

Cxadr Cas9-CKO Strategy

Designer:

JiaYu

Reviewer:

Xiaojing Li

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Project Overview

Project Name

Cxadr

Project type

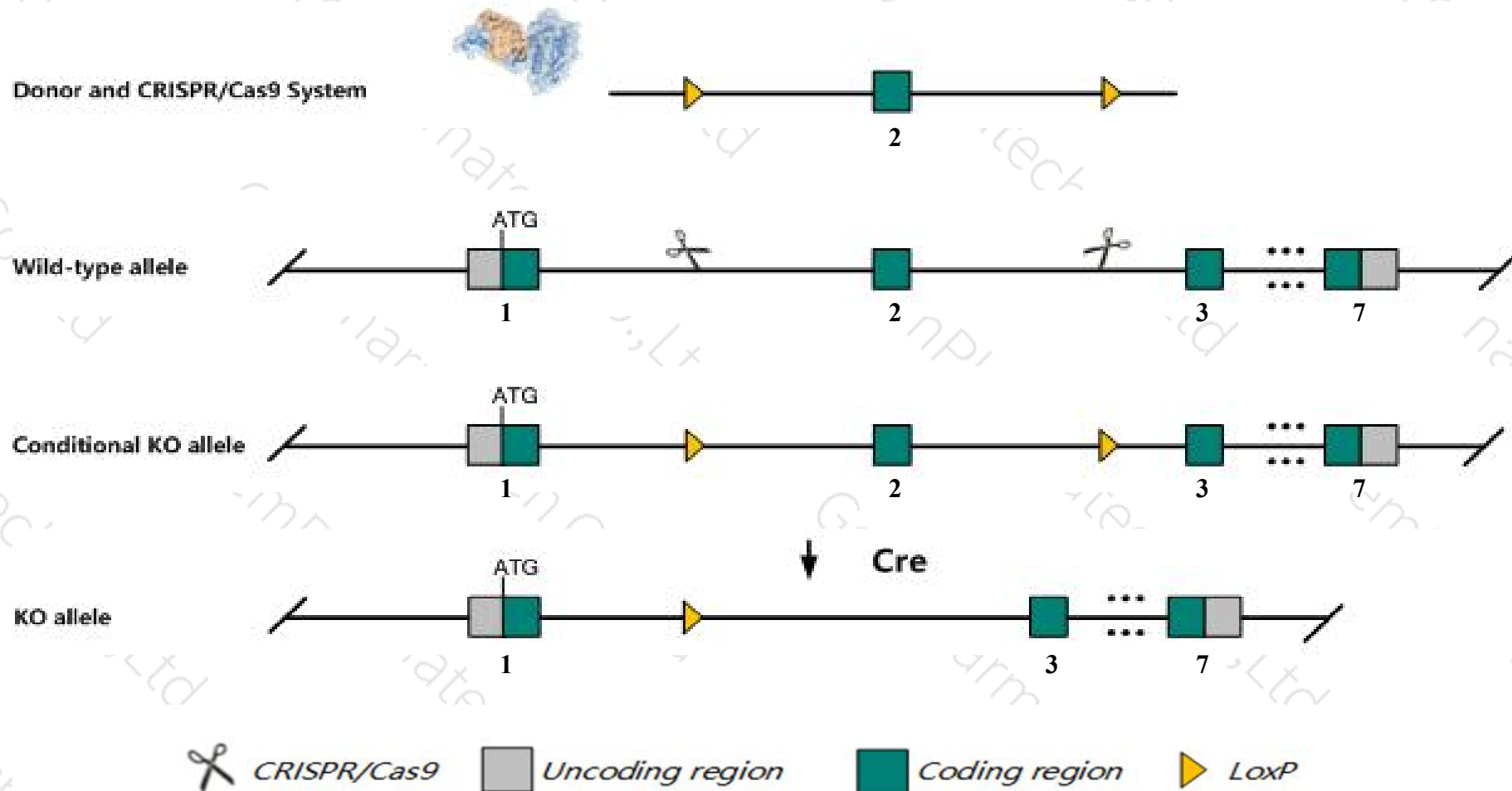
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Cxadr* gene has 6 transcripts. According to the structure of *Cxadr* gene, exon2 of *Cxadr-201* (ENSMUST00000023572.14) transcript is recommended as the knockout region. The region contains 167bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cxadr* 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, Homozygous null mice display embryonic lethality with focal cardiomyocyte apoptosis and extensive thoracic hemorrhaging.
- The *Cxadr* gene is located on the Chr16. 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)

Cxadr coxsackie virus and adenovirus receptor [Mus musculus (house mouse)]

Gene ID: 13052, updated on 19-Feb-2019

Summary



Official Symbol	Cxadr provided by MGI
Official Full Name	coxsackie virus and adenovirus receptor provided by MGI
Primary source	MGI:MGI:1201679
See related	Ensembl:ENSMUSG00000022865
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	2610206D03Rik, AU016810, AW553441, CAR, MCAR, MCVADR
Summary	This gene encodes a protein that is part of the Cortical Thymocyte marker in Xenopus (CTX) subfamily within the immunoglobulin superfamily. Members of this subfamily, predominantly expressed on the surface of endothelial and epithelial cells, help establish cell polarity and provide a barrier function, regulating migration of immune cells. This protein, first identified as the receptor for adenovirus subgroup C and coxsackieviruses group B, is developmentally regulated and plays an important role in cardiac development. Alternative splicing results in multiple transcript variants that encode different protein isoforms. [provided by RefSeq, Jan 2013]
Expression	Broad expression in CNS E18 (RPKM 24.6), whole brain E14.5 (RPKM 17.4) and 23 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

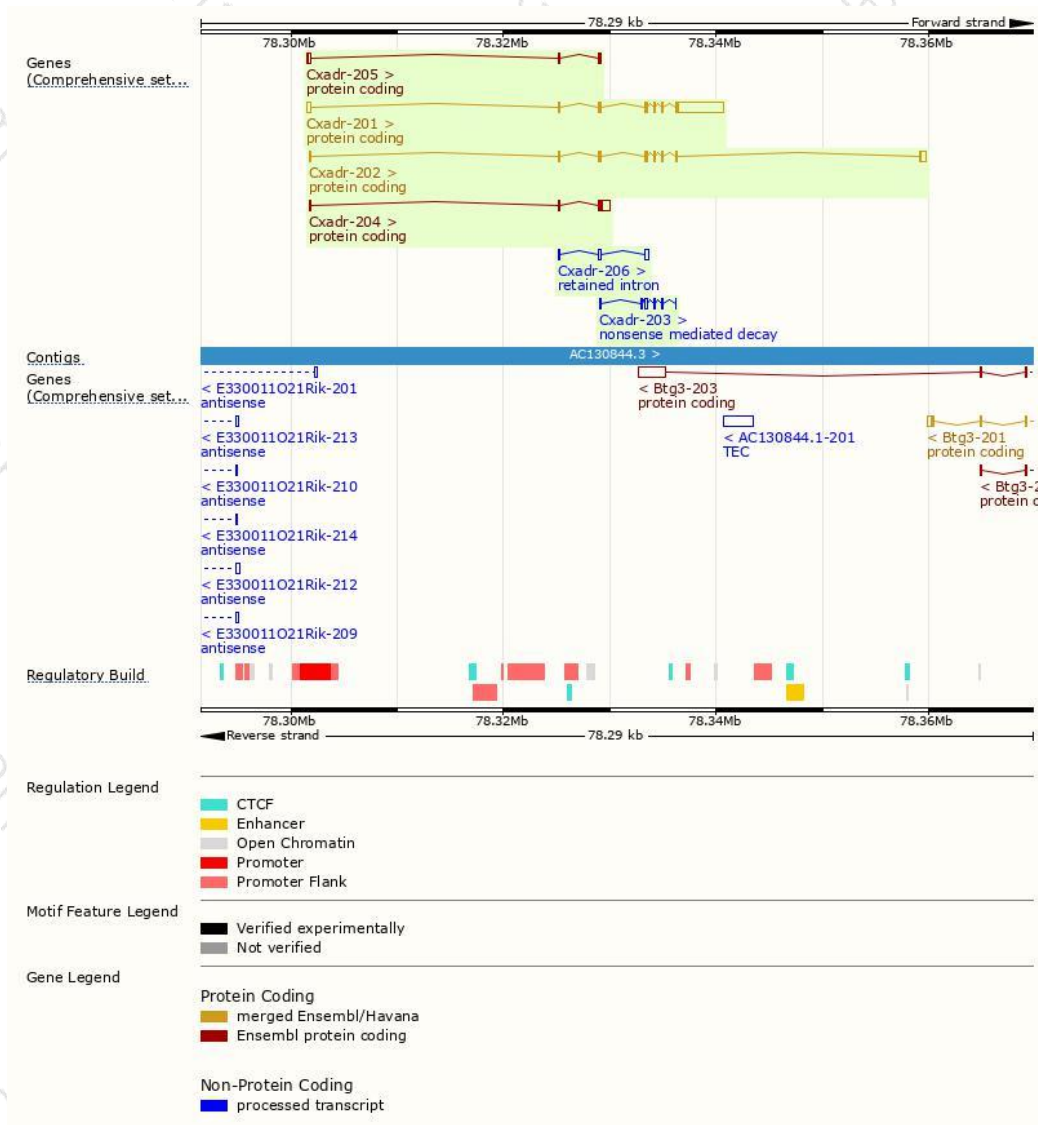
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cxadr-201	ENSMUST00000023572.14	5742	365aa	Protein coding	CCDS28276	P97792	TSL:1 GENCODE basic APPRIS P3
Cxadr-202	ENSMUST00000114229.3	1657	352aa	Protein coding	CCDS37379	P97792	TSL:1 GENCODE basic APPRIS ALT2
Cxadr-204	ENSMUST00000231356.1	1298	164aa	Protein coding	-	P97792	GENCODE basic
Cxadr-205	ENSMUST00000232148.1	650	136aa	Protein coding	-	A0A338P6N1	CDS 3' incomplete
Cxadr-203	ENSMUST00000231251.1	688	52aa	Nonsense mediated decay	-	A0A338P6U1	CDS 5' incomplete
Cxadr-206	ENSMUST00000232189.1	678	No protein	Retained intron	-	-	

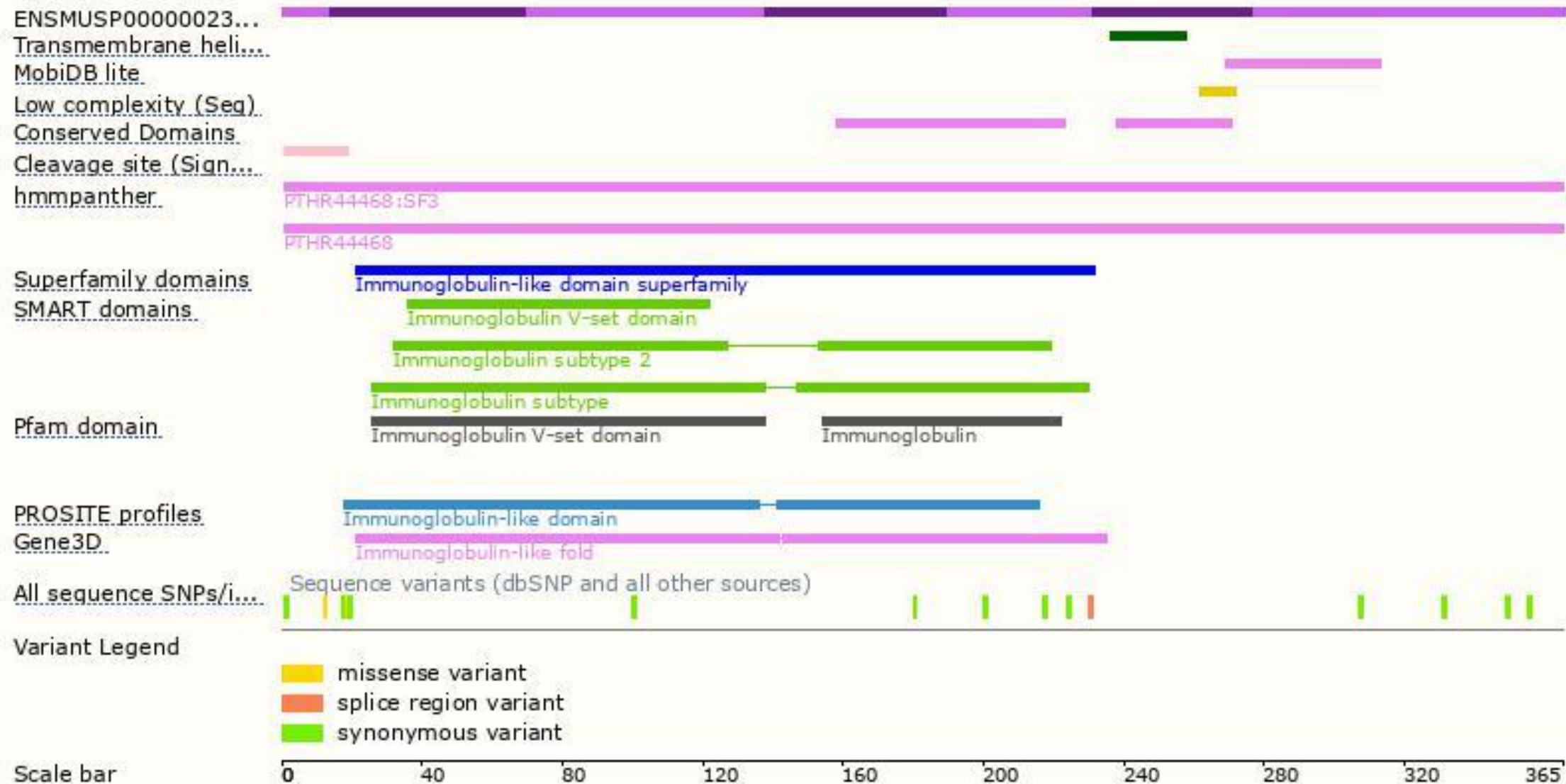
The strategy is based on the design of *Cxadr-201* transcript,The transcription is shown below



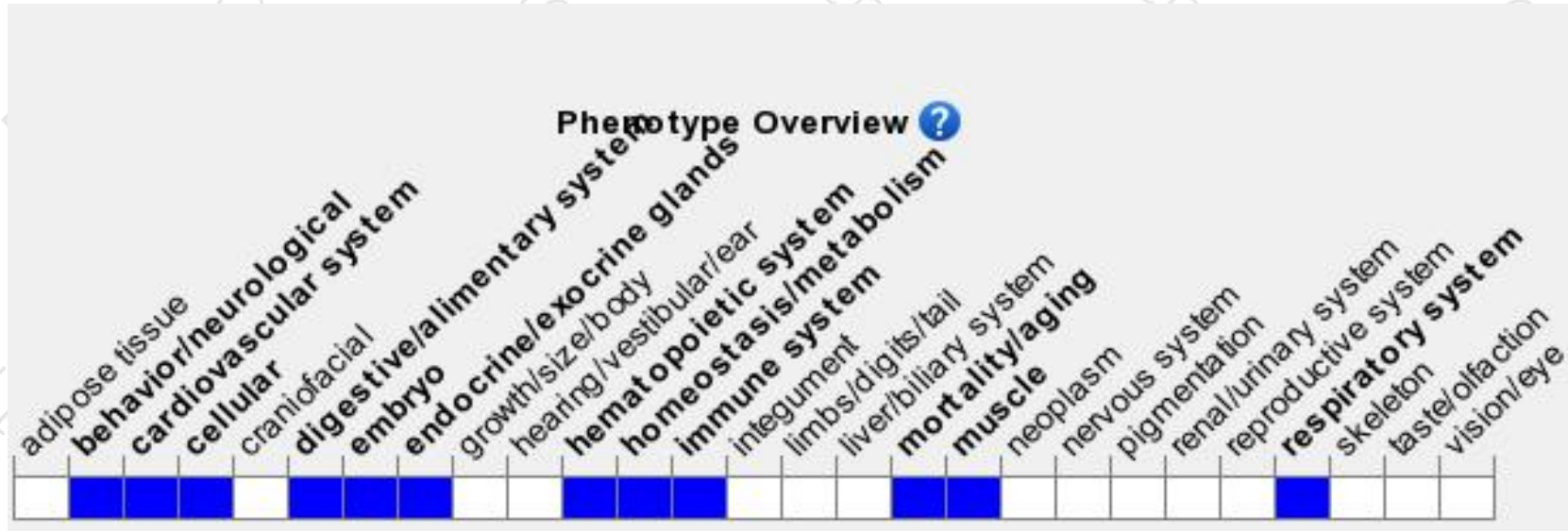
Genomic location distribution



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, Homozygous null mice display embryonic lethality with focal cardiomyocyte apoptosis and extensive thoracic hemorrhaging.

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

Tel: 400-9660890

