

# *Usp53* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Usp53*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Usp53* gene. The schematic diagram is as follows:



- The *Usp53* gene has 10 transcripts. According to the structure of *Usp53* gene, exon3-exon6 of *Usp53-201* (ENSMUST00000090379.6) transcript is recommended as the knockout region. The region contains 425bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Usp53* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for an ENU-induced allele show progressive hearing loss associated with altered cochlear outer hair cell (OHC) morphology, reduced endocochlear potential, and early OHC loss followed by IHC and spiral ganglion degeneration. Heterozygotes are susceptible to noise-induced hearing loss.
- The *Usp53* gene is located on the Chr3. 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)

## Usp53 ubiquitin specific peptidase 53 [Mus musculus (house mouse)]

Gene ID: 99526, updated on 31-Jan-2019

### Summary



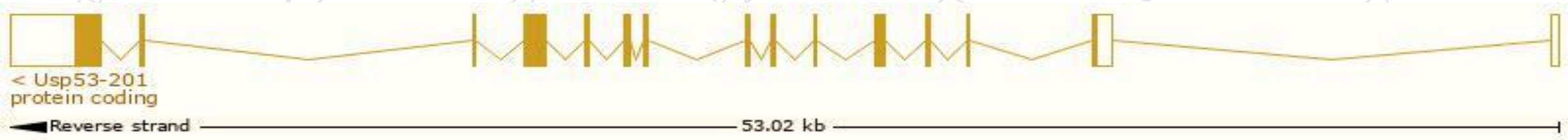
<b>Official Symbol</b>	Usp53 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	ubiquitin specific peptidase 53 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2139607</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000039701</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	PROVISIONAL
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	AA939927, Phxr3, Sp6, mKIAA1350, mbo
<b>Expression</b>	Ubiquitous expression in cerebellum adult (RPKM 3.0), colon adult (RPKM 2.7) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

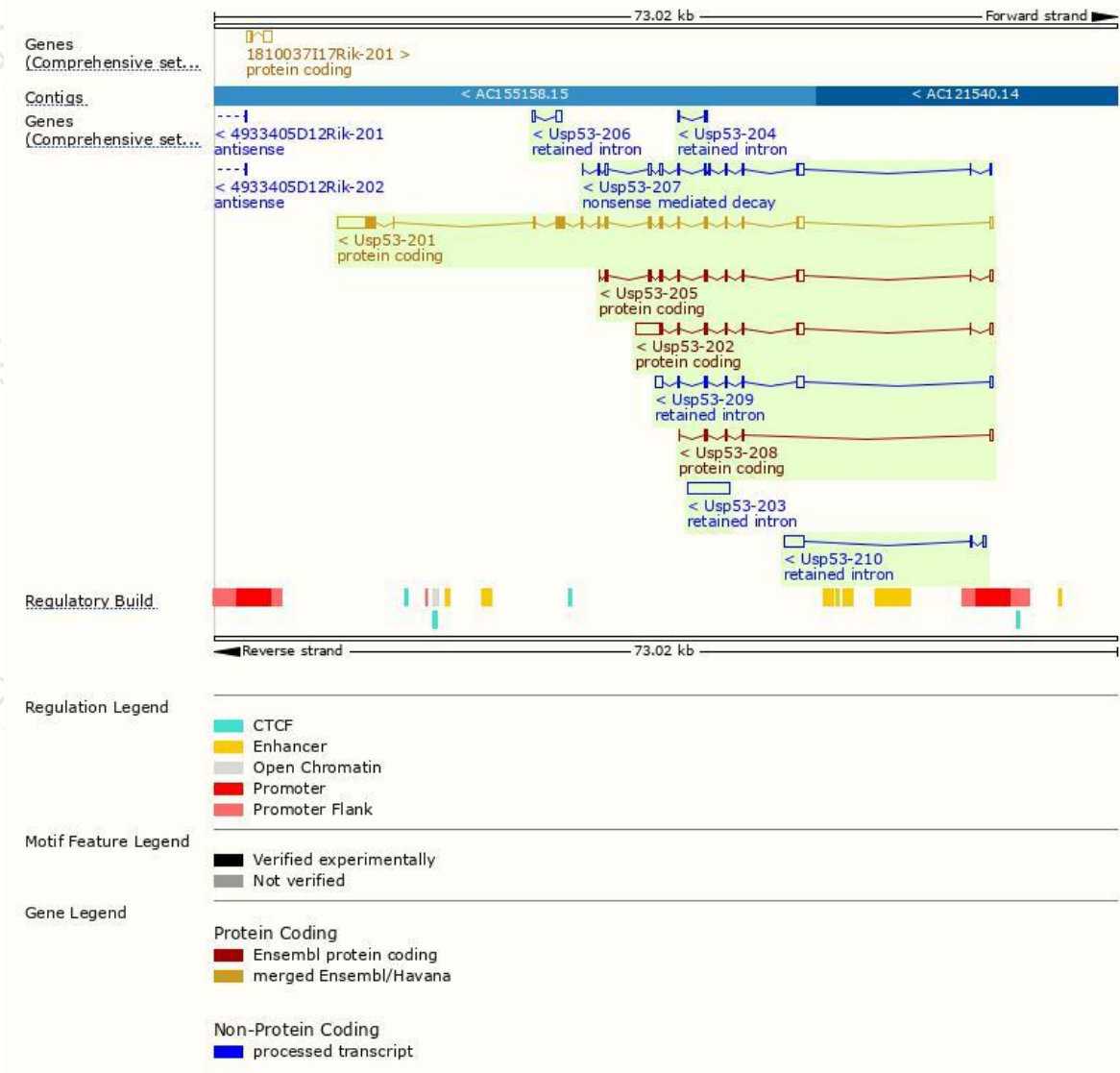
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Usp53-201	<a href="#">ENSMUST00000090379.6</a>	6185	<a href="#">1069aa</a>	Protein coding	<a href="#">CCDS17815</a>	<a href="#">P15975</a>	TSL:1 GENCODE basic APPRIS P1
Usp53-202	<a href="#">ENSMUST00000197314.4</a>	3586	<a href="#">283aa</a>	Protein coding	-	<a href="#">P15975 Q8BSX5</a>	TSL:5 GENCODE basic
Usp53-205	<a href="#">ENSMUST00000197934.4</a>	2048	<a href="#">427aa</a>	Protein coding	-	<a href="#">Q3USD9</a>	CDS 3' incomplete TSL:1
Usp53-208	<a href="#">ENSMUST00000199401.1</a>	664	<a href="#">90aa</a>	Protein coding	-	<a href="#">A0A0G2JG80</a>	CDS 3' incomplete TSL:3
Usp53-207	<a href="#">ENSMUST00000199329.4</a>	1882	<a href="#">128aa</a>	Nonsense mediated decay	-	<a href="#">A0A0G2JFC5</a>	TSL:1
Usp53-203	<a href="#">ENSMUST00000197358.1</a>	3407	No protein	Retained intron	-	-	TSL:NA
Usp53-209	<a href="#">ENSMUST00000199923.4</a>	1984	No protein	Retained intron	-	-	TSL:1
Usp53-210	<a href="#">ENSMUST00000200188.1</a>	1960	No protein	Retained intron	-	-	TSL:1
Usp53-206	<a href="#">ENSMUST00000198814.1</a>	745	No protein	Retained intron	-	-	TSL:3
Usp53-204	<a href="#">ENSMUST00000197801.1</a>	306	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Usp53-201* transcript,The transcription is shown below

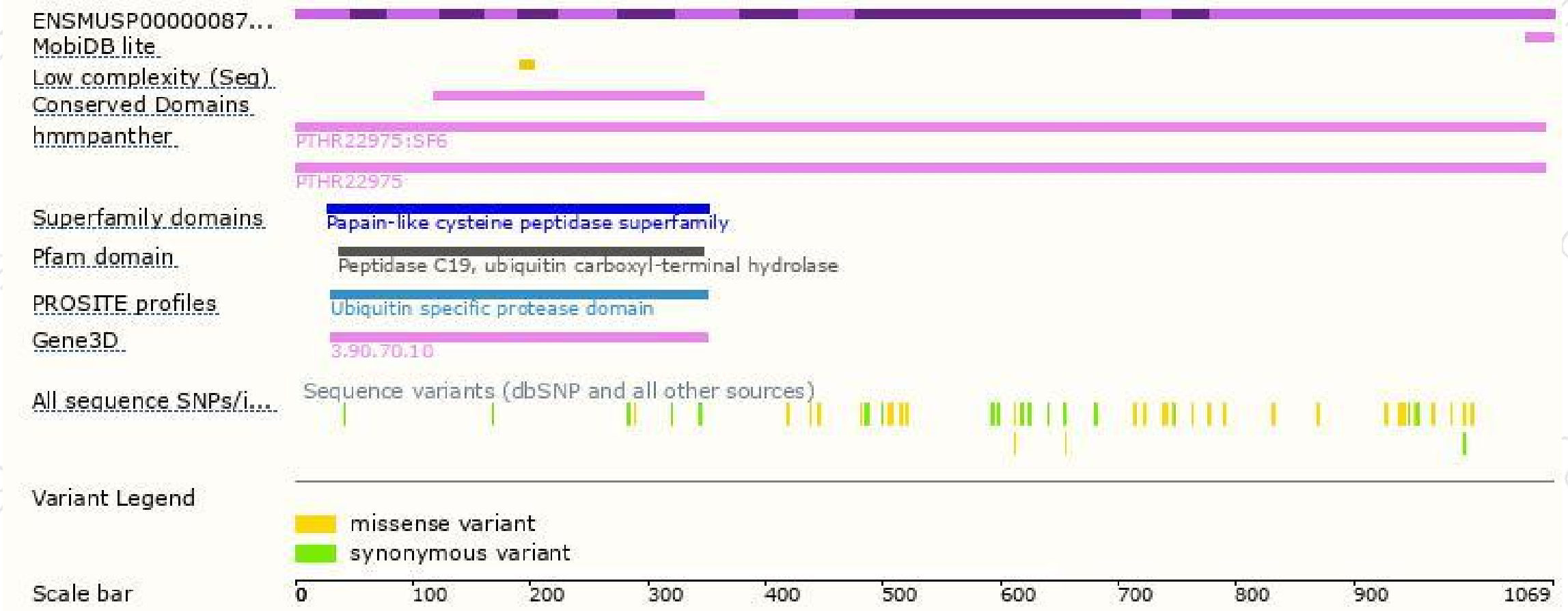


# Genomic location distribution

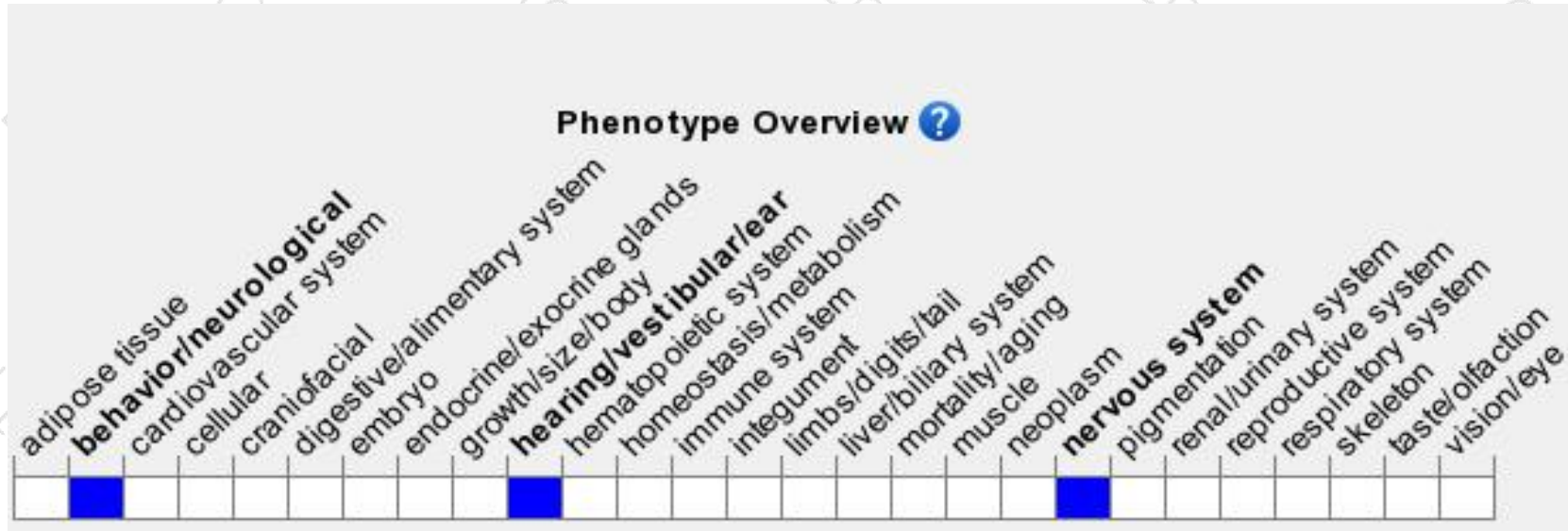




# Protein domain



# 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, Homozygotes for an ENU-induced allele show progressive hearing loss associated with altered cochlear outer hair cell (OHC) morphology, reduced endocochlear potential, and early OHC loss followed by IHC and spiral ganglion degeneration. Heterozygotes are susceptible to noise-induced hearing loss.

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

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