

# *Senp1* Cas9-KO Strategy

**Designer:**

**Baocheng Zhuang**

**Reviewer:**

**Yang Zeng**

**Design Date:**

**2018-6-8**

# Project Overview

**Project Name**

*Senp1*

**Project type**

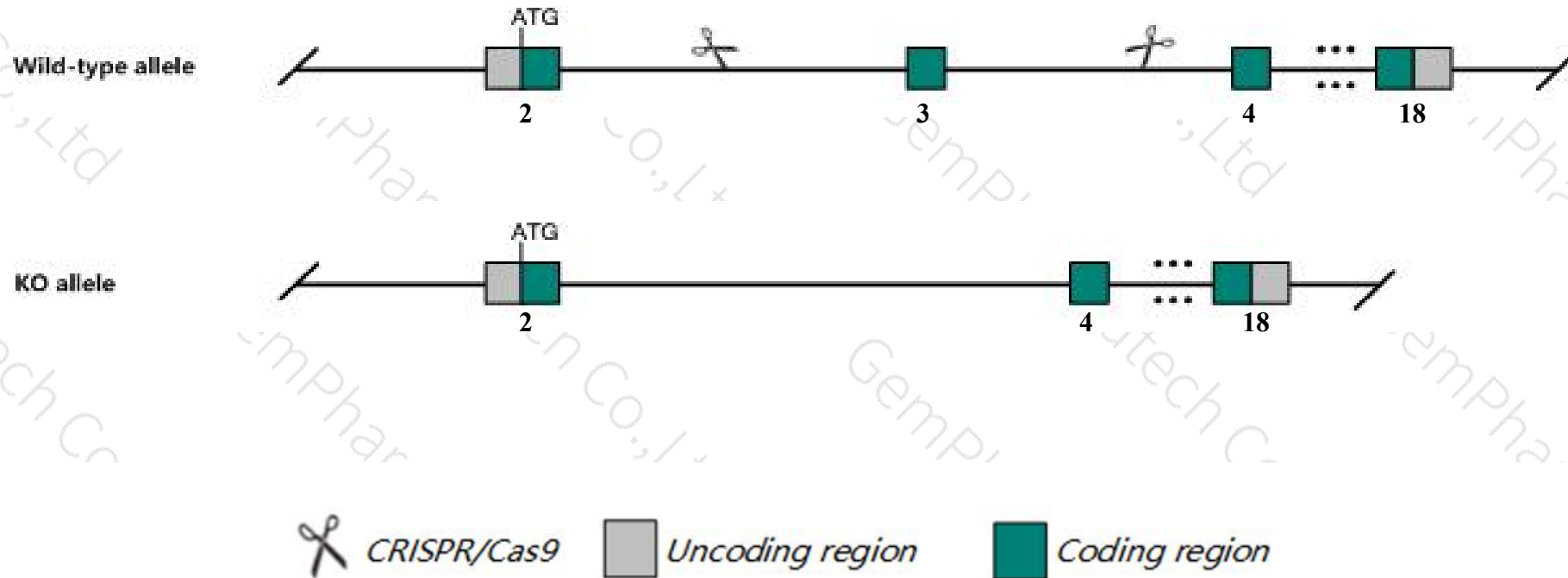
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Senp1* gene. The schematic diagram is as follows:



- The *Senp1* gene has 9 transcripts. According to the structure of *Senp1* gene, exon3 of *Senp1-201* (ENSMUST00000044189.15) transcript is recommended as the knockout region. The region contains 131bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Senp1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutant mice die before birth. Depending on the allele mice may exhibit placental labyrinth defects and widespread cell death or severe anemia and a defect in definitive erythropoiesis in the fetal liver.
- Transcript *Senp1*-202/203/207/208 may not be affected.
- The *Senp1* gene is located on the Chr15. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Senp1 SUMO1/sentrin specific peptidase 1 [ *Mus musculus* (house mouse) ]

Gene ID: 223870, updated on 21-Aug-2019

### Summary

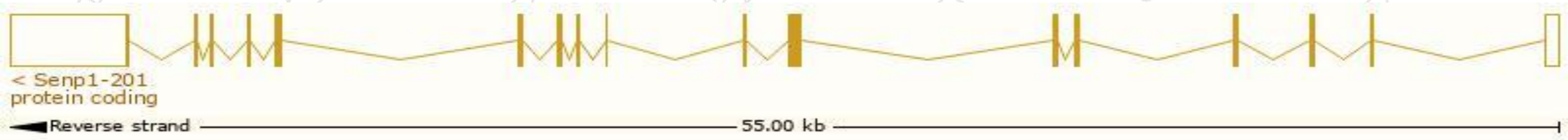
<b>Official Symbol</b>	Senp1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	SUMO1/sentrin specific peptidase 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2445054</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000033075</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	suPr-2; D15Ert528e; 2310046A20Rik; E330036L07Rik
<b>Expression</b>	Ubiquitous expression in testis adult (RPKM 9.4), thymus adult (RPKM 9.2) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

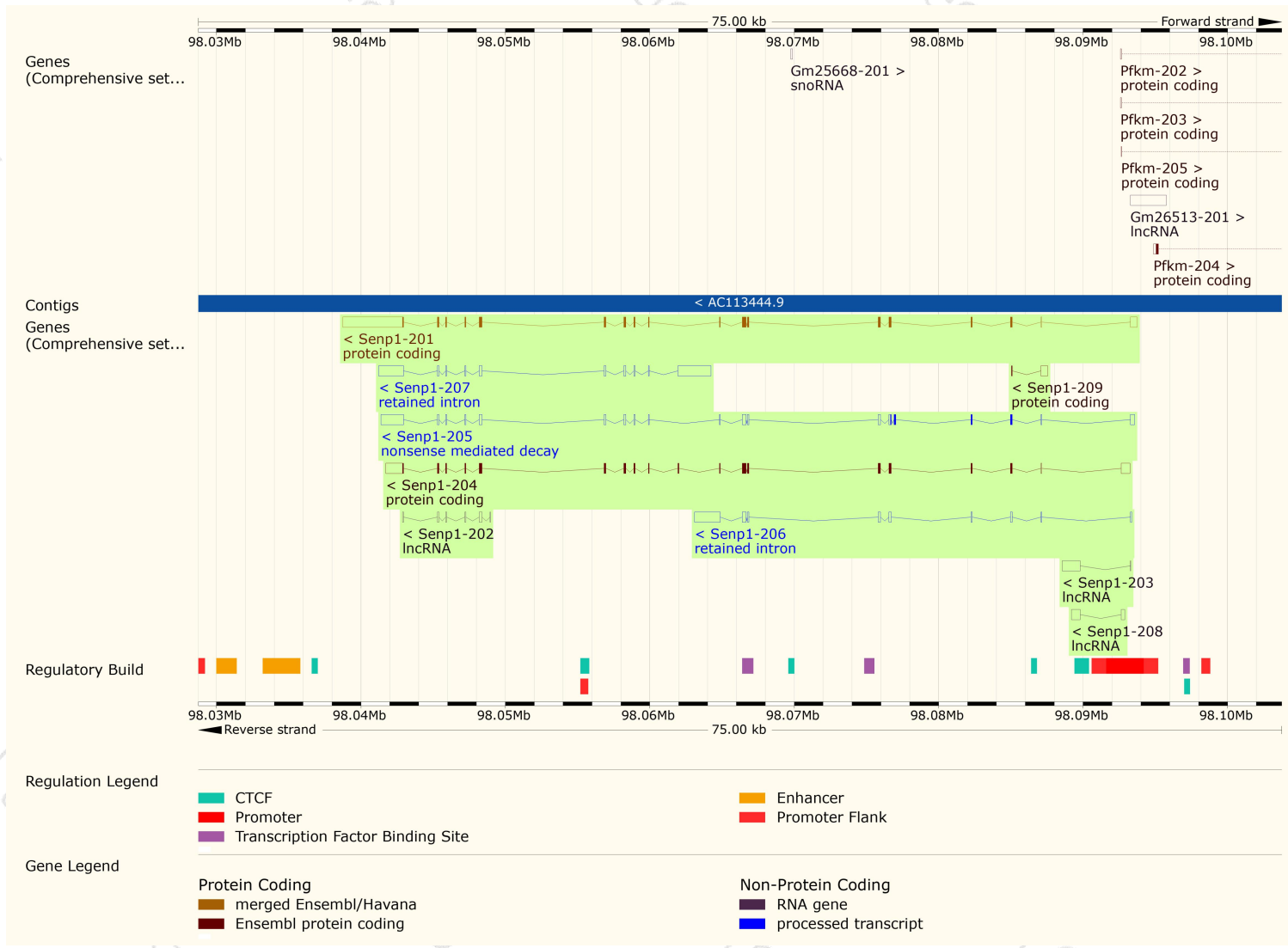
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Senp1-201	<a href="#">ENSMUST00000044189.15</a>	6575	<a href="#">640aa</a>	Protein coding	<a href="#">CCDS49717</a>	<a href="#">P59110</a>	TSL:1 GENCODE basic APPRIS P2
Senp1-204	<a href="#">ENSMUST00000180657.1</a>	3806	<a href="#">666aa</a>	Protein coding	-	<a href="#">M0QWX4</a>	TSL:1 GENCODE basic APPRIS ALT2
Senp1-209	<a href="#">ENSMUST00000183105.1</a>	518	<a href="#">21aa</a>	Protein coding	-	<a href="#">S4R1V9</a>	CDS 3' incomplete TSL:3
Senp1-205	<a href="#">ENSMUST00000180716.7</a>	3882	<a href="#">130aa</a>	Nonsense mediated decay	-	<a href="#">M0QWV7</a>	TSL:5
Senp1-203	<a href="#">ENSMUST00000180531.1</a>	1270	No protein	Processed transcript	-	-	TSL:1
Senp1-208	<a href="#">ENSMUST00000182611.1</a>	853	No protein	Processed transcript	-	-	TSL:3
Senp1-202	<a href="#">ENSMUST00000180461.1</a>	568	No protein	Processed transcript	-	-	TSL:3
Senp1-207	<a href="#">ENSMUST00000181855.7</a>	4886	No protein	Retained intron	-	-	TSL:2
Senp1-206	<a href="#">ENSMUST00000181349.1</a>	2830	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Senp1-201* transcript,The transcription is shown below

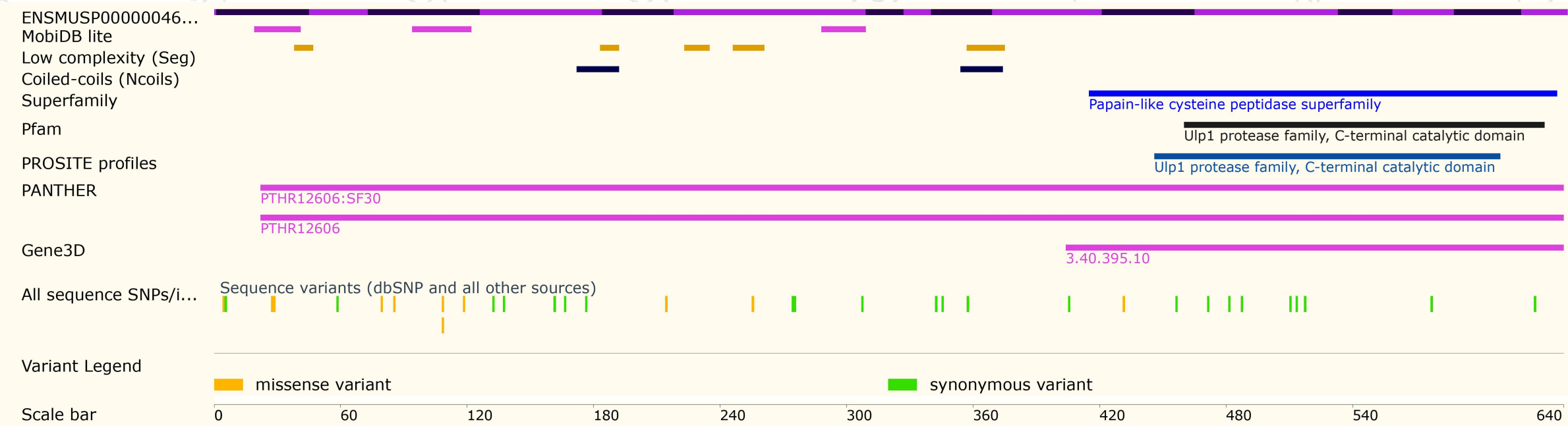


# Genomic location distribution

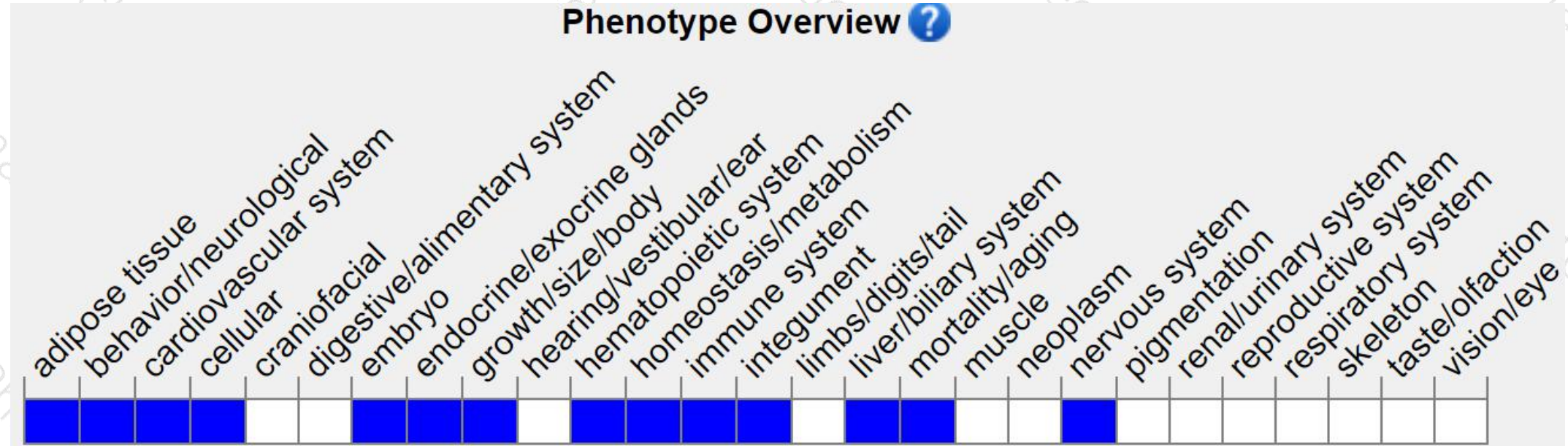




# Protein domain



# 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 mutant mice die before birth. Depending on the allele mice may exhibit placental labyrinth defects and widespread cell death or severe anemia and a defect in definitive erythropoiesis in the fetal liver.

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

Tel: 400-9660890

