Efs Cas9-KO *Strategy*

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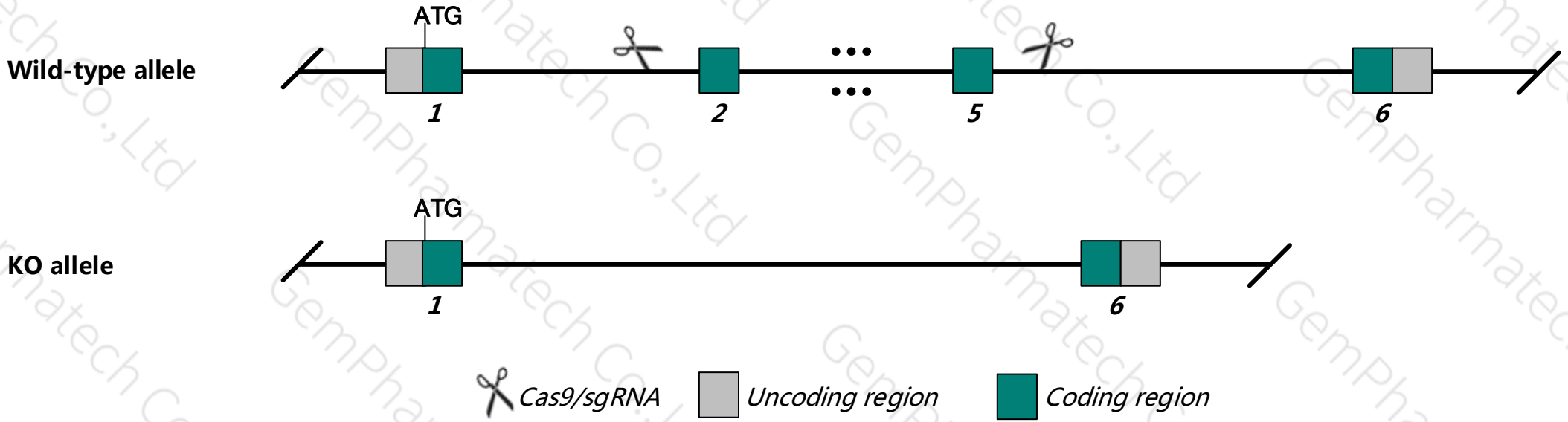
Project Overview

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

Knockout strategy

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



Technical routes

- The *Efs* gene has 3 transcripts.According to the structure of *Efs* gene, exon2~exon5 of *Efs*-201 (ENSMUST00000022813.7)transcript is recommended as the knockout region.The region contains most of coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Efs* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.

Notice

- According to the existing MGI data，mice homozygous for a disruption in this gene display an increased inflammatory response characterized by excessive T cell responses, enhanced cytokine secretion and antibody production, and intestinal, kidney, liver, and lung inflammation.

- The KO region deletes most of the coding sequence, but does not result in frameshift.

- The *Efs* gene is located on the Chr14. 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）

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Efs embryonal Fyn-associated substrate [*Mus musculus* (house mouse)]

Gene ID: 13644, updated on 12-Aug-2019

Summary

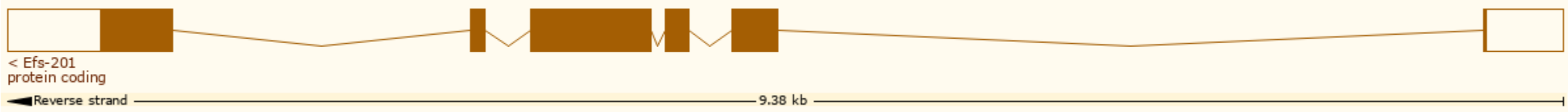
Official Symbol	Efs provided by MGI
Official Full Name	embryonal Fyn-associated substrate provided by MGI
Primary source	MGI:MGI:105311
See related	Ensembl:ENSMUSG00000022203
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Broad expression in limb E14.5 (RPKM 32.5), ovary adult (RPKM 23.9) and 18 other tissues See more
Orthologs	human all

Transcript information（ Ensembl ）

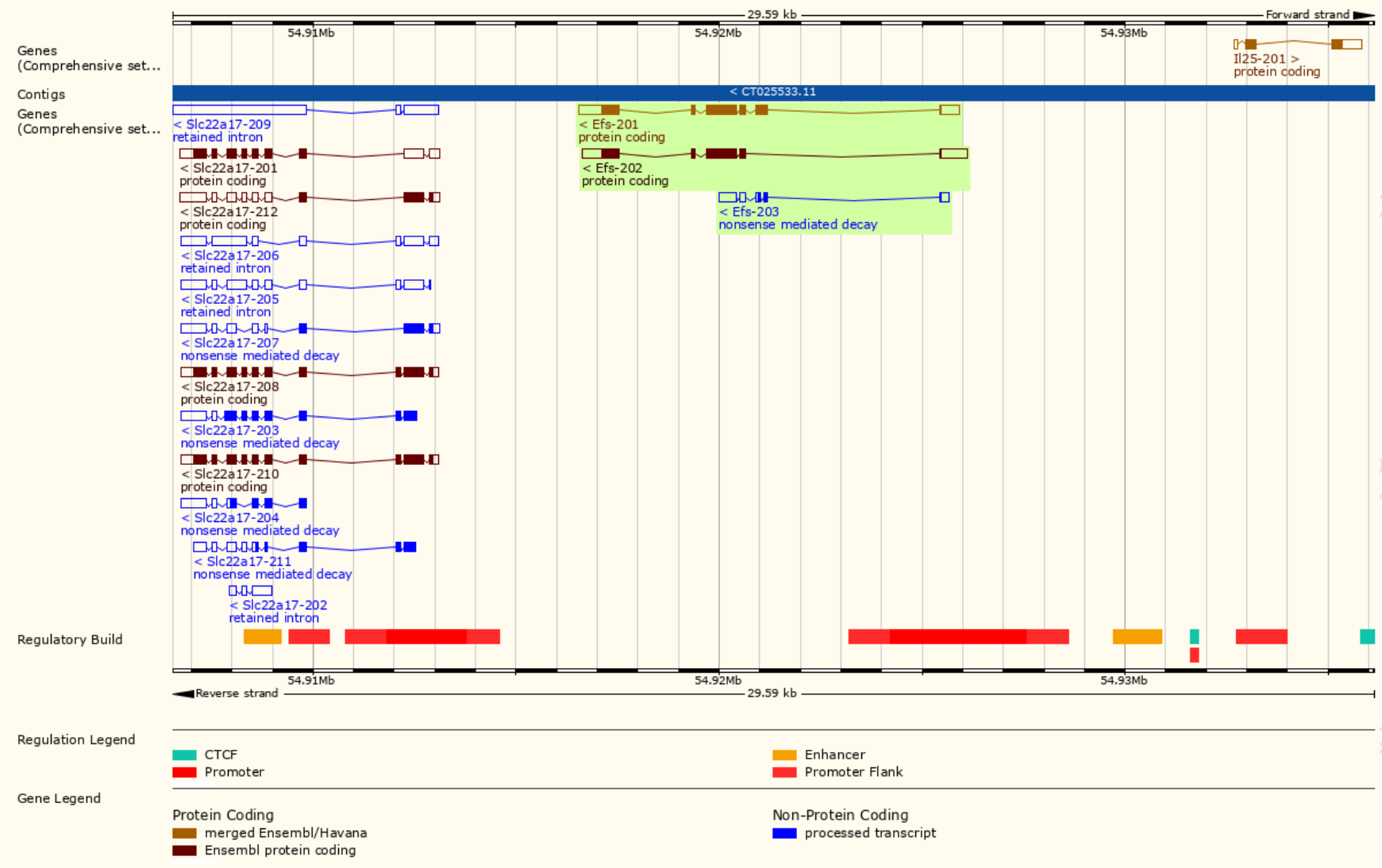
The gene has 3 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Efs-201	ENSMUST00000022813.7	2705	560aa	Protein coding	CCDS36925	Q64355	TSL:1 GENCODE basic APPRIS P1
Efs-202	ENSMUST00000227037.1	2540	467aa	Protein coding	-	A0A2I3BRP5	GENCODE basic
Efs-203	ENSMUST00000227587.1	961	45aa	Nonsense mediated decay	-	A0A2I3BQ52	-

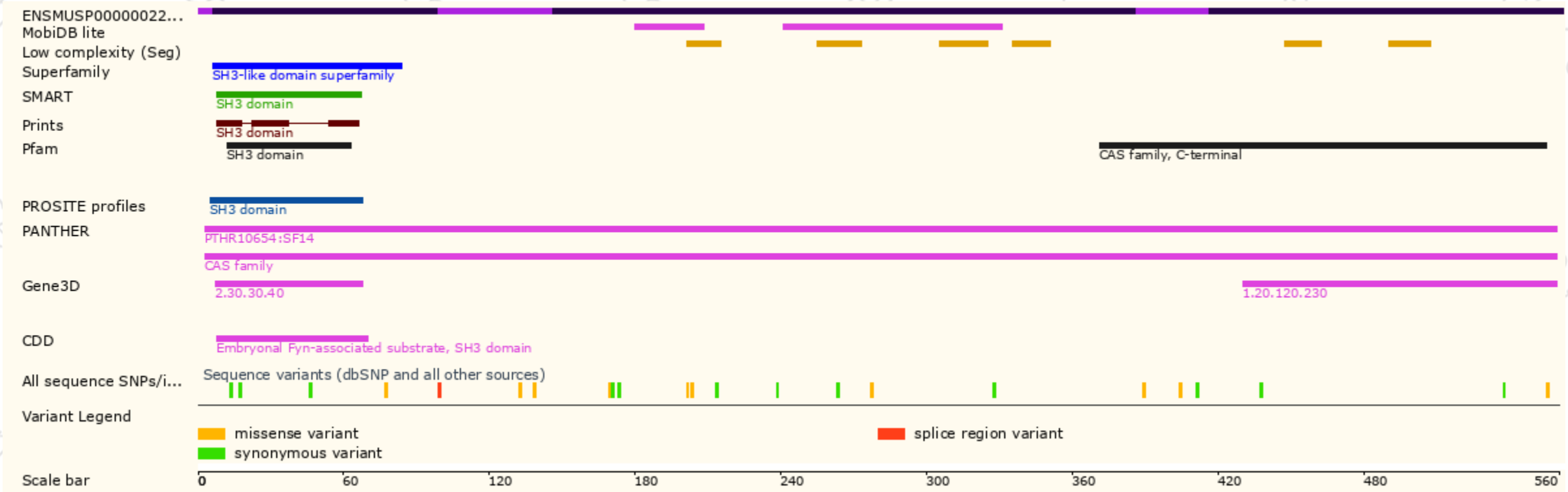
The strategy is based on the design of *Efs-201* transcript,the transcription is shown below:



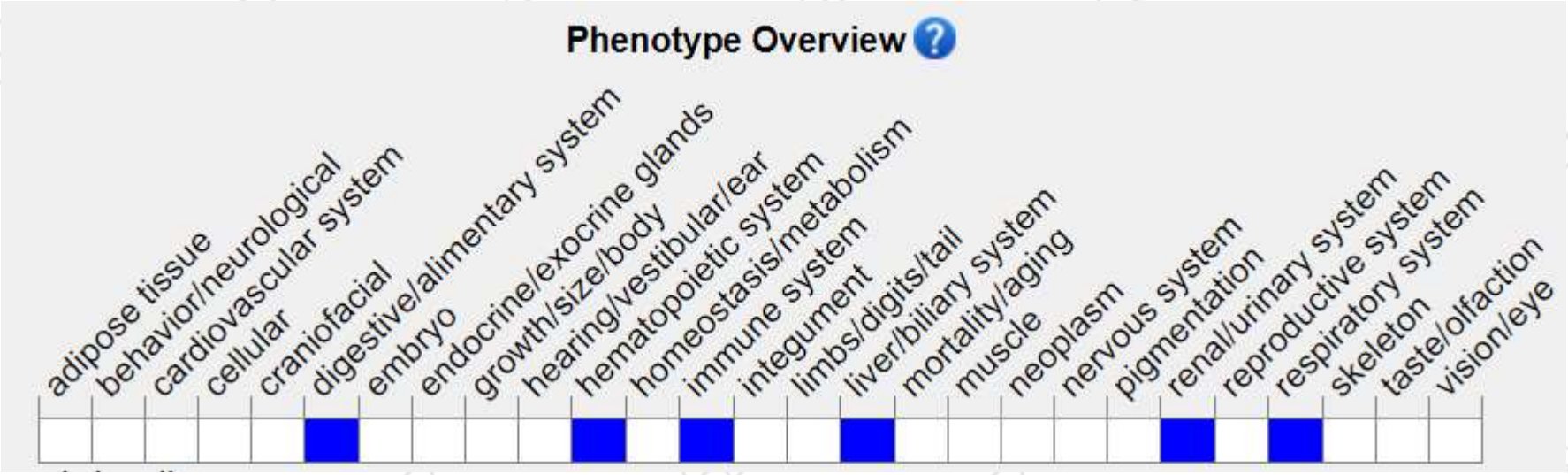
Genomic location (Ensembl)



Protein domain（Ensembl）



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 a disruption in this gene display an increased inflammatory response characterized by excessive T cell responses, enhanced cytokine secretion and antibody production, and intestinal, kidney, liver, and lung inflammation.

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

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