Svil Cas9-CKO Strategy

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Project Overview

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

Conditional Knockout strategy

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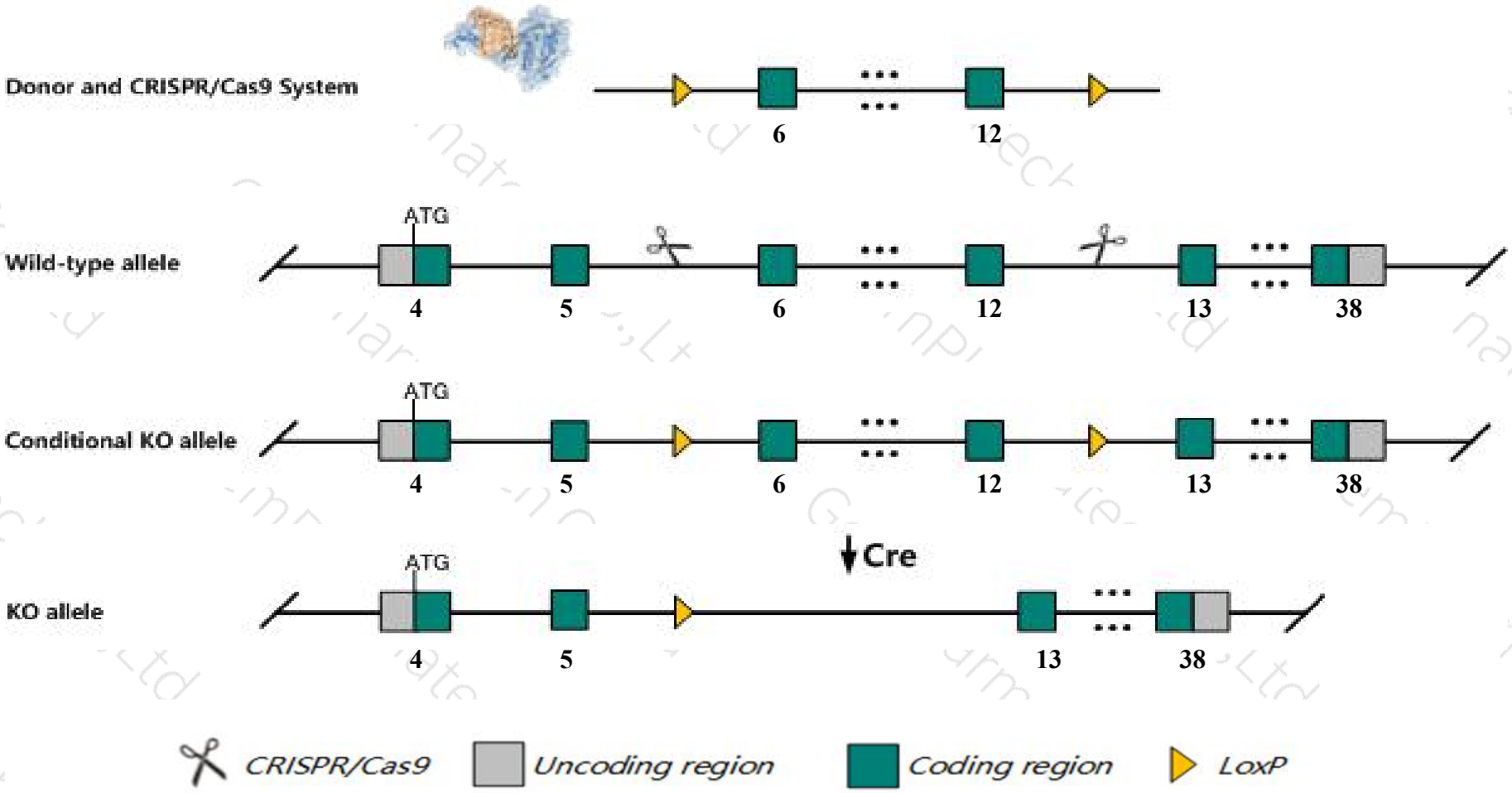
This model will use CRISPR/Cas9 technology to edit the *Svil* gene. The schematic diagram is as follows:



Technical routes

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- The *Svil* gene has 15 transcripts. According to the structure of *Svil* gene, exon6-exon12 of *Svil-203* (ENSMUST00000126977.7) transcript is recommended as the knockout region.The region contains 1963bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Svil* 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.

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele exhibit enhanched adhesion and thrombus formation.

- Transcript 212 CDS 5' and 3' incomplete the influences is unknown. Transcript 214 CDS 3' incomplete the influences is unknown.

- The *Svil* gene is located on the Chr18. 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）

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Svil supervillin [Mus musculus (house mouse)]

Gene ID: 225115, updated on 31-Jan-2019

Summary

Official Symbol	Svil provided by MGI
Official Full Name	supervillin provided byMGI
Primary source	MGI:MGI:2147319
See related	Ensembl:ENSMUSG00000024236
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	AU024053, B430302E16Rik
Expression	Broad expression in bladder adult (RPKM 33.3), heart adult (RPKM 16.5) and 20 other tissuesSee more
Orthologs	human all

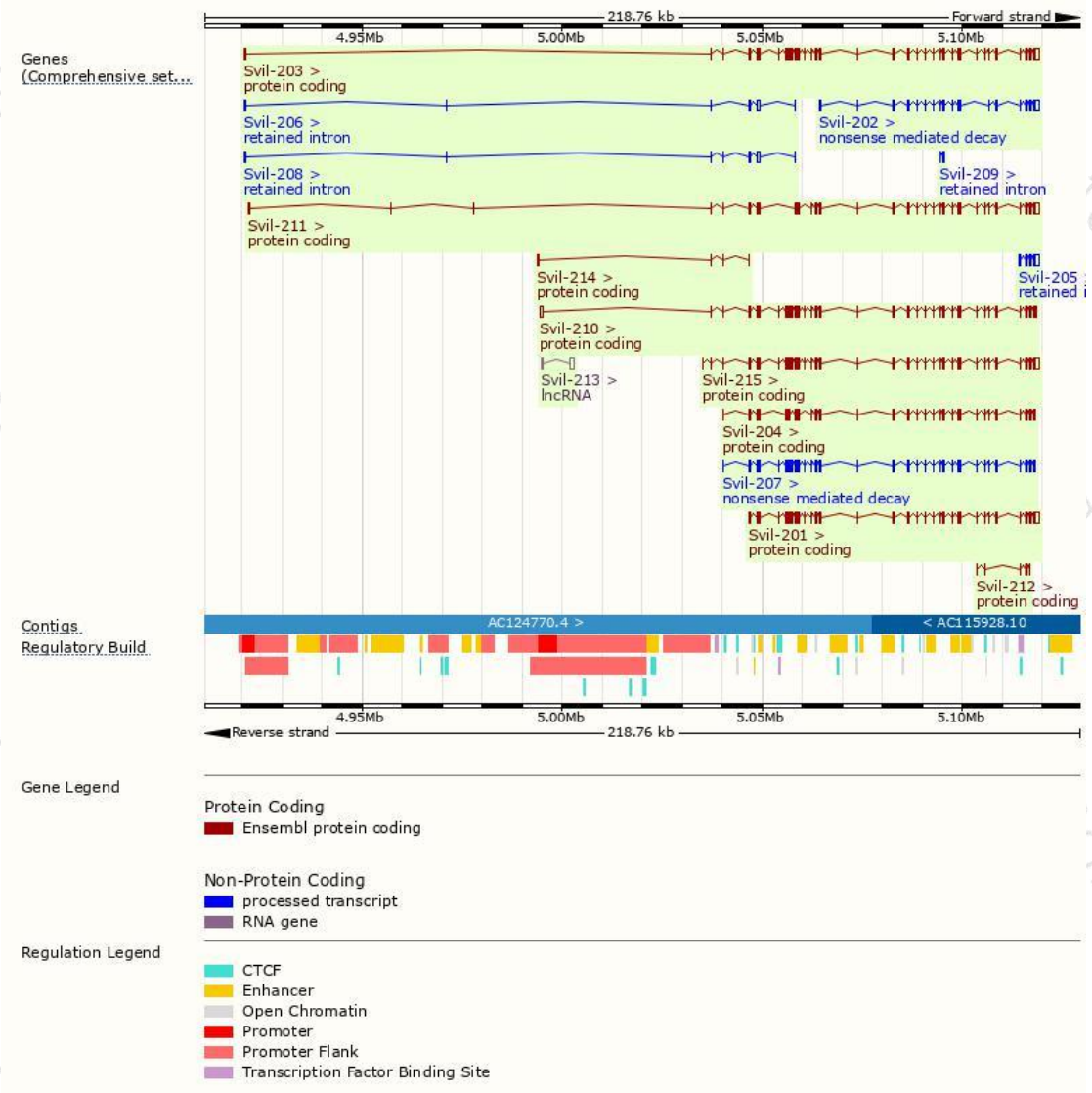
Transcript information（Ensembl）

The gene has 15 transcripts,all transcripts are shown below:

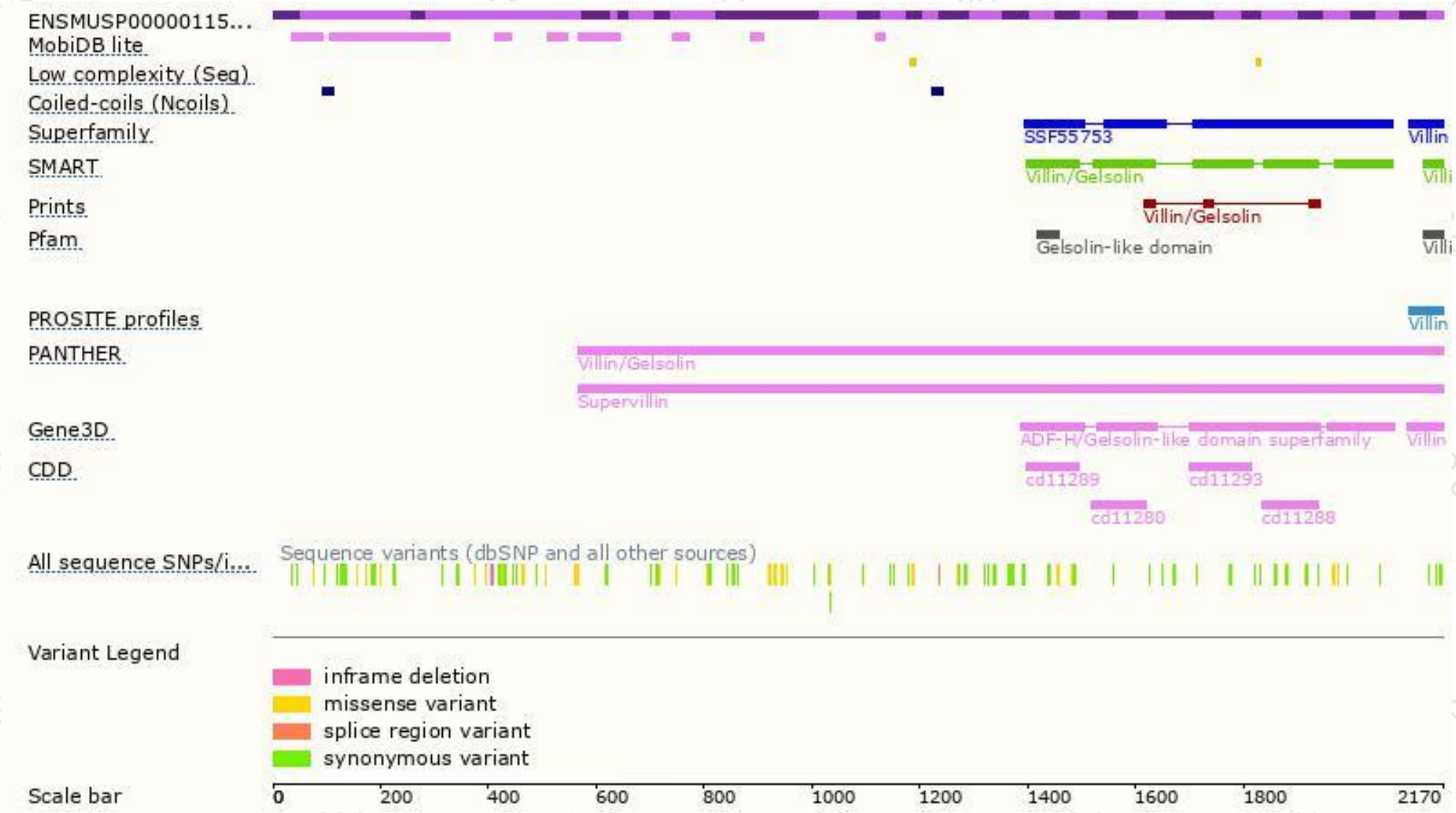
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Svil-203	ENSMUST00000126977.7	7907	2170aa	Protein coding	CCDS37720	Q8K4L3	TSL:5 GENCODE basic APPRIS P3
Svil-201	ENSMUST00000025079.15	7433	2170aa	Protein coding	CCDS37720	Q8K4L3	TSL:1 GENCODE basic APPRIS P3
Svil-210	ENSMUST00000140448.7	7423	2170aa	Protein coding	CCDS37720	Q8K4L3	TSL:5 GENCODE basic APPRIS P3
Svil-211	ENSMUST00000143254.7	6594	1766aa	Protein coding	CCDS84352	Q8K4L3	TSL:5 GENCODE basic APPRIS ALT2
Svil-215	ENSMUST00000210707.1	7633	2257aa	Protein coding	-	A0A1B0GS91	TSL:5 GENCODE basic APPRIS ALT2
Svil-204	ENSMUST00000127297.7	6243	2056aa	Protein coding	-	E9Q3Z5	TSL:5 GENCODE basic APPRIS ALT2
Svil-212	ENSMUST00000146723.1	507	169aa	Protein coding	-	F6TBK9	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Svil-214	ENSMUST00000153016.7	497	40aa	Protein coding	-	D3Z2X9	CDS 3' incomplete TSL:2
Svil-207	ENSMUST00000131609.7	6420	2031aa	Nonsense mediated decay	-	Q8K4L2	TSL:5
Svil-202	ENSMUST00000125512.7	4060	749aa	Nonsense mediated decay	-	F6R6A4	CDS 5' incomplete TSL:5
Svil-205	ENSMUST00000129543.1	1732	No protein	Retained intron	-	-	TSL:2
Svil-206	ENSMUST00000131210.7	1560	No protein	Retained intron	-	-	TSL:1
Svil-208	ENSMUST00000138258.7	1430	No protein	Retained intron	-	-	TSL:5
Svil-209	ENSMUST00000139761.1	523	No protein	Retained intron	-	-	TSL:2
Svil-213	ENSMUST00000148564.1	1218	No protein	lncRNA	-	-	TSL:1

The strategy is based on the design of *Svil-203* transcript,The transcription is shown below

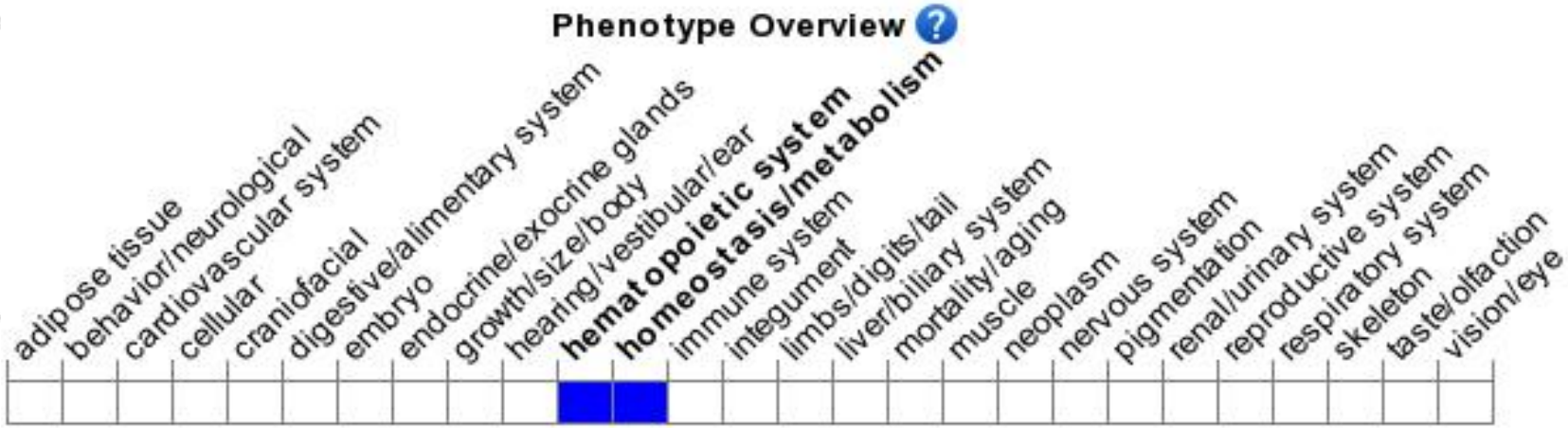
Genomic location distribution



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/).

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