

Apc Cas9-KO Strategy

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Overview

Target Gene Name

• Apc

Project Type

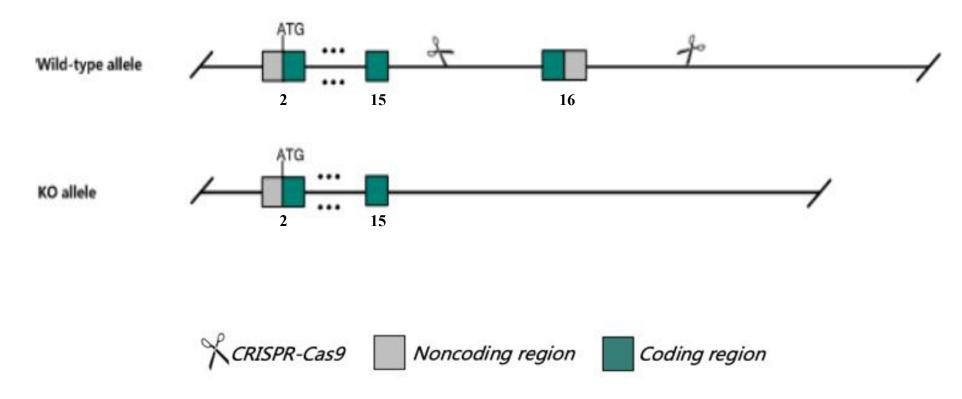
• Cas9-KO

Genetic Background

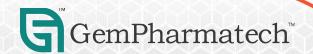
• C57BL/6JGpt



Strain Strategy

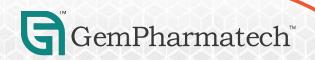


Schematic representation of CRISPR-Cas9 engineering used to edit the Apc gene.



Technical Information

- The *Apc* gene has 9 transcripts. According to the structure of *Apc* gene, exon 16 of *Apc-202* (ENSMUST0000079362.13) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Apc* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.



Gene Information

Apc APC, WNT signaling pathway regulator [Mus musculus (house mouse)]

Gene ID: 11789, updated on 12-Jul-2022

Summary

☆ 1

Official Symbol Apc provided by MGI

Official Full Name APC, WNT signaling pathway regulator provided by MGI

Primary source MGI:MGI:88039

See related Ensembl: ENSMUSG00000005871

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 AI047805, AU020952, AW124434, CC1, Min, mAPC

Expression Broad expression in frontal lobe adult (RPKM 29.9), CNS E18 (RPKM 22.5) and 18 other tissuesSee more

Orthologs human all

Source: https://www.ncbi.nlm.nih.gov/

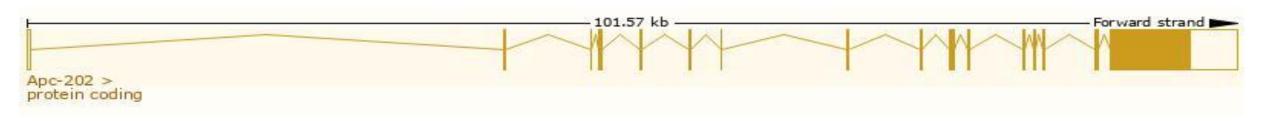


Transcript Information

The gene has 9 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Apc-202	ENSMUST00000079362.13	12811	2842aa	Protein coding	CCDS29125		TSL:1 , GENCODE basic , APPRIS P2 ,
Apc-203	ENSMUST00000115781.10	12346	2808aa	Protein coding	1941		TSL:5 , GENCODE basic , APPRIS ALT2 ,
Apc-209	ENSMUST00000171187.8	3588	<u>1133aa</u>	Protein coding	828		CDS 3' incomplete , TSL:5 ,
Apc-201	ENSMUST00000066133.7	1185	324aa	Protein coding	-		TSL:1 , GENCODE basic ,
Apc-205	ENSMUST00000165590.2	2633	<u>51aa</u>	Nonsense mediated decay	-		CDS 5' incomplete , TSL:5 ,
Apc-204	ENSMUST00000163295.2	608	<u>21aa</u>	Nonsense mediated decay	170		CDS 5' incomplete , TSL:5 ,
Apc-206	ENSMUST00000167136.2	435	No protein	Processed transcript	: - :		TSL:3,
Apc-208	ENSMUST00000170195.2	2732	No protein	Retained intron	12		TSL:1,
Apc-207	ENSMUST00000170023.8	1825	No protein	Retained intron	ASS		TSL:1,

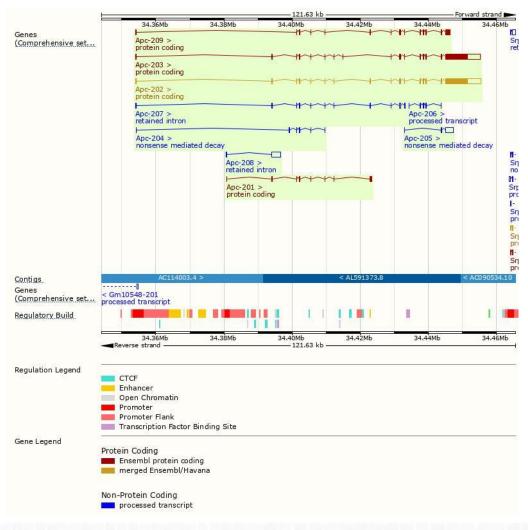
The strategy is based on the design of *Apc-202* transcript, the transcription is shown below:



Source: https://www.ensembl.org



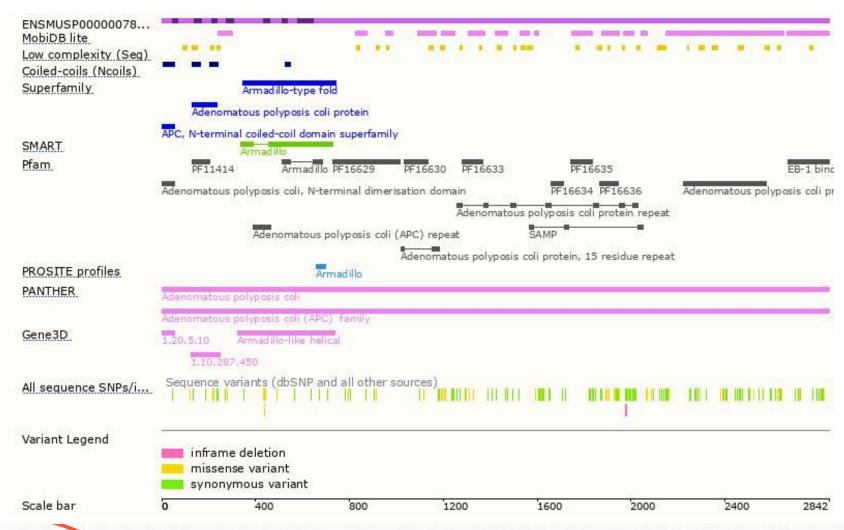
Genomic Information





Source: : https://www.ensembl.org

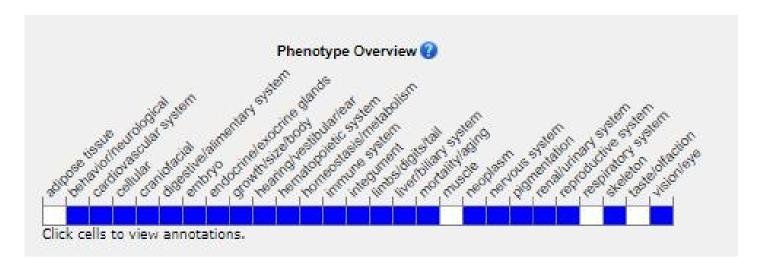
Protein Information





Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



• Most targeted and hypomorphic heterozygous mutants develop intestinal polyps and colorectal cancer, associated with anemia from intestinal bleeding. Homozygotes are embryonic lethal. Homozygotes for a mild alleles survive and have less extreme tumor incidence.



Source: https://www.informatics.jax.org

Important Information

- According to the existing MGI data, most targeted and hypomorphic heterozygous mutants develop intestinal polyps and colorectal cancer, associated with anemia from intestinal bleeding. Homozygotes are embryonic lethal. Homozygotes for a mild alleles survive and have less extreme tumor incidence.
- The effect of this strategy on *Apc-201* transcript is unknown.
- Apc is located on Chr18. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

