

Hdac11 Cas9-CKO Strategy

Designer:

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Project Overview

Project Name

Hdac11

Project type

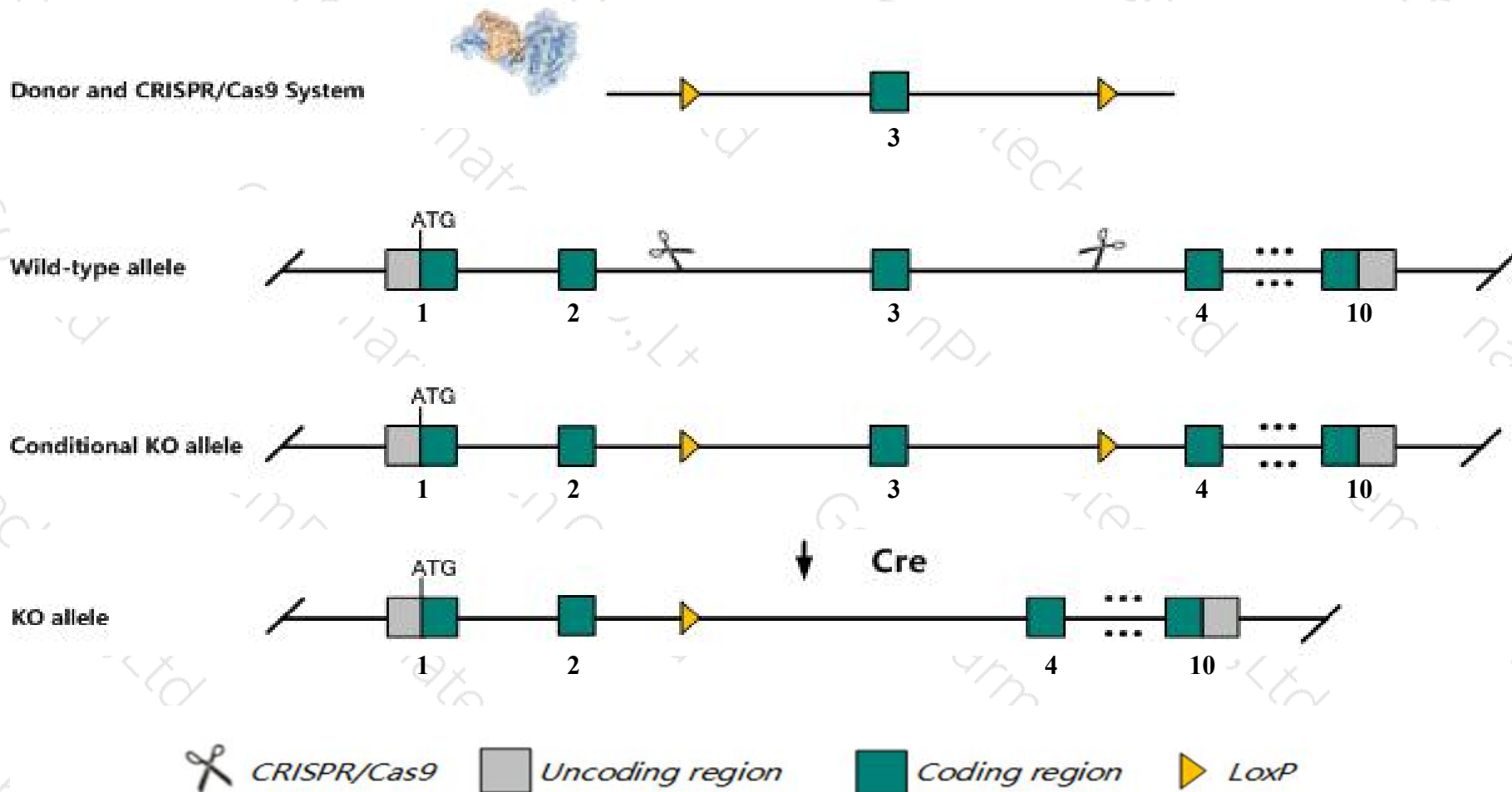
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hdac11* gene. The schematic diagram is as follows:



Technical routes

- The *Hdac11* gene has 7 transcripts. According to the structure of *Hdac11* gene, exon3 of *Hdac11-201* (ENSMUST00000041736.10) transcript is recommended as the knockout region. The region contains 101bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hdac11* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a knockout allele exhibit increased IL10 secretion from peritoneal elicited macrophages stimulated with LPS, more suppressive myeloid-derived suppressive cell population and enhanced tumor growth of injected tumor cells.
- The *Hdac11* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Hdac11 histone deacetylase 11 [Mus musculus (house mouse)]

Gene ID: 232232, updated on 30-Mar-2019

Summary



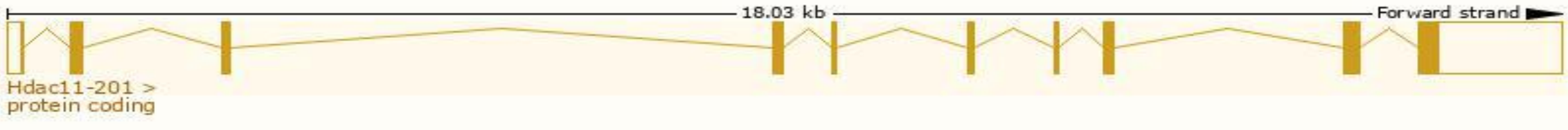
Official Symbol	Hdac11 provided by MGI
Official Full Name	histone deacetylase 11 provided by MGI
Primary source	MGI:MGI:2385252
See related	Ensembl:ENSMUSG000000034245
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Ubiquitous expression in testis adult (RPKM 59.4), cerebellum adult (RPKM 42.4) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

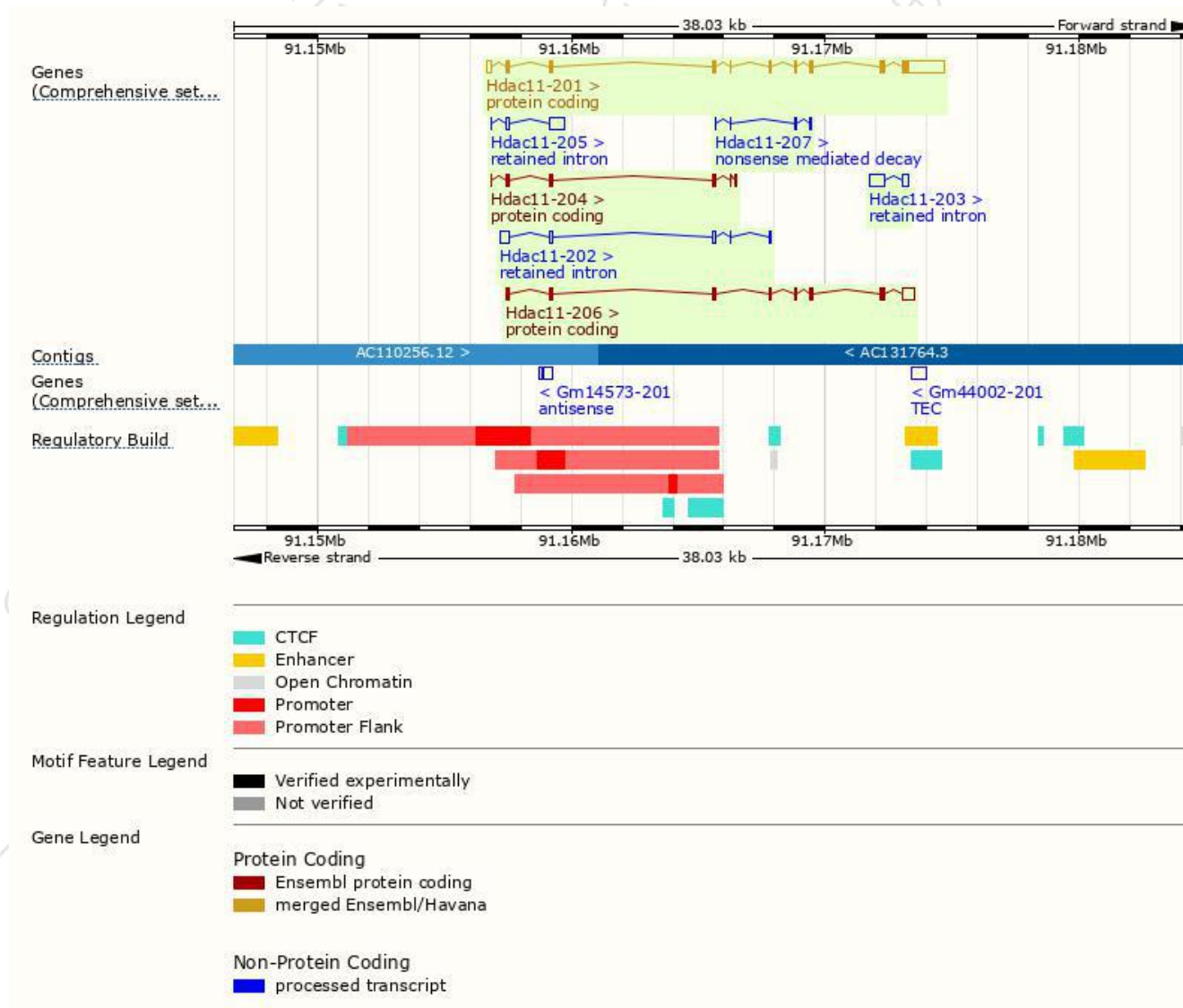
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hdac11-201	ENSMUST00000041736.10	2653	347aa	Protein coding	CCDS20366	Q543U1 Q91WA3	TSL:1 GENCODE basic APPRIS P1
Hdac11-206	ENSMUST00000155007.1	1251	264aa	Protein coding	-	F6UL83	CDS 5' incomplete TSL:5
Hdac11-204	ENSMUST00000143621.7	536	172aa	Protein coding	-	D3Z2G7	CDS 3' incomplete TSL:5
Hdac11-207	ENSMUST00000204776.1	198	26aa	Nonsense mediated decay	-	A0A0N4SVA2	CDS 5' incomplete TSL:1
Hdac11-203	ENSMUST00000134154.1	815	No protein	Retained intron	-	-	TSL:2
Hdac11-205	ENSMUST00000154389.1	738	No protein	Retained intron	-	-	TSL:2
Hdac11-202	ENSMUST00000127768.1	688	No protein	Retained intron	-	-	TSL:3

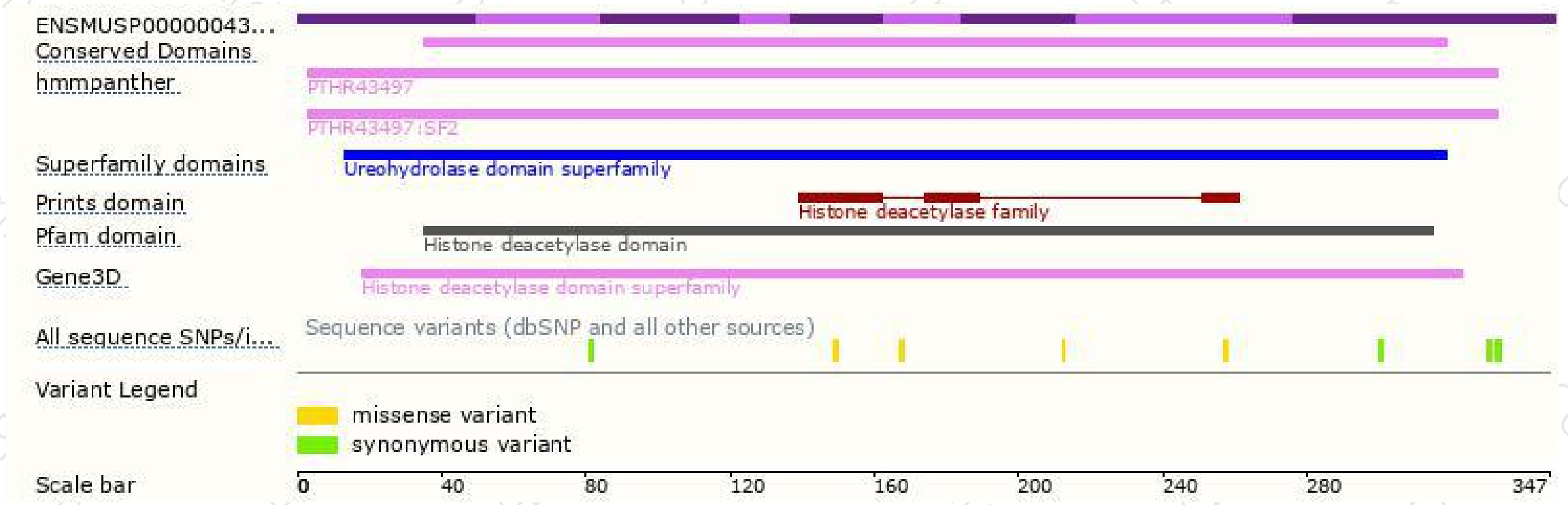
The strategy is based on the design of *Hdac11-201* transcript,The transcription is shown below



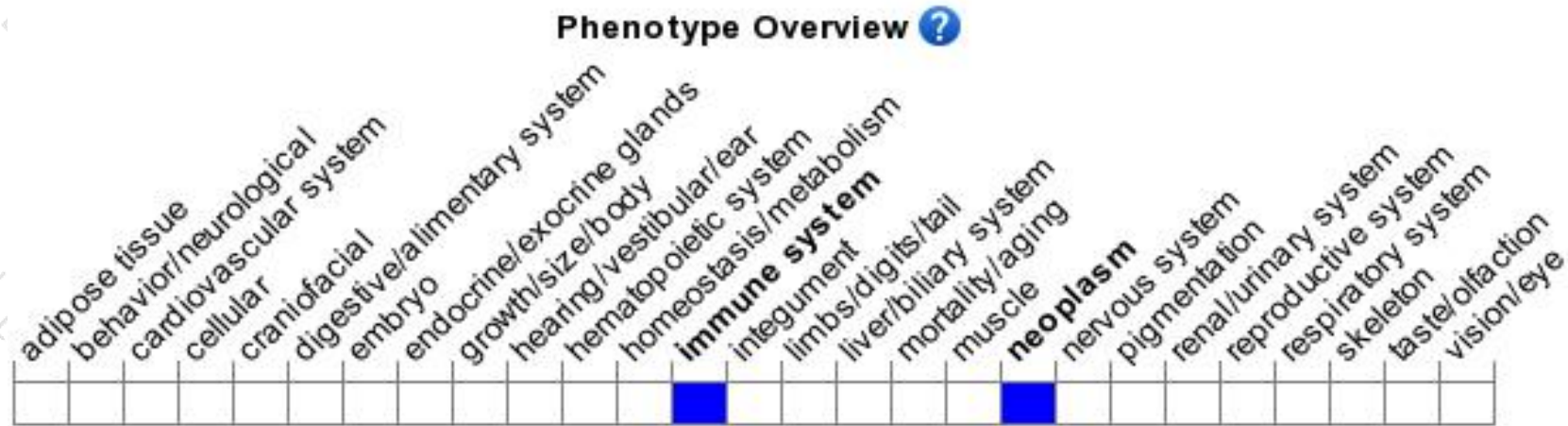
Genomic location distribution



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 knockout allele exhibit increased IL10 secretion from peritoneal elicited macrophages stimulated with LPS, more suppressive myeloid-derived suppressive cell population and enhanced tumor growth of injected tumor cells.

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

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