Espn Cas9-KO Strategy

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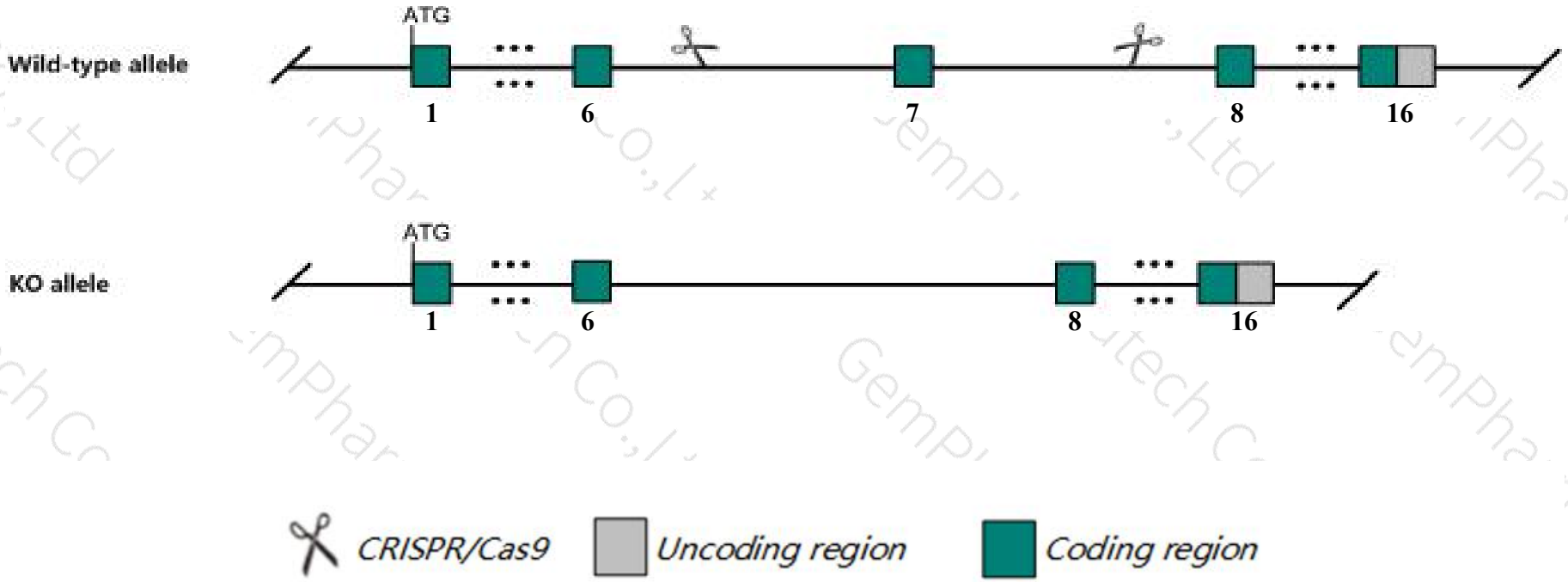
Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Espn* gene has 20 transcripts. According to the structure of *Espn* gene, exon7 of *Espn-201* (ENSMUST00000030785.14) transcript is recommended as the knockout region.The region contains 281bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

- According to the existing MGI data,Homozygotes for a spontaneous mutation exhibit progressive degeneration of both inner and outer hair cells, severe deafness, vestibular dysfunction, and poor mothering ability. Heterozygotes show a progressive, age-related hearing loss.

- The *Espn* gene is located on the Chr4. 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）

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Espn espin [*Mus musculus* (house mouse)]

Gene ID: 56226, updated on 27-Aug-2019

Summary

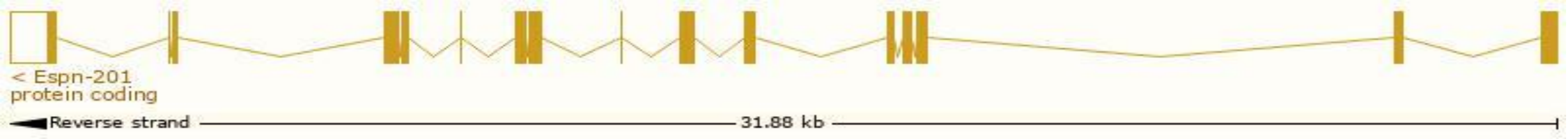
Official Symbol	Espn provided by MGI
Official Full Name	espin provided by MGI
Primary source	MGI:MGI:1861630
See related	Ensembl:ENSMUSG00000028943
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	je
Expression	Biased expression in duodenum adult (RPKM 67.5), small intestine adult (RPKM 49.0) and 9 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 20 transcripts,all transcripts are shown below:

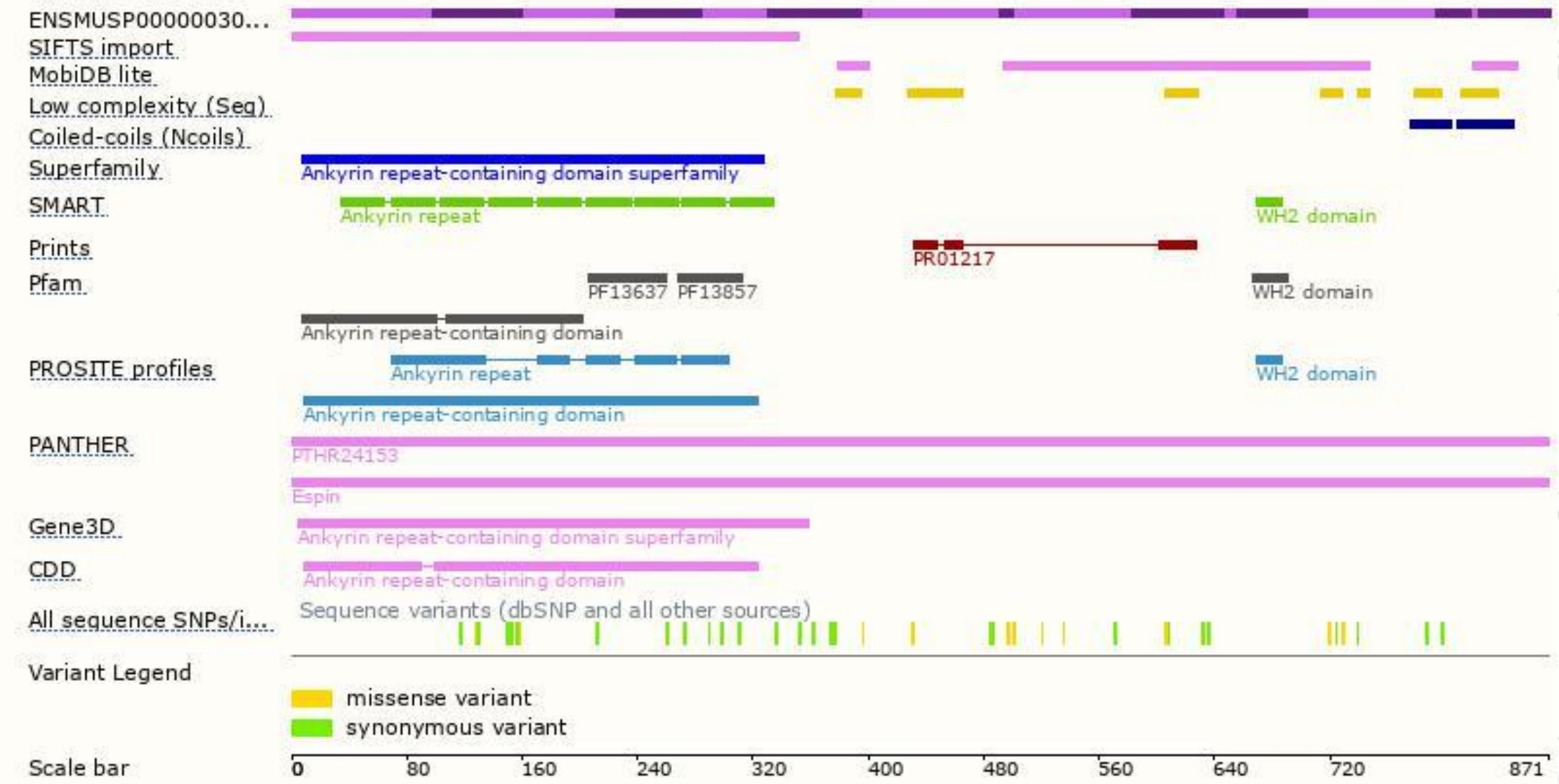
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Espn-201	ENSMUST00000030785.14	3406	871aa	Protein coding	CCDS18989	Q9ET47	TSL:1 GENCODE basic APPRIS P2
Espn-205	ENSMUST00000084114.11	1645	533aa	Protein coding	CCDS18990	Q9ET47	TSL:1 GENCODE basic
Espn-203	ENSMUST00000070018.13	1618	524aa	Protein coding	CCDS18993	Q9ET47	TSL:1 GENCODE basic
Espn-204	ENSMUST00000080042.12	1402	452aa	Protein coding	CCDS18991	Q9ET47	TSL:1 GENCODE basic
Espn-211	ENSMUST00000105657.8	1375	443aa	Protein coding	CCDS18992	Q9ET47	TSL:1 GENCODE basic
Espn-202	ENSMUST00000049305.13	1142	253aa	Protein coding	CCDS18994	Q9DD12	TSL:1 GENCODE basic
Espn-220	ENSMUST00000207676.1	4618	1405aa	Protein coding	-	A0A140LJB0	TSL:5 GENCODE basic APPRIS ALT2
Espn-213	ENSMUST00000105659.8	3595	881aa	Protein coding	-	B1AWQ4	TSL:5 GENCODE basic APPRIS ALT2
Espn-212	ENSMUST00000105658.7	2815	848aa	Protein coding	-	B1AWQ3	TSL:5 GENCODE basic APPRIS ALT2
Espn-214	ENSMUST00000135185.1	2102	700aa	Protein coding	-	B1AWQ1	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Espn-210	ENSMUST00000105656.7	1593	530aa	Protein coding	-	B1AWP8	TSL:5 GENCODE basic
Espn-208	ENSMUST00000105654.7	1566	521aa	Protein coding	-	B1AWQ0	TSL:5 GENCODE basic
Espn-207	ENSMUST00000105653.7	1411	285aa	Protein coding	-	Q9ET47	TSL:5 GENCODE basic
Espn-209	ENSMUST00000105655.7	1350	449aa	Protein coding	-	B1AWP7	TSL:5 GENCODE basic
Espn-206	ENSMUST00000103196.8	1323	440aa	Protein coding	-	B1AWP9	TSL:5 GENCODE basic
Espn-216	ENSMUST00000137937.7	1190	No protein	Retained intron	-	-	TSL:1
Espn-217	ENSMUST00000148075.1	784	No protein	Retained intron	-	-	TSL:3
Espn-218	ENSMUST00000150958.7	2365	No protein	lncRNA	-	-	TSL:1
Espn-219	ENSMUST00000156517.7	1734	No protein	lncRNA	-	-	TSL:1
Espn-215	ENSMUST00000136627.7	882	No protein	lncRNA	-	-	TSL:5

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

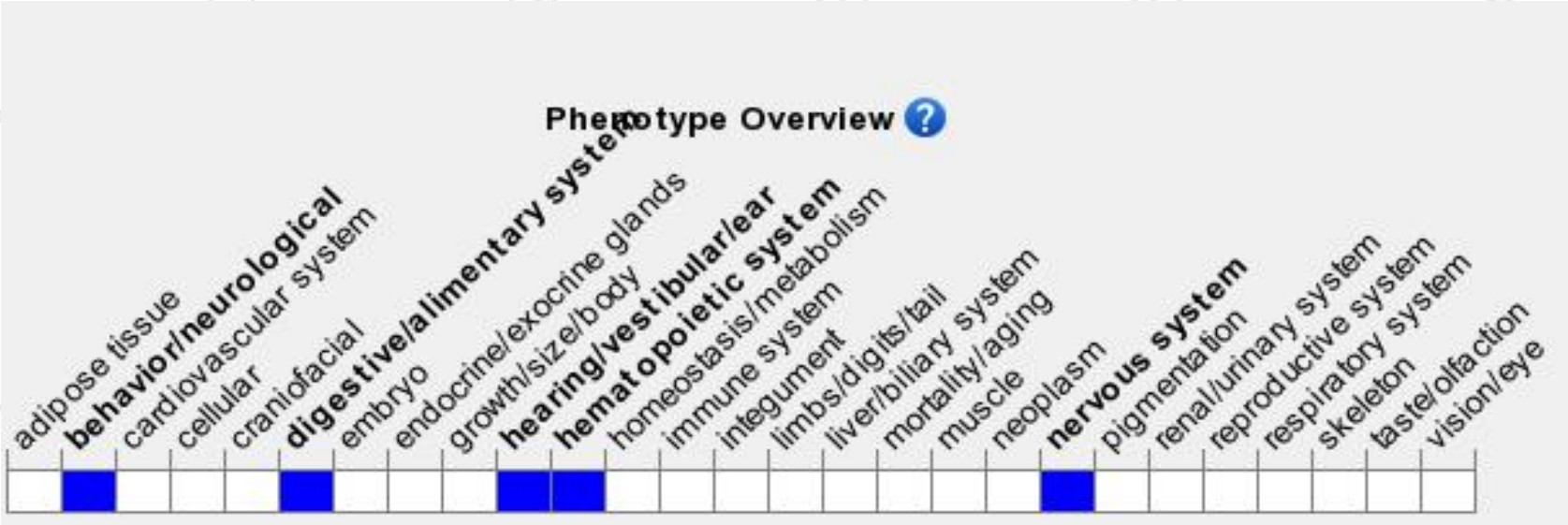


Genomic location distribution

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/).

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

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