Adam23 Cas9-KO Strategy

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Design Date: 20190806

Project Overview

Project Name	***Adam23***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Adam23* gene. The schematic diagram is as follows:

Technical routes

➢ The *Adam23* gene has 12 transcripts. According to the structure of *Adam23* gene, exon3 of *Adam23-201* (ENSMUST00000087374.9) transcript is recommended as the knockout region.The region contains 77bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Adam23* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

➢ According to the existing MGI data,Mice homozygous for an insertional mutation that inactivates the gene are smaller than normal littermates, show delayed lung development, are lethal by postnatal day 14, and display severe tremor and ataxia.

➢ The *Adam23* gene is located on the Chr1. 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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Adam23 a disintegrin and metallopeptidase domain 23 [Mus musculus (house mouse)]

Gene ID: 23792, updated on 31-Jan-2019

Summary

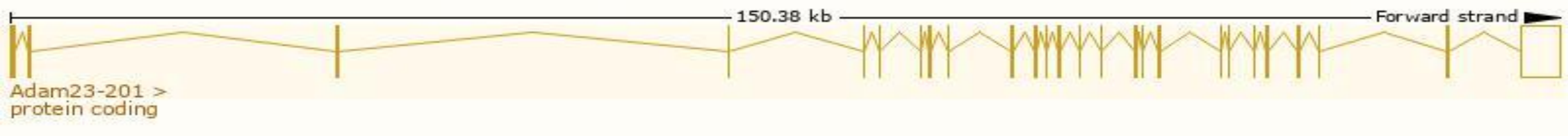
Official Symbol	Adam23 provided by MGI
Official Full Name	a disintegrin and metallopeptidase domain 23 provided by MGI
Primary source	MGI:MGI:1345162
See related	Ensembl:ENSMUSG00000025964
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW046396, MDC3
Summary	This gene encodes a member of the disintegrin family of membrane-anchored proteins that play a role in diverse biological processes such as brain development, fertilization, tumor development and inflammation. The encoded protein undergoes proteolytic processing to generate a mature polypeptide comprised of an inactive metalloprotease and disintegrin domains. Transgenic disruption of this gene in mice results in postnatal neurological defects including tremor and ataxia resulting in death by 2 weeks of age. [provided by RefSeq, Sep 2015]
Expression	Broad expression in cerebellum adult (RPKM 24.9), cortex adult (RPKM 15.1) and 16 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

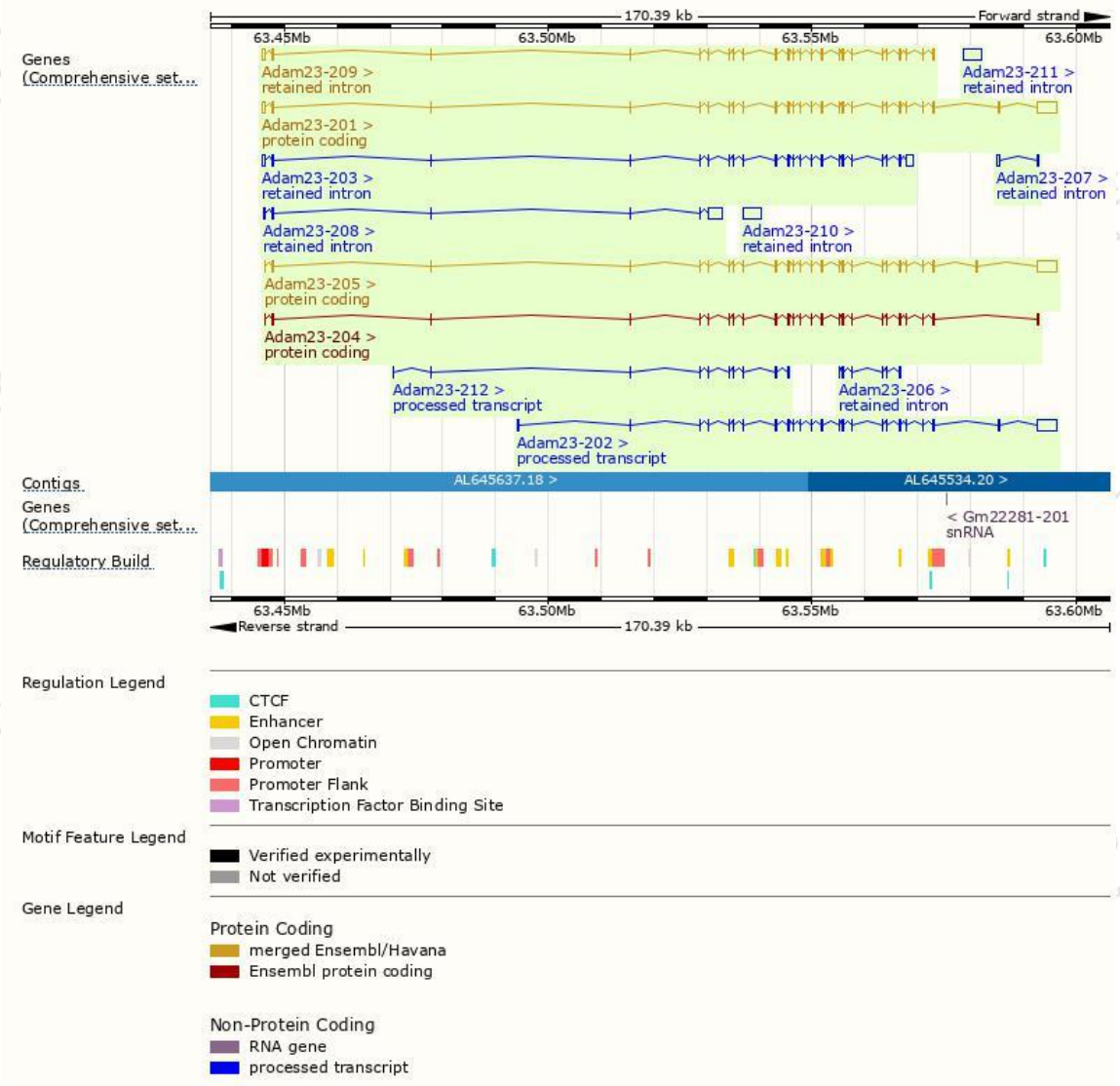
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Adam23-201	ENSMUST00000087374.9	6426	829aa	Protein coding	CCDS14999	Q9R1V7	TSL:1 GENCODE basic APPRIS P2
Adam23-205	ENSMUST00000114107.2	6110	829aa	Protein coding	-	Q9R1V7	TSL:5 GENCODE basic APPRIS ALT2
Adam23-204	ENSMUST00000114103.7	2655	829aa	Protein coding	-	Q9R1V7	TSL:5 GENCODE basic APPRIS ALT2
Adam23-202	ENSMUST00000097717.8	5730	No protein	Processed transcript	-	-	TSL:1
Adam23-212	ENSMUST00000190658.6	740	No protein	Processed transcript	-	-	TSL:5
Adam23-208	ENSMUST00000146403.7	3538	No protein	Retained intron	-	-	TSL:2
Adam23-210	ENSMUST00000185616.1	3507	No protein	Retained intron	-	-	TSL:NA
Adam23-203	ENSMUST00000114101.7	3496	No protein	Retained intron	-	-	TSL:2
Adam23-211	ENSMUST00000187844.1	3388	No protein	Retained intron	-	-	TSL:NA
Adam23-209	ENSMUST00000182642.7	2889	No protein	Retained intron	-	-	TSL:1
Adam23-206	ENSMUST00000134704.2	648	No protein	Retained intron	-	-	TSL:5
Adam23-207	ENSMUST00000141545.2	631	No protein	Retained intron	-	-	TSL:2

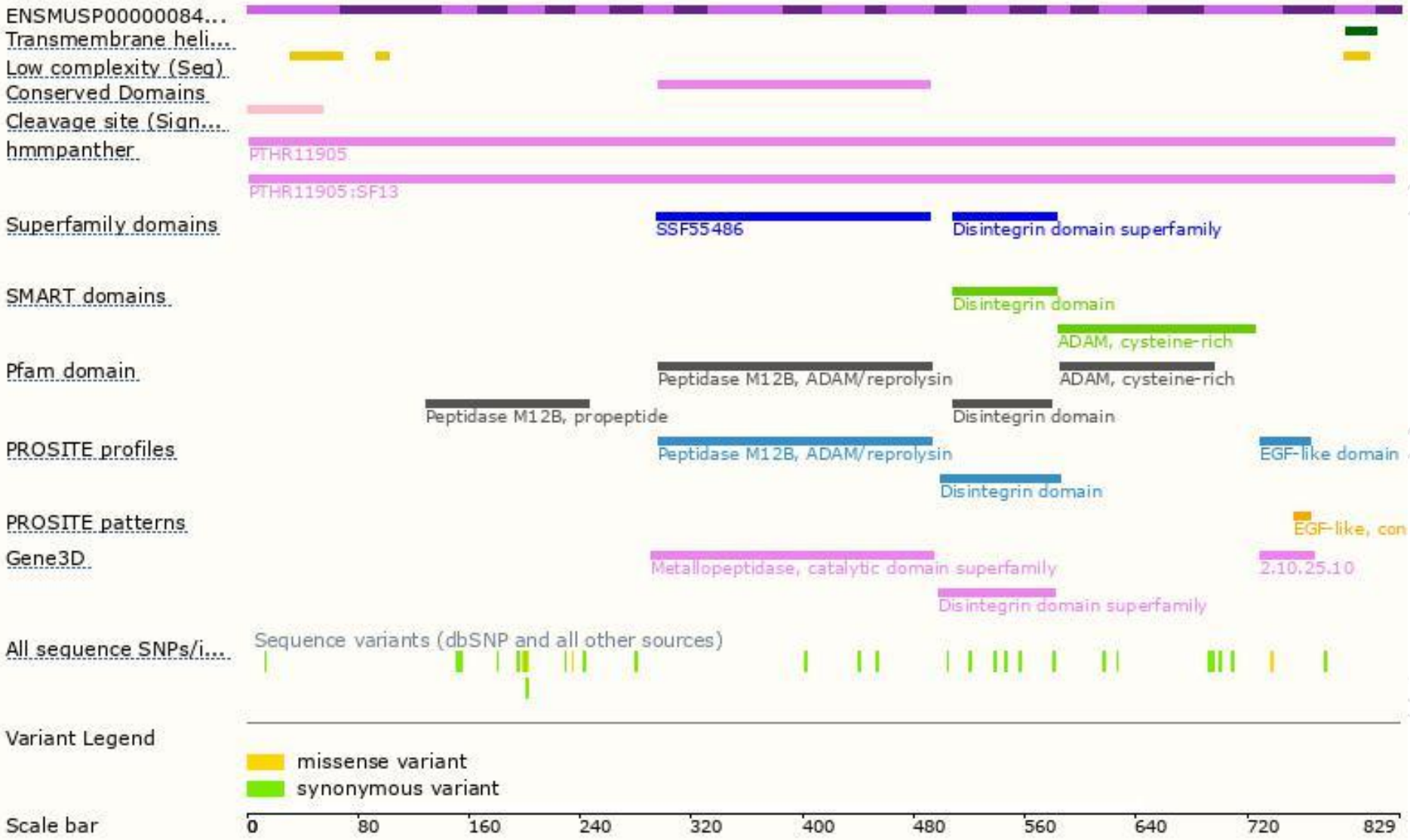
The strategy is based on the design of *Adam23-201* transcript,The transcription is shown below



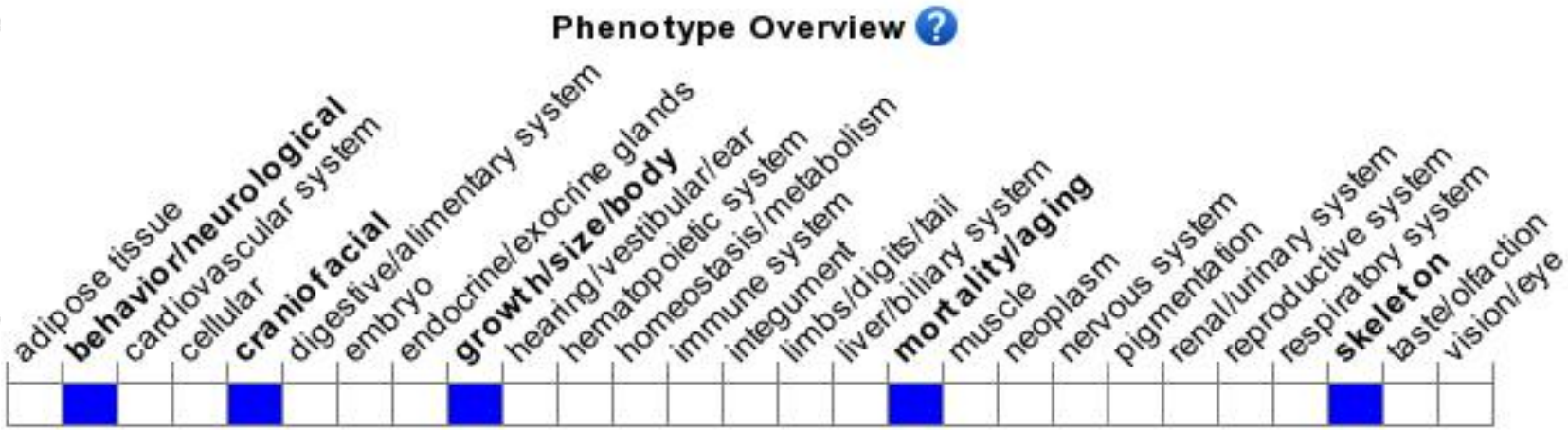
Genomic location distribution



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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