Adam22 Cas9-KO Strategy

Designer: JiaYu

Reviewer: Xiaojing Li

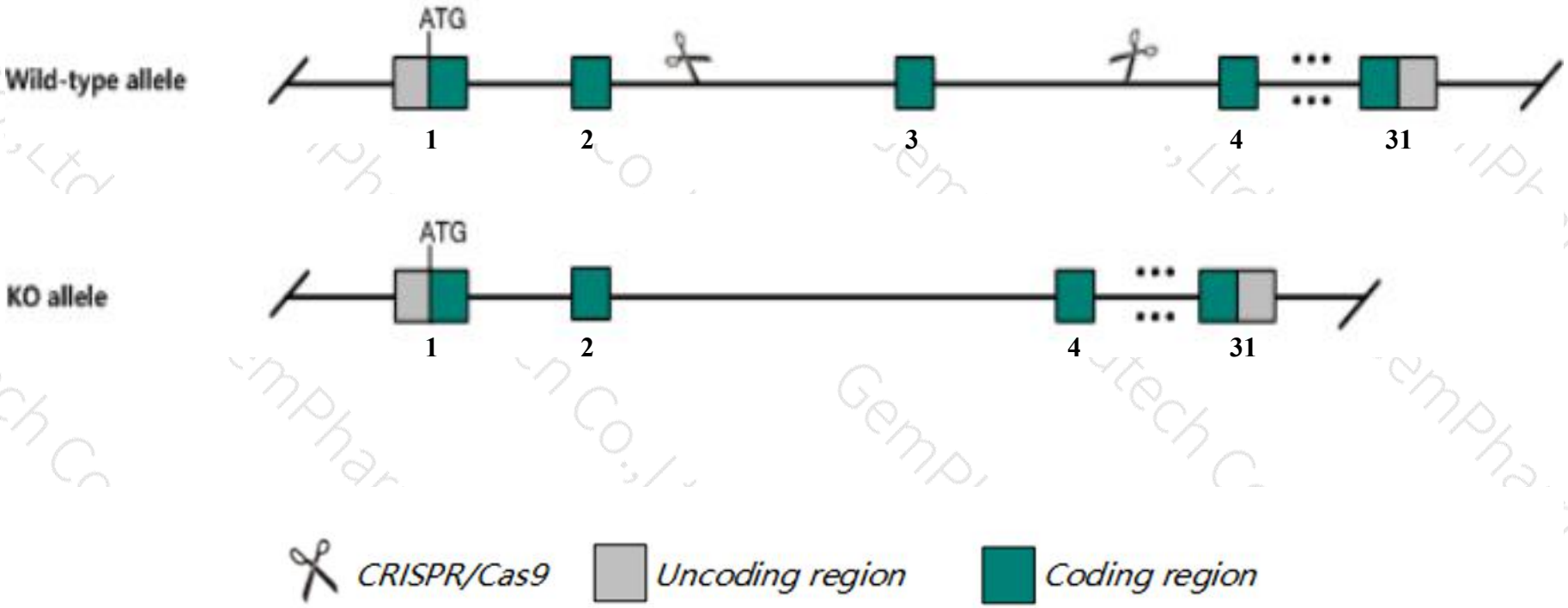
Design Date: 2020-7-28

Project Overview

Project Name	***Adam22***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Adam22* gene. The schematic diagram is as follows:



Technical routes

➢ The *Adam22* gene has 24 transcripts. According to the structure of *Adam22* gene, exon3 of *Adam22-204*(ENSMUST00000088761.10) transcript is recommended as the knockout region.The region contains 77bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Adam22* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➢ According to the existing MGI data,homozygous mutant mice exhibit severe ataxia, die before weaning and have marked hypomyelination of the peripheral nerves.

➢Transcript 206,224 CDS 5' incomplete the influences is unknown.

➢Transcript 205,208,209,210,211,212,213,215,216,219,220,221,223 CDS 5' and 3' incomplete the influences is unknown.

➢ The *Adam22* gene is located on the Chr5. 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）

集萃药康 GemPharmatech

Adam22 a disintegrin and metallopeptidase domain 22 [Mus musculus (house mouse)]

Gene ID: 11496, updated on 13-Mar-2020

Summary

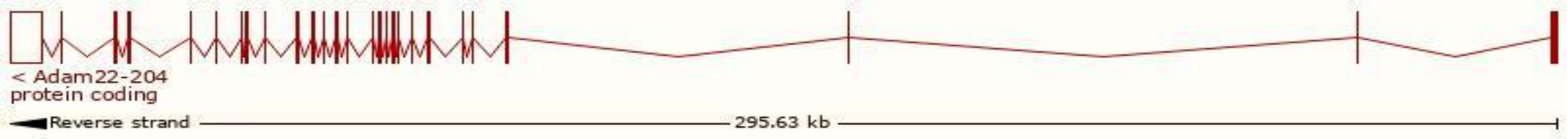
Official Symbol	Adam22 provided by MGI
Official Full Name	a disintegrin and metallopeptidase domain 22 provided by MGI
Primary source	MGI:MGI:1340046
See related	Ensembl:ENSMUSG00000040537
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2900022I03Rik, AI854032, MDC2
Summary	This gene encodes a member of a disintegrin and metalloprotease (ADAM) family of endoproteases that play important roles in various biological processes including cell signaling, adhesion and migration. The encoded preproprotein undergoes proteolytic processing to generate a mature, functional protein. The protein encoded by this gene is believed to lack metalloproteinase activity due to the lack of a critical catalytic motif. Mice lacking the encoded protein exhibit severe ataxia, hypomyelination and premature death. Alternative splicing results in multiple transcript variants encoding different isoforms, some of which may undergo similar processing. [provided by RefSeq, May 2016]
Expression	Biased expression in cerebellum adult (RPKM 18.0), cortex adult (RPKM 14.5) and 7 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

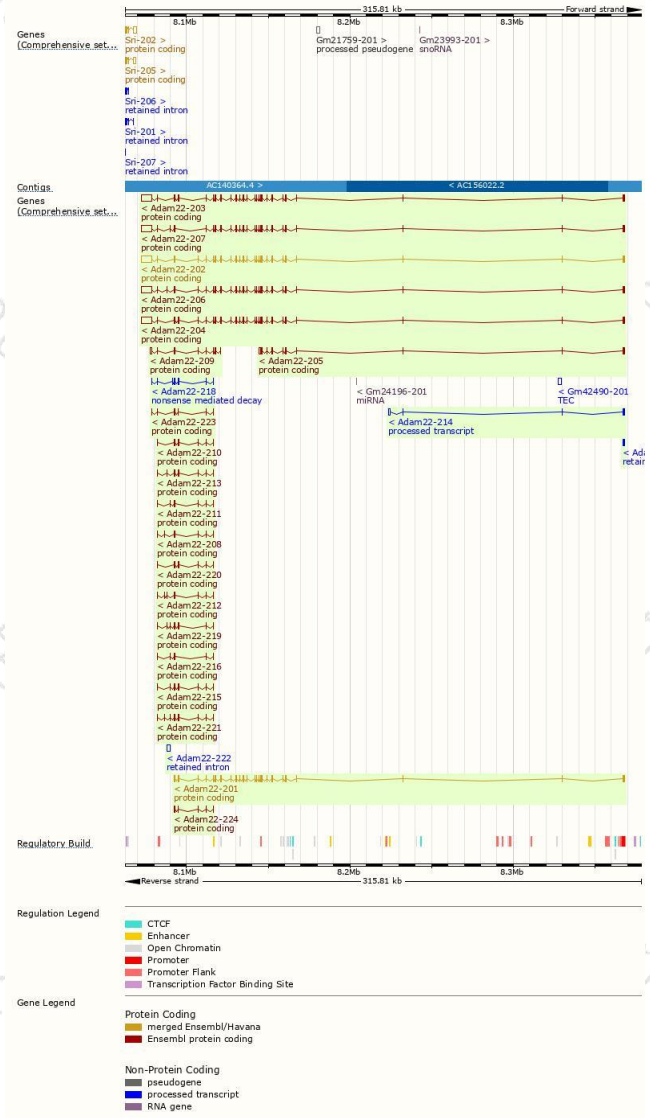
The gene has 24 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Adam22-207	ENSMUST00000115388.8	9161	899aa	Protein coding	CCDS80205	Q9R1V6	TSL:5 GENCODE basic APPRIS ALT2
Adam22-204	ENSMUST00000088761.10	9077	904aa	Protein coding	CCDS80207	D6QSS8 Q9R1V6	TSL:1 GENCODE basic APPRIS ALT2
Adam22-202	ENSMUST00000050166.13	8969	868aa	Protein coding	CCDS51411	Q9R1V6	TSL:5 GENCODE basic APPRIS ALT2
Adam22-201	ENSMUST00000046838.13	2773	857aa	Protein coding	CCDS19080	Q9R1V6	TSL:1 GENCODE basic APPRIS P3
Adam22-203	ENSMUST00000088744.11	9245	927aa	Protein coding	-	Q9R1V6	TSL:5 GENCODE basic APPRIS ALT2
Adam22-206	ENSMUST00000115386.7	9056	897aa	Protein coding	-	D3YUP9	TSL:5 GENCODE basic APPRIS ALT2
Adam22-205	ENSMUST00000115385.1	2318	333aa	Protein coding	-	D3YUQ0	TSL:2 GENCODE basic
Adam22-209	ENSMUST00000124121.7	1601	251aa	Protein coding	-	F7CDH3	CDS 5' incomplete TSL:1
Adam22-221	ENSMUST00000154935.7	801	267aa	Protein coding	-	F6PZ09	CDS 5' and 3' incomplete TSL:5
Adam22-219	ENSMUST00000153427.7	753	251aa	Protein coding	-	F6XIT3	CDS 5' and 3' incomplete TSL:5
Adam22-213	ENSMUST00000136808.7	747	249aa	Protein coding	-	F7DAP1	CDS 5' and 3' incomplete TSL:5
Adam22-215	ENSMUST00000139048.7	684	228aa	Protein coding	-	F7BZ55	CDS 5' and 3' incomplete TSL:5
Adam22-210	ENSMUST00000126384.7	660	220aa	Protein coding	-	F6VJ78	CDS 5' and 3' incomplete TSL:5
Adam22-212	ENSMUST00000136524.7	582	194aa	Protein coding	-	F7AYY9	CDS 5' and 3' incomplete TSL:5
Adam22-211	ENSMUST00000130315.7	576	192aa	Protein coding	-	F6TDF4	CDS 5' and 3' incomplete TSL:5
Adam22-220	ENSMUST00000153889.7	573	191aa	Protein coding	-	F6XRZ6	CDS 5' and 3' incomplete TSL:5
Adam22-216	ENSMUST00000139841.7	558	186aa	Protein coding	-	F6SK63	CDS 5' and 3' incomplete TSL:5
Adam22-223	ENSMUST00000197700.4	527	175aa	Protein coding	-	A0A0G2JE04	CDS 5' and 3' incomplete TSL:1
Adam22-208	ENSMUST00000123168.7	495	165aa	Protein coding	-	F7BXL9	CDS 5' and 3' incomplete TSL:5
Adam22-224	ENSMUST00000199853.1	417	138aa	Protein coding	-	A0A0G2JFA9	CDS 5' incomplete TSL:1
Adam22-218	ENSMUST00000144241.7	631	150aa	Nonsense mediated decay	-	S4R1S5	CDS 5' incomplete TSL:5
Adam22-214	ENSMUST00000138652.1	1620	No protein	Processed transcript	-	-	TSL:1
Adam22-222	ENSMUST00000196356.1	2303	No protein	Retained intron	-	-	TSL:NA
Adam22-217	ENSMUST00000143929.1	705	No protein	Retained intron	-	-	TSL:2

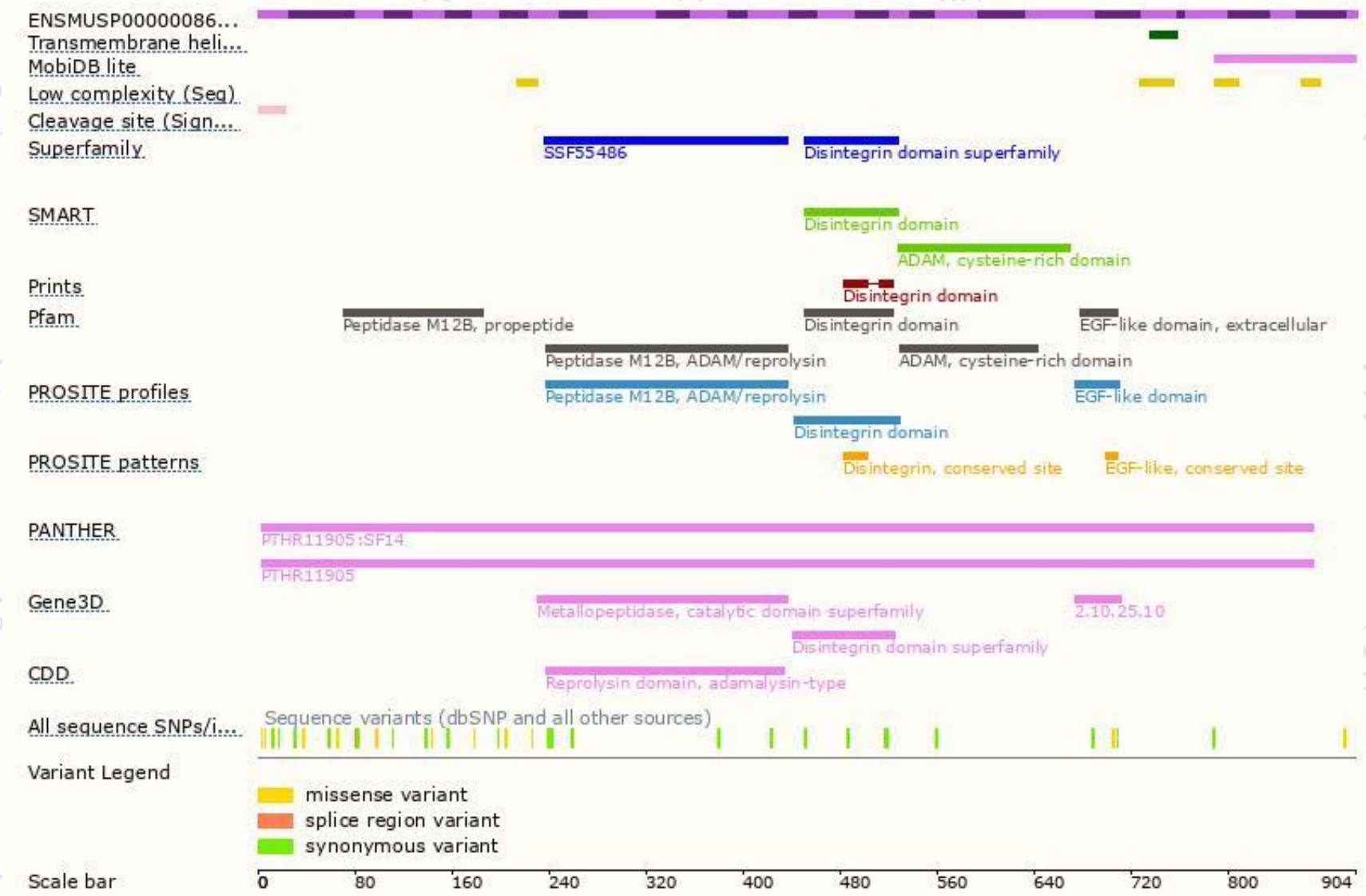
The strategy is based on the design of *Adam22-204* transcript,the transcription is shown below:



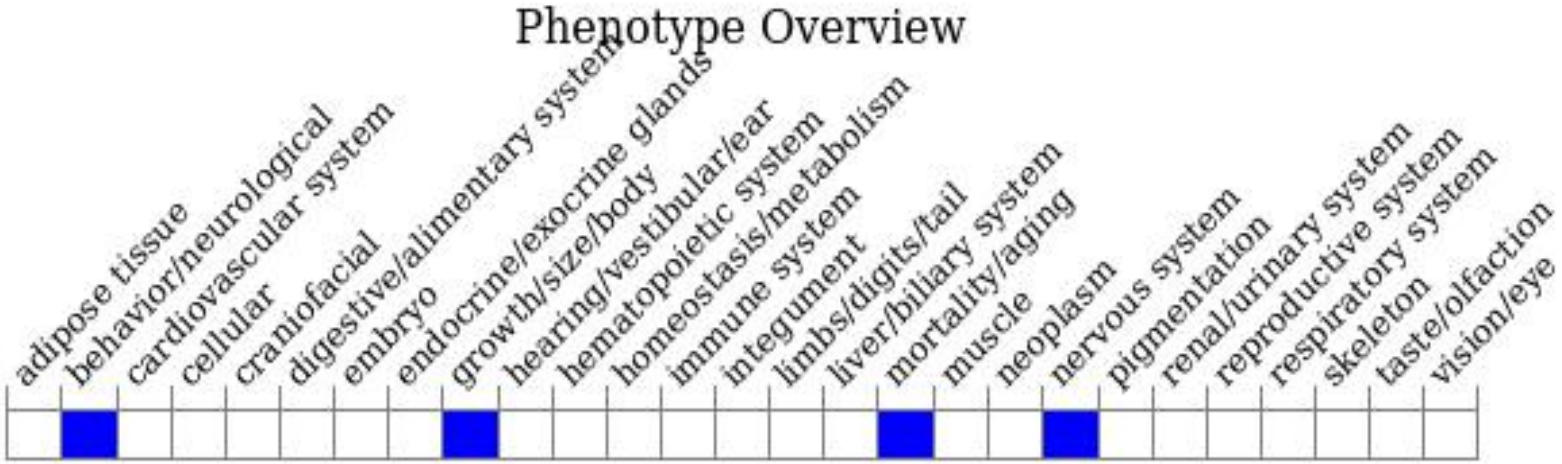
Genomic location distribution



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,homozygous mutant mice exhibit severe ataxia, die before weaning and have marked hypomyelination of the peripheral nerves.

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