

Poglut2 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Poglut2

Project type

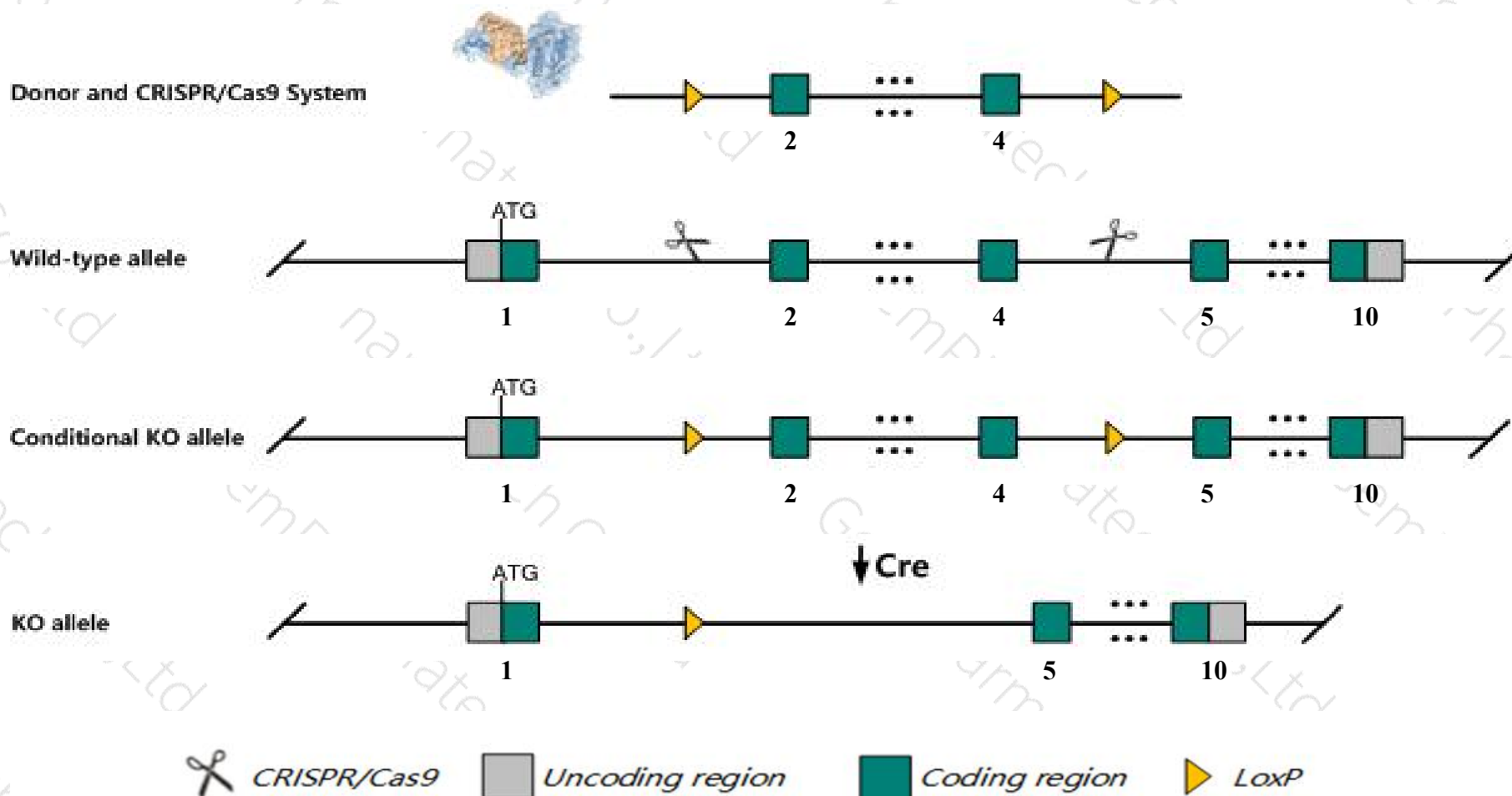
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Poglut2* gene. The schematic diagram is as follows:



- The *Poglut2* gene has 5 transcripts. According to the structure of *Poglut2* gene, exon2-exon4 of *Poglut2*-202 (ENSMUST00000065767.8) transcript is recommended as the knockout region. The region contains 490bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Poglut2* 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 flox region is about 1.6 kb away from the 5th end of the *Bivm* gene, and its effect is unknown.
- The *Poglut2* gene is located on the Chr1. 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)

Poglut2 protein O-glucosyltransferase 2 [Mus musculus (house mouse)]

Gene ID: 72050, updated on 13-Mar-2020

Summary



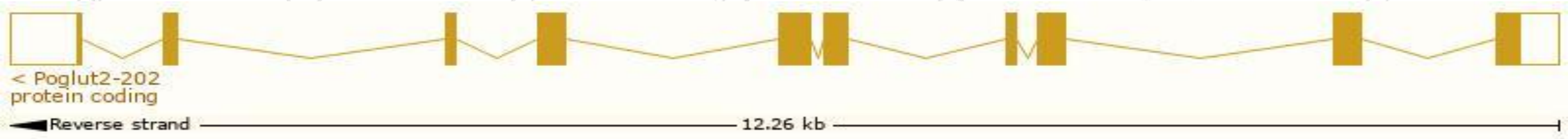
Official Symbol	Poglut2 provided by MGI
Official Full Name	protein O-glucosyltransferase 2 provided by MGI
Primary source	MGI:MGI:1919300
See related	Ensembl:ENSMUSG00000026047
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1810049A15Rik, 5730416C13Rik, EP58, Kdel1, Kdelc1
Expression	Ubiquitous expression in limb E14.5 (RPKM 19.9), ovary adult (RPKM 16.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

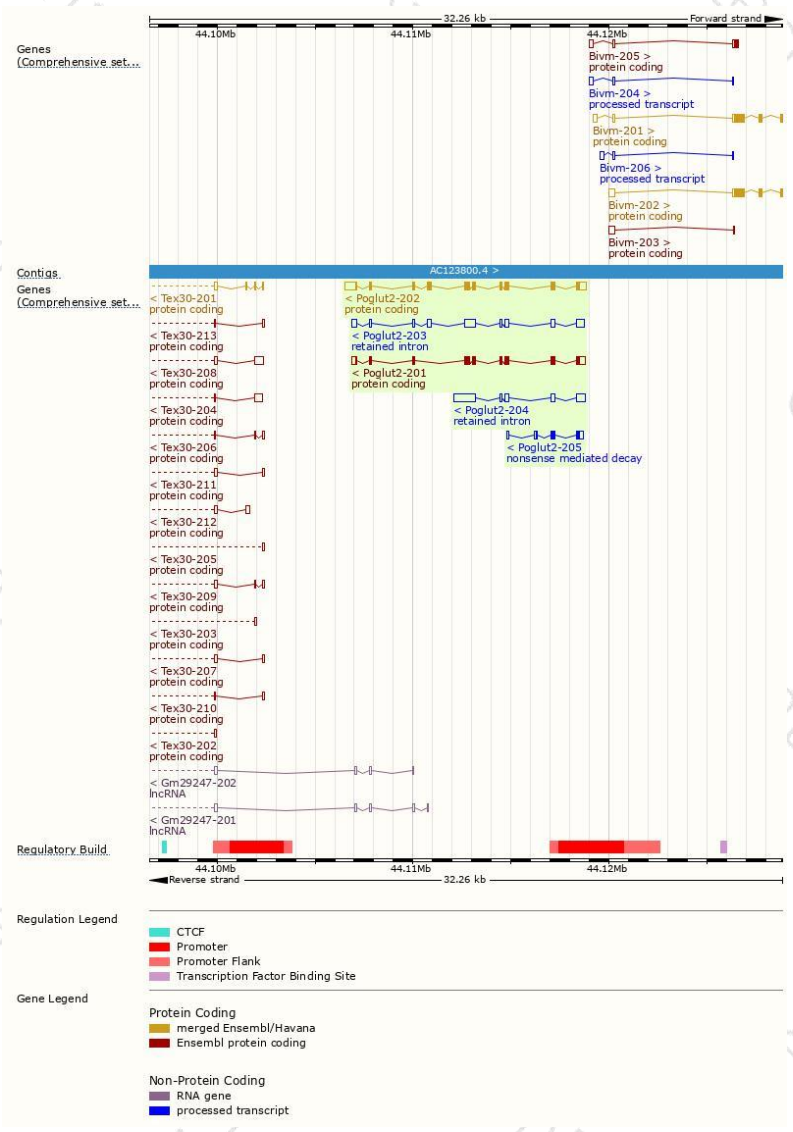
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Poglut2-202	ENSMUST00000065767.8	2359	502aa	Protein coding	CCDS14929	Q9JHP7	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 P1
Poglut2-201	ENSMUST00000027213.13	1765	432aa	Protein coding	-	Q9JHP7	TSL:1 GENCODE basic
Poglut2-205	ENSMUST00000152643.1	864	137aa	Nonsense mediated decay	-	D6RE32	TSL:3
Poglut2-203	ENSMUST00000141125.7	2085	No protein	Retained intron	-	-	TSL:1
Poglut2-204	ENSMUST00000149665.1	2031	No protein	Retained intron	-	-	TSL:1

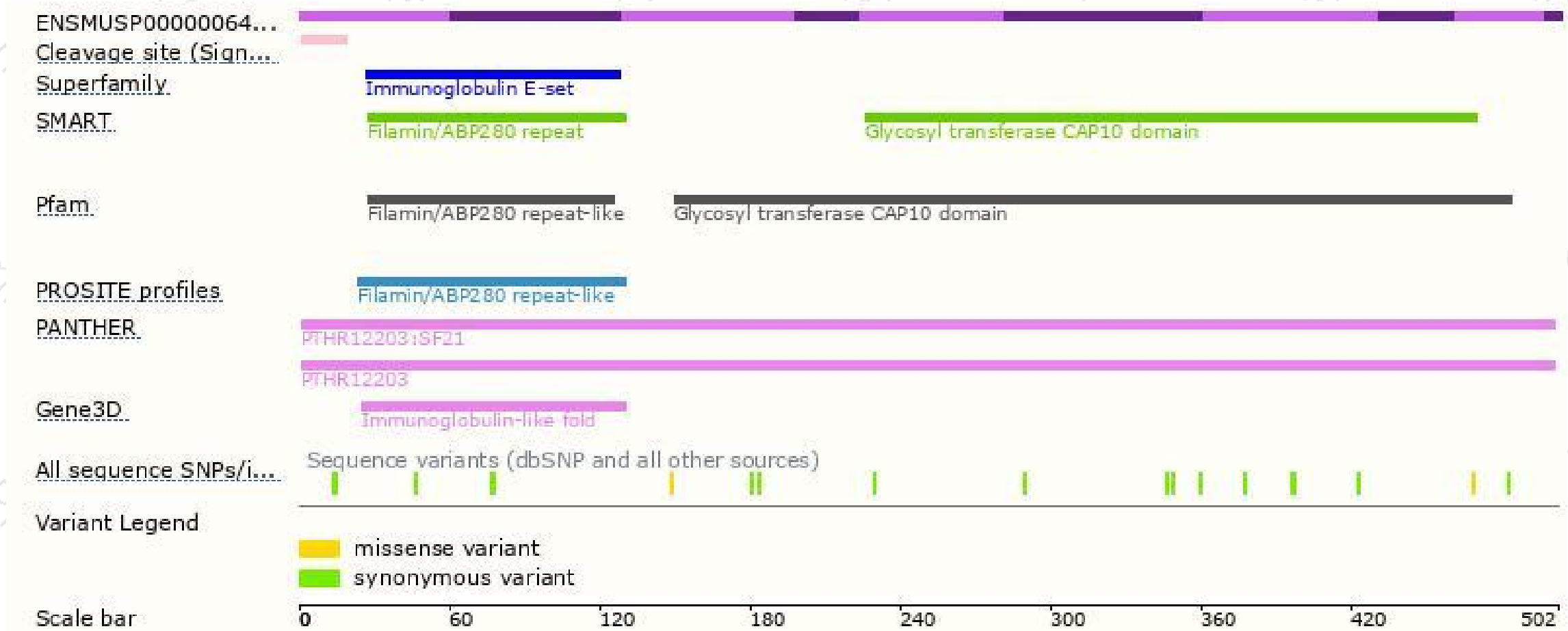
The strategy is based on the design of *Poglut2-202* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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