Lepr Cas9-KO Strategy

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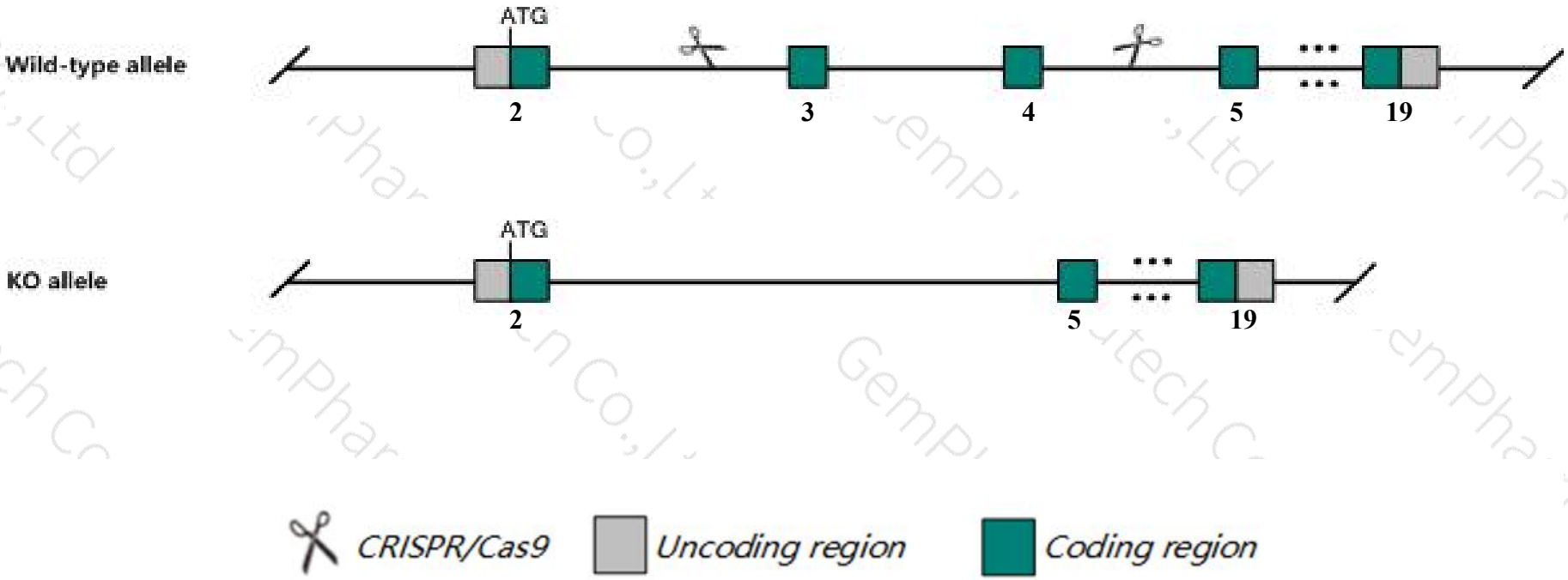
Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Lepr* gene has 7 transcripts. According to the structure of *Lepr* gene, exon3-exon4 of *Lepr-203* (ENSMUST00000106921.8) transcript is recommended as the knockout region.The region contains 454bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

- According to the existing MGI data,Homozygous mutants are hyperphagic, low-activity, poorly cold-adapted, sterile and have enhanced fat conversion. They are obese, hyperinsulinemic and, on certain strains, severely hyperglycemic. Heterozygotes are normal but resistant to prolonged fasting.

- The *Lepr* gene is located on the Chr4. 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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Lepr leptin receptor [Mus musculus (house mouse)]

Gene ID: 16847, updated on 9-Apr-2019

Summary

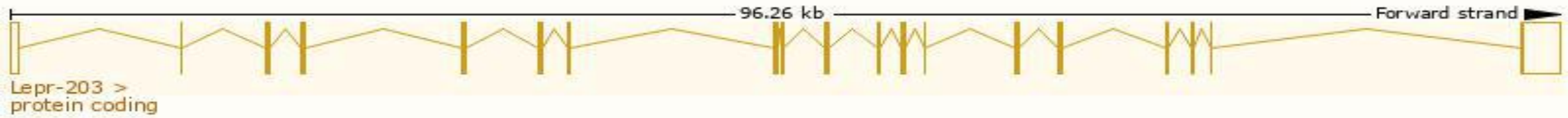
Official Symbol	Lepr provided by MGI
Official Full Name	leptin receptor provided by MGI
Primary source	MGI:MGI:104993
See related	Ensembl:ENSMUSG00000057722
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	LEPROT, Leprb, Modb1, OB-RGRP, Obr, db, diabetes, obese-like, obl
Expression	Broad expression in bladder adult (RPKM 5.0), placenta adult (RPKM 3.3) and 18 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

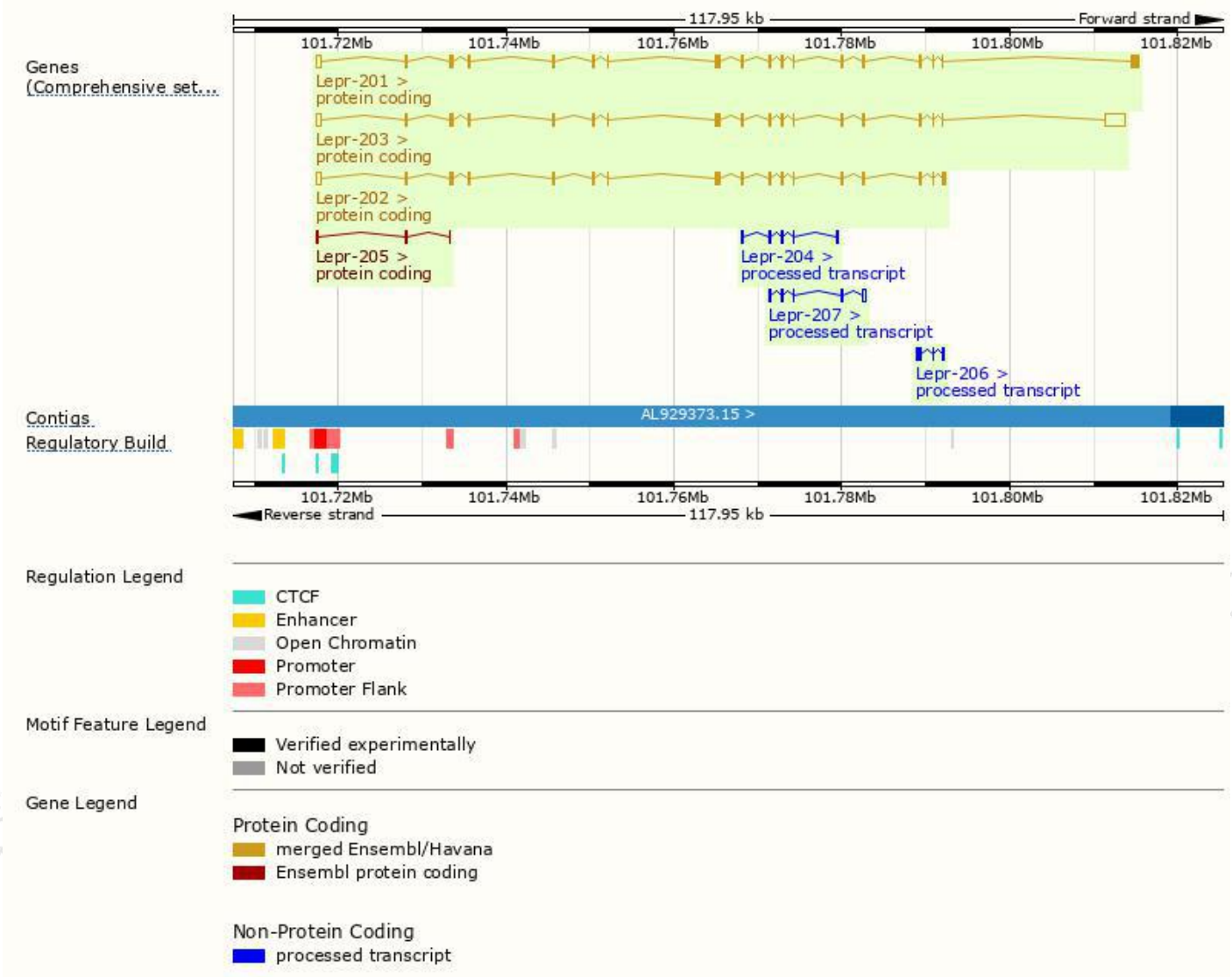
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lepr-203	ENSMUST00000106921.8	5542	894aa	Protein coding	CCDS51239	P48356 Q3US58	TSL:1 GENCODE basic APPRIS ALT2
Lepr-201	ENSMUST00000037552.9	4127	1162aa	Protein coding	CCDS51240	P48356	TSL:1 GENCODE basic APPRIS ALT2
Lepr-202	ENSMUST00000102777.9	3410	892aa	Protein coding	CCDS18397	P48356 Q3UNU8	TSL:1 GENCODE basic APPRIS P3
Lepr-205	ENSMUST00000145024.1	208	30aa	Protein coding	-	A2AV66	CDS 3' incomplete TSL:5
Lepr-207	ENSMUST00000156402.1	889	No protein	Processed transcript	-	-	TSL:2
Lepr-204	ENSMUST00000128948.7	787	No protein	Processed transcript	-	-	TSL:3
Lepr-206	ENSMUST00000151733.1	415	No protein	Processed transcript	-	-	TSL:3

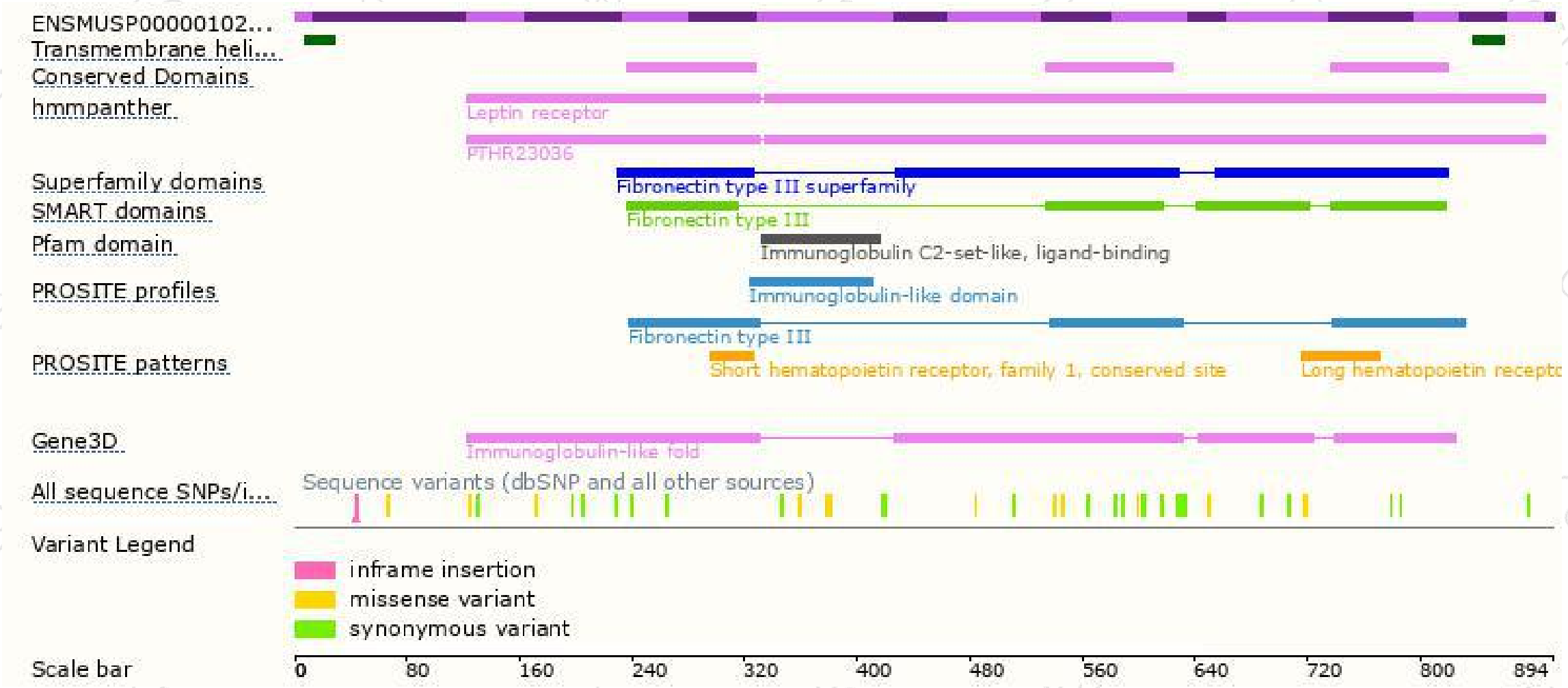
The strategy is based on the design of *Lepr-203* transcript,The transcription is shown below



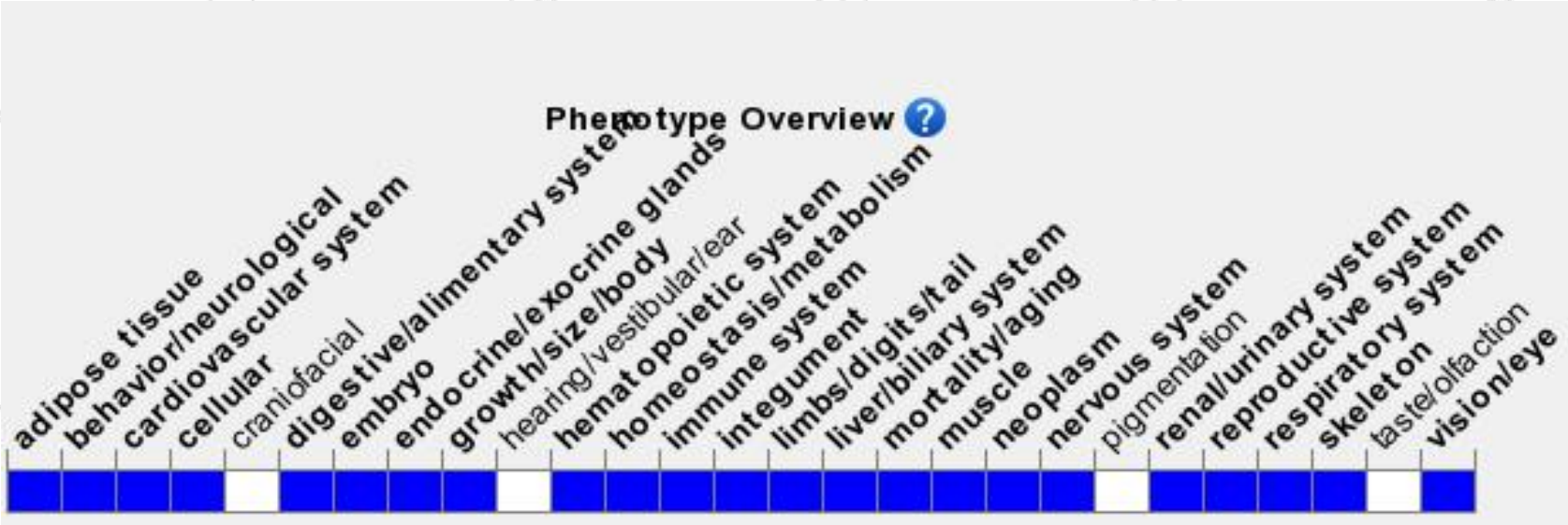
Genomic location distribution



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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