

Ubr4 Cas9-KO Strategy

Designer:

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Project Overview

Project Name

Ubr4

Project type

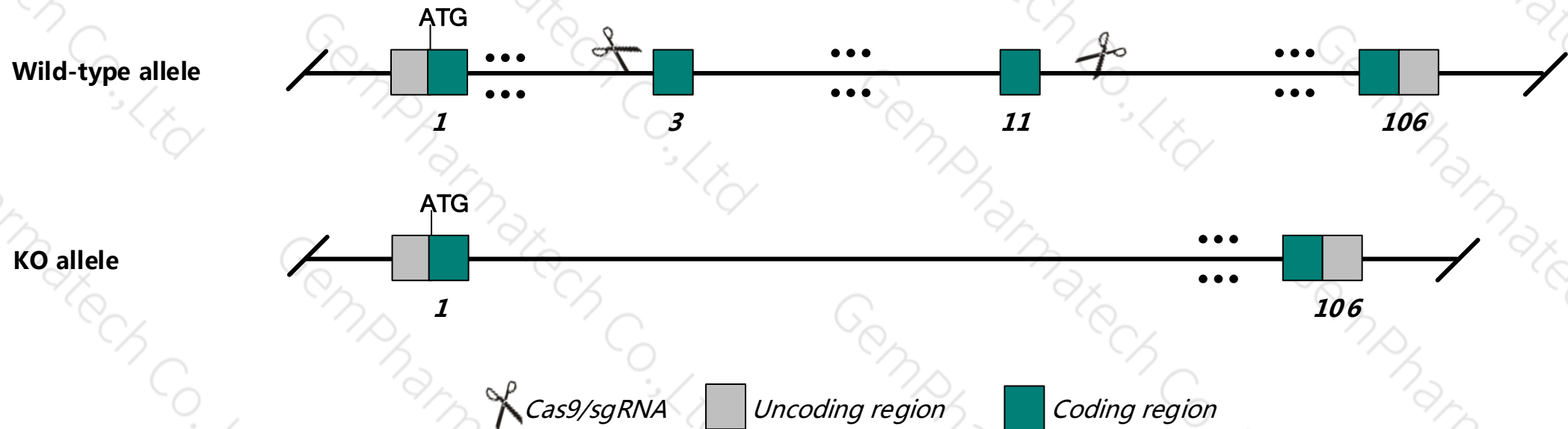
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ubr4* gene. The schematic diagram is as follows:



Technical routes

- The *Ubr4* gene has 12 transcripts. According to the structure of *Ubr4* gene, exon3-exon11 of *Ubr4*-201 (ENSMUST00000097822.9) transcript is recommended as the knockout region. The region contains 1120bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ubr4* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data , Mice homozygous for a transgenic gene disruption exhibit neonatal lethality and decreased body size at birth. Mice homozygous for a null mutation display complete embryonic lethality during organogenesis with arrest of vitelline vascular remodeling.
- The *Ubr4* 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, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Ubr4 ubiquitin protein ligase E3 component n-recognin 4 [*Mus musculus* (house mouse)]

Gene ID: 69116, updated on 12-Aug-2018

Summary

Official Symbol Ubr4 provided by [MGI](#)

Official Full Name ubiquitin protein ligase E3 component n-recognin 4 provided by [MGI](#)

Primary source [MGI:MGI:1916366](#)

See related [Ensembl:ENSMUSG00000066036](#) [Vega:OTTMUSG00000009956](#)

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 p600; Zubr1; Gm1032; Gm1666; N28143; RBAF600; mKIAA0462; 1810009A16Rik; A930005E13Rik; D930005K06Rik

Expression Ubiquitous expression in testis adult (RPKM 30.4), thymus adult (RPKM 22.5) and 28 other tissues [See more](#)

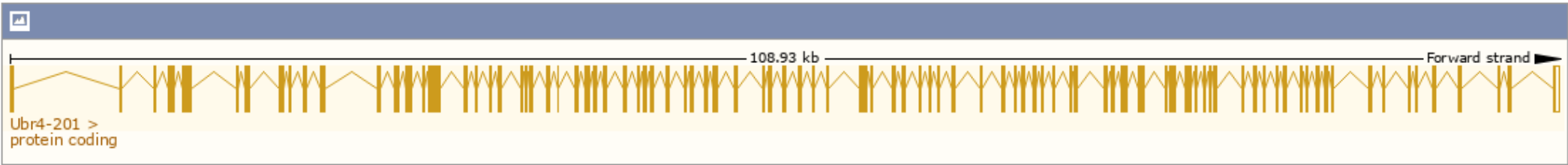
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

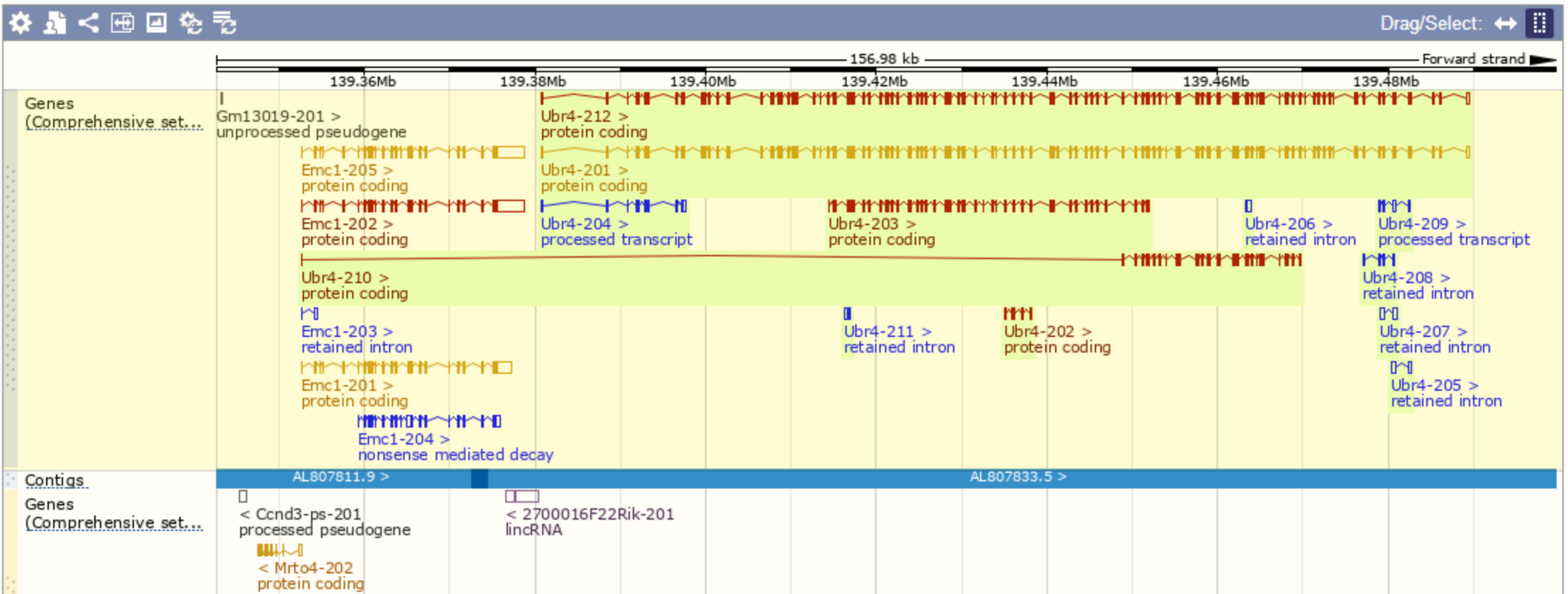
The gene has 12 transcripts, and all transcripts are shown below:

Show/hide columns (1 hidden)								Filter		
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags		
Ubr4-201	ENSMUST00000097822.9	15928	5180aa	 Protein coding	CCDS51340 	A2AN08 	NM_001160319  NP_001153791 	TSL:5	GENCODE basic	APPRIS P1
Ubr4-212	ENSMUST00000165860.7	15798	5156aa	 Protein coding	-	A2AN08 	-	TSL:5	GENCODE basic	
Ubr4-203	ENSMUST00000129949.7	6195	2065aa	 Protein coding	-	F6SSP6 	-	CDS 5' and 3' incomplete	TSL:1	
Ubr4-210	ENSMUST00000147999.7	4061	1301aa	 Protein coding	-	Z4YMA7 	-	CDS 3' incomplete	TSL:2	
Ubr4-202	ENSMUST00000129779.1	612	204aa	 Protein coding	-	Z4YLP1 	-	CDS 5' and 3' incomplete	TSL:2	
Ubr4-204	ENSMUST00000133220.1	1626	No protein	 Processed transcript	-	-	-	TSL:1		
Ubr4-209	ENSMUST00000145659.1	617	No protein	 Processed transcript	-	-	-	TSL:3		
Ubr4-207	ENSMUST00000141327.1	861	No protein	 Retained intron	-	-	-	TSL:3		
Ubr4-205	ENSMUST00000135534.1	682	No protein	 Retained intron	-	-	-	TSL:5		
Ubr4-206	ENSMUST00000136230.1	629	No protein	 Retained intron	-	-	-	TSL:1		
Ubr4-208	ENSMUST00000145273.1	627	No protein	 Retained intron	-	-	-	TSL:2		
Ubr4-211	ENSMUST00000149995.1	614	No protein	 Retained intron	-	-	-	TSL:3		

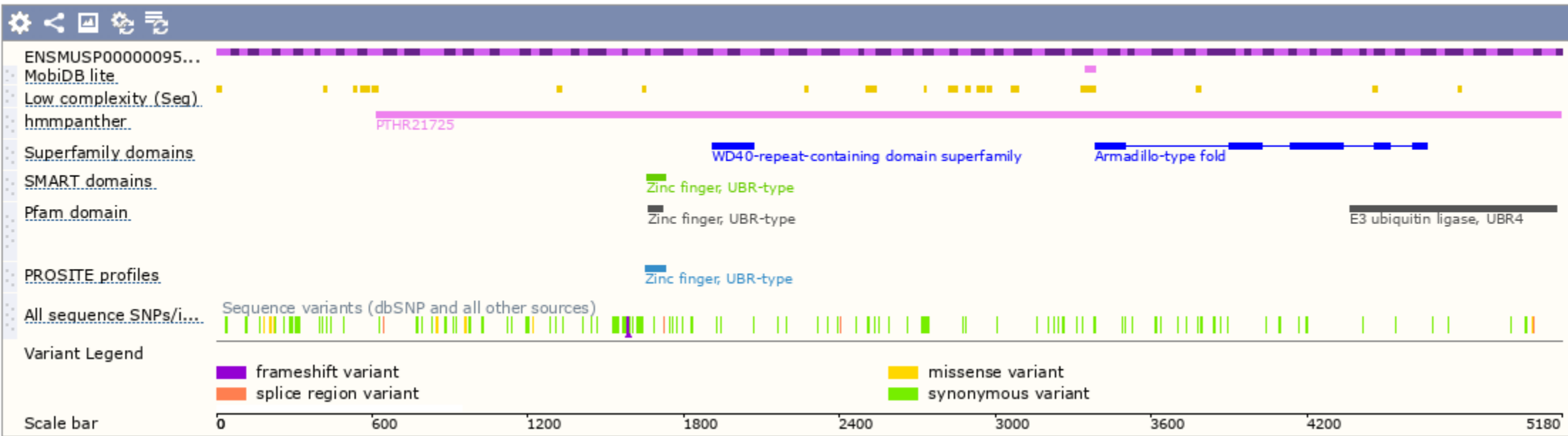
The strategy is based on the design of *Ubr4*-201 transcript,The transcription is shown below



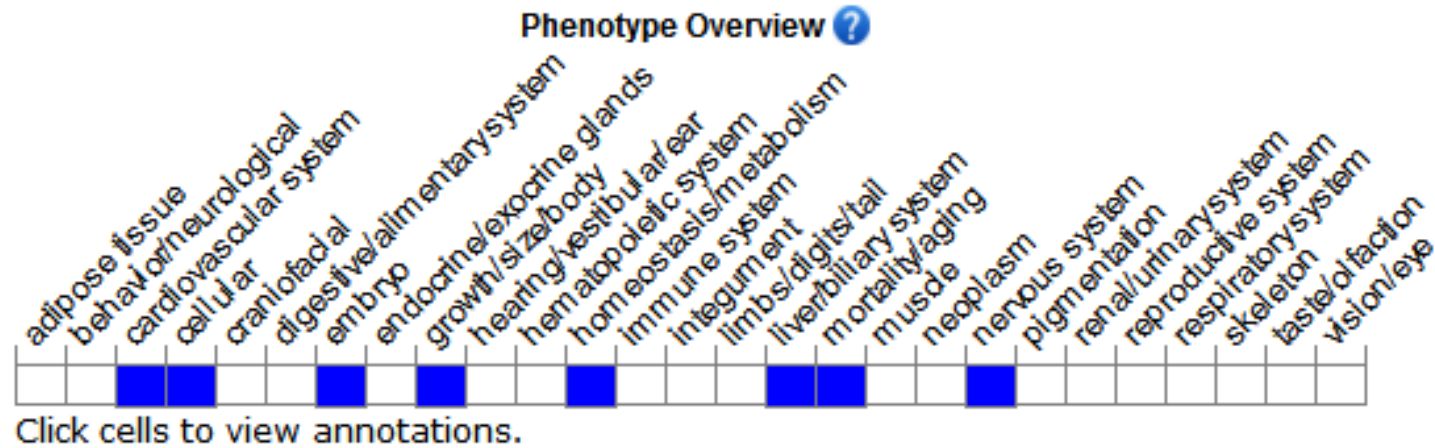
Genomic location distribution



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 transgenic gene disruption exhibit neonatal lethality and decreased body size at birth. Mice homozygous for a null mutation display complete embryonic lethality during organogenesis with arrest of vitelline vascular remodeling.

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