

Sez6 Cas9-CKO Strategy

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Project Overview



Project Name

Sez6

Project type

Cas9-CKO

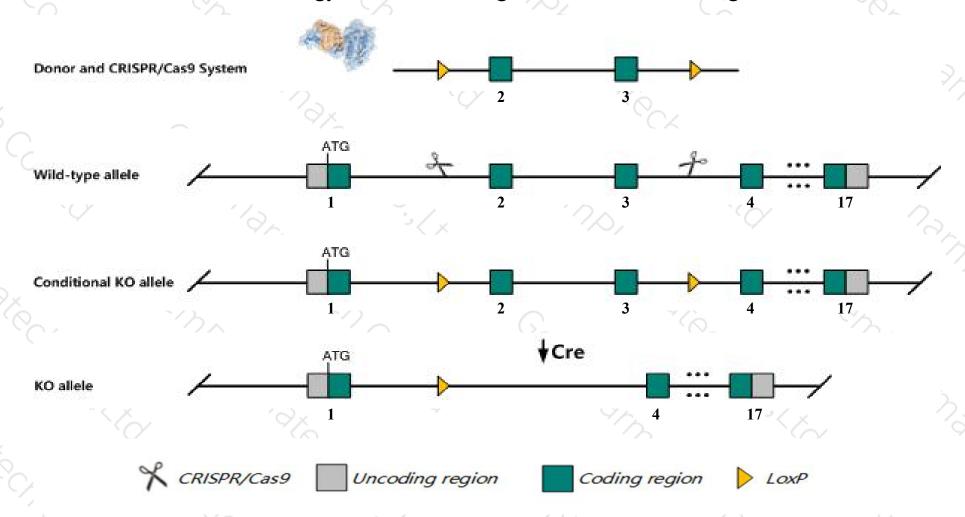
Strain background

C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Sez6 gene. The schematic diagram is as follows:



Technical routes



- ➤ The Sez6 gene has 9 transcripts. According to the structure of Sez6 gene, exon2-exon3 of Sez6-202

 (ENSMUST00000093995.9) transcript is recommended as the knockout region. The region contains 794bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Sez6* 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 increased short dendrites, decreased excitatory synaptic signaling, resistance to pharmacologically induces seizures, decreased activity and impaired learning and coordination.
- ➤ The effect on transcript *Sez6*-206&208 is unknown.
- > Transcript Sez6-203 may not be affected.
- > The Sez6 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)



Sez6 seizure related gene 6 [Mus musculus (house mouse)]

Gene ID: 20370, updated on 12-Aug-2019

Summary

☆ ?

Official Symbol Sez6 provided by MGI

Official Full Name seizure related gene 6 provided by MGI

Primary source MGI:MGI:104745

See related Ensembl:ENSMUSG00000000632

Gene type protein coding
RefSeq status VALIDATED
Organism <u>Mus musculus</u>

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;

Muroidea; Muridae; Murinae; Mus; Mus

Also known as sez-6; BSRP-C; D11Bhm177e

Expression Biased expression in whole brain E14.5 (RPKM 47.2), CNS E14 (RPKM 47.1) and 5 other tissues See more

Orthologs <u>human</u> <u>all</u>

Genomic context



Location: 11 B5; 11 46.74 cM

See Sez6 in Genome Data Viewer

Exon count: 19

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (7793058777979052)
Build 37.2	previous assembly	MGSCv37 (GCF 000001635.18)	11	NC 000077.5 (7774444577792550)

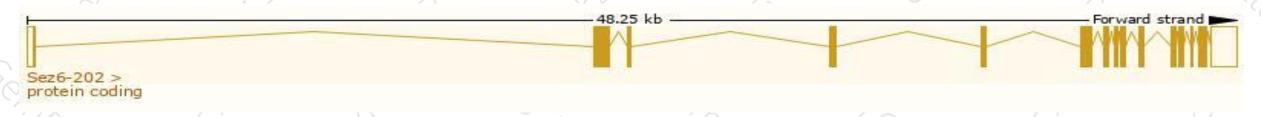
Transcript information (Ensembl)



The gene has 9 transcripts, all transcripts are shown below:

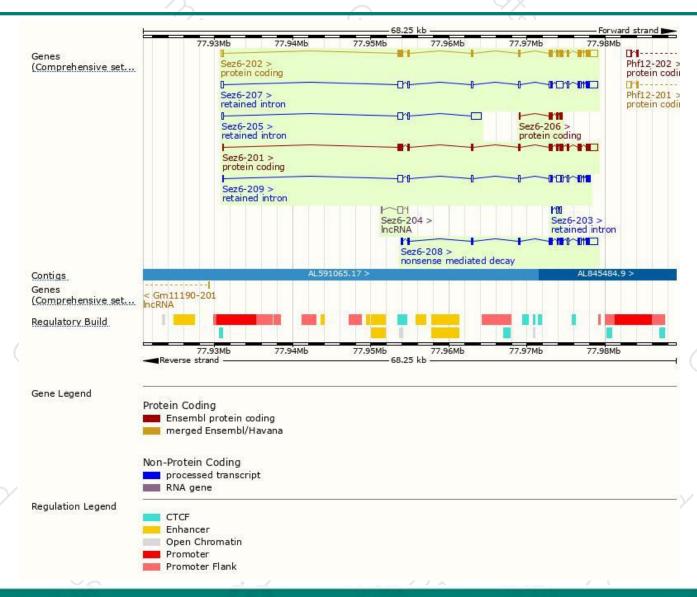
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sez6-202	ENSMUST00000093995.9	4239	991aa	Protein coding	CCDS25087	Q7TSK2	TSL:1 GENCODE basic APPRIS P3
Sez6-201	ENSMUST00000000646.13	3964	<u>977aa</u>	Protein coding	CCDS70255	Q7TSK2	TSL:1 GENCODE basic APPRIS ALT2
Sez6-206	ENSMUST00000140630.1	832	<u>278aa</u>	Protein coding	49	F6SXT0	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
Sez6-208	ENSMUST00000151982.7	3424	452aa	Nonsense mediated decay	20	F6XNR8	CDS 5' incomplete TSL:5
Sez6-207	ENSMUST00000142542.7	4523	No protein	Retained intron	- Tá	-	TSL:2
Sez6-209	ENSMUST00000155087.7	3226	No protein	Retained intron	*8	*	TSL:2
Sez6-205	ENSMUST00000138749.7	2229	No protein	Retained intron	49	~	TSL:1
Sez6-203	ENSMUST00000126866.1	467	No protein	Retained intron	20	20	TSL:3
Sez6-204	ENSMUST00000138346.1	813	No protein	IncRNA	7.6	-	TSL:5

The strategy is based on the design of Sez6-202 transcript, The transcription is shown below



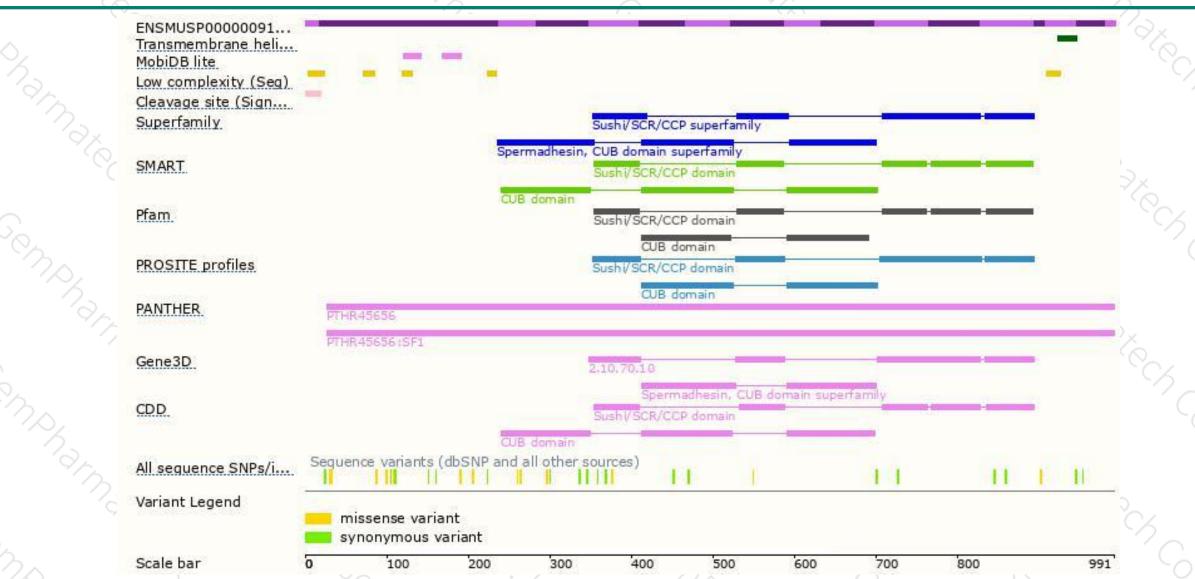
Genomic location distribution





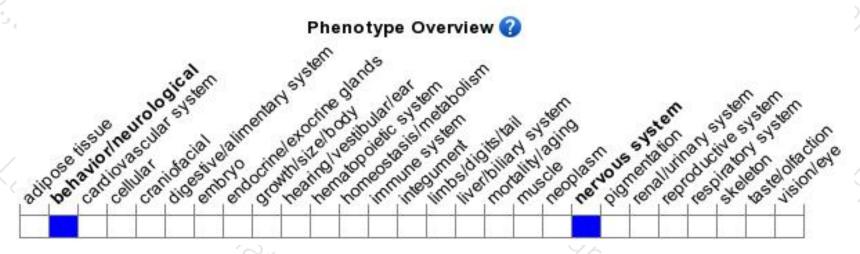
Protein domain





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 increased short dendrites, decreased excitatory synaptic signaling, resistance to pharmacologically induces seizures, decreased activity and impaired learning and coordination.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





