Stard5 Cas9-KO Strategy

Designer:	**Daohua Xu**
Reviewer:	**Huimin Su**
Design Date:	**2020-4-15**

Project Overview

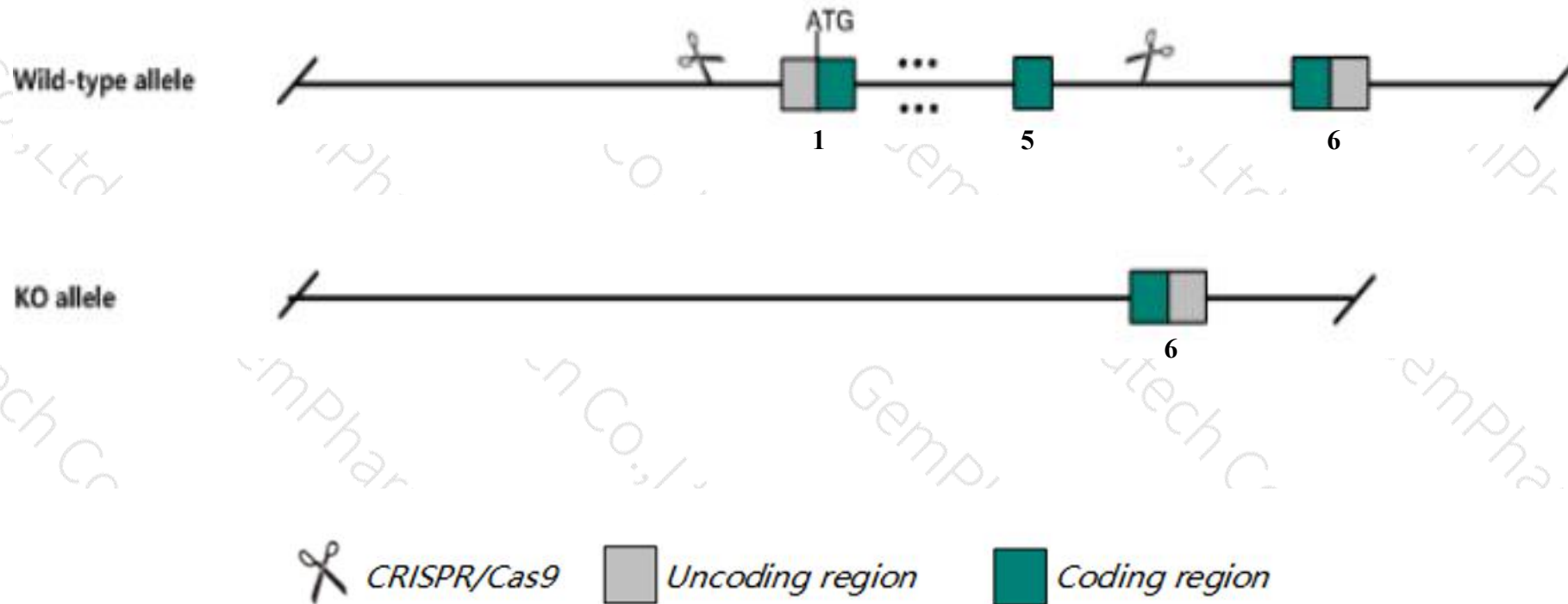|	
Project Name	*Stard5*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

This model will use CRISPR/Cas9 technology to edit the *Stard5* gene. The schematic diagram is as follows:

Technical routes

➢ The *Stard5* gene has 5 transcripts. According to the structure of *Stard5* gene, exon1-exon5 of *Stard5-201* (ENSMUST00000075418.14) 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 *Stard5* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,mice homozygous for a knock-out allele exhibit abnormal vertebral transverse process morphology.

➢ The KO region contains functional region of the *Gm16638* gene.Knockout the region may affect the function of *Gm16638* gene.

➢ The *Stard5* gene is located on the Chr7. 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）

Stard5 StAR-related lipid transfer (START) domain containing 5 [Mus musculus (house mouse)]

Gene ID: 170460, updated on 13-Mar-2020

## Summary

|	
Official Symbol	Stard5 provided by MGI
Official Full Name	StAR-related lipid transfer (START) domain containing 5 provided by MGI
Primary source	MGI:MGI:2156765
See related	Ensembl:ENSMUSG00000046027
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310058G22Rik, AI607880, D7Ertd152e
Expression	Broad expression in kidney adult (RPKM 30.6), liver adult (RPKM 26.0) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 5 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stard5-201	ENSMUST00000075418.14	2483	213aa	Protein coding	CCDS21411	Q9EPQ7	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 P1
Stard5-202	ENSMUST00000117410.1	2832	206aa	Protein coding	-	D3YU00	TSL:1 GENCODE basic
Stard5-203	ENSMUST00000130723.1	369	No protein	Processed transcript	-	-	TSL:3
Stard5-205	ENSMUST00000150174.7	897	No protein	Retained intron	-	-	TSL:2
Stard5-204	ENSMUST00000146469.1	482	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Stard5-201* transcript,the transcription is shown below:
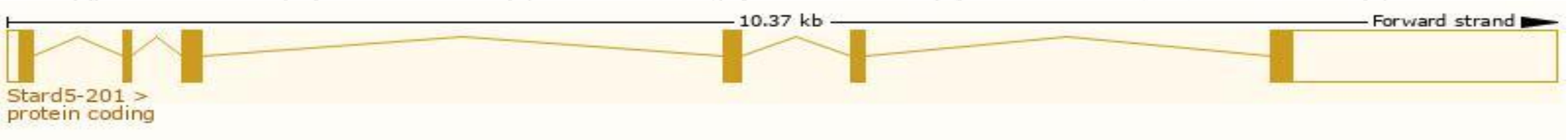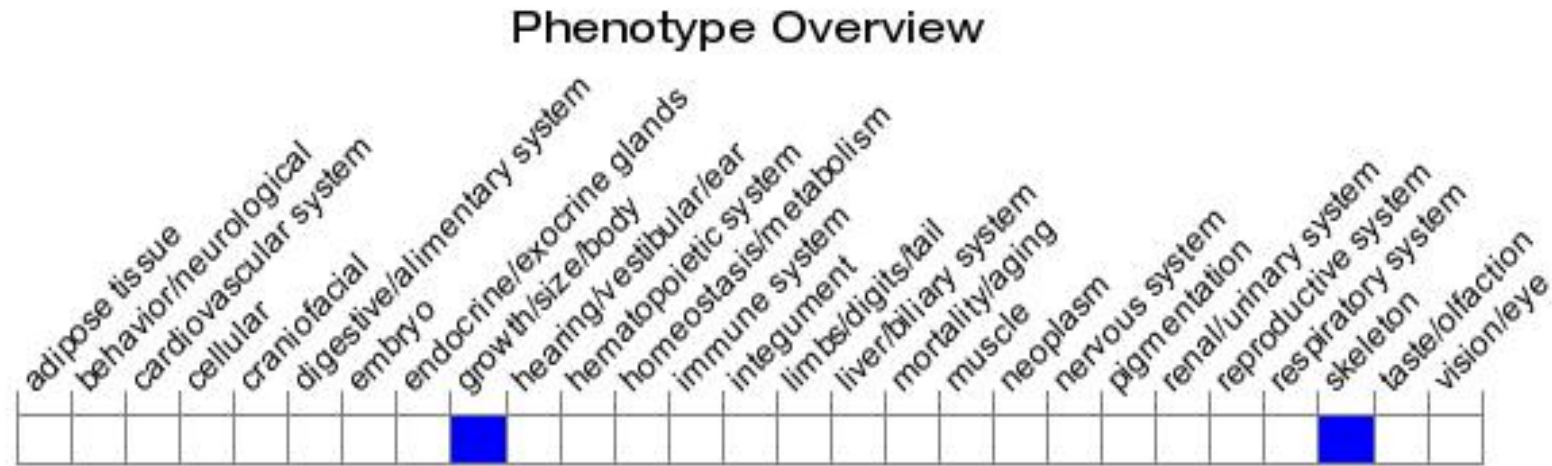
Genomic location distribution
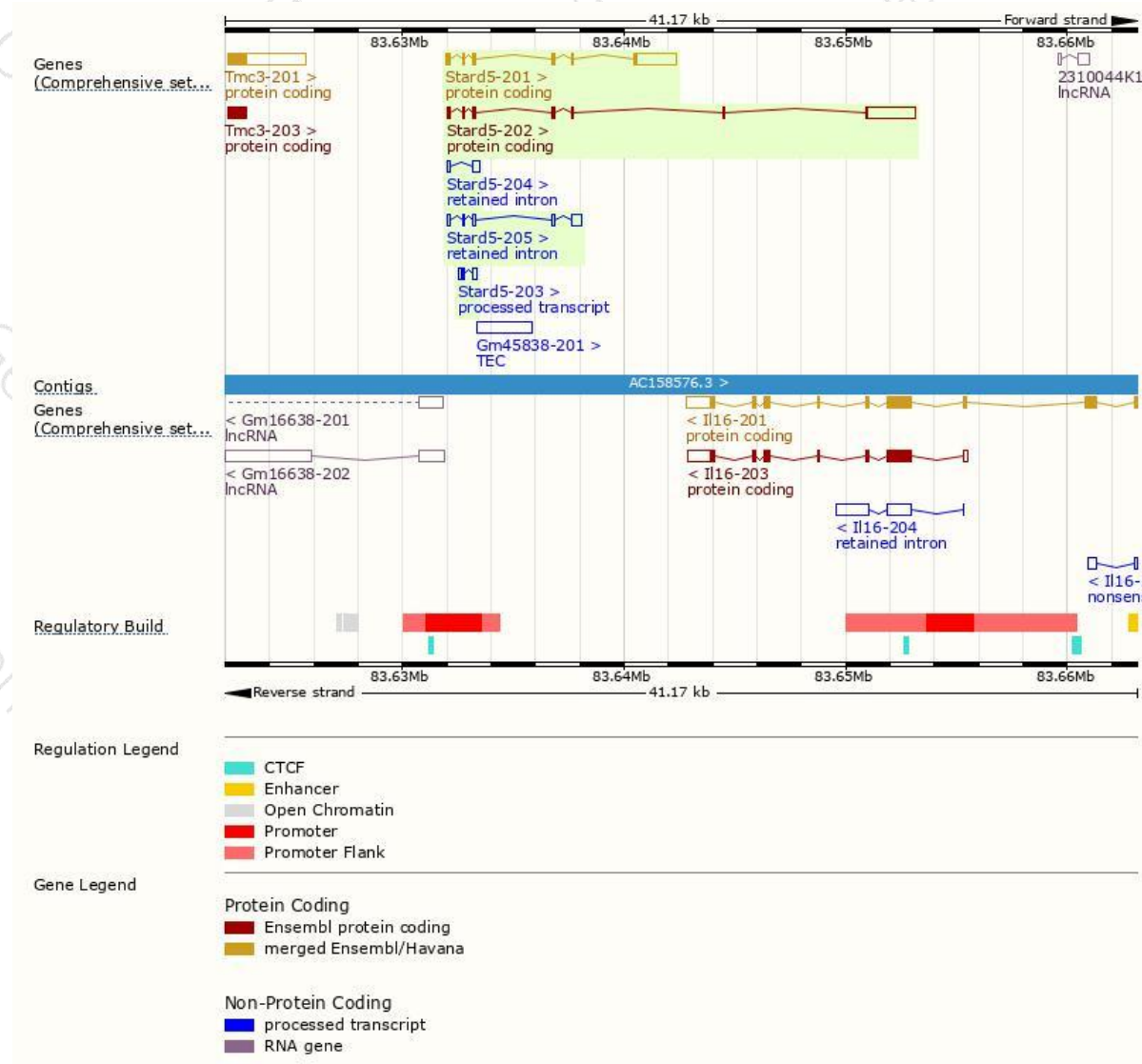
Protein domain
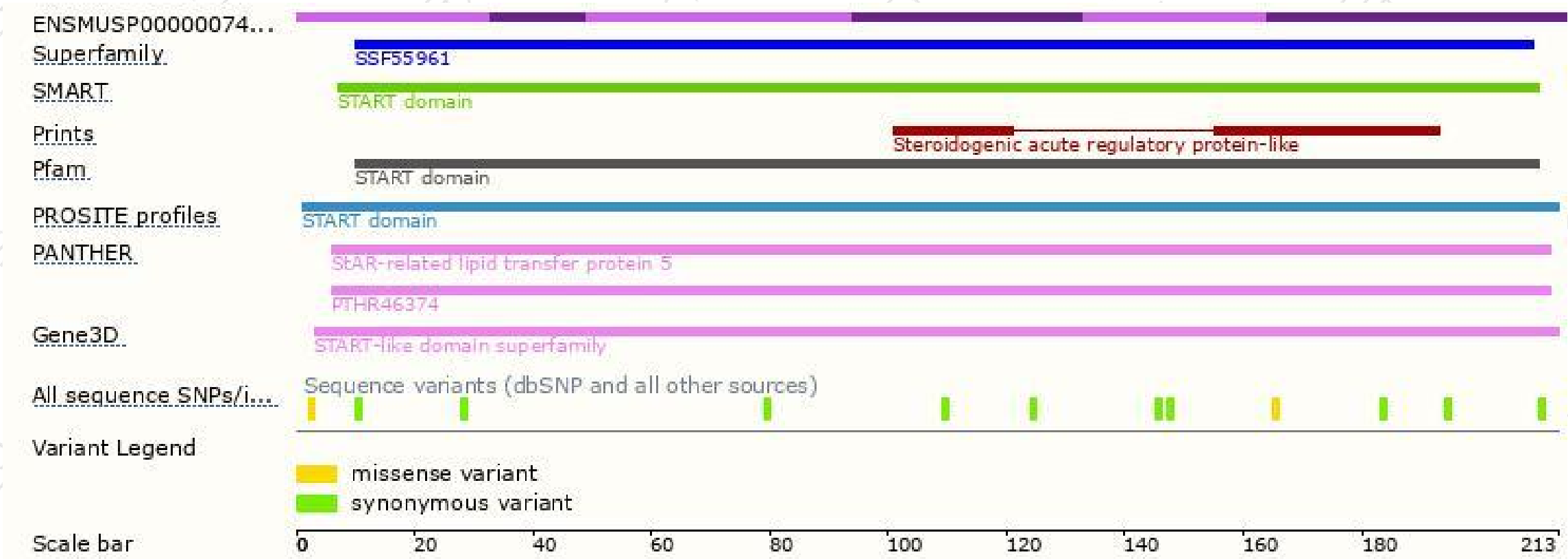
Mouse phenotype description(MGI)

Phenotype Overview

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 knock-out allele exhibit abnormal vertebral transverse process morphology.

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

集萃药康生物科技
GemPharmatech Co.,Ltd