Stat5a Cas9-CKO Strategy

Designer: Xueting Zhang
Design Date: 2019-8-5

Project Overview

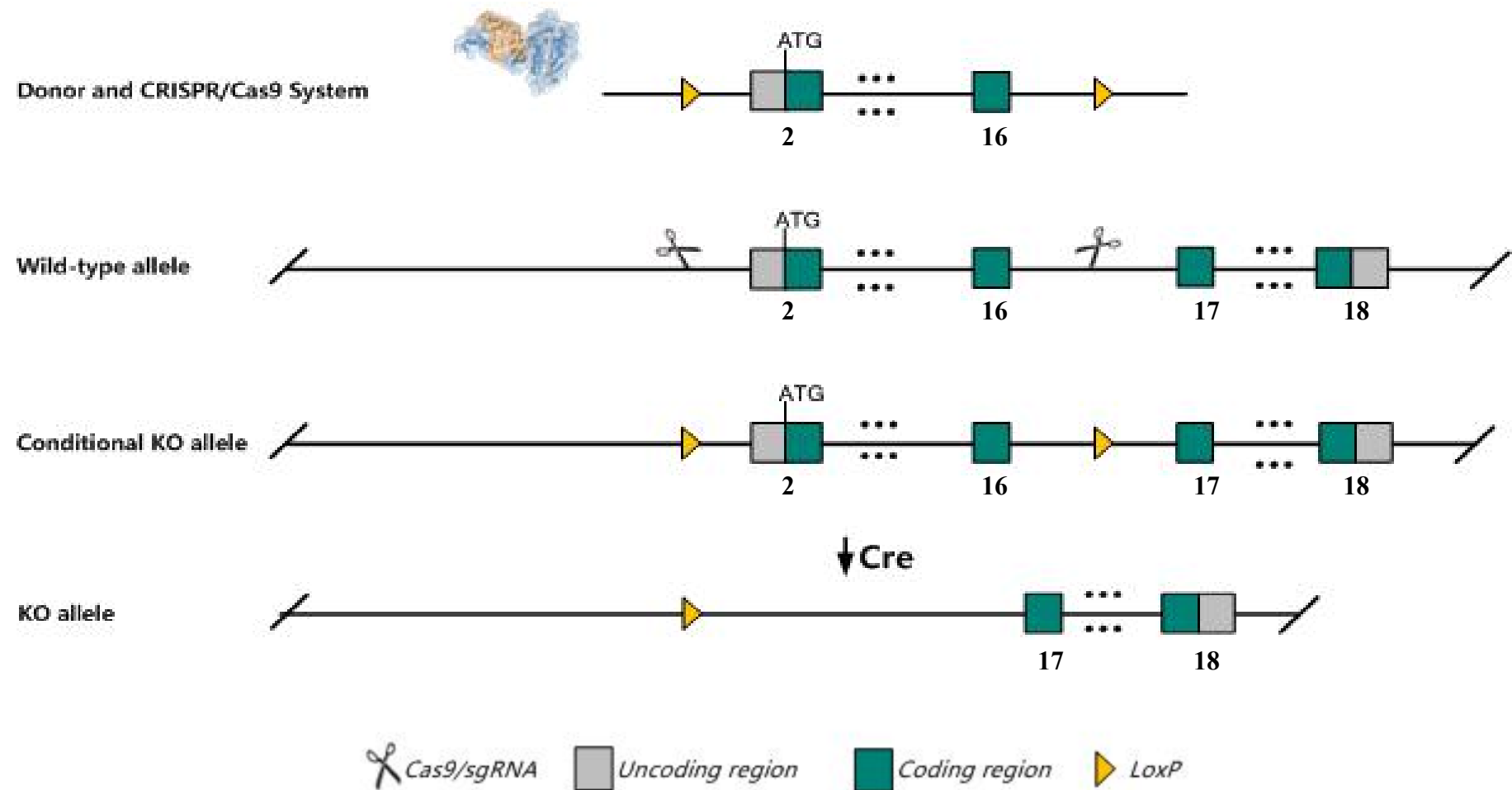|	
Project Name	*Stat5a*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Stat5a* gene. The schematic diagram is as follows:

Technical routes

➤ The *Stat5a* gene has 7 transcripts. According to the structure of *Stat5a* gene, exon2-exon16 of *Stat5a-203* (ENSMUST00000107357.3) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Stat5a* gene. The brief process is as follows:gRNA was transcribed in vitro, donor was constructed.Cas9, gRNA 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

➤ 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.

Notice

➢ According to the existing MGI data,Mice homozygous for disruptions in this gene are reduced in size and display abnormalities in both mammary gland structure and function.

➢ The *Stat5a* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

Stat5a signal transducer and activator of transcription 5A [Mus musculus (house mouse)]
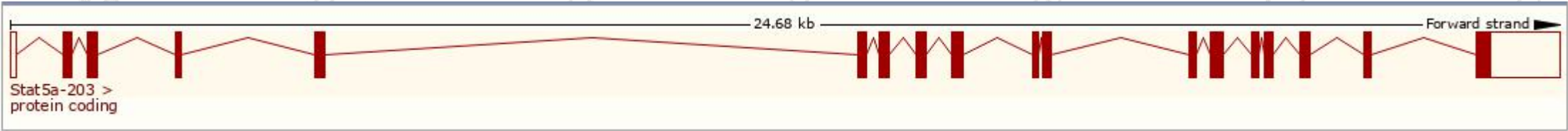
Gene ID: 20850, updated on 25-Mar-2019

▲ Summary

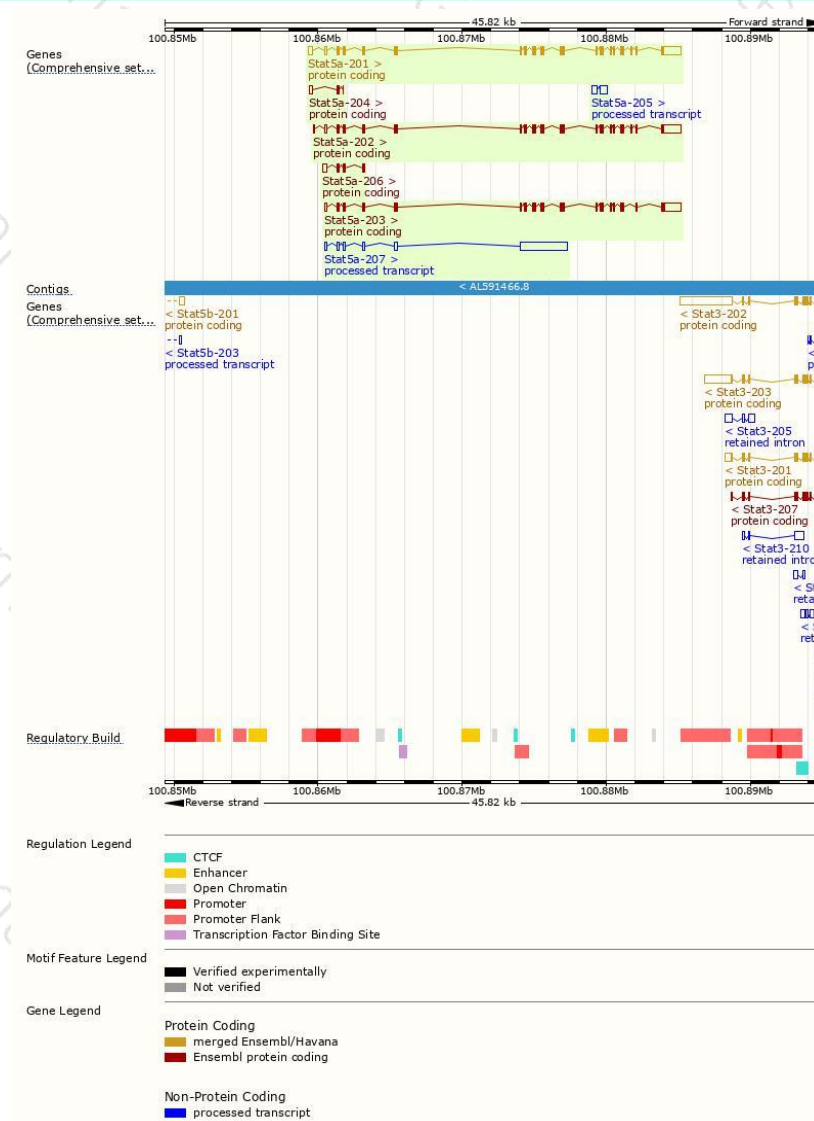|	
Official Symbol	Stat5a provided by MGI
Official Full Name	signal transducer and activator of transcription 5A provided by MGI
Primary source	MGI:MGI:103036
See related	Ensembl:ENSMUSG00000004043
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA959963, STAT5
Expression	Broad expression in thymus adult (RPKM 40.3), mammary gland adult (RPKM 29.6) and 20 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stat5a-201	ENSMUST00000004145.13	3888	793aa	Protein coding	CCDS25439	P42230 Q9JIA0	TSL:1 GENCODE basic APPRIS P1
Stat5a-202	ENSMUST00000107356.7	3738	793aa	Protein coding	CCDS25439	P42230 Q9JIA0	TSL:1 GENCODE basic APPRIS P1
Stat5a-203	ENSMUST00000107357.3	3605	797aa	Protein coding	CCDS48933	B2C3G8	TSL:1 GENCODE basic
Stat5a-206	ENSMUST00000138083.7	617	125aa	Protein coding	-	A2A5D3	CDS 3' incomplete TSL:2
Stat5a-204	ENSMUST00000133036.7	336	51aa	Protein coding	-	A2A5D4	CDS 3' incomplete TSL:3
Stat5a-207	ENSMUST00000154087.1	3958	No protein	Processed transcript	-	-	TSL:1
Stat5a-205	ENSMUST00000135272.1	850	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Stat5a-203* transcript,The transcription is shown below
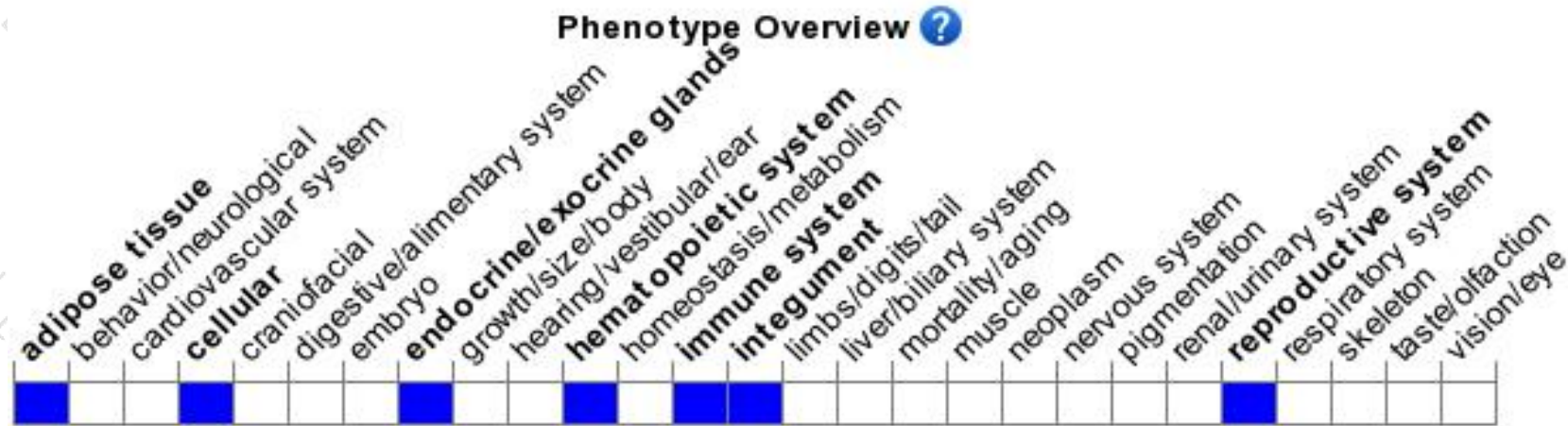
Genomic location distribution

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 disruptions in this gene are reduced in size and display abnormalities in both mammary gland structure and function.

集萃药康
GemPharmatech

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

集萃药康生物科技
GemPharmatech Co.,Ltd