Pard3 Cas9-CKO Strategy

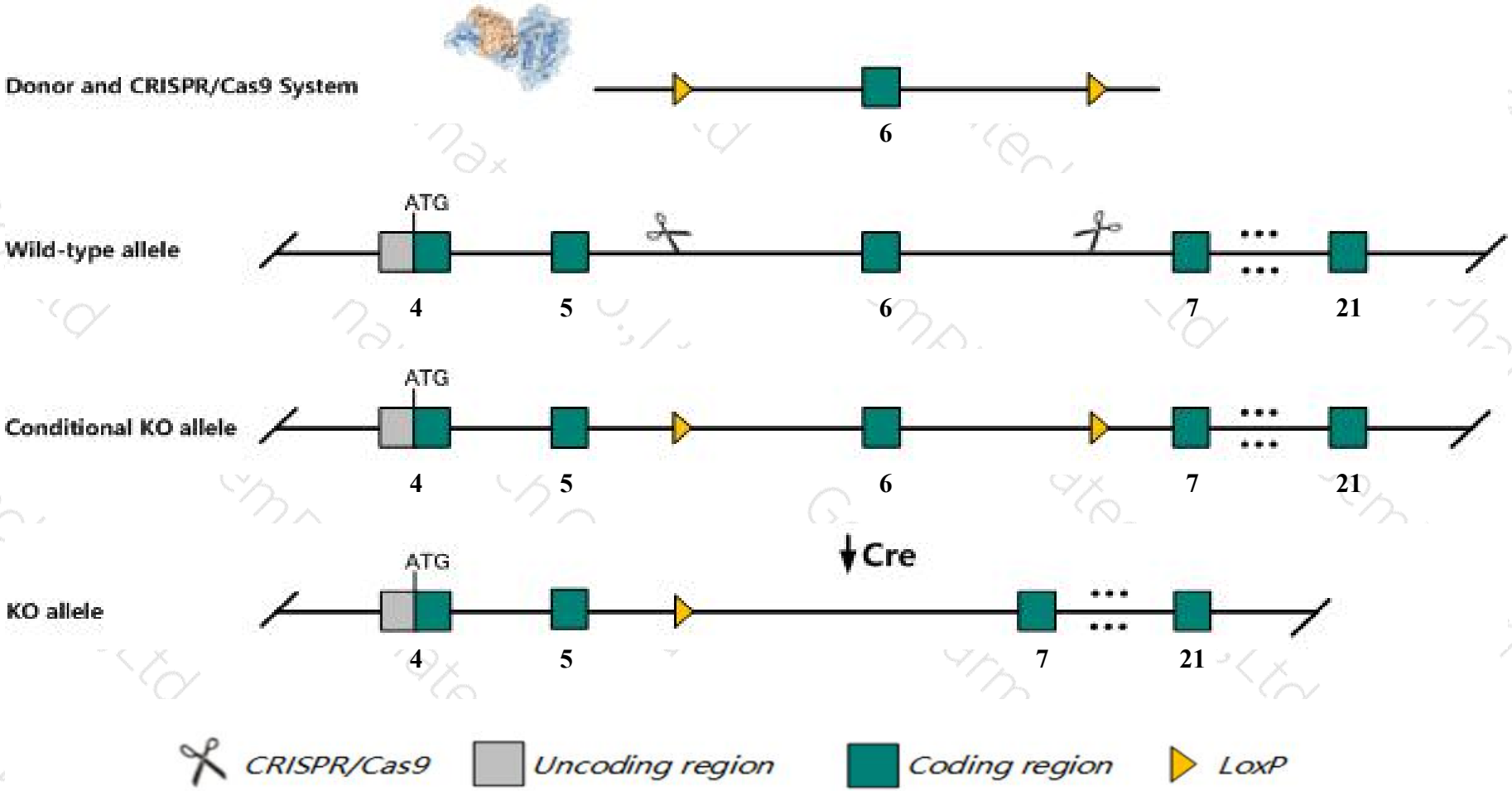
Designer: QiongZhou

Project Overview

Project Name	***Pard3***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pard3* gene. The schematic diagram is as follows:



Technical routes

- The *Pard3* gene has 29 transcripts. According to the structure of *Pard3* gene, exon6 of *Pard3-202* (ENSMUST00000079777.11) transcript is recommended as the knockout region.The region contains 92bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Pard3* 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.

Notice

- According to the existing MGI data,mice homozygous for a null allele exhibit embryonic lethality at e12.5 associated with growth retardation, abnormal heart development, and abnormal epicardial cell development.
- The *Pard3* gene is located on the Chr8. 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）

集萃药康 GemPharmatech

Pard3 par-3 family cell polarity regulator [Mus musculus (house mouse)]

Gene ID: 93742, updated on 7-Apr-2019

Summary

Official Symbol	Pard3 provided by MGI
Official Full Name	par-3 family cell polarity regulator provided by MGI
Primary source	MGI:MGI:2135608
See related	Ensembl:ENSMUSG00000025812
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	AA960621, AI256638, Asip, D8Ertd580e, Par-3, Par3, Pard-3, Pard3a, Phip
Expression	Ubiquitous expression in ovary adult (RPKM 7.1), bladder adult (RPKM 6.3) and 28 other tissues See more
Orthologs	human all

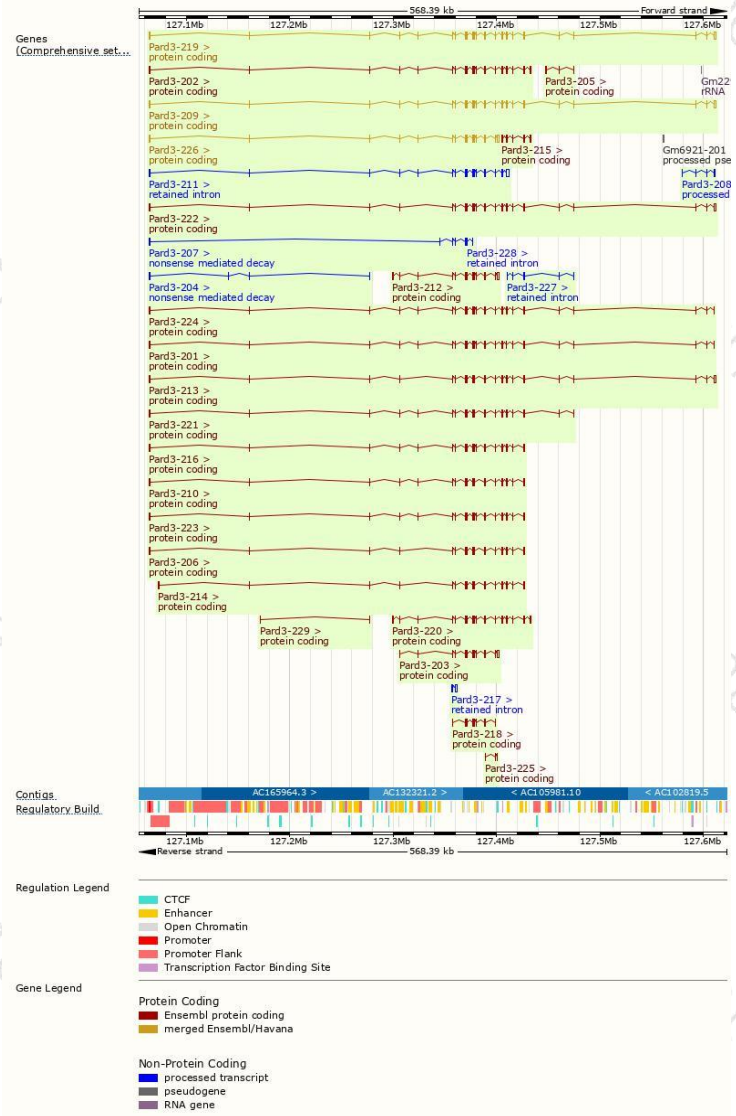
Transcript information（Ensembl）

The gene has 29 transcripts,all transcripts are shown below:

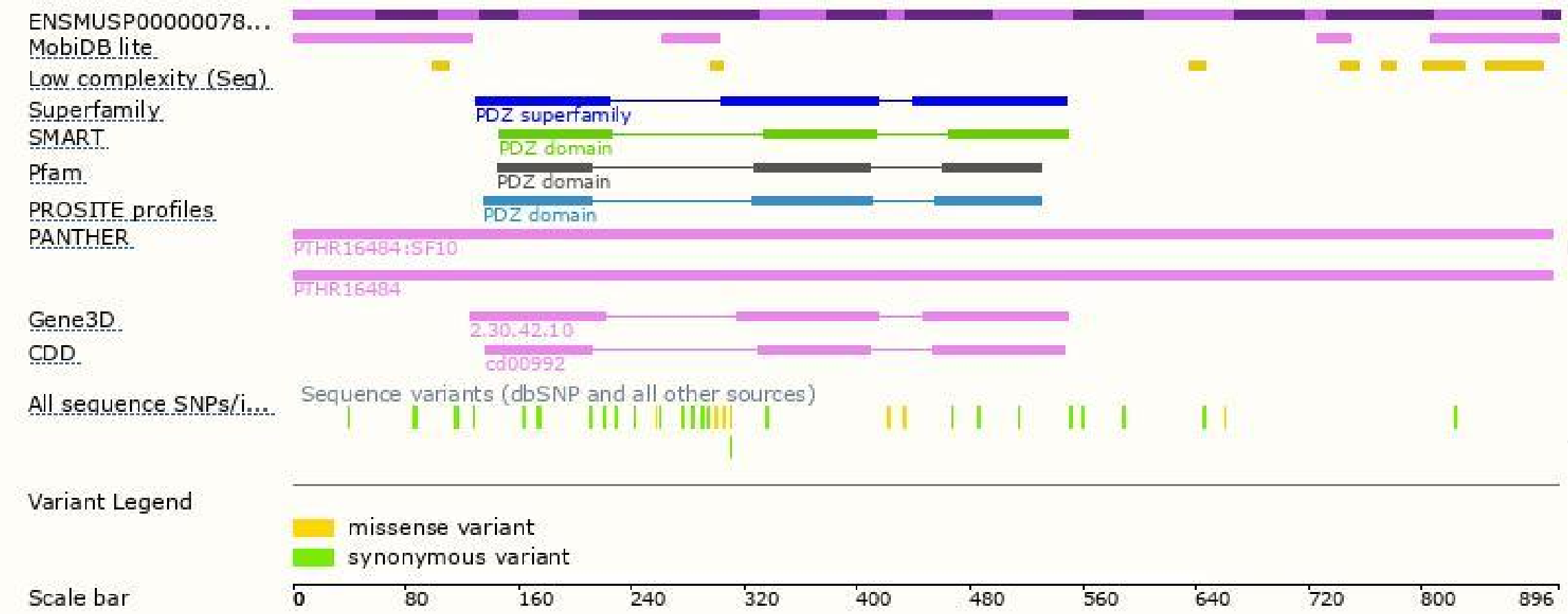
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pard3-209	ENSMUST00000160272.7	5815	1334aa	Protein coding	CCDS80945	A5D6P2	TSL:1 GENCODE basic APPRIS ALT2
Pard3-219	ENSMUST00000162309.7	5659	1333aa	Protein coding	CCDS22788	G3XA13	TSL:1 GENCODE basic APPRIS P3
Pard3-226	ENSMUST00000162907.7	4682	741aa	Protein coding	CCDS52712	E9PYJ2	TSL:1 GENCODE basic APPRIS ALT2
Pard3-212	ENSMUST00000160717.7	4214	606aa	Protein coding	CCDS40523	Q99NH2	TSL:1 GENCODE basic
Pard3-201	ENSMUST00000026921.12	4050	1319aa	Protein coding	CCDS80946	B7ZNY3	TSL:1 GENCODE basic APPRIS ALT2
Pard3-203	ENSMUST00000108752.9	3497	606aa	Protein coding	CCDS40523	Q99NH2	TSL:5 GENCODE basic
Pard3-202	ENSMUST00000079777.11	3394	896aa	Protein coding	CCDS22789	A0A0R4J1Y4	TSL:5 GENCODE basic
Pard3-220	ENSMUST00000162456.7	3204	896aa	Protein coding	CCDS22789	A0A0R4J1Y4	TSL:1 GENCODE basic
Pard3-222	ENSMUST00000162536.7	5175	1289aa	Protein coding	-	E0CXL4	TSL:5 GENCODE basic APPRIS ALT2
Pard3-213	ENSMUST00000160766.7	4949	1247aa	Protein coding	-	E0CY24	TSL:5 GENCODE basic APPRIS ALT2
Pard3-224	ENSMUST00000162665.7	4005	1324aa	Protein coding	-	F6S7Z1	CDS 5' incomplete TSL:1
Pard3-221	ENSMUST00000162531.7	3293	1094aa	Protein coding	-	E0CZ83	CDS 3' incomplete TSL:5
Pard3-223	ENSMUST00000162602.7	3083	1024aa	Protein coding	-	E0CZE2	CDS 3' incomplete TSL:5
Pard3-216	ENSMUST00000161355.7	2981	990aa	Protein coding	-	E0CXR8	CDS 3' incomplete TSL:5
Pard3-210	ENSMUST00000160581.7	2954	984aa	Protein coding	-	F6TSJ9	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 APPRIS ALT2
Pard3-206	ENSMUST00000159537.7	2838	943aa	Protein coding	-	E0CX45	CDS 3' incomplete TSL:5
Pard3-214	ENSMUST00000161277.7	2758	919aa	Protein coding	-	F6UGU7	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Pard3-218	ENSMUST00000162176.1	1266	422aa	Protein coding	-	Q4JJC0	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:1
Pard3-215	ENSMUST00000161348.2	1124	269aa	Protein coding	-	F6URI7	CDS 5' incomplete TSL:5
Pard3-225	ENSMUST00000162727.1	622	116aa	Protein coding	-	F6TB42	CDS 5' incomplete TSL:2
Pard3-205	ENSMUST00000159511.1	307	102aa	Protein coding	-	F6T4Y3	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Pard3-207	ENSMUST00000159818.1	568	44aa	Nonsense mediated decay	-	E0CYB6	TSL:5
Pard3-204	ENSMUST00000159141.7	520	59aa	Nonsense mediated decay	-	E0CXD3	TSL:2
Pard3-208	ENSMUST00000159940.1	746	No protein	Processed transcript	-	-	TSL:2
Pard3-211	ENSMUST00000160593.7	5310	No protein	Retained intron	-	-	TSL:1
Pard3-217	ENSMUST00000162035.1	3017	No protein	Retained intron	-	-	TSL:1
Pard3-227	ENSMUST00000163002.1	815	No protein	Retained intron	-	-	TSL:3
Pard3-228	ENSMUST00000163021.1	614	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Pard3-202* transcript,the transcription is shown below:

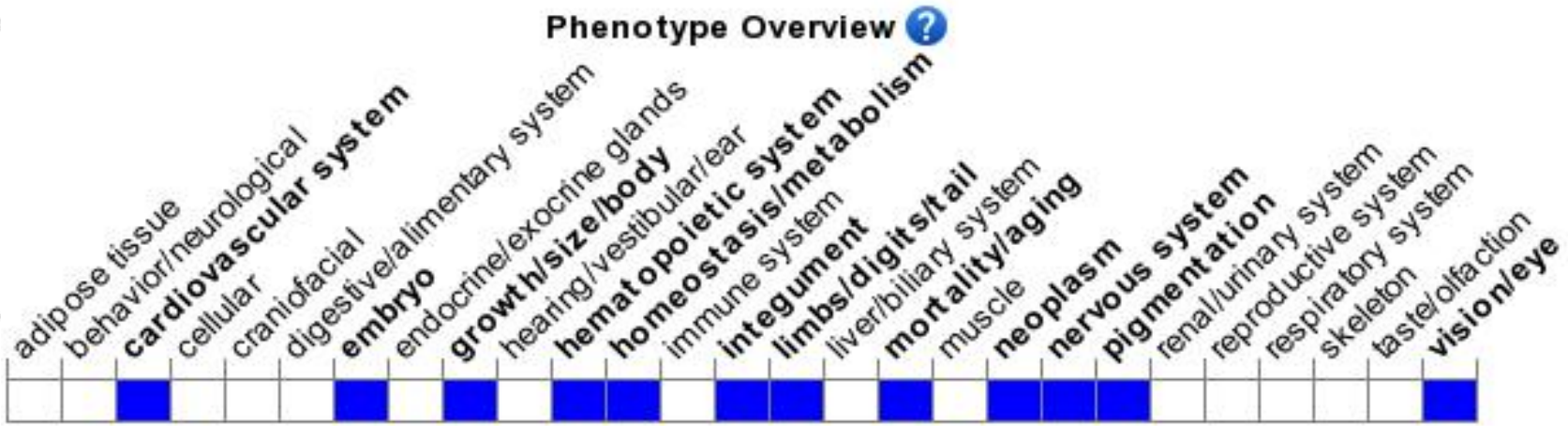
Genomic location distribution



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 null allele exhibit embryonic lethality at E12.5 associated with growth retardation, abnormal heart development, and abnormal epicardial cell development.

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