

Gga2 Cas9-CKO Strategy

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Project Overview

Project Name

Gga2

Project type

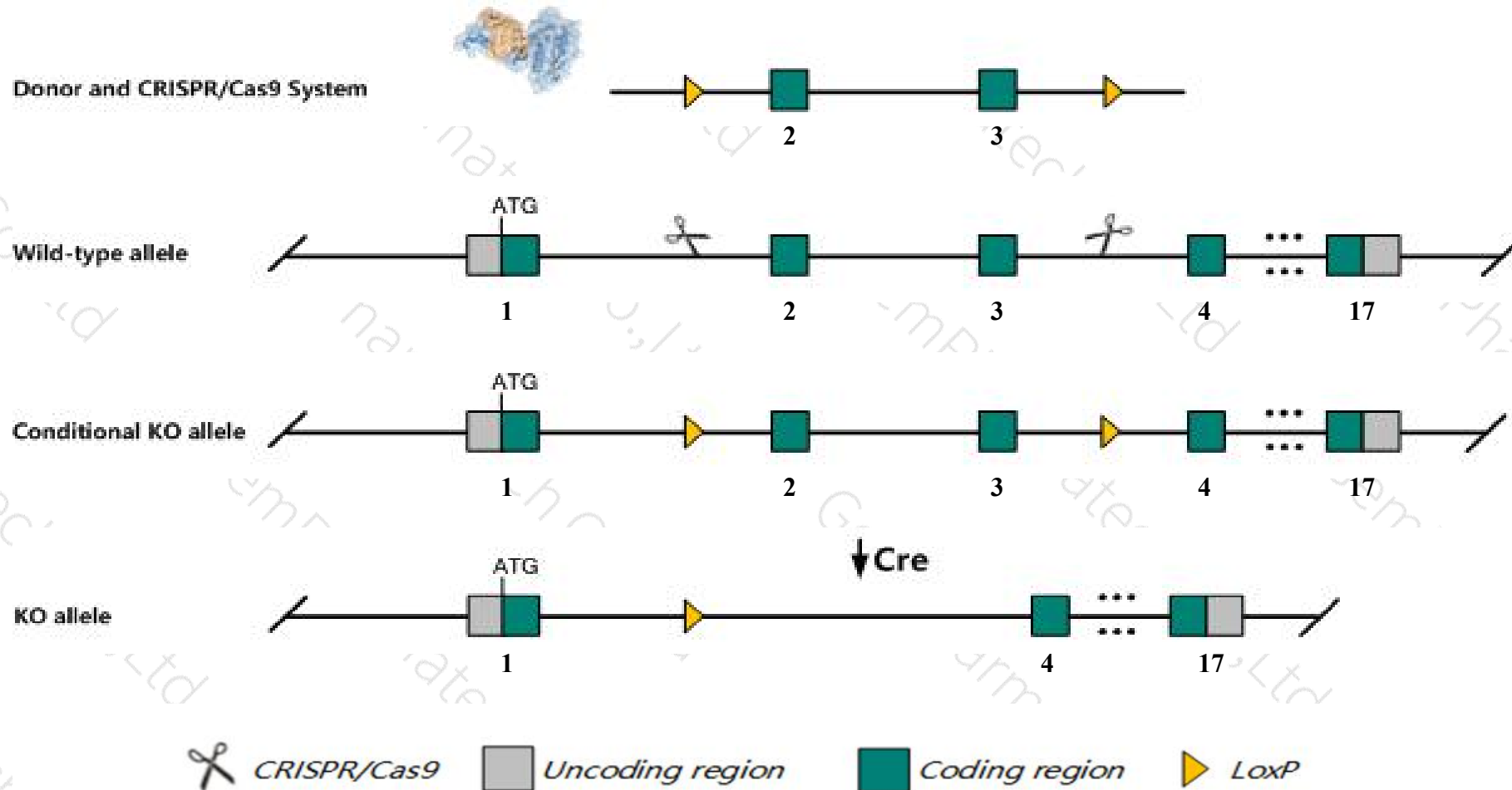
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gga2* gene. The schematic diagram is as follows:



Technical routes

- The *Gga2* gene has 6 transcripts. According to the structure of *Gga2* gene, exon2-exon3 of *Gga2-201* (ENSMUST00000033160.14) transcript is recommended as the knockout region. The region contains 161bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gga2* 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.

- According to the existing MGI data, mice homozygous for a gene trapped allele exhibit complete embryonic lethality. mice homozygous for a different gene trapped allele show decreased birth weight, hypoglycemia and partial neonatal lethality, with all remaining mice dying within the first three weeks of life.
- The *Gga2* gene is located on the Chr7. 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)

Gga2 golgi associated, gamma adaptin ear containing, ARF binding protein 2 [Mus musculus (house mouse)]

Gene ID: 74105, updated on 13-Mar-2020

Summary



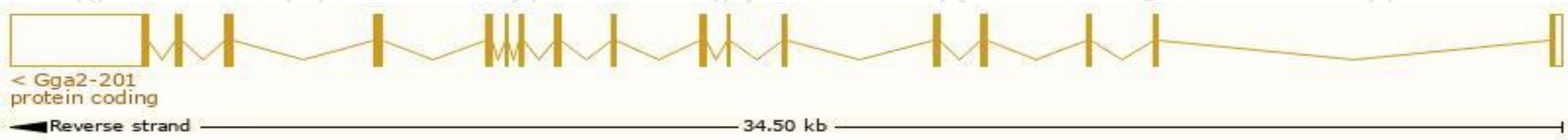
Official Symbol	Gga2 provided by MGI
Official Full Name	golgi associated, gamma adaptin ear containing, ARF binding protein 2 provided by MGI
Primary source	MGI:MGI:1921355
See related	Ensembl:ENSMUSG00000030872
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1200007E24Rik, mKIAA1080
Expression	Broad expression in placenta adult (RPKM 61.9), limb E14.5 (RPKM 23.5) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

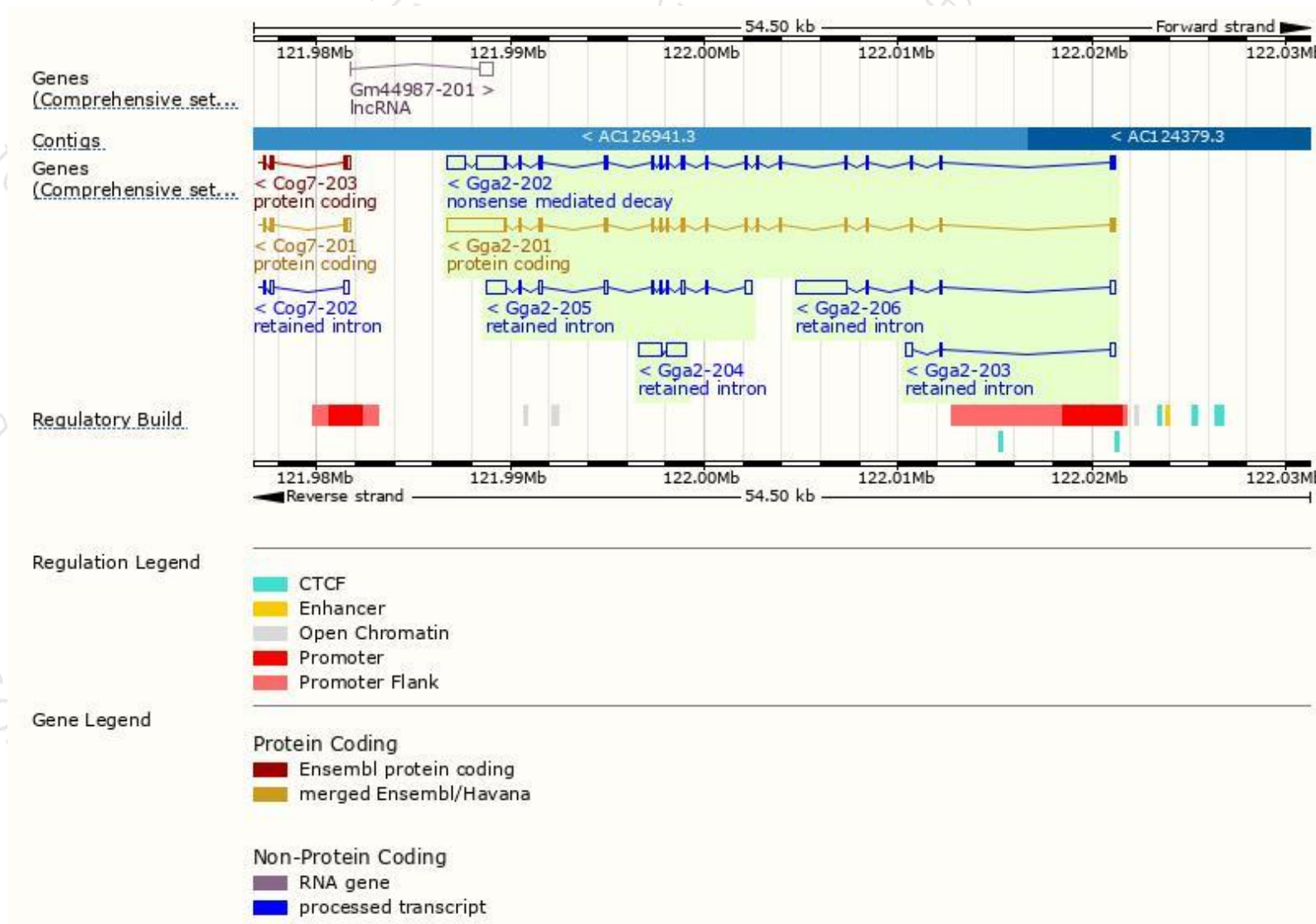
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gga2-201	ENSMUST00000033160.14	4915	603aa	Protein coding	CCDS40116	Q6P5E6	TSL:1 GENCODE basic APPRIS P1
Gga2-202	ENSMUST00000124566.1	4251	603aa	Nonsense mediated decay	-	Q6P5E6	TSL:2
Gga2-206	ENSMUST00000145277.7	3086	No protein	Retained intron	-	-	TSL:2
Gga2-205	ENSMUST00000144779.1	2351	No protein	Retained intron	-	-	TSL:1
Gga2-204	ENSMUST00000138441.1	2181	No protein	Retained intron	-	-	TSL:1
Gga2-203	ENSMUST00000131081.1	620	No protein	Retained intron	-	-	TSL:2

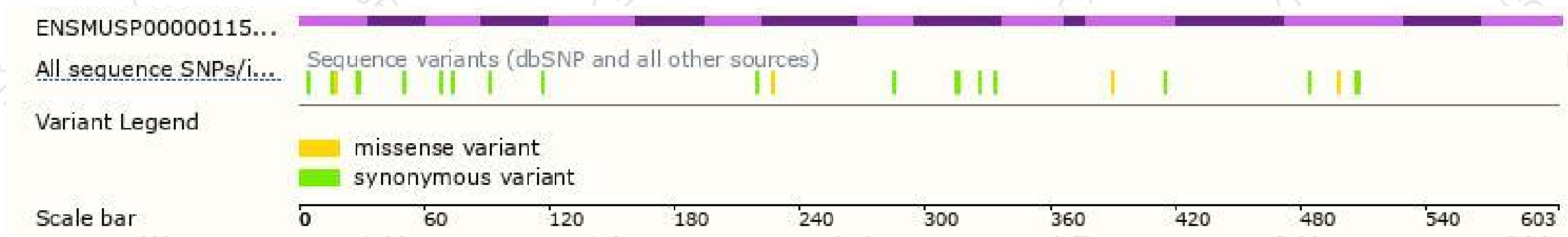
The strategy is based on the design of *Gga2-201* transcript,the transcription is shown below:



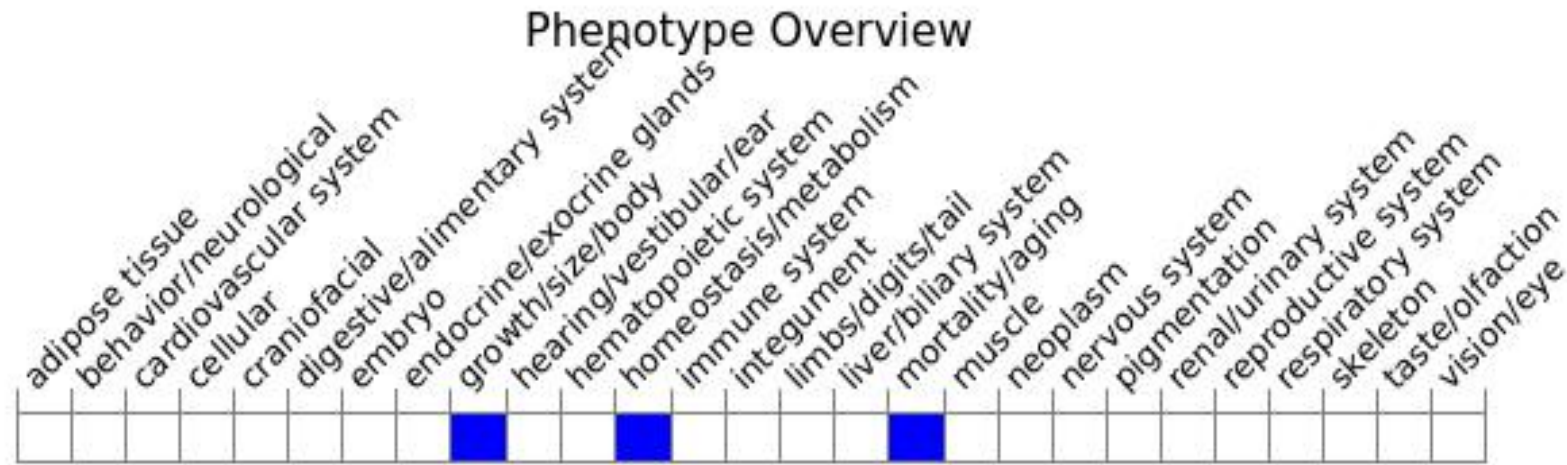
Genomic location distribution



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/>).

According to the existing MGI data, mice homozygous for a gene trapped allele exhibit complete embryonic lethality. Mice homozygous for a different gene trapped allele show decreased birth weight, hypoglycemia and partial neonatal lethality, with all remaining mice dying within the first three weeks of life.

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

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