

Osbp11 Cas9-KO Strategy

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Project Overview

Project Name

Osbpl11

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Osbpl11* gene. The schematic diagram is as follows:



- The *Osbpl11* gene has 4 transcripts. According to the structure of *Osbpl11* gene, exon3-exon4 of *Osbpl11-201* (ENSMUST00000039733.9) transcript is recommended as the knockout region. The region contains 256bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Osbpl11* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Osbp11* gene is located on the Chr16. 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)

Osbpl11 oxysterol binding protein-like 11 [Mus musculus (house mouse)]

Gene ID: 106326, updated on 13-Mar-2020

Summary



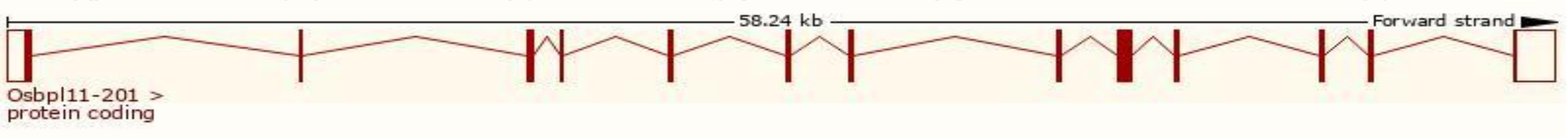
Official Symbol	Osbpl11 provided by MGI
Official Full Name	oxysterol binding protein-like 11 provided by MGI
Primary source	MGI:MGI:2146553
See related	Ensembl:ENSMUSG00000022807
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9430097N02Rik, A132306, AU019795, ORP-11
Expression	Ubiquitous expression in subcutaneous fat pad adult (RPKM 10.9), thymus adult (RPKM 8.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

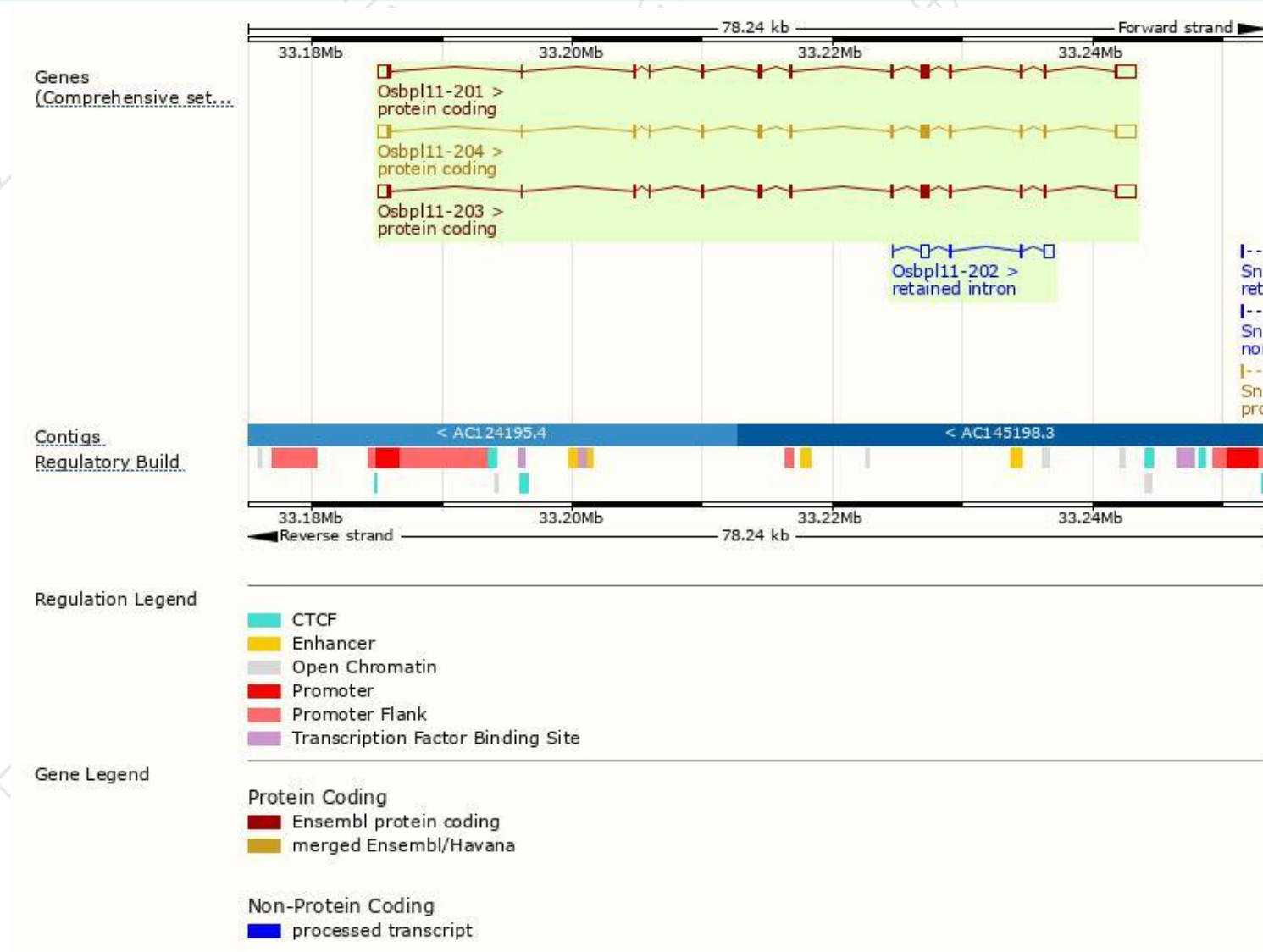
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Osbp11-201	ENSMUST00000039733.9	4521	757aa	Protein coding	CCDS28128	G5E8A0	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 P2
Osbp11-204	ENSMUST000000232181.1	4475	757aa	Protein coding	CCDS28128	G5E8A0	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 P2
Osbp11-203	ENSMUST000000232100.1	4475	751aa	Protein coding	-	A0A338P6F2	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 ALT2
Osbp11-202	ENSMUST000000231617.1	1676	No protein	Retained intron	-	-	

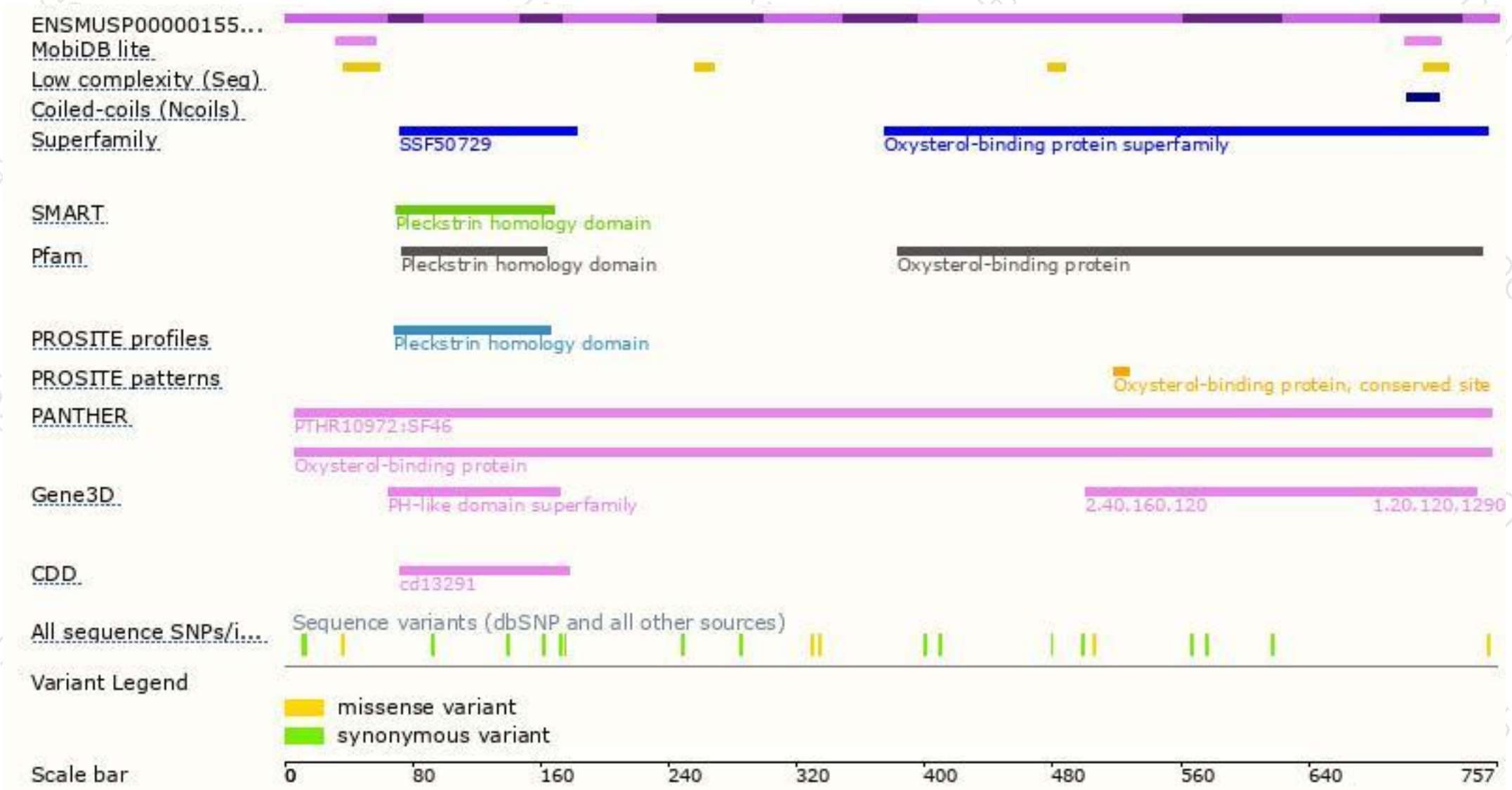
The strategy is based on the design of *Osbp11-201* transcript,the transcription is shown below:



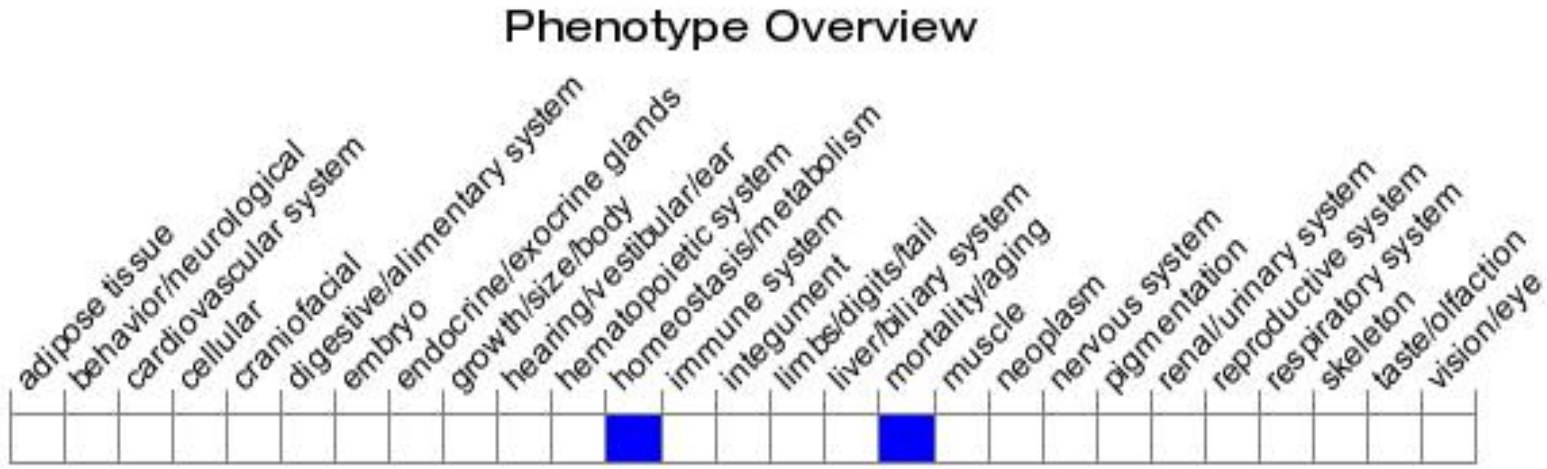
Genomic location distribution



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/>).

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

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