

# **Brca2** Cas9-KO Strategy

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**Design Date:** 2019-7-19

# **Project Overview**



**Project Name** 

Brca2

**Project type** 

Cas9-KO

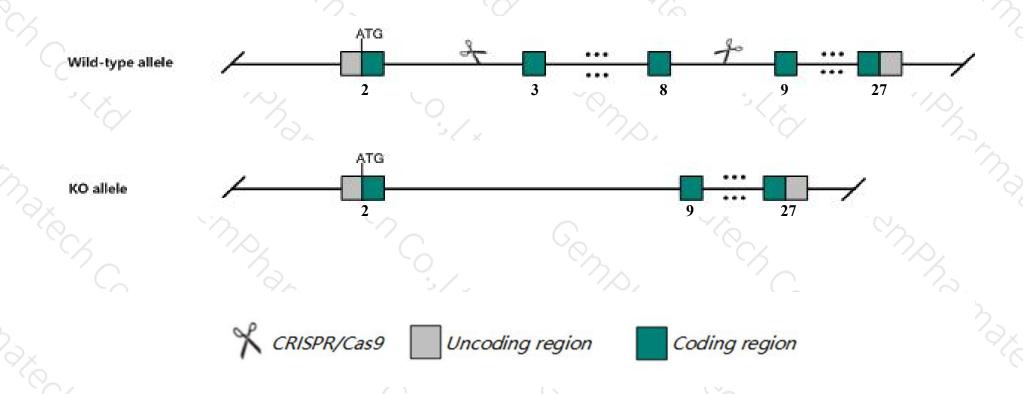
Strain background

C57BL/6JGpt

# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Brca2* gene. The schematic diagram is as follows:



### **Technical routes**



- ➤ The *Brca2* gene has 14 transcripts. According to the structure of *Brca2* gene, exon3-exon8 of *Brca2-201* (ENSMUST00000044620.10) transcript is recommended as the knockout region. The region contains 590bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Brca2* 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 BRCA2 protein survive, are small, infertile, show improper tissue differentiation and develop lymphomas and carcinomas.
- The *Brca2* gene is located on the Chr5. 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)



#### Brca2 breast cancer 2, early onset [Mus musculus (house mouse)]

Gene ID: 12190, updated on 9-Apr-2019

#### Summary

☆ ?

Official Symbol Brca2 provided by MGI

Official Full Name breast cancer 2, early onset provided by MGI

Primary source MGI:MGI:109337

See related Ensembl: ENSMUSG00000041147

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 Fancd1, RAB163

Expression Broad expression in CNS E11.5 (RPKM 2.0), liver E14 (RPKM 1.6) and 24 other tissuesSee more

Orthologs human all

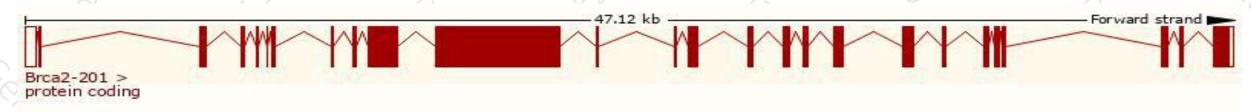
# Transcript information (Ensembl)



The gene has 14 transcripts, all transcripts are shown below:

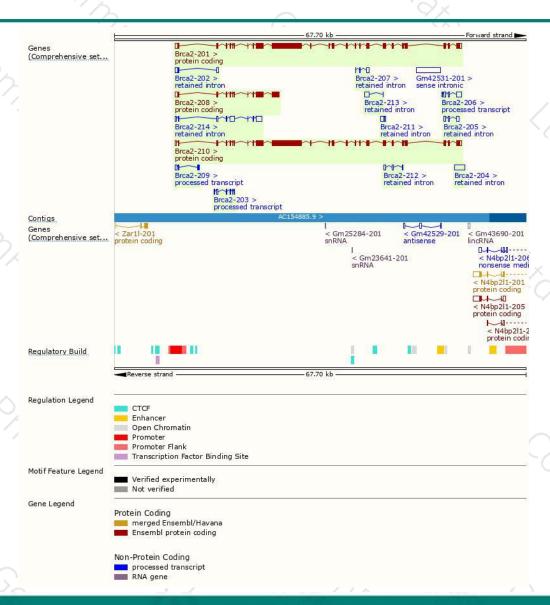
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Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Brca2-201	ENSMUST00000044620.10	10724	3329aa	Protein coding	CCDS39411	P97929	TSL:5 GENCODE basic APPRIS P1
Brca2-210	ENSMUST00000202313.1	10517	3329aa	Protein coding	CCDS39411	P97929	TSL:1 GENCODE basic APPRIS P
Brca2-208	ENSMUST00000202003.3	3473	992aa	Protein coding	0.20	A0A0J9YVI7	CDS 3' incomplete TSL:1
Brca2-206	ENSMUST00000201309.3	1340	No protein	Processed transcript	128	2	TSL:1
Brca2-203	ENSMUST00000201149.1	634	No protein	Processed transcript	-		TSL:5
Brca2-209	ENSMUST00000202192.1	588	No protein	Processed transcript	-	-	TSL:2
Brca2-214	ENSMUST00000202975.3	2534	No protein	Retained intron	0.20	ų.	TSL:2
Brca2-204	ENSMUST00000201165.1	1742	No protein	Retained intron	120	2	TSL:NA
Brca2-202	ENSMUST00000200686.3	937	No protein	Retained intron	-	5	TSL:2
Brca2-205	ENSMUST00000201226.1	864	No protein	Retained intron	-	-	TSL:2
Brca2-211	ENSMUST00000202693.1	688	No protein	Retained intron	0.20	ų.	TSL:3
Brca2-213	ENSMUST00000202837.1	669	No protein	Retained intron		2	TSL:3
Brca2-207	ENSMUST00000201678.1	646	No protein	Retained intron	1.51	54	TSL:3
Brca2-212	ENSMUST00000202727.1	479	No protein	Retained intron		-	TSL:2

The strategy is based on the design of *Brca2-201* transcript, The transcription is shown below



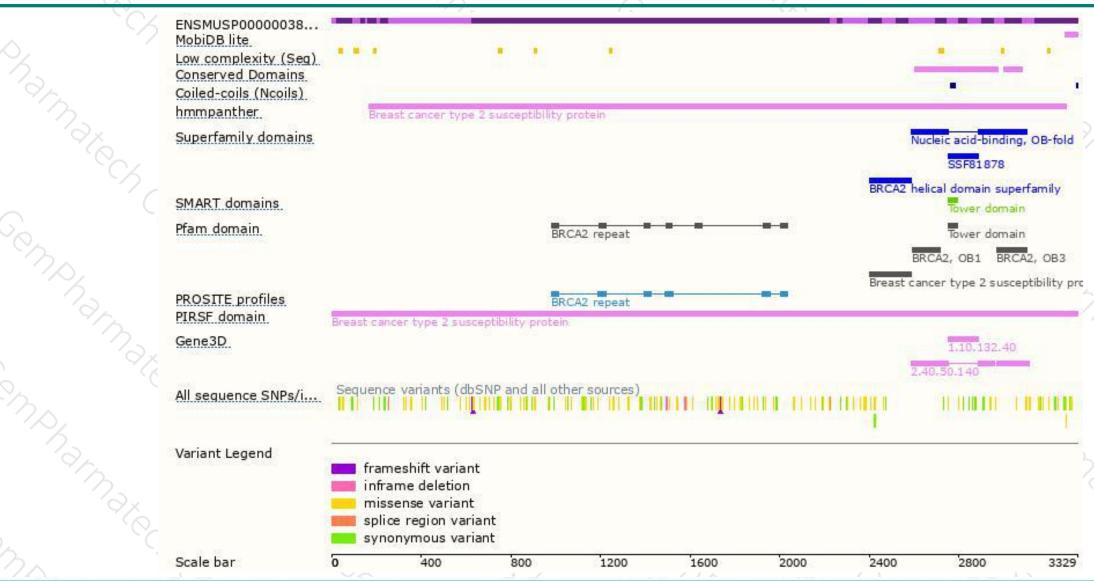
### Genomic location distribution





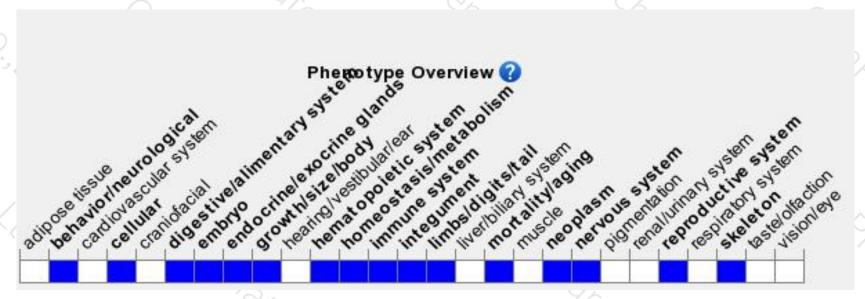
### Protein domain





## 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, 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 BRCA2 protein survive, are small, infertile, show improper tissue differentiation and develop lymphomas and carcinomas.



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





