

Adgrl3 Cas9-KO Strategy

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Project Overview

Project Name

Adgrl3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Adgrl3* gene. The schematic diagram is as follows:



- The *Adgrl3* gene has 35 transcripts. According to the structure of *Adgrl3* gene, exon4 of *Adgrl3-202* (ENSMUST00000072521.10) transcript is recommended as the knockout region. The region contains 110bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Adgrl3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a gene trap allele exhibit increased dopamine and serotonin levels in the dorsal striatum, hyperactivity, increased stereotypic behavior and enhanced hyperactivity in response to cocaine.
- Transcript 220 maybe unaffected.
- The *Adgrl3* 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)

Adgrl3 adhesion G protein-coupled receptor L3 [Mus musculus (house mouse)]

Gene ID: 319387, updated on 31-Jan-2019

Summary



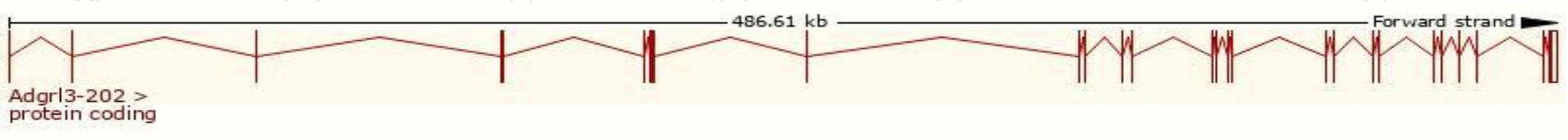
Official Symbol	Adgrl3 provided by MGI
Official Full Name	adhesion G protein-coupled receptor L3 provided by MGI
Primary source	MGI:MGI:2441950
See related	Ensembl:ENSMUSG000000037605
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5430402I23Rik, CIRL-3, D130075K09Rik, Gm1379, LEC3, Lphn3, mKIAA0768
Expression	Broad expression in CNS E18 (RPKM 5.1), whole brain E14.5 (RPKM 4.6) and 17 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

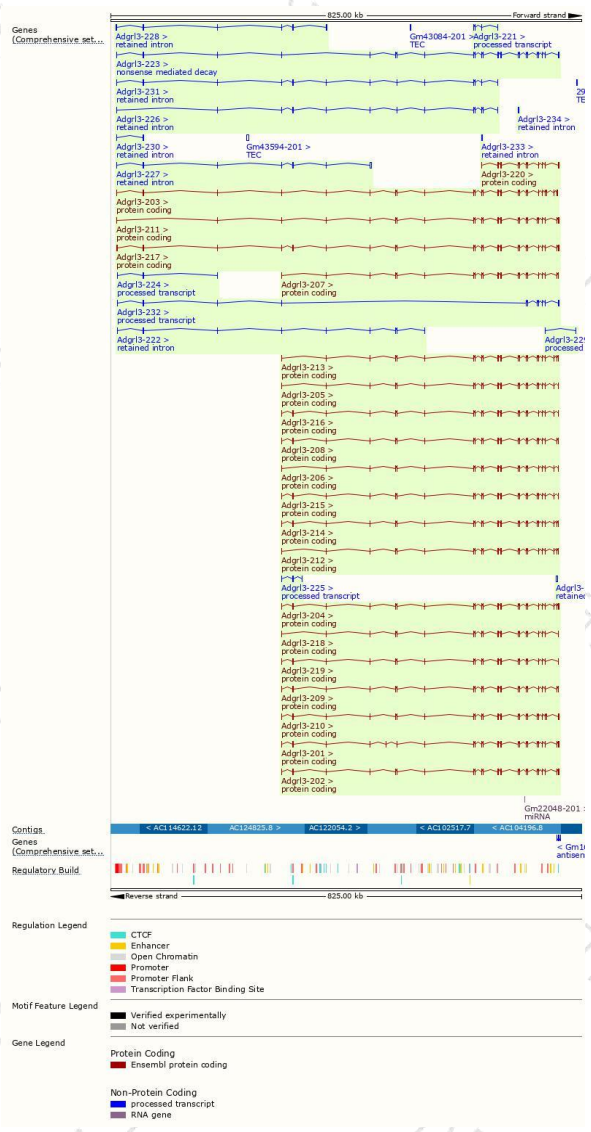
The gene has 35 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Adgrl3-202	ENSMUST00000072621.10	6203	1543aa	Protein coding	CCDS39122	Q80TS3	TSL5 GENCODE basic APPRIS P2
Adgrl3-208	ENSMUST00000118442.7	5101	1308aa	Protein coding	CCDS44991	O3Z3X6	TSL5 GENCODE basic
Adgrl3-209	ENSMUST00000119385.7	4905	1299aa	Protein coding	CCDS44993	O3Z8H6	TSL5 GENCODE basic
Adgrl3-219	ENSMUST00000122356.7	4853	1528aa	Protein coding	CCDS44984	Q80TS3	TSL5 GENCODE basic
Adgrl3-218	ENSMUST00000122037.7	4649	1460aa	Protein coding	CCDS44995	O3Z634	TSL5 GENCODE basic
Adgrl3-217	ENSMUST00000121707.7	6690	1534aa	Protein coding	-	O3YTW7	TSL5 GENCODE basic
Adgrl3-211	ENSMUST00000120128.7	6370	1240aa	Protein coding	-	O3Z6J2	TSL5 GENCODE basic
Adgrl3-201	ENSMUST00000038068.14	6203	1543aa	Protein coding	-	K3W4M8	TSL5 GENCODE basic APPRIS ALT1
Adgrl3-204	ENSMUST00000117407.7	5705	1342aa	Protein coding	-	Q80TS3	TSL5 GENCODE basic
Adgrl3-210	ENSMUST00000119788.7	5394	1550aa	Protein coding	-	O3YV19	TSL5 GENCODE basic
Adgrl3-214	ENSMUST00000120445.7	5230	1351aa	Protein coding	-	O3Z8H7	TSL5 GENCODE basic
Adgrl3-215	ENSMUST00000120673.7	5178	1580aa	Protein coding	-	O3Z5M6	TSL5 GENCODE basic APPRIS ALT1
Adgrl3-216	ENSMUST00000121641.7	5151	1571aa	Protein coding	-	O3Z457	TSL5 GENCODE basic
Adgrl3-213	ENSMUST00000120282.7	5026	1283aa	Protein coding	-	O3YH81	TSL5 GENCODE basic
Adgrl3-212	ENSMUST00000120144.7	4999	1274aa	Protein coding	-	O3Z4V0	TSL5 GENCODE basic
Adgrl3-205	ENSMUST00000117985.7	4974	1512aa	Protein coding	-	O3Z3G4	TSL5 GENCODE basic
Adgrl3-206	ENSMUST00000118034.7	4947	1503aa	Protein coding	-	O3Z593	TSL5 GENCODE basic
Adgrl3-207	ENSMUST00000118078.7	4871	1231aa	Protein coding	-	O3YU23	TSL5 GENCODE basic
Adgrl3-203	ENSMUST00000117283.7	4764	1268aa	Protein coding	-	O3YWR3	TSL1 GENCODE basic
Adgrl3-220	ENSMUST00000124117.1	4191	873aa	Protein coding	-	F6WMY5	CDS 5' incomplete TSL5
Adgrl3-223	ENSMUST00000132375.7	6793	67aa	Nonsense mediated decay	-	Q8RFB0	TSL1
Adgrl3-232	ENSMUST00000153264.7	3279	No protein	Processed transcript	-	-	TSL5
Adgrl3-225	ENSMUST00000134587.1	887	No protein	Processed transcript	-	-	TSL3
Adgrl3-221	ENSMUST00000128227.1	675	No protein	Processed transcript	-	-	TSL5
Adgrl3-224	ENSMUST00000132634.7	445	No protein	Processed transcript	-	-	TSL5
Adgrl3-229	ENSMUST00000148830.1	241	No protein	Processed transcript	-	-	TSL5
Adgrl3-227	ENSMUST00000140356.7	3287	No protein	Retained intron	-	-	TSL1
Adgrl3-226	ENSMUST00000136104.7	3140	No protein	Retained intron	-	-	TSL1
Adgrl3-231	ENSMUST00000149280.7	3138	No protein	Retained intron	-	-	TSL1
Adgrl3-228	ENSMUST00000147226.7	2728	No protein	Retained intron	-	-	TSL1
Adgrl3-234	ENSMUST00000201055.1	2082	No protein	Retained intron	-	-	TSLNA
Adgrl3-235	ENSMUST00000201803.1	2035	No protein	Retained intron	-	-	TSLNA
Adgrl3-222	ENSMUST00000127046.1	1680	No protein	Retained intron	-	-	TSL1
Adgrl3-233	ENSMUST00000200930.1	1356	No protein	Retained intron	-	-	TSLNA
Adgrl3-230	ENSMUST00000148923.1	614	No protein	Retained intron	-	-	TSL3

The strategy is based on the design of *Adgrl3-202* transcript,The transcription is shown below



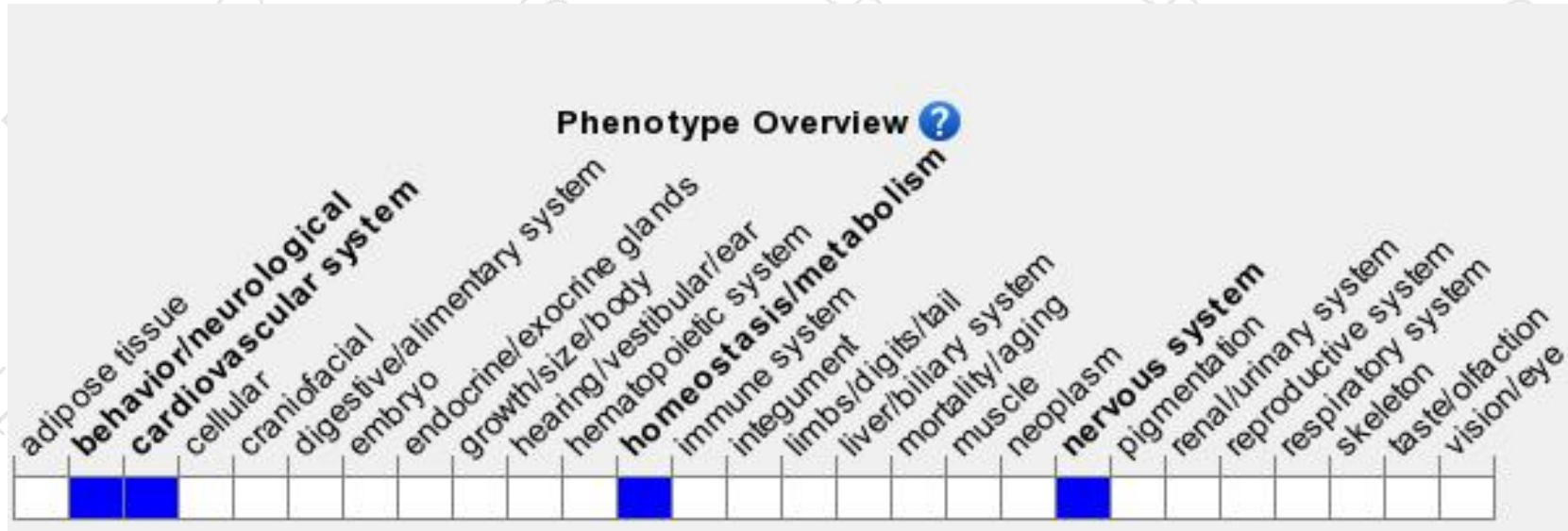
Genomic location distribution



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, Mice homozygous for a gene trap allele exhibit increased dopamine and serotonin levels in the dorsal striatum, hyperactivity, increased stereotypic behavior and enhanced hyperactivity in response to cocaine.

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

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