Nbea Cas9-KO Strategy

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Design Date: 2019-9-19
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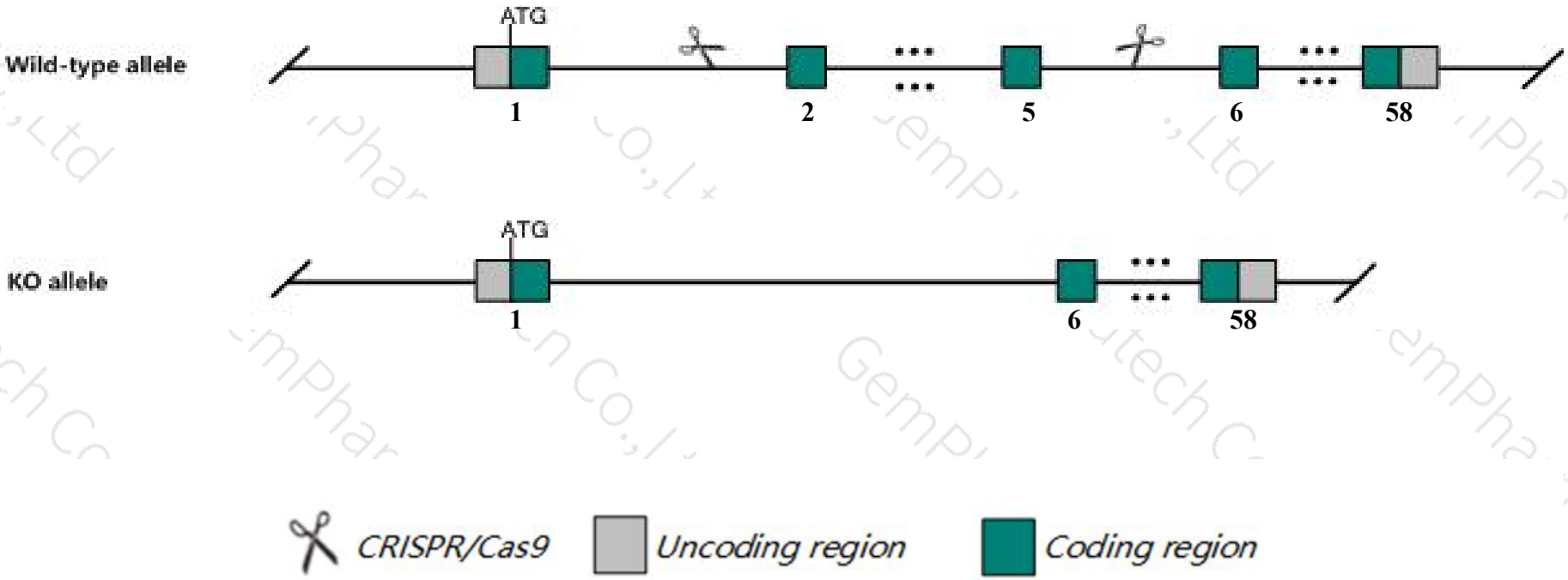
Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Nbea* gene has 10 transcripts. According to the structure of *Nbea* gene, exon2-exon5 of *Nbea-201* (ENSMUST00000029374.7) transcript is recommended as the knockout region.The region contains 551bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

➢ According to the existing MGI data,Mice homozygous for a gene trapped allele or transgene insertion die shortly after birth, are cyanotic, and exhibit no response to tactile stimuli, no spontaneous movement, and impaired CNS synaptic transmission.

➢ The *Nbea* gene is located on the Chr3. 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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Nbea neurobeachin [Mus musculus (house mouse)]

Gene ID: 26422, updated on 31-Jan-2019

Summary

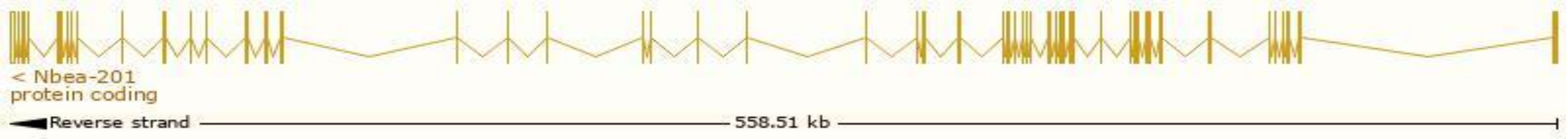
Official Symbol	Nbea provided by MGI
Official Full Name	neurobeachin provided by MGI
Primary source	MGI:MGI:1347075
See related	Ensembl:ENSMUSG00000027799
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Lyst2, mKIAA1544
Expression	Broad expression in CNS E18 (RPKM 19.0), whole brain E14.5 (RPKM 15.5) and 16 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

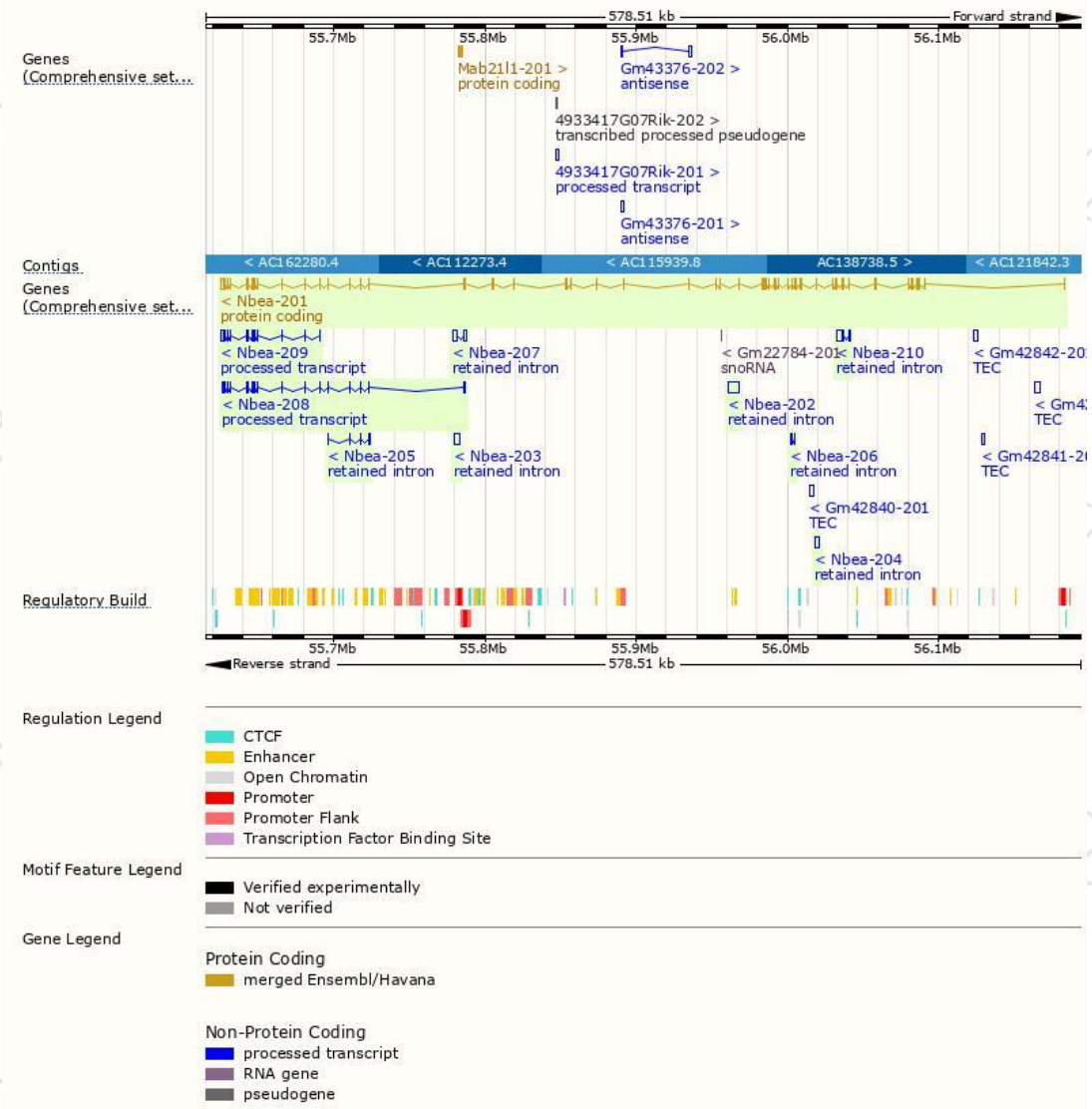
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nbea-201	ENSMUST00000029374.7	10986	2936aa	Protein coding	CCDS50911	Q9EPN1	TSL:5 GENCODE basic APPRIS P1
Nbea-209	ENSMUST00000199803.4	3433	No protein	Processed transcript	-	-	TSL:5
Nbea-208	ENSMUST00000199535.4	2936	No protein	Processed transcript	-	-	TSL:1
Nbea-202	ENSMUST00000196577.1	7326	No protein	Retained intron	-	-	TSL:NA
Nbea-207	ENSMUST00000199126.1	4717	No protein	Retained intron	-	-	TSL:2
Nbea-203	ENSMUST00000196612.1	3860	No protein	Retained intron	-	-	TSL:NA
Nbea-210	ENSMUST00000200526.1	3740	No protein	Retained intron	-	-	TSL:1
Nbea-204	ENSMUST00000197395.1	3158	No protein	Retained intron	-	-	TSL:NA
Nbea-206	ENSMUST00000198315.1	833	No protein	Retained intron	-	-	TSL:2
Nbea-205	ENSMUST00000198259.1	811	No protein	Retained intron	-	-	TSL:5

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

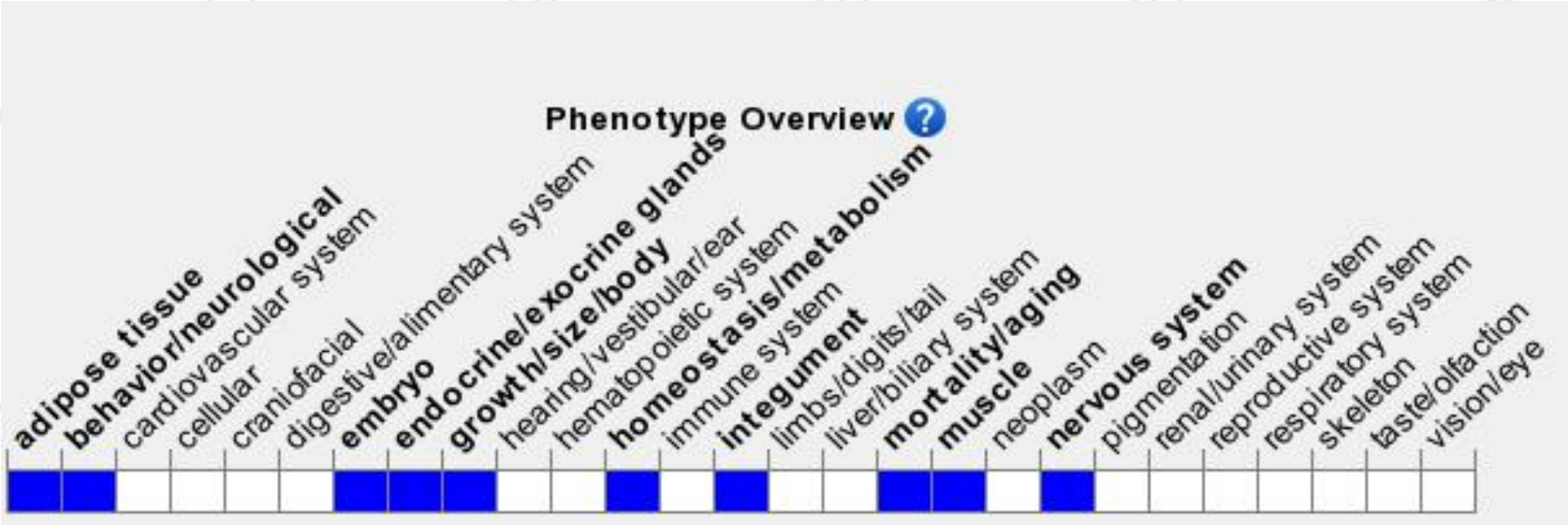


Genomic location distribution



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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