

# *Dcc Cas9-KO Strategy*

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**Reviewer:**

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**Design Date:**

**2019/12/18**

# Project Overview



**Project Name**

***Dcc***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Dcc* gene has 3 transcripts. According to the structure of *Dcc* gene, exon4 of *Dcc-202* (ENSMUST00000114943.10) transcript is recommended as the knockout region. The region contains 151bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dcc* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous animals show defects in axonal projections and hypothalamic development affecting both visual and neuroendocrine systems. Incidence of tumors increases in mutations preventing netrin-1 binding.
- The *Dcc* gene is located on the Chr18. 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)

## Dcc deleted in colorectal carcinoma [ *Mus musculus* (house mouse) ]

Gene ID: 13176, updated on 4-Dec-2019

### Summary

Official Symbol	Dcc provided by <a href="#">MGI</a>
Official Full Name	deleted in colorectal carcinoma provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MG1:94869</a>
See related	<a href="#">Ensembl:ENSMUSG00000060534</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Igdcc1; C030036D22Rik
Expression	Biased expression in whole brain E14.5 (RPKM 7.6), CNS E14 (RPKM 7.4) and 5 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

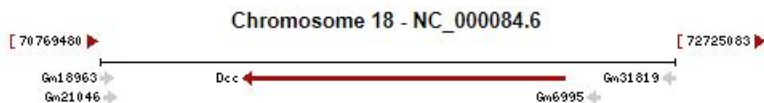
### Genomic context

Location: 18 E2; 18 45.24 cM

See Dcc in [Genome Data Viewer](#)

Exon count: 29

Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	18	NC_000084.6 (71253613..72351228, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	18	NC_000084.5 (71413286..72510723, complement)

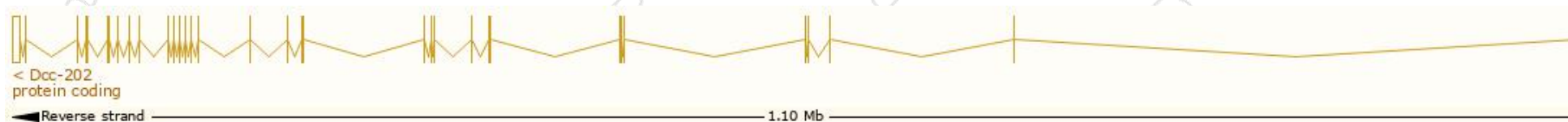


# Transcript information (Ensembl)

The gene has 3 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dcc-202	<a href="#">ENSMUST00000114943.10</a>	10323	<a href="#">1447aa</a>	Protein coding	<a href="#">CCDS29336</a>	<a href="#">P70211</a>	TSL:1 GENCODE basic APPRIS P1
Dcc-201	<a href="#">ENSMUST00000073379.5</a>	4855	<a href="#">1427aa</a>	Protein coding	-	<a href="#">P70211</a>	TSL:5 GENCODE basic
Dcc-203	<a href="#">ENSMUST00000126030.1</a>	3855	No protein	Retained intron	-	-	TSL:1

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

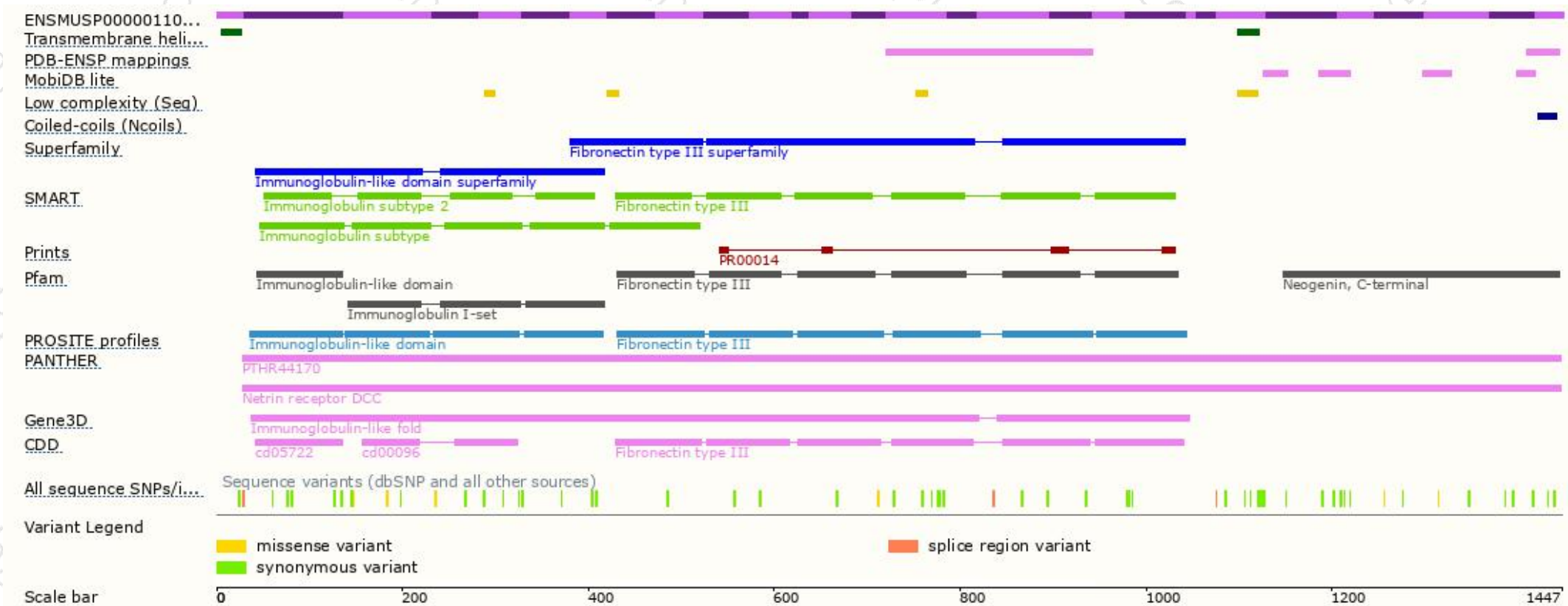


# Genomic location distribution

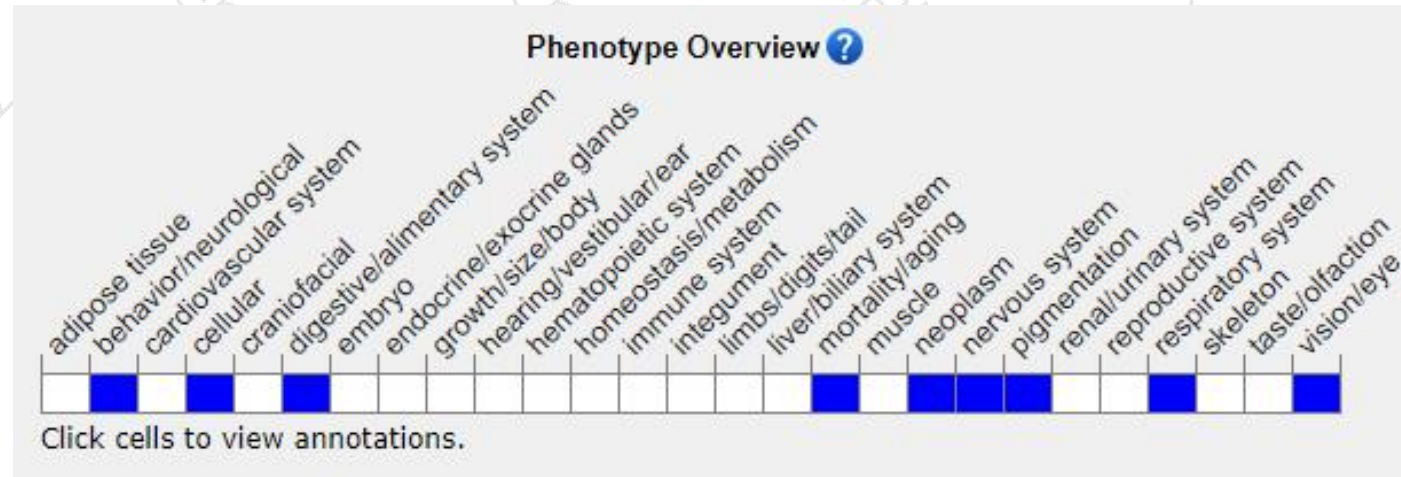




# Protein domain



# 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, Homozygous animals show defects in axonal projections and hypothalamic development affecting both visual and neuroendocrine systems. Incidence of tumors increases in mutations preventing netrin-1 binding.

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

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