# *Smarce1* Cas9-KO Strategy

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# Project Overview

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|---|---|
| **Project Name** | *Smarce1* |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Smarce1* gene. The schematic diagram is as follows:

# Technical routes

➢ The *Smarce1* gene has 6 transcripts. According to the structure of *Smarce1* gene, exon5-exon7 of *Smarce1-201* (ENSMUST00000103133.3) transcript is recommended as the knockout region.The region contains 385bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Smarce1* gene. The brief process is as follows: CRISPR/Cas9 syste

# Notice

➢ According to the existing MGI data, mice homozygous for a knock-out allele exhibit prenatal lethality.

➢ The *Smarce1* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information （NCBI）

**Smarce1** SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 [ *Mus musculus* (house mouse) ]

Gene ID: 57376, updated on 29-Oct-2019

## ▲ Summary

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|---|---|
| **Official Symbol** | Smarce1 provided by MGI |
| **Official Full Name** | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 provided by MGI |
| **Primary source** | MGI:MGI:1927347 |
| **See related** | Ensembl:ENSMUSG00000037935 |
| **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** | Baf27; 2810417B20Rik; 5830412H02Rik; 9030408N19Rik |
| **Expression** | Broad expression in CNS E11.5 (RPKM 73.8), CNS E14 (RPKM 55.2) and 23 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

The gene has 6 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------|---------------|-----|---------|---------|------|---------|-------|
| Smarce1-201 | ENSMUST00000103133.3 | 2919 | 411aa | Protein coding | CCDS25374 | O54941 | TSL:1　GENCODE basic　APPRIS P1 |
| Smarce1-202 | ENSMUST00000128215.1 | 3117 | No protein | lncRNA | - | - | TSL:1 |
| Smarce1-203 | ENSMUST00000128707.7 | 456 | No protein | lncRNA | - | - | TSL:5 |
| Smarce1-204 | ENSMUST00000135040.7 | 761 | No protein | lncRNA | - | - | TSL:1 |
| Smarce1-205 | ENSMUST00000155062.1 | 481 | No protein | lncRNA | - | - | TSL:2 |
| Smarce1-206 | ENSMUST00000156160.1 | 610 | No protein | lncRNA | - | - | TSL:2 |

The strategy is based on the design of *Smarce1-201* transcript,The transcription is shown below



< Smarce1-201
protein coding

◀ Reverse strand ——————————————— 21.97 kb ———————————————
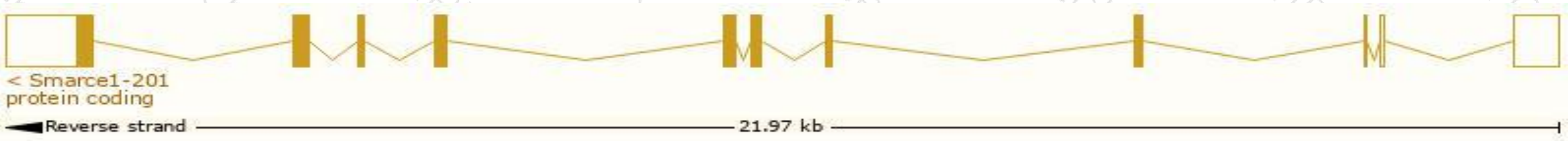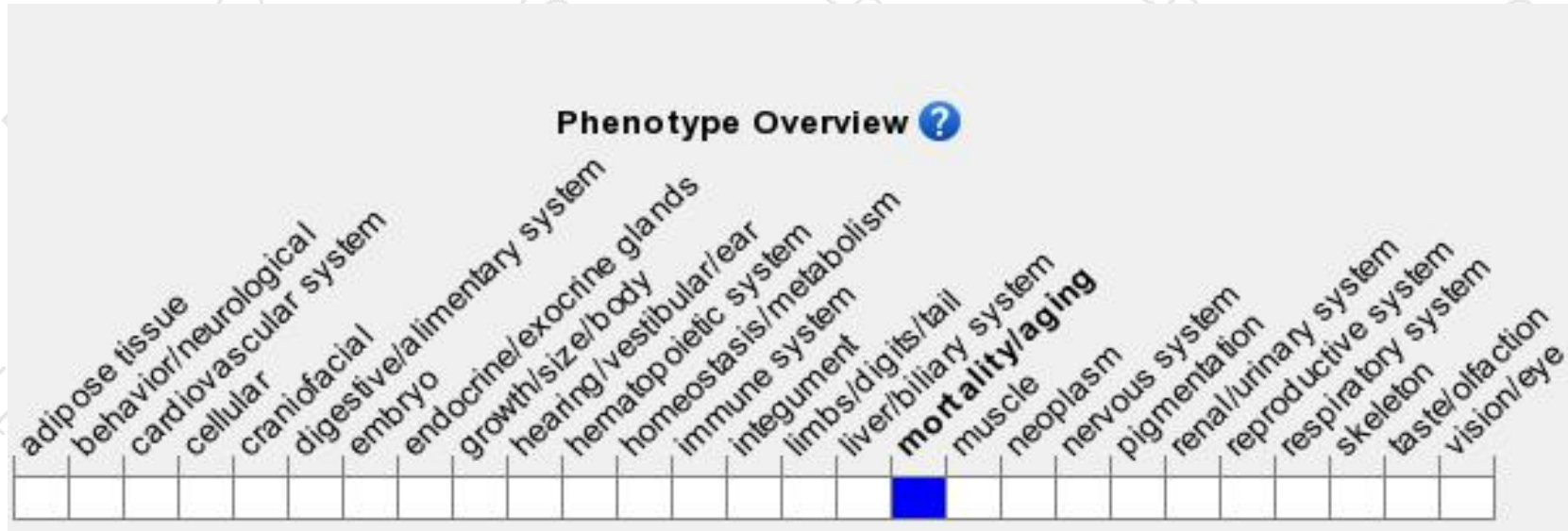
# Genomic location distribution
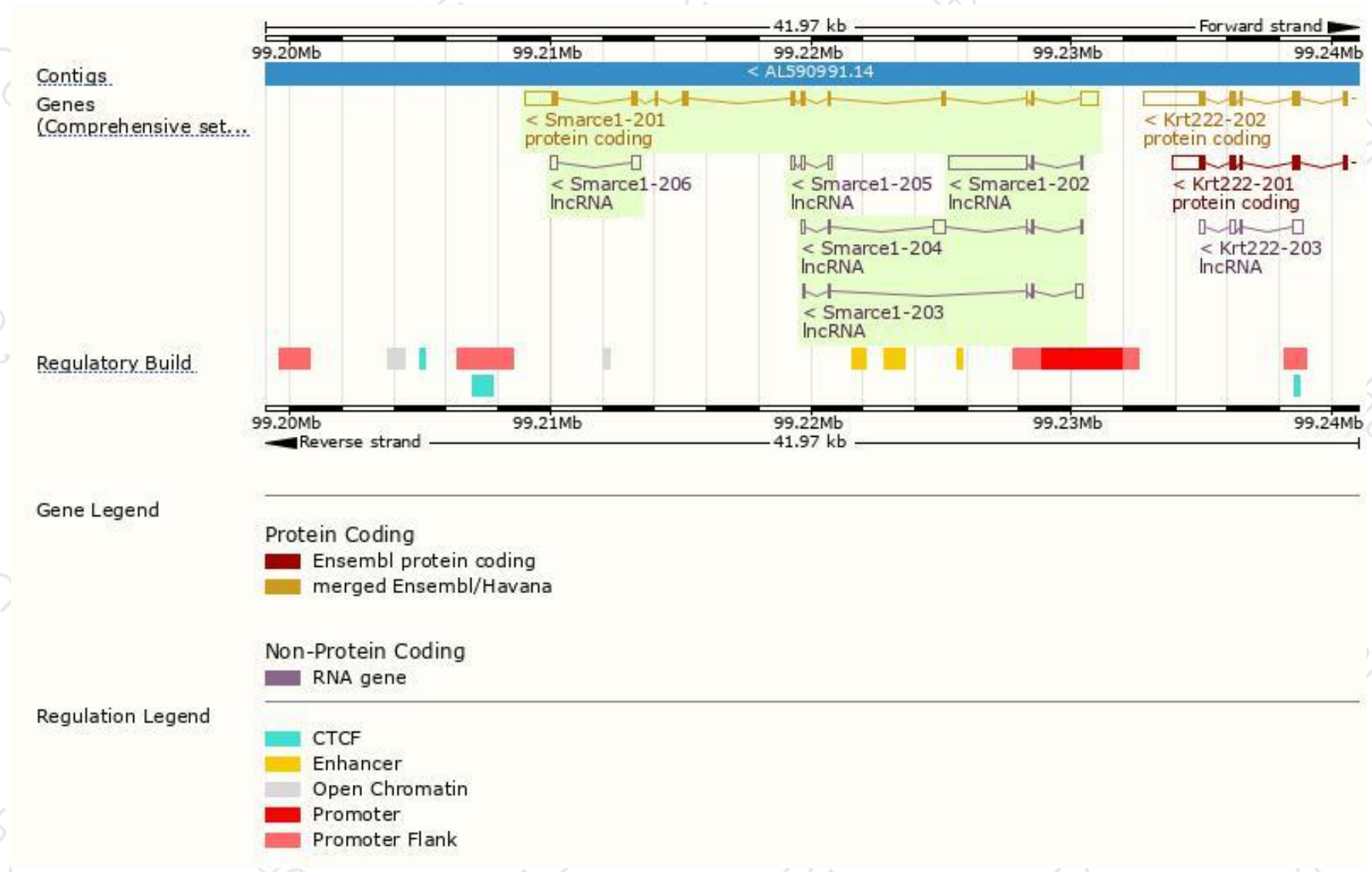
# Protein domain
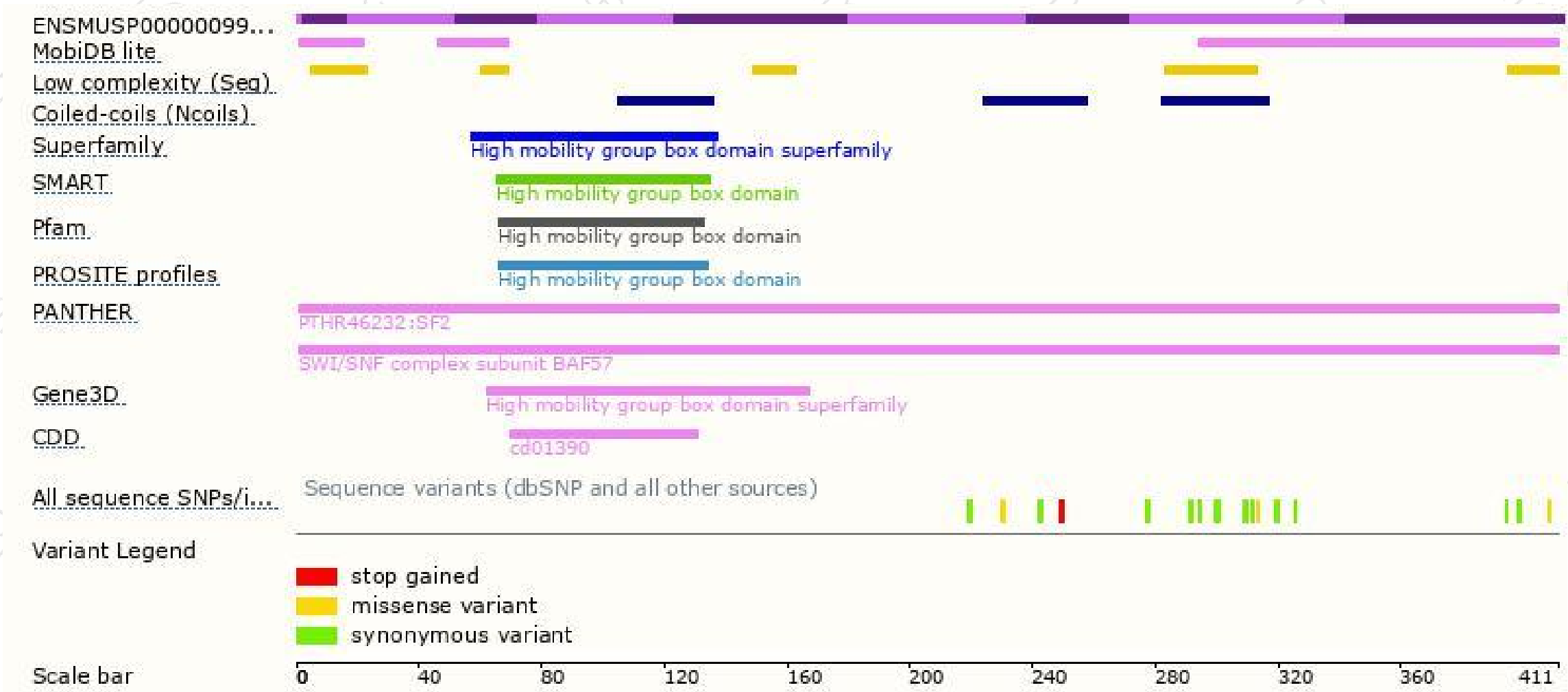
# Mouse phenotype description(MGI )



*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 knock-out allele exhibit prenatal lethality.

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