Ubtf Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Daohua Xu

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Project Overview

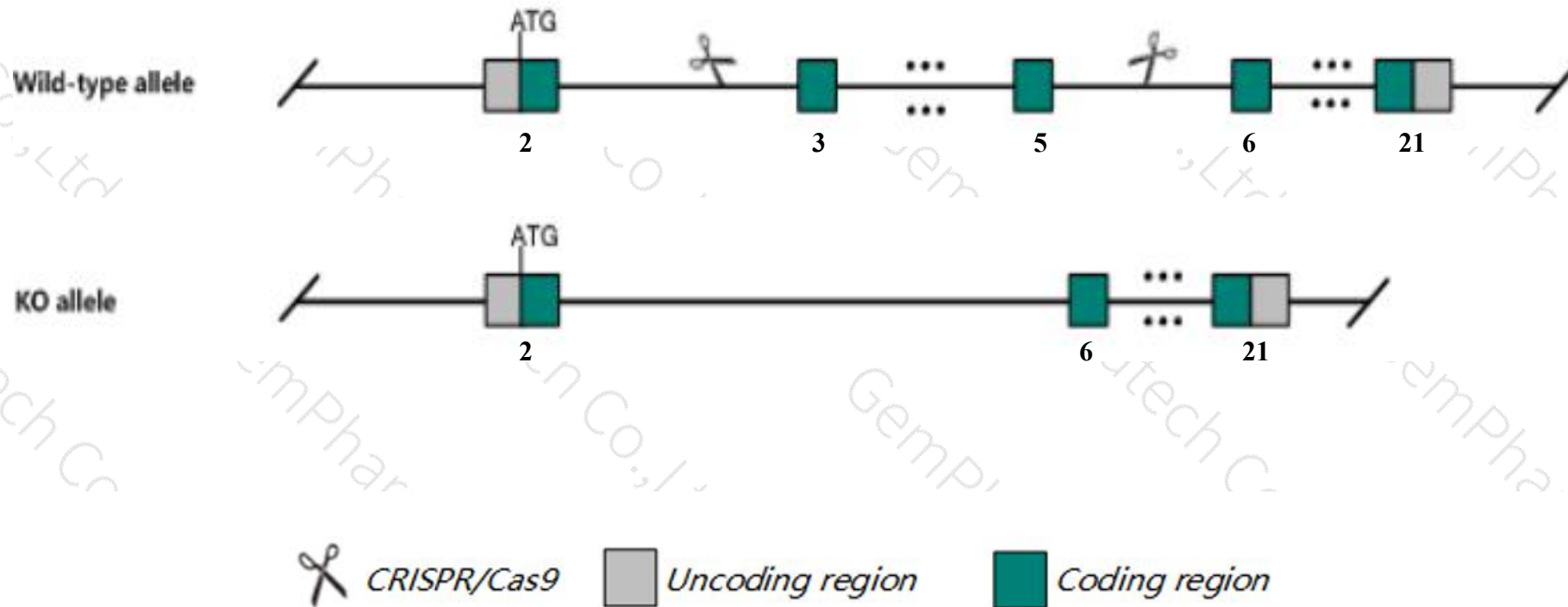|	
Project Name	*Ubtf*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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

Technical routes

➢ The *Ubtf* gene has 13 transcripts. According to the structure of *Ubtf* gene, exon3-exon5 of *Ubtf-210*(ENSMUST00000174302.7) transcript is recommended as the knockout region.The region contains 416bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

➢ According to the existing MGI data,mice homozygous for a knock-out allele exhibit embryonic lethality before implantation with embryonic growth arrest.

➢ Transcript *Ubtf*-211&212 may not be affected.

➢ The *Ubtf* gene is located on the Chr11. 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）

Ubtf upstream binding transcription factor, RNA polymerase I [Mus musculus (house mouse)]

Gene ID: 21429, updated on 13-Mar-2020

▲ Summary

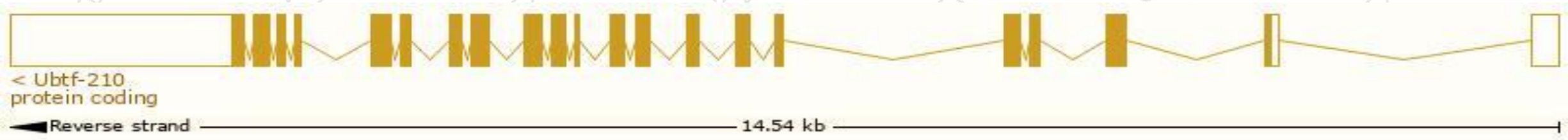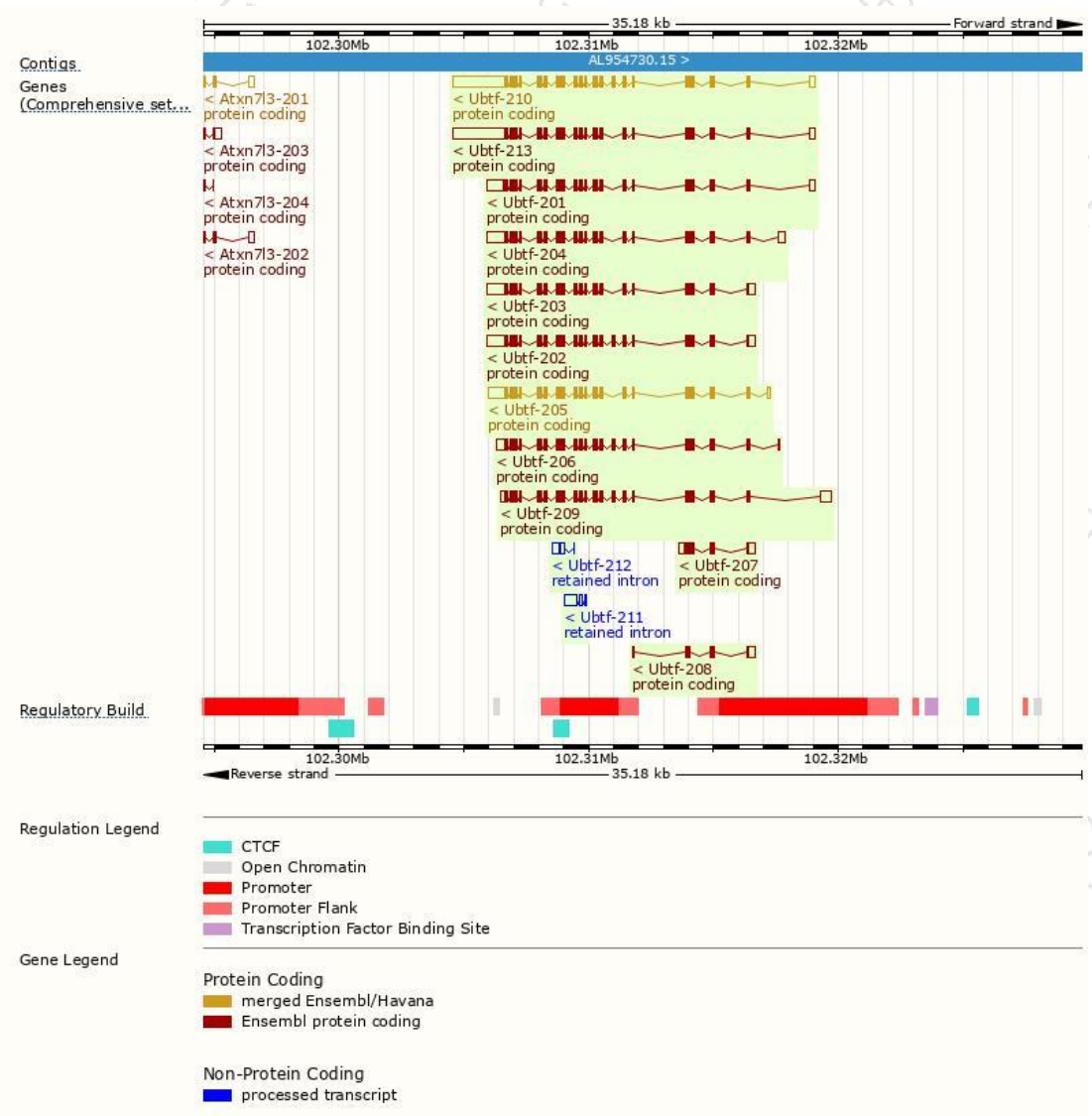|	
Official Symbol	Ubtf provided by MGI
Official Full Name	upstream binding transcription factor, RNA polymerase I provided by MGI
Primary source	MGI:MGI:98512
See related	Ensembl:ENSMUSG00000020923
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A930005G04Rik, NOR-90, Tcfubf, UBF, UBF-1, UBF1
Expression	Ubiquitous expression in CNS E11.5 (RPKM 28.0), liver E14 (RPKM 15.9) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ubtf-210	ENSMUST00000174302.7	4692	764aa	Protein coding	CCDS25495	A2AWT5	TSL:5 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 P3
Ubtf-213	ENSMUST00000178839.7	4580	727aa	Protein coding	CCDS36343	A2AWT6	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 ALT2
Ubtf-202	ENSMUST00000079589.10	3286	764aa	Protein coding	CCDS25495	A2AWT5	TSL:5 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 P3
Ubtf-204	ENSMUST00000107117.8	3258	727aa	Protein coding	CCDS36343	A2AWT6	TSL:5 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
Ubtf-201	ENSMUST00000006754.13	3213	752aa	Protein coding	CCDS79056	A2AWT7	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 ALT2
Ubtf-203	ENSMUST00000107115.7	3199	727aa	Protein coding	CCDS36343	A2AWT6	TSL:5 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
Ubtf-205	ENSMUST00000107119.8	3013	727aa	Protein coding	CCDS36343	A2AWT6	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 ALT2
Ubtf-209	ENSMUST00000173870.7	2936	764aa	Protein coding	CCDS25495	A2AWT5	TSL:5 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 P3
Ubtf-206	ENSMUST00000107123.9	2759	764aa	Protein coding	CCDS25495	A2AWT5	TSL:5 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 P3
Ubtf-207	ENSMUST00000128016.1	1062	169aa	Protein coding	-	E9Q4A8	TSL:2 GENCODE basic
Ubtf-208	ENSMUST00000146896.8	723	151aa	Protein coding	-	G3UZW9	CDS 3' incomplete TSL:5
Ubtf-211	ENSMUST00000174400.1	668	No protein	Retained intron	-	-	TSL:2
Ubtf-212	ENSMUST00000174726.1	480	No protein	Retained intron	-	-	TSL:5

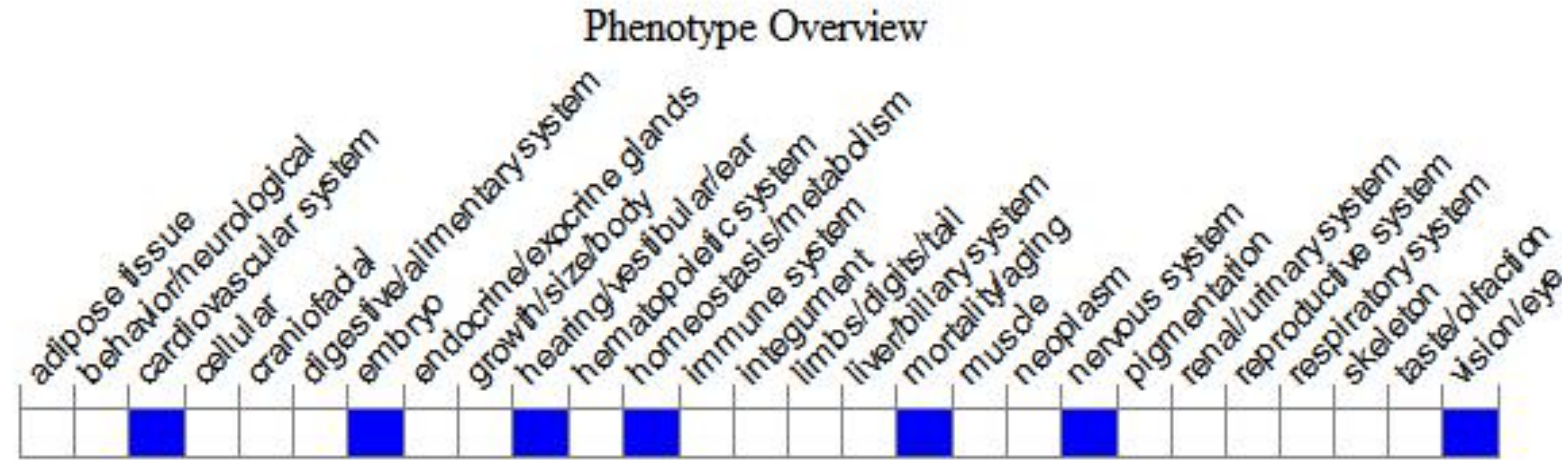The strategy is based on the design of *Ubtf-210* transcript,the transcription is shown below:

< Ubtf-210
protein coding

◀ Reverse strand   14.54 kb

Genomic location distribution

Protein domain

ENSMUSP00000133...	
MobiDB lite	
Low complexity (Seg)	
Coiled-coils (Ncoils)	
Superfamily	High mobility group box domain superfamily
SMART	High mobility group box domain
Pfam	High mobility group box domain
	High mobility group box domain High mobility group box domain 5
PROSITE profiles	High mobility group box domain
PANTHER	PTHR46318
	PTHR46318:SF4
Gene3D	
CDD	High mobility group box domain superfamily
	cd01390
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)

Variant Legend

- inframe insertion
- missense variant
- synonymous variant

Scale bar   0   80   160   240   320   400   480   560   640   764

Mouse phenotype description(MGI)

Phenotype Overview

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 knock-out allele exhibit embryonic lethality before implantation with embryonic growth arrest.

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

集萃药康生物科技
GemPharmatech Co.,Ltd