Cep290 Cas9-KO Strategy

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Project Overview

Project Name	***Cep290***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cep290* gene. The schematic diagram is as follows:

Technical routes

➢ The *Cep290* gene has 10 transcripts. According to the structure of *Cep290* gene, exon7-exon15 of *Cep290-210* (ENSMUST00000220346.1) transcript is recommended as the knockout region.The region contains 1084bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cep290* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,Mutant mice display mislocalization of ciliary and phototransduction proteins resulting in early-onset retinal degeneration. Heterotaxy with transposition of the great arteries (TGA), atrioventricular septal defect (AVSD), left bronchial isomerism, and hypoplastic spleen is also seen.

- The *Cep290* gene is located on the Chr10. 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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Cep290 centrosomal protein 290 [Mus musculus (house mouse)]

Gene ID: 216274, updated on 5-Mar-2019

Summary

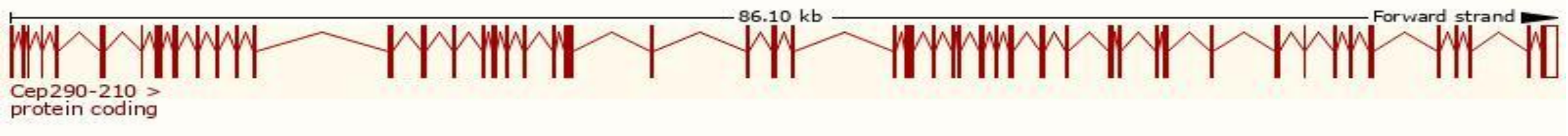
Official Symbol	Cep290 provided by MGI
Official Full Name	centrosomal protein 290 provided by MGI
Primary source	MGI:MGI:2384917
See related	Ensembl:ENSMUSG00000019971
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BC004690, Nphp6, b2b1454Clo, b2b1752Clo
Expression	Biased expression in CNS E11.5 (RPKM 1.5), testis adult (RPKM 1.4) and 14 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

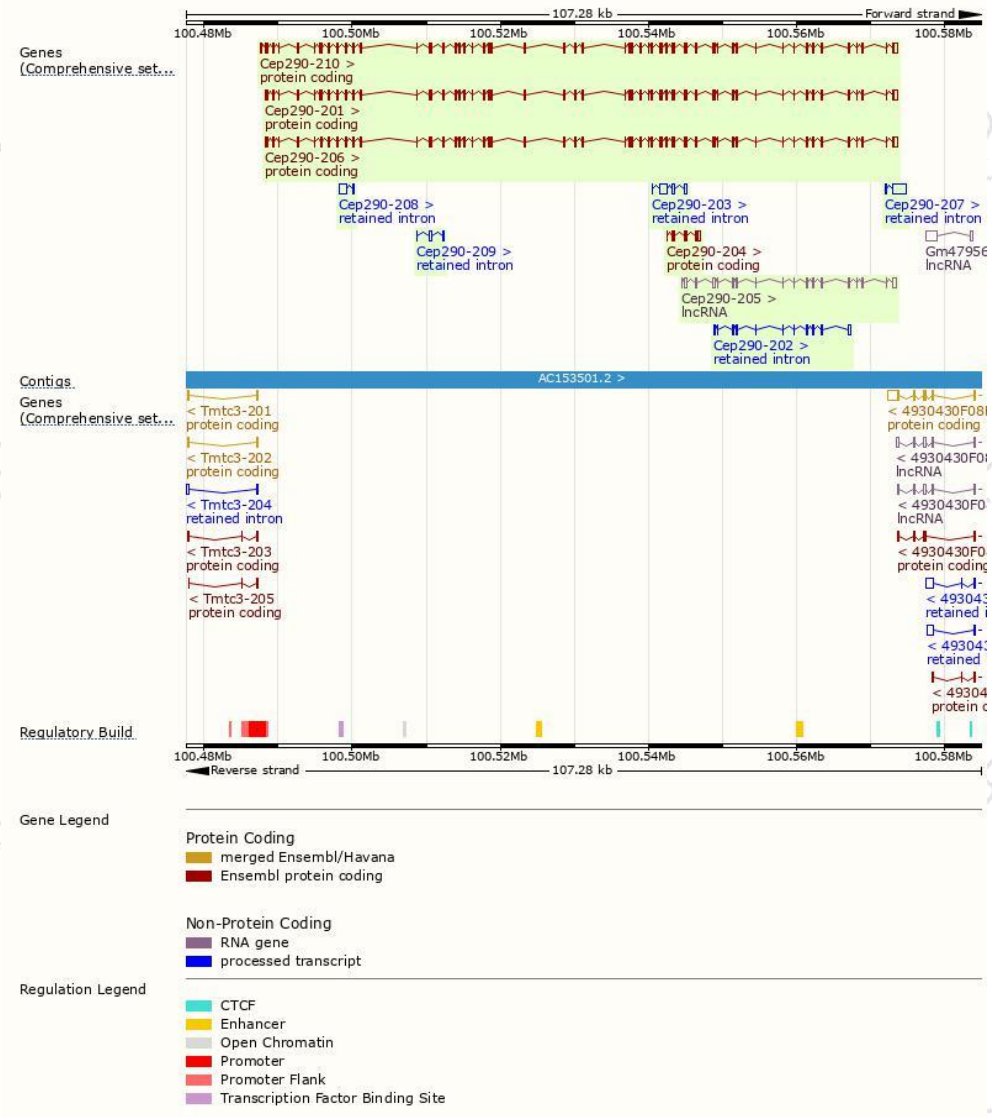
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cep290-210	ENSMUST00000220346.1	8211	2479aa	Protein coding	CCDS48685	E9Q9M0	TSL:5 GENCODE basic APPRIS P2
Cep290-201	ENSMUST00000164751.1	8006	2479aa	Protein coding	CCDS48685	E9Q9M0	TSL:5 GENCODE basic APPRIS P2
Cep290-206	ENSMUST00000219765.1	7985	2472aa	Protein coding	-	Q6A078	TSL:5 GENCODE basic APPRIS ALT2
Cep290-204	ENSMUST00000219408.1	1177	237aa	Protein coding	-	A0A1W2P6U7	CDS 5' incomplete TSL:2
Cep290-207	ENSMUST00000219889.1	2170	No protein	Retained intron	-	-	TSL:1
Cep290-202	ENSMUST00000218000.1	1567	No protein	Retained intron	-	-	TSL:5
Cep290-203	ENSMUST00000218703.1	1406	No protein	Retained intron	-	-	TSL:5
Cep290-208	ENSMUST00000220231.1	903	No protein	Retained intron	-	-	TSL:5
Cep290-209	ENSMUST00000220331.1	423	No protein	Retained intron	-	-	TSL:3
Cep290-205	ENSMUST00000219643.1	2738	No protein	lncRNA	-	-	TSL:1

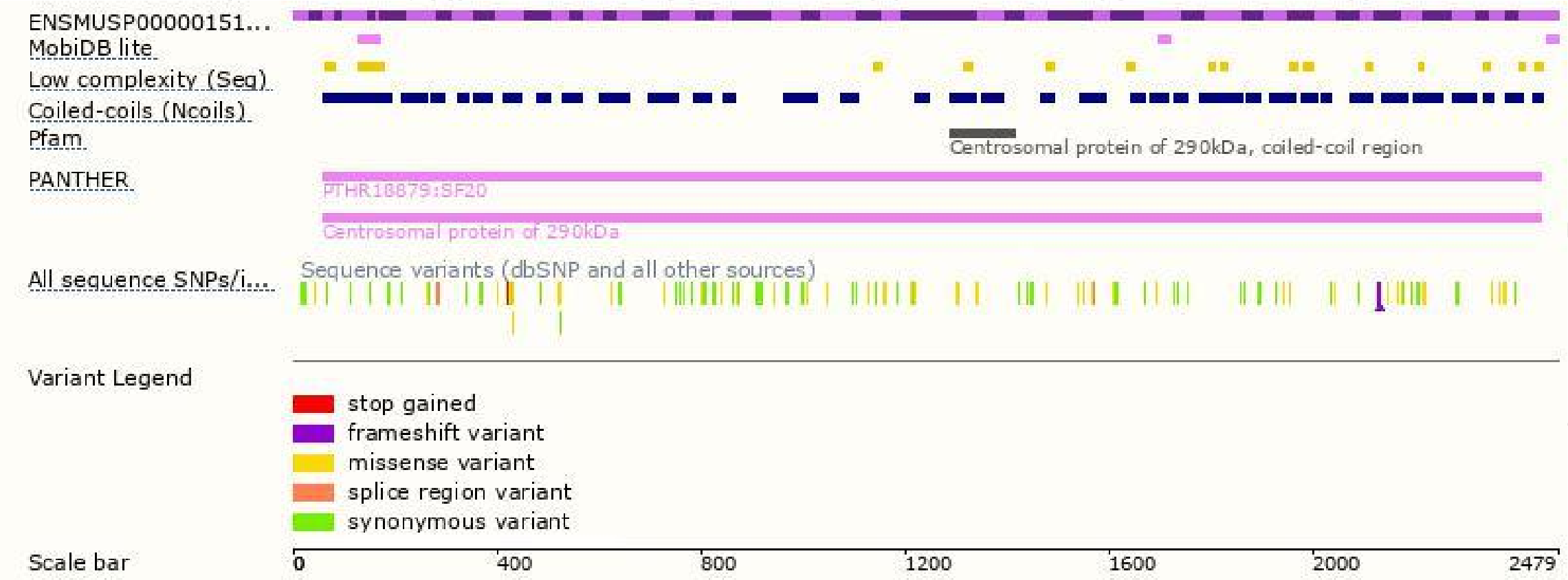
The strategy is based on the design of *Cep290-210* transcript,The transcription is shown below



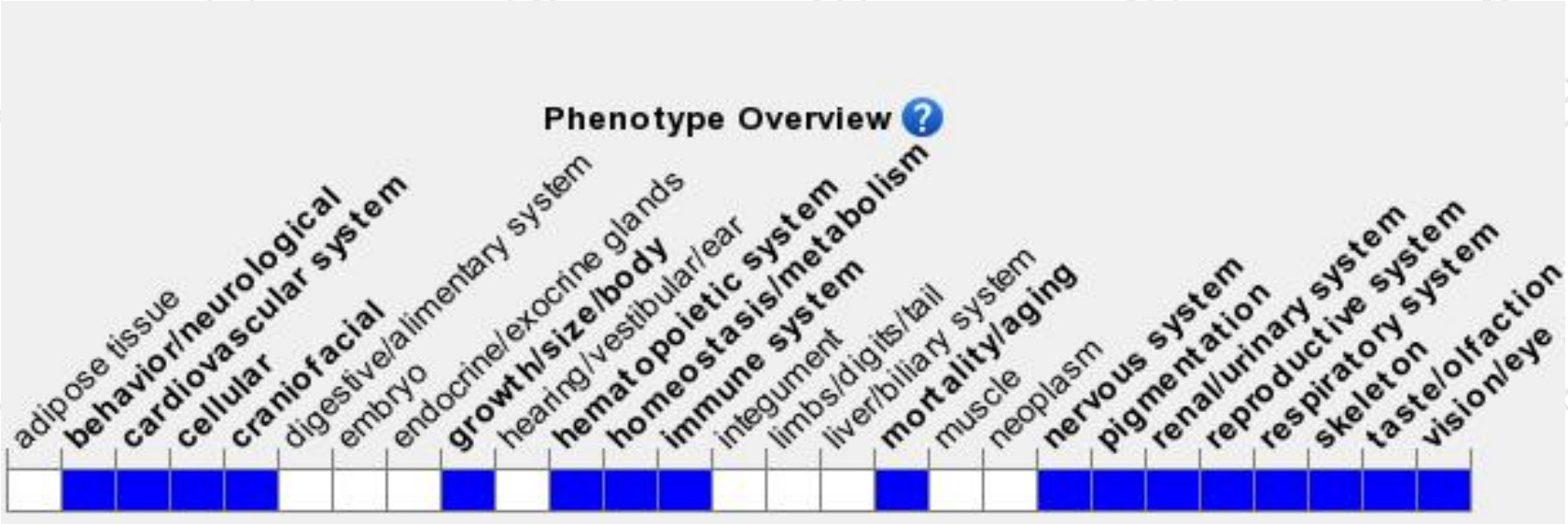
Genomic location distribution



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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