

Nr5a2 Cas9-KO Strategy

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Design Date:	2019-12-16

Project Overview

Project Name

Nr5a2

Project type

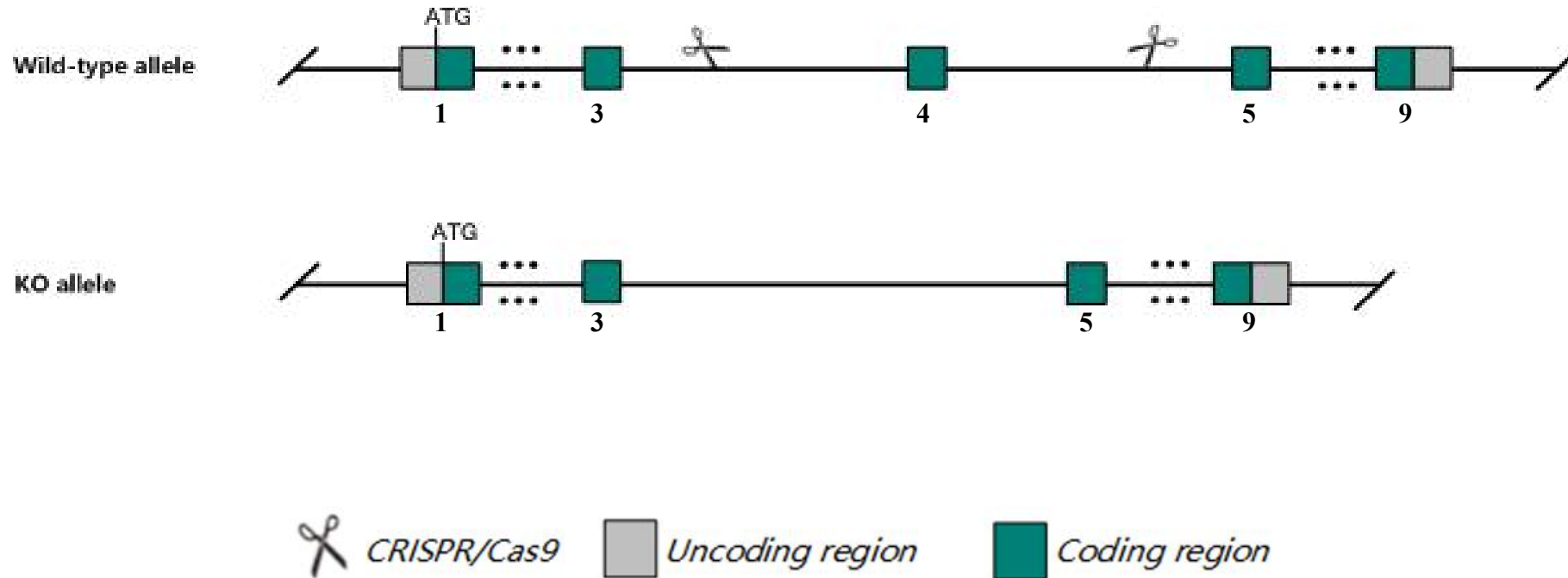
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nr5a2* gene. The schematic diagram is as follows:



The *Nr5a2* gene has 6 transcripts. According to the structure of *Nr5a2* gene, exon4 of *Nr5a2-201* (ENSMUST00000027649.13) transcript is recommended as the knockout region. The region contains 119bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Nr5a2* gene. The brief process is as follows: CRISPR/Cas9 system

According to the existing MGI data, Mice homozygous for disruptions in this gene die around embryonic day 7.5. Heterozygotes are essentially normal but with lower plasma cholesterol, increased bile acids, and shorter intestinal crypt length.

The *Nr5a2* gene is located on the Chr1. 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.

Nr5a2 nuclear receptor subfamily 5, group A, member 2 [Mus musculus (house mouse)]

Gene ID: 26424, updated on 20-Mar-2019

Summary



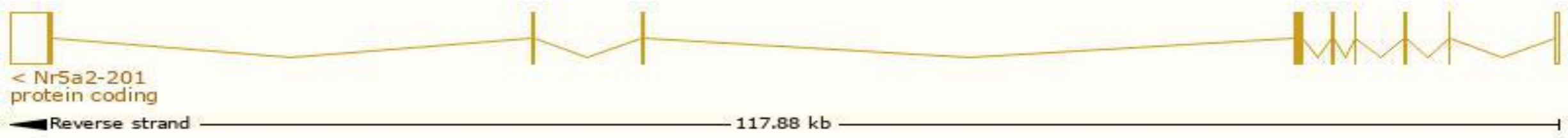
Official Symbol	Nr5a2 provided by MGI
Official Full Name	nuclear receptor subfamily 5, group A, member 2 provided by MGI
Primary source	MGI:MGI:1346834
See related	Ensembl:ENSMUSG00000026398
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AU020803, D1Etd308e, Ftf, LRH-1, UF2-H3B
Expression	Biased expression in ovary adult (RPKM 23.7), liver adult (RPKM 4.6) and 7 other tissues See more
Orthologs	human all

Transcript information Ensembl

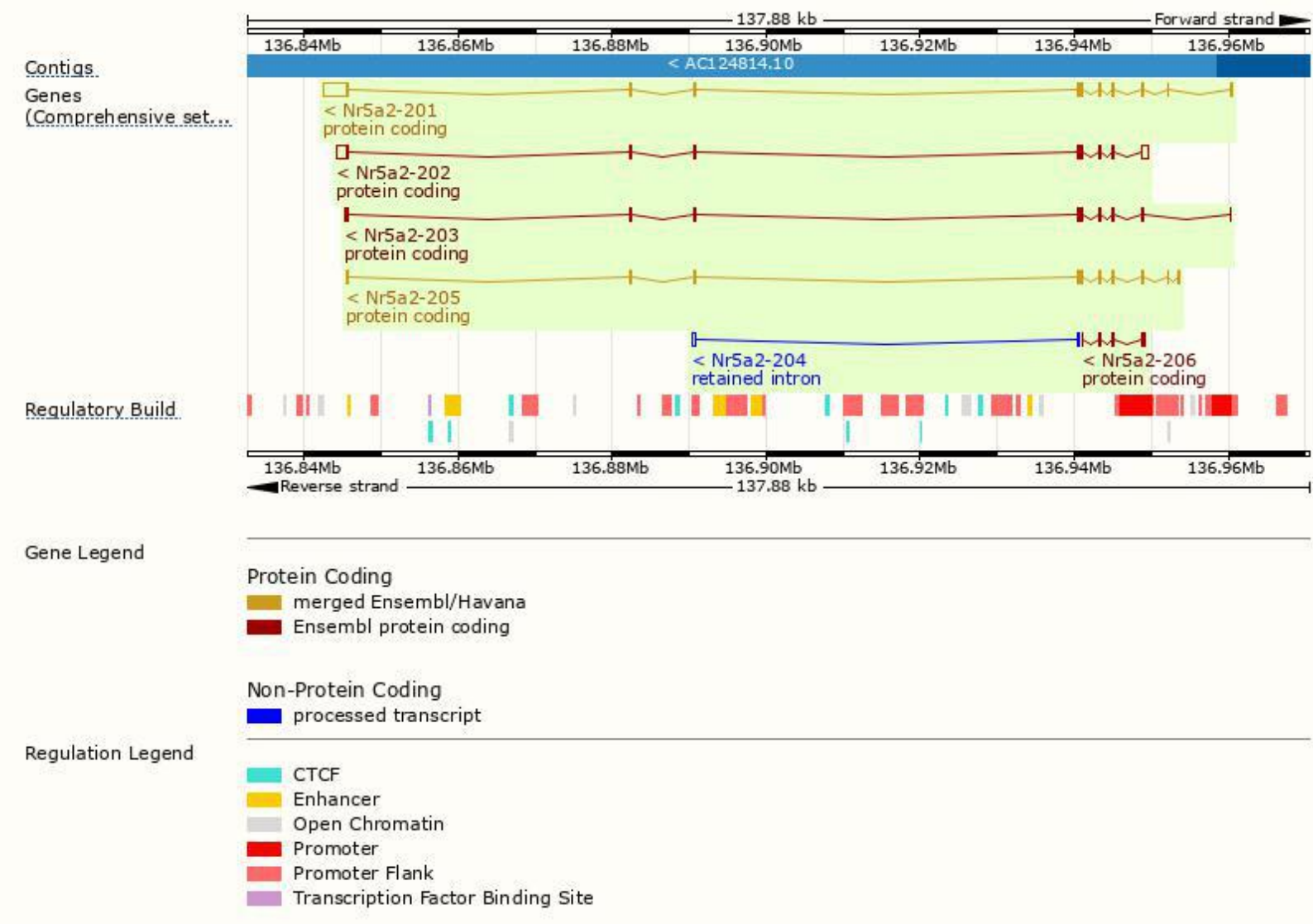
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nr5a2-201	ENSMUST00000027649.13	4733	560aa	Protein coding	CCDS15328	P45448	TSL:1 GENCODE basic
Nr5a2-202	ENSMUST00000168126.6	3446	499aa	Protein coding	CCDS48382	Q1WLP7	TSL:5 GENCODE basic
Nr5a2-205	ENSMUST00000192929.5	1756	499aa	Protein coding	CCDS48382	Q1WLP7	TSL:1 GENCODE basic
Nr5a2-203	ENSMUST00000192357.5	1859	539aa	Protein coding	-	A0A0A6YY04	TSL:5 GENCODE basic APPRIS P1
Nr5a2-206	ENSMUST00000195428.1	679	136aa	Protein coding	-	A0A0A6YWQ4	CDS 3' incomplete TSL:5
Nr5a2-204	ENSMUST00000192587.1	621	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Nr5a2-201* 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 disruptions in this gene die around embryonic day 7.5.

Heterozygotes are essentially normal but with lower plasma cholesterol, increased bile acids, and shorter intestinal crypt length.

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