

Sptan1 Cas9-KO Strategy

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Project Overview

Project Name

Sptan1

Project type

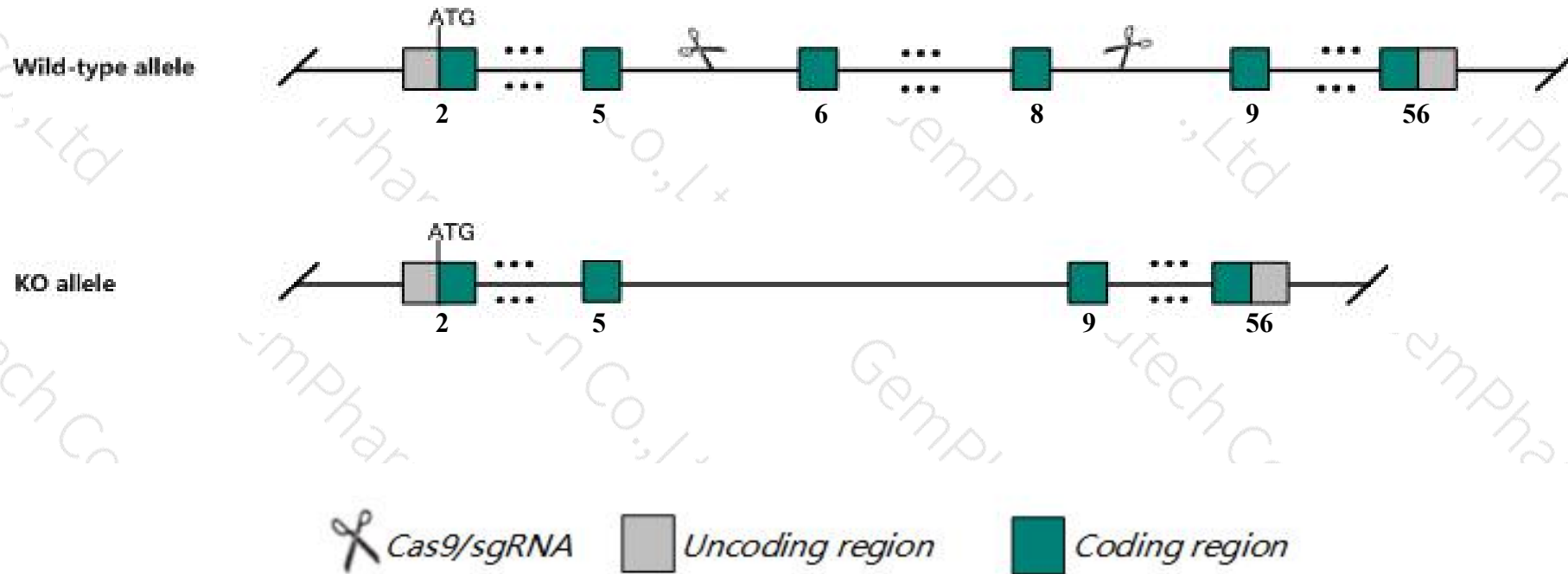
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sptan1* gene. The schematic diagram is as follows:



- The *Sptan1* gene has 16 transcripts. According to the structure of *Sptan1* gene, exon6-exon8 of *Sptan1*-204 (ENSMUST00000113717.7) transcript is recommended as the knockout region. The region contains 434bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sptan1* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, homozygous deletion of the exons encoding the CCC region are normal. Mice homozygous for a gene trap allele exhibit embryonic lethality and abnormal nervous system, heart and craniofacial morphology.
- The *Sptan1* gene is located on the Chr2. 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)

Sptan1 spectrin alpha, non-erythrocytic 1 [Mus musculus (house mouse)]

Gene ID: 20740, updated on 7-Apr-2019

Summary



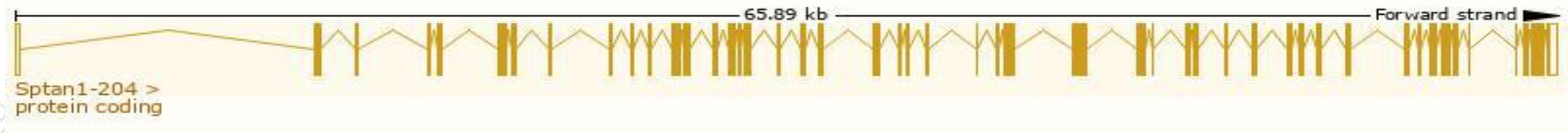
Official Symbol	Sptan1 provided by MGI
Official Full Name	spectrin alpha, non-erythrocytic 1 provided by MGI
Primary source	MGI:MGI:98386
See related	Ensembl:ENSMUSG00000057738
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610027H02Rik, Spna-2, Spna2
Expression	Broad expression in CNS E18 (RPKM 112.4), cerebellum adult (RPKM 102.7) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

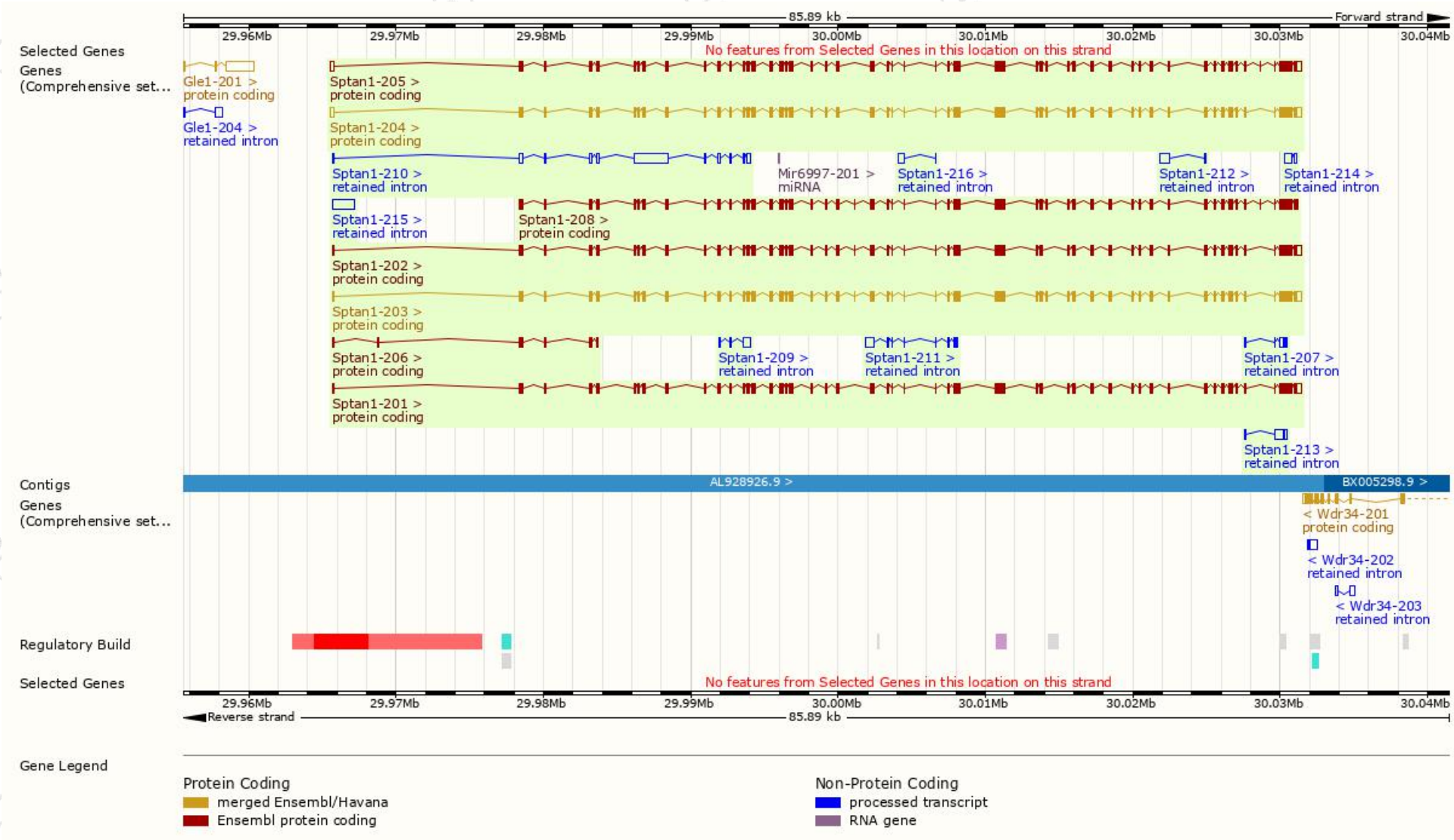
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sptan1-204	ENSMUST00000113717.7	7958	2457aa	Protein coding	CCDS50559	A3KGU5	TSL:1 GENCODE basic
Sptan1-203	ENSMUST00000100225.8	7892	2477aa	Protein coding	CCDS50558	A3KGU7	TSL:1 GENCODE basic APPRIS ALT 1
Sptan1-208	ENSMUST00000129241.2	7585	2498aa	Protein coding	CCDS38094	A3KGU9	TSL:5 GENCODE basic APPRIS P3
Sptan1-205	ENSMUST00000113719.8	8018	2478aa	Protein coding	-	E9Q447	TSL:5 GENCODE basic
Sptan1-202	ENSMUST00000095083.10	7883	2472aa	Protein coding	-	P16546	TSL:5 GENCODE basic APPRIS ALT 1
Sptan1-201	ENSMUST00000046257.13	7820	2452aa	Protein coding	-	P16546	TSL:5 GENCODE basic APPRIS ALT 1
Sptan1-206	ENSMUST00000113741.7	781	219aa	Protein coding	-	A3KGU4	CDS 3' incomplete TSL:5
Sptan1-210	ENSMUST00000143918.7	3735	No protein	Retained intron	-	-	TSL:2
Sptan1-215	ENSMUST00000202286.1	1471	No protein	Retained intron	-	-	TSL:NA
Sptan1-211	ENSMUST00000149038.2	1025	No protein	Retained intron	-	-	TSL:5
Sptan1-213	ENSMUST00000152453.2	814	No protein	Retained intron	-	-	TSL:5
Sptan1-212	ENSMUST00000149846.1	800	No protein	Retained intron	-	-	TSL:3
Sptan1-214	ENSMUST00000201758.1	719	No protein	Retained intron	-	-	TSL:2
Sptan1-209	ENSMUST00000131827.2	570	No protein	Retained intron	-	-	TSL:3
Sptan1-216	ENSMUST00000202844.1	477	No protein	Retained intron	-	-	TSL:5
Sptan1-207	ENSMUST00000124494.4	457	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Sptan1-204* transcript,The transcription is shown below:



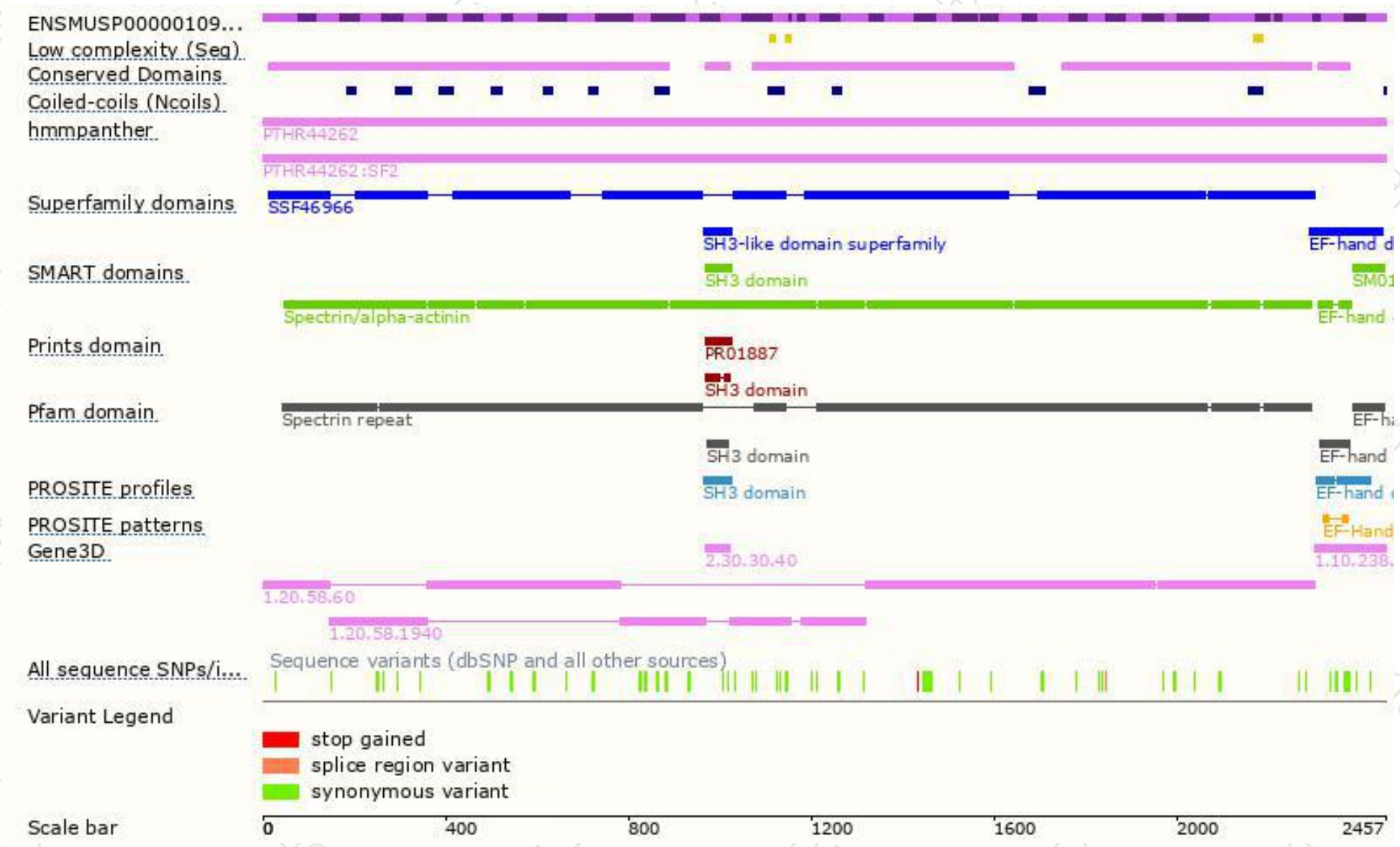
Genomic location distribution



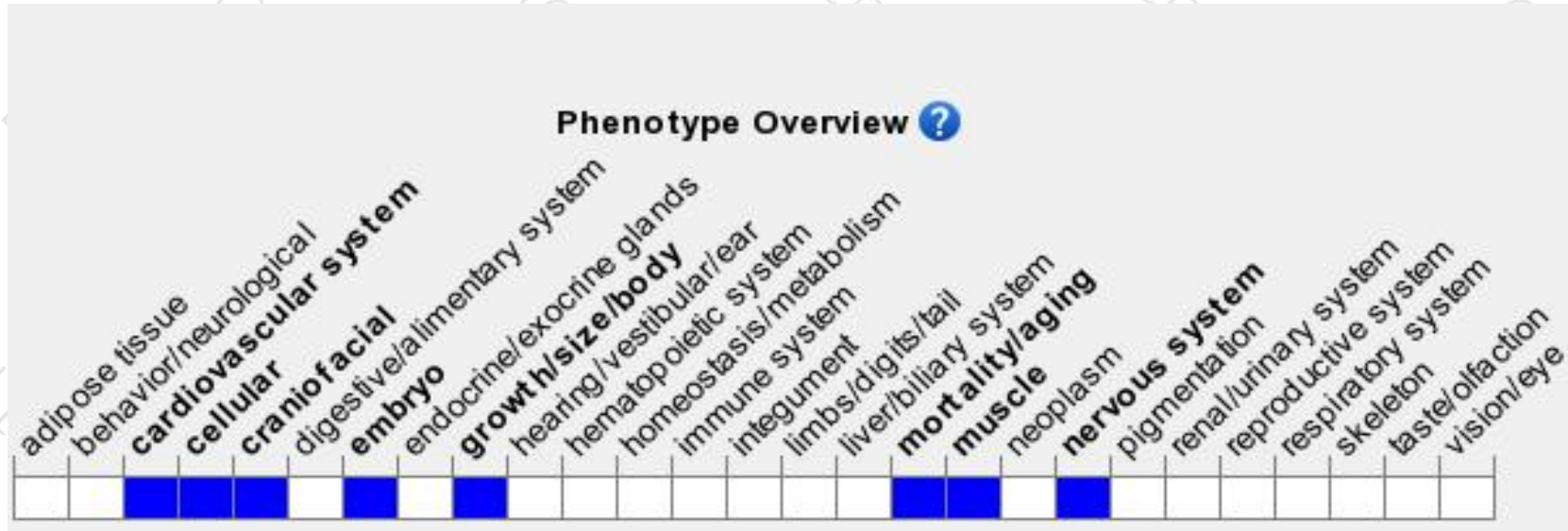
Protein domain



集萃药康
GemPharmatech



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 deletion of the exons encoding the CCC region are normal. Mice homozygous for a gene trap allele exhibit embryonic lethality and abnormal nervous system, heart and craniofacial morphology.

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

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