Chrdl1 Cas9-KO Strategy

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Project Overview

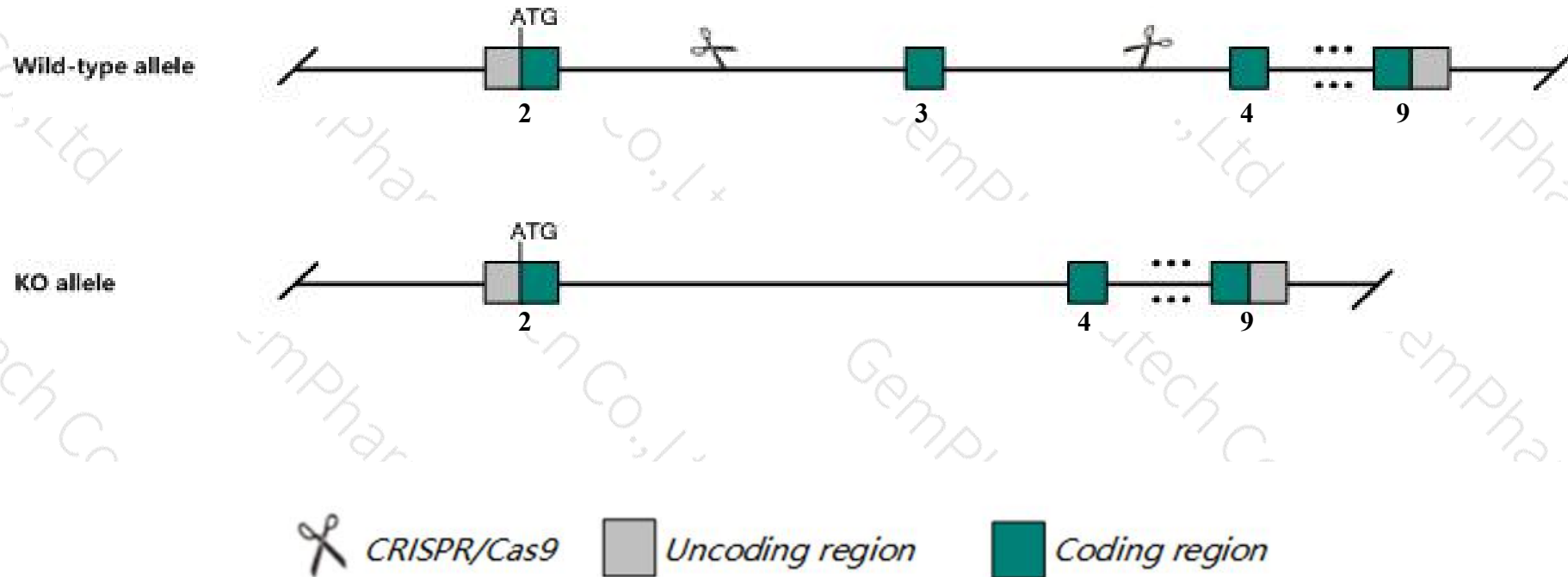|	
Project Name	*Chrdl1*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Chrdl1* gene. The schematic diagram is as follows:

Technical routes

➢ The *Chrdl1* gene has 5 transcripts. According to the structure of *Chrdl1* gene, exon3 of *Chrdl1-202* (ENSMUST00000074660.11) transcript is recommended as the knockout region.The region contains 113bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Chrdl1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ The *Chrdl1* gene is located on the ChrX. 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）

Chrdl1   chordin-like 1 [*Mus musculus* (house mouse)]

Gene ID: 83453, updated on 24-Aug-2019

⌃ Summary

Official Symbol	Chrdl1 provided by MGI
Official Full Name	chordin-like 1 provided by MGI
Primary source	MGI:MGI:1933172
See related	Ensembl:ENSMUSG00000031283
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	CHL; CHL1; VOPT; Nrln1
Expression	Broad expression in genital fat pad adult (RPKM 5.5), bladder adult (RPKM 4.9) and 18 other tissues See more
Orthologs	human all

⌃ Genomic context

Location: X; X F2

See Chrdl1 in Genome Data Viewer
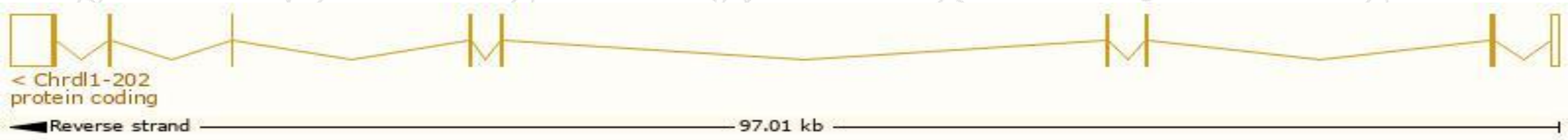
Exon count: 12

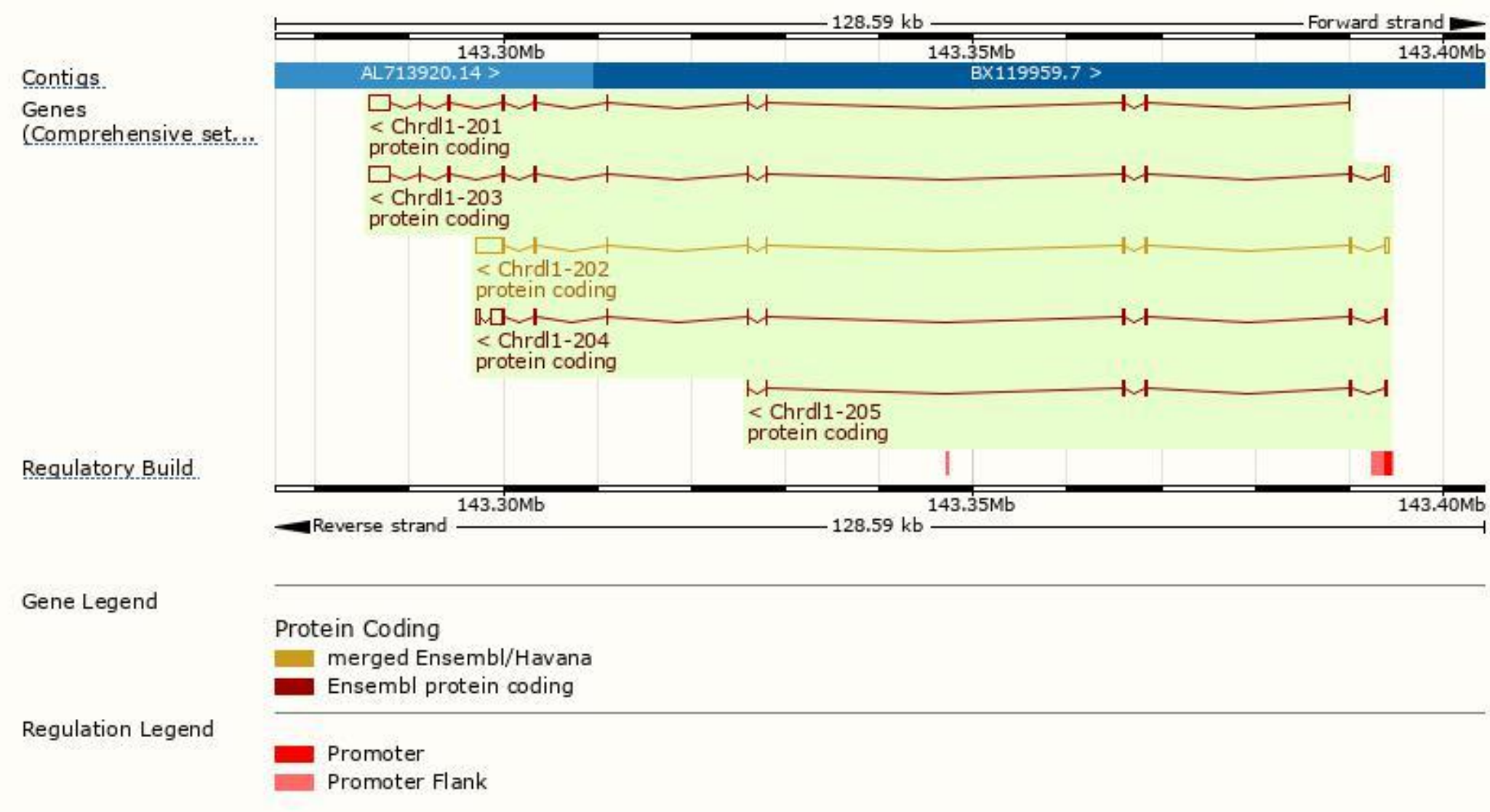| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	X	NC_000086.7 (143285674..143394263, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	X	NC_000086.6 (139720217..139828805, complement)

Transcript information（Ensembl）

The gene has 5 transcripts,all transcripts are shown below:

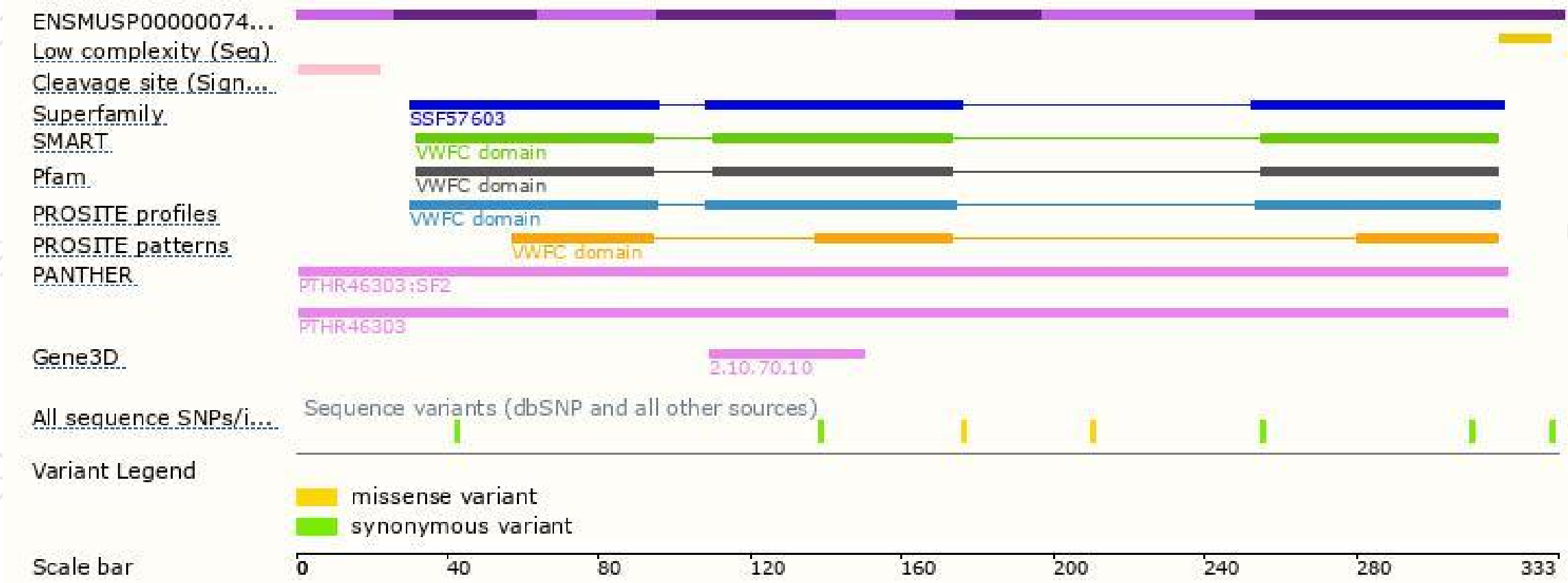| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Chrdl1-202	ENSMUST00000074660.11	4096	333aa	Protein coding	CCDS30453	Q3TP73 Q920C1	TSL:1 GENCODE basic APPRIS P3
Chrdl1-203	ENSMUST00000112878.8	4050	447aa	Protein coding	CCDS53208	Q920C1	TSL:5 GENCODE basic APPRIS ALT2
Chrdl1-201	ENSMUST00000063029.12	3550	447aa	Protein coding	CCDS53208	Q920C1	TSL:1 GENCODE basic APPRIS ALT2
Chrdl1-204	ENSMUST0000166406.2	2605	333aa	Protein coding	CCDS30453	Q3TP73 Q920C1	TSL:1 GENCODE basic APPRIS P3
Chrdl1-205	ENSMUST0000207415.1	640	159aa	Protein coding	-	A0A140LIV5	CDS 3' incomplete TSL:3

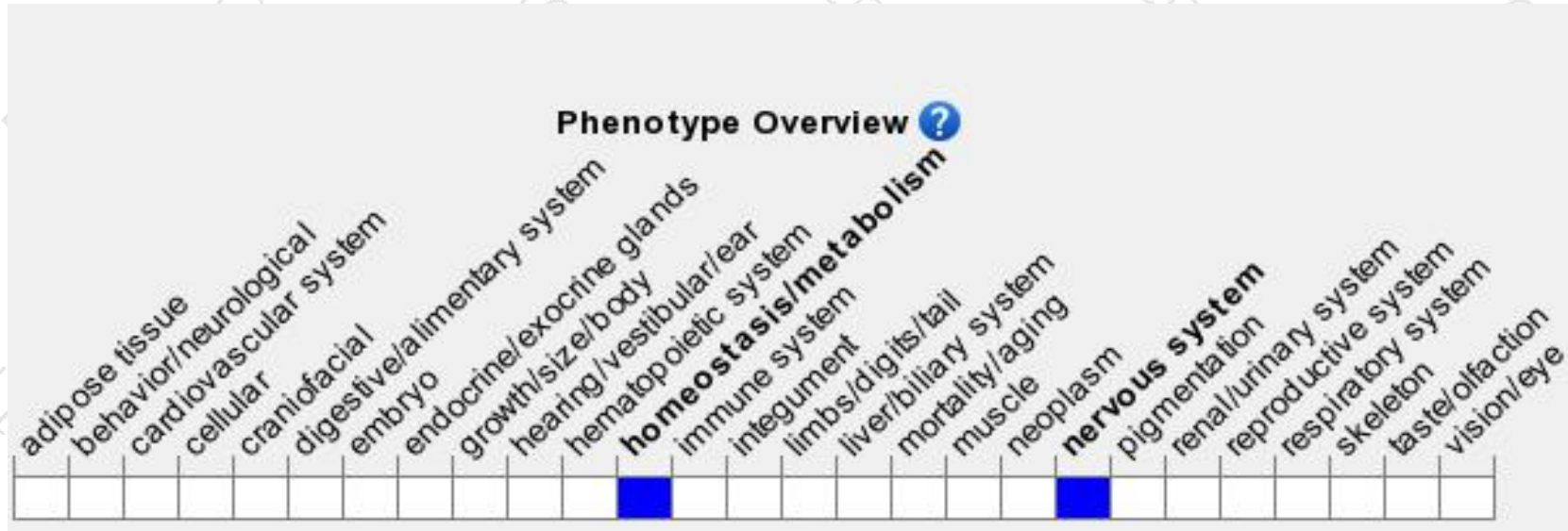The strategy is based on the design of *Chrdl1-202* transcript,The transcription is shown below

< Chrdl1-202
protein coding

◄ Reverse strand

—— 97.01 kb ——

Genomic location distribution

Protein domain

ENSMUSP00000074...		
Low complexity (Seg)		
Cleavage site (Sign...		
Superfamily	SSF57603	
SMART	VWFC domain	
Pfam	VWFC domain	
PROSITE profiles	VWFC domain	
PROSITE patterns	VWFC domain	
PANTHER	PTHR46303:SF2	
	PTHR46303	
Gene3D	2.10.70.10	
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)	

Variant Legend

- ▬ missense variant
- ▬ synonymous variant

Scale bar

0   40   80   120   160   200   240   280   333

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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