

Abcg4 Cas9-KO Strategy

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Project Overview

Project Name

Abcg4

Project type

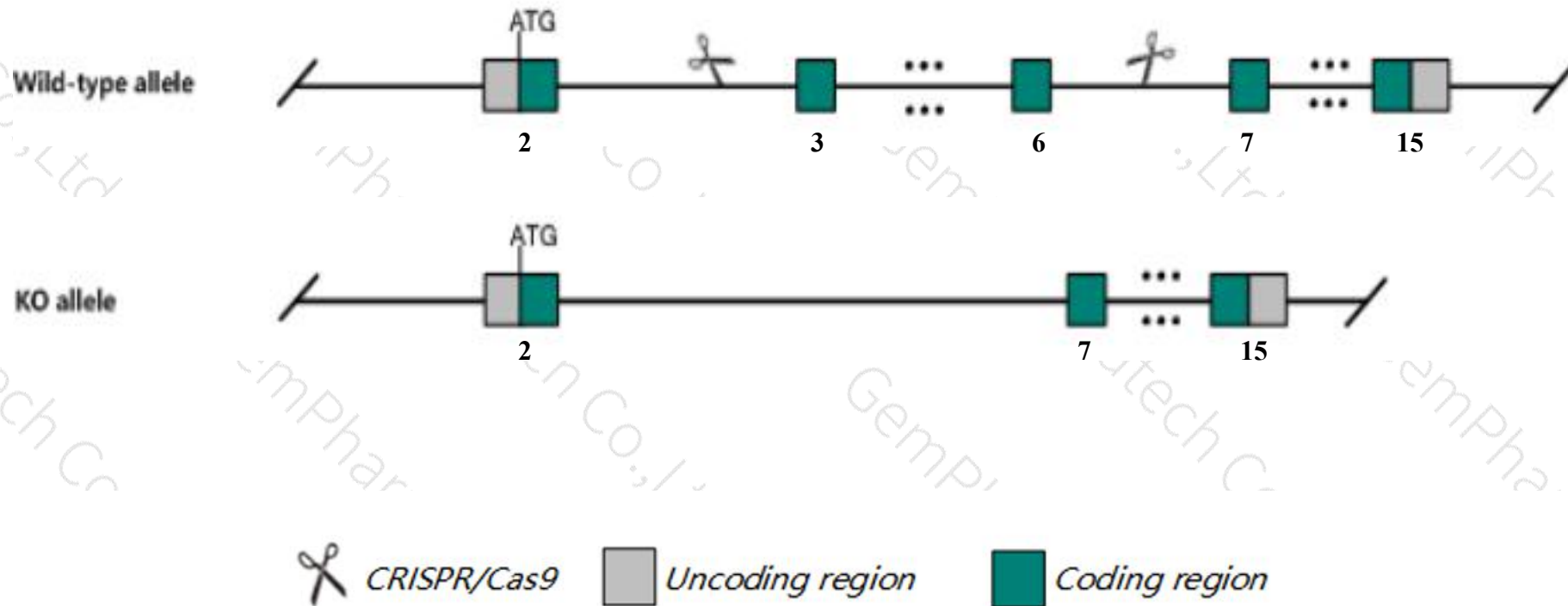
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abcg4* gene. The schematic diagram is as follows:



- The *Abcg4* gene has 10 transcripts. According to the structure of *Abcg4* gene, exon3-exon6 of *Abcg4-208* (ENSMUST00000161354.8) transcript is recommended as the knockout region. The region contains 448bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Abcg4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a report allele exhibit increased brain lathosterol levels.
- The *Abcg4* gene is located on the Chr9. 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)

Abcg4 ATP binding cassette subfamily G member 4 [Mus musculus (house mouse)]

Gene ID: 192663, updated on 13-Mar-2020

Summary



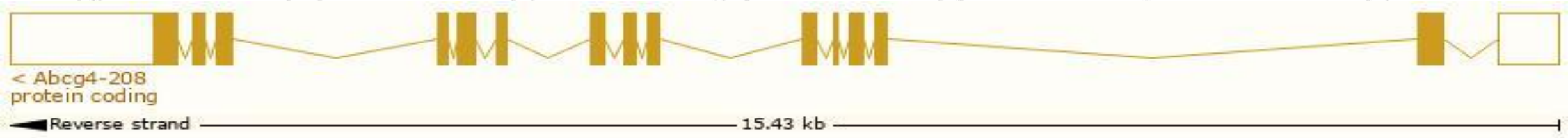
Official Symbol	Abcg4 provided by MGI
Official Full Name	ATP binding cassette subfamily G member 4 provided by MGI
Primary source	MGI:MGI:1890594
See related	Ensembl:ENSMUSG00000032131
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	6430517O04Rik
Expression	Broad expression in adrenal adult (RPKM 20.5), cerebellum adult (RPKM 15.8) and 15 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

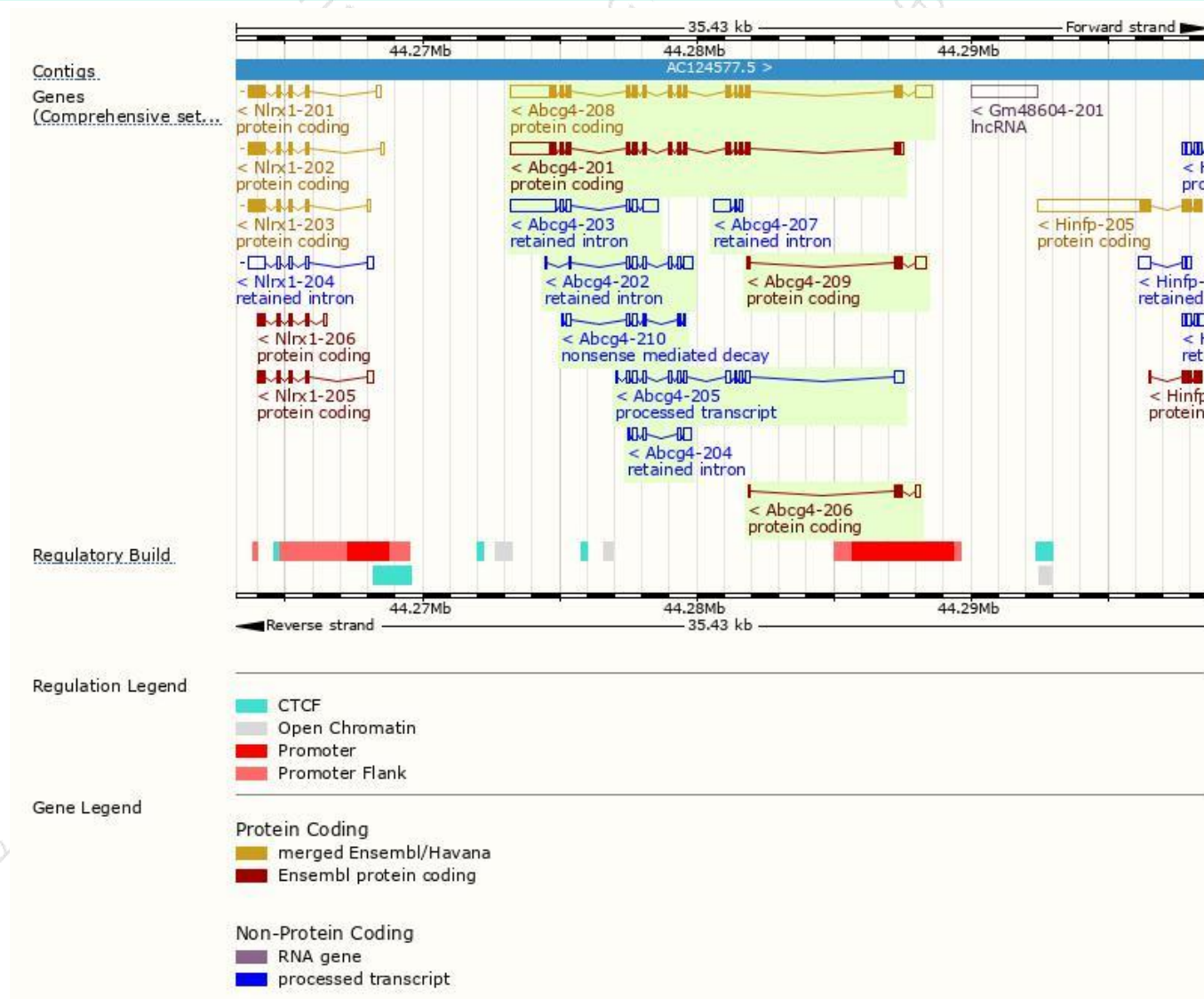
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abcg4-208	ENSMUST00000161354.8	3999	646aa	Protein coding	CCDS23101	Q91WA9	TSL:1 GENCODE basic APPRIS P1
Abcg4-201	ENSMUST00000034648.15	3476	646aa	Protein coding	CCDS23101	Q91WA9	TSL:1 GENCODE basic APPRIS P1
Abcg4-209	ENSMUST00000161408.1	678	104aa	Protein coding	-	E0CYI8	CDS 3' incomplete TSL:5
Abcg4-206	ENSMUST00000160384.1	402	83aa	Protein coding	-	E0CY02	CDS 3' incomplete TSL:5
Abcg4-210	ENSMUST00000162783.7	749	65aa	Nonsense mediated decay	-	F6XWY6	CDS 5' incomplete TSL:5
Abcg4-205	ENSMUST00000160323.7	1547	No protein	Processed transcript	-	-	TSL:1
Abcg4-203	ENSMUST00000159385.7	2801	No protein	Retained intron	-	-	TSL:1
Abcg4-202	ENSMUST00000085979.10	1017	No protein	Retained intron	-	-	TSL:5
Abcg4-207	ENSMUST00000161206.1	731	No protein	Retained intron	-	-	TSL:3
Abcg4-204	ENSMUST00000159997.1	696	No protein	Retained intron	-	-	TSL:3

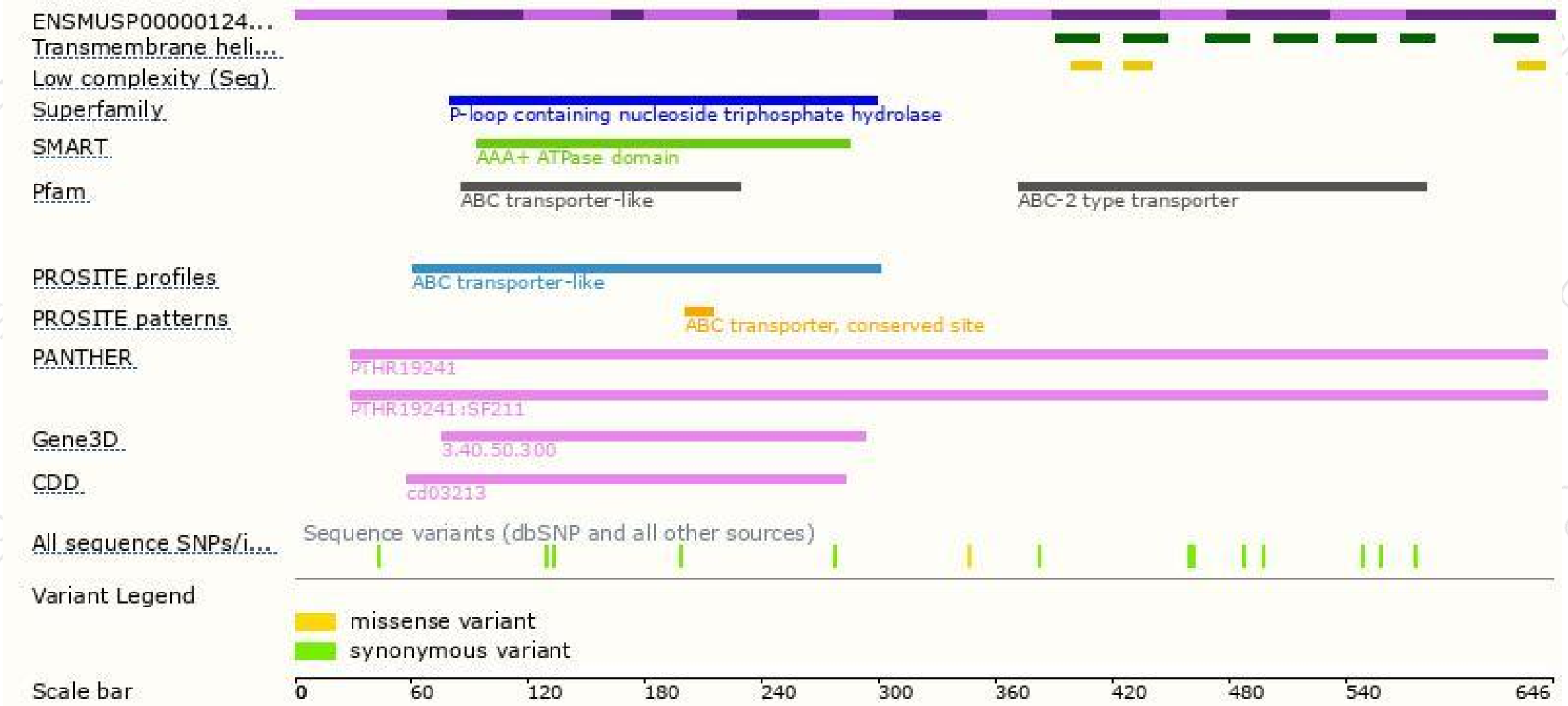
The strategy is based on the design of *Abcg4-208* transcript,the transcription is shown below:



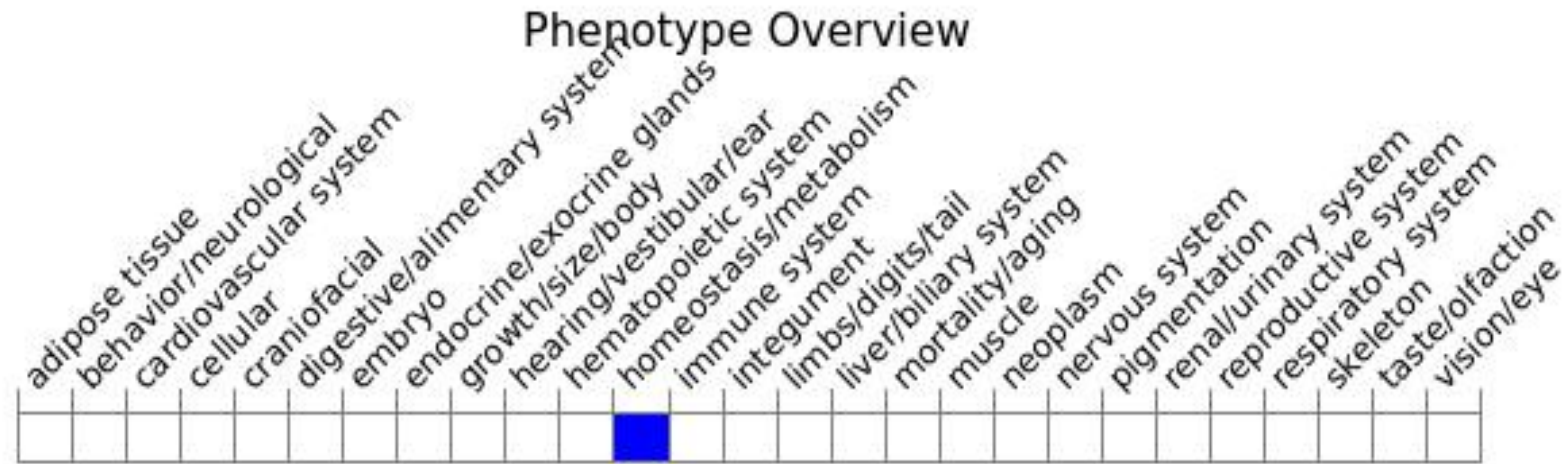
Genomic location distribution



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 report allele exhibit increased brain lathosterol levels.

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

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