Usp28 Cas9-KO Strategy

Designer: Qiong Zhou

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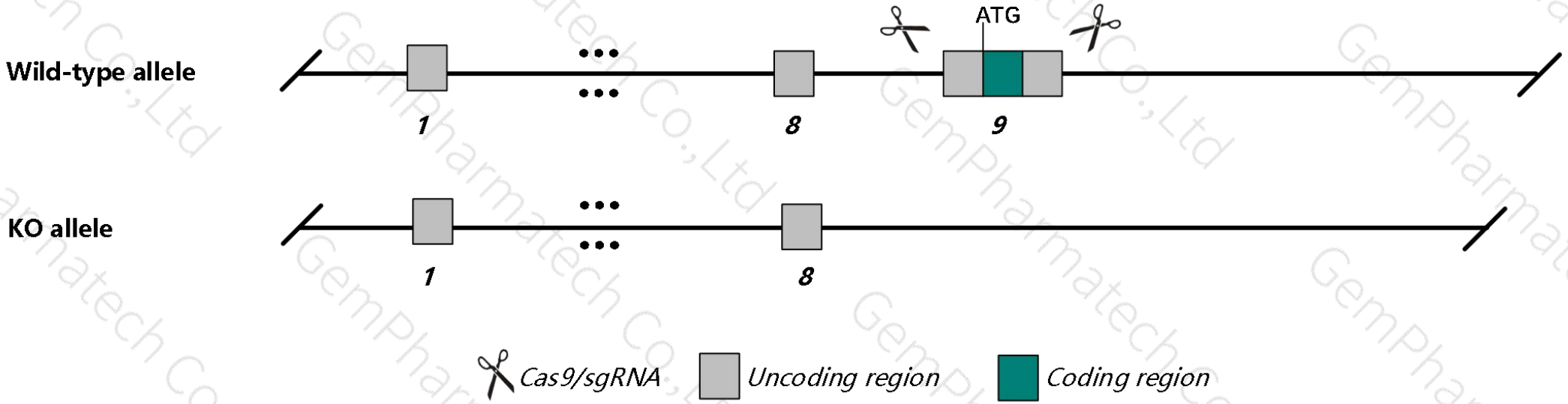
集萃药康 GemPharmatech
GemPharmatech Co.,Ltd

Project Overview

Project Name	***Usp28***
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Usp28* gene. The schematic diagram is as follows:



Technical routes

- The *Usp28* gene has 9 transcripts. According to the structure of *Usp29* gene, exon9 of *Usp29-204* (ENSMUST00000200535.5) transcript is recommended as the knockout region.The region contains all of the coding sequenc Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Usp28* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

Notice

➢ According to the MGI date, Paternal inheritance of a KO allele results in decreased birth weight and changes in chromosome methylation. Fathers carrying a KO allele sire smaller litters.

➢ The *Zim3* gene and *Usp29* are partly overlap, so the *Zim3* gene may be affected together.

➢ The *Usp28* 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）

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Usp29 ubiquitin specific peptidase 29 [*Mus musculus* (house mouse)]

Gene ID: 57775, updated on 31-Jan-2019

Summary

Official Symbol	Usp29 provided by MGI
Official Full Name	ubiquitin specific peptidase 29 provided by MGI
Primary source	MGI:MGI:1888998
See related	Ensembl:ENSMUSG00000051527
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	Ocat
Expression	Biased expression in CNS E18 (RPKM 4.9), whole brain E14.5 (RPKM 4.2) and 7 other tissues See more
Orthologs	human all

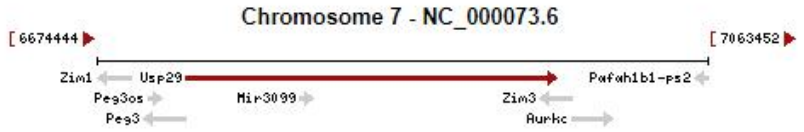
Genomic context

Location: 7 A1; 7 4.04 cM

See Usp29 in Genome Data Viewer

Exon count: 13

Annotation release	Status	Assembly	Chr	Location
106	current	GRCm38.p4 (GCF_000001635.24)	7	NC_000073.6 (6730560..6967220)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (6683452..6919931)



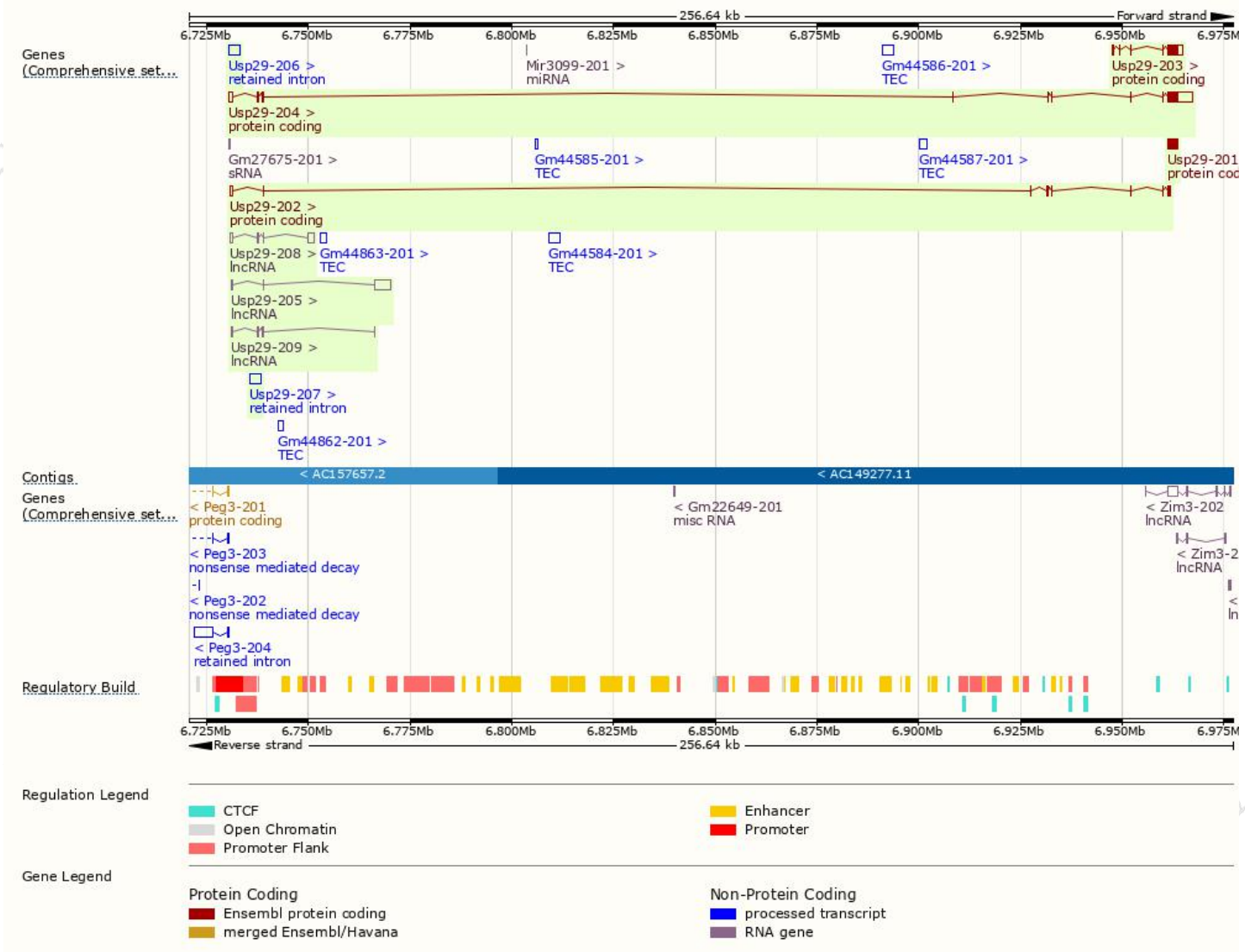
Transcript information（Ensembl）

The gene has 9 transcripts,all transcripts are shown below:

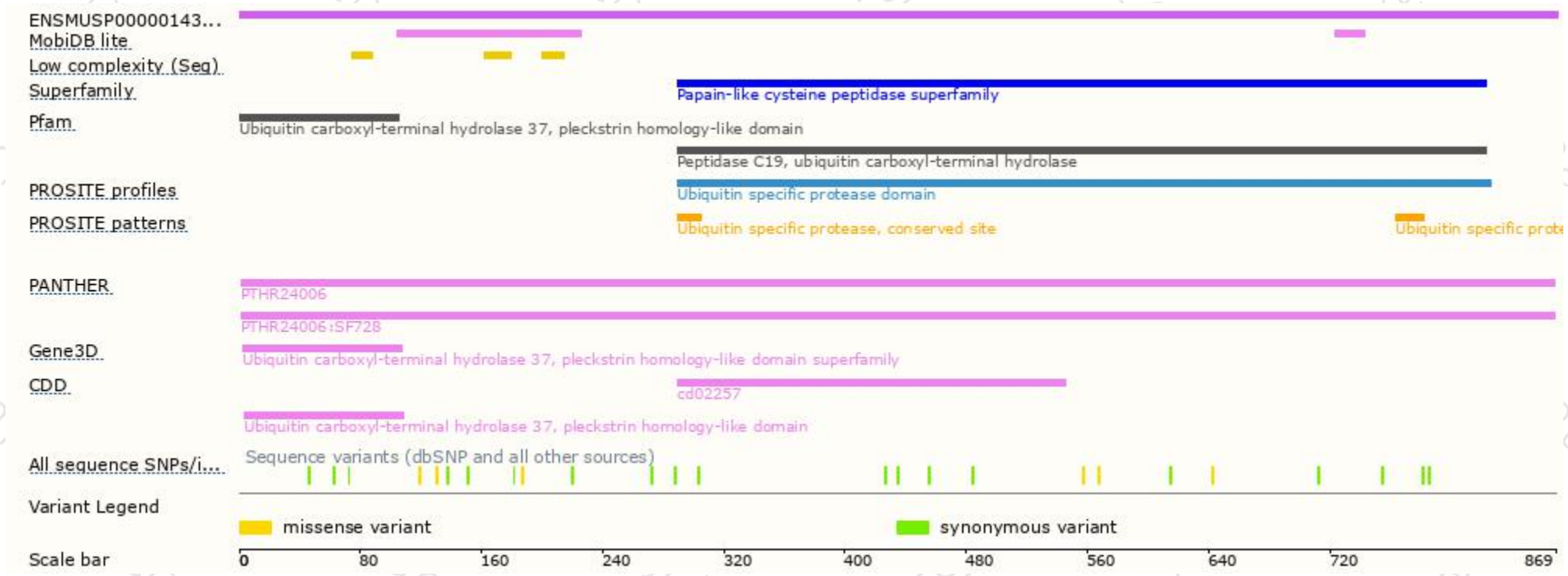
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Usp29-204	ENSMUST00000200535.5	7540	869aa	Protein coding	CCDS20784	Q9ES63	TSL:5 GENCODE basic APPRIS P1
Usp29-203	ENSMUST00000198068.2	4420	869aa	Protein coding	CCDS20784	Q9ES63	TSL:5 GENCODE basic APPRIS P1
Usp29-201	ENSMUST00000054055.6	2610	869aa	Protein coding	CCDS20784	Q9ES63	TSL:NA GENCODE basic APPRIS P1
Usp29-202	ENSMUST00000197117.4	1853	198aa	Protein coding	-	Q8CAH4	CDS 3' incomplete TSL:1
Usp29-206	ENSMUST00000208195.1	2660	No protein	Retained intron	-	-	TSL:NA
Usp29-207	ENSMUST00000208642.1	2610	No protein	Retained intron	-	-	TSL:NA
Usp29-205	ENSMUST00000207899.1	4348	No protein	lncRNA	-	-	TSL:1
Usp29-208	ENSMUST00000208662.1	2232	No protein	lncRNA	-	-	TSL:1
Usp29-209	ENSMUST00000208952.1	447	No protein	lncRNA	-	-	TSL:1

The strategy is based on the design of *Usp29-204* transcript,The transcription is shown below

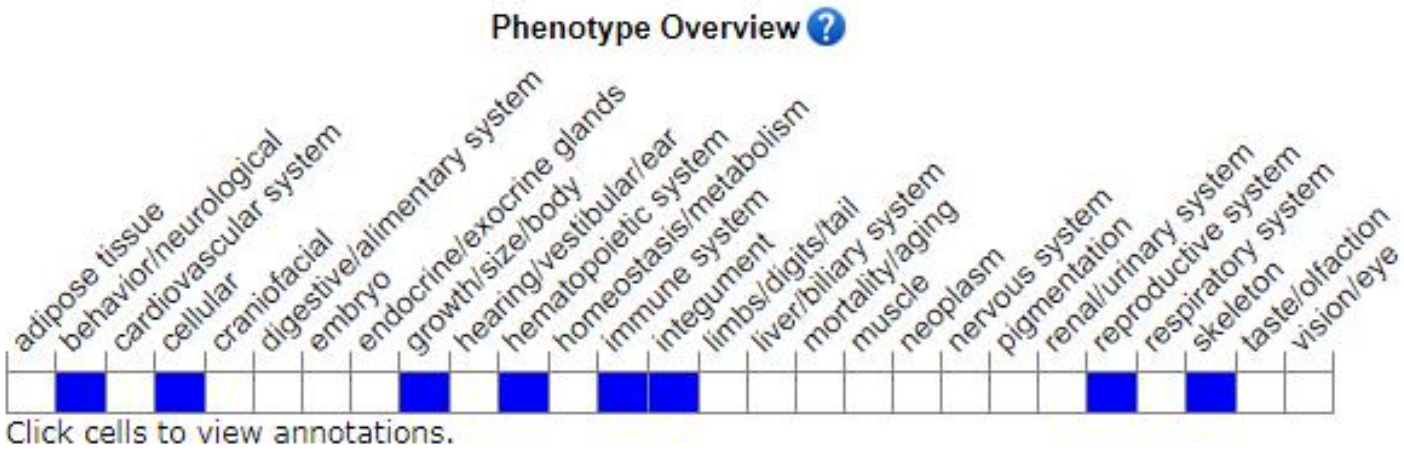
Genomic location distribution



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/).

Paternal inheritance of a KO allele results in decreased birth weight and changes in chromosome methylation. Fathers carrying a KO allele sire smaller litters.

集萃药康
GemPharmatech

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

Tel: 025-5864 1534

集萃药康生物科技
GemPharmatech Co.,Ltd

GemPharmatech Co.,Ltd