

Etv1 Cas9-KO Strategy

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Project Overview



Project Name Etv1

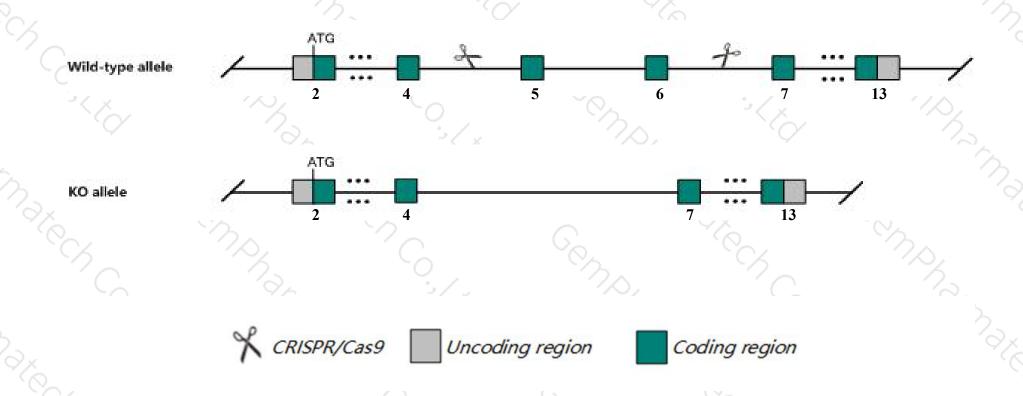
Project type Cas9-KO

Strain background C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Etv1* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Etv1* gene has 13 transcripts. According to the structure of *Etv1* gene, exon5-exon6 of *Etv1-201* (ENSMUST00000095767.10) transcript is recommended as the knockout region. The region contains 184bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Etv1* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice



- > According to the existing MGI data, Homozygous inactivation of this gene leads to premature death, ataxia, impaired limb coordination, defects in muscle innervation, muscle spindle differentiation and sensory-motor connectivity, deficient golgi tendon organs, and absence of Pacinian corpuscles and their afferents.
- > The *Etv1* gene is located on the Chr12. 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)



Etv1 ets variant 1 [Mus musculus (house mouse)]

Gene ID: 14009, updated on 2-Apr-2019

Summary

☆ ?

Official Symbol Etv1 provided by MGI

Official Full Name ets variant 1 provided by MGI

Primary source MGI:MGI:99254

See related Ensembl: ENSMUSG00000004151

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 ER81, Etsrp81

Expression Biased expression in cerebellum adult (RPKM 13.2), frontal lobe adult (RPKM 4.0) and 9 other tissuesSee more

Orthologs human all

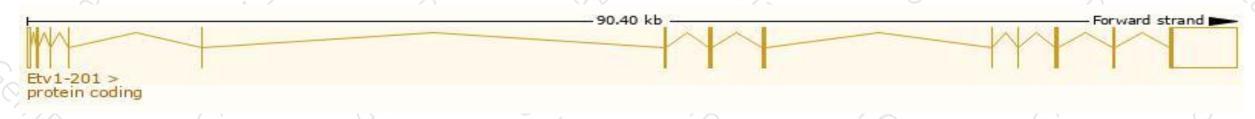
Transcript information (Ensembl)



The gene has 13 transcripts, all transcripts are shown below:

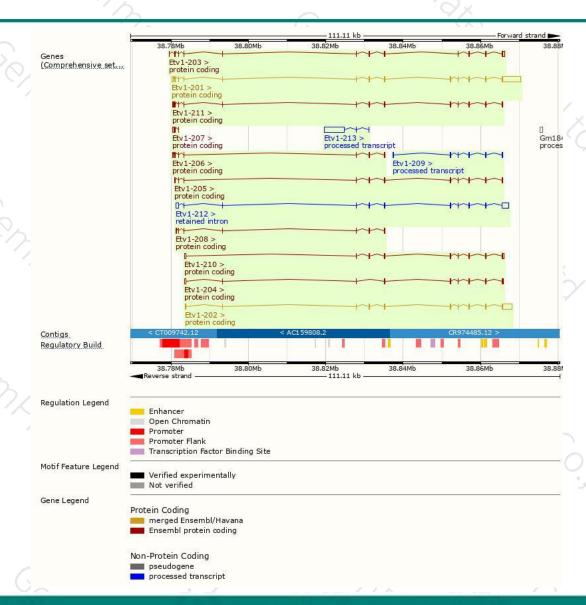
			· / ` / ` .			
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000095767.10	6576	477aa	Protein coding	CCDS49053	P41164 Q549J8	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000159334.7	3981	<u>437aa</u>	Protein coding	CCDS49054	Q8CCR6	TSL:1 GENCODE basic
ENSMUST00000162563.7	1865	<u>477aa</u>	Protein coding	CCDS49053	P41164 Q549J8	TSL:5 GENCODE basic APPRIS P1
ENSMUST00000160856.7	1474	459aa	Protein coding	CCDS83959	E0CZ54	TSL:5 GENCODE basic
ENSMUST00000160244.7	2032	454aa	Protein coding	Tá	E0CZ37	TSL:5 GENCODE basic
ENSMUST00000161980.7	1939	419aa	Protein coding		E0CXD2	TSL:5 GENCODE basic
ENSMUST00000160701.7	1578	374aa	Protein coding	20	E0CYN8	TSL:5 GENCODE basic
ENSMUST00000160996.7	850	230aa	Protein coding	29	E0CXE6	CDS 3' incomplete TSL:3
ENSMUST00000161513.8	828	249aa	Protein coding	Ŧá	E0CYI1	CDS 3' incomplete TSL:5
ENSMUST00000161164.7	544	<u>20aa</u>	Protein coding	-	E0CXX3	CDS 3' incomplete TSL:5
ENSMUST00000220492.1	5482	No protein	Processed transcript	20	#1	TSL:2
ENSMUST00000161591.1	670	No protein	Processed transcript	29	20	TSL:5
ENSMUST00000162730.9	3605	No protein	Retained intron	-	7.0	TSL:1
	ENSMUST0000095767.10 ENSMUST00000159334.7 ENSMUST00000162563.7 ENSMUST00000160856.7 ENSMUST00000160244.7 ENSMUST00000161980.7 ENSMUST00000160701.7 ENSMUST00000160996.7 ENSMUST00000161513.8 ENSMUST00000161164.7 ENSMUST00000161164.7 ENSMUST00000161591.1	ENSMUST00000095767.10 6576 ENSMUST00000159334.7 3981 ENSMUST00000162563.7 1865 ENSMUST00000160856.7 1474 ENSMUST00000160244.7 2032 ENSMUST00000161980.7 1939 ENSMUST00000160701.7 1578 ENSMUST00000160996.7 850 ENSMUST00000161513.8 828 ENSMUST00000161164.7 544 ENSMUST00000220492.1 5482 ENSMUST00000161591.1 670	ENSMUST00000159334.7 3981 437aa ENSMUST00000159334.7 1865 477aa ENSMUST00000162563.7 1865 477aa ENSMUST00000160856.7 1474 459aa ENSMUST00000160244.7 2032 454aa ENSMUST00000161980.7 1939 419aa ENSMUST00000160701.7 1578 374aa ENSMUST00000160996.7 850 230aa ENSMUST00000161513.8 828 249aa ENSMUST00000161164.7 544 20aa ENSMUST00000161591.1 5482 No protein ENSMUST00000161591.1 670 No protein	ENSMUST00000095767.10 6576 477aa Protein coding ENSMUST00000159334.7 3981 437aa Protein coding ENSMUST00000162563.7 1865 477aa Protein coding ENSMUST00000160856.7 1474 459aa Protein coding ENSMUST00000160244.7 2032 454aa Protein coding ENSMUST00000161980.7 1939 419aa Protein coding ENSMUST00000160701.7 1578 374aa Protein coding ENSMUST00000160996.7 850 230aa Protein coding ENSMUST00000161513.8 828 249aa Protein coding ENSMUST00000161164.7 544 20aa Protein coding ENSMUST00000161591.1 5482 No protein Processed transcript ENSMUST00000161591.1 670 No protein Processed transcript	ENSMUST00000095767.10 6576 477aa Protein coding CCDS49053 ENSMUST00000159334.7 3981 437aa Protein coding CCDS49054 ENSMUST00000162563.7 1865 477aa Protein coding CCDS49053 ENSMUST00000160856.7 1474 459aa Protein coding CCDS83959 ENSMUST00000160244.7 2032 454aa Protein coding - ENSMUST00000161980.7 1939 419aa Protein coding - ENSMUST00000160701.7 1578 374aa Protein coding - ENSMUST00000160996.7 850 230aa Protein coding - ENSMUST00000161513.8 828 249aa Protein coding - ENSMUST00000161164.7 544 20aa Protein coding - ENSMUST000000220492.1 5482 No protein Processed transcript - ENSMUST00000161591.1 670 No protein Processed transcript -	ENSMUST00000095767.10 6576 477aa Protein coding CCDS49053 P41164 Q549J8 ENSMUST00000159334.7 3981 437aa Protein coding CCDS49054 Q8CCR6 ENSMUST00000162563.7 1865 477aa Protein coding CCDS49053 P41164 Q549J8 ENSMUST00000160856.7 1474 459aa Protein coding CCDS83959 E0CZ54 ENSMUST00000160244.7 2032 454aa Protein coding - E0CZ37 ENSMUST00000161980.7 1939 419aa Protein coding - E0CXD2 ENSMUST00000160701.7 1578 374aa Protein coding - E0CYN8 ENSMUST00000160996.7 850 230aa Protein coding - E0CXE6 ENSMUST00000161513.8 828 249aa Protein coding - E0CXX3 ENSMUST00000161164.7 544 20aa Protein coding - E0CXX3 ENSMUST00000161591.1 670 No protein Processed transcript - -

The strategy is based on the design of *Etv1-201* transcript, The transcription is shown below



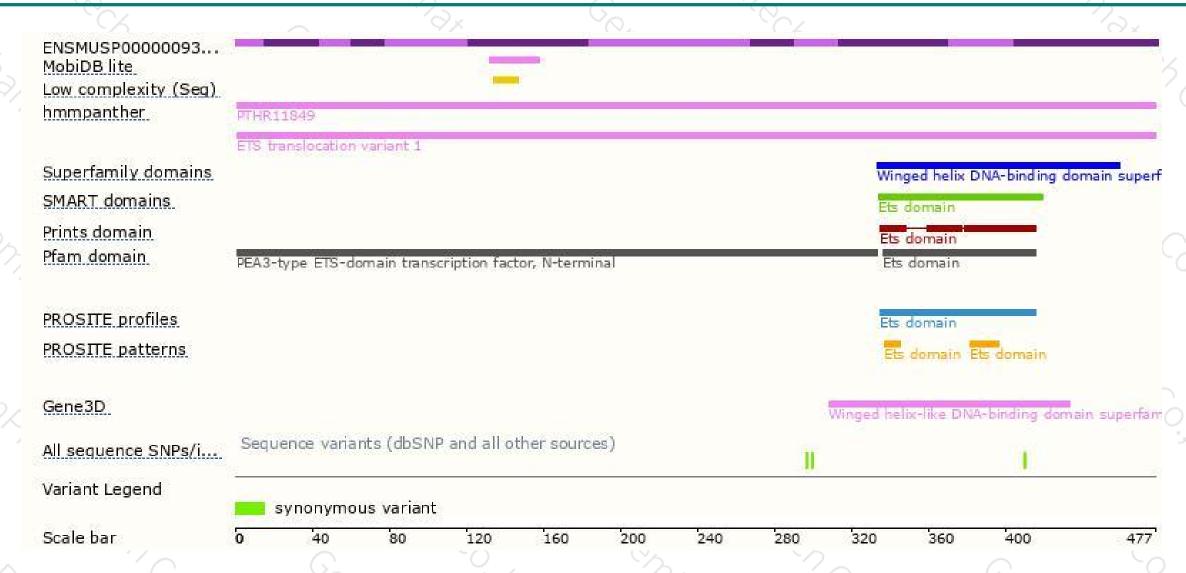
Genomic location distribution





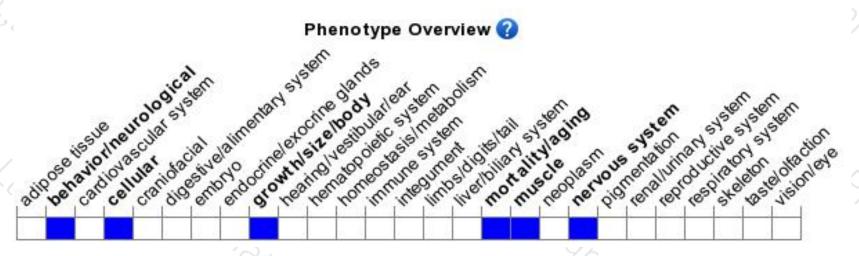
Protein domain





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 inactivation of this gene leads to premature death, ataxia, impaired limb coordination, defects in muscle innervation, muscle spindle differentiation and sensory-motor connectivity, deficient golgi tendon organs, and absence of Pacinian corpuscles and their afferents.



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





