

Mdga2 Cas9-KO Strategy

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Project Overview

Project Name

Mdga2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mdga2* gene. The schematic diagram is as follows:



- The *Mdga2* gene has 14 transcripts. According to the structure of *Mdga2* gene, exon2 of *Mdga2-210* (ENSMUST00000222167.1) transcript is recommended as the knockout region. The region contains 140bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mdga2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice that paternally inherit an allele disrupted by transgene insertion exhibit varying degrees of abnormalities in the skull, paw, and tail.
- The *Mdga2* gene is located on the Chr12. 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)

Mdga2 MAM domain containing glycosylphosphatidylinositol anchor 2 [Mus musculus (house mouse)]

Gene ID: 320772, updated on 19-Mar-2019

Summary



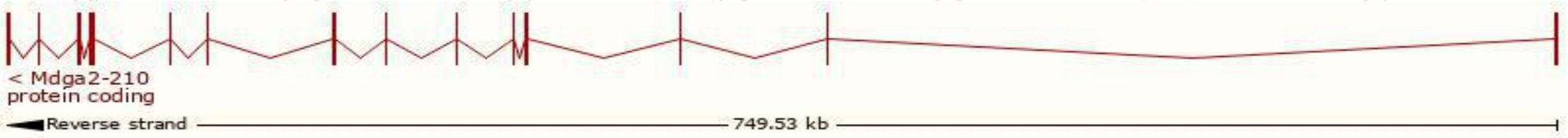
| | |
|---------------------------|---|
| Official Symbol | Mdga2 provided by MGI |
| Official Full Name | MAM domain containing glycosylphosphatidylinositol anchor 2 provided by MGI |
| Primary source | MGI:MGI:2444706 |
| See related | Ensembl:ENSMUSG000000034912 |
| Gene type | protein coding |
| 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 | 6720489L24Rik, 9330209L04Rik, Adp, Mamdc1, Tg(Pmp-PFN1*G118V)838Kiae |
| Expression | Biased expression in CNS E18 (RPKM 2.1), cortex adult (RPKM 1.5) and 7 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

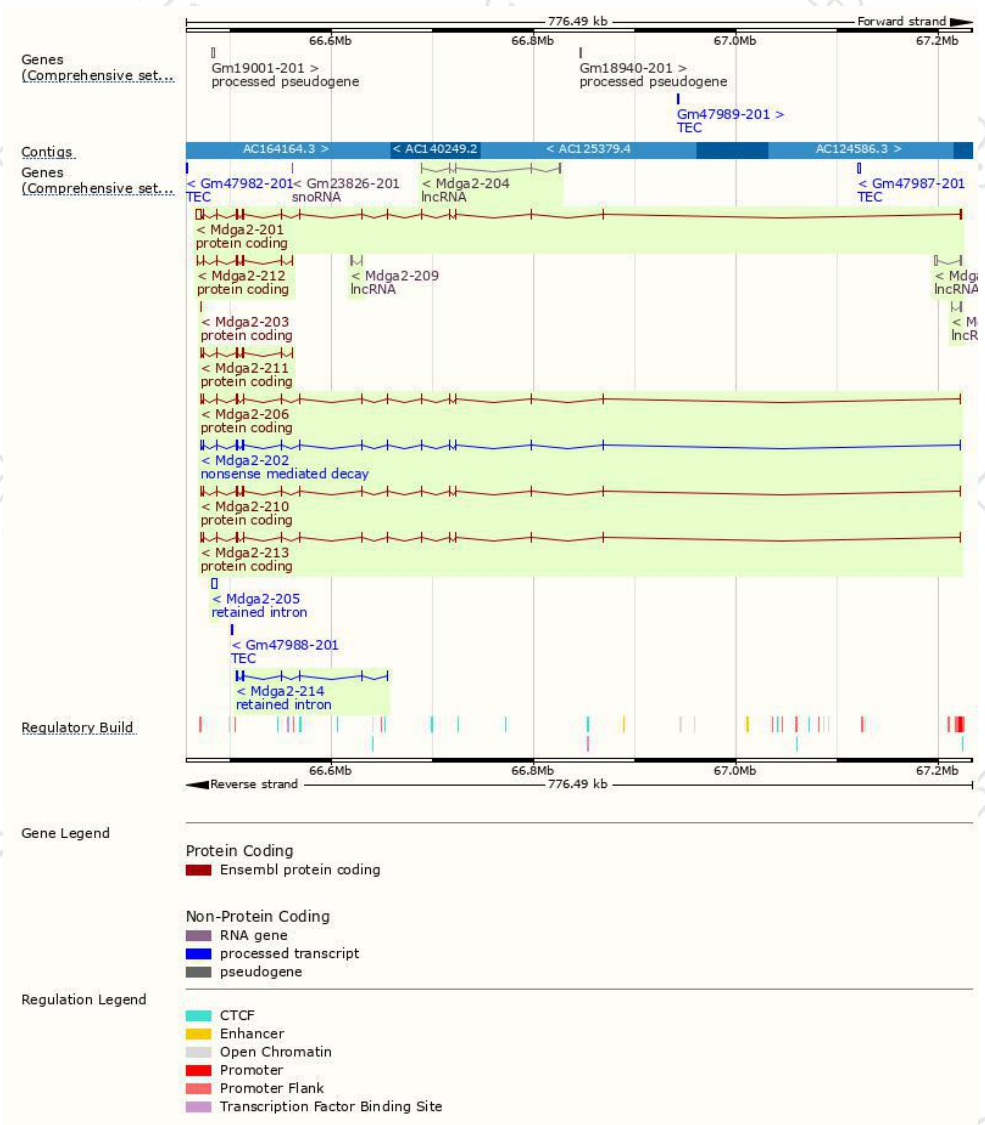
The gene has 14 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|---------------------------------------|------|------------------------|-------------------------|---------------------------|----------------------------|---------------------------------|
| Mdga2-210 | ENSMUST00000222167.1 | 2871 | 956aa | Protein coding | CCDS56842 | B2RQF5 | TSL:1 GENCODE basic APPRIS P2 |
| Mdga2-213 | ENSMUST00000223141.1 | 2850 | 949aa | Protein coding | CCDS25945 | P60755 | TSL:2 GENCODE basic |
| Mdga2-201 | ENSMUST00000037181.15 | 9833 | 1025aa | Protein coding | - | Q3UV20 | TSL:1 GENCODE basic APPRIS ALT1 |
| Mdga2-206 | ENSMUST00000178814.8 | 3362 | 1009aa | Protein coding | - | A0A217FL82 | CDS 5' incomplete TSL:2 |
| Mdga2-211 | ENSMUST00000222623.1 | 1449 | 297aa | Protein coding | - | A0A1Y7VJM7 | TSL:5 GENCODE basic |
| Mdga2-212 | ENSMUST00000222987.1 | 1388 | 319aa | Protein coding | - | A0A1Y7VIL8 | TSL:5 GENCODE basic |
| Mdga2-203 | ENSMUST00000113942.2 | 423 | 140aa | Protein coding | - | Q3UUB8 | TSL:NA GENCODE basic |
| Mdga2-202 | ENSMUST00000101379.9 | 3072 | 134aa | Nonsense mediated decay | - | F6UYI7 | CDS 5' incomplete TSL:1 |
| Mdga2-205 | ENSMUST00000178724.1 | 5217 | No protein | Retained intron | - | - | TSL:NA |
| Mdga2-214 | ENSMUST00000223289.1 | 1428 | No protein | Retained intron | - | - | TSL:5 |
| Mdga2-208 | ENSMUST00000179577.2 | 3997 | No protein | lncRNA | - | - | TSL:2 |
| Mdga2-207 | ENSMUST00000179025.1 | 1684 | No protein | lncRNA | - | - | TSL:2 |
| Mdga2-204 | ENSMUST00000177690.1 | 631 | No protein | lncRNA | - | - | TSL:3 |
| Mdga2-209 | ENSMUST00000179729.1 | 594 | No protein | lncRNA | - | - | TSL:2 |

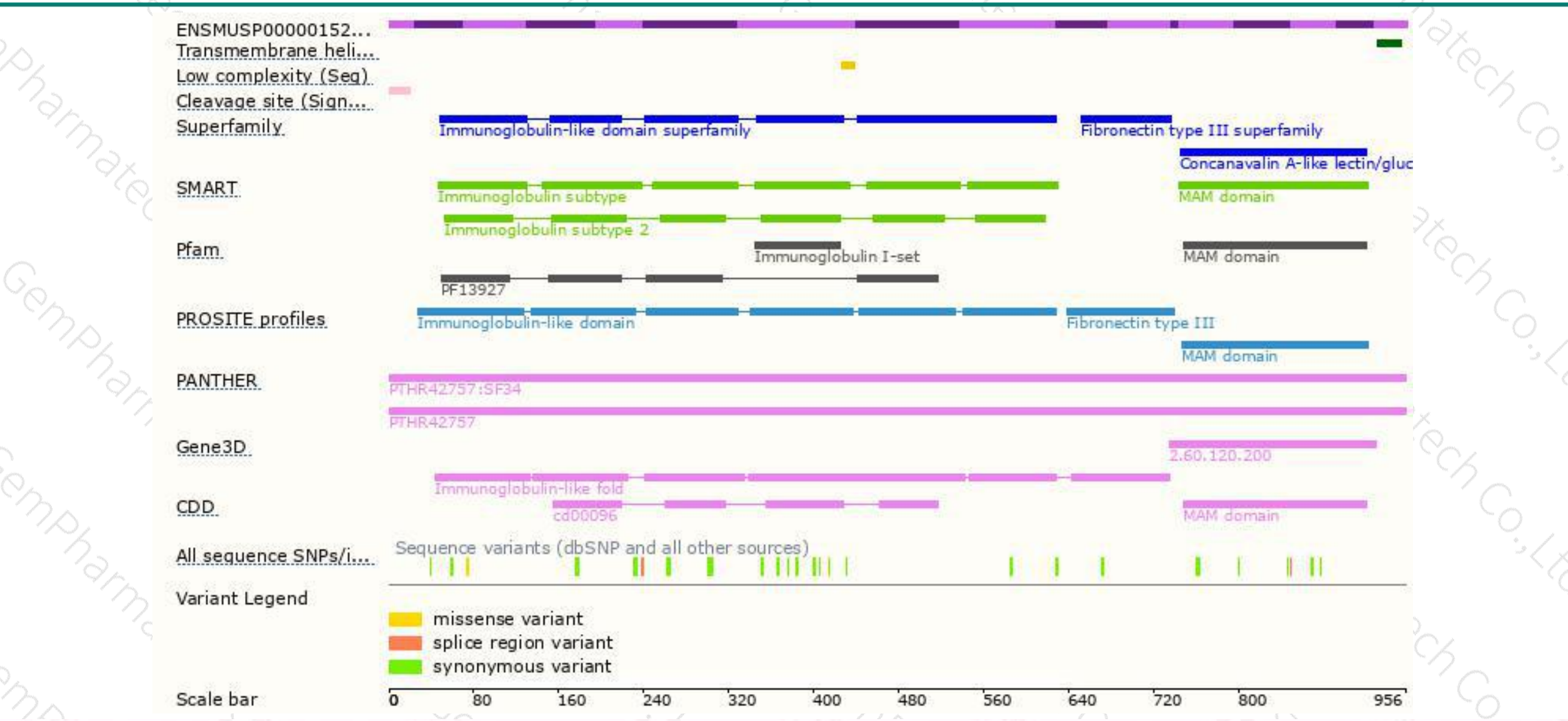
The strategy is based on the design of *Mdga2-210* transcript,The transcription is shown below



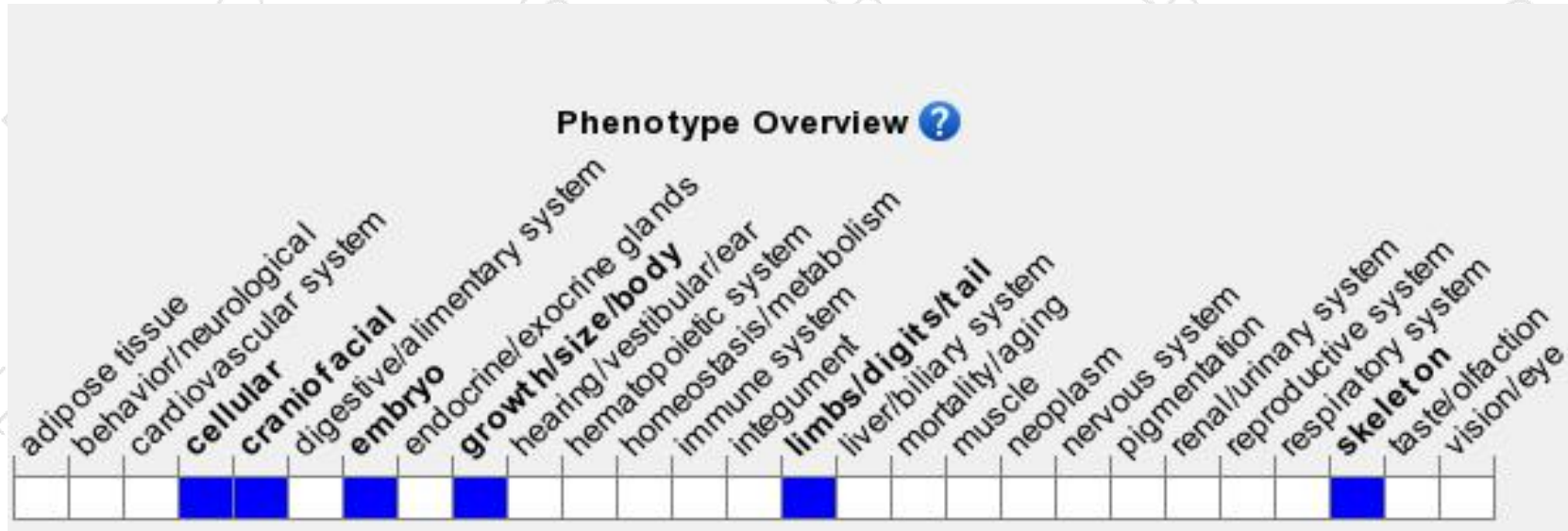
Genomic location distribution



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, Mice that paternally inherit an allele disrupted by transgene insertion exhibit varying degrees of abnormalities in the skull, paw, and tail.

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

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