Rnf14 Cas9-KO Strategy

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Project Overview

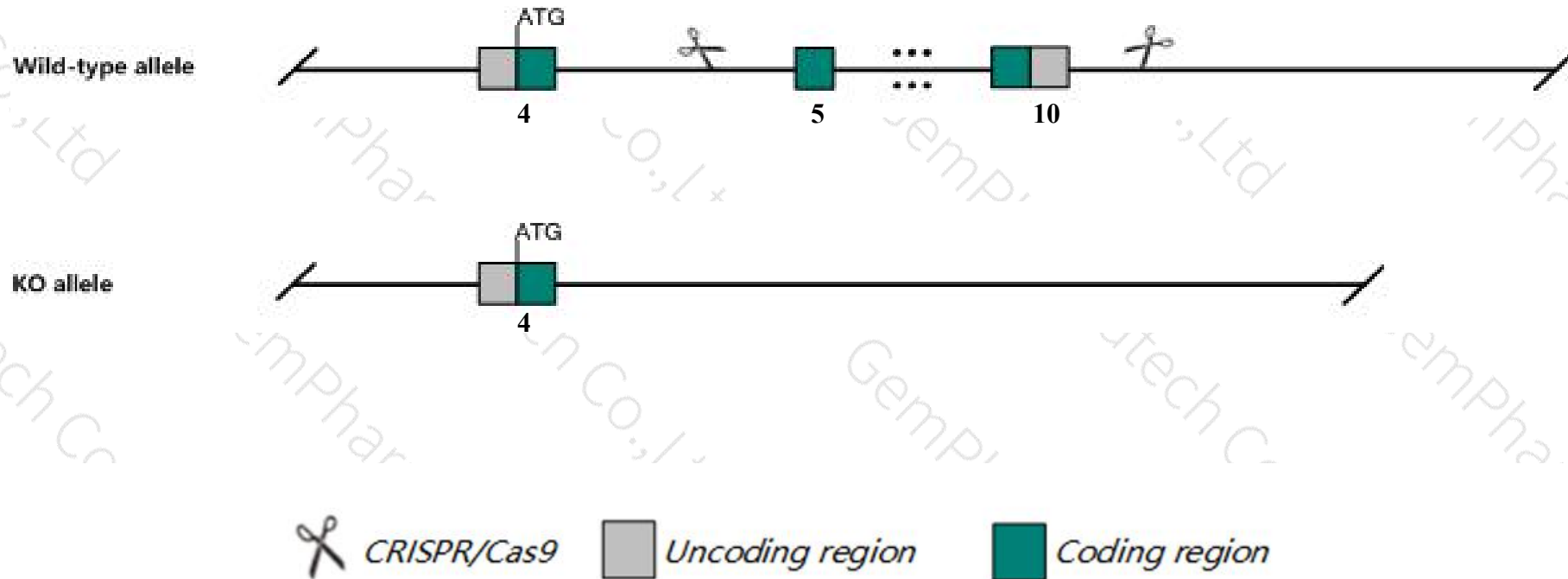|	
Project Name	***Rnf14***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnf14* gene. The schematic diagram is as follows:

Technical routes

➤ The *Rnf14* gene has 21 transcripts. According to the structure of *Rnf14* gene, exon5-exon10 of *Rnf14-203* (ENSMUST00000171461.2) transcript is recommended as the knockout region.The region contains most of the coding sequence.Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Rnf14* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

➢ The effect on transcript *Rnf14*-206&210 is unknown.

➢ Transcript *Rnf14*-207&213&221 may not be affected.

➢ The *Rnf14* gene is located on the Chr18. 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）

Rnf14 ring finger protein 14 [*Mus musculus* (house mouse)]

Gene ID: 56736, updated on 24-Oct-2019

▲ Summary

Official Symbol	Rnf14 provided by MGI
Official Full Name	ring finger protein 14 provided by MGI
Primary source	MGI:MGI:1929668
See related	Ensembl:ENSMUSG00000060450
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	Triad2; AA986456; AU041447; D7Bwg0165e; D18Ertd188e; 2310075C09Rik; 2610005D23Rik
Expression	Ubiquitous expression in CNS E18 (RPKM 51.1), cortex adult (RPKM 38.6) and 28 other tissues See more
Orthologs	human all

▲ Genomic context

Location: 18 B3; 18 20.2 cM

See Rnf14 in Genome Data Viewer

Exon count: 15

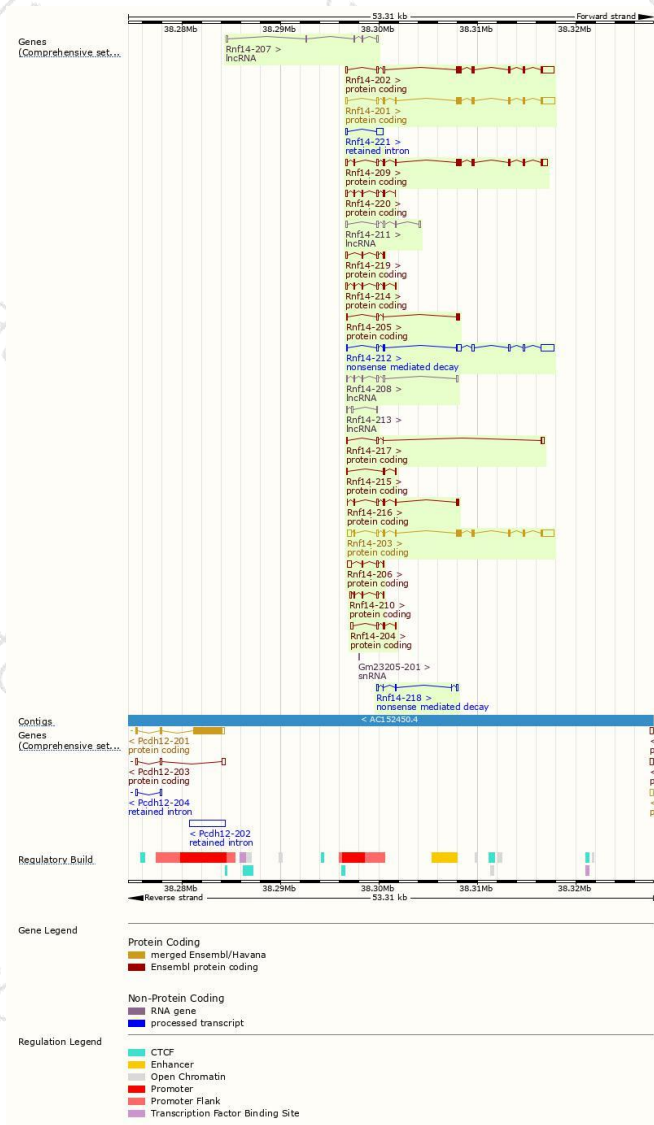| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	18	NC_000084.6 (38277460..38317852)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	18	NC_000084.5 (38456289..38477503)

Transcript information（Ensembl）

The gene has 21 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf14-203	ENSMUST00000171461.2	3340	485aa	Protein coding	CCDS29200	Q9JI90	TSL:1 GENCODE basic APPRIS P1
Rnf14-201	ENSMUST00000072376.12	3040	485aa	Protein coding	CCDS29200	Q9JI90	TSL:1 GENCODE basic APPRIS P1
Rnf14-202	ENSMUST00000170811.7	2886	359aa	Protein coding	CCDS50261	G3XA54	TSL:1 GENCODE basic
Rnf14-209	ENSMUST00000236116.1	2410	485aa	Protein coding	CCDS29200	-	GENCODE basic APPRIS P1
Rnf14-216	ENSMUST00000237211.1	864	183aa	Protein coding	-	-	CDS 3' incomplete
Rnf14-214	ENSMUST00000236982.1	776	94aa	Protein coding	-	-	CDS 3' incomplete
Rnf14-204	ENSMUST00000235491.1	767	102aa	Protein coding	-	-	CDS 3' incomplete
Rnf14-206	ENSMUST00000235811.1	740	28aa	Protein coding	-	-	CDS 3' incomplete
Rnf14-205	ENSMUST00000235549.1	717	142aa	Protein coding	-	-	CDS 3' incomplete
Rnf14-210	ENSMUST00000236319.1	684	40aa	Protein coding	-	-	CDS 3' incomplete
Rnf14-220	ENSMUST00000237903.1	662	65aa	Protein coding	-	-	CDS 3' incomplete
Rnf14-217	ENSMUST00000237416.1	618	23aa	Protein coding	-	-	GENCODE basic
Rnf14-219	ENSMUST00000237824.1	530	49aa	Protein coding	-	-	CDS 3' incomplete
Rnf14-215	ENSMUST00000237089.1	364	87aa	Protein coding	-	-	CDS 3' incomplete
Rnf14-212	ENSMUST00000236649.1	2822	79aa	Nonsense mediated decay	-	-	
Rnf14-218	ENSMUST00000237667.1	674	39aa	Nonsense mediated decay	-	-	
Rnf14-221	ENSMUST00000238031.1	796	No protein	Retained intron	-	-	
Rnf14-208	ENSMUST00000236032.1	778	No protein	lncRNA	-	-	
Rnf14-211	ENSMUST00000236353.1	743	No protein	lncRNA	-	-	
Rnf14-207	ENSMUST00000235812.1	548	No protein	lncRNA	-	-	
Rnf14-213	ENSMUST00000236690.1	424	No protein	lncRNA	-	-	

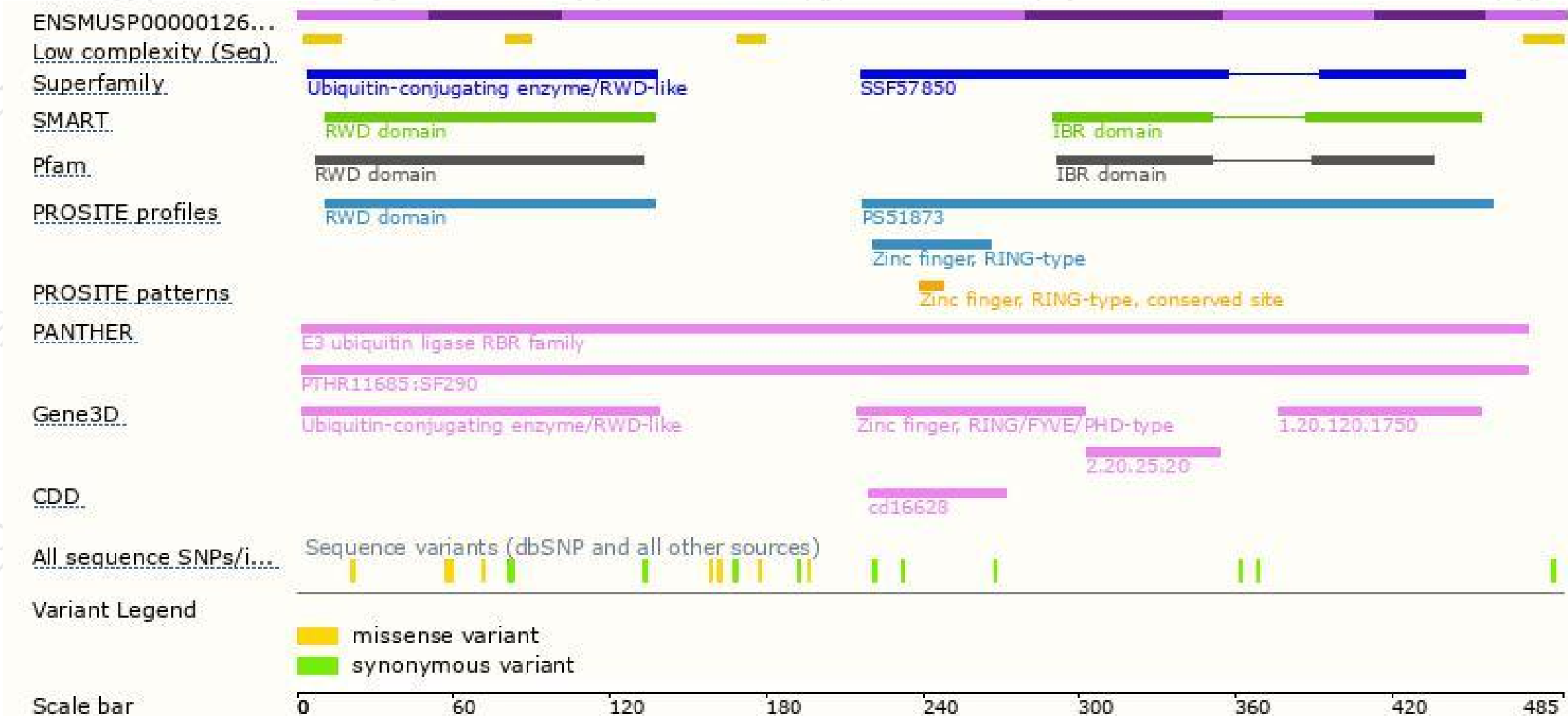The strategy is based on the design of *Rnf14-203* transcript,The transcription is shown below
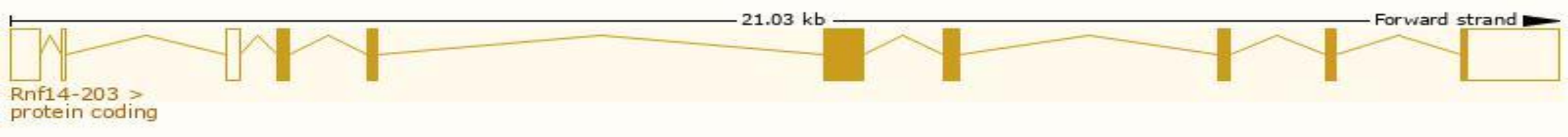
Genomic location distribution

Protein domain

ENSMUSP00000126...								
Low complexity (Seg)								
Superfamily	Ubiquitin-conjugating enzyme/RWD-like			SSF57850				
SMART	RWD domain					IBR domain		
Pfam	RWD domain					IBR domain		
PROSITE profiles	RWD domain			PS51873				
				Zinc finger, RING-type				
PROSITE patterns				Zinc finger, RING-type, conserved site				
PANTHER	E3 ubiquitin ligase RBR family							
	PTHR11685:SF290							
Gene3D	Ubiquitin-conjugating enzyme/RWD-like			Zinc finger, RING/FYVE/PHD-type			1.20.120.1750	
					2.20.25.20			
CDD				cd16628				
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)							

Variant Legend

🟨 missense variant
🟩 synonymous variant

Scale bar	0	60	120	180	240	300	360	420	485

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