Nup160 Cas9-KO Strategy

Designer:Xueting Zhang
Reviewer:Yanhua Shen
Design Date:2019-8-22

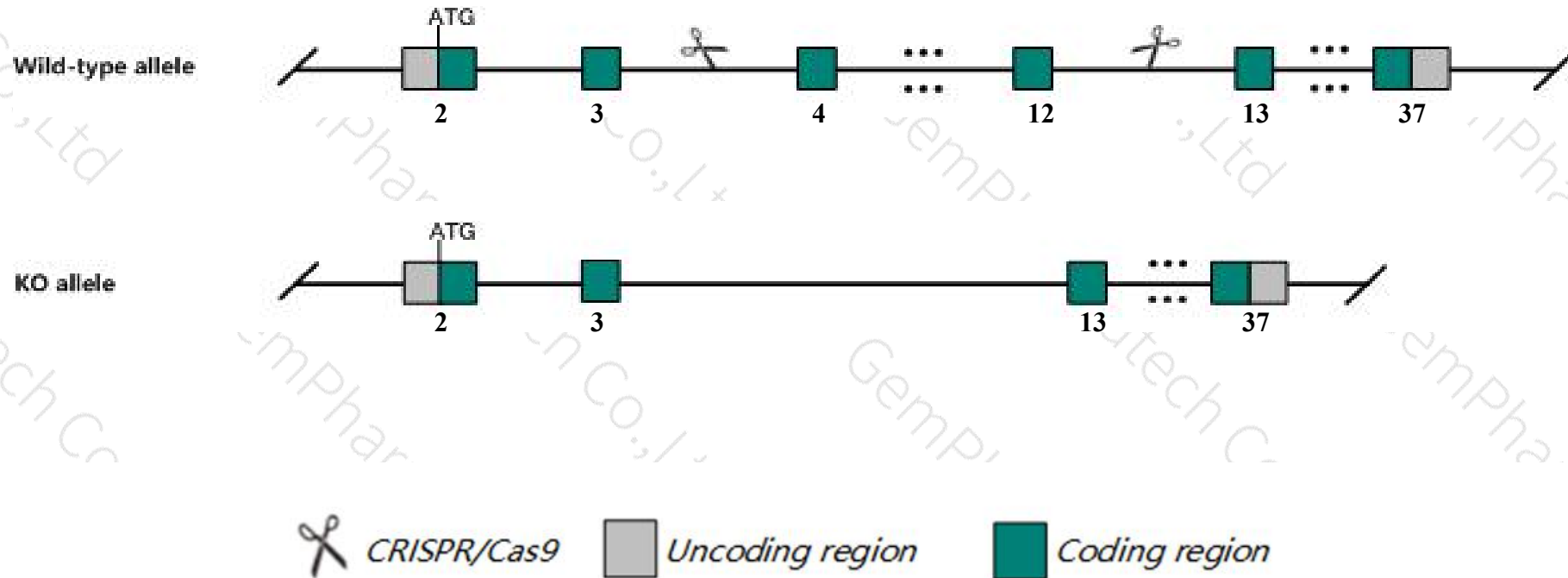|	
Project Name	*Nup160*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nup160* gene. The schematic diagram is as follows:

Technical routes

➢ The *Nup160* gene has 7 transcripts. According to the structure of *Nup160* gene, exon4-exon12 of *Nup160-201* (ENSMUST00000057481.6) transcript is recommended as the knockout region.The region contains 1117bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Nup160* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

➢ The *Nup160* 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.

➢ Transcript *Nup160*-202&203&204 may not be affected.

➢ 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）

Nup160 nucleoporin 160 [*Mus musculus* (house mouse)]

Gene ID: 59015, updated on 12-Aug-2019

Summary

Official Symbol	Nup160 provided by MGI
Official Full Name	nucleoporin 160 provided by MGI
Primary source	MGI:MGI:1926227
See related	Ensembl:ENSMUSG00000051329
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Gtl13; 160kDa; Gtl-13; Gtl1-13; AA414952; AU020188; mKIAA0197; 2810011M03Rik
Expression	Ubiquitous expression in liver E14 (RPKM 4.4), CNS E11.5 (RPKM 4.3) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 2; 2 E1
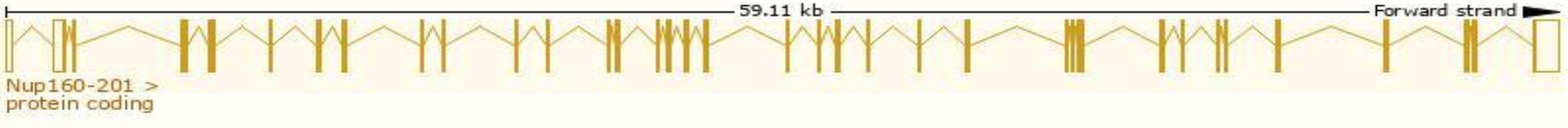
See Nup160 in Genome Data Viewer

Exon count: 37

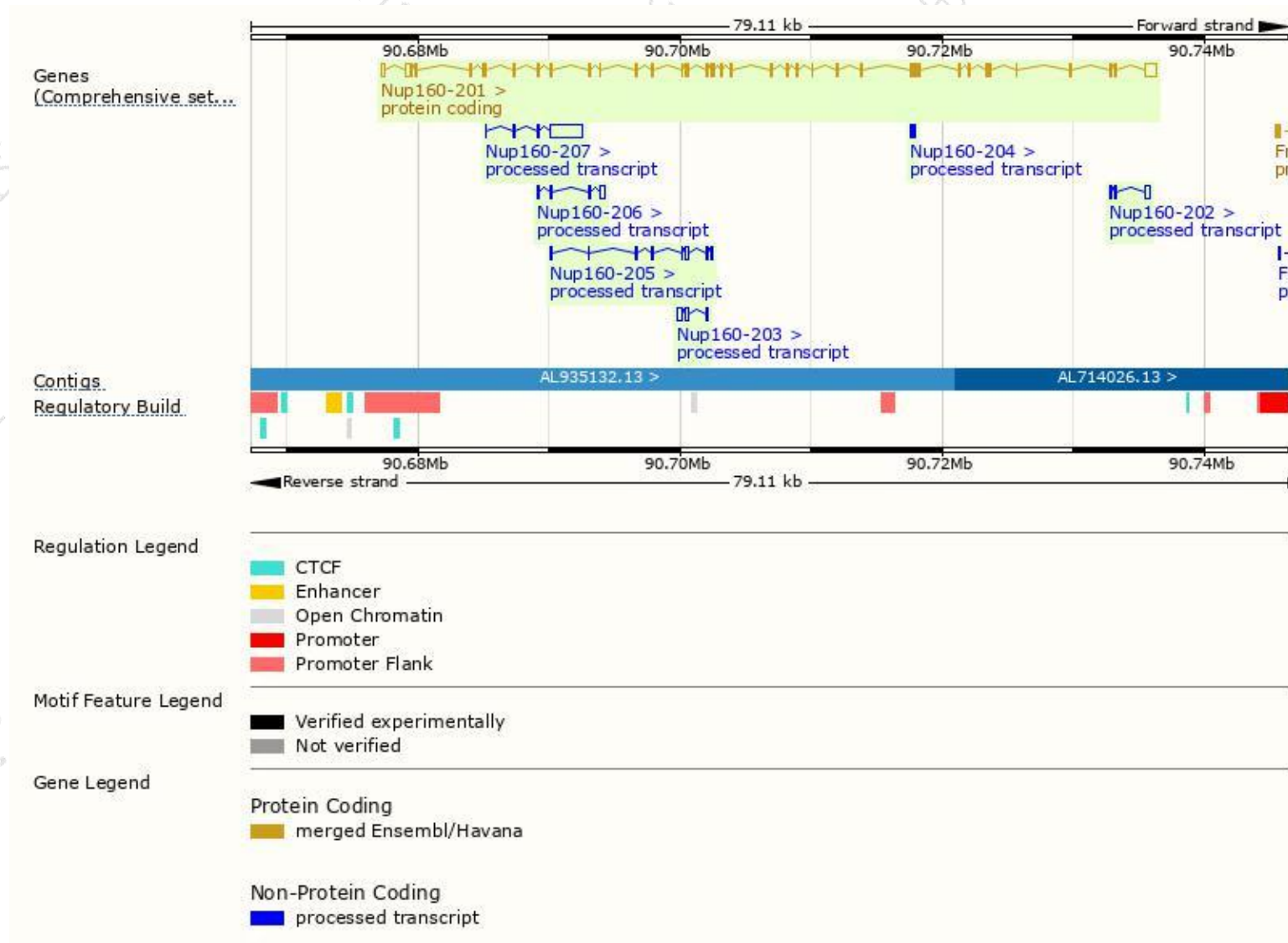| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (90677215..90739327)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (90517372..90576485)

Transcript information（Ensembl）

The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nup160-201	ENSMUST00000057481.6	5684	1402aa	Protein coding	CCDS16413	Q9Z0W3	TSL:1 GENCODE basic APPRIS P1
Nup160-207	ENSMUST00000154036.1	2673	No protein	Processed transcript	-	-	TSL:1
Nup160-206	ENSMUST00000145669.1	762	No protein	Processed transcript	-	-	TSL:3
Nup160-205	ENSMUST00000136739.7	726	No protein	Processed transcript	-	-	TSL:3
Nup160-203	ENSMUST00000130629.1	687	No protein	Processed transcript	-	-	TSL:3
Nup160-202	ENSMUST00000126503.1	658	No protein	Processed transcript	-	-	TSL:2
Nup160-204	ENSMUST00000132595.1	229	No protein	Processed transcript	-	-	TSL:3

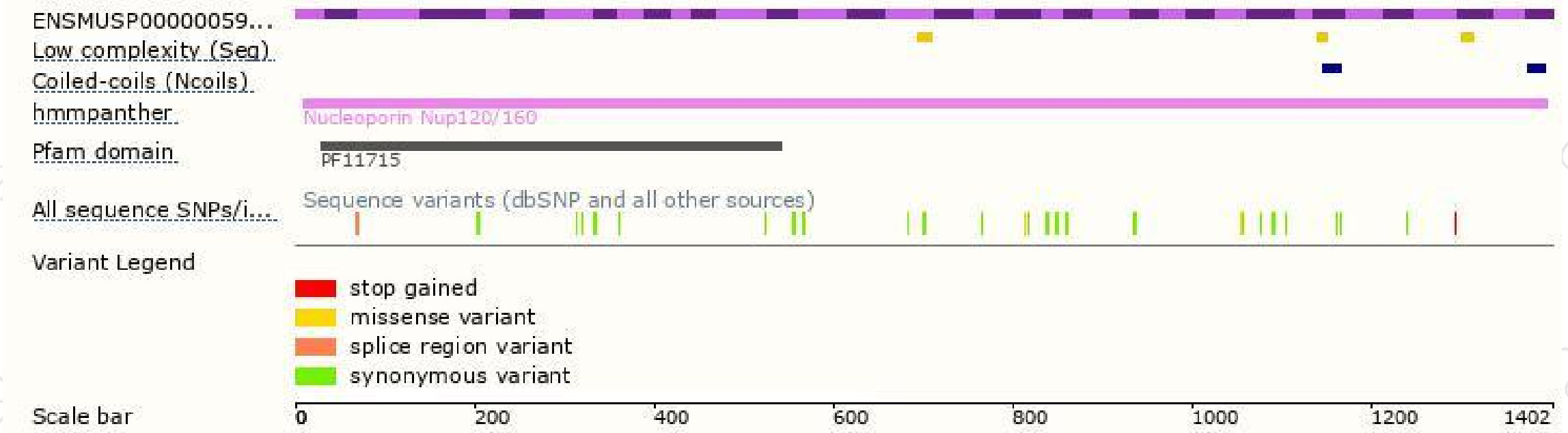The strategy is based on the design of *Nup160-201* transcript,The transcription is shown below

Genomic location distribution

Protein domain

ENSMUSP00000059...	
Low complexity (Seg)	
Coiled-coils (Ncoils)	
hmmpanther	Nucleoporin Nup120/160
Pfam domain	PF11715
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)

Variant Legend

- stop gained
- missense variant
- splice region variant
- synonymous variant

Scale bar: 0 200 400 600 800 1000 1200 1402

If you have any questions, you are welcome to inquire.
Tel: 400-9660890