Pars2 Cas9-CKO Strategy

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Project Overview

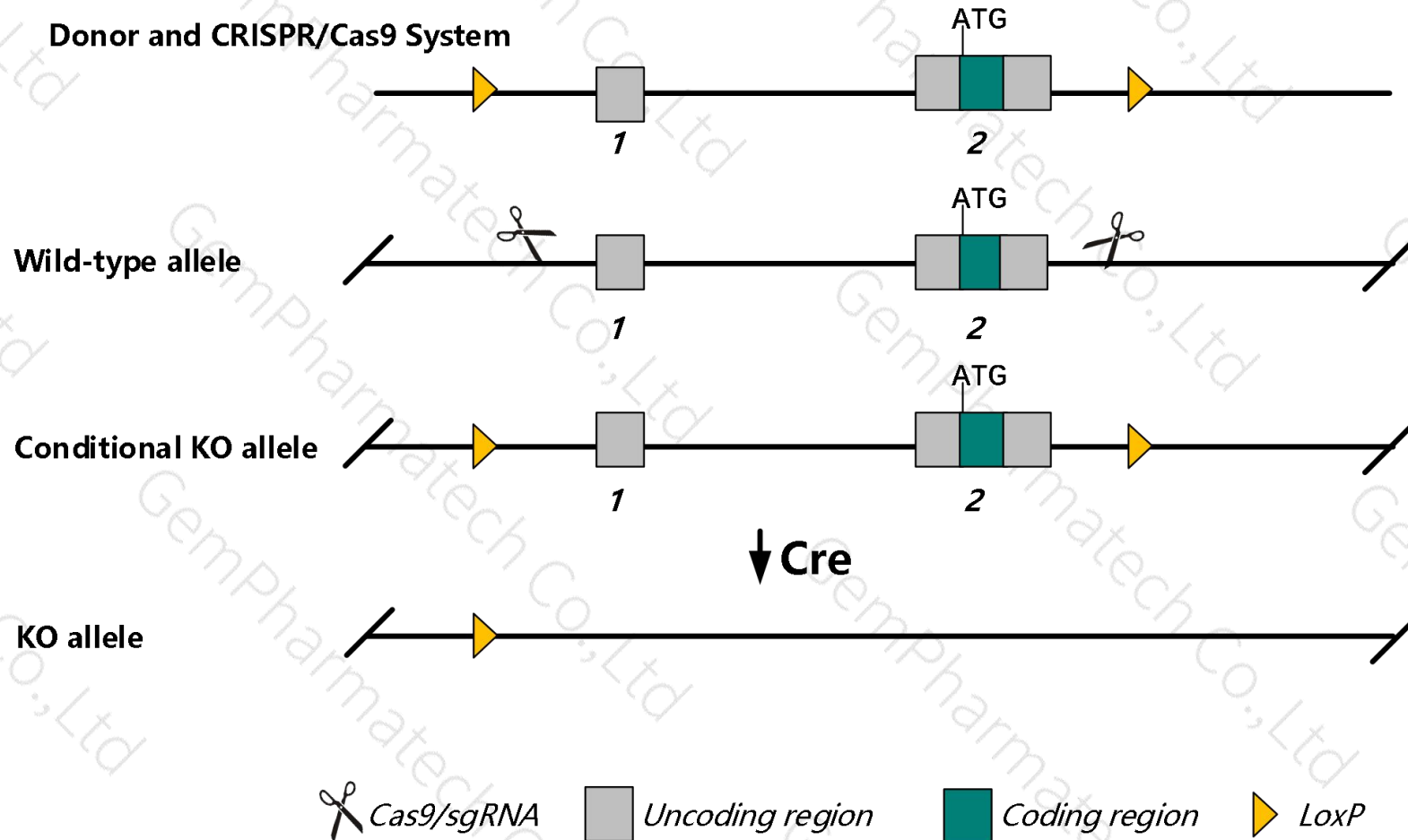|	
Project Name	***Pars2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pars2* gene. The schematic diagram is as follows:

Technical routes

➢ The *Pars2* gene has 4 transcripts. According to the structure of *Pars2* gene, exon1-exon2 of *Pars2-202* (ENSMUST00000106781.1) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Pars2* 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.

Notice

➢ The *Pars2* 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, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

Pars2 prolyl-tRNA synthetase (mitochondrial)(putative) [Mus musculus (house mouse)]

Gene ID: 230577, updated on 13-Mar-2020

▲ Summary   ⌃ ?

|	
Official Symbol	Pars2 provided by MGI
Official Full Name	prolyl-tRNA synthetase (mitochondrial)(putative) provided by MGI
Primary source	MGI:MGI:2386296
See related	Ensembl:ENSMUSG00000043572
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	BC027073
Expression	Ubiquitous expression in thymus adult (RPKM 2.6), ovary adult (RPKM 2.6) and 28 other tissuesSee 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
Pars2-202	ENSMUST00000106781.1	3046	511aa	Protein coding	CCDS38828	A8Y5T6	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
Pars2-201	ENSMUST00000058905.7	2191	475aa	Protein coding	CCDS18423	Q8CFI5	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 P3
Pars2-203	ENSMUST00000106782.1	502	163aa	Protein coding	-	A2AVQ7	CDS 3' incomplete TSL:2
Pars2-204	ENSMUST00000146966.1	644	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Pars2-202* transcript,the transcription is shown below:

4.18 kb   Forward strand ▶

Pars2-202 >
protein coding
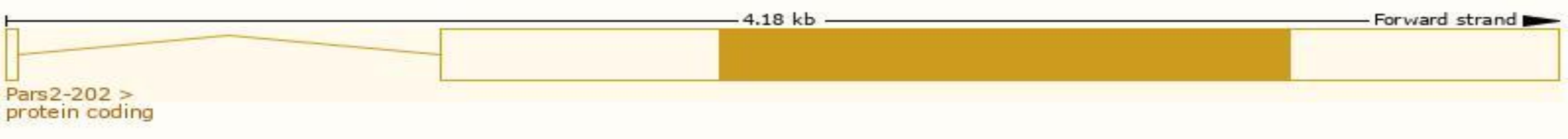
Genomic location distribution
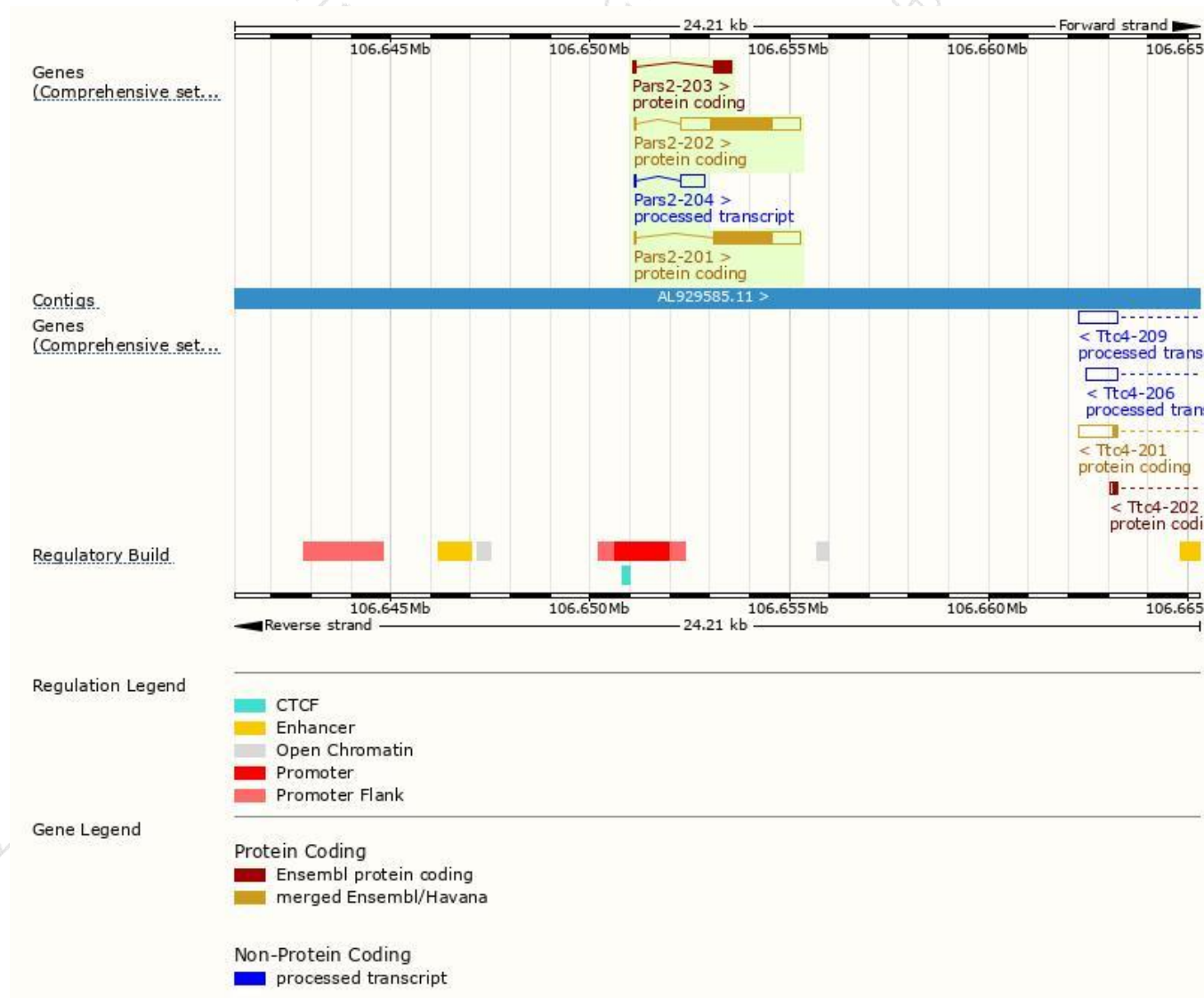
Protein domain
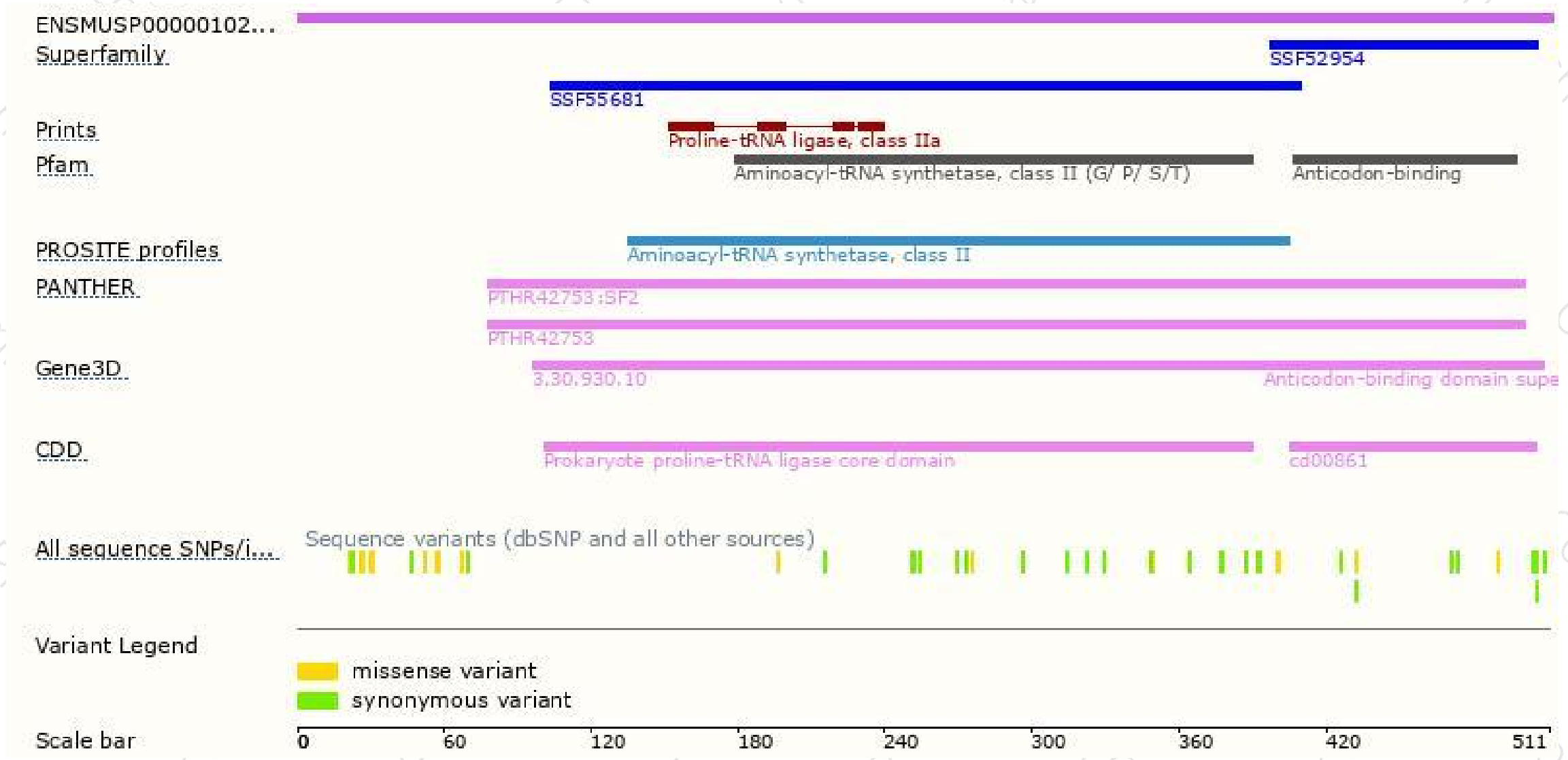
If you have any questions, you are welcome to inquire.
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