

Tiam1 Cas9-CKO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

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Project Overview

Project Name

Tiam1

Project type

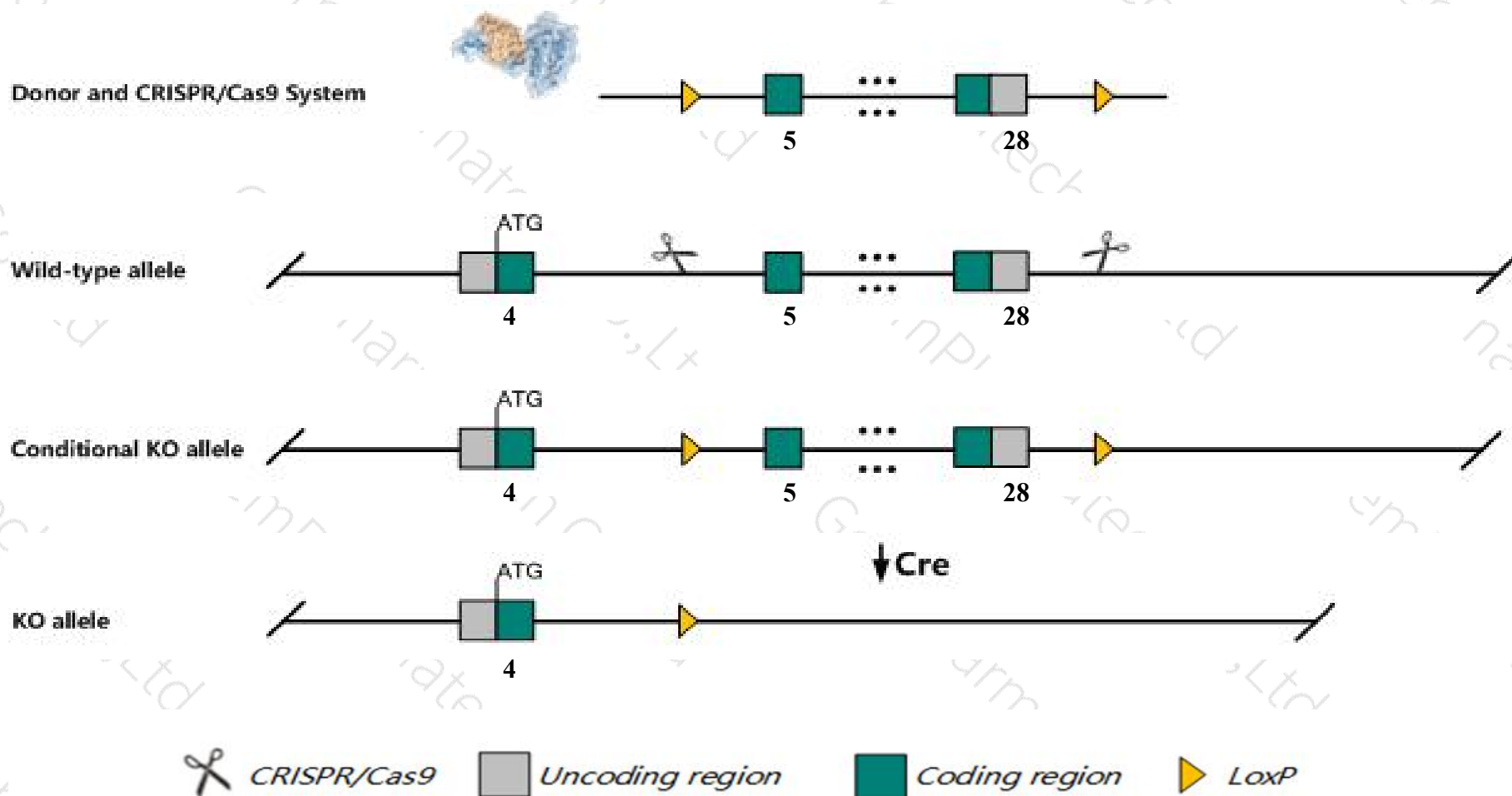
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tiam1* gene. The schematic diagram is as follows:



- The *Tiam1* gene has 15 transcripts. According to the structure of *Tiam1* gene, exon5-exon28 of *Tiam1*-201 (ENSMUST00000002588.10) transcript is recommended as the knockout region. The region contains most 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 *Tiam1* 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 targeted null allele display resistance to chemically-induced tumors, however, tumors that do develop progress to malignancy. Mice homozygous for a gene trap allele display anencephaly, exencephaly and/or neural tube defects.
- The *Tiam1* 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)

Tiam1 T cell lymphoma invasion and metastasis 1 [Mus musculus (house mouse)]

Gene ID: 21844, updated on 31-Jan-2019

Summary



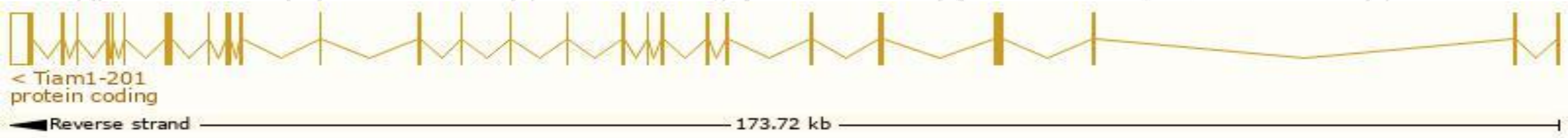
Official Symbol	Tiam1 provided by MGI
Official Full Name	T cell lymphoma invasion and metastasis 1 provided by MGI
Primary source	MGI:MGI:103306
See related	Ensembl:ENSMUSG000000002489
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI847750, D16lum10, D16lum10e
Expression	Broad expression in cerebellum adult (RPKM 9.6), frontal lobe adult (RPKM 5.9) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

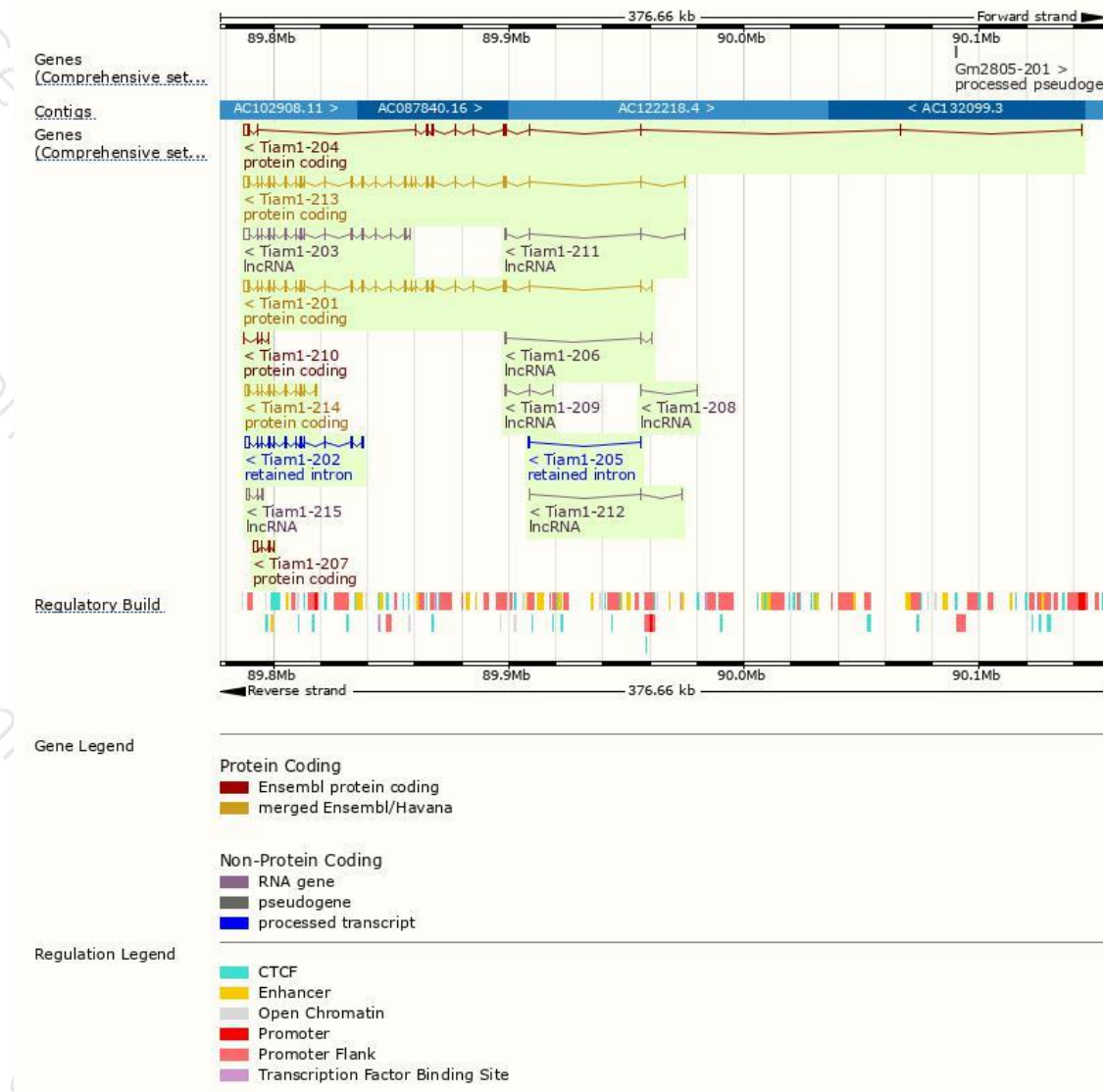
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tiam1-201	ENSMUST0000002588.10	7289	1591aa	Protein coding	CCDS28314	G3UWG2	TSL:1 GENCODE basic APPRIS P1
Tiam1-213	ENSMUST00000163370.7	7255	1591aa	Protein coding	CCDS28314	G3UWG2	TSL:1 GENCODE basic APPRIS P1
Tiam1-214	ENSMUST00000164263.8	3569	622aa	Protein coding	CCDS49904	E9Q1R7	TSL:1 GENCODE basic
Tiam1-204	ENSMUST00000114124.8	5203	900aa	Protein coding	-	Q6P1D6	TSL:5 GENCODE basic
Tiam1-207	ENSMUST00000134021.1	1770	168aa	Protein coding	-	J3QQ55	CDS 5' incomplete TSL:1
Tiam1-210	ENSMUST00000144691.8	321	92aa	Protein coding	-	J3QMH1	CDS 5' incomplete TSL:5
Tiam1-202	ENSMUST00000089084.11	3495	No protein	Retained intron	-	-	TSL:1
Tiam1-205	ENSMUST00000124433.7	667	No protein	Retained intron	-	-	TSL:1
Tiam1-203	ENSMUST00000114122.7	4596	No protein	lncRNA	-	-	TSL:1
Tiam1-215	ENSMUST00000178095.1	1465	No protein	lncRNA	-	-	TSL:1
Tiam1-211	ENSMUST00000151655.7	726	No protein	lncRNA	-	-	TSL:2
Tiam1-209	ENSMUST00000139544.1	503	No protein	lncRNA	-	-	TSL:3
Tiam1-206	ENSMUST00000130951.7	461	No protein	lncRNA	-	-	TSL:2
Tiam1-212	ENSMUST00000155915.1	446	No protein	lncRNA	-	-	TSL:2
Tiam1-208	ENSMUST00000136760.1	241	No protein	lncRNA	-	-	TSL:5

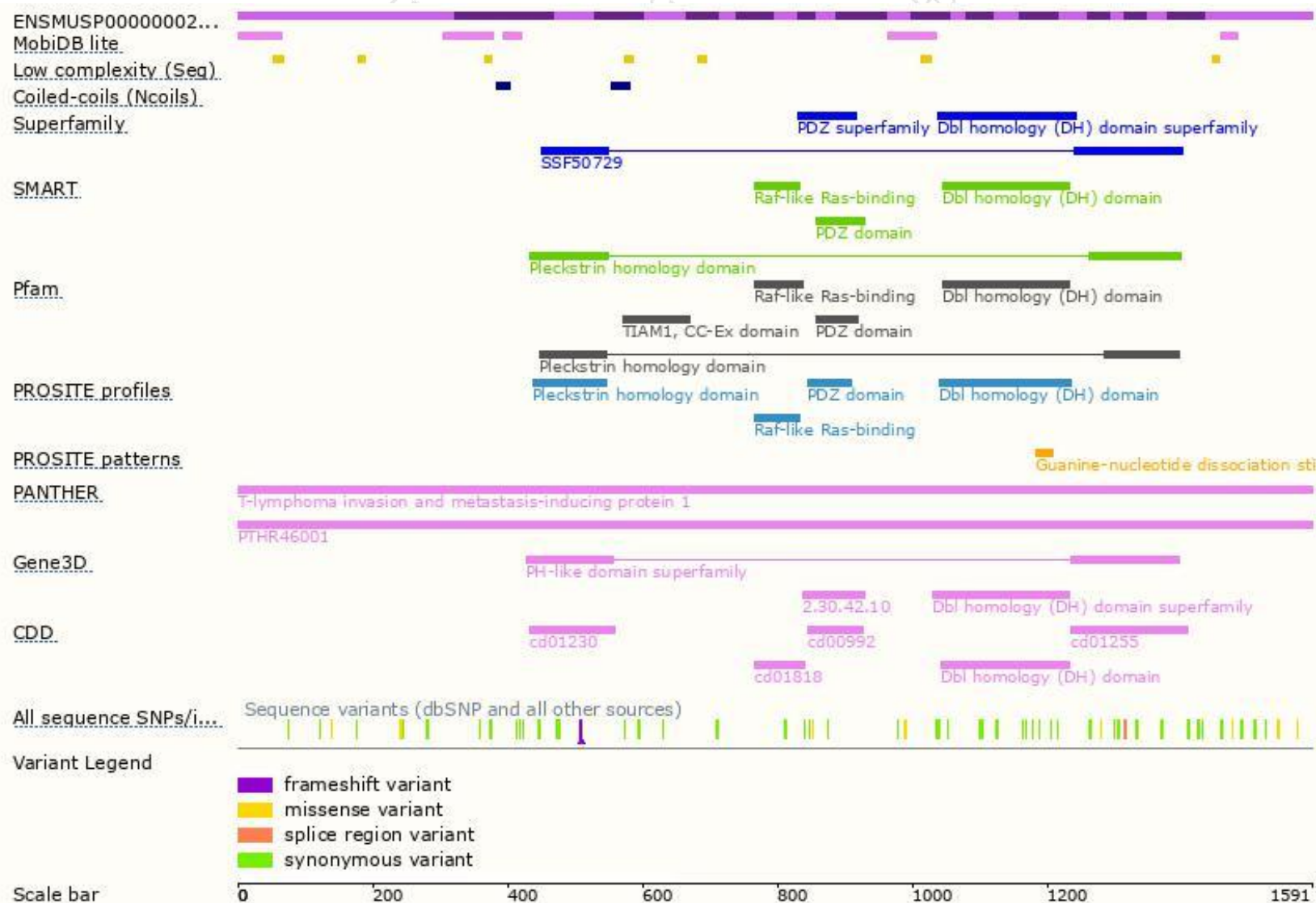
The strategy is based on the design of *Tiam1-201* transcript,The transcription is shown below



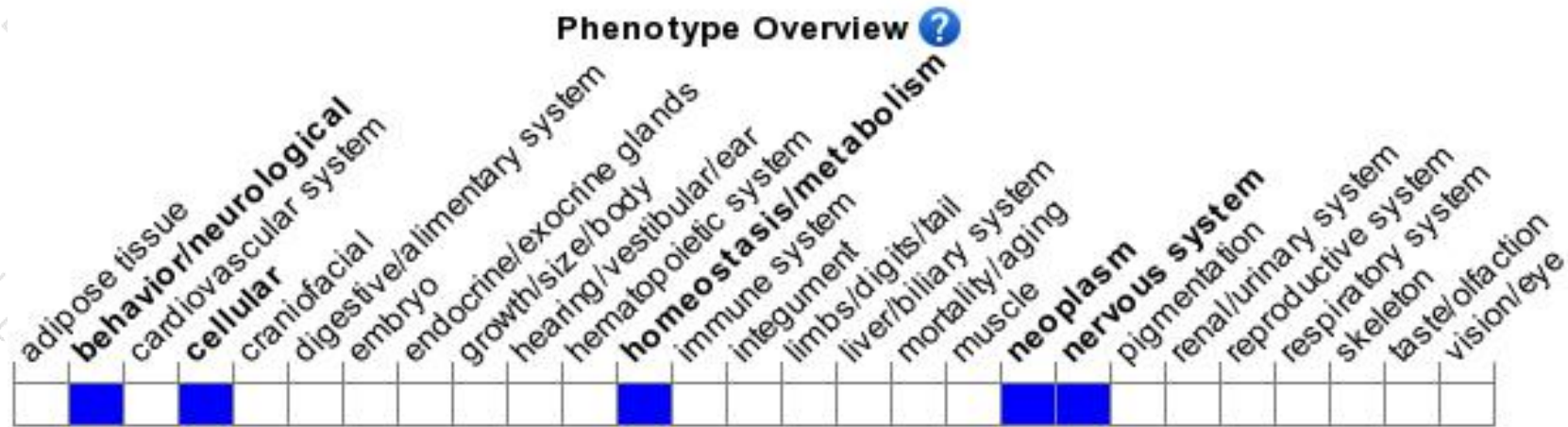
Genomic location distribution



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 targeted null allele display resistance to chemically-induced tumors, however, tumors that do develop progress to malignancy. Mice homozygous for a gene trap allele anencephaly, exencephaly and/or neural tube defects.

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

Tel: 400-9660890

