Lyst Cas9-KO Strategy

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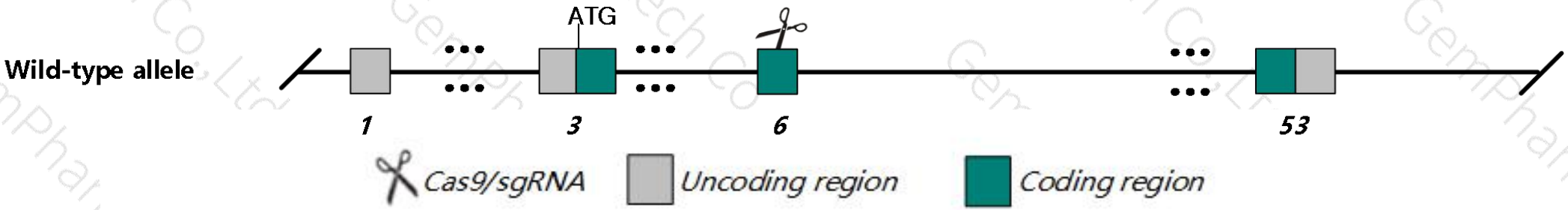
Project Overview

Project Name	***Lyst***
Project type	**Cas9-KO**
Strain background	**NOD/ShiLtJ**

Knockout strategy

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



Technical routes

➢ The *Lyst* gene has 2 transcripts. According to the structure of *Lyst* gene, exon6 part of the coding area of MGP_NODShiLtJ_T0036056.1 transcript is recommended as the knockout region.The region contains key coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Lyst* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of NOD/ShiLtJ mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with NOD/ShiLtJ mice.

Notice

➢

➢ The *Lyst* gene is located on the Chr13. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information（NCBI）

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Lyst lysosomal trafficking regulator [*Mus musculus* (house mouse)]

Gene ID: 17101, updated on 5-Mar-2019

Summary

Official Symbol	Lyst provided by MGI
Official Full Name	lysosomal trafficking regulator provided by MGI
Primary source	MGI:MGI:107448
See related	Ensembl:ENSMUSG00000019726
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	bg; beige; D13Sfk13
Expression	Ubiquitous expression in thymus adult (RPKM 5.4), spleen adult (RPKM 3.5) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 2 transcripts,all transcripts are shown below:

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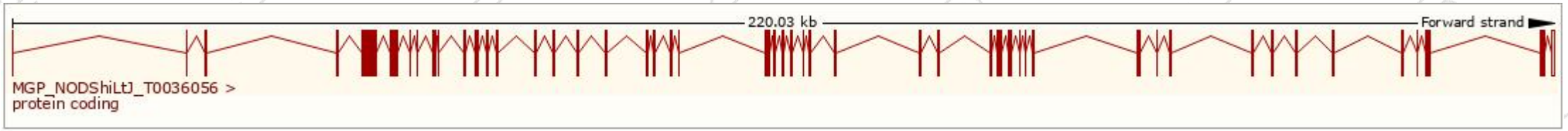
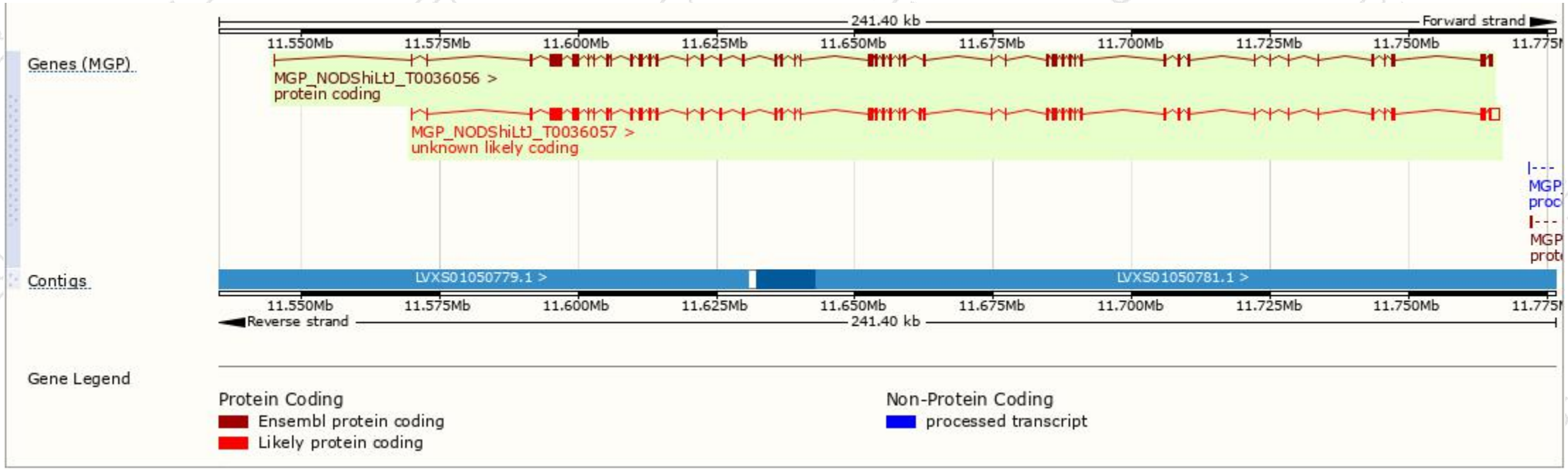
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
-	MGP_NODShiLtJ_T0036056.1	11806	3787aa	Protein coding	CCDS36597	G5E8Q0	-
-	MGP_NODShiLtJ_T0036057.1	13238	3839aa	Unknown likely coding	-	-	-

The strategy is based on the design of *MGP_NODShiLtJ_T0036056.1* transcript,The transcription is shown below

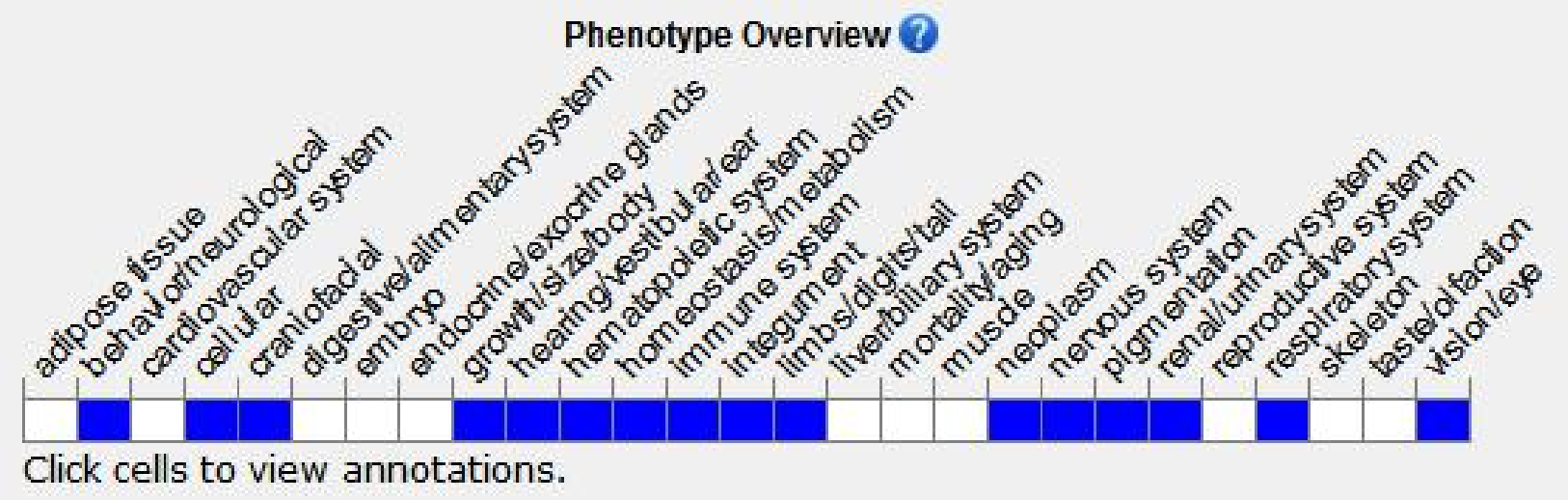


Genomic location distribution



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,Homozygous mice have a phenotype similar to human Chediak-Higashi syndrome patients, exhibiting lysosomal dysfunction with resultant protein storage; diluted coat color; abnormal melanogenesis; immune cell dysfunction resulting in increased susceptibility to bacterial, viral, and parasitic infections and decreased cytotoxic activity against tumor cells.

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

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