

Sdk2 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Sdk2

Project type

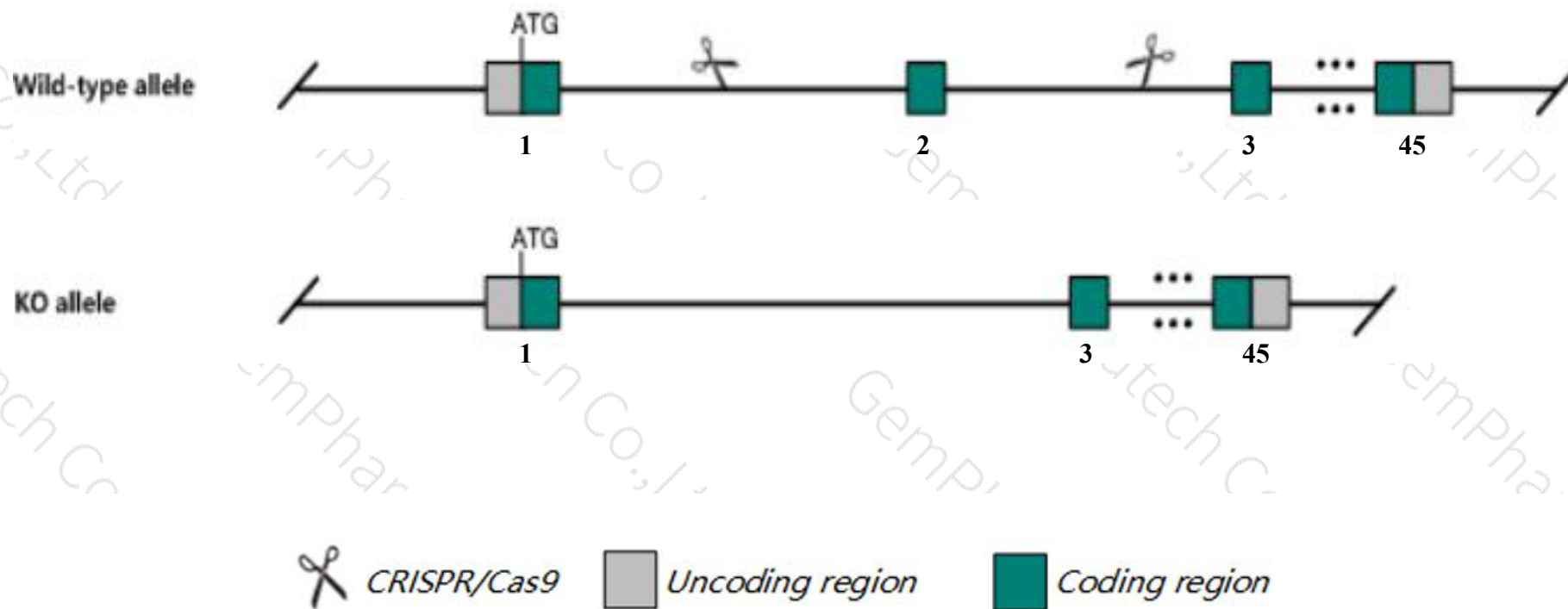
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sdk2* gene. The schematic diagram is as follows:



- The *Sdk2* gene has 6 transcripts. According to the structure of *Sdk2* gene, exon2 of *Sdk2-201* (ENSMUST00000041627.13) transcript is recommended as the knockout region. The region contains 160bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sdk2* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit impaired interconnectivity between VG3 amacrine cells and W3B retinal ganglion cells.
- The *Sdk2* gene is located on the Chr11. 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)

Sdk2 sidekick cell adhesion molecule 2 [Mus musculus (house mouse)]

Gene ID: 237979, updated on 13-Mar-2020

Summary



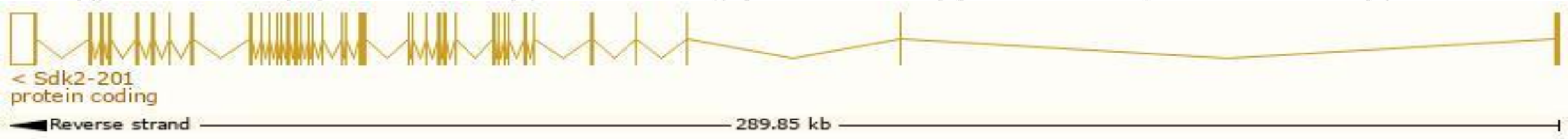
Official Symbol	Sdk2 provided by MGI
Official Full Name	sidekick cell adhesion molecule 2 provided by MGI
Primary source	MGI:MGI:2443847
See related	Ensembl:ENSMUSG00000041592
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4632412F08Rik, 5330435L01Rik, Sdk-2, mKIAA1514
Expression	Broad expression in limb E14.5 (RPKM 3.2), frontal lobe adult (RPKM 1.8) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

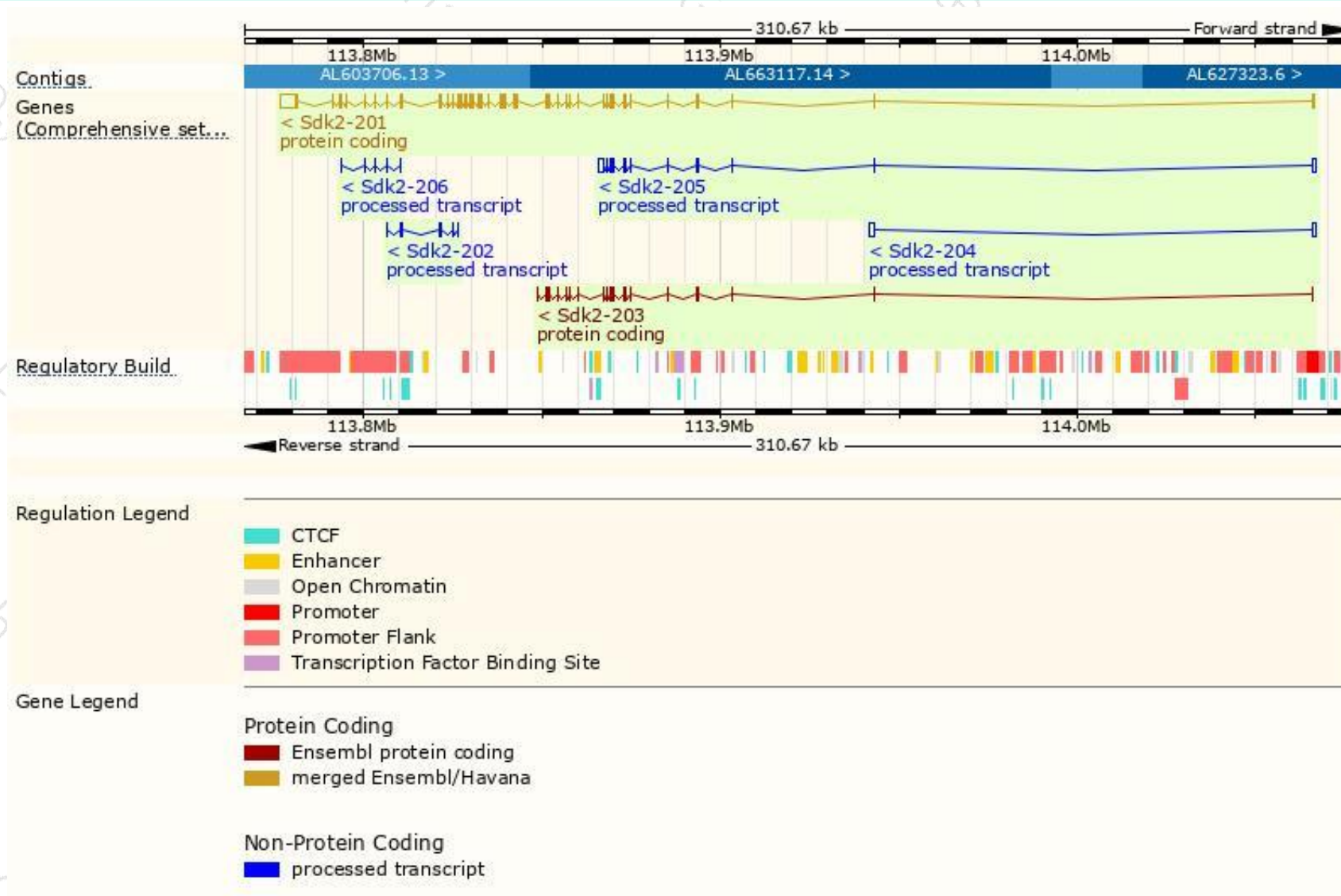
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sdk2-201	ENSMUST00000041627.13	11287	2176aa	Protein coding	CCDS25605	Q6V4S5	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Sdk2-203	ENSMUST00000141943.1	2783	895aa	Protein coding	-	B1ASR7	CDS 3' incomplete TSL:1
Sdk2-205	ENSMUST00000155651.1	4155	No protein	Processed transcript	-	-	TSL:1
Sdk2-204	ENSMUST00000144301.1	3083	No protein	Processed transcript	-	-	TSL:1
Sdk2-202	ENSMUST00000125879.1	681	No protein	Processed transcript	-	-	TSL:3
Sdk2-206	ENSMUST00000156955.1	546	No protein	Processed transcript	-	-	TSL:3

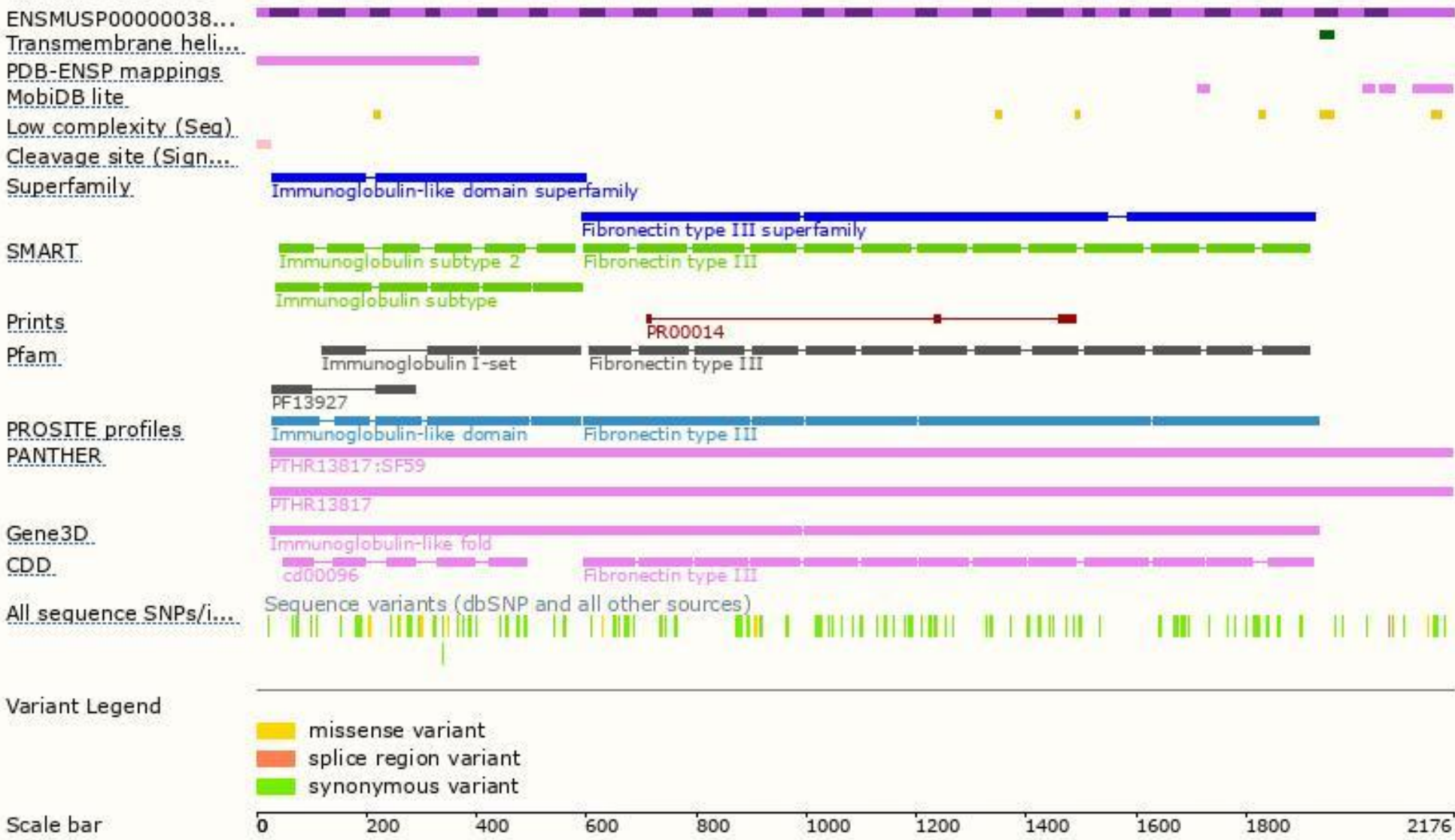
The strategy is based on the design of *Sdk2-201* transcript,The transcription is shown below



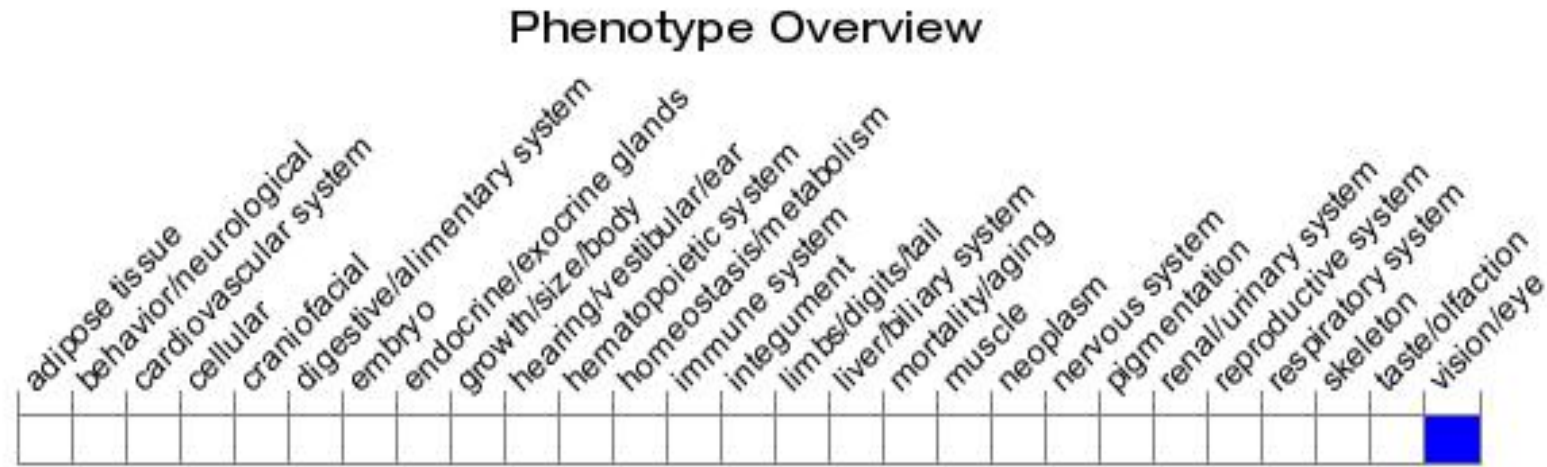
Genomic location distribution



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 a knock-out allele exhibit impaired interconnectivity between VG3 amacrine cells and W3B retinal ganglion cells.

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

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