Rdh12 Cas9-KO Strategy

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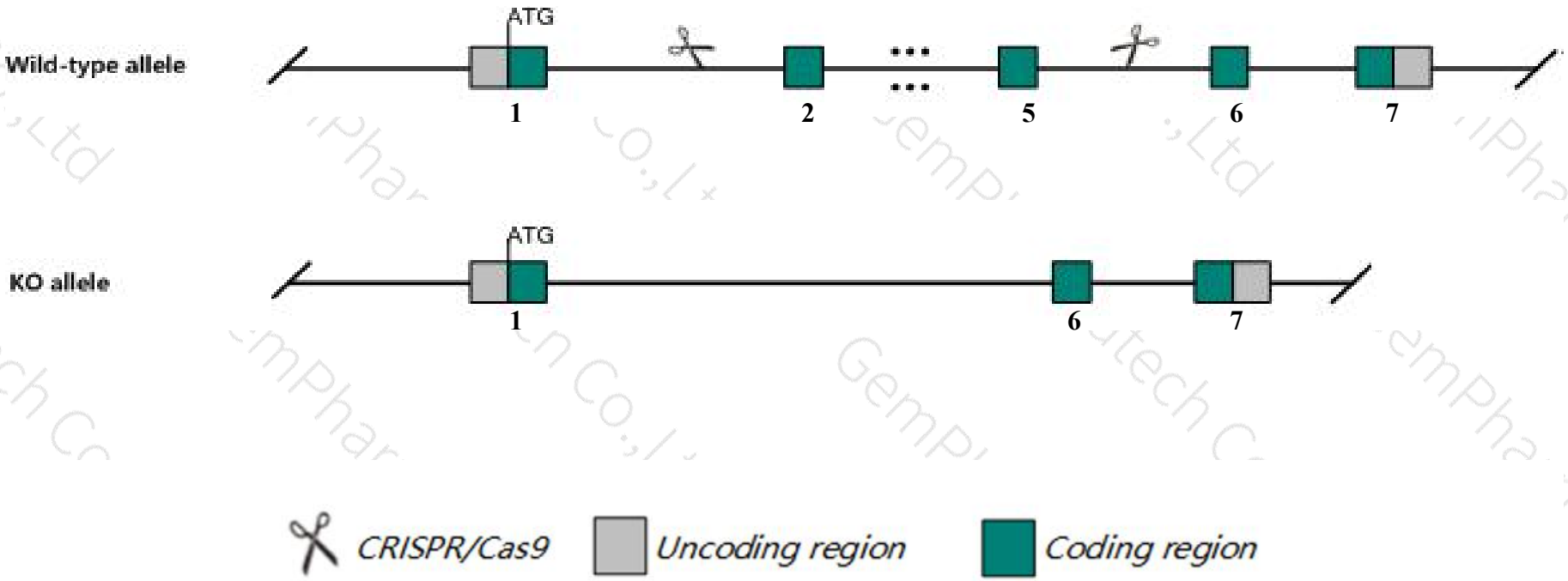
Project Overview

Project Name	***Rdh12***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rdh12* gene. The schematic diagram is as follows:



Technical routes

➢ The *Rdh12* gene has 4 transcripts. According to the structure of *Rdh12* gene, exon2-exon5 of *Rdh12-201* (ENSMUST00000021548.11) transcript is recommended as the knockout region.The region contains 590bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rdh12* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Deletion of this gene in mice results in slowed kinetics of all-trans-retinal reduction leading to delayed dark adaptation and increased susceptibility to light-induced photoreceptor apoptosis from accelerated 11-cis-retinal production.

- The coding transcript 203 is incomplete and the effect is unknown.

- The *Rdh12* 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）

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Rdh12 retinol dehydrogenase 12 [Mus musculus (house mouse)]

Gene ID: 77974, updated on 17-Feb-2019

Summary

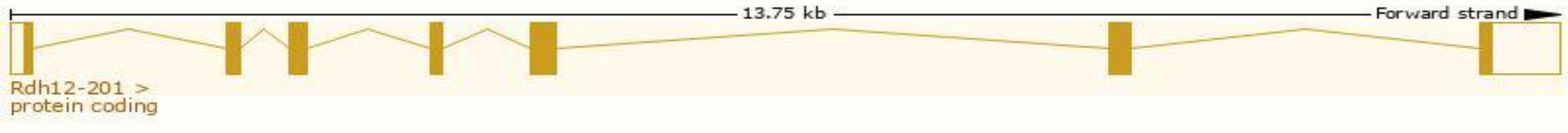
Official Symbol	Rdh12 provided by MGI
Official Full Name	retinol dehydrogenase 12 provided by MGI
Primary source	MGI:MGI:1925224
See related	Ensembl:ENSMUSG00000021123
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Summary	The protein encoded by this gene is an NADPH-dependent retinal reductase whose highest activity is toward 9-cis and all-trans-retinol. The encoded enzyme also plays a role in the metabolism of short-chain aldehydes but does not exhibit steroid dehydrogenase activity. Defects in the human gene are associated with Leber congenital amaurosis type 13, and Retinitis Pigmentosa 53. [provided by RefSeq, Sep 2015]
Expression	Broad expression in stomach adult (RPKM 6.7), placenta adult (RPKM 6.2) and 17 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

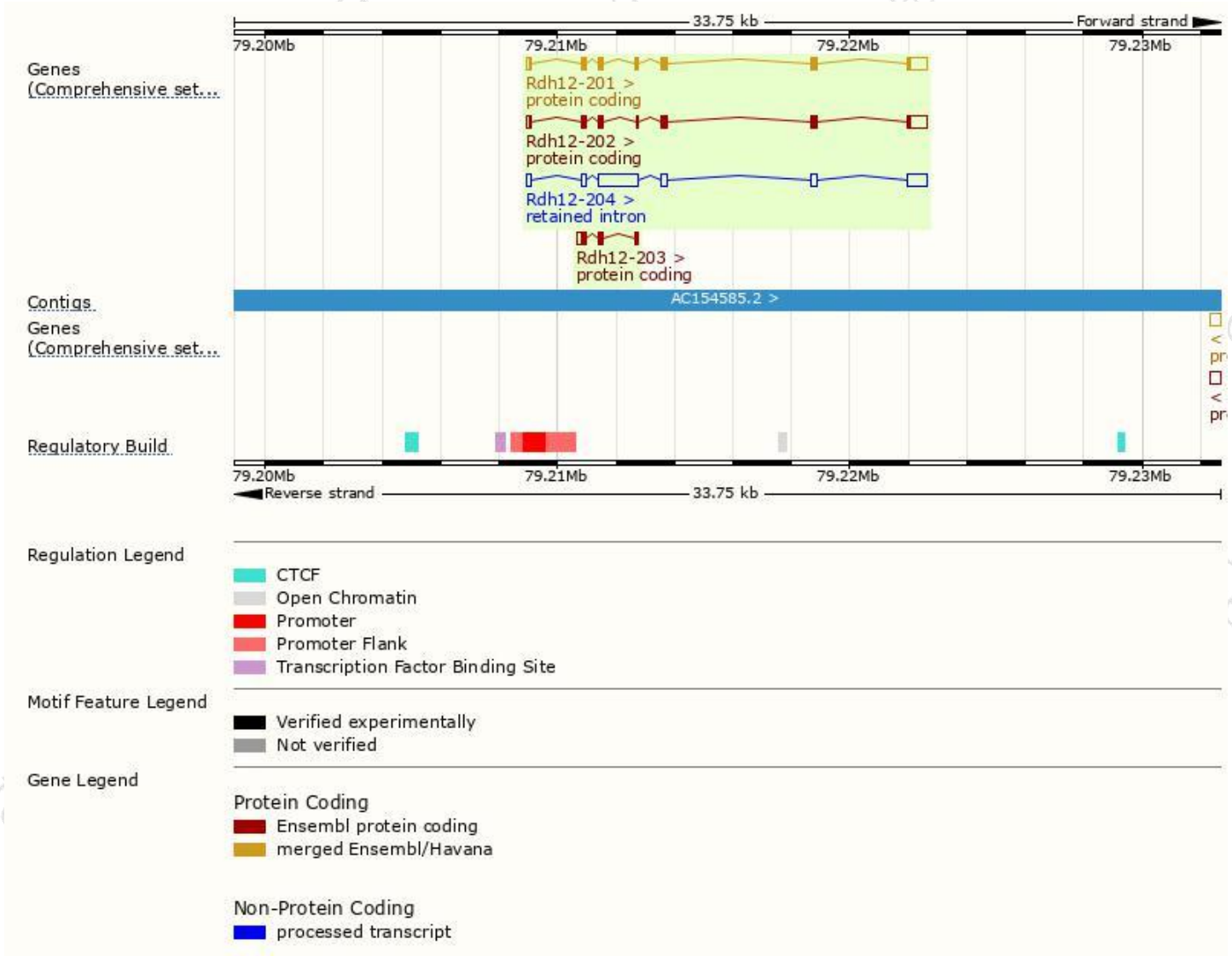
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rdh12-201	ENSMUST00000021548.11	1678	316aa	Protein coding	CCDS26009	Q8BYK4	TSL:1 GENCODE basic APPRIS P1
Rdh12-202	ENSMUST00000122227.7	1624	304aa	Protein coding	CCDS83971	A0A0R4J1M3	TSL:1 GENCODE basic
Rdh12-203	ENSMUST00000140823.1	558	136aa	Protein coding	-	D3YY80	CDS 3' incomplete TSL:3
Rdh12-204	ENSMUST00000151980.1	2753	No protein	Retained intron	-	-	TSL:2

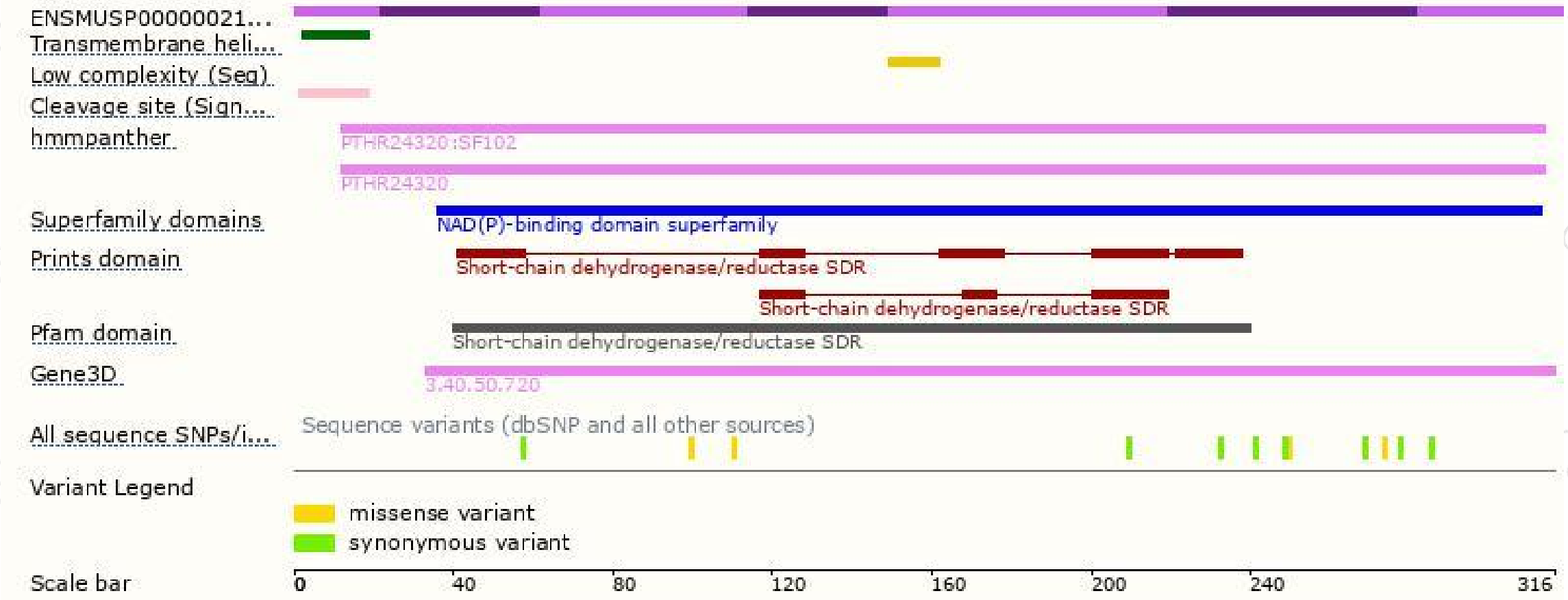
The strategy is based on the design of *Rdh12-201* transcript,The transcription is shown below



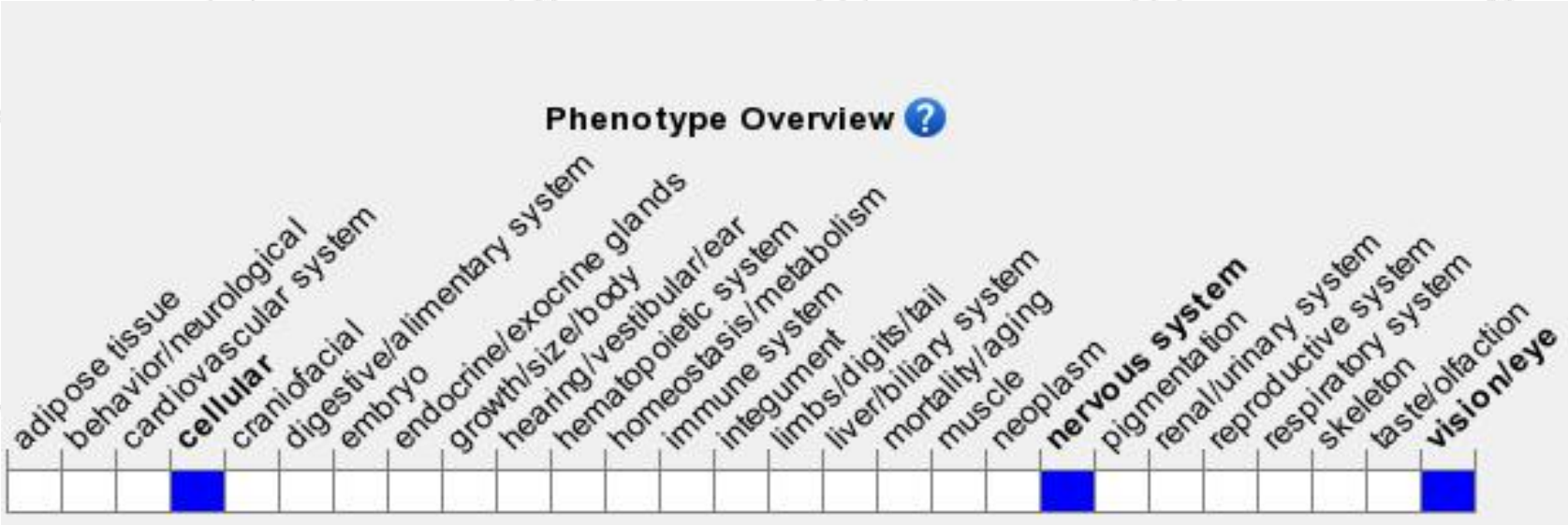
Genomic location distribution



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,Deletion of this gene in mice results in slowed kinetics of all-trans-retinal reduction leading to delayed dark adaptation and increased susceptibility to light-induced photoreceptor apoptosis from accelerated 11-cis-retinal production.

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

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