

Cwc22 Cas9-KO Strategy

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Design Date:

2019-12-11

Project Overview

Project Name

Cwc22

Project type

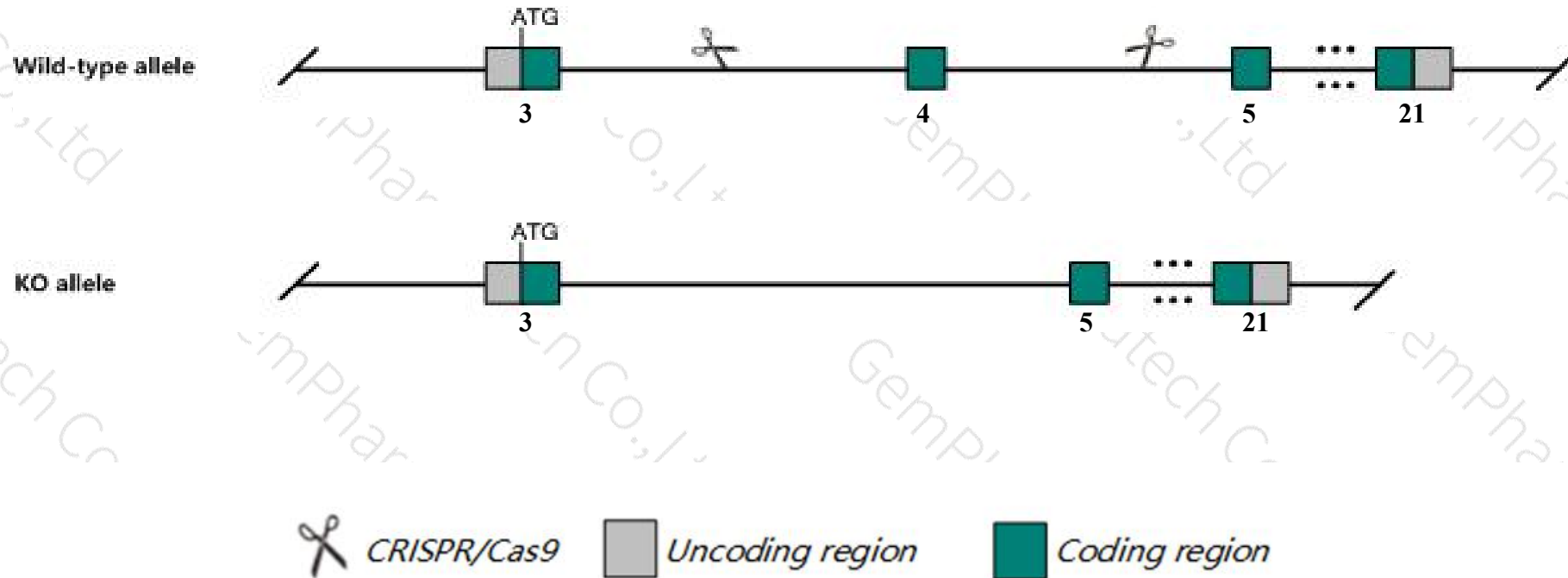
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cwc22* gene. The schematic diagram is as follows:



- The *Cwc22* gene has 13 transcripts. According to the structure of *Cwc22* gene, exon4 of *Cwc22-201* (ENSMUST00000065889.9) transcript is recommended as the knockout region. The region contains 65bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cwc22* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Cwc22* gene is located on the Chr2. 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)

Cwc22 CWC22 spliceosome-associated protein [Mus musculus (house mouse)]

Gene ID: 80744, updated on 3-Feb-2019

Summary



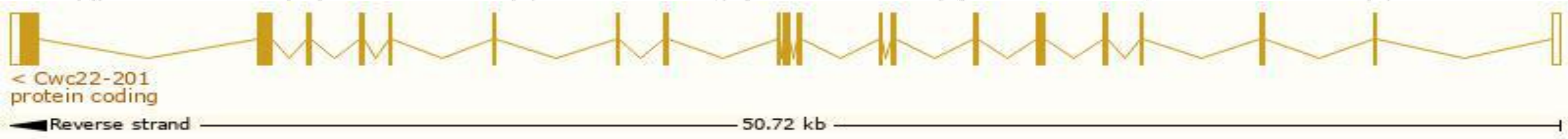
Official Symbol	Cwc22 provided by MGI
Official Full Name	CWC22 spliceosome-associated protein provided by MGI
Primary source	MGI:MGI:2136773
See related	Ensembl:ENSMUSG00000027014
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA684037, AI173004, AL022752, B230213M24, mKIAA1604
Expression	Broad expression in CNS E11.5 (RPKM 12.6), liver E14 (RPKM 8.0) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

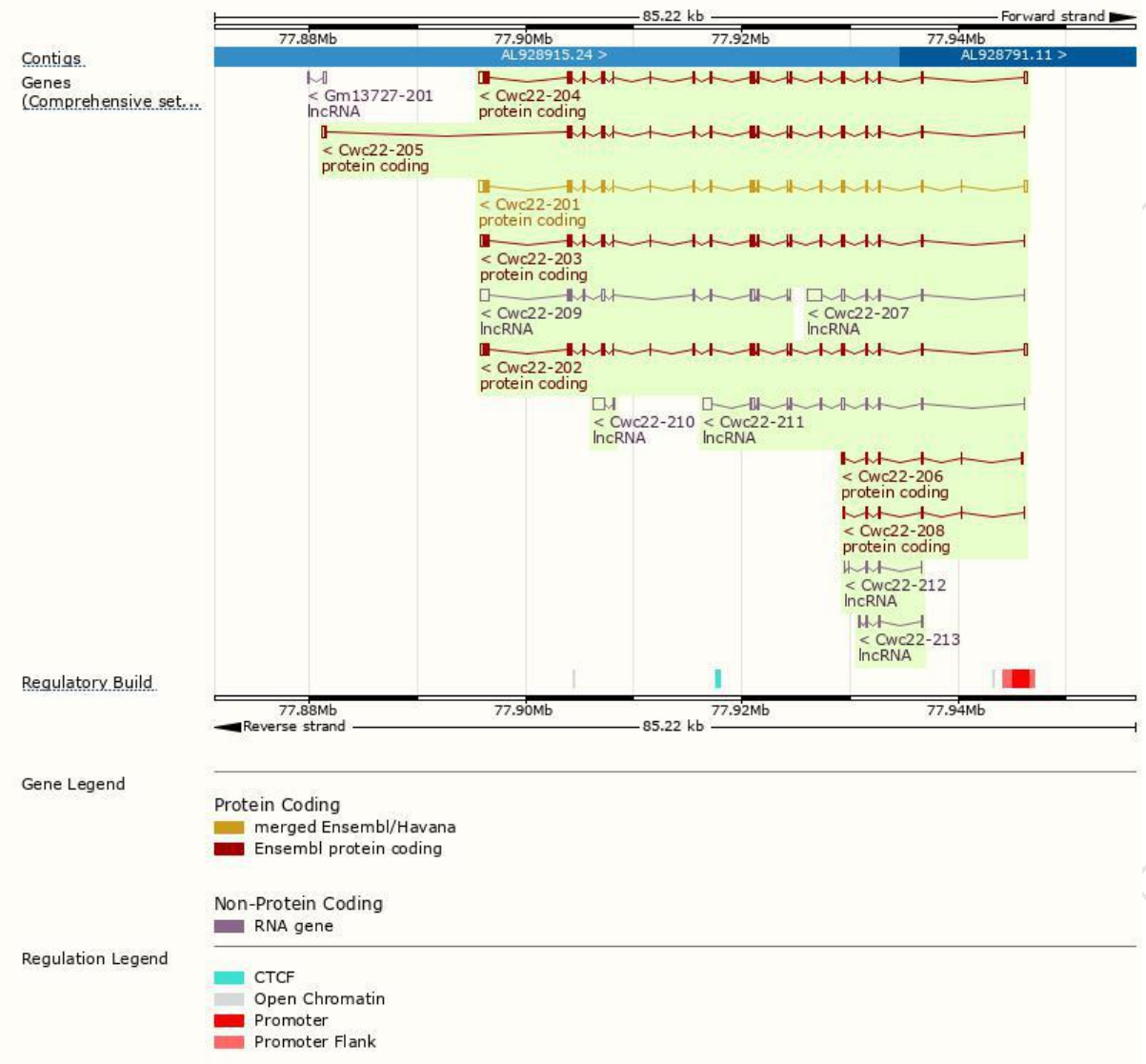
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cwc22-201	ENSMUST00000065889.9	3471	908aa	Protein coding	CCDS16165	Q8C5N3	TSL:1 GENCODE basic APPRIS P3
Cwc22-204	ENSMUST00000111821.8	3388	908aa	Protein coding	CCDS16165	Q8C5N3	TSL:5 GENCODE basic APPRIS P3
Cwc22-202	ENSMUST00000111818.7	3255	902aa	Protein coding	CCDS57178	Q8C5N3	TSL:1 GENCODE basic APPRIS ALT2
Cwc22-203	ENSMUST00000111819.7	3090	903aa	Protein coding	CCDS71080	B1AYU7	TSL:1 GENCODE basic APPRIS ALT2
Cwc22-205	ENSMUST00000111824.7	2603	723aa	Protein coding	-	B1AYU4	TSL:1 GENCODE basic APPRIS ALT2
Cwc22-206	ENSMUST00000127289.7	678	139aa	Protein coding	-	B1AYU8	CDS 3' incomplete TSL:5
Cwc22-208	ENSMUST00000128963.1	533	109aa	Protein coding	-	B1AYU9	CDS 3' incomplete TSL:2
Cwc22-209	ENSMUST00000137494.7	2205	No protein	lncRNA	-	-	TSL:1
Cwc22-211	ENSMUST00000144727.7	2094	No protein	lncRNA	-	-	TSL:1
Cwc22-207	ENSMUST00000127351.7	1877	No protein	lncRNA	-	-	TSL:1
Cwc22-210	ENSMUST00000139842.1	1066	No protein	lncRNA	-	-	TSL:1
Cwc22-213	ENSMUST00000156863.1	511	No protein	lncRNA	-	-	TSL:3
Cwc22-212	ENSMUST00000149012.7	409	No protein	lncRNA	-	-	TSL:3

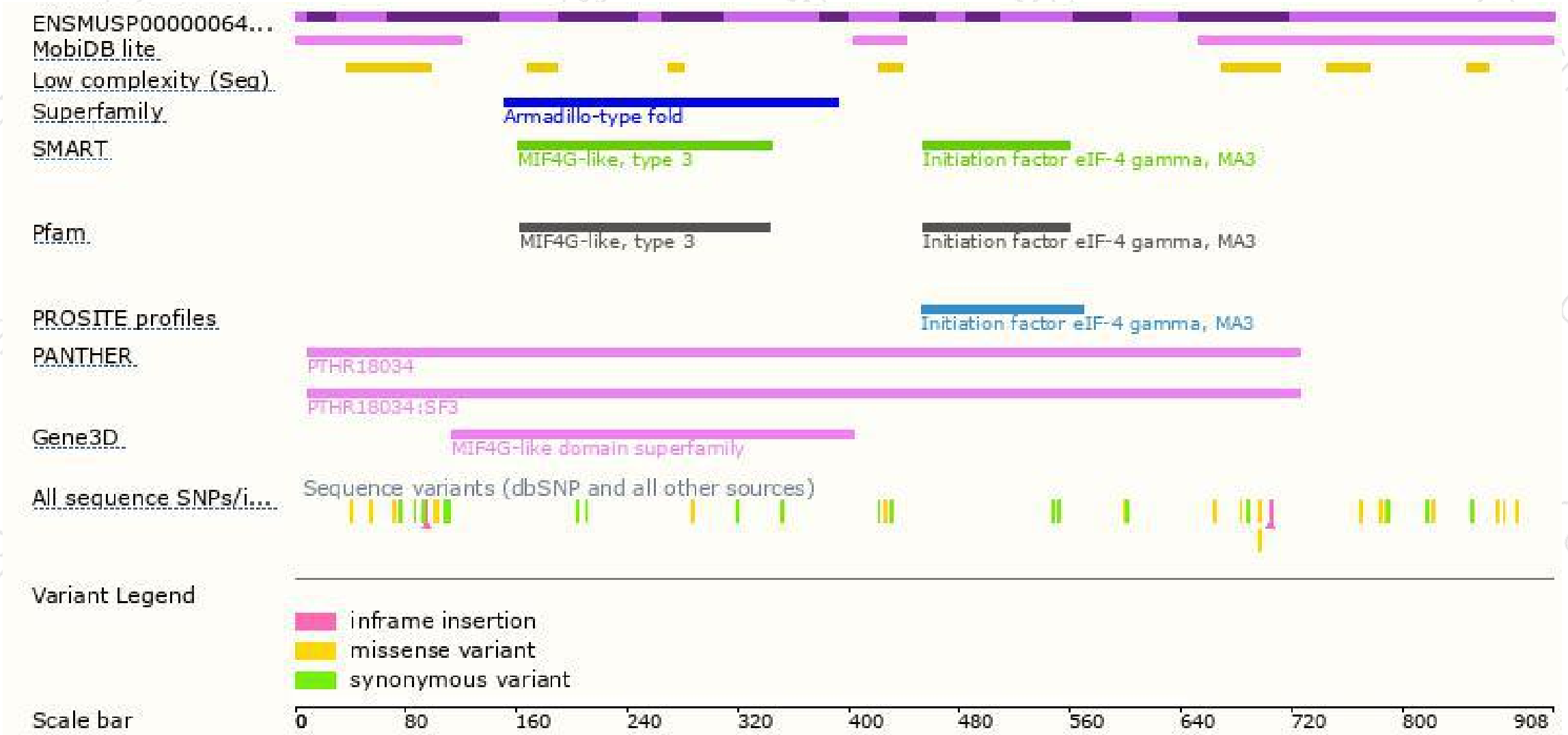
The strategy is based on the design of *Cwc22-201* transcript,The transcription is shown below



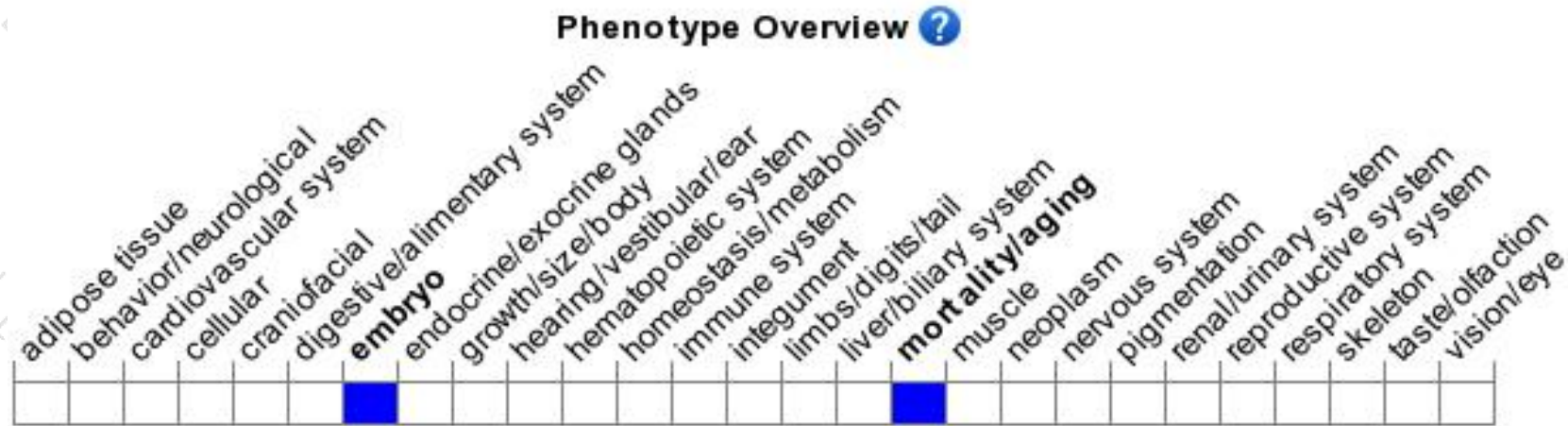
Genomic location distribution



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/>).

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

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