

Atp2a2 Cas9-CKO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

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Project Overview

Project Name

Atp2a2

Project type

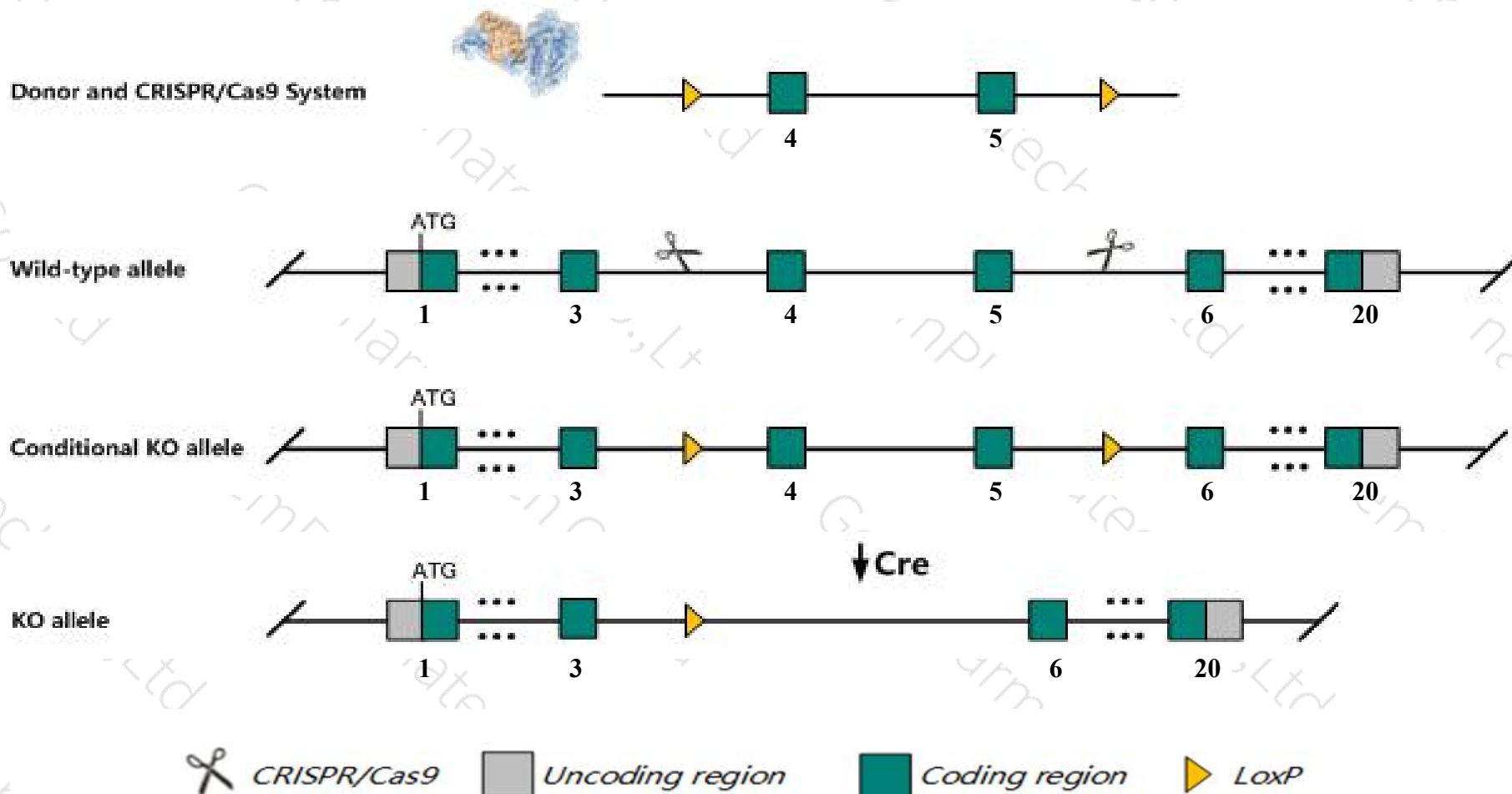
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp2a2* gene. The schematic diagram is as follows:



Technical routes

- The *Atp2a2* gene has 5 transcripts. According to the structure of *Atp2a2* gene, exon4-exon5 of *Atp2a2-201* (ENSMUST00000031423.9) transcript is recommended as the knockout region. The region contains 244bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp2a2* 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, Targeted homozygous mutants are embryonic lethal while heterozygotes show reduced blood pressure and mildly impaired cardiac contractility and relaxation. Aged heterozygotes for one targeted mutation develop squamous cell tumors of the forestomach, esophagus, oral mucosa, tongue, and skin.
- The KO region contains functional region of the *Gm43360* gene. Knockout the region may affect the function of *Gm43360* gene.
- The *Atp2a2* gene is located on the Chr5. 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)

Atp2a2 ATPase, Ca⁺⁺ transporting, cardiac muscle, slow twitch 2 [Mus musculus (house mouse)]

Gene ID: 11938, updated on 7-Apr-2019

Summary



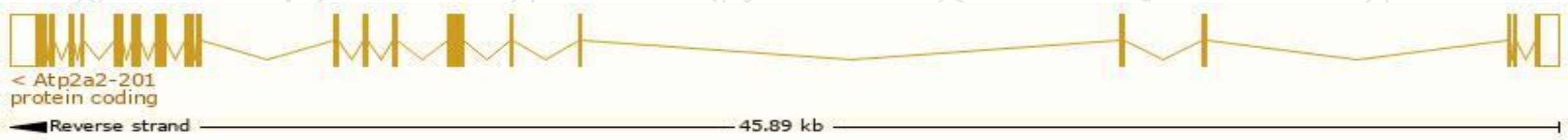
Official Symbol	Atp2a2 provided by MGI
Official Full Name	ATPase, Ca ⁺⁺ transporting, cardiac muscle, slow twitch 2 provided by MGI
Primary source	MGI:MGI:88110
See related	Ensembl:ENSMUSG00000029467
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9530097L16Rik, D5Wsu150e, SERCA2, SERCA2B, Serca2a, mKIAA4195
Expression	Biased expression in heart adult (RPKM 1140.8), bladder adult (RPKM 124.3) and 3 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

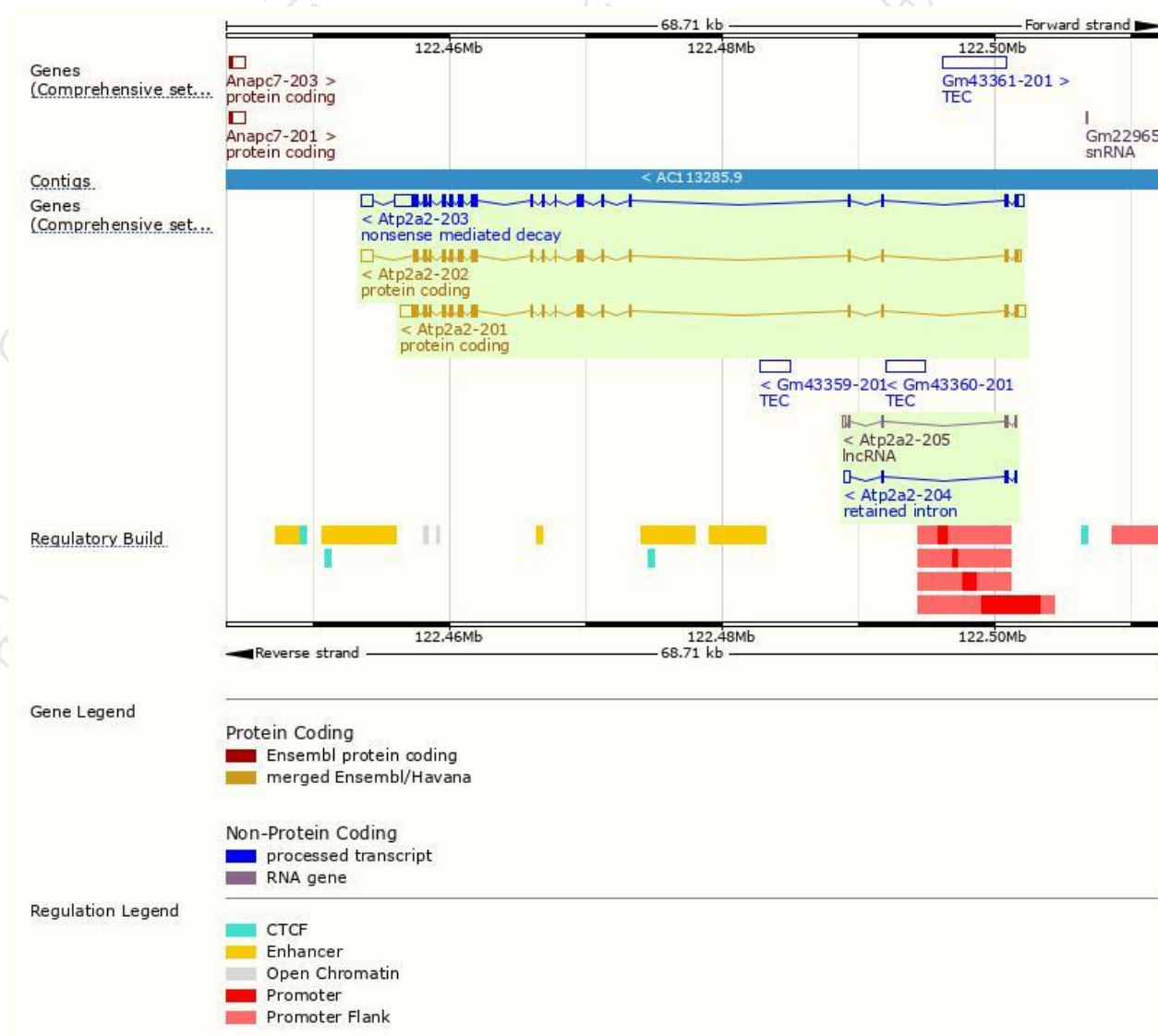
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp2a2-201	ENSMUST00000031423.9	4486	1044aa	Protein coding	CCDS57378	O55143	TSL:1 GENCODE basic APPRIS P4
Atp2a2-202	ENSMUST00000177974.7	3984	998aa	Protein coding	CCDS57379	O55143	TSL:1 GENCODE basic APPRIS ALT 1
Atp2a2-203	ENSMUST00000179939.7	5674	1044aa	Nonsense mediated decay	-	O55143	TSL:1
Atp2a2-205	ENSMUST00000197415.4	615	No protein	Processed transcript	-	-	TSL:3
Atp2a2-204	ENSMUST00000196490.1	698	No protein	Retained intron	-	-	TSL:2

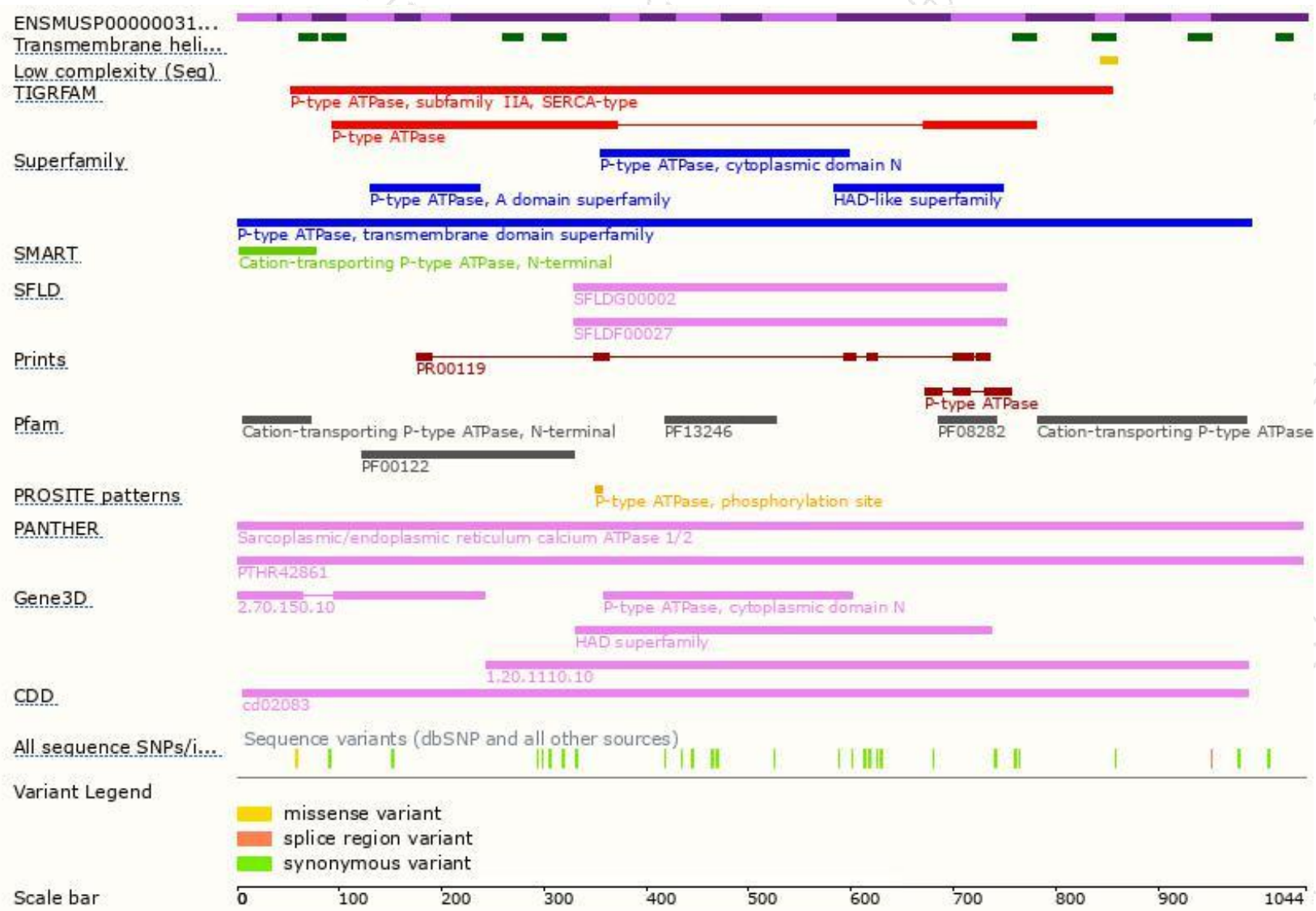
The strategy is based on the design of *Atp2a2-201* transcript,The transcription is shown below



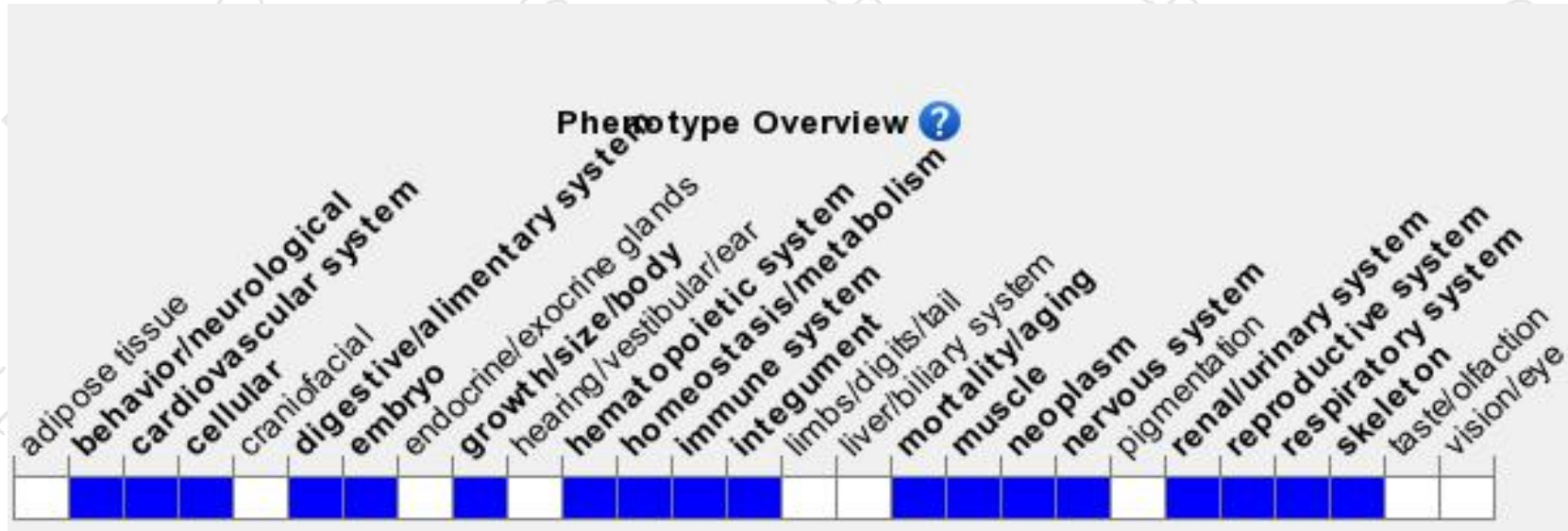
Genomic location distribution



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/>).

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

Tel: 400-9660890

