

Zyx Cas9-KO Strategy

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Project Overview



Project Name Zyx

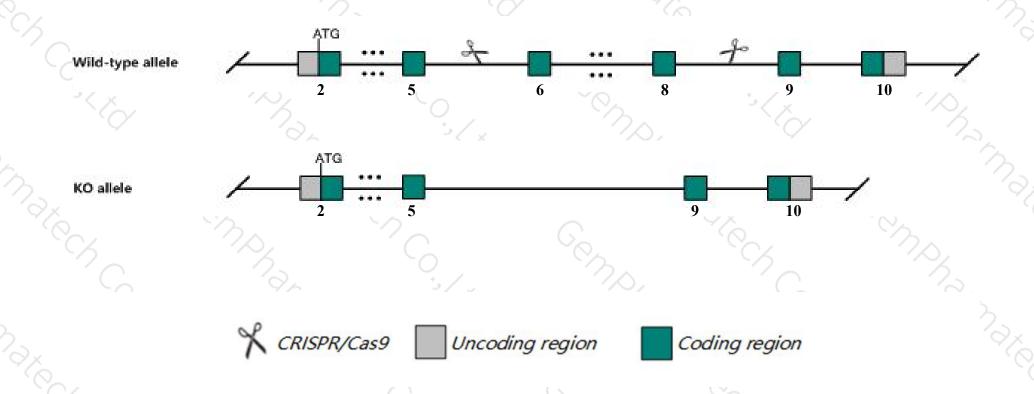
Project type Cas9-KO

Strain background C57BL/6JGpt

Knockout strategy



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



Technical routes



- The Zyx gene has 11 transcripts. According to the structure of Zyx gene, exon6-exon8 of Zyx-202 (ENSMUST00000164375.3) transcript is recommended as the knockout region. The region contains 470bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify Zyx gene. The brief process is as follows: CRISPR/Cas9 system we

Notice



- ➤ According to the existing MGI data, Mice lacking functional copies of this gene are viable, fertile, and develop normally.
- Transcript Zyx-204/206/ 208/209 may not be affected. The KO region is close to Epha1 gene, Knockout the region may affect the regulatory function of Epha1 gene.
- > The Zyx gene is located on the Chr6. 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)



Zyx zyxin [Mus musculus (house mouse)]

Gene ID: 22793, updated on 3-Sep-2019

Summary

☆? -

Official Symbol Zyx provided by MGI
Official Full Name zyxin provided by MGI
Primary source MGI:MGI:103072

See related Ensembl: ENSMUSG00000029860

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 R75157; 9530098H06Rik

Expression Ubiquitous expression in lung adult (RPKM 88.7), ovary adult (RPKM 71.5) and 28 other tissues See more

Orthologs human all



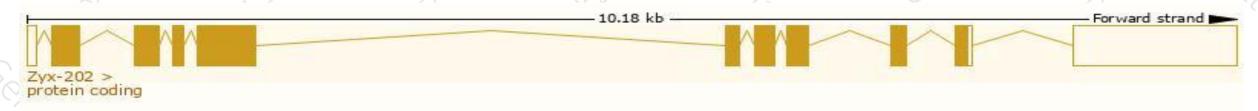
Transcript information (Ensembl)



The gene has 11 transcripts, all transcripts are shown below:

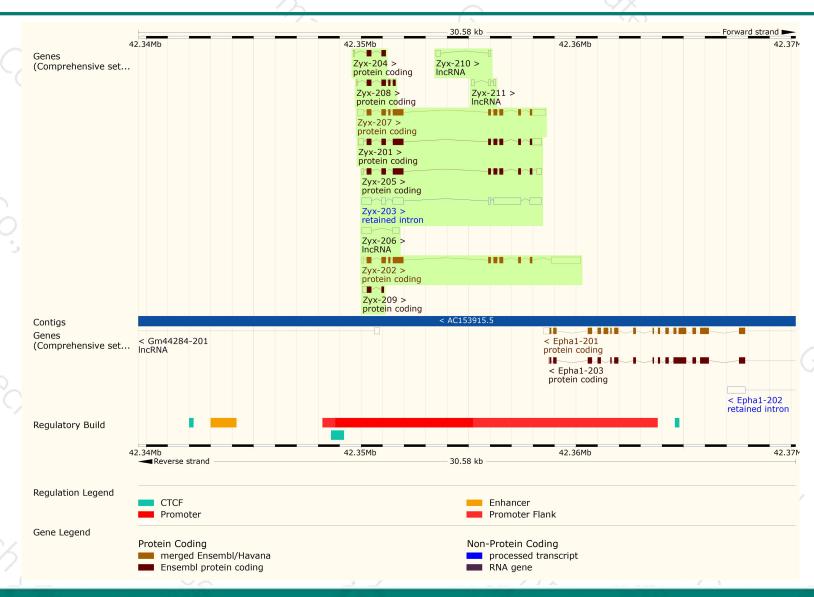
| | | | | | - dia | | | |
|---------|-----------------------|------|--------------|----------------------|-----------------|-------------|-------------------|---------------------------------|
| Name 🍦 | Transcript ID | bp 🛊 | Protein | Translation ID | Biotype | CCDS | UniProt | Flags |
| Zyx-202 | ENSMUST00000164375.3 | 3188 | <u>564aa</u> | ENSMUSP00000126622.1 | Protein coding | CCDS20066 ₺ | <u>Q62523</u> ₽ | TSL:1 GENCODE basic APPRIS P3 |
| Zyx-207 | ENSMUST00000203652.2 | 2605 | <u>564aa</u> | ENSMUSP00000145451.1 | Protein coding | CCDS20066 ₺ | <u>Q62523</u> ₽ | TSL:1 GENCODE basic APPRIS P3 |
| Zyx-201 | ENSMUST00000070635.12 | 2301 | <u>533aa</u> | ENSMUSP00000070427.7 | Protein coding | CCDS85034₺ | Q7TQE2₽ | TSL:1 GENCODE basic APPRIS ALT2 |
| Zyx-205 | ENSMUST00000203401.2 | 1954 | <u>533aa</u> | ENSMUSP00000145236.1 | Protein coding | CCDS85034 € | Q7TQE2® | TSL:1 GENCODE basic APPRIS ALT2 |
| Zyx-208 | ENSMUST00000203846.2 | 695 | 212aa | ENSMUSP00000145189.1 | Protein coding | 5 | A0A0N4SVP4₽ | CDS 3' incomplete TSL:3 |
| Zyx-209 | ENSMUST00000203849.1 | 525 | <u>109aa</u> | ENSMUSP00000145052.1 | Protein coding | - | A0A0N4SVD2₽ | CDS 3' incomplete TSL:2 |
| Zyx-204 | ENSMUST00000203329.2 | 499 | <u>137aa</u> | ENSMUSP00000144863.1 | Protein coding | | A0A0N4SUX7₺ | CDS 3' incomplete TSL:3 |
| Zyx-203 | ENSMUST00000203290.2 | 3076 | No protein | = | Retained intron | - | 3 12 3 | TSL:2 |
| Zyx-206 | ENSMUST00000203626.1 | 729 | No protein | ā | IncRNA | a a | (5) | TSL:2 |
| Zyx-211 | ENSMUST00000204480.1 | 351 | No protein | = | IncRNA | - | 3 12 3 | TSL:3 |
| Zyx-210 | ENSMUST00000204270.2 | 344 | No protein | ā | IncRNA | 1.7 | (5) | TSL:2 |

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



Genomic location distribution





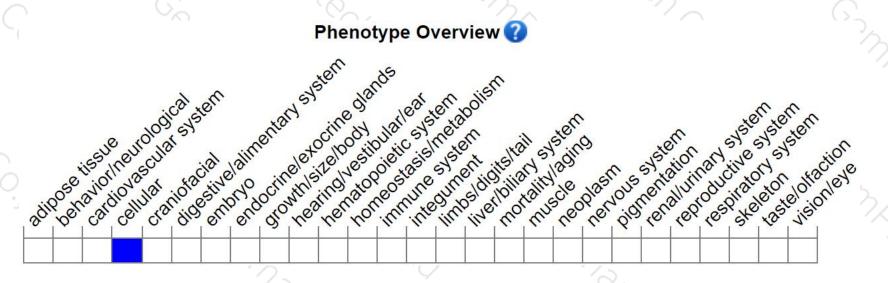
Protein domain





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 lacking functional copies of this gene are viable, fertile, and develop normally.



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





