# *Brca1* Cas9-KO Strategy

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**Design Date:** 2019-7-17

# Project Overview

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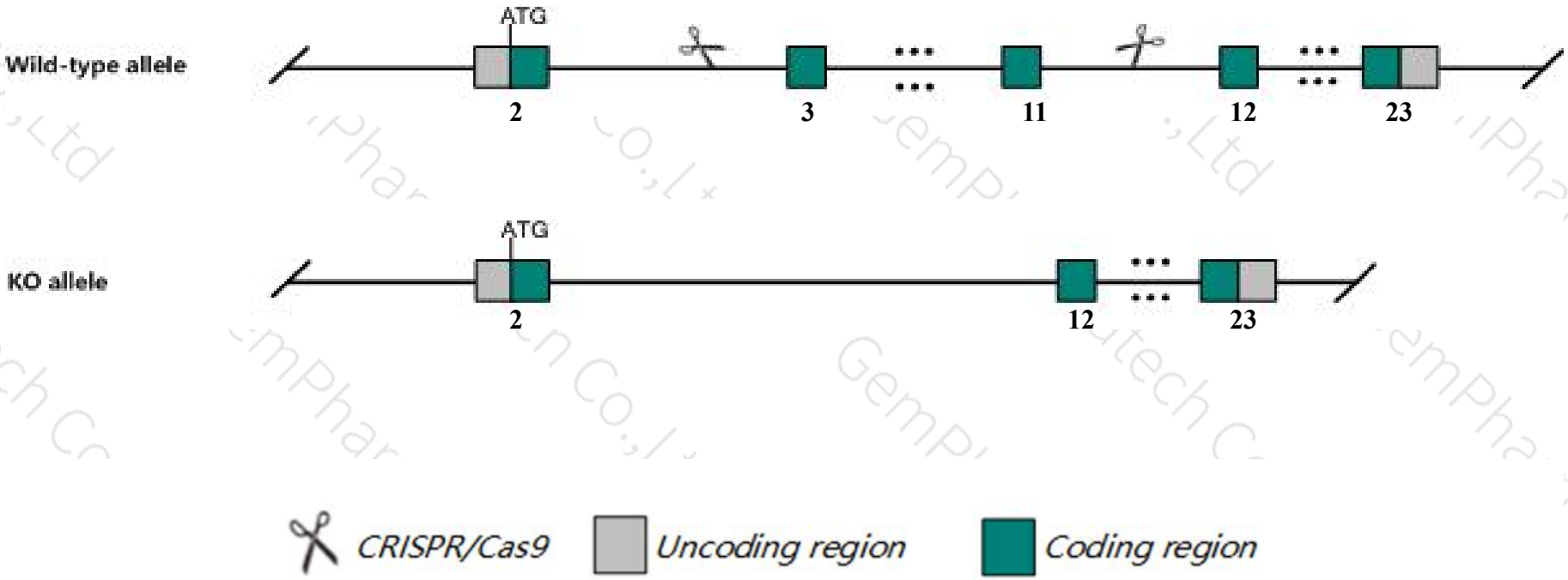
| **Project Name** | ***Brca1*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Brca1* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Brca1* gene has 7 transcripts. According to the structure of *Brca1* gene, exon3-exon11 of *Brca1-201* (ENSMUST00000017290.10) transcript is recommended as the knockout region.The region contains 3973bp coding sequenc Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Brca1* gene. The brief process is as follows: CRISPR/Cas9 system

# Notice

- According to the existing MGI data,Homozygous null mutants are embryonic lethal with abnormalities including growth retardation, neural tube defects, and mesoderm abnormalities; conditional mutations cause genetic instability and enhanced tumor formation; mutants with truncated BRCA1 protein survive, have a kinky tail, pigmentation anomalies, male infertility and increased tumor incidence.

- The *Brca1* 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）

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## Brca1 breast cancer 1, early onset [Mus musculus (house mouse)]

Gene ID: 12189, updated on 9-Apr-2019

### Summary

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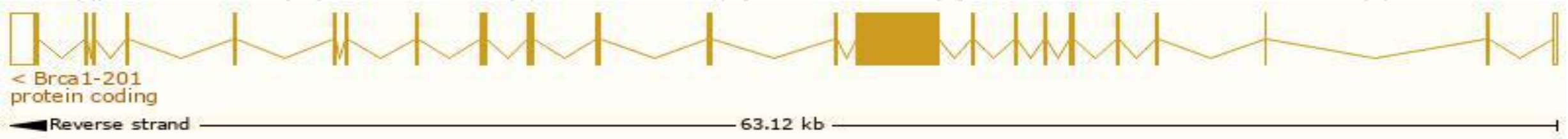
|---|---|
| **Official Symbol** | Brca1 provided by MGI |
| **Official Full Name** | breast cancer 1, early onset provided byMGI |
| **Primary source** | MGI:MGI:104537 |
| **See related** | Ensembl:ENSMUSG00000017146 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Expression** | Biased expression in liver E14 (RPKM 5.9), CNS E11.5 (RPKM 5.7) and 12 other tissuesSee more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

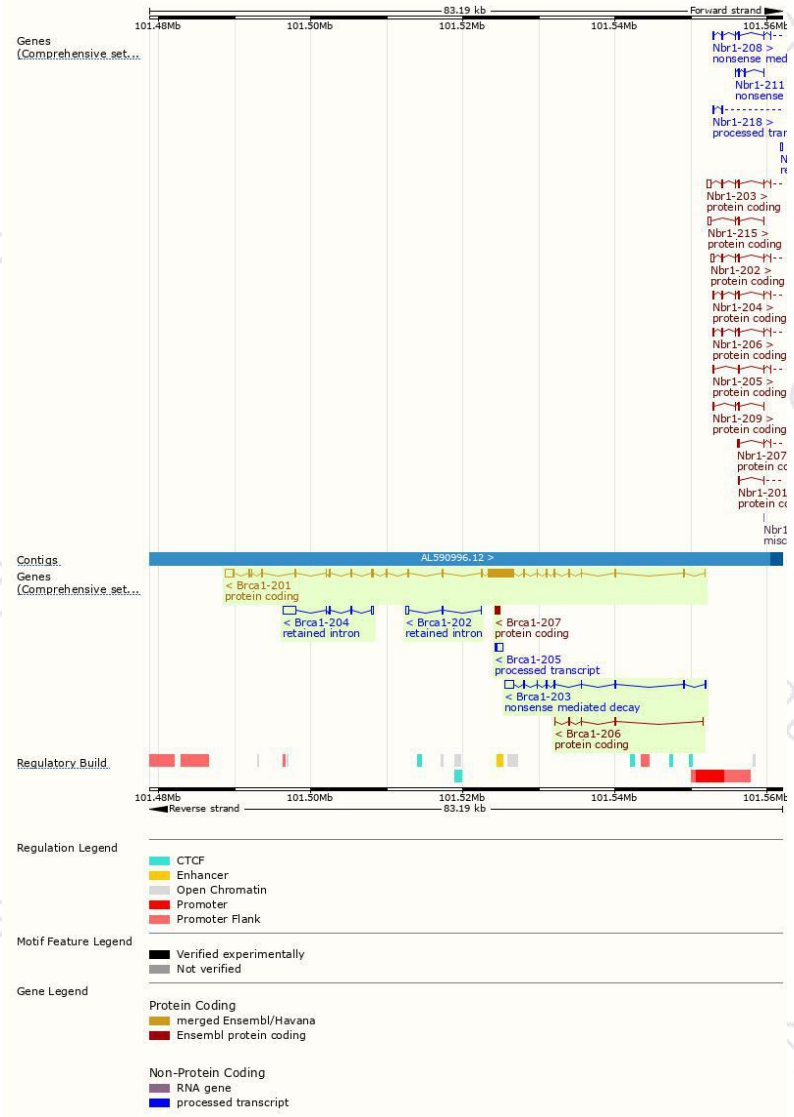
The gene has 7 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Brca1-201 | ENSMUST00000017290.10 | 6572 | 1812aa | Protein coding | CCDS25474 | P48754 | TSL:1 GENCODE basic APPRIS P1 |
| Brca1-207 | ENSMUST00000191198.1 | 531 | 177aa | Protein coding | - | A0A087WPE1 | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3 |
| Brca1-206 | ENSMUST00000190862.1 | 355 | 79aa | Protein coding | - | A0A087WP26 | CDS 3' incomplete TSL:5 |
| Brca1-203 | ENSMUST00000142086.2 | 1917 | 75aa | Nonsense mediated decay | - | A0A087WPK5 | TSL:1 |
| Brca1-205 | ENSMUST00000188168.1 | 852 | No protein | Processed transcript | - | - | TSL:3 |
| Brca1-204 | ENSMUST00000156843.1 | 2136 | No protein | Retained intron | - | - | TSL:1 |
| Brca1-202 | ENSMUST00000131460.1 | 539 | No protein | Retained intron | - | - | TSL:3 |

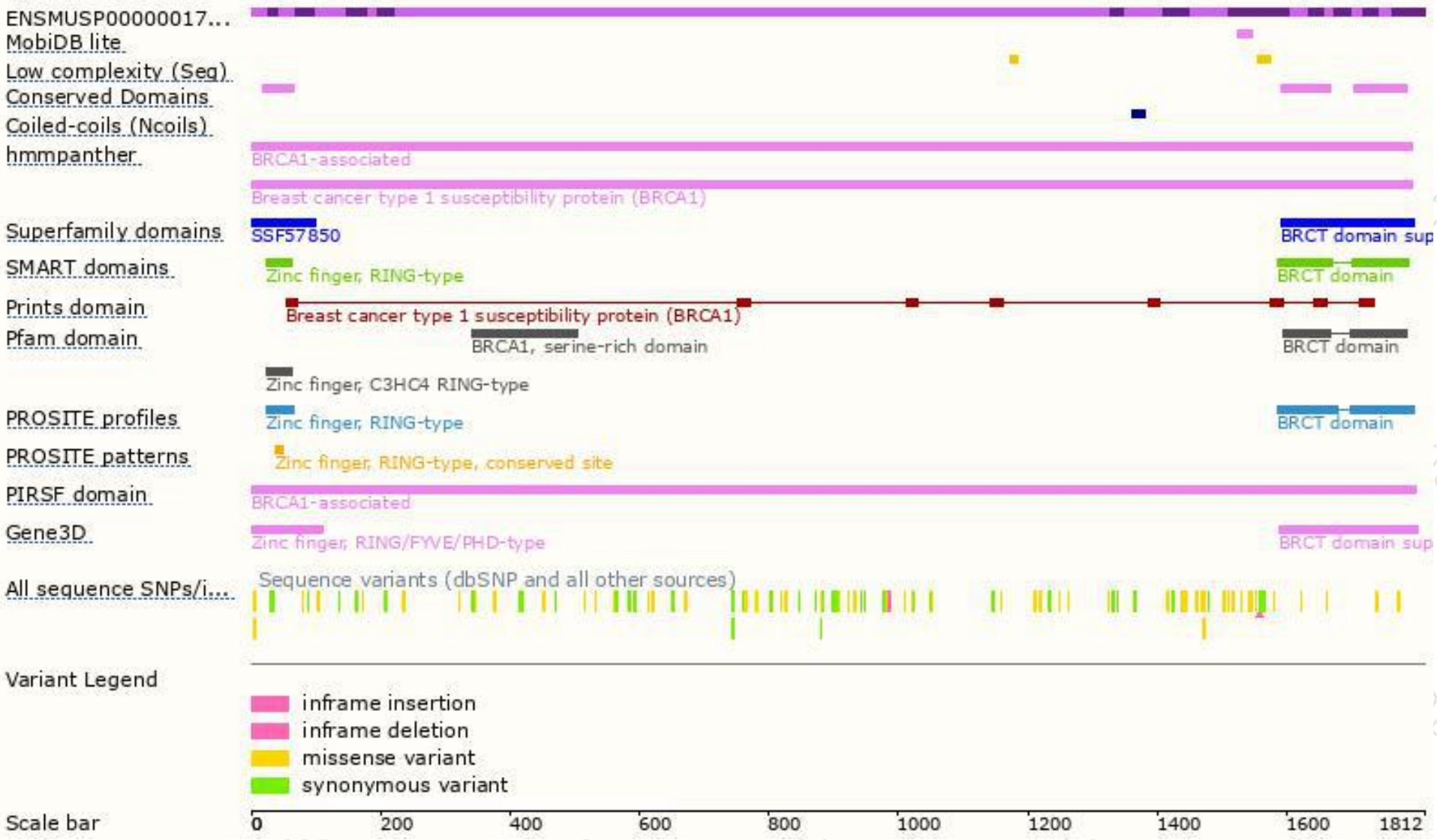
The strategy is based on the design of *Brca1-201* transcript,The transcription is shown below



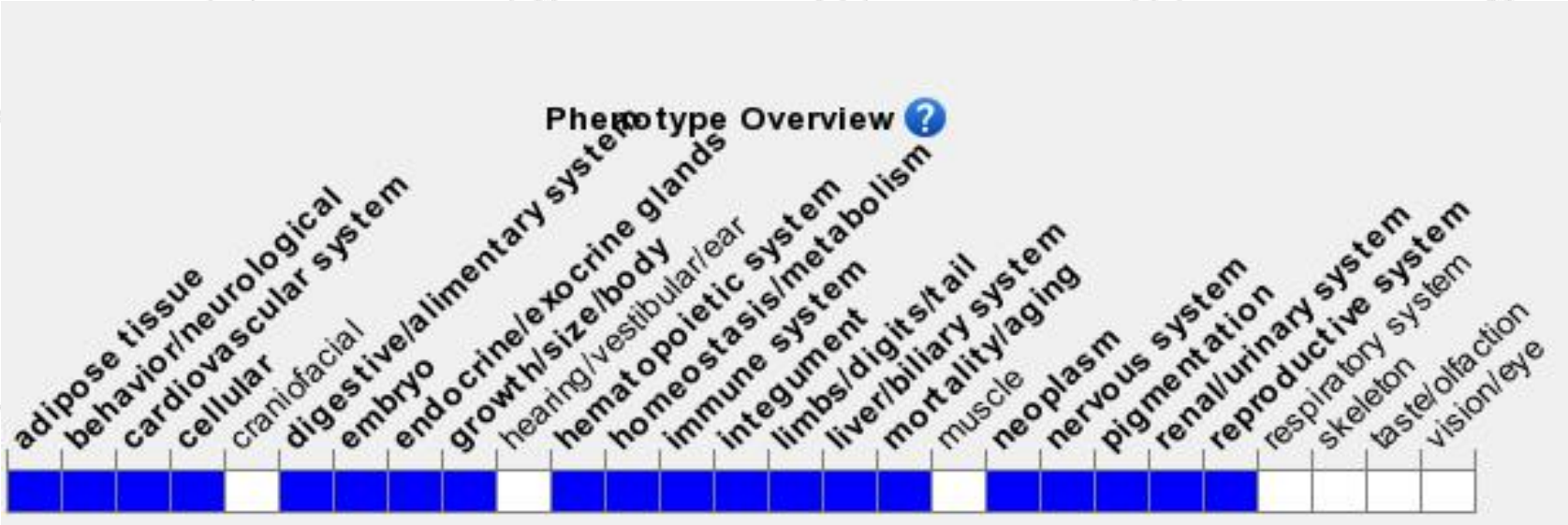
# Genomic location distribution



# 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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