Ret Cas9-KO Strategy

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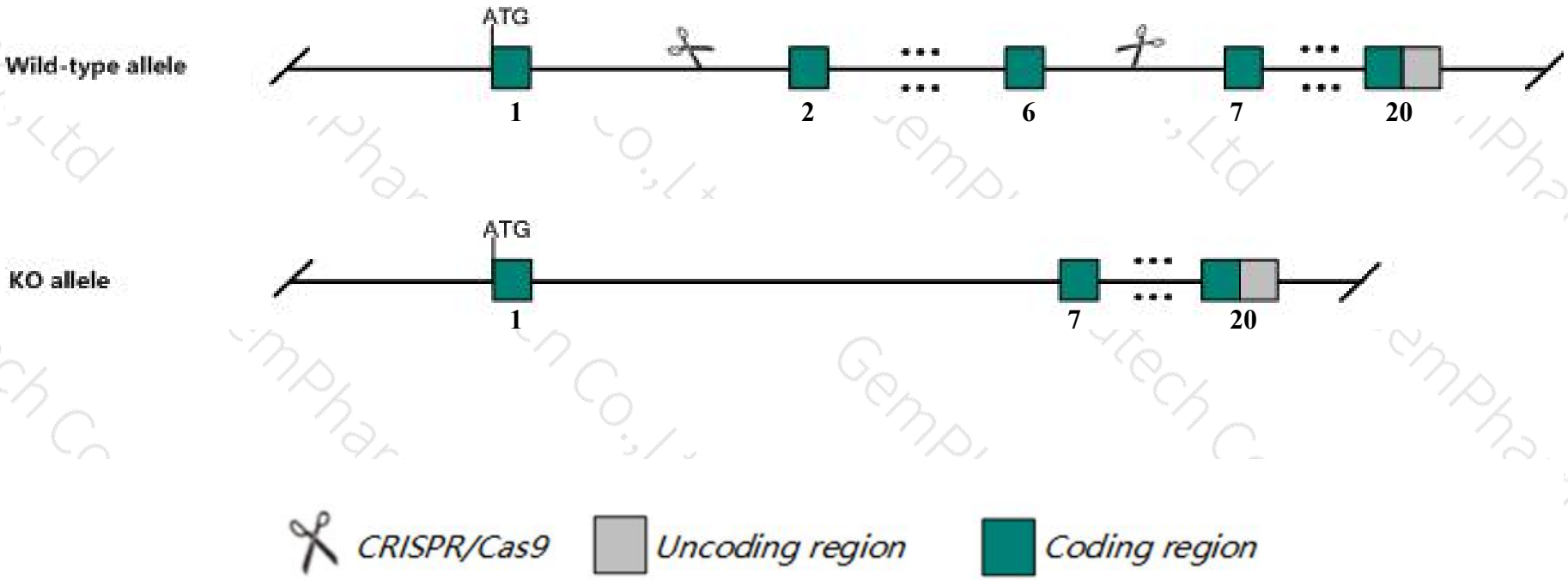
Design Date: 2019-7-31

Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Ret* gene has 2 transcripts. According to the structure of *Ret* gene, exon2-exon6 of *Ret-201* (ENSMUST00000032201.7) transcript is recommended as the knockout region.The region contains 1196bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

- According to the existing MGI data,Mice homozygous for some point mutations or knock-out alleles exhibit premature lethality, defects in neurogenesis, and abnormal kidney, ureter, ovary, muscle, and intestine morphology.

- The *Ret* gene is located on the Chr6. 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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Ret ret proto-oncogene [Mus musculus (house mouse)]

Gene ID: 19713, updated on 26-Mar-2019

Summary

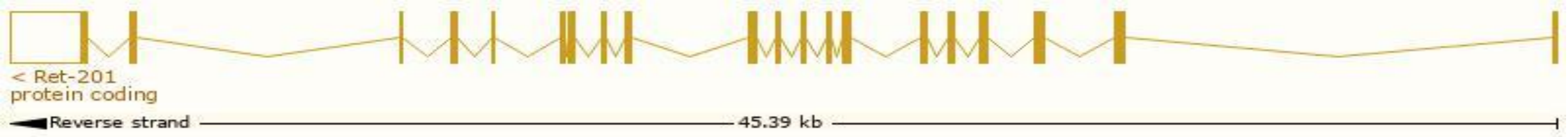
Official Symbol	Ret provided by MGI
Official Full Name	ret proto-oncogene provided by MGI
Primary source	MGI:MGI:97902
See related	Ensembl:ENSMUSG00000030110
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	PTC, RET51, RET9, c-Ret
Expression	Broad expression in cerebellum adult (RPKM 5.3), subcutaneous fat pad adult (RPKM 4.5) and 18 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

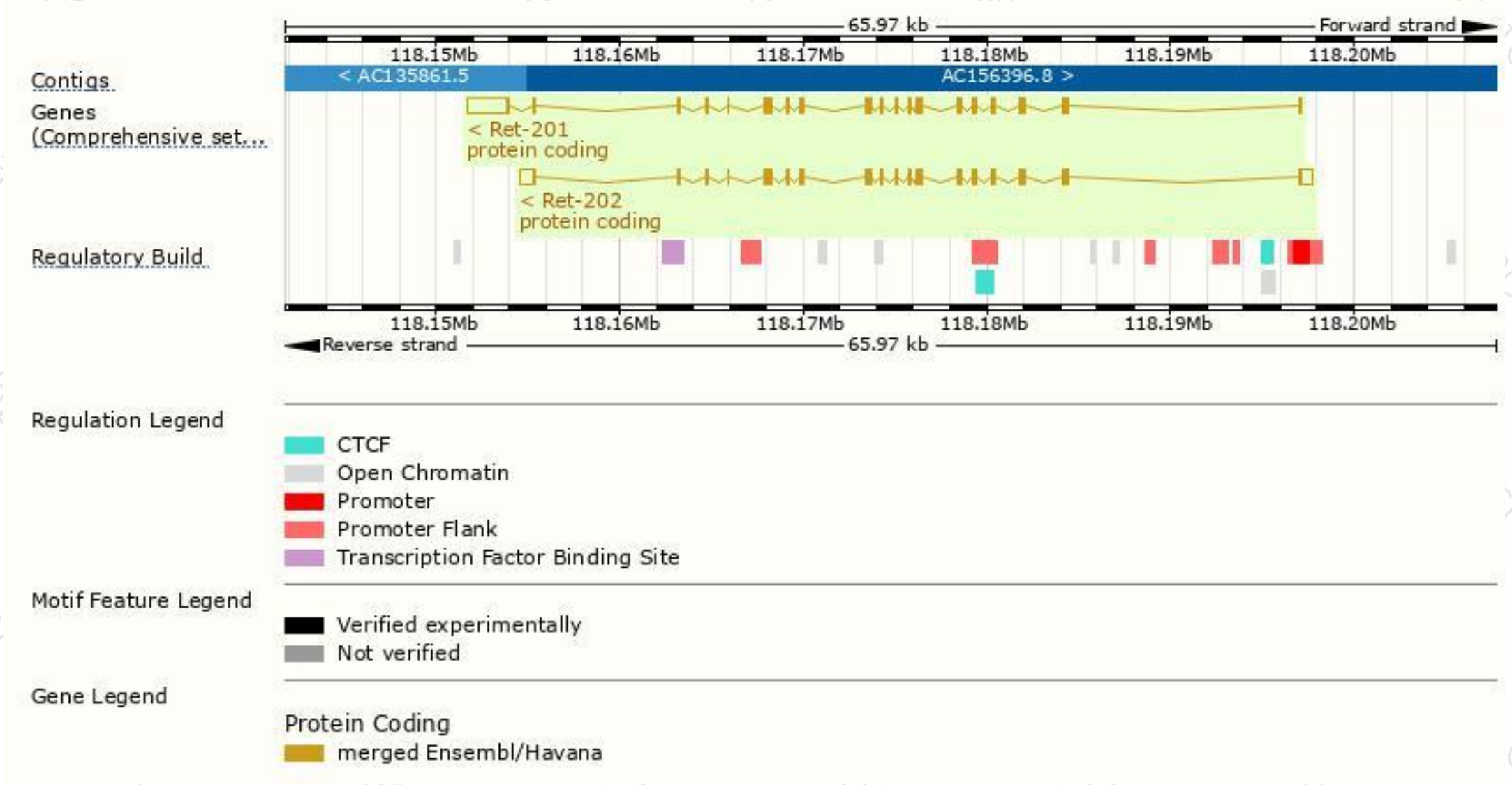
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ret-201	ENSMUST00000032201.7	5456	1115aa	Protein coding	CCDS20470	P35546	TSL:1 GENCODE basic APPRIS P3
Ret-202	ENSMUST00000088790.8	4497	1073aa	Protein coding	CCDS39608	P35546	TSL:1 GENCODE basic APPRIS ALT2

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

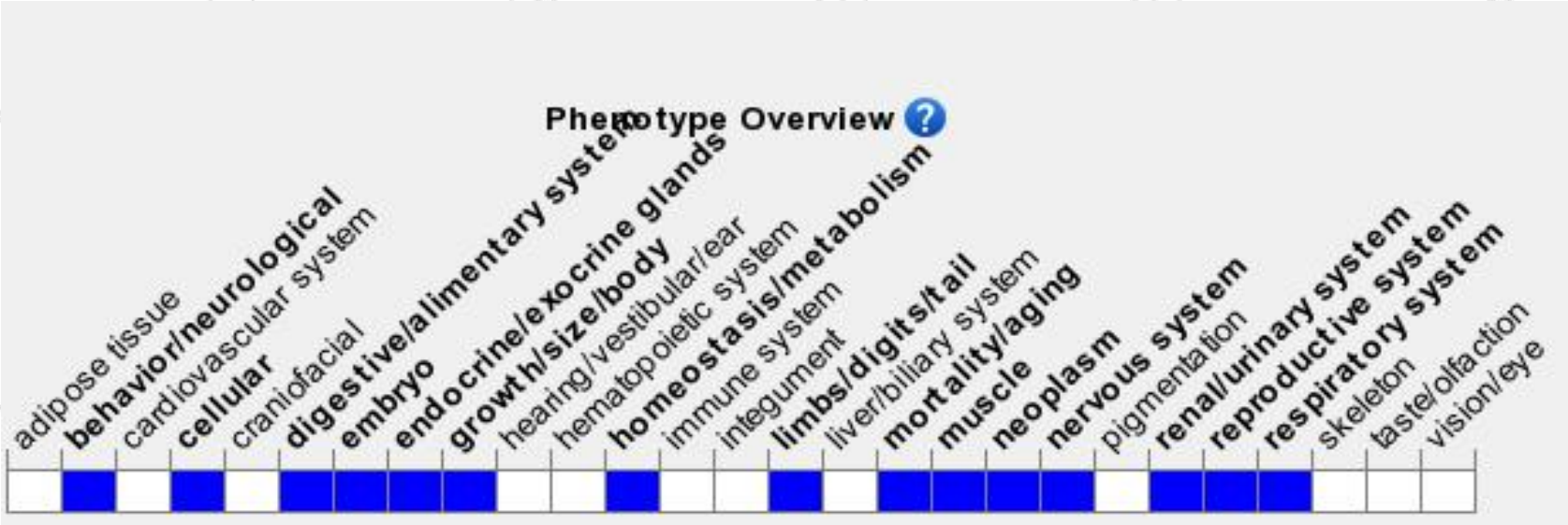


Genomic location distribution



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/).

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

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