Zfp354a Cas9-CKO Strategy

Designer:	**Daohua Xu**
Reviewer:	**Huimin Su**
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Project Overview

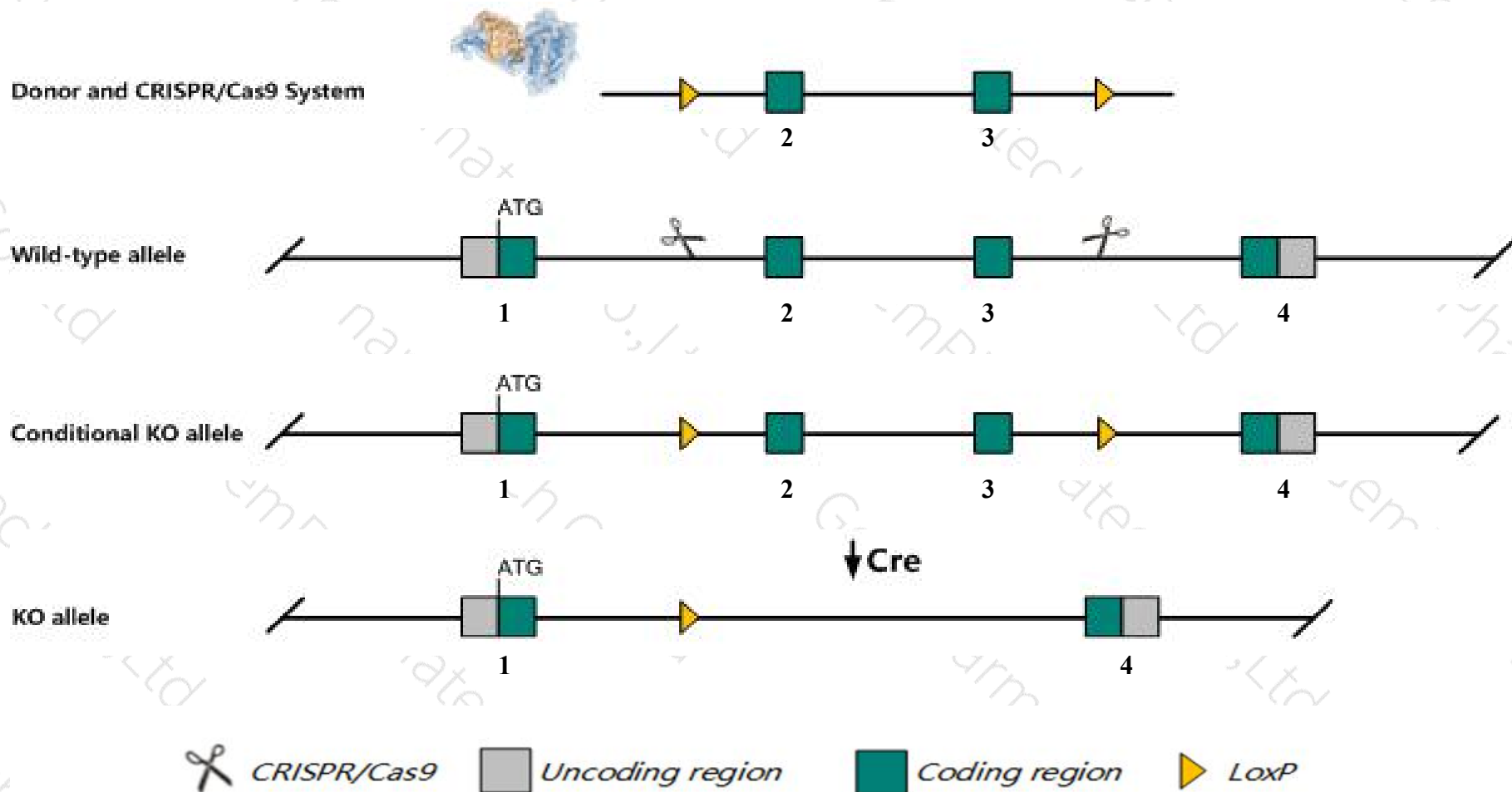|	
Project Name	*Zfp354a*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp354a* gene. The schematic diagram is as follows:

Technical routes

➤ The *Zfp354a* gene has 5 transcripts. According to the structure of *Zfp354a* gene, exon2-exon3 of *Zfp354a-203* (ENSMUST00000109119.7) transcript is recommended as the knockout region.The region contains Ens 226bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Zfp354a* 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

➢ The *Zfp354a* gene is located on the Chr11. 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）

Zfp354a zinc finger protein 354A [Mus musculus (house mouse)]

Gene ID: 21408, updated on 13-Mar-2020

Summary

|	
Official Symbol	Zfp354a provided by MGI
Official Full Name	zinc finger protein 354A provided by MGI
Primary source	MGI:MGI:103172
See related	Ensembl:ENSMUSG00000020364
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	AW488485, Tcf17, Znf354a, kid1
Expression	Broad expression in CNS E18 (RPKM 2.5), CNS E14 (RPKM 2.0) and 22 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
Zfp354a-204	ENSMUST00000109122.7	4165	571aa	Protein coding	CCDS83802	Q5PPR4	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Zfp354a-202	ENSMUST00000102766.9	2592	572aa	Protein coding	CCDS24648	Q61751	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Zfp354a-203	ENSMUST00000109119.7	2078	573aa	Protein coding	CCDS83803	B1ATG3	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Zfp354a-201	ENSMUST00000020628.5	1719	572aa	Protein coding	CCDS24648	Q61751	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Zfp354a-205	ENSMUST00000156914.1	430	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Zfp354a-203* transcript,the transcription is shown below:
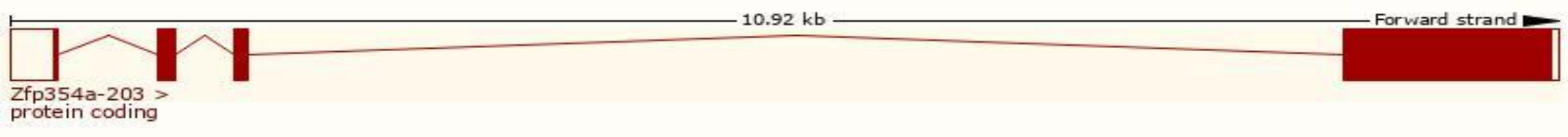
Genomic location distribution
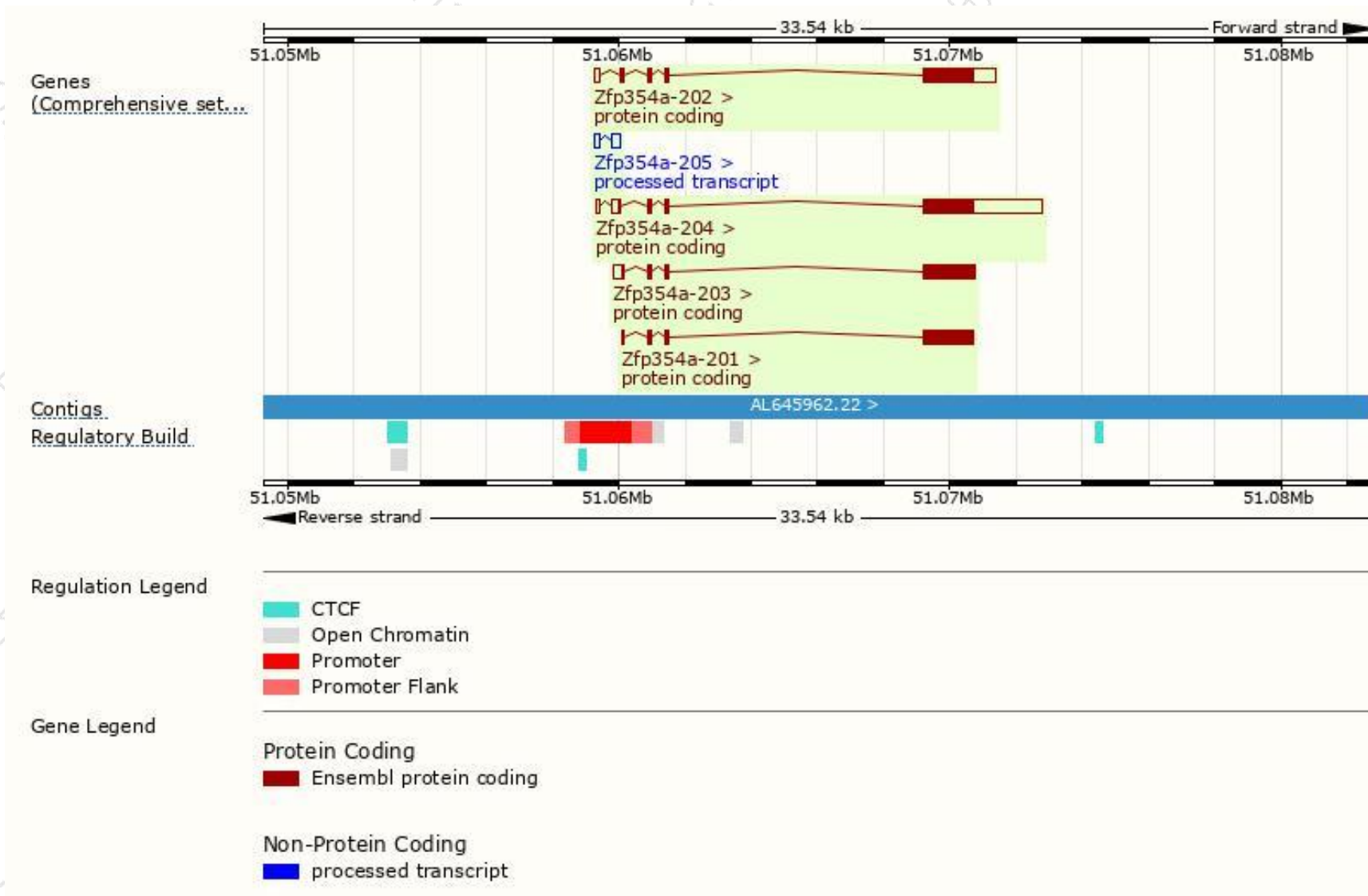
Protein domain
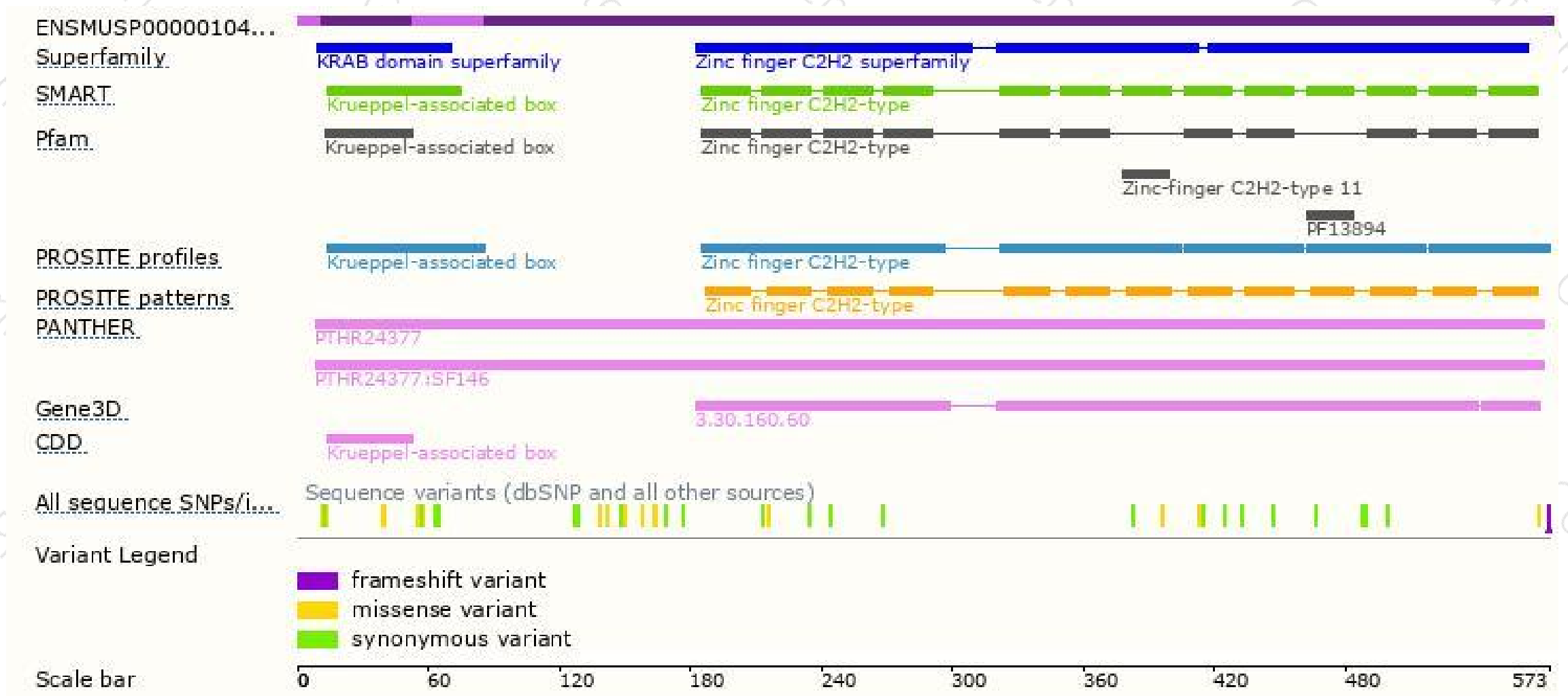
If you have any questions, you are welcome to inquire.
Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd