Lyst Cas9-CKO Strategy

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Overview

Target Gene Name

- Lyst

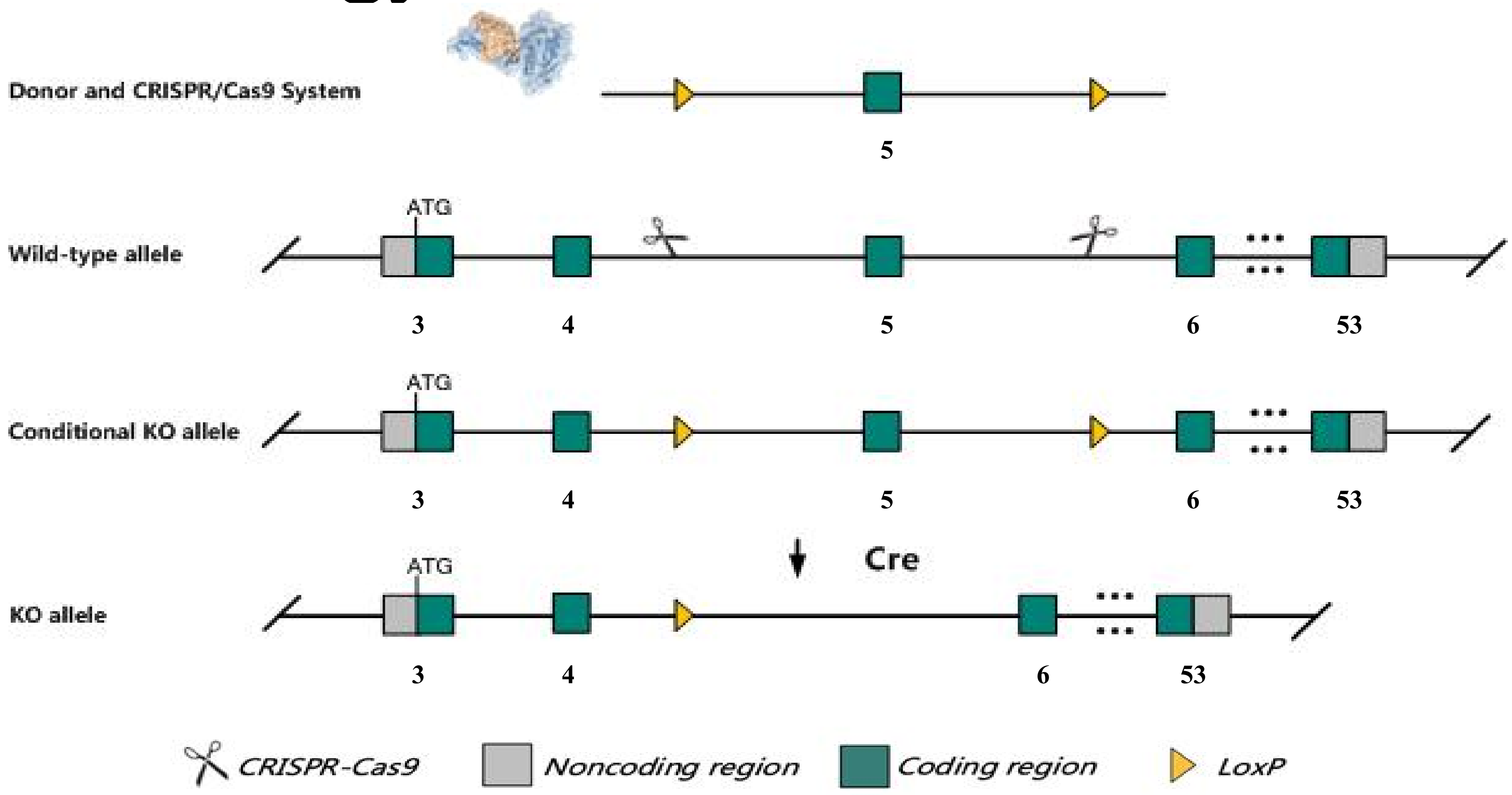
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Lyst* gene.

Technical Information

- The *Lyst* gene has 8 transcripts. According to the structure of *Lyst* gene, exon 5 of *Lyst*-201 (ENSMUST00000110559.3) transcript is recommended as the knockout region. The region contains 2080 bp coding sequence. Knocking 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: CRISPR-Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Gene Information

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

Gene ID: 17101, updated on 14-Nov-2024

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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 AllianceGenome:MGI:107448
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
Summary	Predicted to enable protein kinase binding activity. Acts upstream of or within several processes, including defense response to other organism; phospholipid homeostasis; and vesicle organization. Located in cytosol. Is expressed in axial skeleton. Used to study Chediak-Higashi syndrome; exfoliation syndrome; and platelet storage pool deficiency. Human ortholog(s) of this gene implicated in Chediak-Higashi syndrome. Orthologous to human LYST (lysosomal trafficking regulator). [provided by Alliance of Genome Resources, Nov 2024]
Expression	Ubiquitous expression in thymus adult (RPKM 5.4), spleen adult (RPKM 3.5) and 27 other tissues See more
Orthologs	human all
NEW	**Try the new** Gene table **Try the new** Transcript table

Genomic context

Location: 13 A1; 13 5.28 cM

See Lyst in Genome Data Viev

Exon count: 55

Annotation release	Status	Assembly	Chr	Location
RS_2024_02	current	GRCm39 (GCF_000001635.27)	13	NC_000079.7 (13764896..13953388)
108.20200622	previous assembly	GRCm38.p6 (GCF_000001635.26)	13	NC_000079.6 (13590311..13778803)

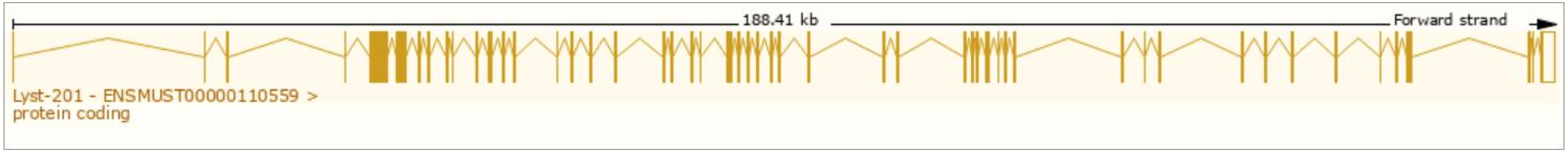
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

The gene has 8 transcripts,all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000110559.3	Lyst-201	13181	3787aa	Protein coding	CCDS36597	G5E8Q0	Ensembl Canonical GENCODE Basic APPRIS P1 TSL:1
ENSMUST00000220937.2	Lyst-202	5854	No protein	Retained intron		-	TSL:1
ENSMUST00000221483.2	Lyst-203	2097	No protein	Retained intron		-	TSL:3
ENSMUST00000221587.2	Lyst-204	306	No protein	Retained intron		-	TSL:3
ENSMUST00000221717.2	Lyst-205	2237	No protein	Retained intron		-	TSL:1
ENSMUST00000223053.2	Lyst-206	2706	No protein	Retained intron		-	TSL:1
ENSMUST00000223527.2	Lyst-207	591	No protein	Retained intron		-	TSL:5
ENSMUST00000231064.2	Lyst-208	178	60aa	Protein coding		A0A2R8W6Q6	CDS 5' and 3' incomplete

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



Source: https://www.ensembl.org

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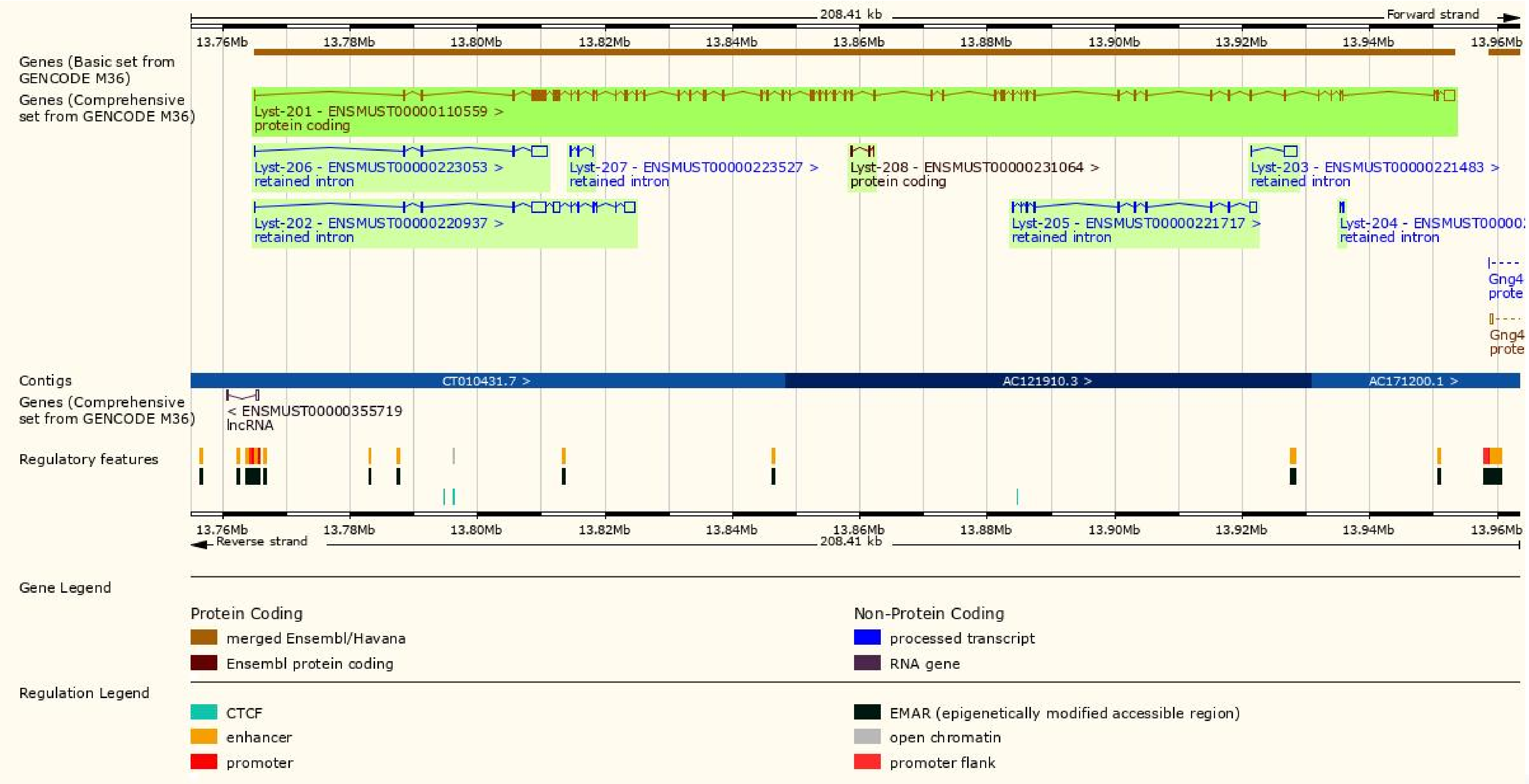
Genomic Information

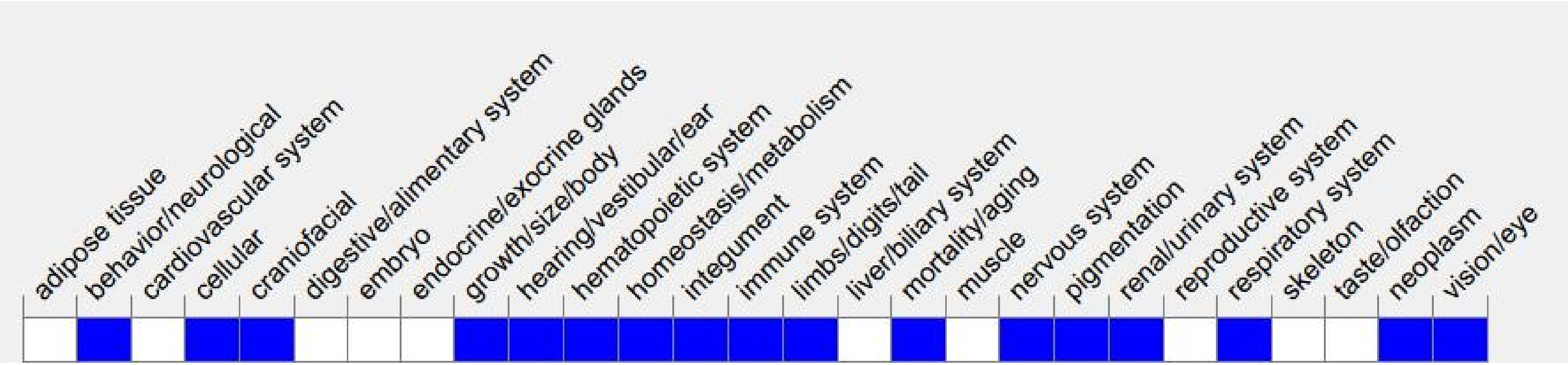


Source: : https://www.ensembl.org

Protein Information

Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



- 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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Source: https://www.informatics.jax.org

Important Information

- 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.
- Transcript *Lyst*-208 may not be affected.
- *Lyst* is located on Chr13. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.