

E2f8 Cas9-KO Strategy

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Design Date:2020-2-11

Project Overview



Project Name

E2f8

Project type

Cas9-KO

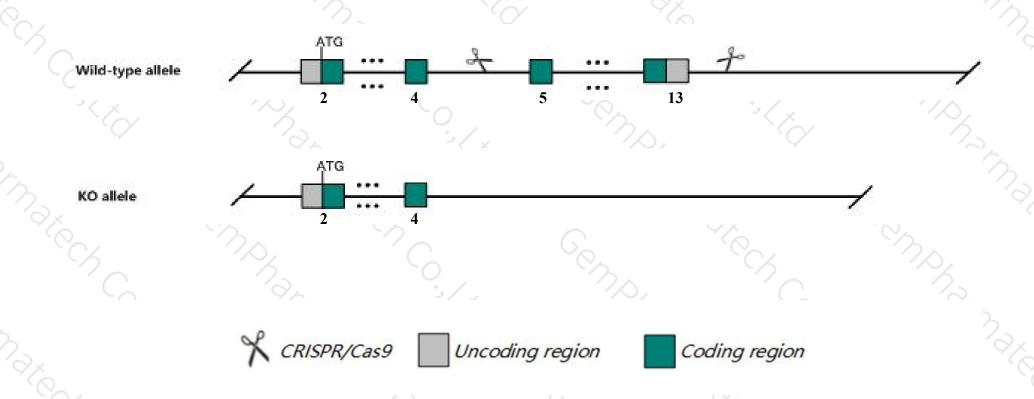
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *E2f8* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *E2f8* gene has 4 transcripts. According to the structure of *E2f8* gene, exon5-exon13 of *E2f8-201*(ENSMUST00000058745.14) transcript is recommended as the knockout region. The region contains 2132bp coding sequence Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *E2f8* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice



- > According to the existing MGI data, Mice homozygous for a knock-out allele develop normally through puberty and live to old age.
- ➤ The knockout area of this strategy is about 2KB from the 5 ends of Gm2788, which may affect its regulation.
- The *E2f8* gene is located on the Chr7. 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)



E2f8 E2F transcription factor 8 [Mus musculus (house mouse)]

Gene ID: 108961, updated on 24-Oct-2019

Summary

Official Symbol E2f8 provided by MGI

Official Full Name E2F transcription factor 8 provided by MGI

Primary source MGI:MGI:1922038

See related Ensembl: ENSMUSG00000046179

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 AA410048; 4432406C08Rik

Expression Broad expression in liver E14.5 (RPKM 17.2), liver E14 (RPKM 16.7) and 16 other tissues See more

Orthologs human all

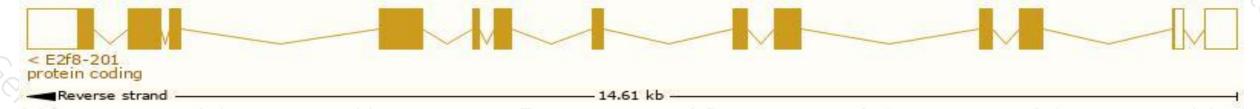
Transcript information (Ensembl)



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

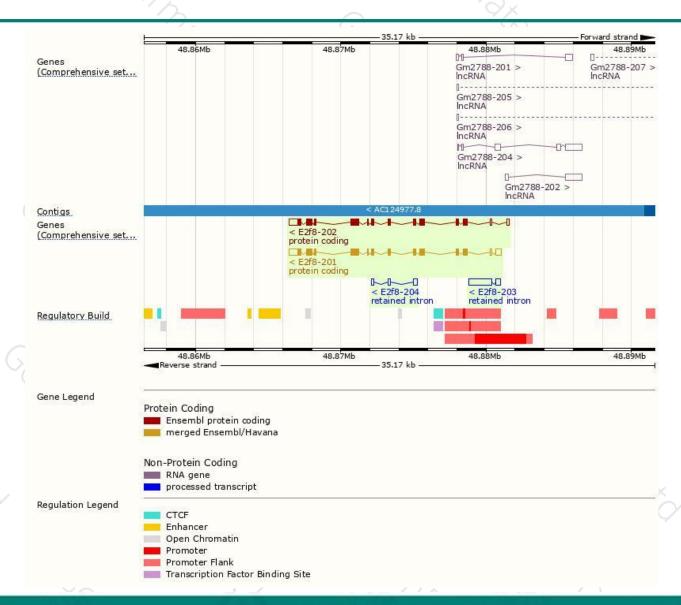
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
CONTRACTOR NAMED OF THE PROPERTY OF THE PARTY OF THE PART					01111101	riags
NSMUST00000058745.14	3691	860aa	Protein coding	CCDS39967	Q58FA4	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000119223.1	3499	<u>860aa</u>	Protein coding	CCDS39967	Q58FA4	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000136142.1	1913	No protein	Retained intron	ų.	0.20	TSL:1
ENSMUST00000151139.1	598	No protein	Retained intron	-	358	TSL:3
	NSMUST00000119223.1 NSMUST00000136142.1	NSMUST00000119223.1 3499 NSMUST00000136142.1 1913	NSMUST00000119223.1 3499 860aa NSMUST00000136142.1 1913 No protein	NSMUST00000119223.1 3499 860aa Protein coding NSMUST00000136142.1 1913 No protein Retained intron	NSMUST00000119223.1 3499 860aa Protein coding CCDS39967 NSMUST00000136142.1 1913 No protein Retained intron -	NSMUST00000119223.1 3499 860aa Protein coding CCDS39967 Q58FA4 NSMUST00000136142.1 1913 No protein Retained intron - -

The strategy is based on the design of *E2f8-201* transcript, The transcription is shown below



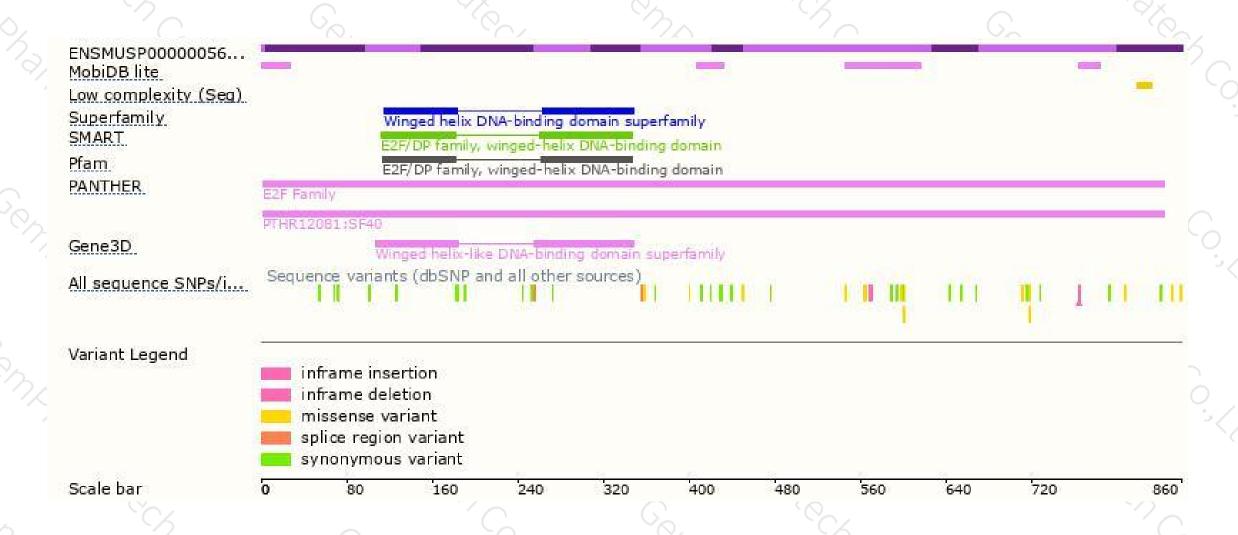
Genomic location distribution





Protein domain







If you have any questions, you are welcome to inquire. Tel: 400-9660890





