

Erp29 Cas9-CKO Strategy

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Design Date:2020-2-19

Project Overview

Project Name

Erp29

Project type

Cas9-CKO

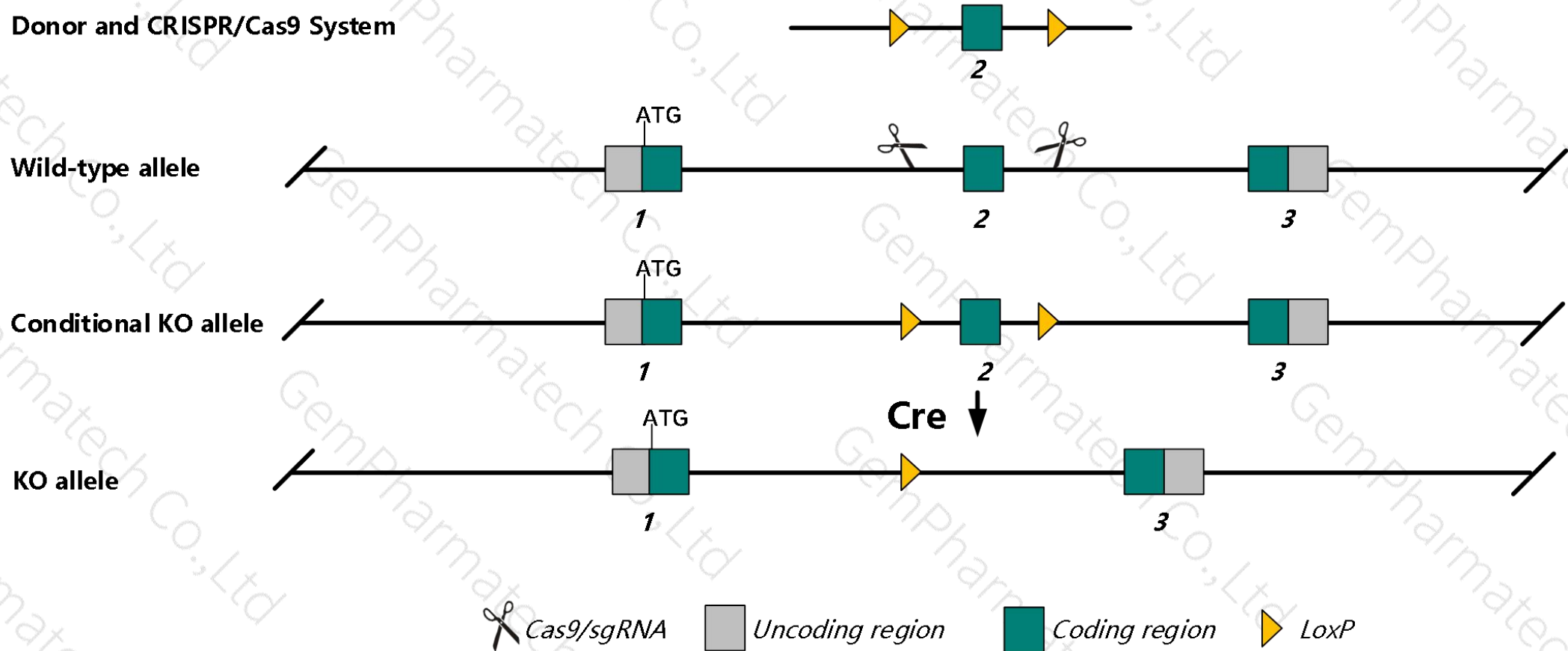
Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Erp29* gene. The schematic diagram is as follows:

Donor and CRISPR/Cas9 System



- The *Erp29* gene has 4 transcripts. According to the structure of *Erp29* gene, exon2 of *Erp29-203* (ENSMUST00000130451.1) transcript is recommended as the knockout region. The region contains 139bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Erp29* 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 null allele exhibit decreased thyrocyte and dermal fibroblast apoptosis sensitivities to induced ER stress and slightly reduced litter sizes.
- The knockout region is located at the 5-terminal of Tmem116 about 4kb, which may affect its 5-terminal regulation after knockout.
- This strategy has no impact on Erp29-201.
- The Erp29 gene is located on the Chr5. 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)

Erp29 endoplasmic reticulum protein 29 [*Mus musculus* (house mouse)]

Gene ID: 67397, updated on 20-Aug-2019

Summary

Official Symbol Erp29 provided by [MGI](#)

Official Full Name endoplasmic reticulum protein 29 provided by [MGI](#)

Primary source [MGI:MGI:1914647](#)

See related [Ensembl:ENSMUSG00000029616](#)

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

Also known as Erp28; Erp31; PDI-Db; AW209030; 1200015M03Rik; 2810446M09Rik

Expression Ubiquitous expression in placenta adult (RPKM 91.8), ovary adult (RPKM 52.5) and 28 other tissues [See more](#)

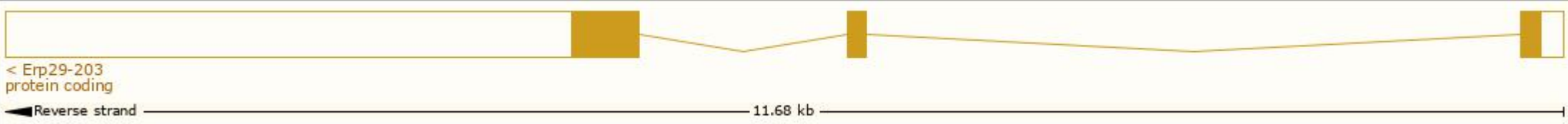
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

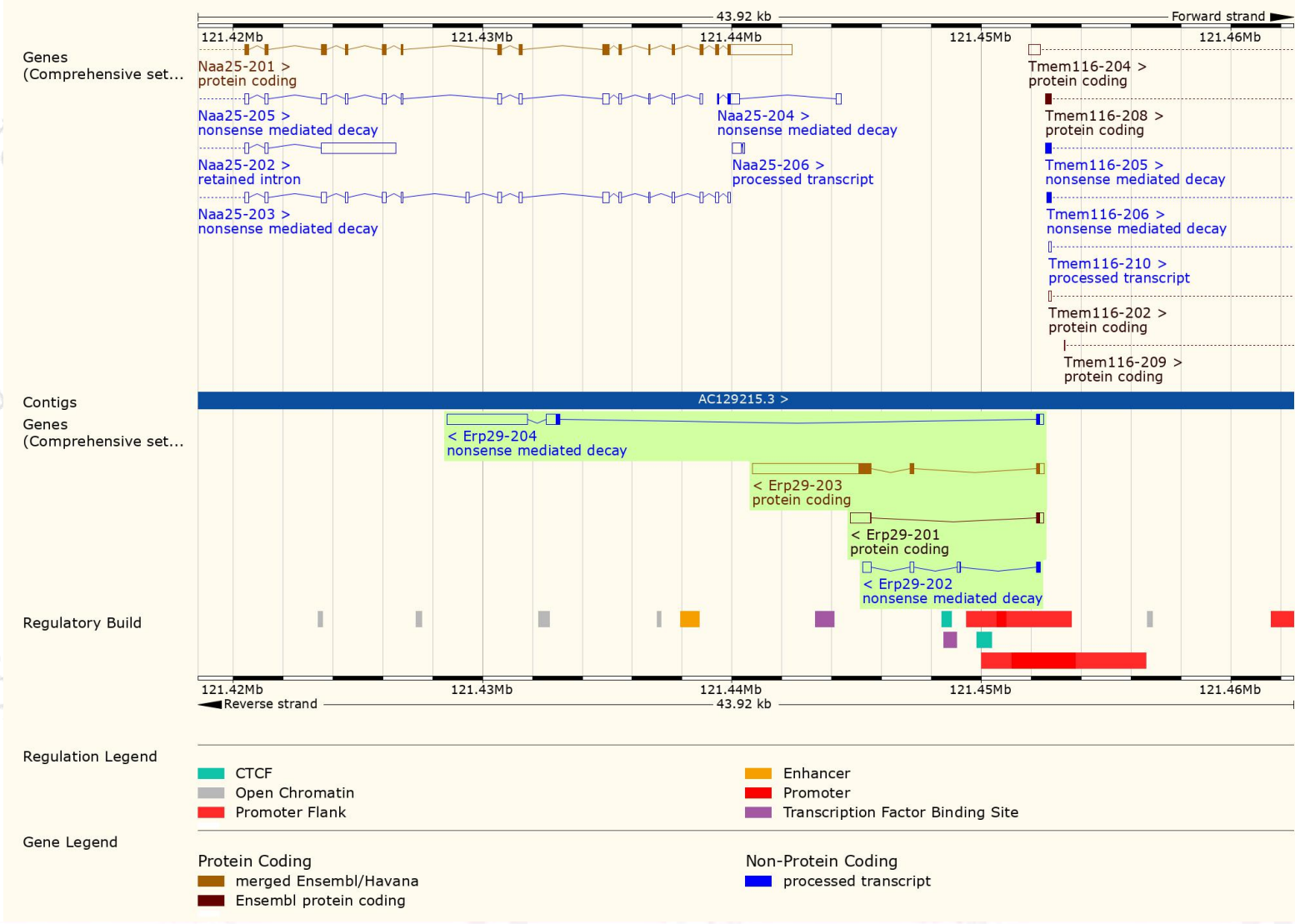
The gene has 4 transcripts,all transcripts are shown below:

Name ▲	Transcript ID ▲	bp ▲	Protein ▲	Biotype ▲	CCDS ▲	UniProt ▲	Flags ▲
Erp29-201	ENSMUST00000052590.7	1123	55aa	Protein coding	-	F8WJI4	TSL:1 Gencode basic
Erp29-202	ENSMUST00000111802.3	748	57aa	Nonsense mediated decay	-	F8WIM7	TSL:2
Erp29-203	ENSMUST00000130451.1	5204	262aa	Protein coding	CCDS19634	P57759	TSL:1 Gencode basic APPRIS P1
Erp29-204	ENSMUST00000153758.1	4034	95aa	Nonsense mediated decay	-	D6RG87	TSL:1

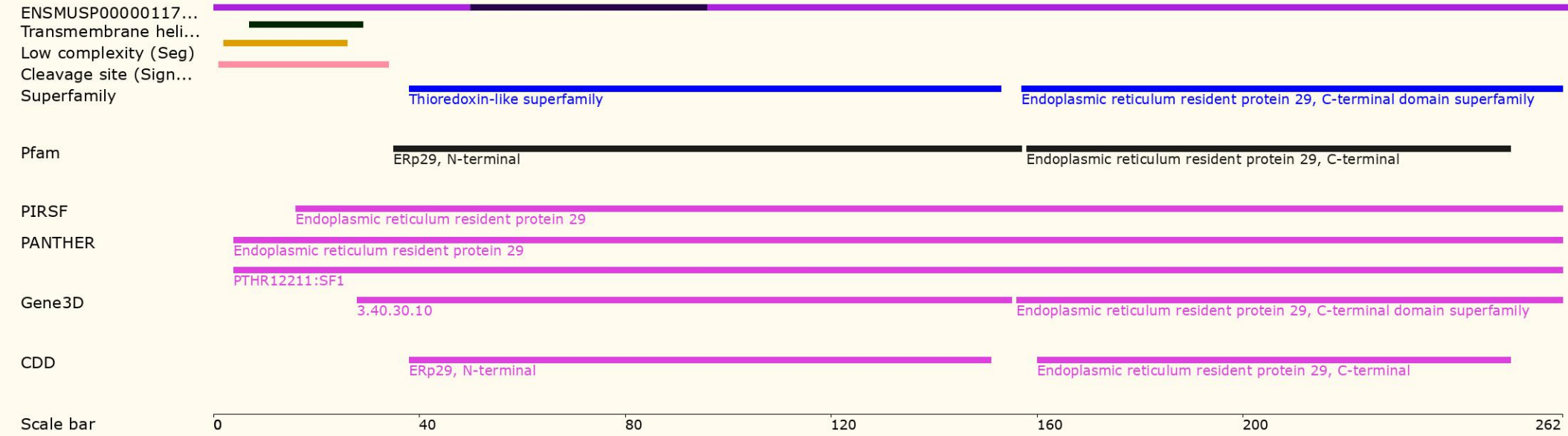
The strategy is based on the design of *Erp29-203* transcript,The transcription is shown below



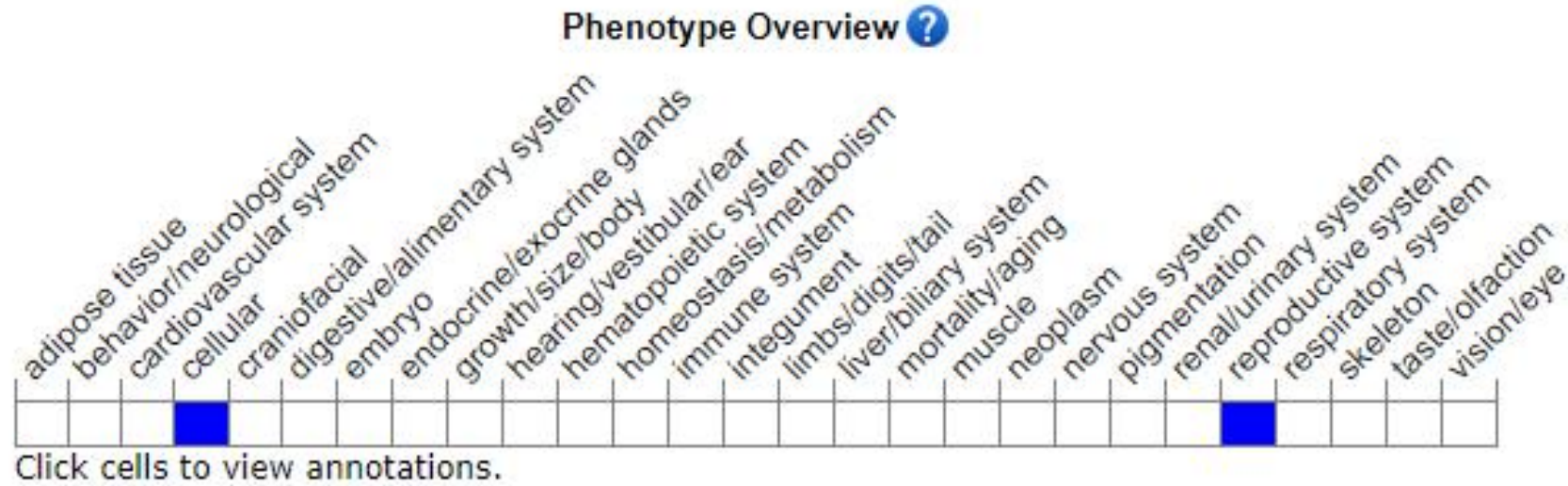
Genomic location distribution



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/>).

Mice homozygous for a null allele exhibit decreased thyrocyte and dermal fibroblast apoptosis sensitivities to induced ER stress and slightly reduced litter sizes.

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

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