

Ano10 Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Ano10

Project type

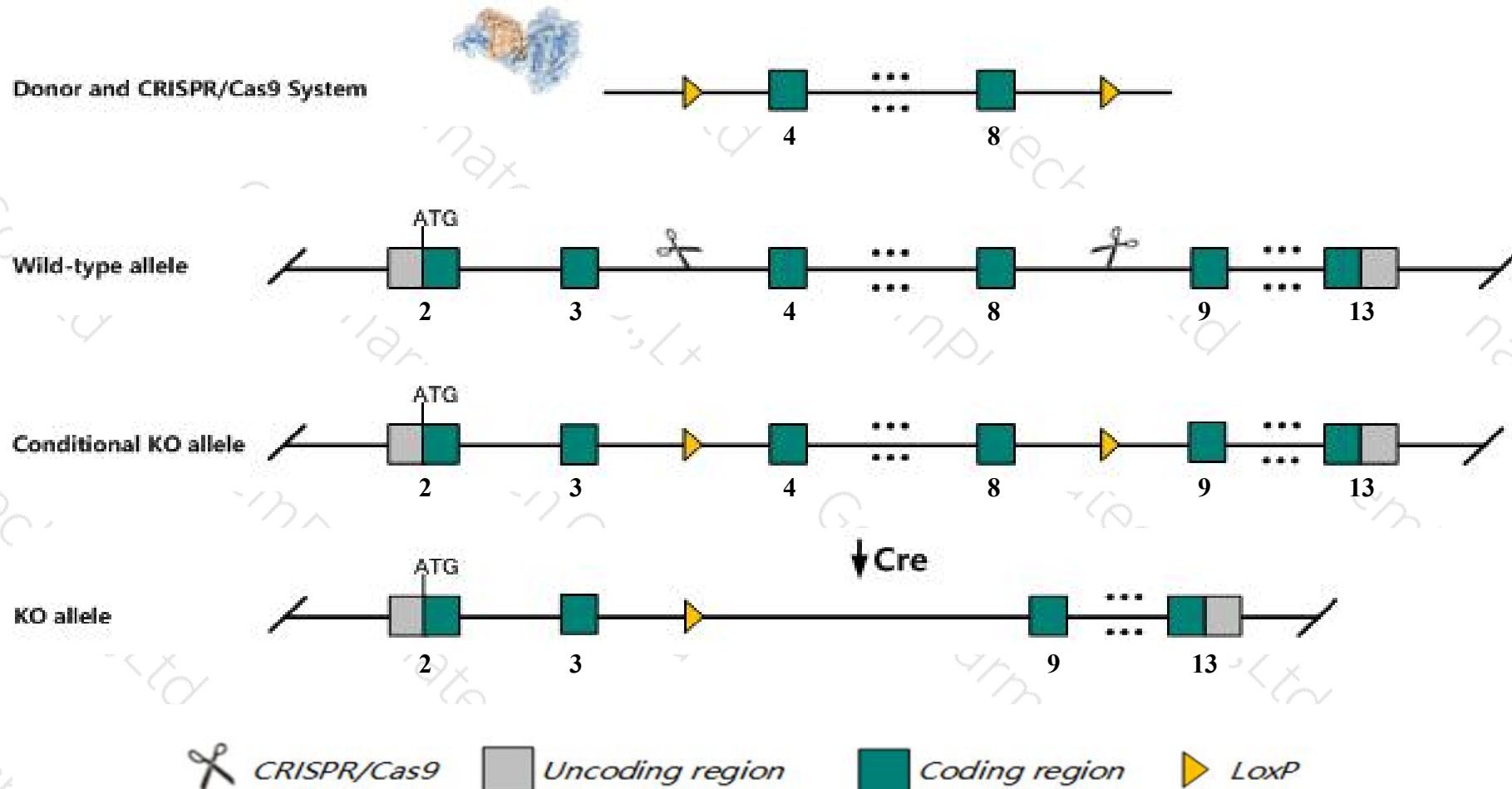
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ano10* gene. The schematic diagram is as follows:



Technical routes

- The *Ano10* gene has 8 transcripts. According to the structure of *Ano10* gene, exon4-exon8 of *Ano10-201* (ENSMUST00000042546.3) transcript is recommended as the knockout region. The region contains 956bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ano10* 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 knock-out allele fail to exhibit calcium-activated chloride ion secretion in the jejunum.
- Transcript 204,207 CDS 3' incomplete the influences is unknown.
- The *Ano10* gene is located on the Chr9. 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)

Ano10 anoctamin 10 [Mus musculus (house mouse)]

Gene ID: 102566, updated on 31-Jan-2019

Summary



Official Symbol Ano10 provided by [MGI](#)

Official Full Name anoctamin 10 provided by [MGI](#)

Primary source [MGI:MGI:2143103](#)

See related [Ensembl:ENSMUSG00000037949](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as AI604832, Tmem16k

Summary This gene encodes a member of the anoctamin family, which in mammals is comprised of 10 members. Anoctamin proteins are proposed to have eight transmembrane domains with both termini facing the cytoplasm and a C-terminal domain of unknown function. While some members have been characterized as calcium-activated chloride channels, this protein is reported to inhibit anion conductance. Alternative splicing results in multiple transcript variants that encode different protein isoforms. [provided by RefSeq, Dec 2012]

Expression Ubiquitous expression in genital fat pad adult (RPKM 24.2), subcutaneous fat pad adult (RPKM 23.2) and 28 other tissues [See more](#)

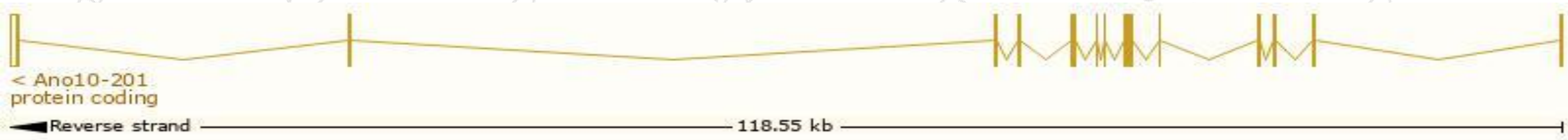
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

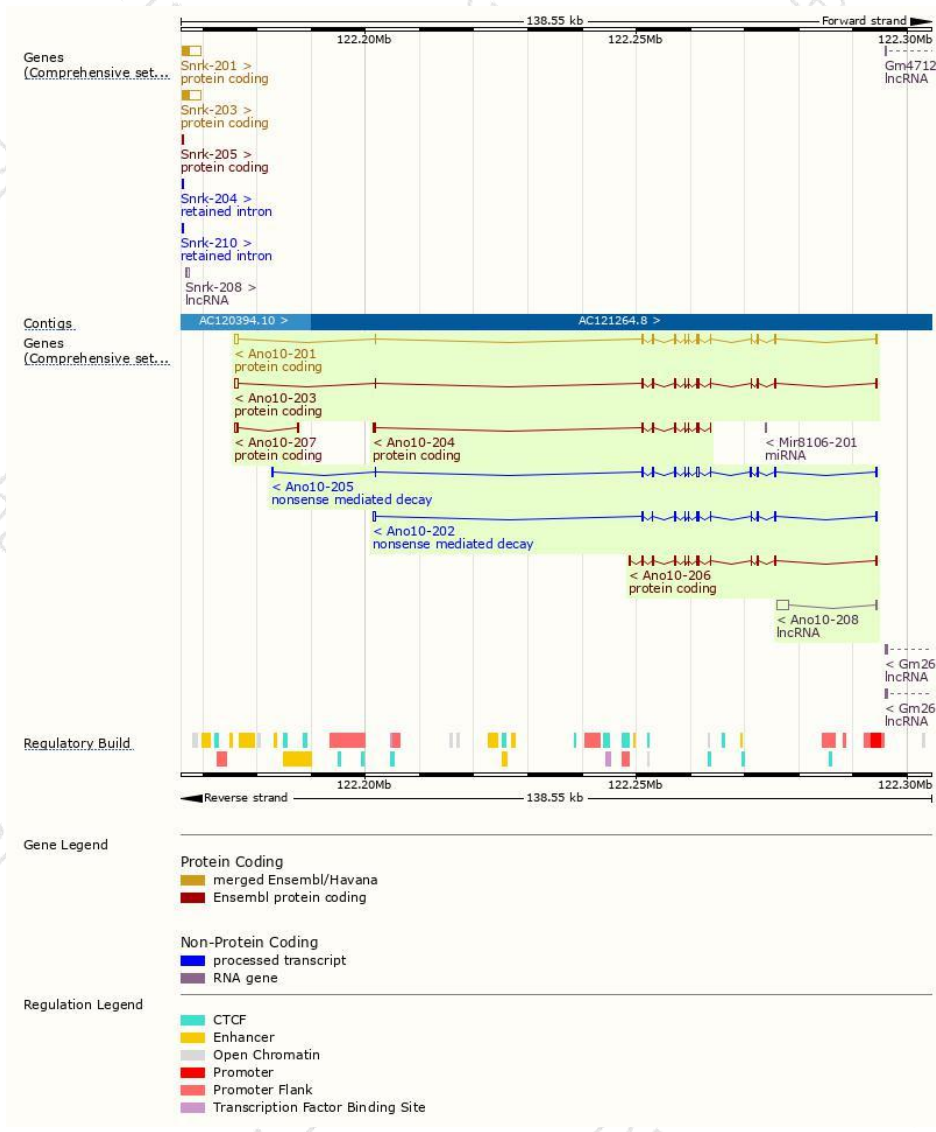
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ano10-201	ENSMUST00000042546.3	2653	659aa	Protein coding	CCDS23645	Q8BH79	TSL:1 GENCODE basic APPRIS P1
Ano10-203	ENSMUST00000214409.1	2384	601aa	Protein coding	-	Q8BH79	TSL:1 GENCODE basic
Ano10-206	ENSMUST00000216670.1	2108	612aa	Protein coding	-	Q8BH79	TSL:1 GENCODE basic
Ano10-204	ENSMUST00000214507.1	1770	478aa	Protein coding	-	A0A1L1SV36	CDS 5' incomplete TSL:1
Ano10-207	ENSMUST00000216738.1	680	100aa	Protein coding	-	A0A1L1SRJ0	CDS 5' incomplete TSL:2
Ano10-202	ENSMUST00000214283.1	2342	498aa	Nonsense mediated decay	-	A0A1L1SS60	TSL:1
Ano10-205	ENSMUST00000216081.1	2329	176aa	Nonsense mediated decay	-	A0A1L1SR14	TSL:2
Ano10-208	ENSMUST00000217606.1	2280	No protein	lncRNA	-	-	TSL:2

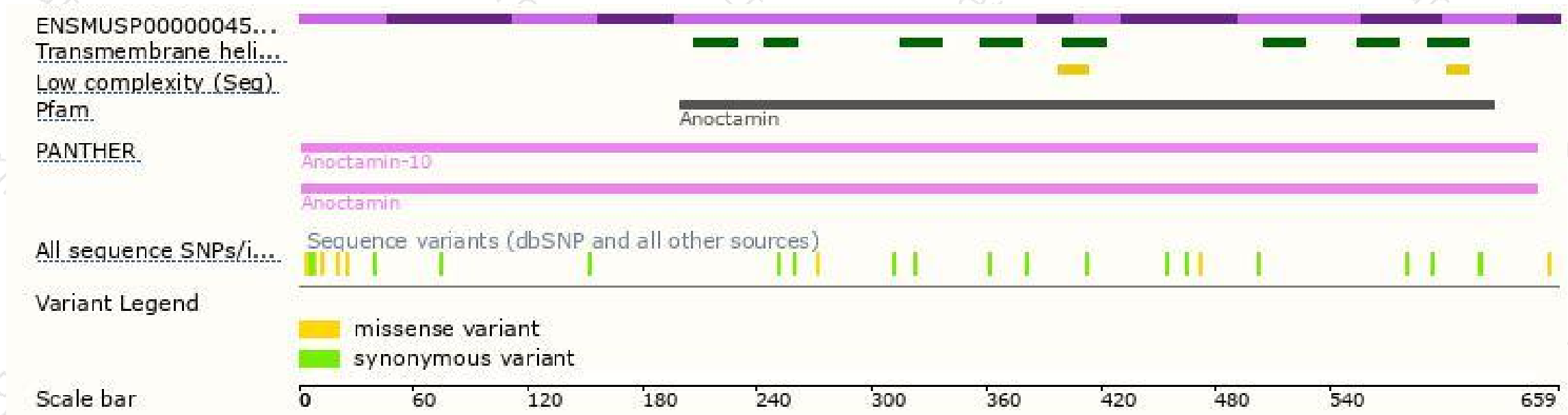
The strategy is based on the design of *Ano10-201* transcript,The transcription is shown below



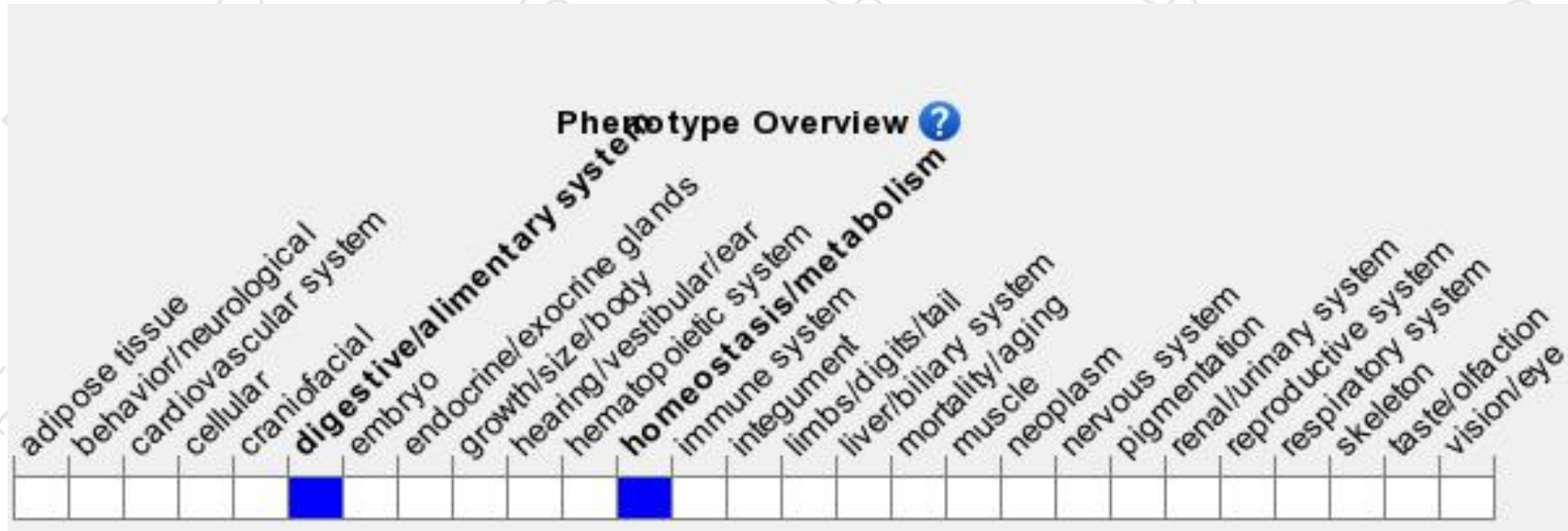
Genomic location distribution



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 knock-out allele fail to exhibit calcium-activated chloride ion secretion in the jejunum.

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

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