

Olfr417 Cas9-CKO Strategy

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Project Overview

Project Name

Olfr417

Project type

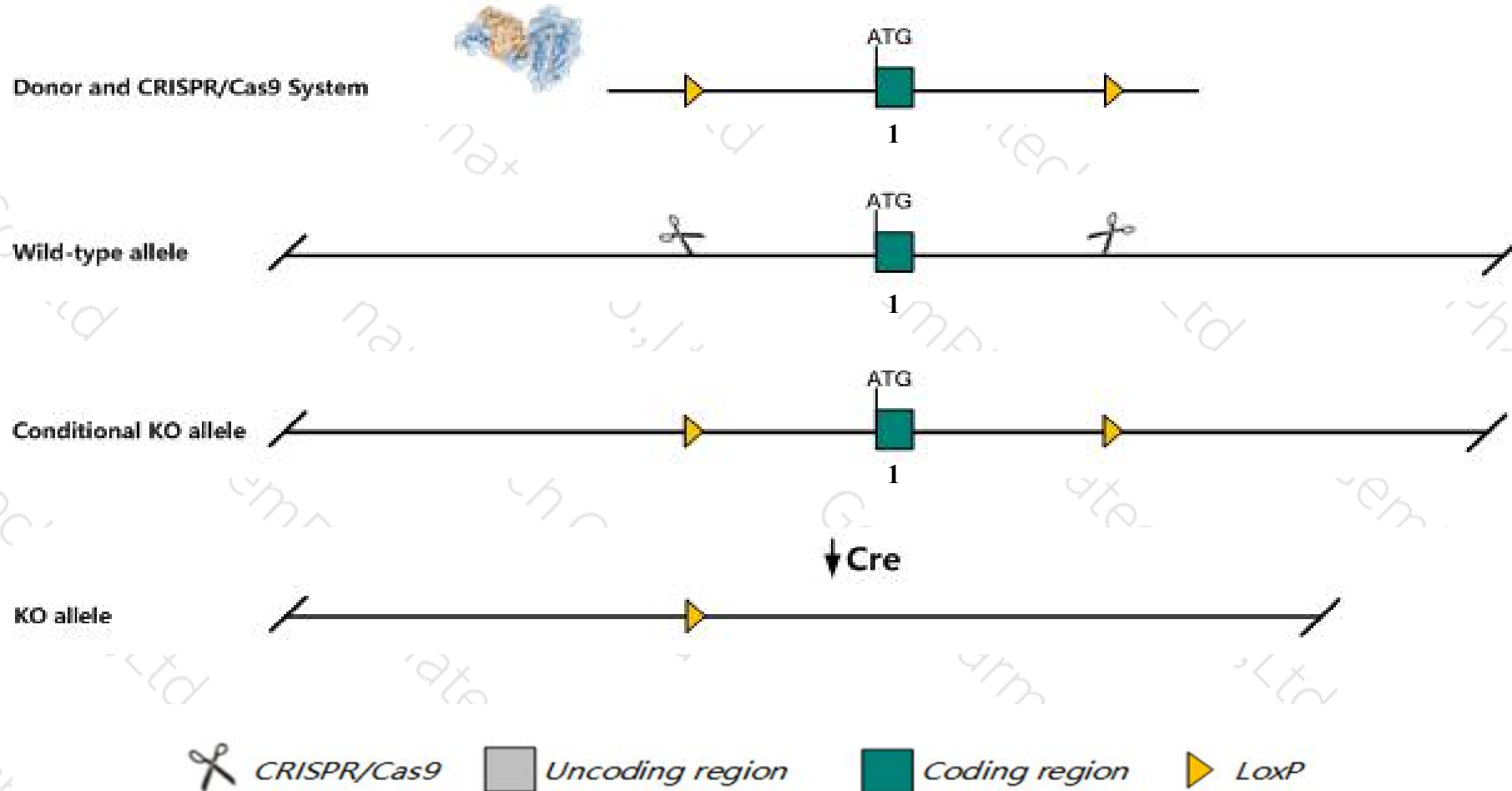
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Olfr417* gene. The schematic diagram is as follows:



Technical routes

- The *Olfr417* gene has 3 transcripts. According to the structure of *Olfr417* gene, exon1 of *Olfr417*-201(ENSMUST00000085862.1) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Olfr417* 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 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.

- The KO region contains functional region of the *Olfr416-ps1* gene. Knockout the region may affect the function of *Olfr416-ps1* gene.
- The *Olfr417* gene is located on the Chr1. 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)

Olfr417 olfactory receptor 417 [Mus musculus (house mouse)]

Gene ID: 258238, updated on 13-Mar-2020

Summary



Official Symbol	Olfr417 provided by MGI
Official Full Name	olfactory receptor 417 provided by MGI
Primary source	MGI:MGI:3030251
See related	Ensembl:ENSMUSG00000066672
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	GA_x5J8B7W3B3M-312879-313274, GA_x6K02T2P20D-20787051-20786119, MOR267-11
Summary	Olfactory receptors interact with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell. The olfactory receptor proteins are members of a large family of G-protein-coupled receptors (GPCR) arising from single coding-exon genes. Olfactory receptors share a 7-transmembrane domain structure with many neurotransmitter and hormone receptors and are responsible for the recognition and G protein-mediated transduction of odorant signals. The olfactory receptor gene family is the largest in the genome. The nomenclature assigned to the olfactory receptor genes and proteins for this organism is independent of other organisms. [provided by RefSeq, Jul 2008]

Transcript information (Ensembl)

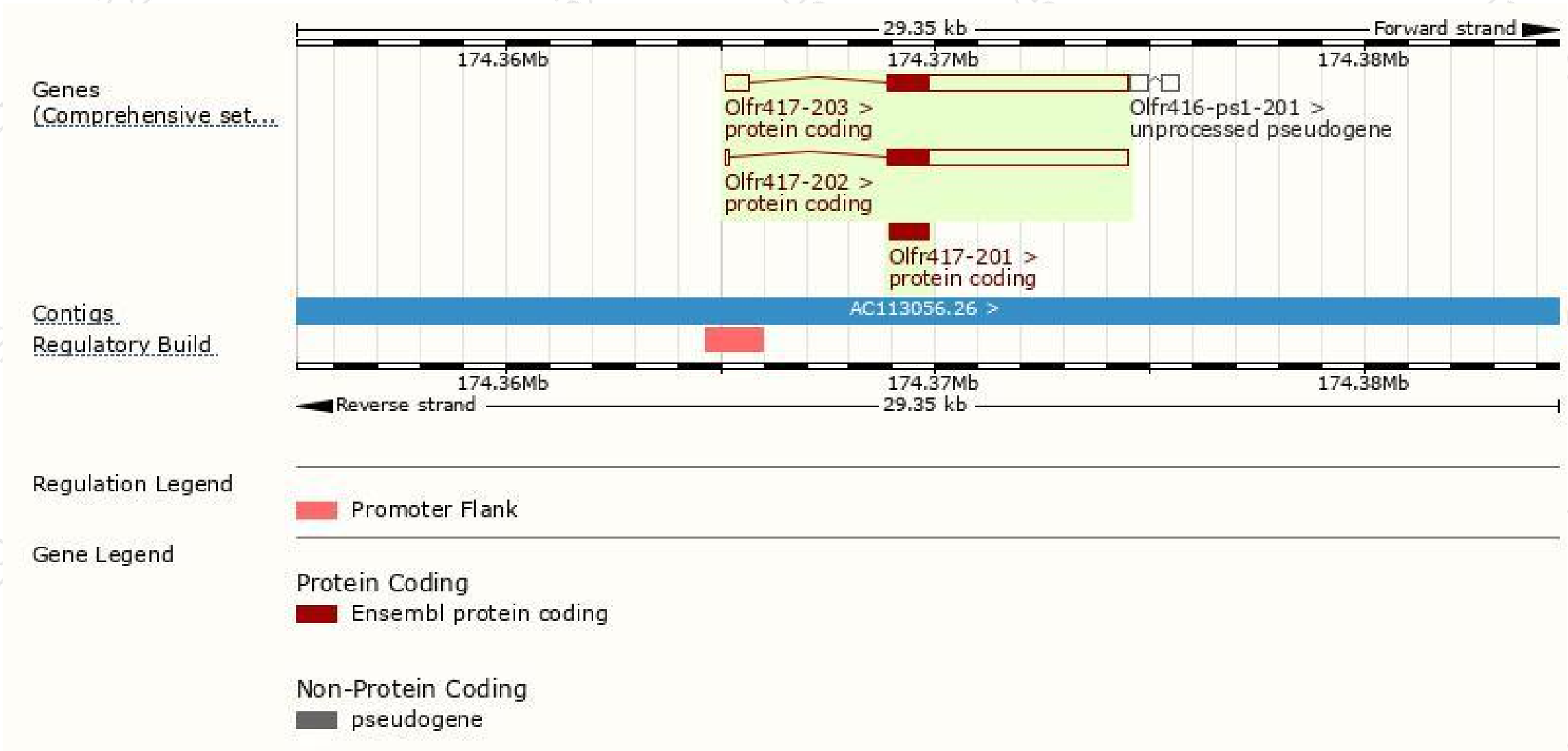
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Olfr417-203	ENSMUST00000220394.1	6080	309aa	Protein coding	CCDS15542	F8VQB1	TSL:5 GENCODE basic APPRIS P1
Olfr417-202	ENSMUST00000217962.1	5662	309aa	Protein coding	CCDS15542	F8VQB1	TSL:5 GENCODE basic APPRIS P1
Olfr417-201	ENSMUST00000085862.1	930	309aa	Protein coding	CCDS15542	F8VQB1	TSL:NA GENCODE basic APPRIS P1

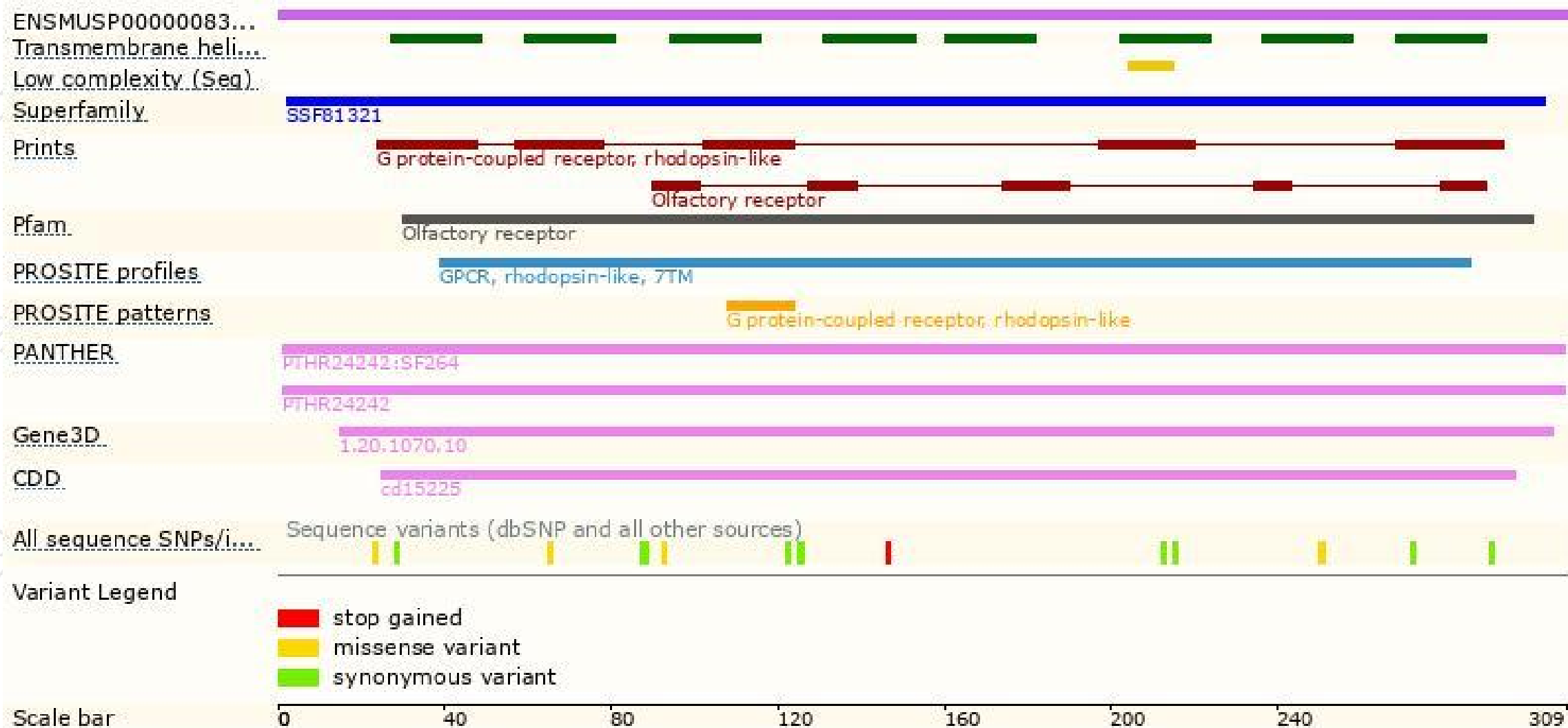
The strategy is based on the design of *Olfr417-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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