

***Grb10* Cas9-KO Strategy**

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Design Date: 2019-4-4

Project Overview

Project Name

Grb10

Project type

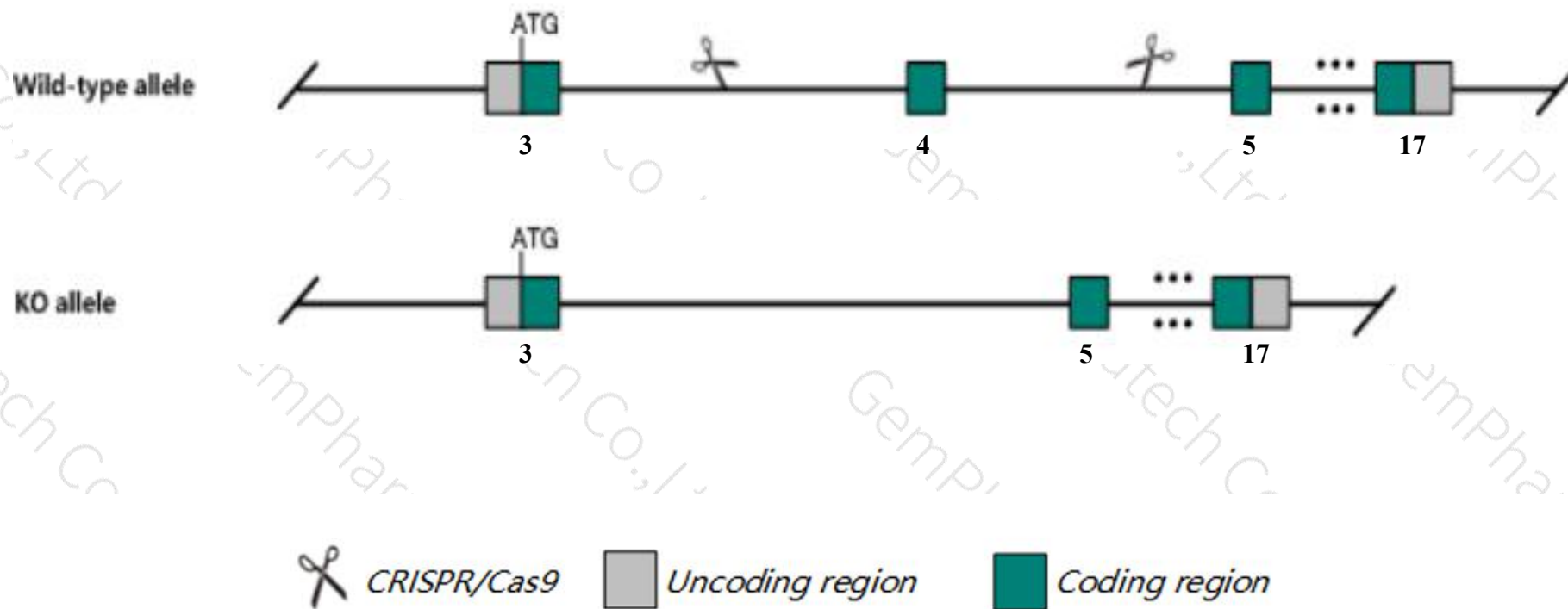
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Grb10* gene. The schematic diagram is as follows:



- The *Grb10* gene has 9 transcripts. According to the structure of *Grb10* gene, exon4 of *Grb10-201* (ENSMUST00000093321.11) transcript is recommended as the knockout region. The region contains 154bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Grb10* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, maternal transmission of a mutant allele results in both fetal and placental overgrowth. disproportionate overgrowth of the liver is observed. paternal transmission of an allele lacking the differentially methylated region results in growth retardation.
- The KO region contains functional region of the *Grb10* gene. Knockout the region may affect the function of LOC102631979
- The *Grb10* gene is located on the Chr11. 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)

Grb10 growth factor receptor bound protein 10 [Mus musculus (house mouse)]

Gene ID: 14783, updated on 13-Mar-2020

Summary



Official Symbol Grb10 provided by [MGI](#)

Official Full Name growth factor receptor bound protein 10 provided by [MGI](#)

Primary source [MGI:MGI:103232](#)

See related [Ensembl:ENSMUSG00000020176](#)

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 5730571D09Rik, AI325020, Meg1, mKIAA0207

Expression Biased expression in limb E14.5 (RPKM 223.2), liver E18 (RPKM 212.5) and 13 other tissues [See more](#)

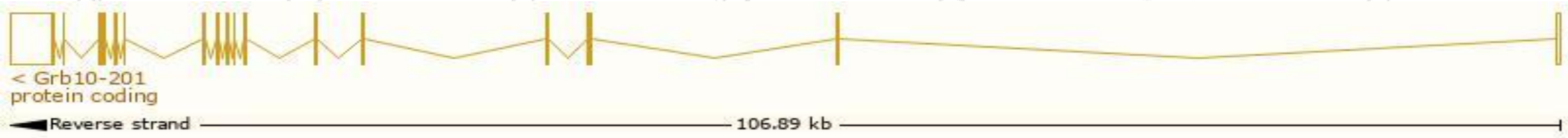
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

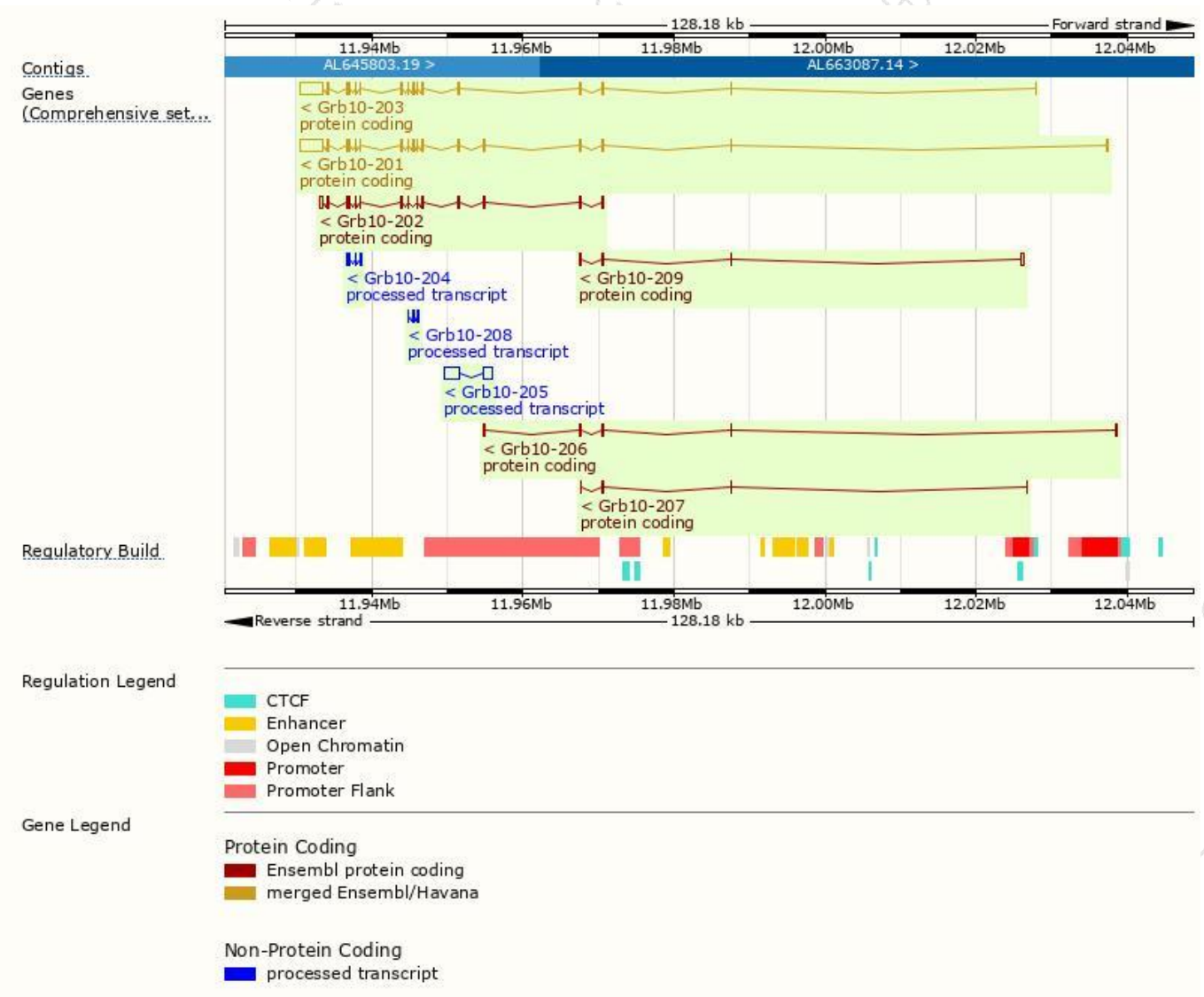
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Grb10-201	ENSMUST00000093321.11	5061	596aa	Protein coding	CCDS24440	Q60760	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Grb10-203	ENSMUST00000109654.7	4755	541aa	Protein coding	CCDS48754	Q60760	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Grb10-202	ENSMUST00000109653.7	2048	550aa	Protein coding	-	Q5SUW3	TSL:5 GENCODE basic
Grb10-209	ENSMUST00000150972.7	940	116aa	Protein coding	-	B1ATS7	CDS 3' incomplete TSL:5
Grb10-206	ENSMUST00000143386.7	761	171aa	Protein coding	-	Q5SUW0	CDS 3' incomplete TSL:3
Grb10-207	ENSMUST00000143915.1	430	84aa	Protein coding	-	B1ATS8	CDS 3' incomplete TSL:5
Grb10-205	ENSMUST00000142877.1	3341	No protein	Processed transcript	-	-	TSL:1
Grb10-204	ENSMUST00000124587.1	479	No protein	Processed transcript	-	-	TSL:5
Grb10-208	ENSMUST00000148254.1	351	No protein	Processed transcript	-	-	TSL:3

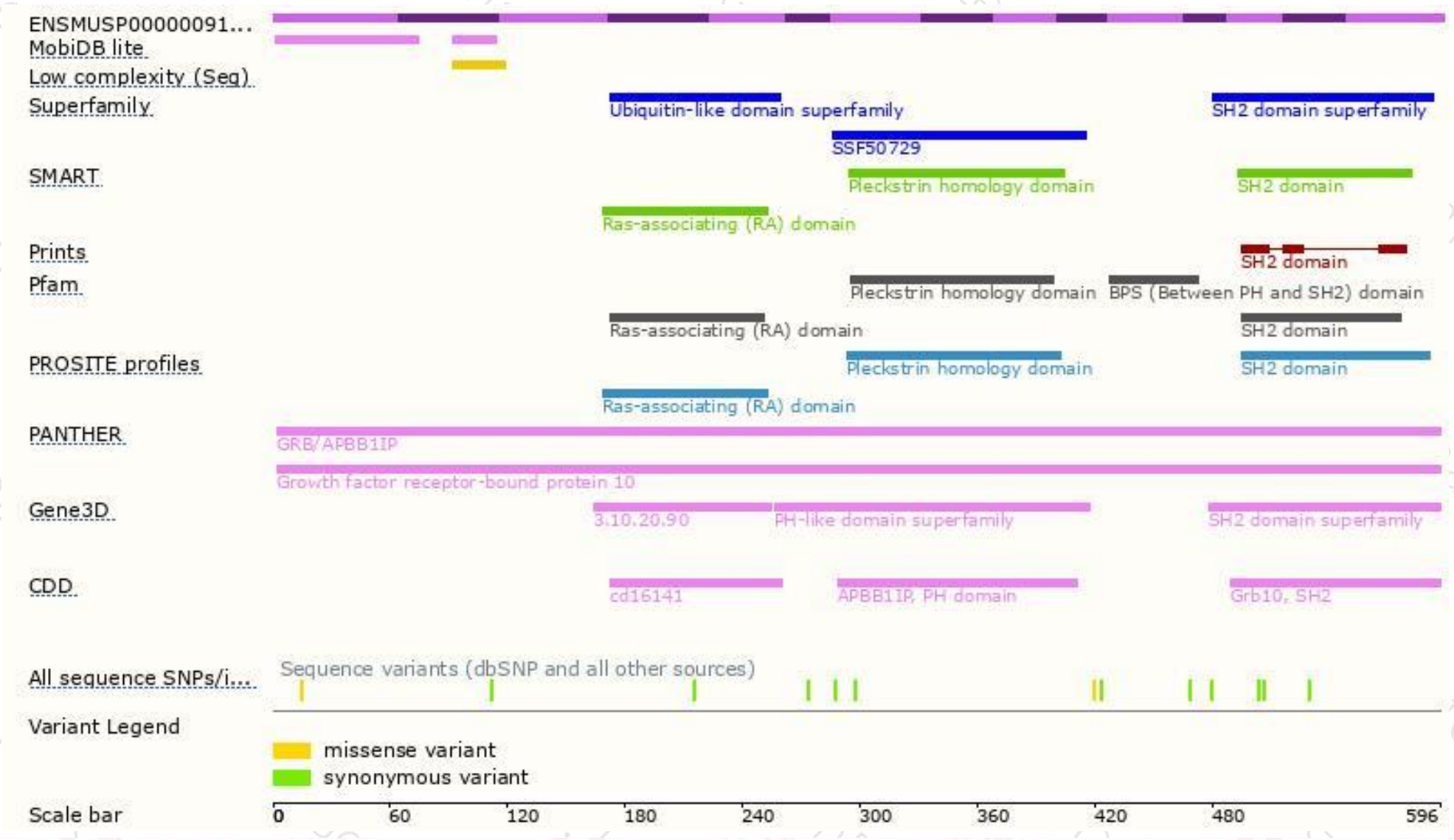
The strategy is based on the design of *Grb10-201* transcript,the transcription is shown below:



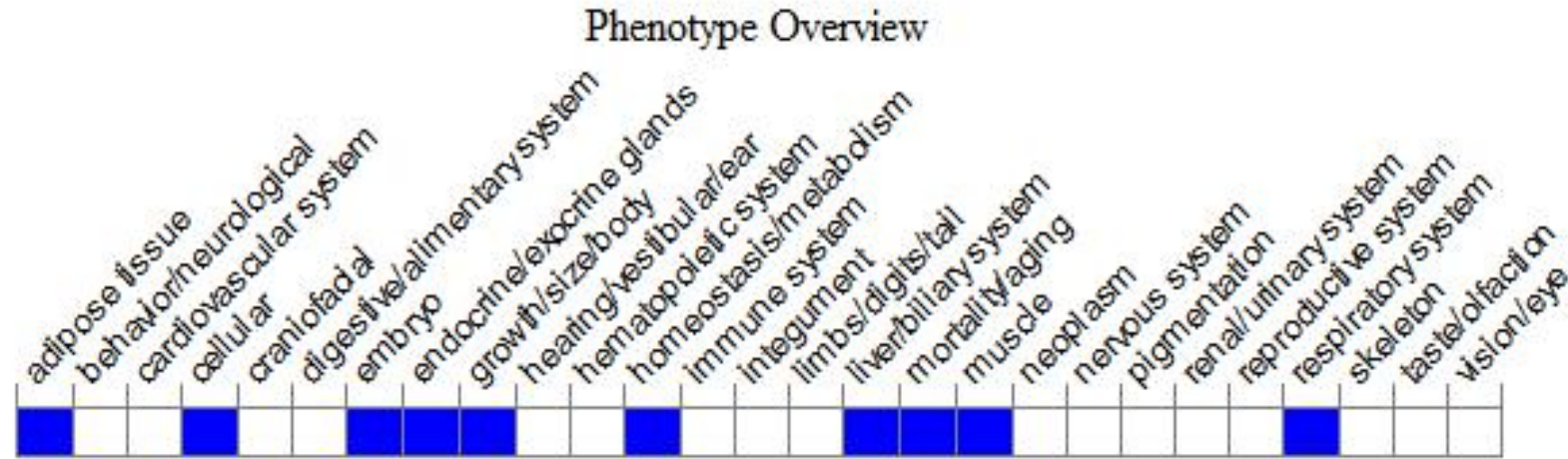
Genomic location distribution



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/>).

According to the existing MGI data, maternal transmission of a mutant allele results in both fetal and placental overgrowth. Disproportionate overgrowth of the liver is observed. Paternal transmission of an allele lacking the differentially methylated region results in growth retardation.

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

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