Senp7 Cas9-KO Strategy

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Project Overview

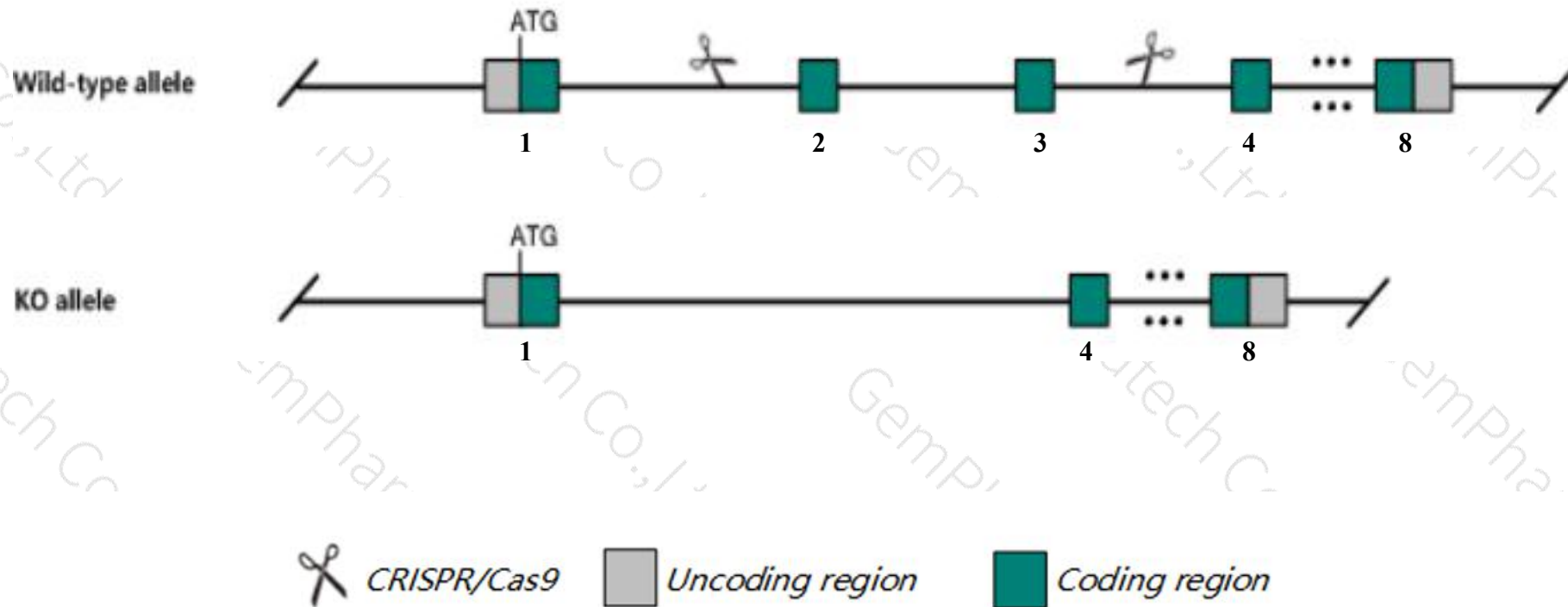|	
Project Name	***Senp7***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Senp7* gene. The schematic diagram is as follows:

Technical routes

➢ The *Senp7* gene has 15 transcripts. According to the structure of *Senp7* gene, exon2-exon3 of *Senp7-211*
(ENSMUST00000202000.1) transcript is recommended as the knockout region.The region contains 134bp coding sequence.
Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Senp7* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ The *Senp7* gene is located on the Chr16. 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）

Senp7 SUMO1/sentrin specific peptidase 7 [Mus musculus (house mouse)]

Gene ID: 66315, updated on 13-Mar-2020

▲ Summary

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Official Symbol	Senp7 provided by MGI
Official Full Name	SUMO1/sentrin specific peptidase 7 provided by MGI
Primary source	MGI:MGI:1913565
See related	Ensembl:ENSMUSG00000052917
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	2410152H17Rik, 2810413I22Rik, 2900036C23Rik, 6030449K19Rik, AI790676
Summary	This gene encodes a SUMO deconjugating enzyme of the Sentrin/SUMO-specific protease (SENP) family. The encoded protein is a protease that exhibits deSUMOylating activity towards proteins involved in chromatin remodeling and promotes chromatin relaxation for DNA repair or transcription. Alternative splicing of this gene results in multiple transcript variants. [provided by RefSeq, Jan 2015]
Expression	Broad expression in whole brain E14.5 (RPKM 4.4), CNS E18 (RPKM 4.3) and 22 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Senp7-203	ENSMUST00000089362.8	4825	1037aa	Protein coding	CCDS28222	Q8BUH8	TSL:1 GENCODE basic APPRIS P2
Senp7-211	ENSMUST00000202000.1	3218	291aa	Protein coding	CCDS84243	A0A0J9YUC9	TSL:2 GENCODE basic
Senp7-201	ENSMUST00000049128.10	1130	254aa	Protein coding	CCDS28223	Q9CQN9	TSL:1 GENCODE basic
Senp7-202	ENSMUST00000089360.9	4802	1010aa	Protein coding	-	E9Q1L5	TSL:5 GENCODE basic APPRIS ALT2
Senp7-205	ENSMUST00000201011.1	914	227aa	Protein coding	-	Q9CX65	TSL:1 GENCODE basic
Senp7-215	ENSMUST00000202799.3	698	211aa	Protein coding	-	Q9CRF0	CDS 3' incomplete TSL:1
Senp7-209	ENSMUST00000201476.1	1169	No protein	Processed transcript	-	-	TSL:1
Senp7-206	ENSMUST00000201218.1	1136	No protein	Processed transcript	-	-	TSL:1
Senp7-210	ENSMUST00000201915.4	855	No protein	Processed transcript	-	-	TSL:1
Senp7-213	ENSMUST00000202159.1	667	No protein	Processed transcript	-	-	TSL:3
Senp7-207	ENSMUST00000201391.1	389	No protein	Processed transcript	-	-	TSL:5
Senp7-214	ENSMUST00000202272.3	3602	No protein	Retained intron	-	-	TSL:2
Senp7-208	ENSMUST00000201418.3	2407	No protein	Retained intron	-	-	TSL:2
Senp7-204	ENSMUST00000200714.3	1330	No protein	Retained intron	-	-	TSL:3
Senp7-212	ENSMUST00000202108.3	421	No protein	Retained intron	-	-	TSL:1

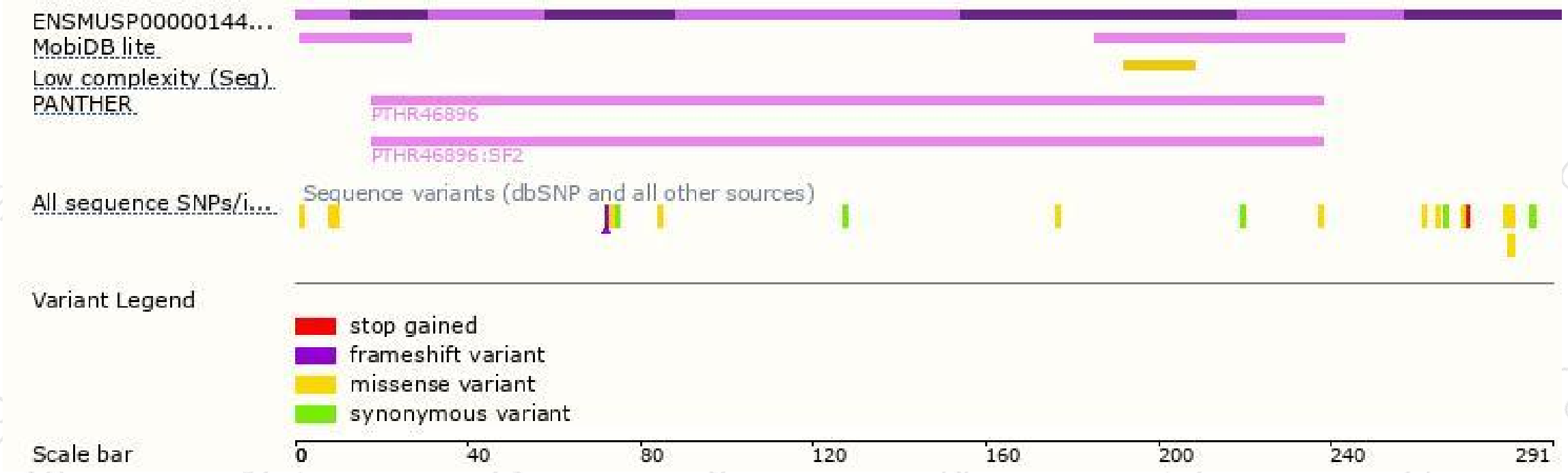The strategy is based on the design of *Senp7-211* transcript,the transcription is shown below:
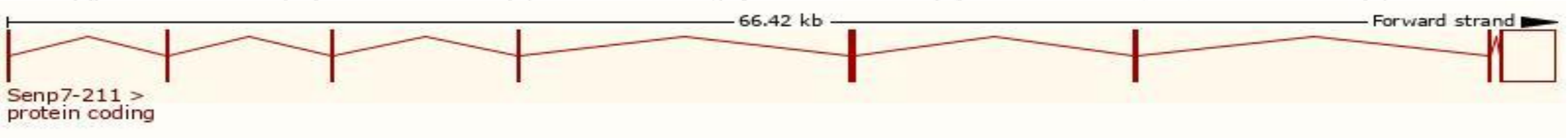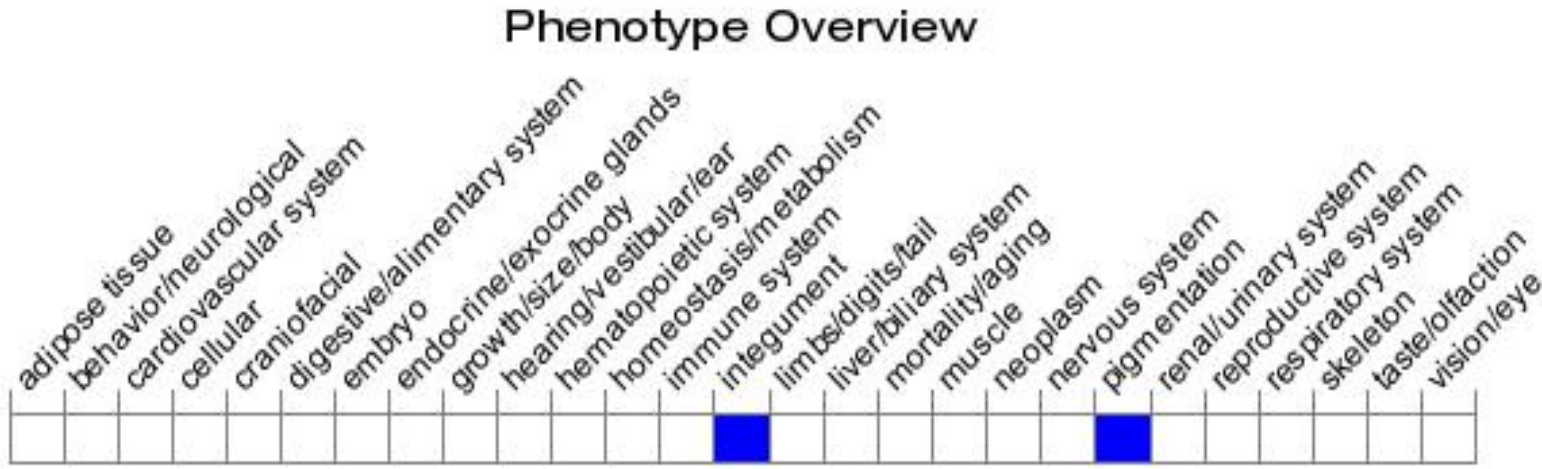
Genomic location distribution
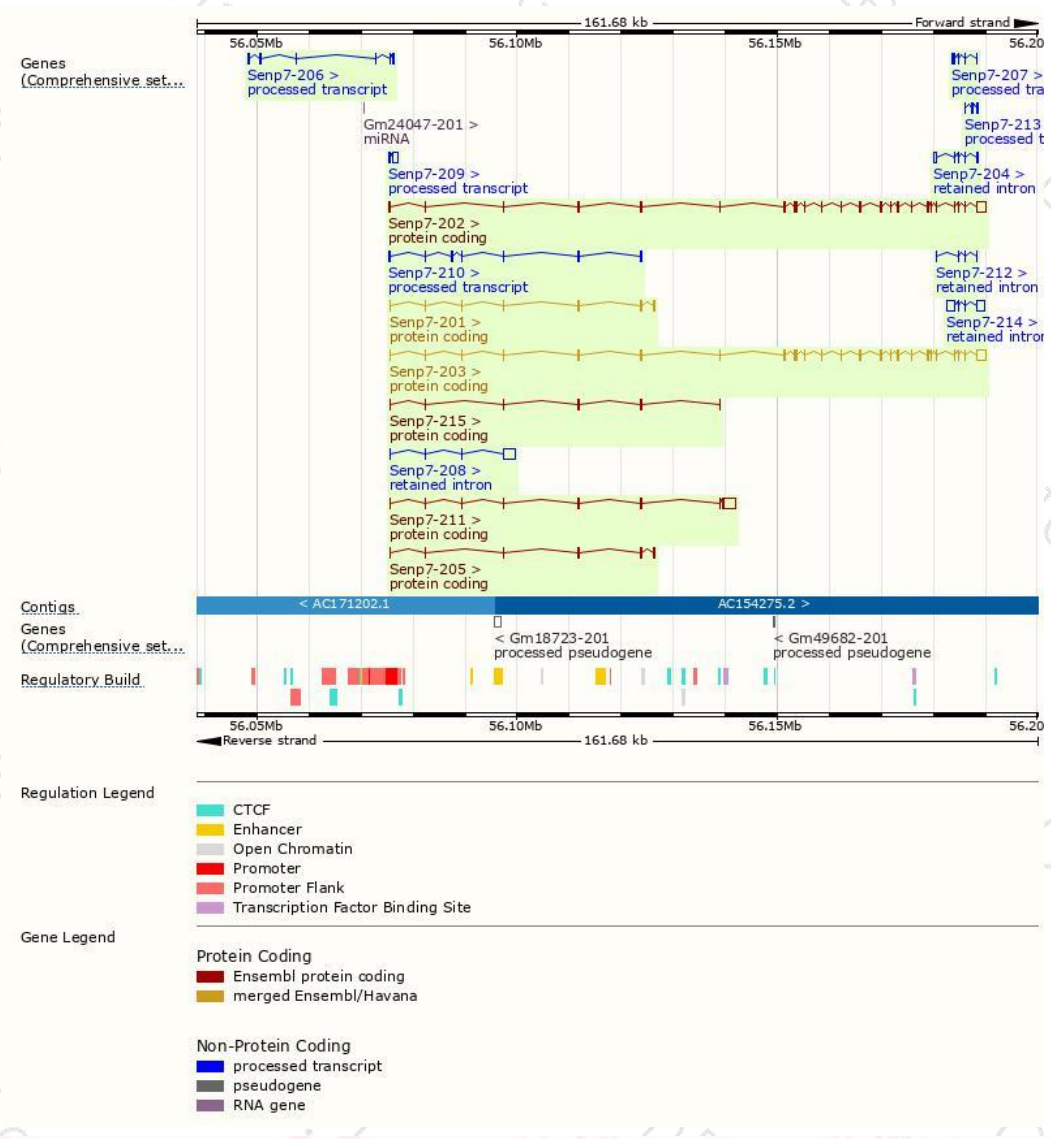
Protein domain

Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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