Mcf2l Cas9-KO Strategy

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Project Overview

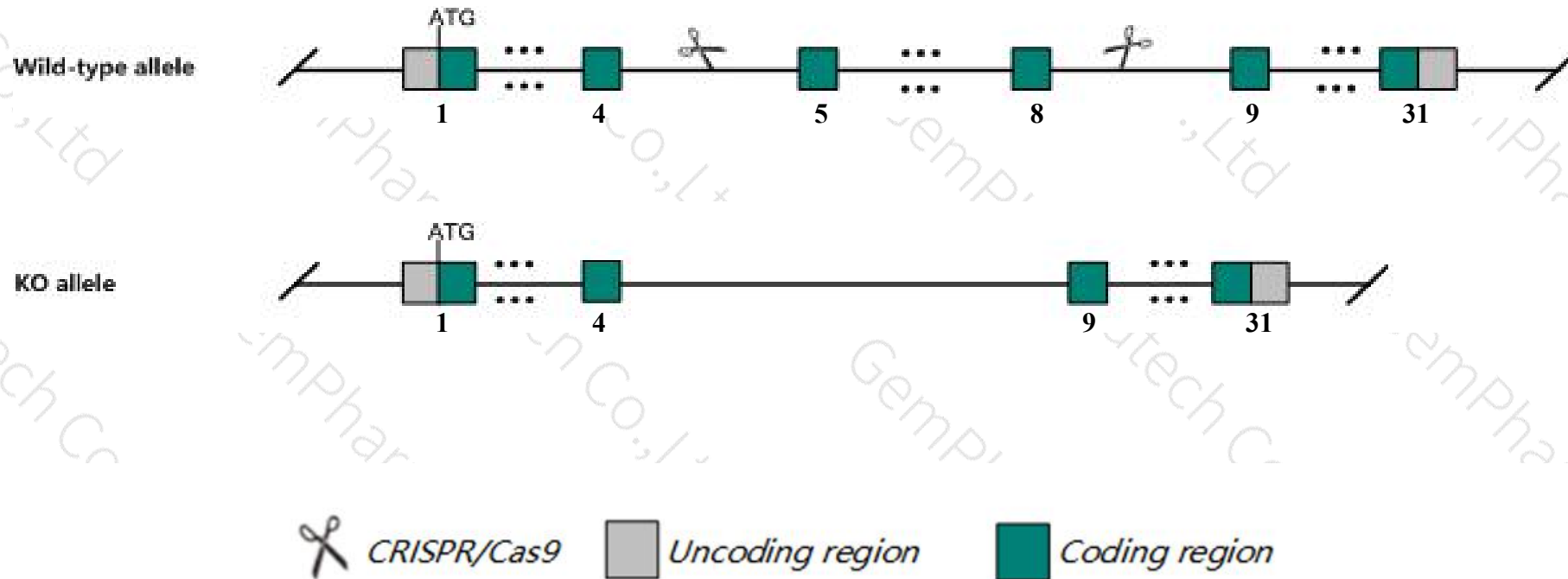|	
Project Name	*Mcf2l*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mcf2l* gene. The schematic diagram is as follows:

Technical routes

➢ The *Mcf2l* gene has 23 transcripts. According to the structure of *Mcf2l* gene, exon5-exon8 of *Mcf2l-207* (ENSMUST00000110876.8) transcript is recommended as the knockout region.The region contains 512bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mcf2l* gene. The brief process is as follows: CRISPR/Cas9 system

➢ The *Mcf2l* gene is located on the Chr8. 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.

➢ Some amino acids will remain at the N-terminus and some functions may be retained.

➢ Transcript 220,223 CDS 3' incomplete the influences is unknown; Transcript 209,210 CDS 3' incomplete the influences is unknown; Transcript 213,216 CDS 5' and 3' incomplete the influences is unknown.

➢ 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）

Mcf2l mcf.2 transforming sequence-like [Mus musculus (house mouse)]

Gene ID: 17207, updated on 31-Jan-2019

▲Summary

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Official Symbol	Mcf2l provided by MGI
Official Full Name	mcf.2 transforming sequence-like provided by MGI
Primary source	MGI:MGI:103263
See related	Ensembl:ENSMUSG00000031442
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	C130040G20Rik, Dbs, Ost, mKIAA0362
Expression	Broad expression in CNS E18 (RPKM 14.7), frontal lobe adult (RPKM 13.1) and 22 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 23 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mcf2l-207	ENSMUST00000110876.8	5253	1175aa	Protein coding	CCDS40225	E9PXE2	TSL:1 GENCODE basic APPRIS P3
Mcf2l-203	ENSMUST00000110866.8	5108	1097aa	Protein coding	CCDS52483	E9PY13	TSL:1 GENCODE basic APPRIS ALT2
Mcf2l-204	ENSMUST00000110867.8	3864	1101aa	Protein coding	CCDS52482	E9PY12	TSL:1 GENCODE basic APPRIS ALT2
Mcf2l-222	ENSMUST00000173099.7	6081	1059aa	Protein coding	-	G3UXP9	TSL:5 GENCODE basic
Mcf2l-217	ENSMUST00000145067.7	5313	1118aa	Protein coding	-	G3UX72	TSL:1 GENCODE basic APPRIS ALT2
Mcf2l-210	ENSMUST00000126905.7	4061	807aa	Protein coding	-	F6VR53	CDS 5' incomplete TSL:1
Mcf2l-201	ENSMUST00000095456.9	3926	1149aa	Protein coding	-	E9QPM7	TSL:1 GENCODE basic APPRIS ALT2
Mcf2l-208	ENSMUST00000110879.8	3664	1125aa	Protein coding	-	E9PXE1	TSL:5 GENCODE basic APPRIS ALT2
Mcf2l-205	ENSMUST00000110871.7	3401	1046aa	Protein coding	-	D3YUF4	TSL:5 GENCODE basic
Mcf2l-202	ENSMUST00000098927.9	3215	1067aa	Protein coding	-	E9Q863	TSL:5 GENCODE basic
Mcf2l-206	ENSMUST00000110873.9	3169	866aa	Protein coding	-	D3YUF3	CDS 3' incomplete TSL:5
Mcf2l-221	ENSMUST00000173006.7	2500	757aa	Protein coding	-	G3UYM8	CDS 3' incomplete TSL:5
Mcf2l-209	ENSMUST00000123811.8	2390	295aa	Protein coding	-	F6WPM5	CDS 5' incomplete TSL:5
Mcf2l-213	ENSMUST00000134227.7	761	254aa	Protein coding	-	F7BZ65	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Mcf2l-216	ENSMUST00000139776.3	565	188aa	Protein coding	-	F6UKC6	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Mcf2l-220	ENSMUST00000156560.1	521	55aa	Protein coding	-	D3Z3S7	CDS 3' incomplete TSL:2
Mcf2l-218	ENSMUST00000145892.2	452	151aa	Protein coding	-	F6ZFQ8	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Mcf2l-223	ENSMUST00000238472.1	419	97aa	Protein coding	-	-	CDS 3' incomplete
Mcf2l-212	ENSMUST00000130302.1	3760	No protein	Retained intron	-	-	TSL:1
Mcf2l-214	ENSMUST00000134989.2	718	No protein	Retained intron	-	-	TSL:2
Mcf2l-211	ENSMUST00000127229.1	666	No protein	Retained intron	-	-	TSL:5
Mcf2l-219	ENSMUST00000156405.7	951	No protein	lncRNA	-	-	TSL:1
Mcf2l-215	ENSMUST00000138387.1	385	No protein	lncRNA	-	-	TSL:3

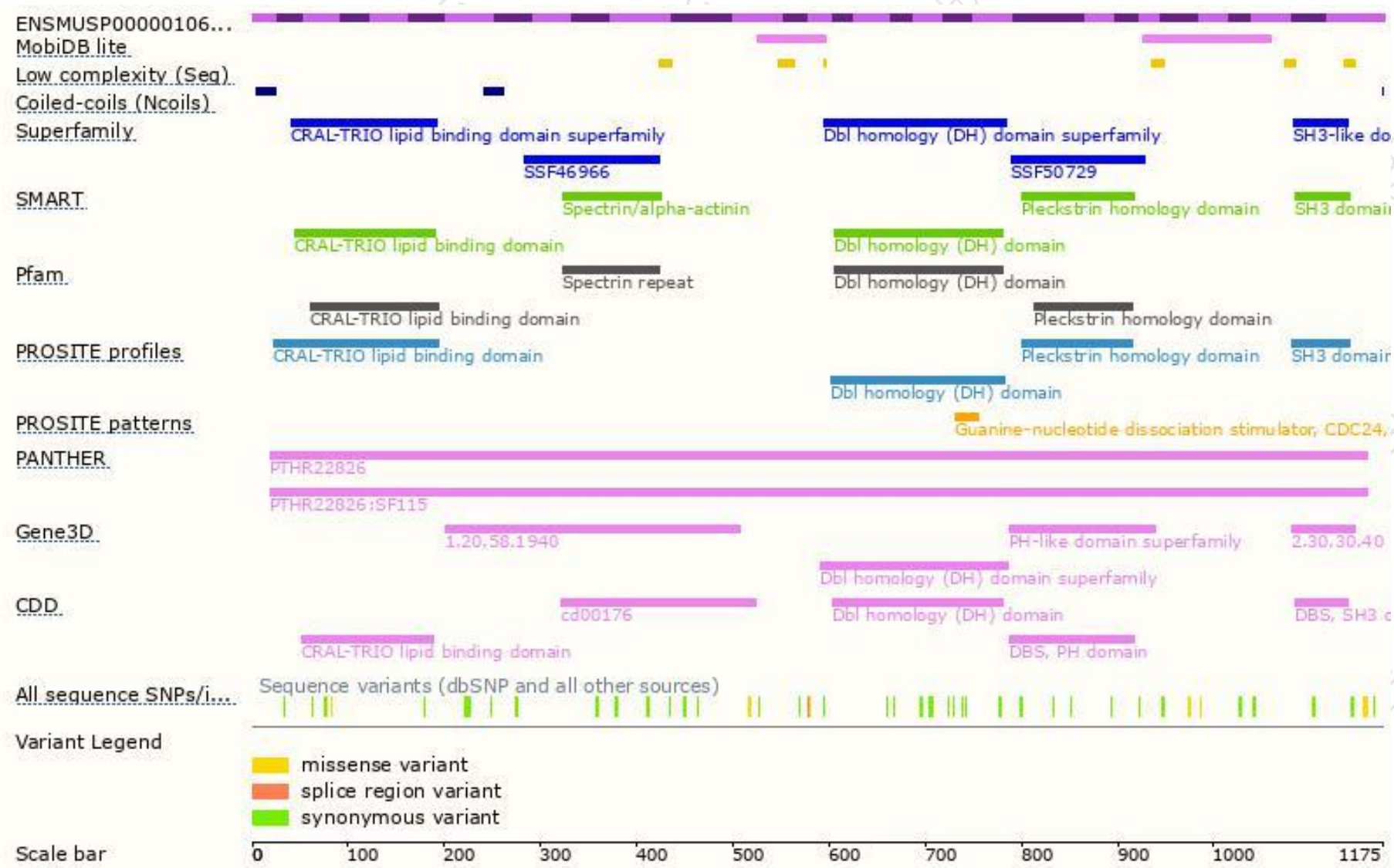The strategy is based on the design of *Mcf2l-207* transcript,The transcription is shown below
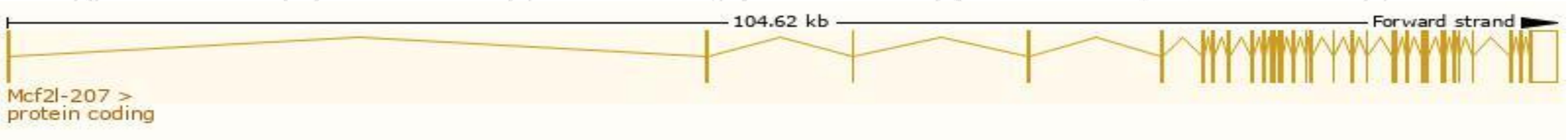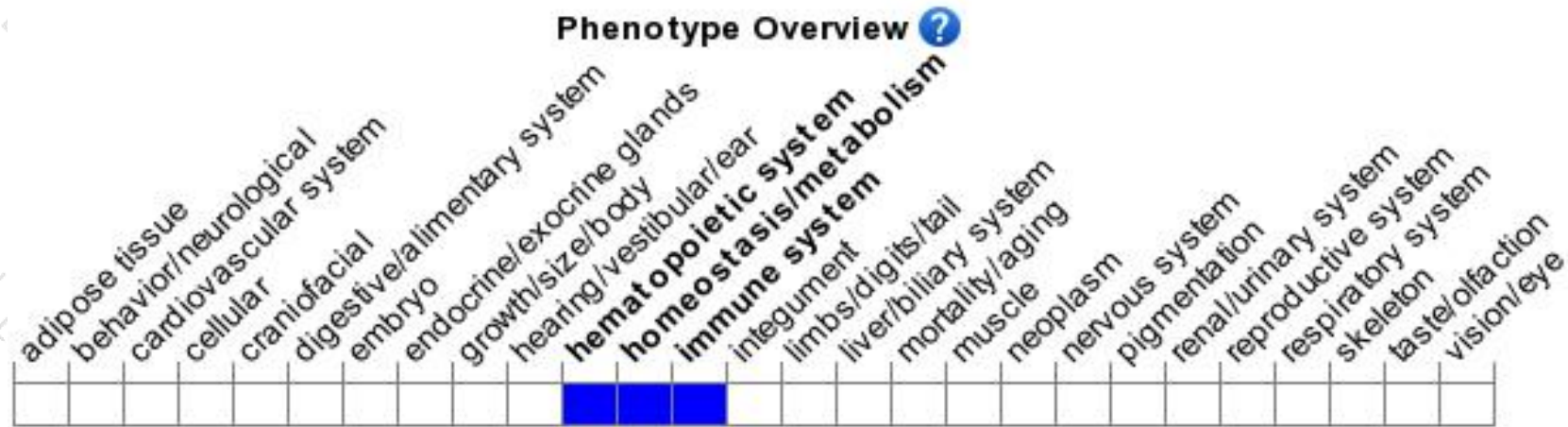
Genomic location distribution
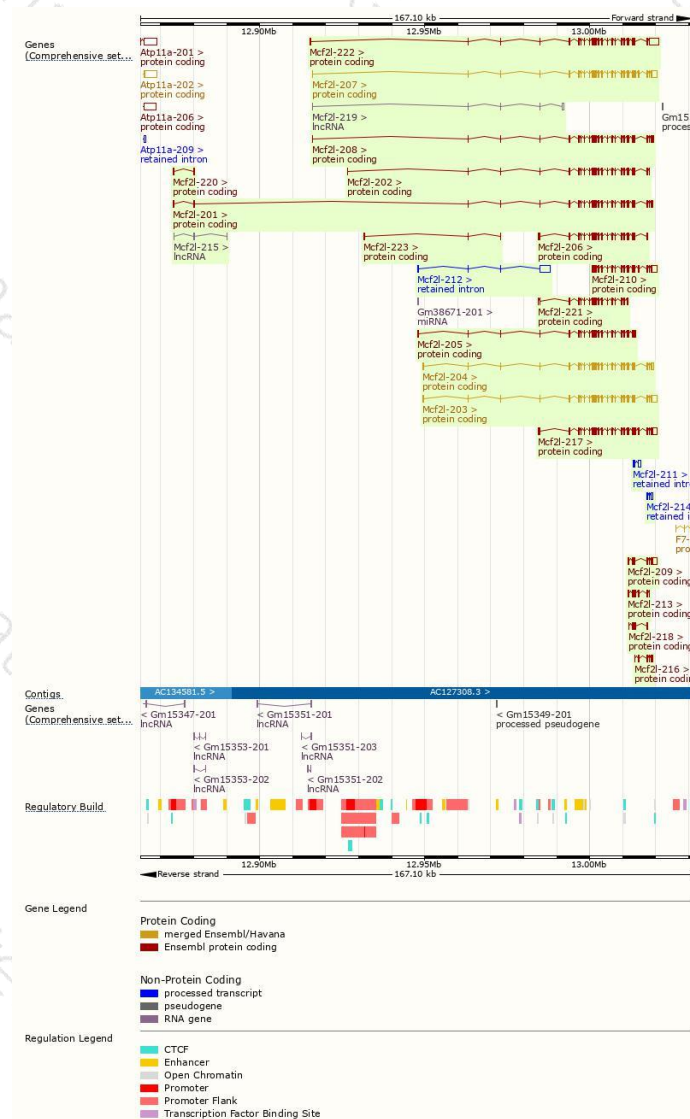
Protein domain

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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