Prmt2 Cas9-KO Strategy

Designer: Longyun Hu
Reviewer: Yun Li
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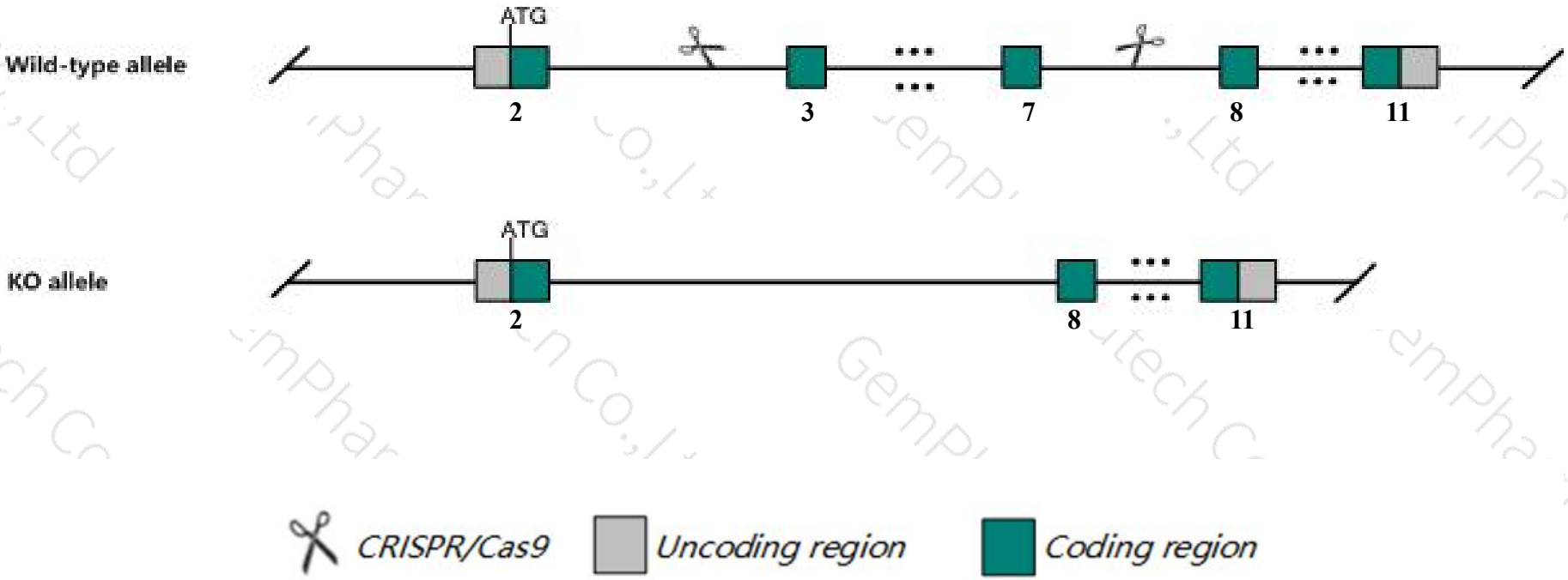
Project Overview

Project Name	***Prmt2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prmt2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Prmt2* gene has 9 transcripts. According to the structure of *Prmt2* gene, exon3-exon7 of *Prmt2-203* (ENSMUST00000099572.9) transcript is recommended as the knockout region.The region contains 812bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Prmt2* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele display a hyperplastic response to vascular injury while mutant mouse embryonic fibroblasts show an earlier S phase entry following release of serum starvation.

- The *Prmt2* gene is located on the Chr10. 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）

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Prmt2 protein arginine N-methyltransferase 2 [Mus musculus (house mouse)]

Gene ID: 15468, updated on 31-Jan-2019

Summary

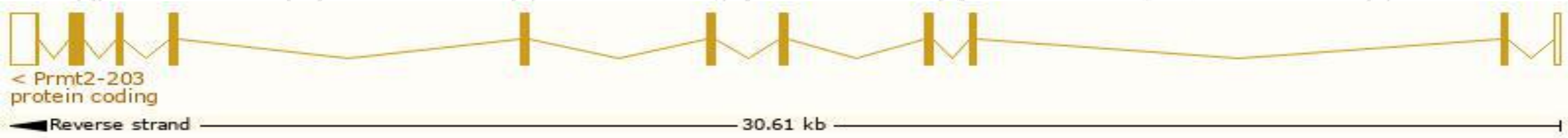
Official Symbol	Prmt2 provided by MGI
Official Full Name	protein arginine N-methyltransferase 2 provided by MGI
Primary source	MGI:MGI:1316652
See related	Ensembl:ENSMUSG00000020230
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI504737, Hrmt1l1
Expression	Broad expression in CNS E18 (RPKM 82.6), whole brain E14.5 (RPKM 68.0) and 23 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

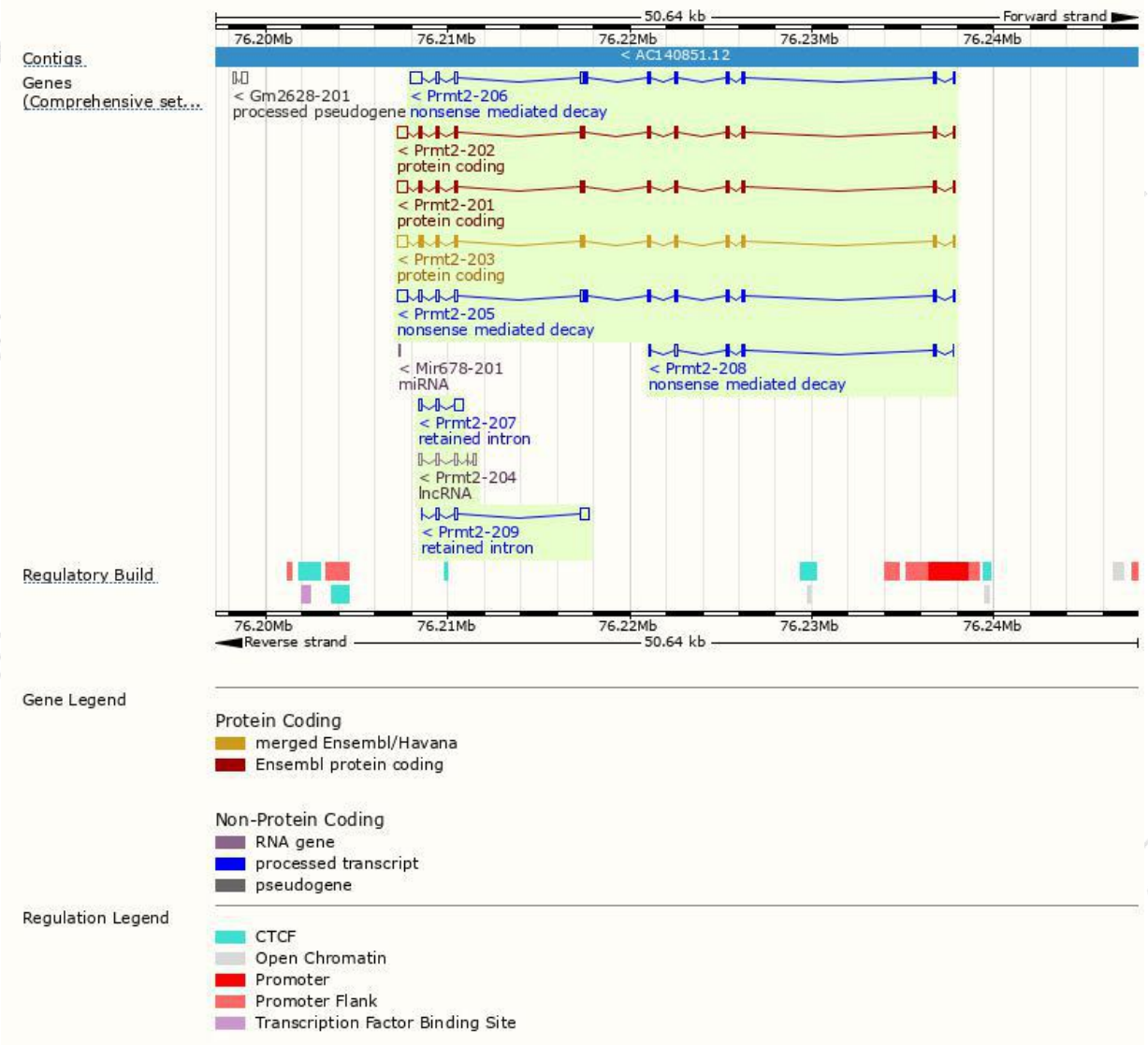
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prmt2-203	ENSMUST00000099572.9	2100	475aa	Protein coding	CCDS78836	Q3UID4	TSL:1 GENCODE basic APPRIS ALT2
Prmt2-202	ENSMUST00000099571.9	2052	445aa	Protein coding	CCDS35942	Q3UKX1	TSL:1 GENCODE basic APPRIS P3
Prmt2-201	ENSMUST00000020452.11	2016	445aa	Protein coding	CCDS35942	Q3UKX1	TSL:1 GENCODE basic APPRIS P3
Prmt2-205	ENSMUST00000128099.7	2066	254aa	Nonsense mediated decay	-	M0QW88	TSL:1
Prmt2-206	ENSMUST00000137857.7	1967	254aa	Nonsense mediated decay	-	M0QW88	TSL:2
Prmt2-208	ENSMUST00000217726.1	725	127aa	Nonsense mediated decay	-	A0A1W2P6Z3	TSL:3
Prmt2-207	ENSMUST00000144670.7	769	No protein	Retained intron	-	-	TSL:2
Prmt2-209	ENSMUST00000220116.1	751	No protein	Retained intron	-	-	TSL:5
Prmt2-204	ENSMUST00000128048.1	608	No protein	lncRNA	-	-	TSL:3

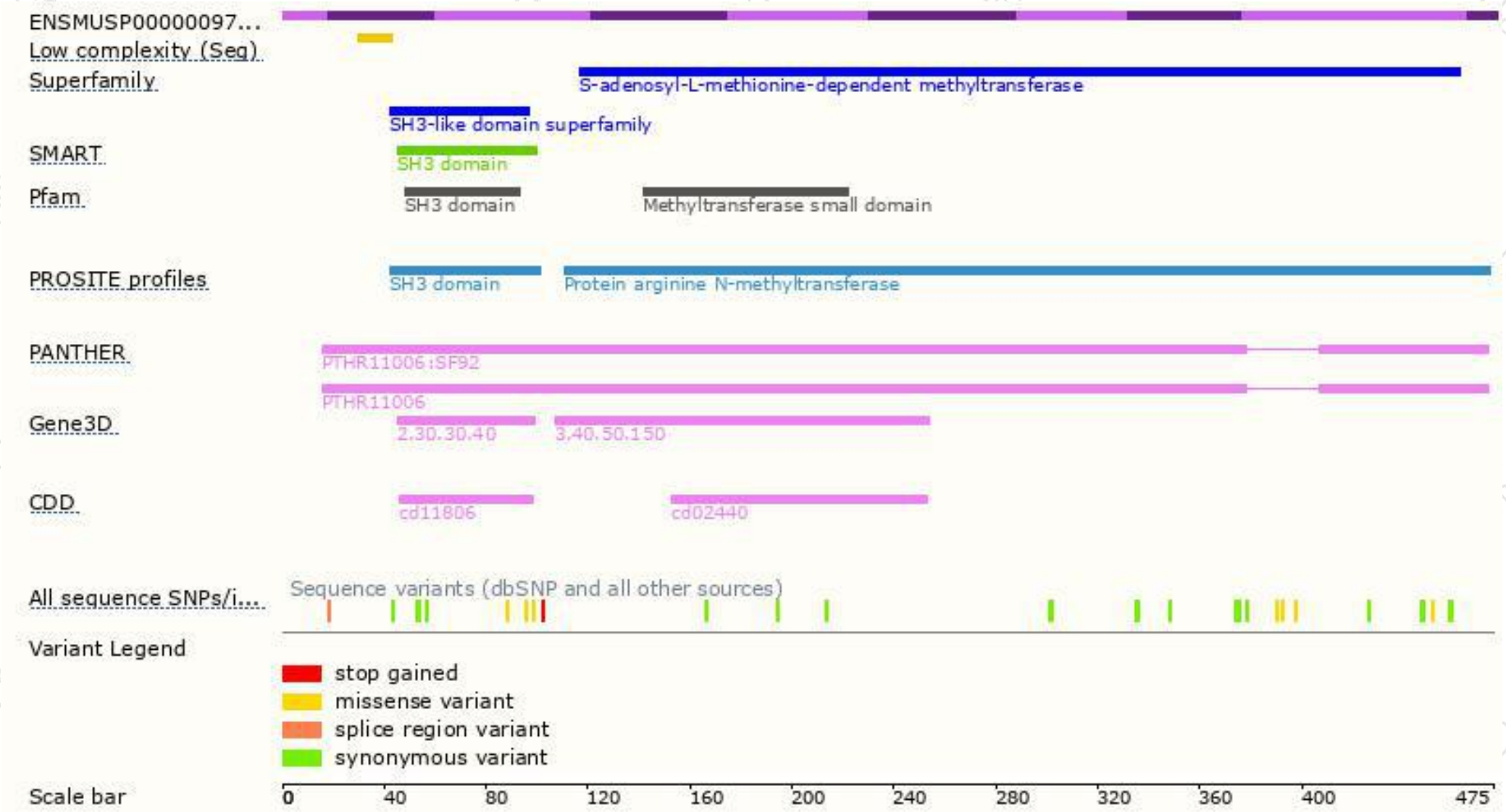
The strategy is based on the design of *Prmt2-203* transcript,The transcription is shown below



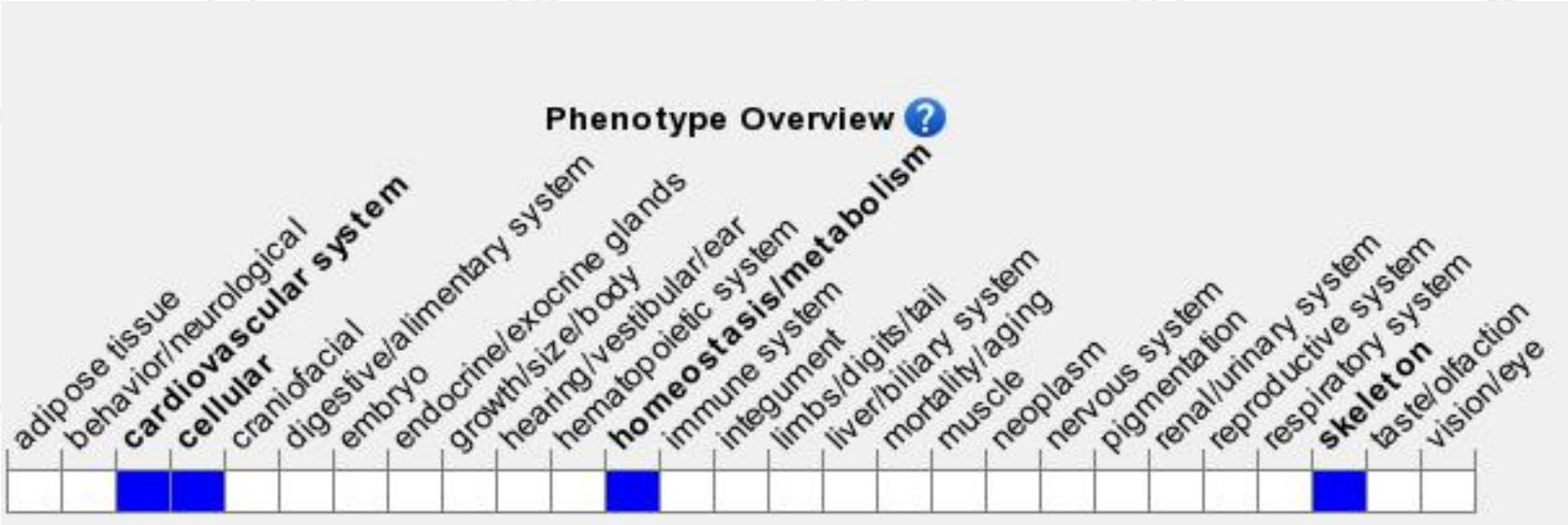
Genomic location distribution



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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集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd