

Eya1 Cas9-KO Strategy

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Project Overview



Project Name

Eya1

Project type

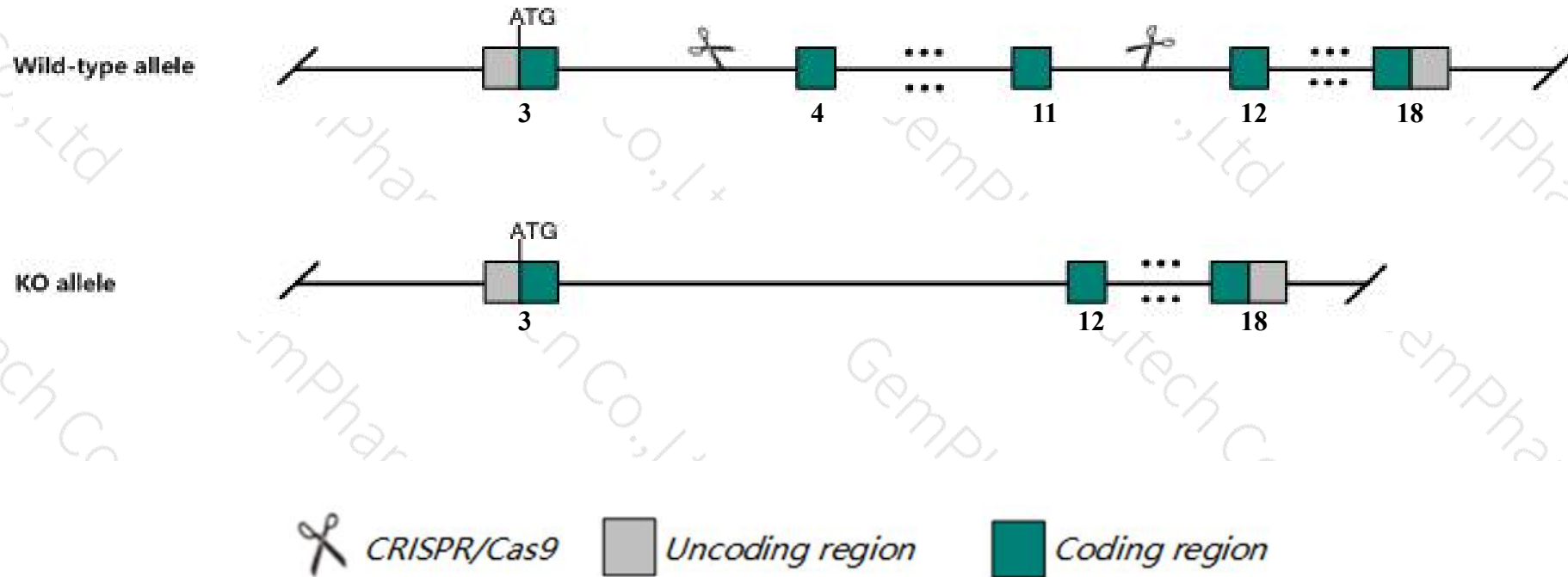
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Eyal* gene has 9 transcripts. According to the structure of *Eyal* gene, exon4-exon11 of *Eyal-203* (ENSMUST00000168081.8) transcript is recommended as the knockout region. The region contains 911bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eyal* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mutations in this locus affect inner ear morphology and hearing, and result in dysmorphic or absent kidneys. Hypomorphs are deaf and circle. Null homozygotes additionally show agenesis of thymus and parathyroid and thyroid hypoplasia.
- The *Eyal* 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.

Gene information (NCBI)

Eya1 EYA transcriptional coactivator and phosphatase 1 [Mus musculus (house mouse)]

Gene ID: 14048, updated on 19-Mar-2019

Summary



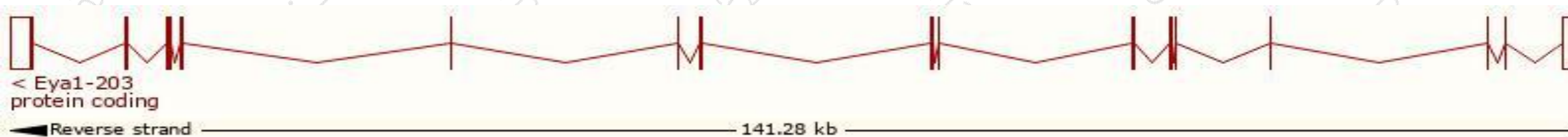
Official Symbol	Eya1 provided by MGI
Official Full Name	EYA transcriptional coactivator and phosphatase 1 provided by MGI
Primary source	MGI:MGI:109344
See related	Ensembl:ENSMUSG000000025932
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	bor
Expression	Broad expression in CNS E11.5 (RPKM 1.6), limb E14.5 (RPKM 1.5) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

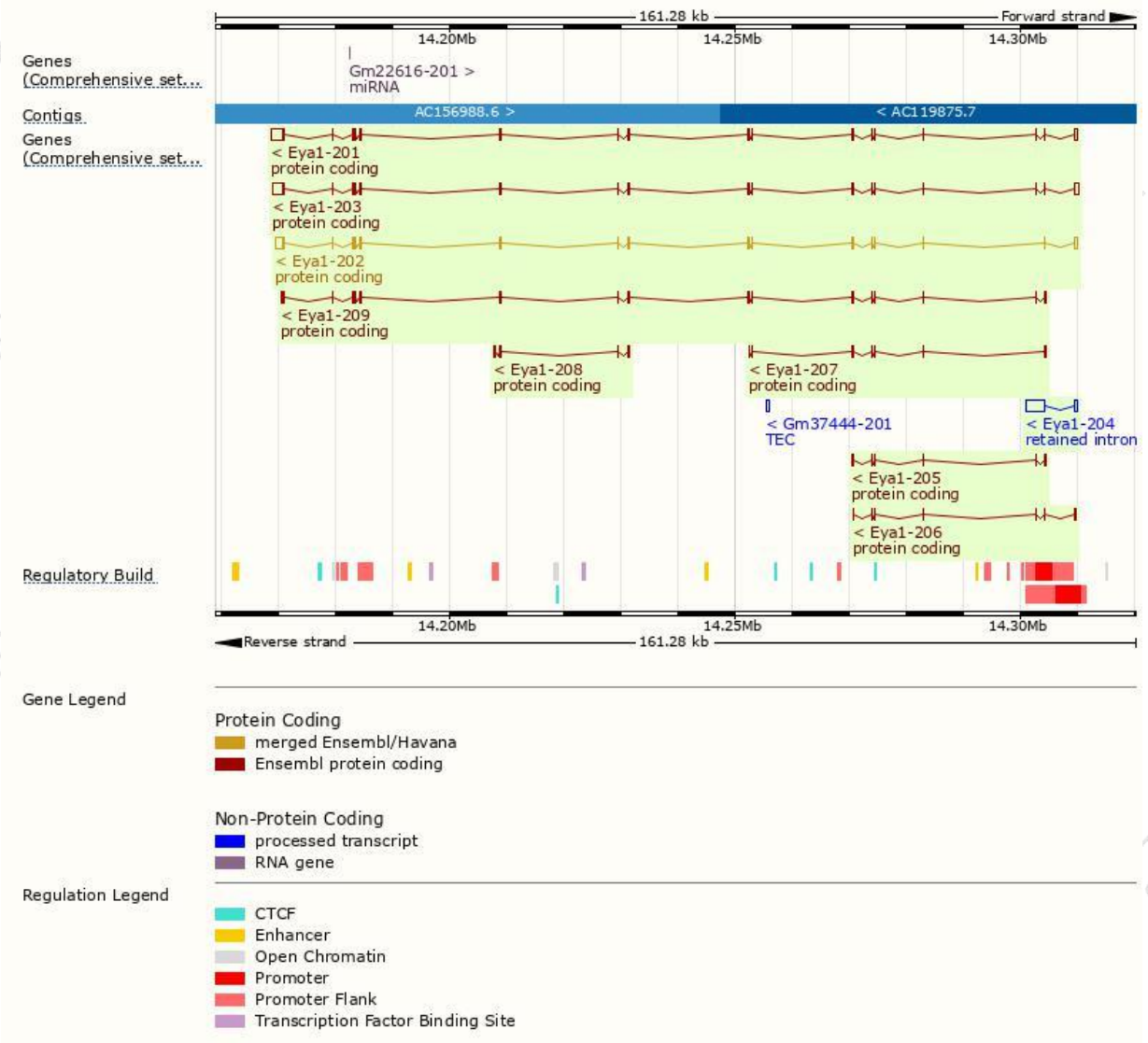
The gene has 9 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eya1-203	ENSMUST00000168081.8	4366	587aa	Protein coding	CCDS78546	F6YST4	TSL:1 GENCODE basic
Eya1-201	ENSMUST0000027066.12	4347	591aa	Protein coding	CCDS78545	P97767	TSL:5 GENCODE basic APPRIS P1
Eya1-202	ENSMUST0000080664.13	3426	558aa	Protein coding	CCDS56621	Q8C9D0	TSL:1 GENCODE basic
Eya1-209	ENSMUST00000190337.6	2199	591aa	Protein coding	CCDS78545	P97767	TSL:1 GENCODE basic APPRIS P1
Eya1-207	ENSMUST00000188857.6	725	185aa	Protein coding	-	A0A087WQF4	CDS 3' incomplete TSL:3
Eya1-205	ENSMUST00000185453.6	664	184aa	Protein coding	-	A0A087WSJ4	CDS 3' incomplete TSL:3
Eya1-206	ENSMUST00000187790.1	664	139aa	Protein coding	-	A0A087WNY3	CDS 3' incomplete TSL:3
Eya1-208	ENSMUST00000189526.1	430	118aa	Protein coding	-	A0A087WRG6	CDS 5' incomplete TSL:2
Eya1-204	ENSMUST00000185329.1	3677	No protein	Retained intron	-	-	TSL:1

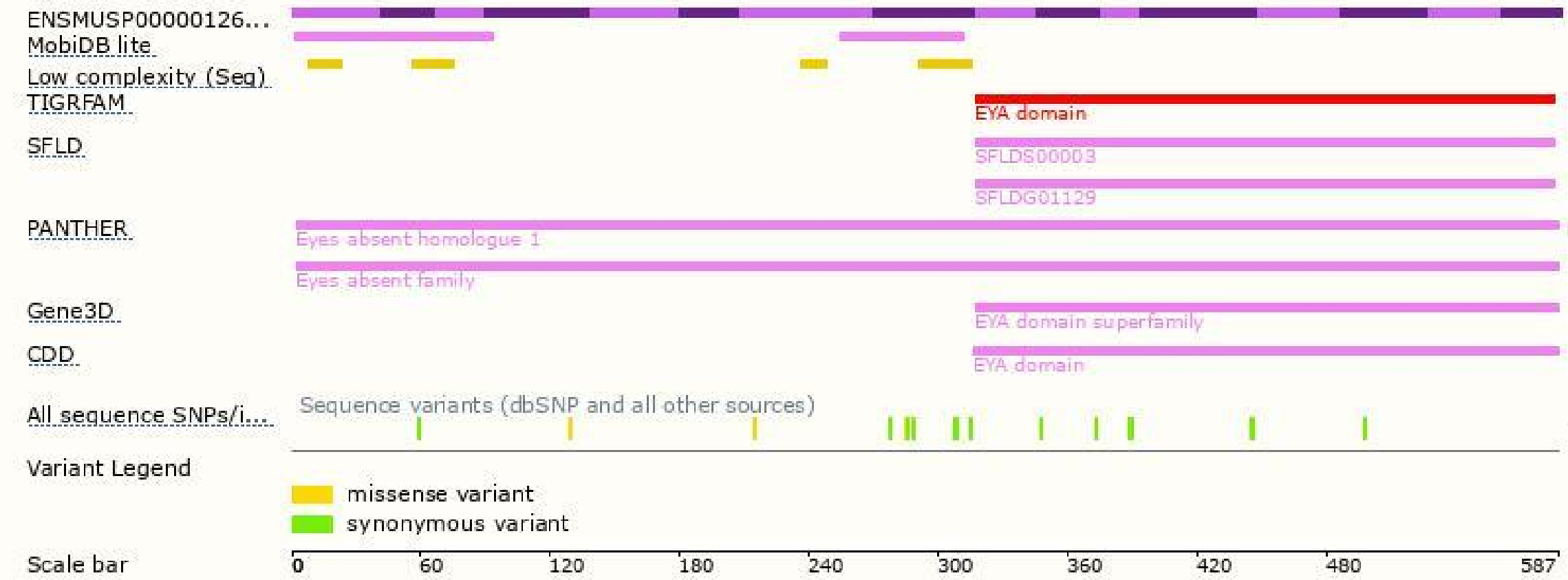
The strategy is based on the design of *Eya1-203* transcript, The transcription is shown below



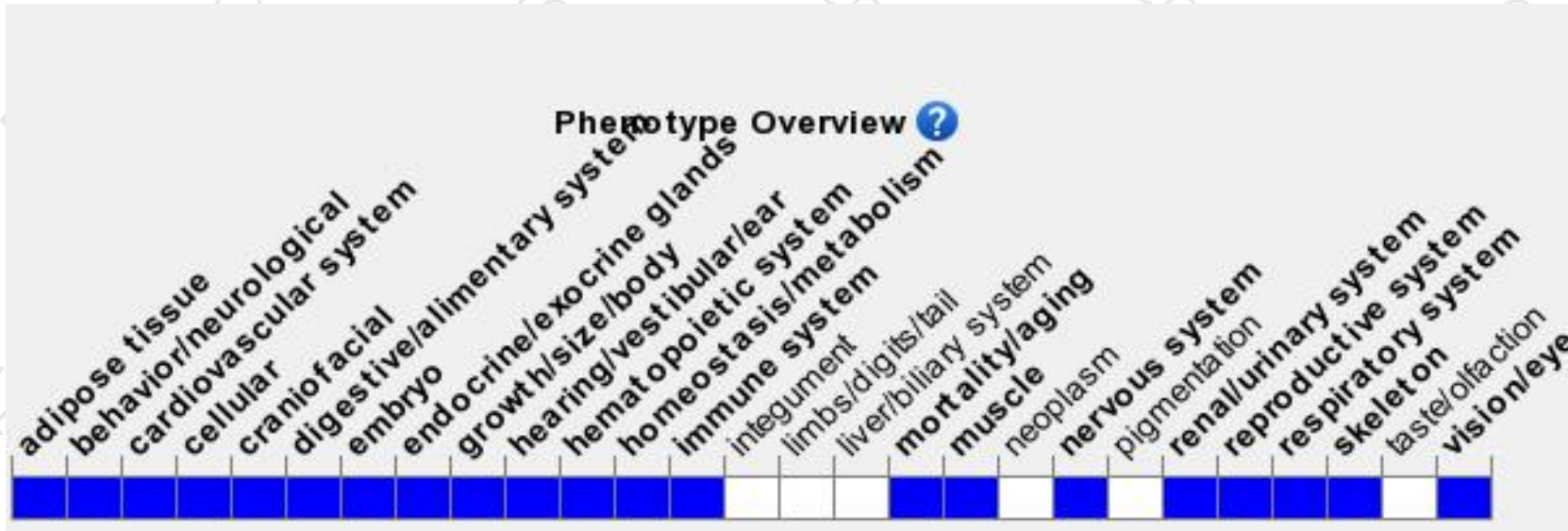
Genomic location distribution



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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