Scyl1 Cas9-CKO Strategy

Designer: JiaYu

Reviewer: Xiaojing Li

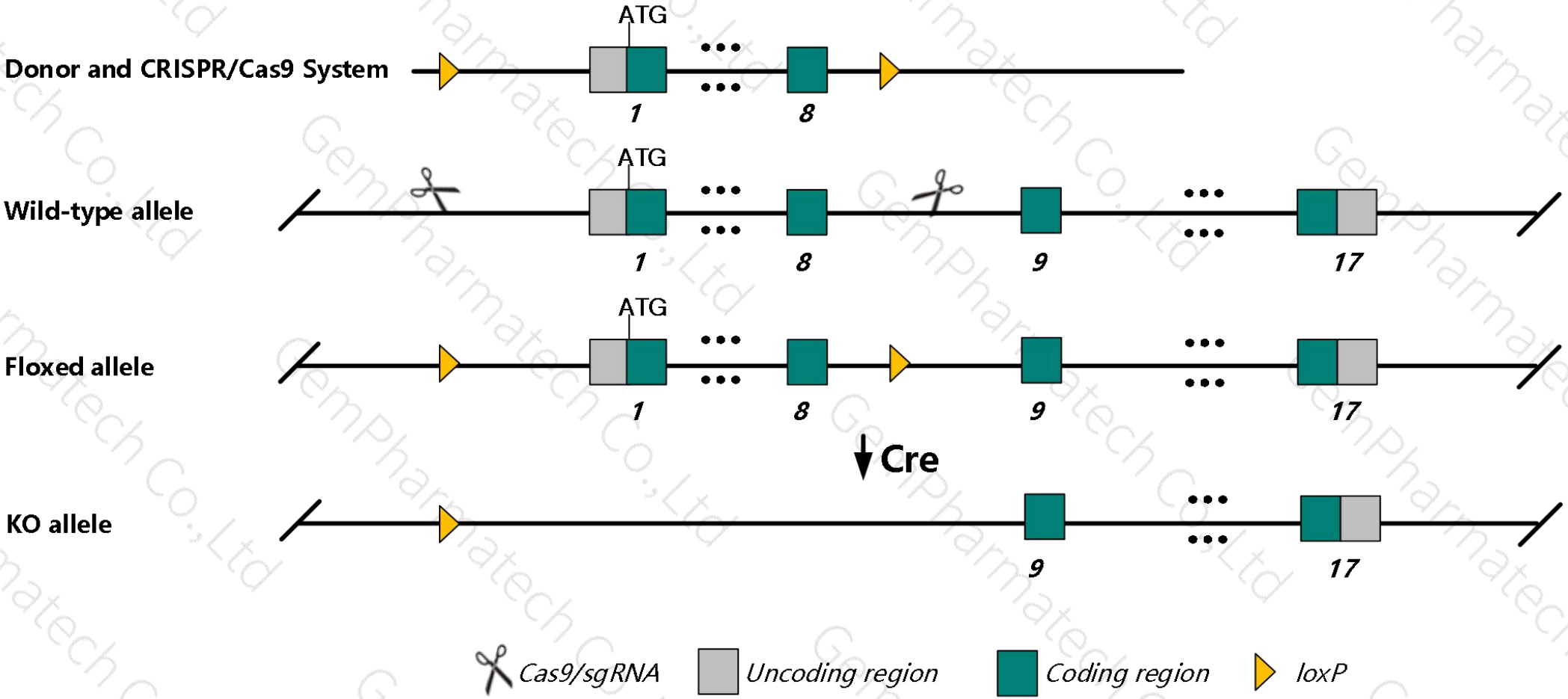
Design Date: 2020-3-9

Project Overview

Project Name	***Scyl1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Scyl1* gene. The schematic diagram is as follows:



Technical routes

- The *Scyl1* gene has 13 transcripts. According to the structure of *Scyl1* gene, exon1-exon8 of *Scyl1-210* (ENSMUST00000236978.1) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Scyl1* 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 spontaneous mutation or a knock-out allele develop a motoneuron disease characterized by gait ataxia, reduced grip strength, tremors, progressive hindlimb paralysis, muscular atrophy, and motoneuron degeneration.

➢Transcript 212 CDS 5' and 3' incomplete the influences is unknown.

➢ The Scyl1 gene is located on the Chr19. 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

Scyl1 SCY1-like 1 (S. cerevisiae) [*Mus musculus* (house mouse)]

Gene ID: 78891, updated on 24-Oct-2019

Summary

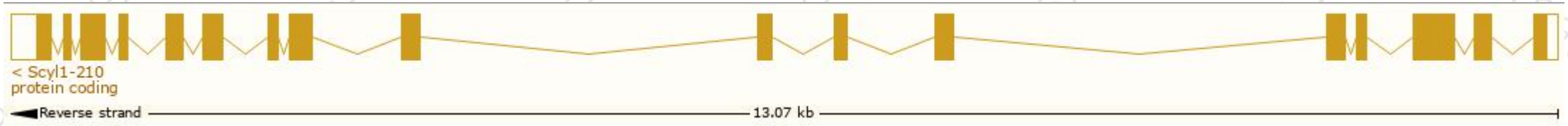
Official Symbol	Scyl1 provided by MGI
Official Full Name	SCY1-like 1 (S. cerevisiae) provided by MGI
Primary source	MGI:MGI:1931787
See related	Ensembl:ENSMUSG00000024941
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	mdf; mfd; Ntkl; p105; C85140; 2810011O19Rik
Expression	Ubiquitous expression in ovary adult (RPKM 46.3), genital fat pad adult (RPKM 42.0) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

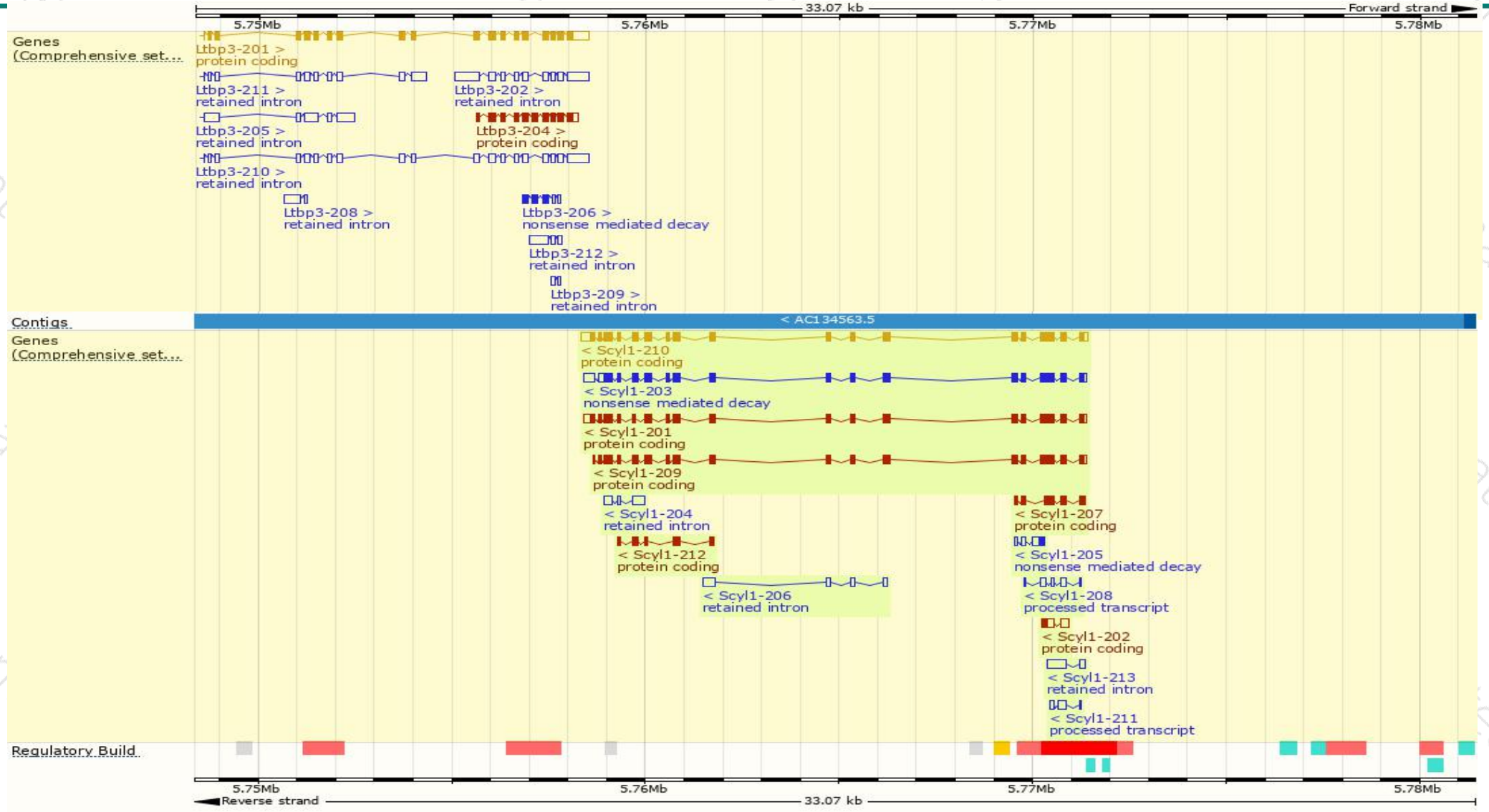
The gene has 13 transcripts,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Scyl1-210	ENSMUST00000236978.1	2731	806aa	Protein coding	CCDS29480	Q9EQC5	GENCODE basic APPRIS P2
Scyl1-201	ENSMUST00000025890.9	2586	789aa	Protein coding	-	R4H4Y7	TSL:1 GENCODE basic APPRIS ALT2
Scyl1-209	ENSMUST00000236773.1	2395	775aa	Protein coding	-	A0A494BBD3	CDS 3' incomplete
Scyl1-207	ENSMUST00000236297.1	717	226aa	Protein coding	-	A0A494BBM6	CDS 3' incomplete
Scyl1-212	ENSMUST00000237453.1	585	195aa	Protein coding	-	A0A494B997	CDS 5' and 3' incomplete
Scyl1-202	ENSMUST00000235561.1	548	48aa	Protein coding	-	A0A494BAG4	CDS 3' incomplete
Scyl1-203	ENSMUST00000235599.1	2719	749aa	Nonsense mediated decay	-	R4H4V1	-
Scyl1-205	ENSMUST00000235698.1	467	39aa	Nonsense mediated decay	-	A0A494B9K7	CDS 5' incomplete
Scyl1-208	ENSMUST00000236568.1	423	No protein	Processed transcript	-	-	-
Scyl1-211	ENSMUST00000237133.1	360	No protein	Processed transcript	-	-	-
Scyl1-206	ENSMUST00000236275.1	622	No protein	Retained intron	-	-	-
Scyl1-213	ENSMUST00000238178.1	606	No protein	Retained intron	-	-	-
Scyl1-204	ENSMUST00000235615.1	588	No protein	Retained intron	-	-	-

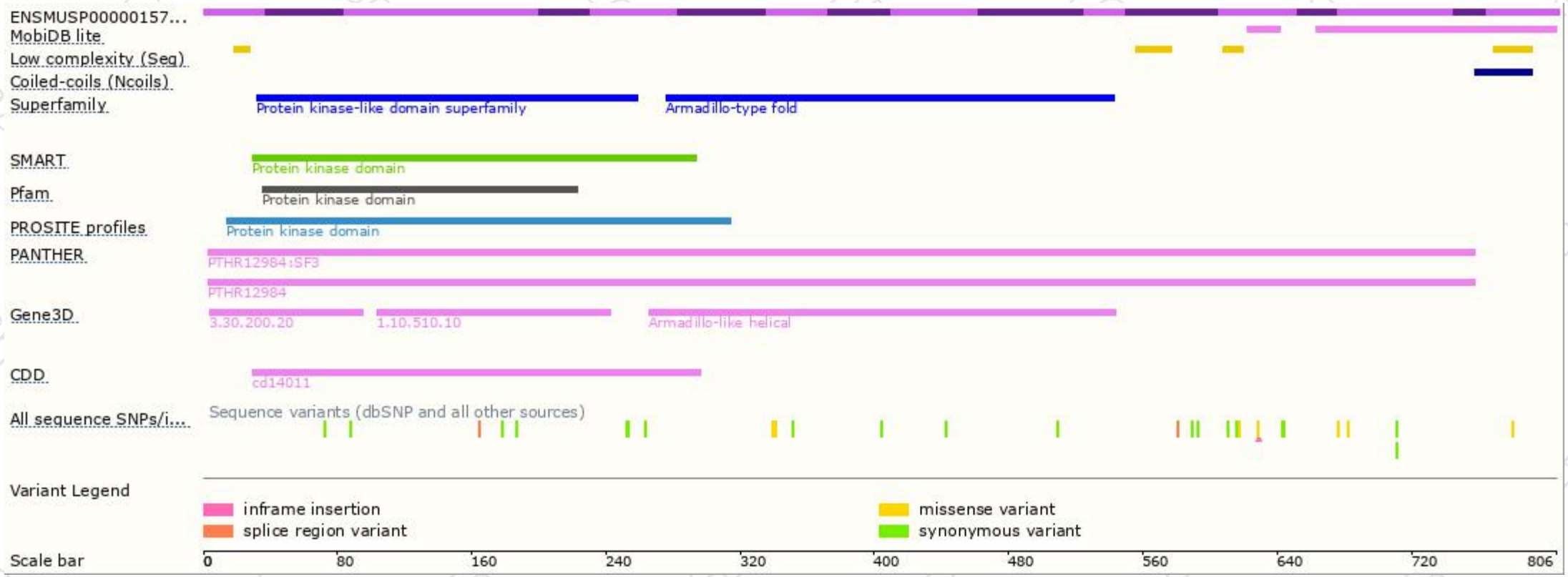
The strategy is based on the design of *Scyl1-210* transcript,The transcription is shown below



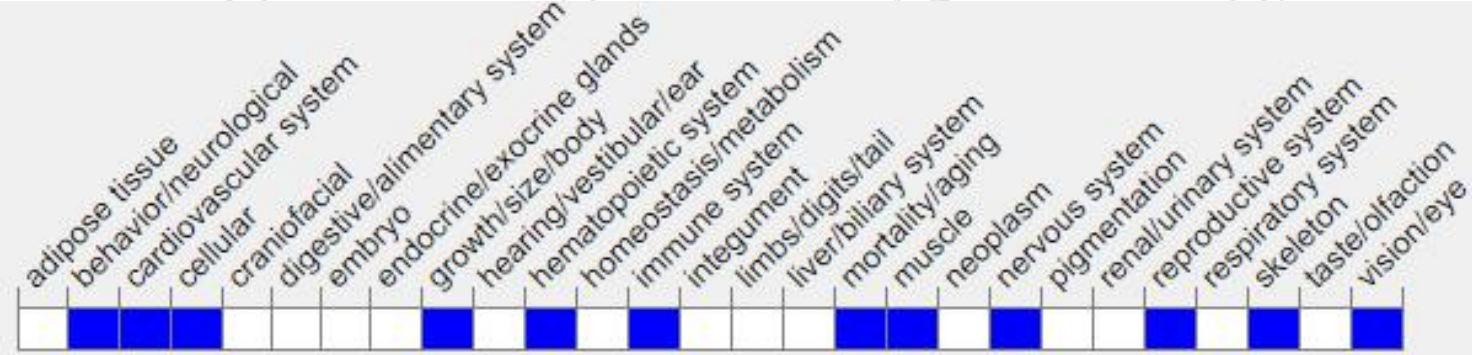
Genomic location distribution



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 spontaneous mutation or a knock-out allele develop a motoneuron disease characterized by gait ataxia, reduced grip strength, tremors, progressive hindlimb paralysis, muscular atrophy, and motoneuron degeneration.

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