Zfp207 Cas9-KO Strategy

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Project Overview

Project Name	***Zfp207***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp207* gene. The schematic diagram is as follows:

Technical routes

➢ The *Zfp207* gene has 8 transcripts. According to the structure of *Zfp207* gene, exon3 of *Zfp207-201* (ENSMUST00000017567.13) transcript is recommended as the knockout region.The region contains 139bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Zfp207* gene. The brief process is as follows: CRISPR/Cas9 systen

Notice

➢ The *Zfp207* gene is located on the Chr11. 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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Zfp207 zinc finger protein 207 [Mus musculus (house mouse)]

Gene ID: 22680, updated on 31-Jan-2019

Summary

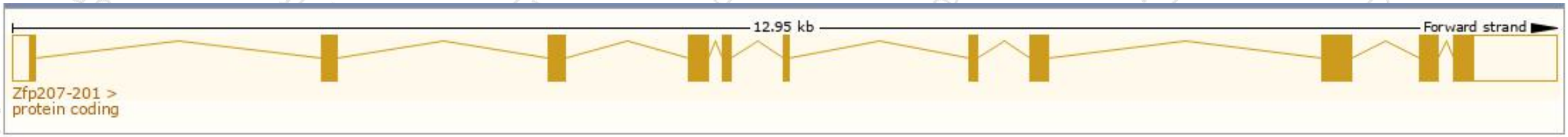
Official Symbol	Zfp207 provided by MGI
Official Full Name	zinc finger protein 207 provided byMGI
Primary source	MGI:MGI:1340045
See related	Ensembl:ENSMUSG00000017421
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	8430401D15Rik, BuGZ, Zep, Znf207
Expression	Ubiquitous expression in CNS E14 (RPKM 25.2), limb E14.5 (RPKM 24.2) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

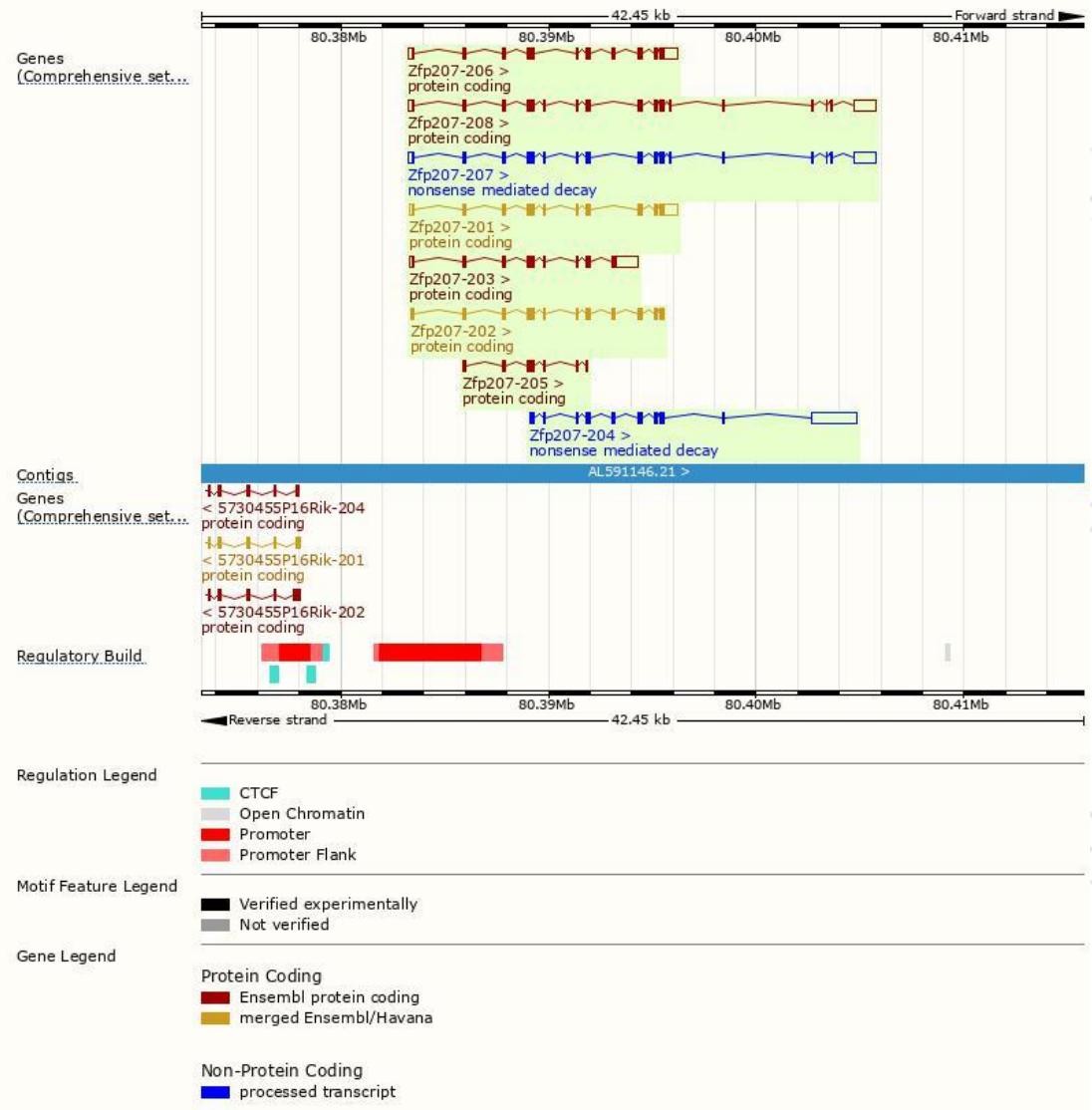
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp207-208	ENSMUST00000188489.6	2898	464aa	Protein coding	CCDS48864	Q9JMD0	TSL:2 GENCODE basic APPRIS ALT1
Zfp207-206	ENSMUST00000165565.7	2311	479aa	Protein coding	CCDS48865	Q9JMD0	TSL:1 GENCODE basic
Zfp207-201	ENSMUST00000017567.13	2245	464aa	Protein coding	CCDS48864	Q9JMD0	TSL:1 GENCODE basic APPRIS ALT1
Zfp207-202	ENSMUST00000053740.14	1562	495aa	Protein coding	CCDS48863	Q9JMD0	TSL:1 GENCODE basic APPRIS P4
Zfp207-203	ENSMUST00000108216.7	2152	329aa	Protein coding	-	Q8CCB2	TSL:2 GENCODE basic
Zfp207-205	ENSMUST00000153824.7	720	227aa	Protein coding	-	B1AQG7	CDS 3' incomplete TSL:2
Zfp207-204	ENSMUST00000123726.1	3279	342aa	Nonsense mediated decay	-	M0QWF0	CDS 5' incomplete TSL:5
Zfp207-207	ENSMUST00000178665.7	2898	464aa	Nonsense mediated decay	-	Q9JMD0	TSL:2

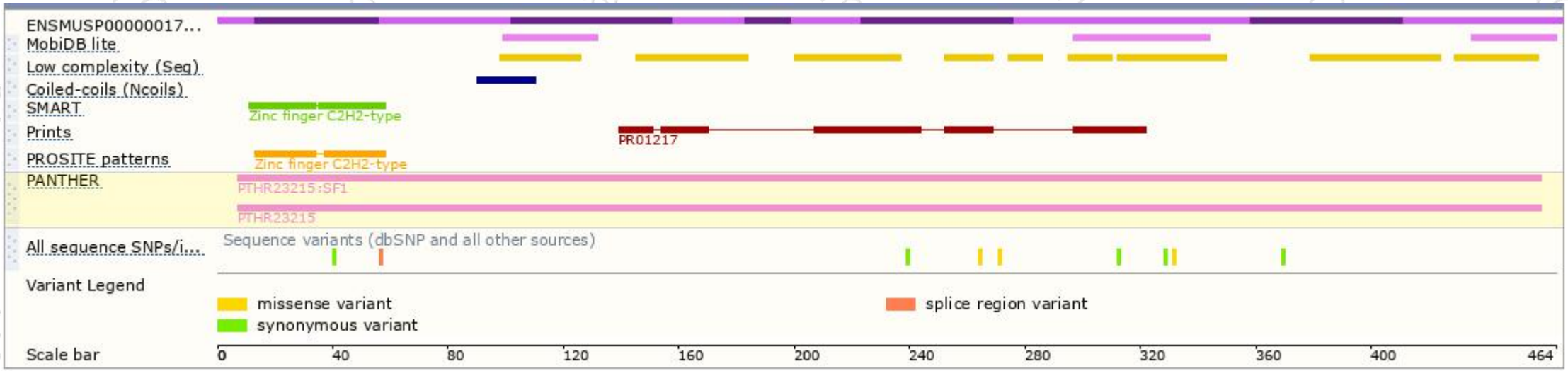
The strategy is based on the design of *Zfp207-201* transcript,The transcription is shown below



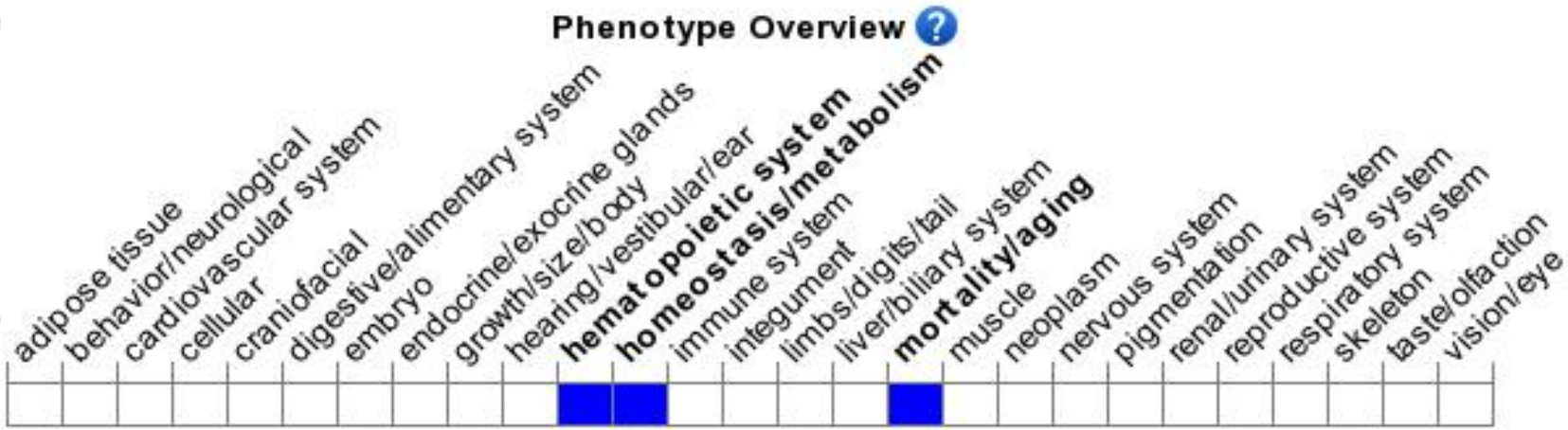
Genomic location distribution



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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