GemPharmatech™

Sgf29 Cas9-CKO Strategy

Designer: Mingzhu Xu

Reviewer: Qian Chen

Design Date: 2024-4-22

Overview

Target Gene Name

- Sgf29

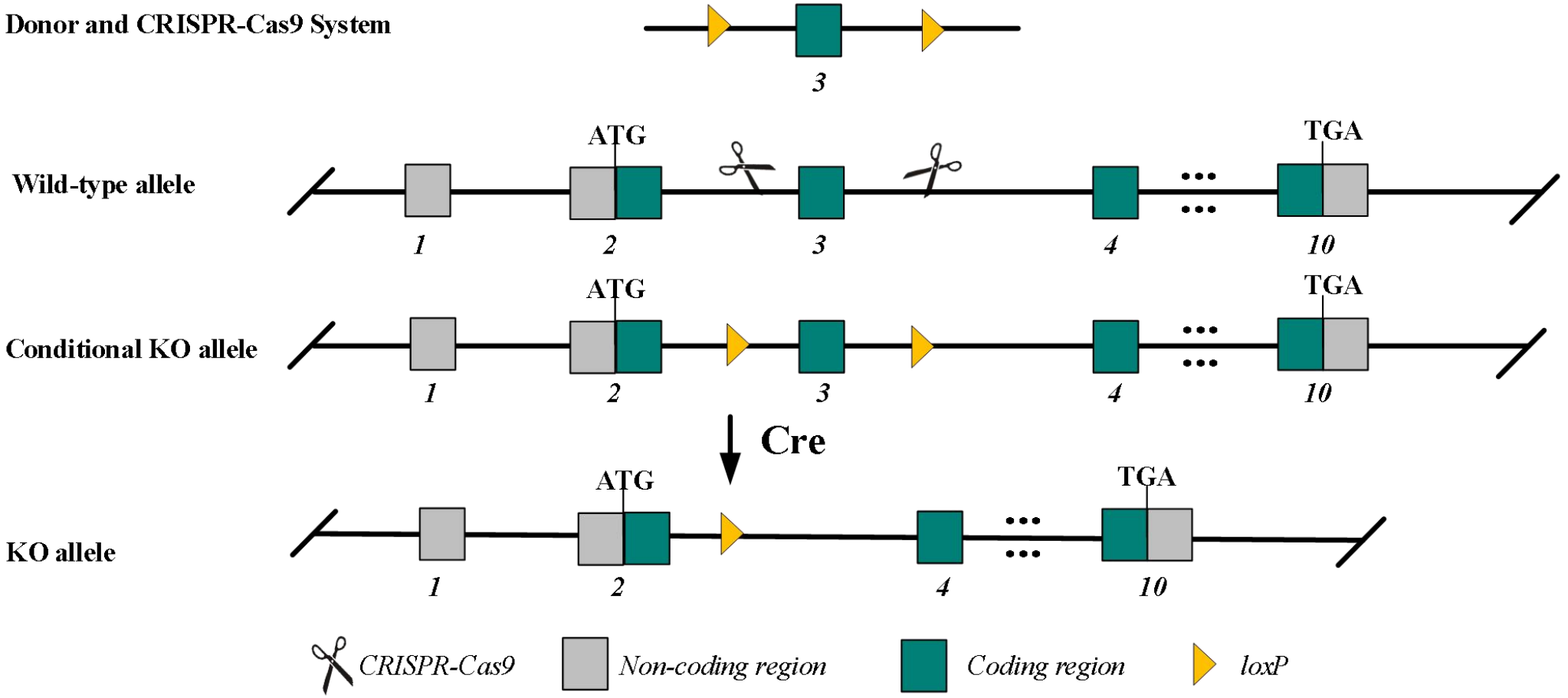
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Sgf29* gene.

Technical Information

- The *Sgf29* gene has 10 transcripts. According to the structure of *Sgf29* gene, exon 3 of *Sgf29*-201 (ENSMUST00000032956.10) transcript is recommended as the knockout region. The region contains 76 bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Sgf29* 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

Sgf29 SAGA complex associated factor 29 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 75565, updated on 5-Mar-2024

Summary

Official Symbol	Sgf29 provided by MGI
Official Full Name	SAGA complex associated factor 29 provided by MGI
Primary source	MGI:MGI:1922815
See related	Ensembl:ENSMUSG00000030714 AllianceGenome:MGI:1922815
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	Ccdc101; 1700023O11Rik; 9530025I05Rik
Summary	Predicted to enable enzyme binding activity; methylated histone binding activity; and protein N-terminus binding activity. Predicted to be involved in histone H3 acetylation. Predicted to act upstream of or within chromatin organization. Part of ATAC complex. Is expressed in genital tubercle; limb; and limb mesenchyme. Human ortholog(s) of this gene implicated in diabetic retinopathy. Orthologous to human SGF29 (SAGA complex associated factor 29). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Broad expression in testis adult (RPKM 127.2), colon adult (RPKM 18.3) and 23 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**

Try the new Transcript table

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

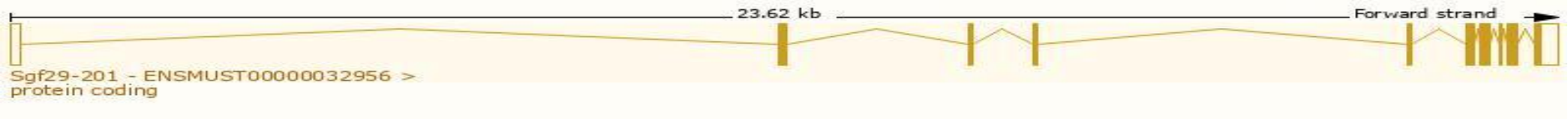
Transcript Information

The gene has 10 transcripts,all transcripts are shown below:

Show/hide columns (1 hidden) Filter

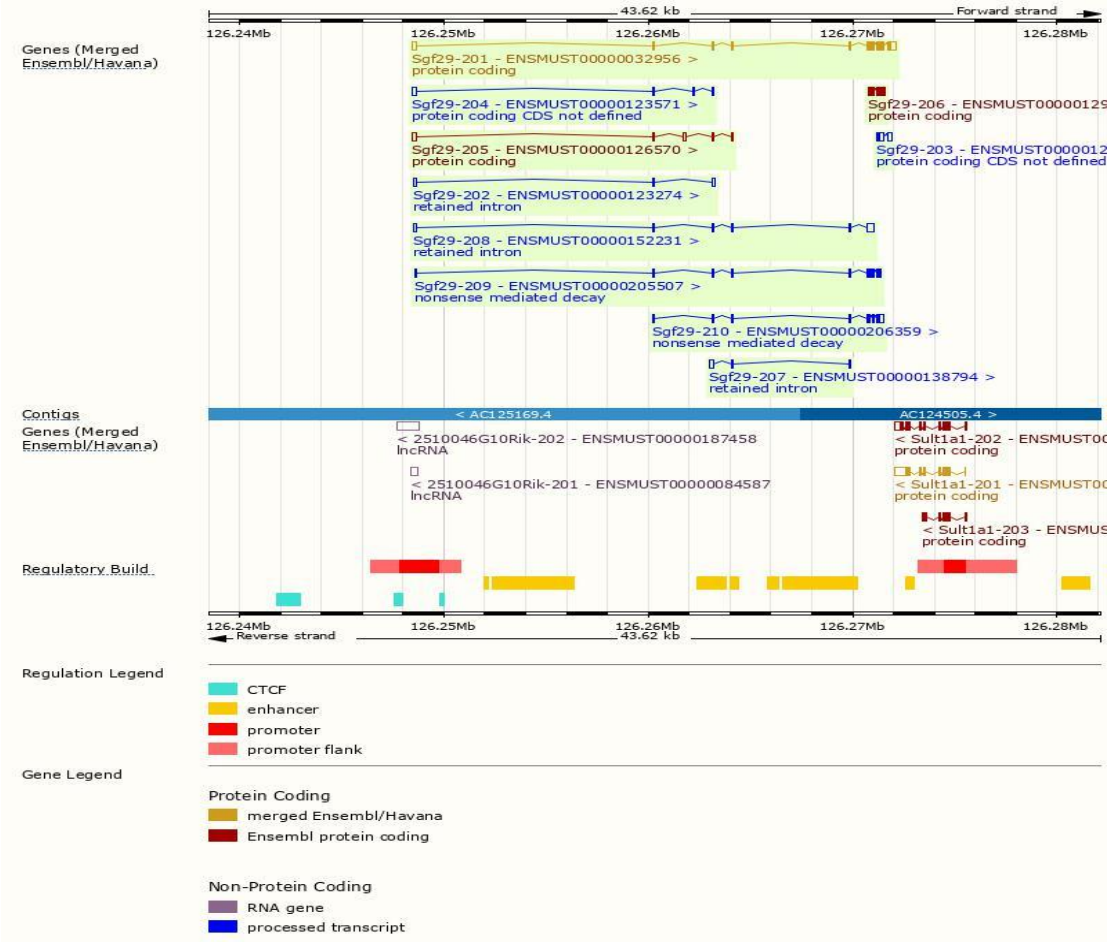
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000032956.10	Sgf29-201	1312	293aa	Protein coding	CCDS21837	Q9DA08	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000123274.8	Sgf29-202	424	No protein	Retained intron		-	TSL:2
ENSMUST00000123382.2	Sgf29-203	416	No protein	Protein coding CDS not defined		-	TSL:2
ENSMUST00000123571.8	Sgf29-204	367	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000126570.8	Sgf29-205	460	18aa	Protein coding		A0A0U1RNP8	TSL:5 CDS 3' incomplete
ENSMUST00000129786.3	Sgf29-206	511	160aa	Protein coding		A0A0U1RNS1	TSL:2 CDS 5' incomplete
ENSMUST00000138794.3	Sgf29-207	344	No protein	Retained intron		-	TSL:3
ENSMUST00000152231.8	Sgf29-208	786	No protein	Retained intron		-	TSL:2
ENSMUST00000205507.2	Sgf29-209	777	163aa	Nonsense mediated decay		A0A0U1RPT9	TSL:5
ENSMUST00000206359.2	Sgf29-210	732	152aa	Nonsense mediated decay		A0A0U1RNH1	TSL:5

The strategy is based on the design of *Sgf29*-201 transcript, the transcription is shown below:



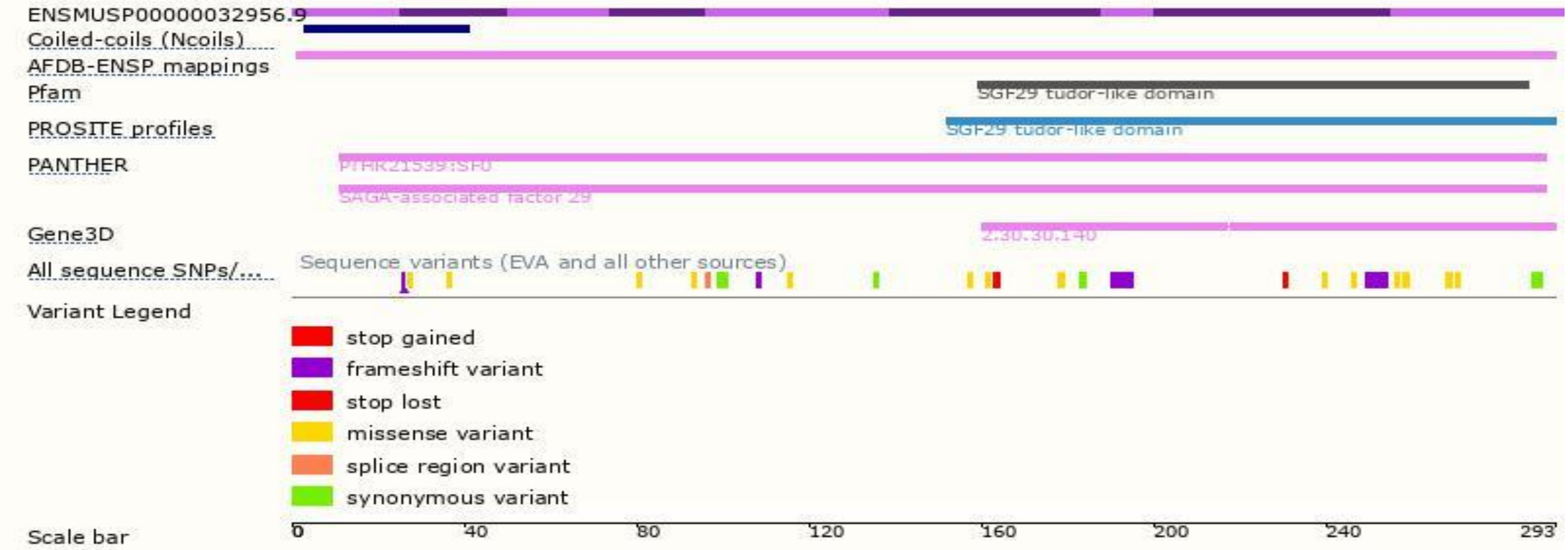
Source: https://www.ensembl.org

Genomic Information



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

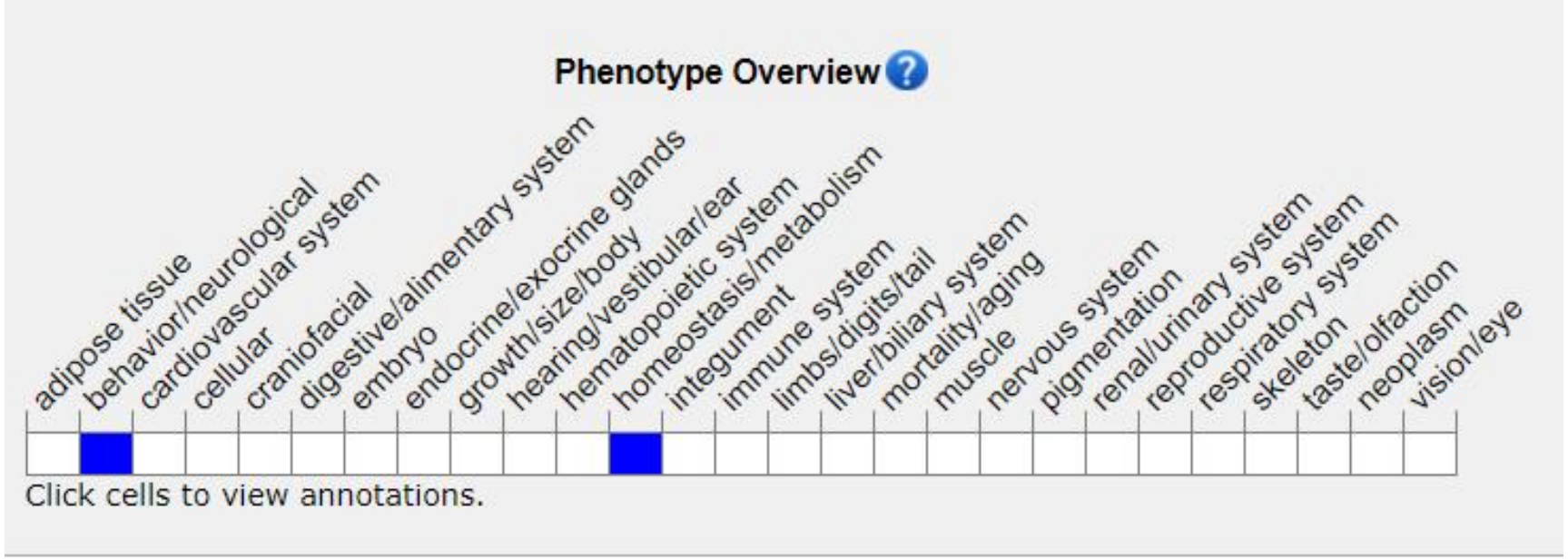
Protein Information



GemPharmatech™

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

Mouse Phenotype Information (MGI)



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

Important Information

- *Sgf29* is located on Chr7. 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.
- Transcript *Sgf29*-203&*Sgf29*-204&*Sgf29*-206 may not be affected.
- 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.