Homer3 Cas9-KO Strategy

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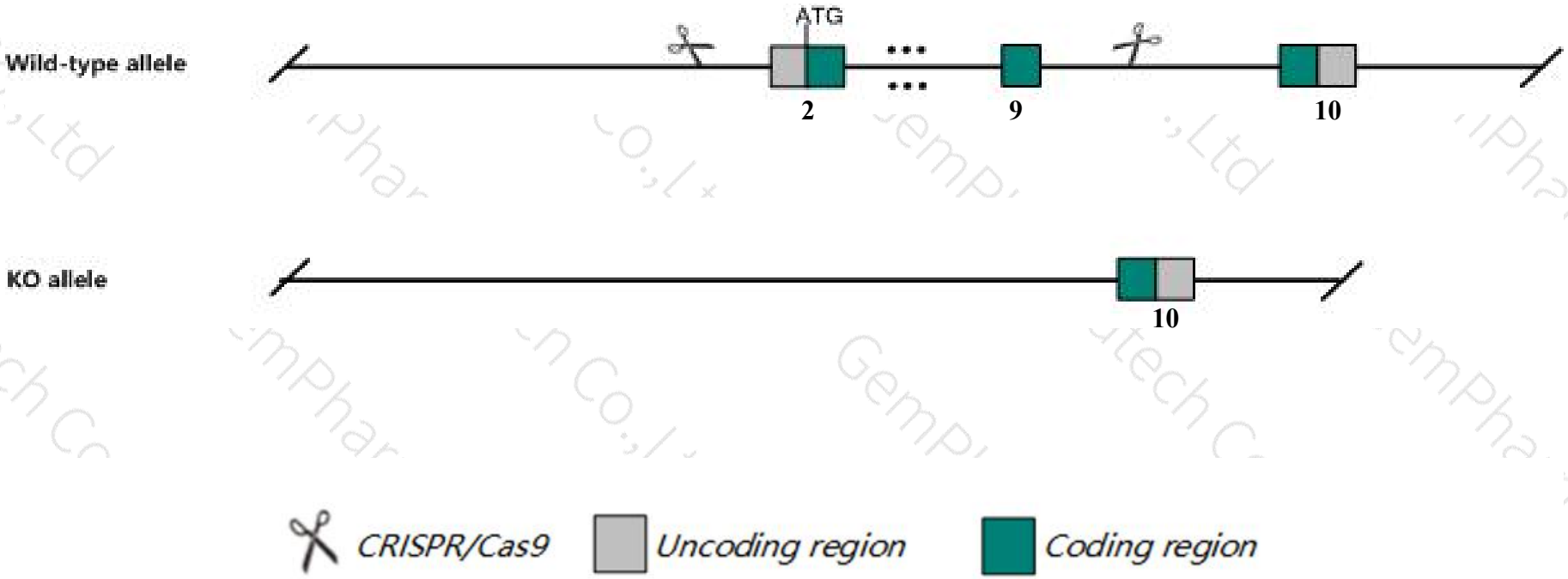
Project Overview

Project Name	***Homer3***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Homer3* gene. The schematic diagram is as follows:



Technical routes

➢ The *Homer3* gene has 8 transcripts. According to the structure of *Homer3* gene, exon2-exon9 of *Homer3-206* (ENSMUST00000140212.7) 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 *Homer3* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

➢ The floxed region is near to the C-terminal of *Ddx49* gene,this strategy may influence the regulatory function of the C-terminal of *Ddx49* gene.

➢ According to the existing MGI data,Homozygous mutants exhibit normal sensitivity to cocaine.

➢ The *Homer3* gene is located on the Chr8. 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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Homer3 homer scaffolding protein 3 [Mus musculus (house mouse)]

Gene ID: 26558, updated on 9-Apr-2019

Summary

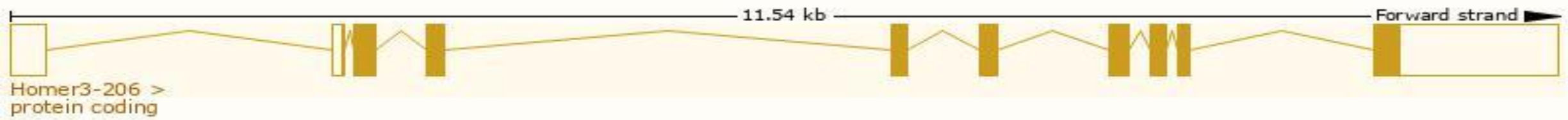
Official Symbol	Homer3 provided by MGI
Official Full Name	homer scaffolding protein 3 provided byMGI
Primary source	MGI:MGI:1347359
See related	Ensembl:ENSMUSG00000003573
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW146114
Expression	Ubiquitous expression in cerebellum adult (RPKM 62.8), ovary adult (RPKM 38.6) and 27 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

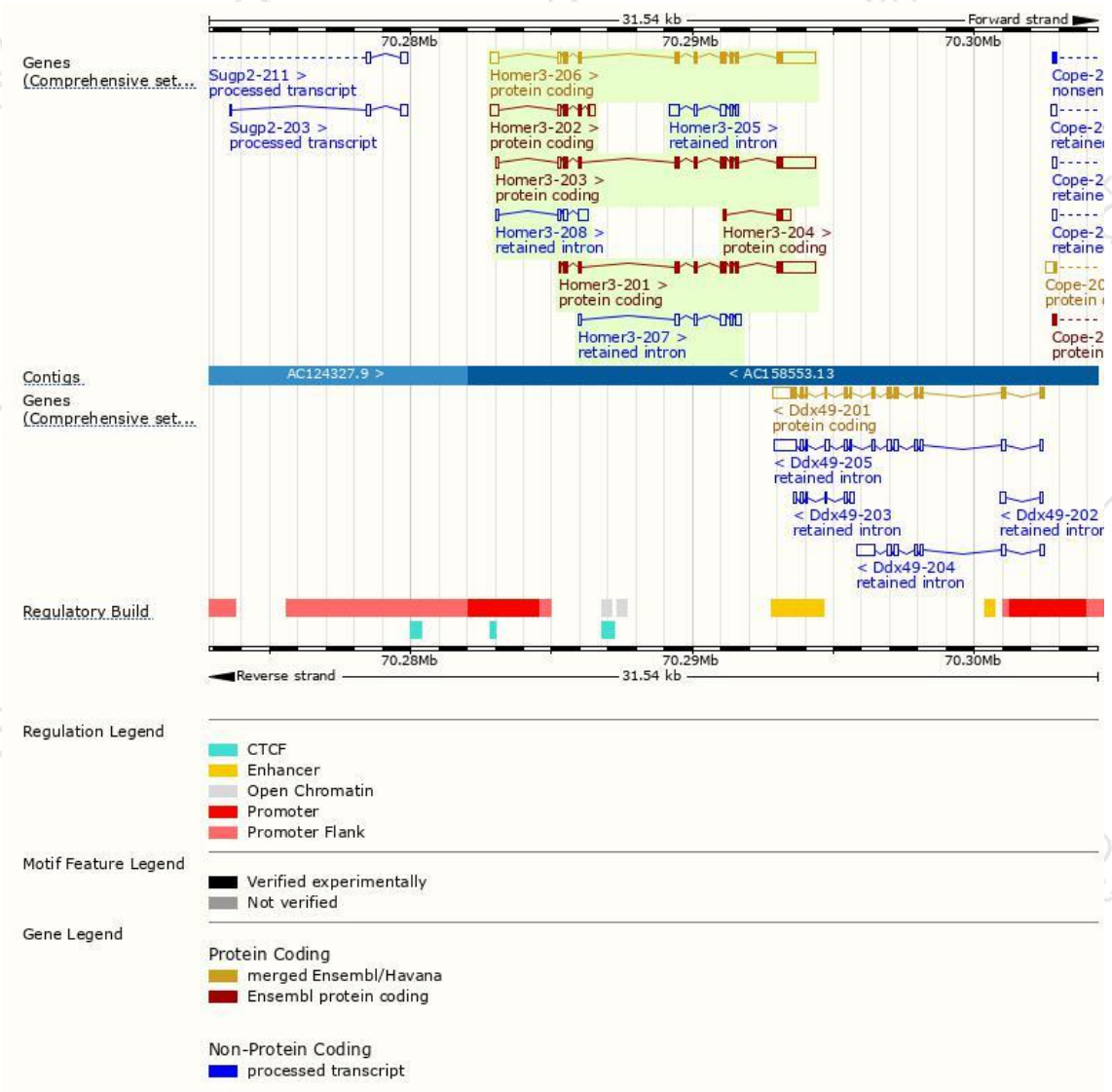
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Homer3-206	ENSMUST00000140212.7	2608	356aa	Protein coding	CCDS22363	Q99JP6	TSL:1 GENCODE basic APPRIS P3
Homer3-203	ENSMUST00000110124.8	2445	359aa	Protein coding	CCDS52569	Q99JP6	TSL:5 GENCODE basic APPRIS ALT1
Homer3-201	ENSMUST00000003669.7	2323	359aa	Protein coding	CCDS52569	Q99JP6	TSL:1 GENCODE basic APPRIS ALT1
Homer3-202	ENSMUST00000087467.11	880	122aa	Protein coding	-	Q501M9	TSL:1 GENCODE basic
Homer3-204	ENSMUST00000135368.1	583	93aa	Protein coding	-	J3QQ00	CDS 5' incomplete TSL:3
Homer3-207	ENSMUST00000143528.7	852	No protein	Retained intron	-	-	TSL:3
Homer3-205	ENSMUST00000135692.1	805	No protein	Retained intron	-	-	TSL:3
Homer3-208	ENSMUST00000155711.1	678	No protein	Retained intron	-	-	TSL:2

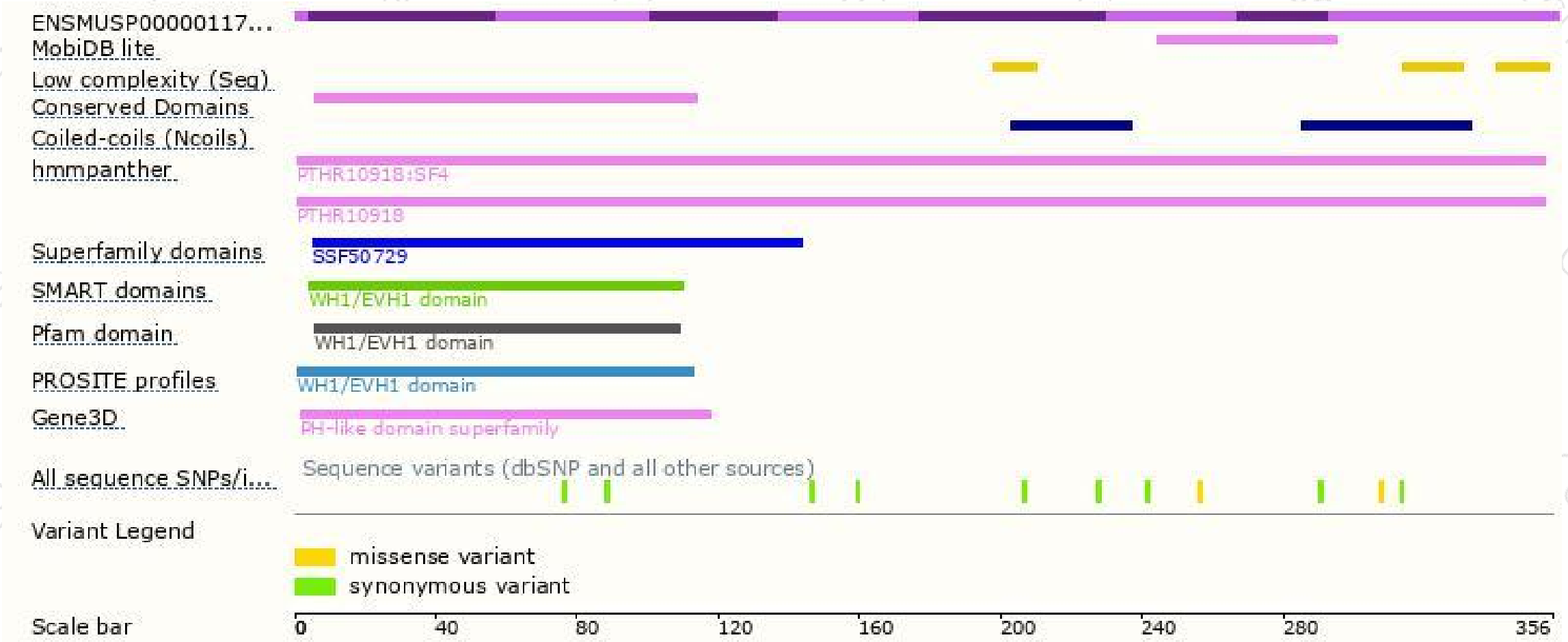
The strategy is based on the design of *Homer3-206* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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