Llgl2 Cas9-KO Strategy

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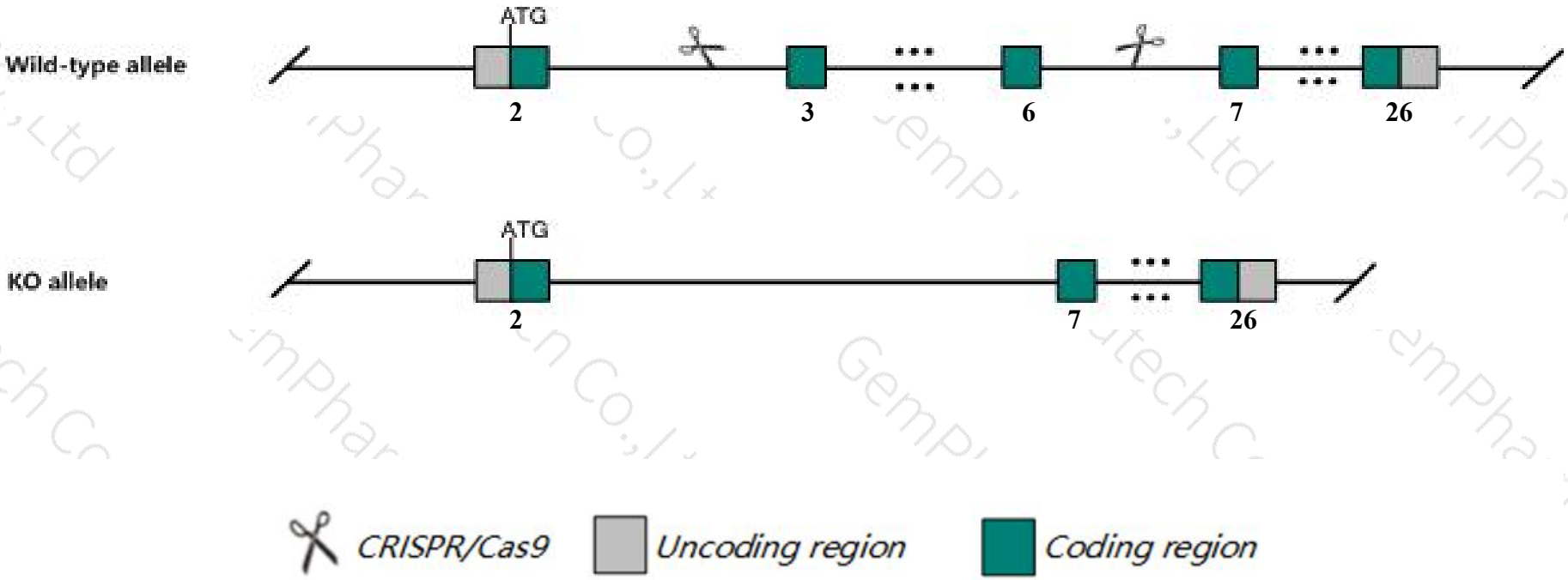
Project Overview

Project Name	***Llgl2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Llgl2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Llgl2* gene has 12 transcripts. According to the structure of *Llgl2* gene, exon3-exon6 of *Llgl2-212* (ENSMUST00000177736.7) transcript is recommended as the knockout region.The region contains 455bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Llgl2* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a gene-trapped allele exhibit abnormal branching morphogenesis of the placental labyrinth layer and are born as runts but catch up in size by adulthood.

- The *Llgl2* 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）

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Llgl2 LLGL2 scribble cell polarity complex component [Mus musculus (house mouse)]

Gene ID: 217325, updated on 31-Jan-2019

Summary

Official Symbol	Llgl2 provided by MGI
Official Full Name	LLGL2 scribble cell polarity complex component provided by MGI
Primary source	MGI:MGI:1918843
See related	Ensembl:ENSMUSG00000020782
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	9130006H11Rik, Llglh2
Expression	Broad expression in colon adult (RPKM 75.1), duodenum adult (RPKM 44.0) and 16 other tissues See more
Orthologs	human all

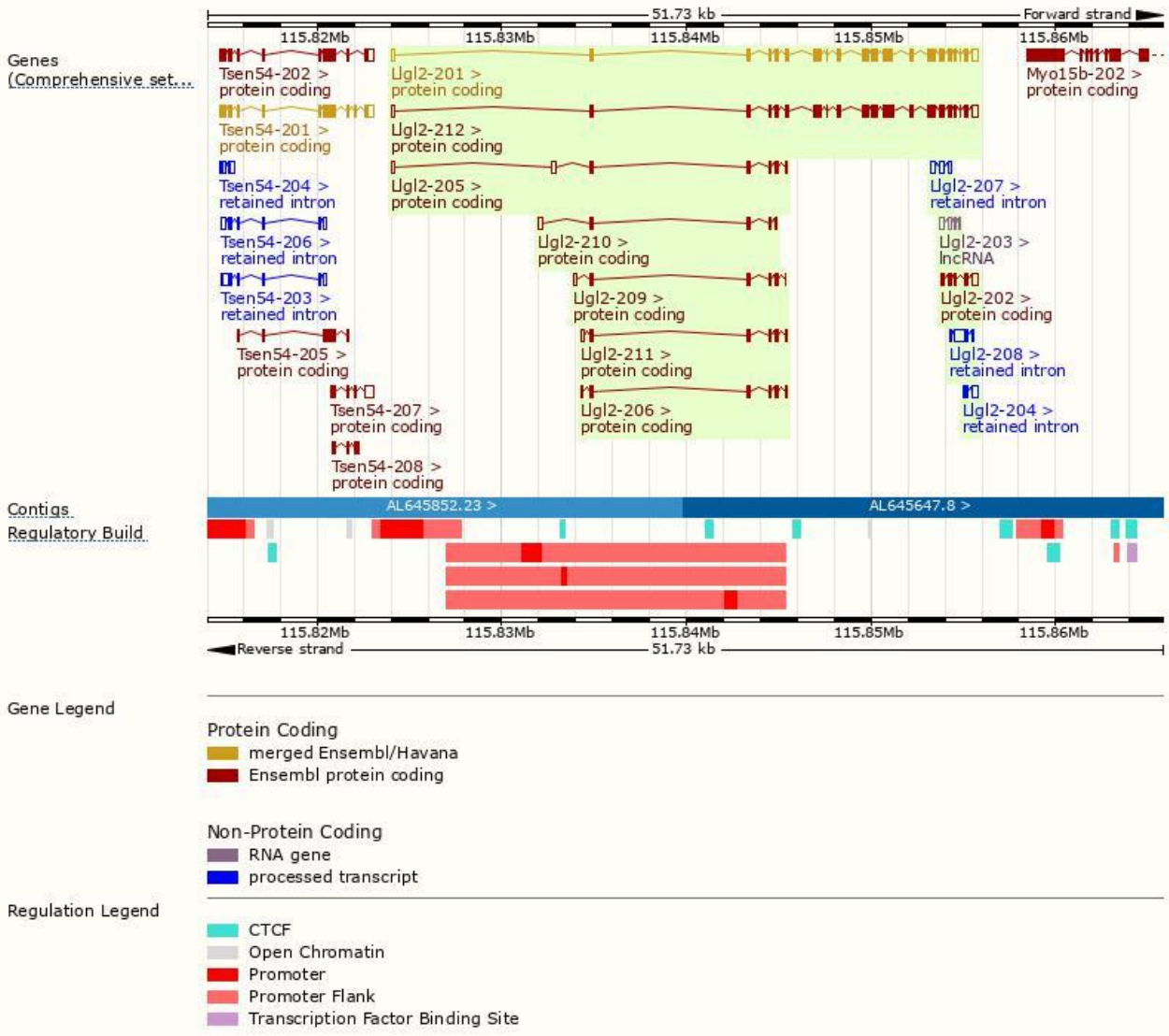
Transcript information（Ensembl）

The gene has 12 transcripts,all transcripts are shown below:

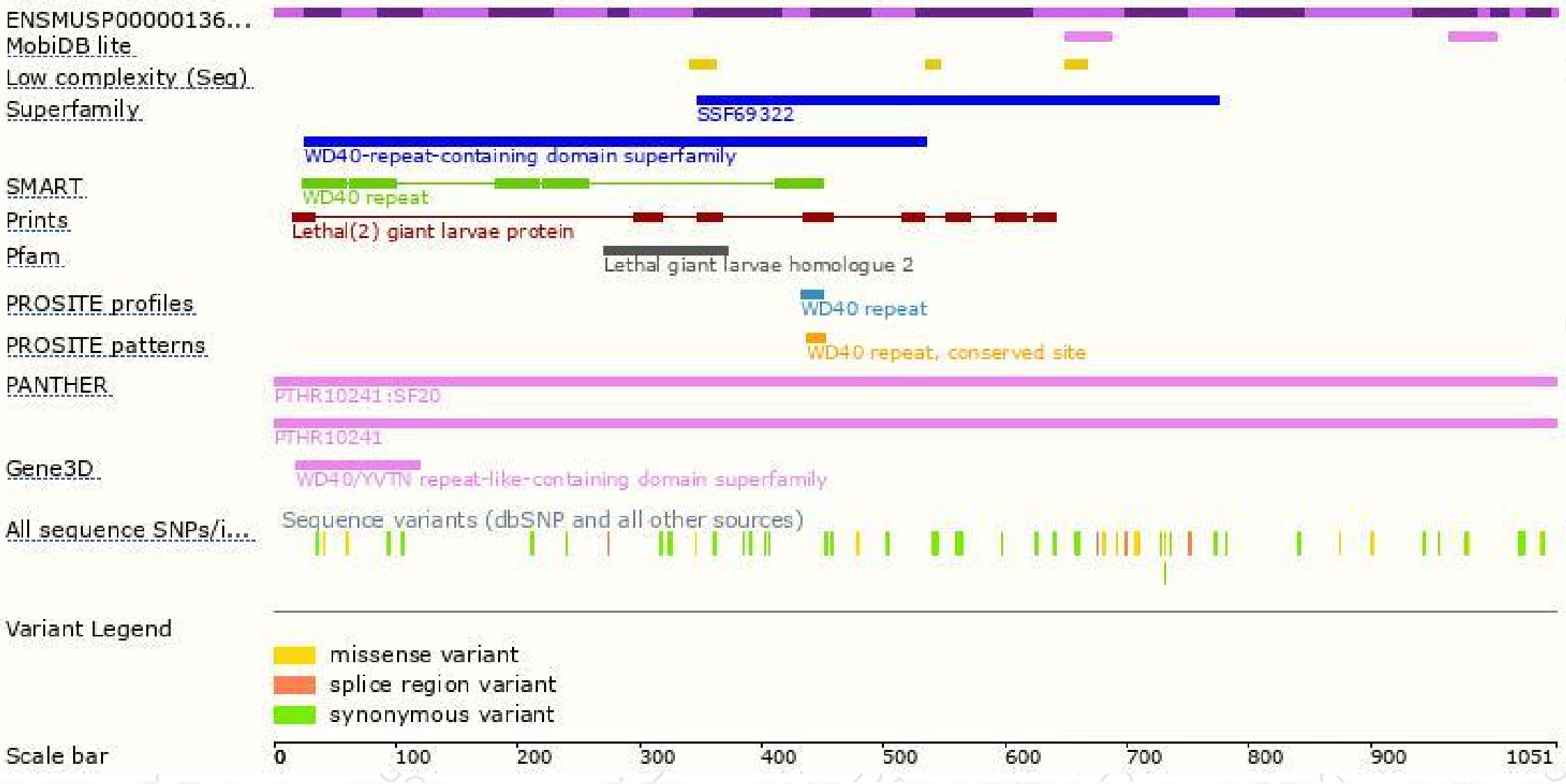
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Llgl2-212	ENSMUST00000177736.7	3612	1051aa	Protein coding	CCDS56820	J3QJU5	TSL:2 GENCODE basic APPRIS ALT2
Llgl2-201	ENSMUST00000103032.10	3551	1027aa	Protein coding	CCDS25649	Q3TJ91	TSL:1 GENCODE basic APPRIS P3
Llgl2-205	ENSMUST00000133250.7	847	146aa	Protein coding	-	B1ATA8	CDS 3' incomplete TSL:5
Llgl2-202	ENSMUST00000128826.1	791	161aa	Protein coding	-	F6X6X1	CDS 5' incomplete TSL:3
Llgl2-211	ENSMUST00000173289.7	643	148aa	Protein coding	-	G3UXR0	CDS 3' incomplete TSL:5
Llgl2-210	ENSMUST00000172552.7	550	101aa	Protein coding	-	G3UXS2	CDS 3' incomplete TSL:3
Llgl2-206	ENSMUST00000137900.1	548	158aa	Protein coding	-	B1ATA9	CDS 3' incomplete TSL:2
Llgl2-209	ENSMUST00000155878.7	545	128aa	Protein coding	-	B1ATA7	CDS 3' incomplete TSL:3
Llgl2-208	ENSMUST00000147878.7	863	No protein	Retained intron	-	-	TSL:3
Llgl2-207	ENSMUST00000137951.1	576	No protein	Retained intron	-	-	TSL:2
Llgl2-204	ENSMUST00000132999.1	451	No protein	Retained intron	-	-	TSL:2
Llgl2-203	ENSMUST00000130518.1	566	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Llgl2-212* transcript,The transcription is shown below

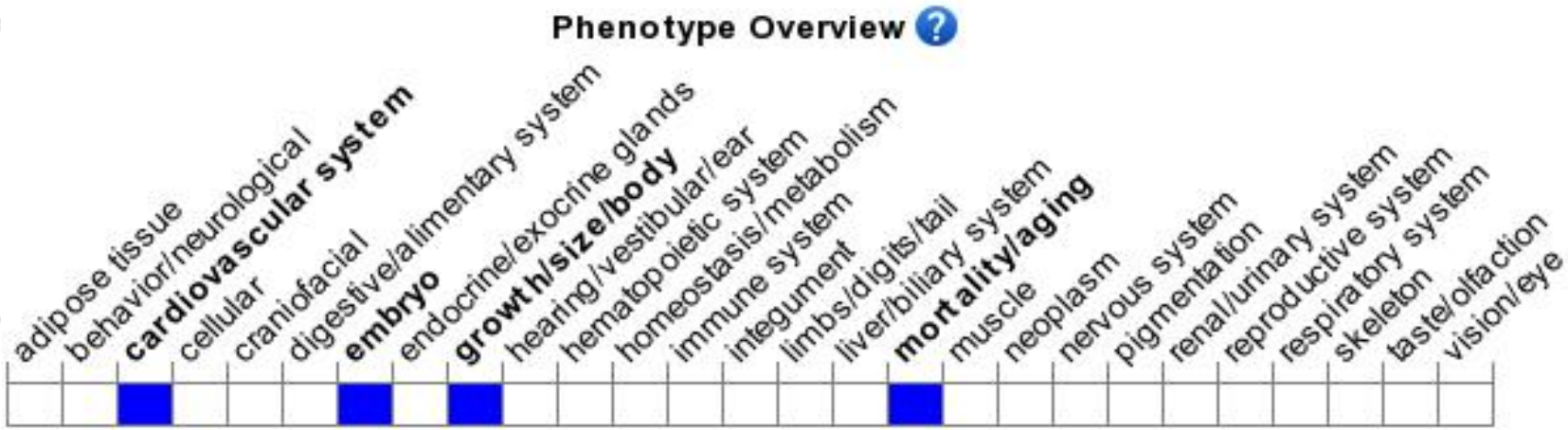
Genomic location distribution



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,Mice homozygous for a gene-trapped allele exhibit abnormal branching morphogenesis of the placental labyrinth layer and are born as runts but catch up in size by adulthood.

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

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