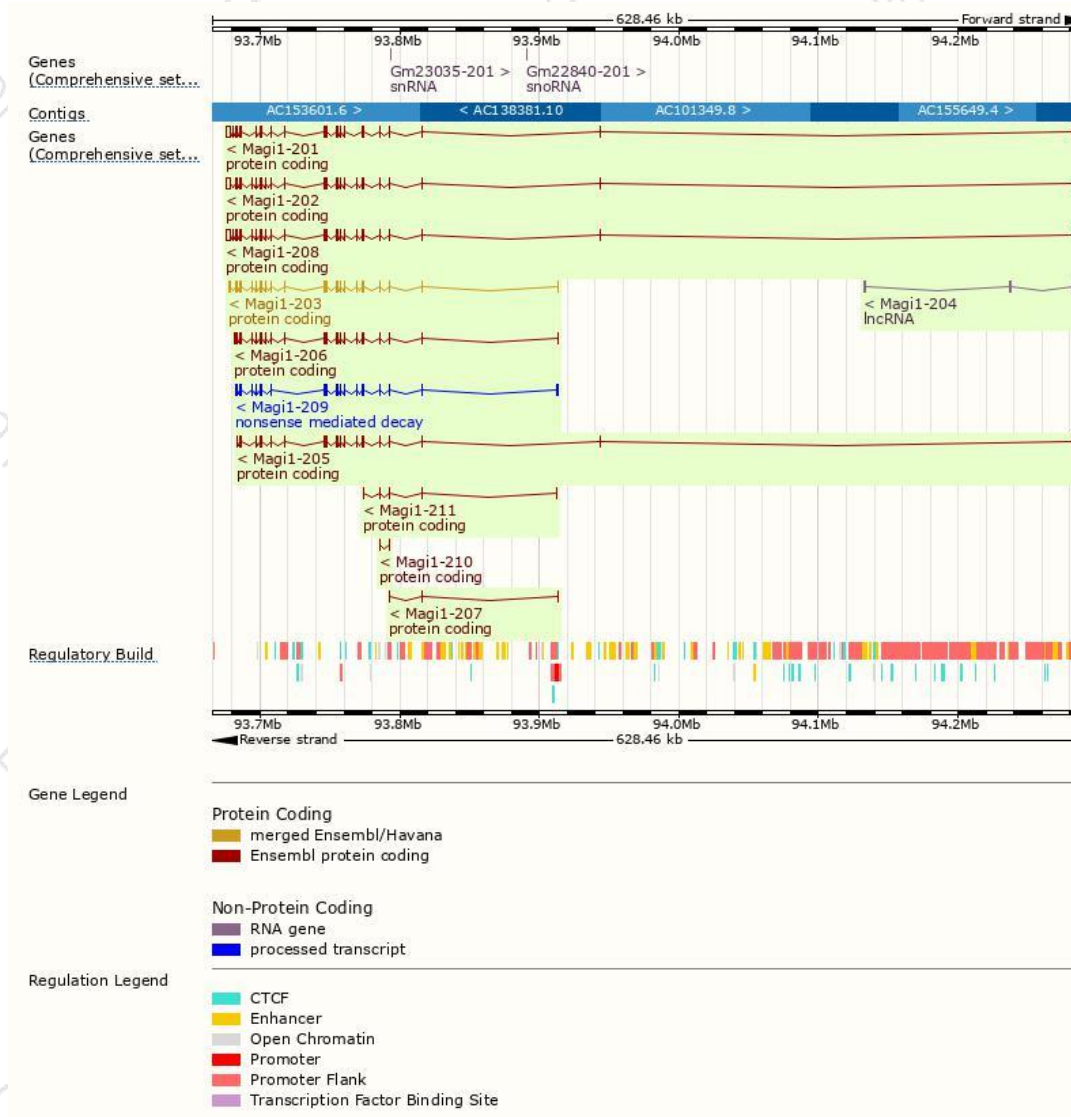
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Magi1-208	ENSMUST00000204347.2	7929	1280aa	Protein coding	CCDS85099	A0A0N4SUZ0	TSL:1 GENCODE basic APPRIS ALT 2
Magi1-202	ENSMUST00000089317.11	7209	1471aa	Protein coding	CCDS20377	Q6RHR9	TSL:1 GENCODE basic APPRIS P3
Magi1-201	ENSMUST00000055224.14	7007	1171aa	Protein coding	CCDS20378	A0A0R4J0S6	TSL:1 GENCODE basic
Magi1-206	ENSMUST00000203688.2	4969	1020aa	Protein coding	CCDS85098	A0A0N4SWH0	TSL:1 GENCODE basic
Magi1-203	ENSMUST00000093769.7	4598	1255aa	Protein coding	CCDS39573	E9PZ12	TSL:1 GENCODE basic
Magi1-205	ENSMUST00000203519.2	3920	1115aa	Protein coding	-	Q4VBG2	CDS 3' incomplete TSL:1
Magi1-211	ENSMUST00000205116.2	745	117aa	Protein coding	-	A0A0N4SVU9	CDS 3' incomplete TSL:2
Magi1-210	ENSMUST00000204788.1	537	132aa	Protein coding	-	A0A0N4SWA1	CDS 5' incomplete TSL:2
Magi1-207	ENSMUST00000204167.1	322	6aa	Protein coding	-	-	CDS 3' incomplete TSL:3
Magi1-209	ENSMUST00000204532.2	4078	496aa	Nonsense mediated decay	-	A0A0N4SUP9	TSL:1
Magi1-204	ENSMUST00000203034.1	408	No protein	lncRNA	-	-	TSL:1

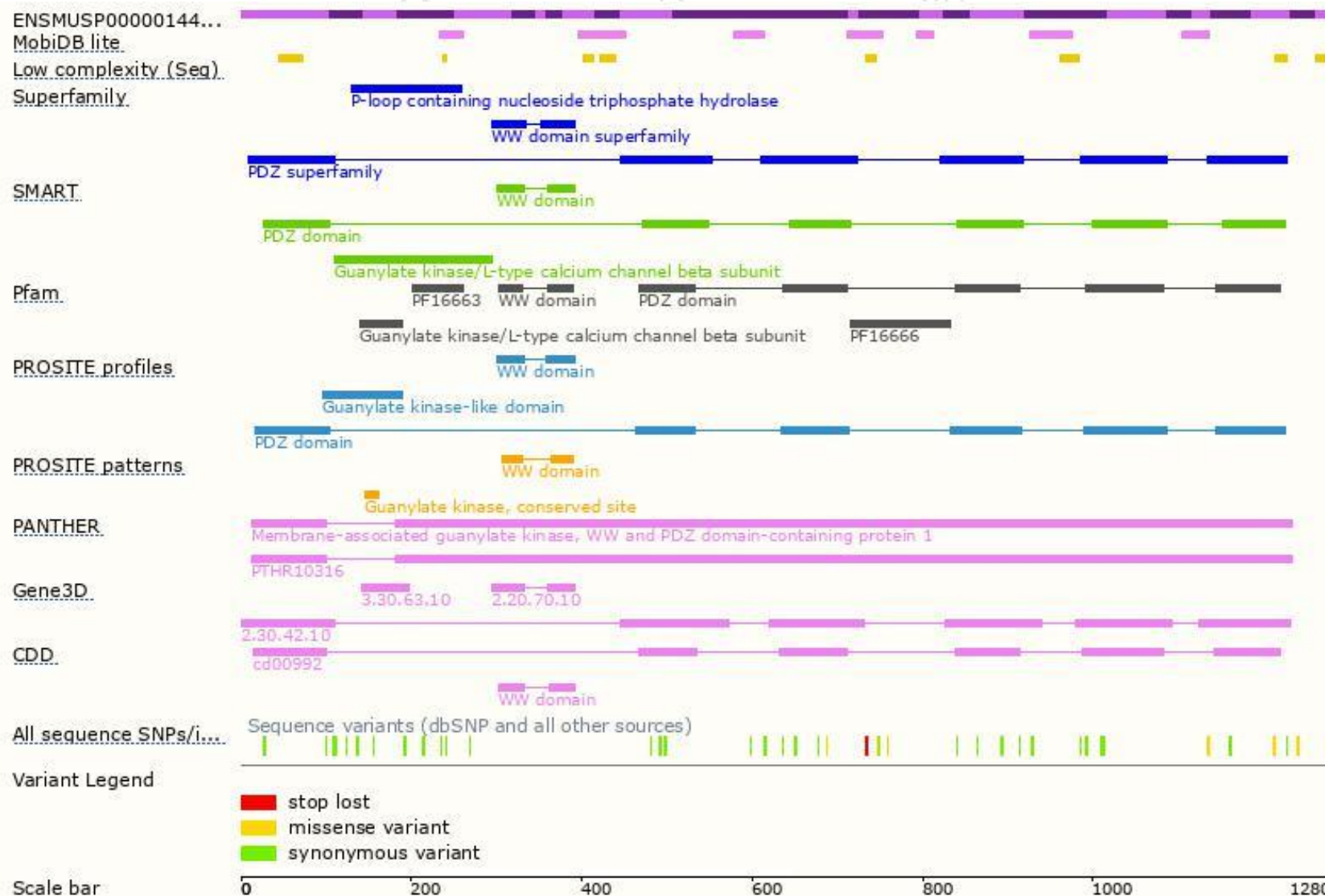
The strategy is based on the design of *Magi1-208* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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