Adgrg1 Cas9-KO Strategy

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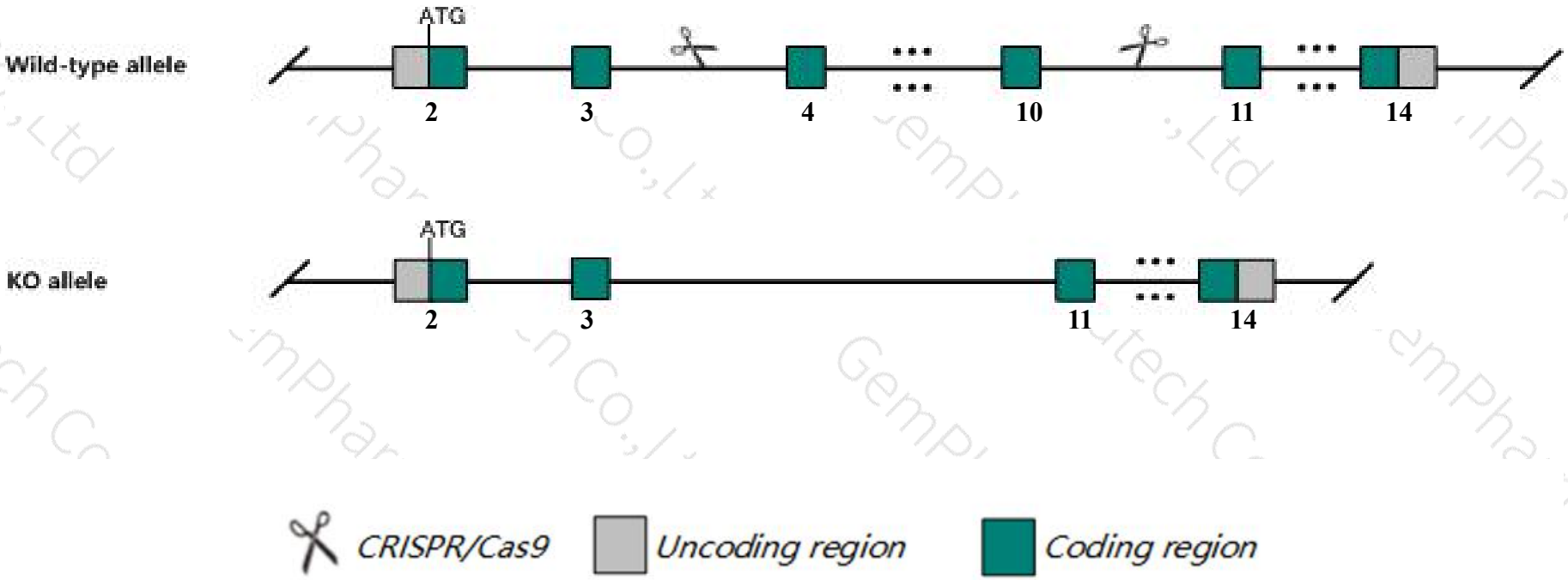
Design Date: 2019-7-18

Project Overview

Project Name	***Adgrg1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Adgrg1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Adgrg1* gene has 16 transcripts. According to the structure of *Adgrg1* gene, exon4-exon10 of *Adgrg1-202* (ENSMUST00000179619.8) transcript is recommended as the knockout region.The region contains 799bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Adgrg1* gene. The brief process is as follows: CRISPR/Cas9 syster

Notice

- According to the existing MGI data,Mice homozygous for a null allele exhibit defects in basement membranes of mutltiple tissues, resulting in neuronal ectopias in the frontoparietal cortex, male subfertility and testis defects, brain development, and hematopoietic stem cell development.

- The *Adgrg1* gene is located on the Chr8. 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）

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Adgrg1 adhesion G protein-coupled receptor G1 [Mus musculus (house mouse)]

Gene ID: 14766, updated on 9-Apr-2019

Summary

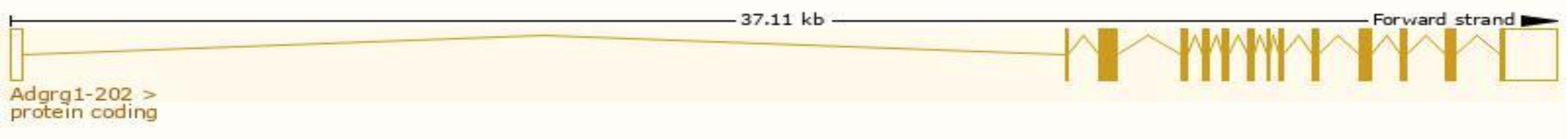
Official Symbol	Adgrg1 provided by MGI
Official Full Name	adhesion G protein-coupled receptor G1 provided byMGI
Primary source	MGI:MGI:1340051
See related	Ensembl:ENSMUSG00000031785
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cyt28, Gpr56, TM7LN4, TM7XN1
Expression	Ubiquitous expression in kidney adult (RPKM 93.7), ovary adult (RPKM 80.7) and 27 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

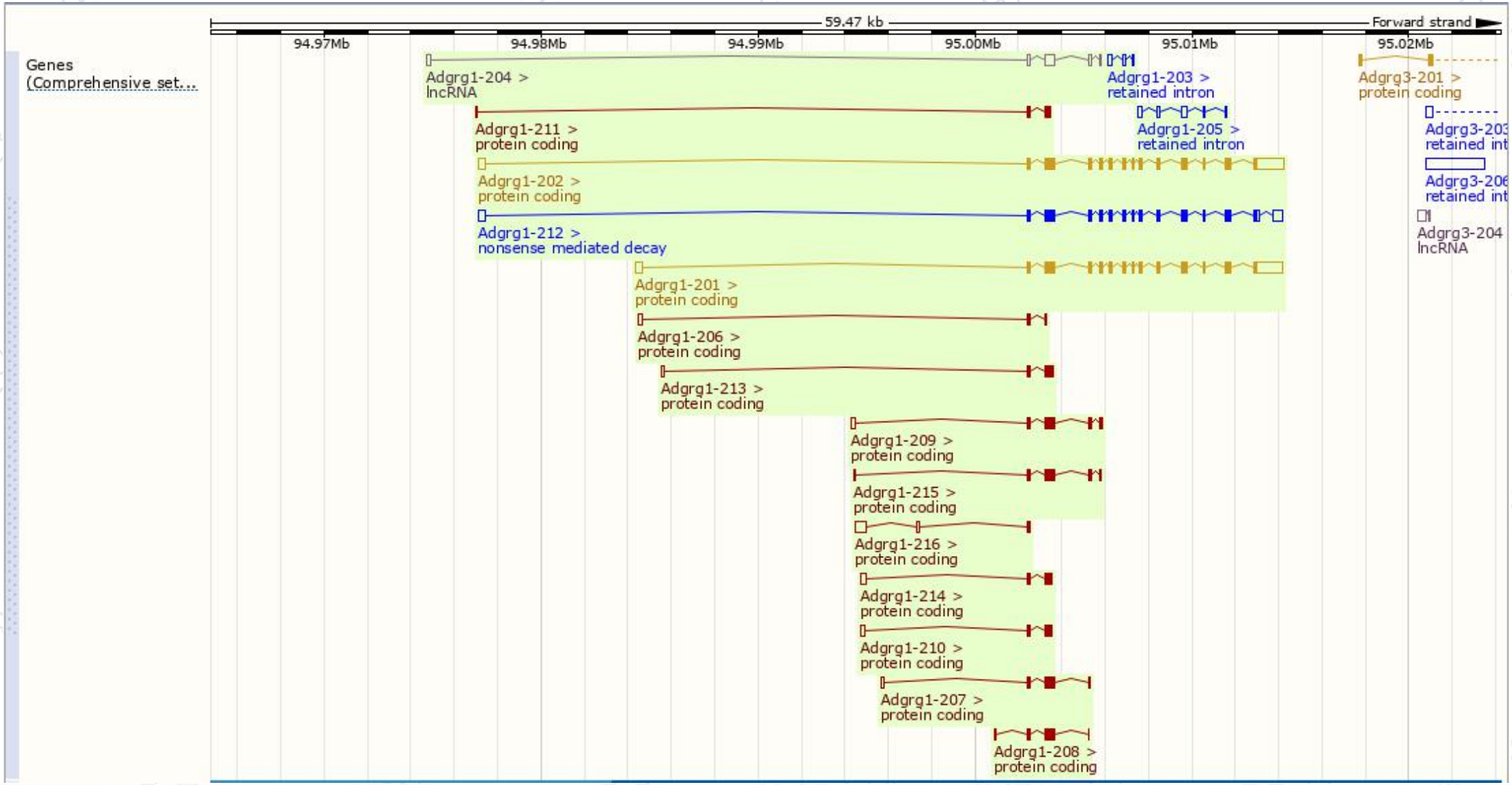
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Adgrg1-202	ENSMUST00000179619.8	3616	687aa	Protein coding	CCDS22553	Q8K209	TSL:1 GENCODE basic APPRIS P1
Adgrg1-201	ENSMUST00000093271.7	3574	687aa	Protein coding	CCDS22553	Q8K209	TSL:1 GENCODE basic APPRIS P1
Adgrg1-209	ENSMUST00000212141.1	995	256aa	Protein coding	-	A0A1D5RLE2	CDS 3' incomplete TSL:2
Adgrg1-215	ENSMUST00000212976.1	774	229aa	Protein coding	-	A0A1D5RLN4	CDS 3' incomplete TSL:3
Adgrg1-216	ENSMUST00000212995.1	709	20aa	Protein coding	-	A0A1D5RLC4	CDS 3' incomplete TSL:3
Adgrg1-207	ENSMUST00000211984.1	705	185aa	Protein coding	-	A0A1D5RLK9	CDS 3' incomplete TSL:5
Adgrg1-208	ENSMUST00000212118.1	614	167aa	Protein coding	-	A0A1D5RLB9	CDS 3' incomplete TSL:5
Adgrg1-214	ENSMUST00000212956.1	598	112aa	Protein coding	-	A0A1D5RLH8	CDS 3' incomplete TSL:3
Adgrg1-213	ENSMUST00000212799.1	575	149aa	Protein coding	-	A0A1D5RLF7	CDS 3' incomplete TSL:3
Adgrg1-210	ENSMUST00000212531.1	499	118aa	Protein coding	-	A0A1D5RM68	CDS 3' incomplete TSL:3
Adgrg1-211	ENSMUST00000212581.1	384	105aa	Protein coding	-	A0A1D5RME3	CDS 3' incomplete TSL:3
Adgrg1-206	ENSMUST00000211944.1	296	32aa	Protein coding	-	A0A1D5RLI8	CDS 3' incomplete TSL:5
Adgrg1-212	ENSMUST00000212660.1	3011	687aa	Nonsense mediated decay	CCDS22553	Q8K209	TSL:1
Adgrg1-205	ENSMUST00000211911.1	713	No protein	Retained intron	-	-	TSL:2
Adgrg1-203	ENSMUST00000211806.1	343	No protein	Retained intron	-	-	TSL:1
Adgrg1-204	ENSMUST00000211850.1	829	No protein	lncRNA	-	-	TSL:5

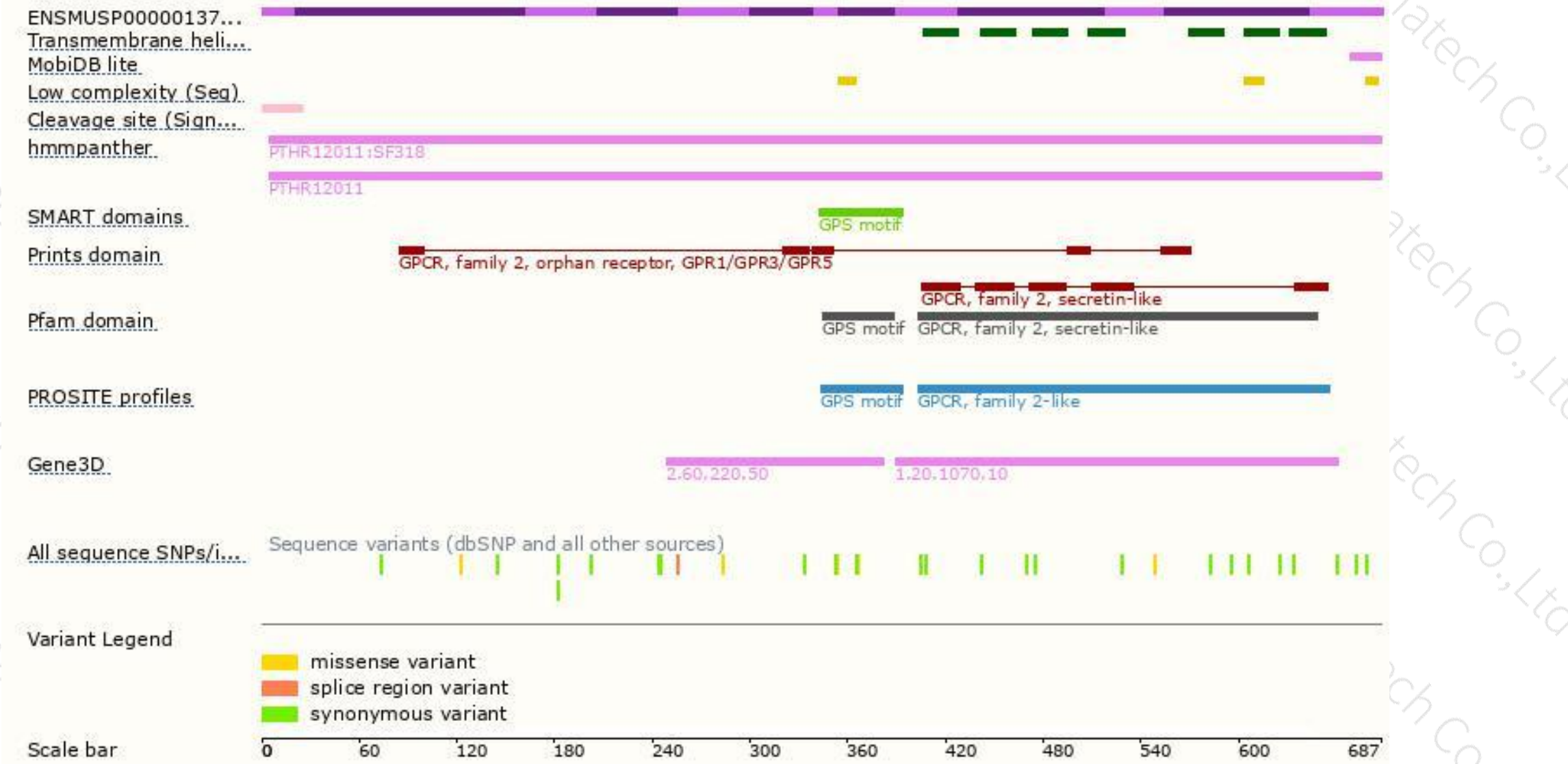
The strategy is based on the design of *Adgrg1-202* transcript,The transcription is shown below



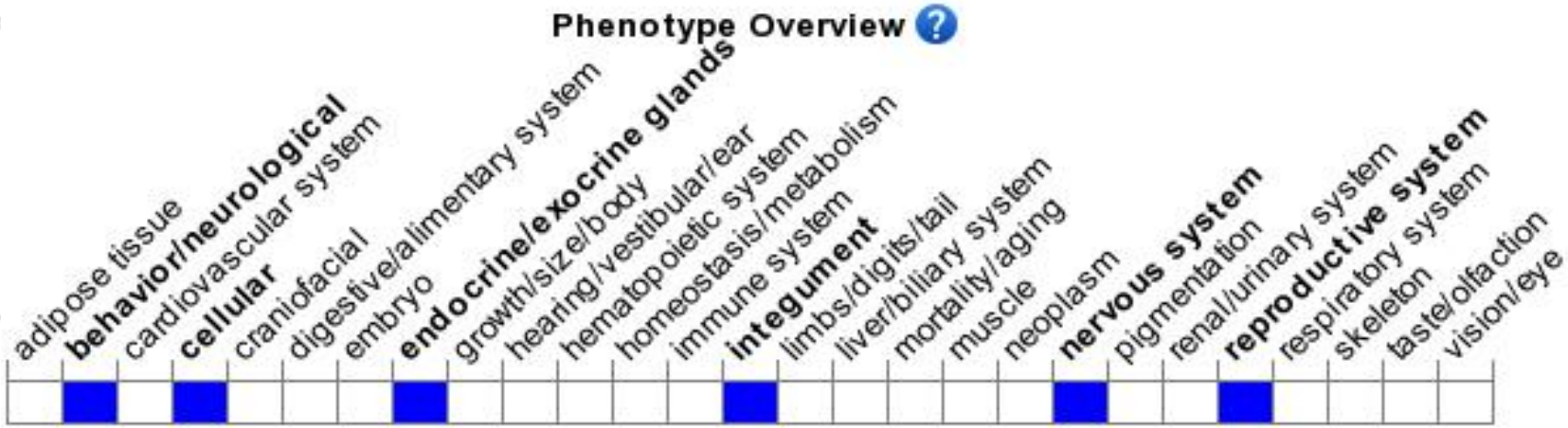
Genomic location distribution



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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