Samhd1 Cas9-KO Strategy

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Project Overview

Project Name	*Samhd1*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

This model will use CRISPR/Cas9 technology to edit the *Samhd1* gene. The schematic diagram is as follows:

Technical routes

➢ The *Samhd1* gene has 10 transcripts. According to the structure of *Samhd1* gene, exon2 of *Samhd1-201* (ENSMUST00000057725.9) transcript is recommended as the knockout region.The region contains 67bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Samhd1* gene. The brief process is as follows: CRISPR/Cas9 syste

➢ According to the existing MGI data,Mice homozygous for a knock-out allele exhibit increased susceptibility to infection with pseudotyped HIV-1.

➢ The *Samhd1* gene is located on the Chr2. 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）

Samhd1 SAM domain and HD domain, 1 [Mus musculus (house mouse)]

Gene ID: 56045, updated on 19-Mar-2019

▲ Summary

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Official Symbol	Samhd1 provided by MGI
Official Full Name	SAM domain and HD domain, 1 provided by MGI
Primary source	MGI:MGI:1927468
See related	Ensembl:ENSMUSG00000027639
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	E330031J07Rik, Mg11, mSAMHD1
Expression	Ubiquitous expression in spleen adult (RPKM 38.6), lung adult (RPKM 21.3) and 26 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Samhd1-201	ENSMUST00000057725.9	3926	658aa	Protein coding	CCDS16973	Q60710	TSL:1 GENCODE basic APPRIS P3
Samhd1-202	ENSMUST00000088523.10	1996	651aa	Protein coding	CCDS50783	Q60710	TSL:5 GENCODE basic APPRIS ALT2
Samhd1-203	ENSMUST00000109549.2	3245	582aa	Protein coding	-	E9PYG9	TSL:1 GENCODE basic APPRIS ALT2
Samhd1-206	ENSMUST00000139263.7	2036	631aa	Protein coding	-	F6TVP2	CDS 5' incomplete TSL:1
Samhd1-204	ENSMUST00000123932.7	3753	150aa	Nonsense mediated decay	-	E0CXZ5	TSL:2
Samhd1-208	ENSMUST00000149313.7	1375	No protein	Retained intron	-	-	TSL:1
Samhd1-210	ENSMUST00000160213.1	681	No protein	Retained intron	-	-	TSL:3
Samhd1-205	ENSMUST00000139149.1	678	No protein	Retained intron	-	-	TSL:2
Samhd1-209	ENSMUST00000152866.1	542	No protein	Retained intron	-	-	TSL:2
Samhd1-207	ENSMUST00000142508.1	473	No protein	Retained intron	-	-	TSL:3

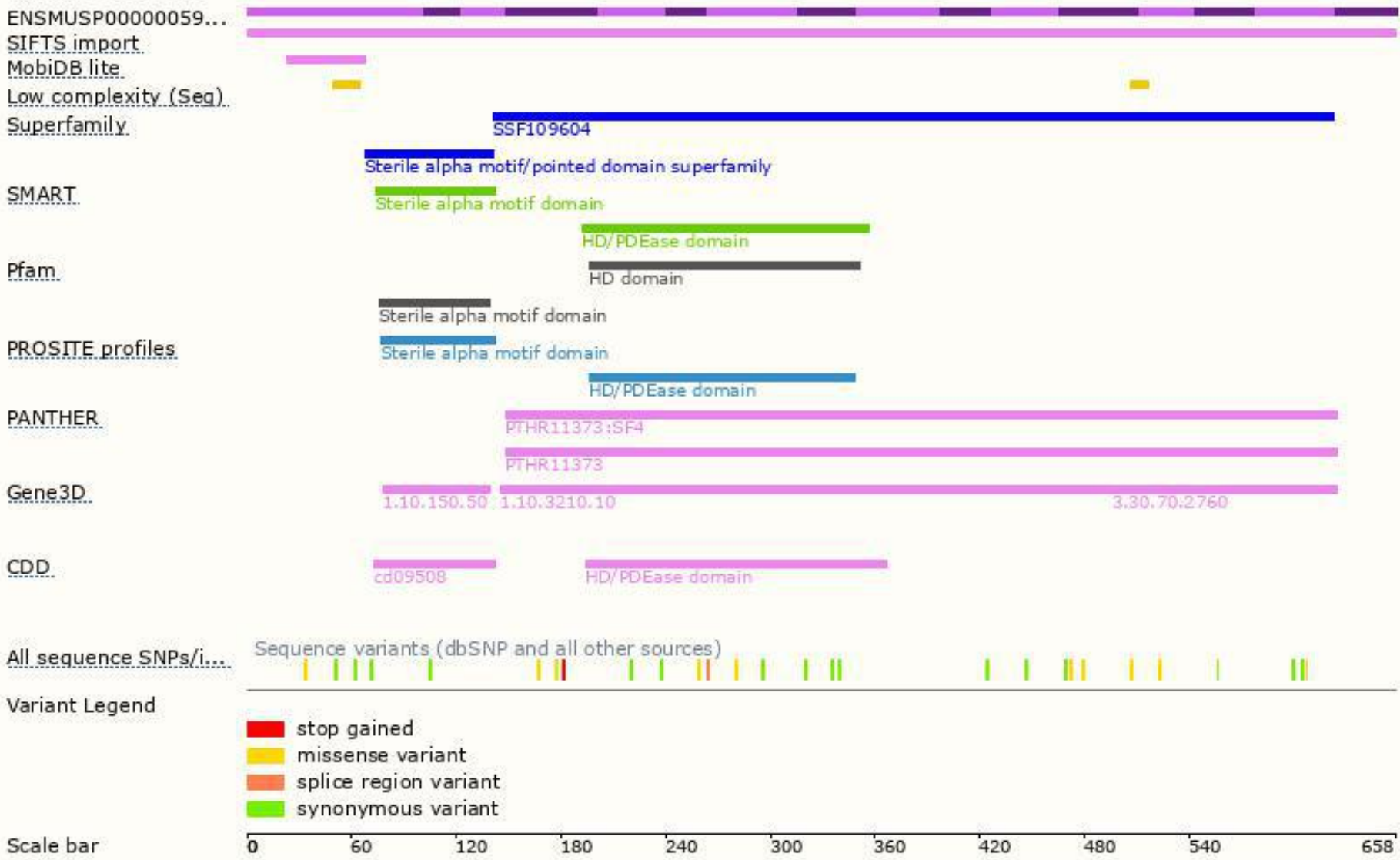The strategy is based on the design of *Samhd1-201* transcript,The transcription is shown below

< Samhd1-201
protein coding

Reverse strand

37.73 kb
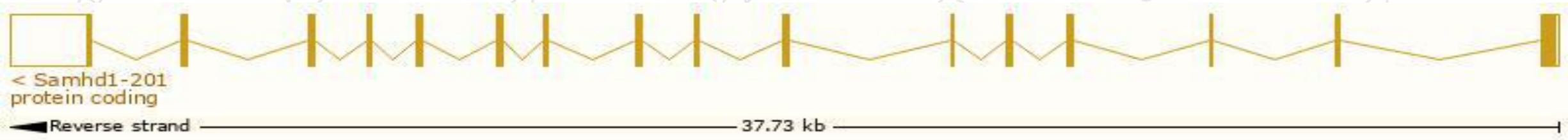
Genomic location distribution
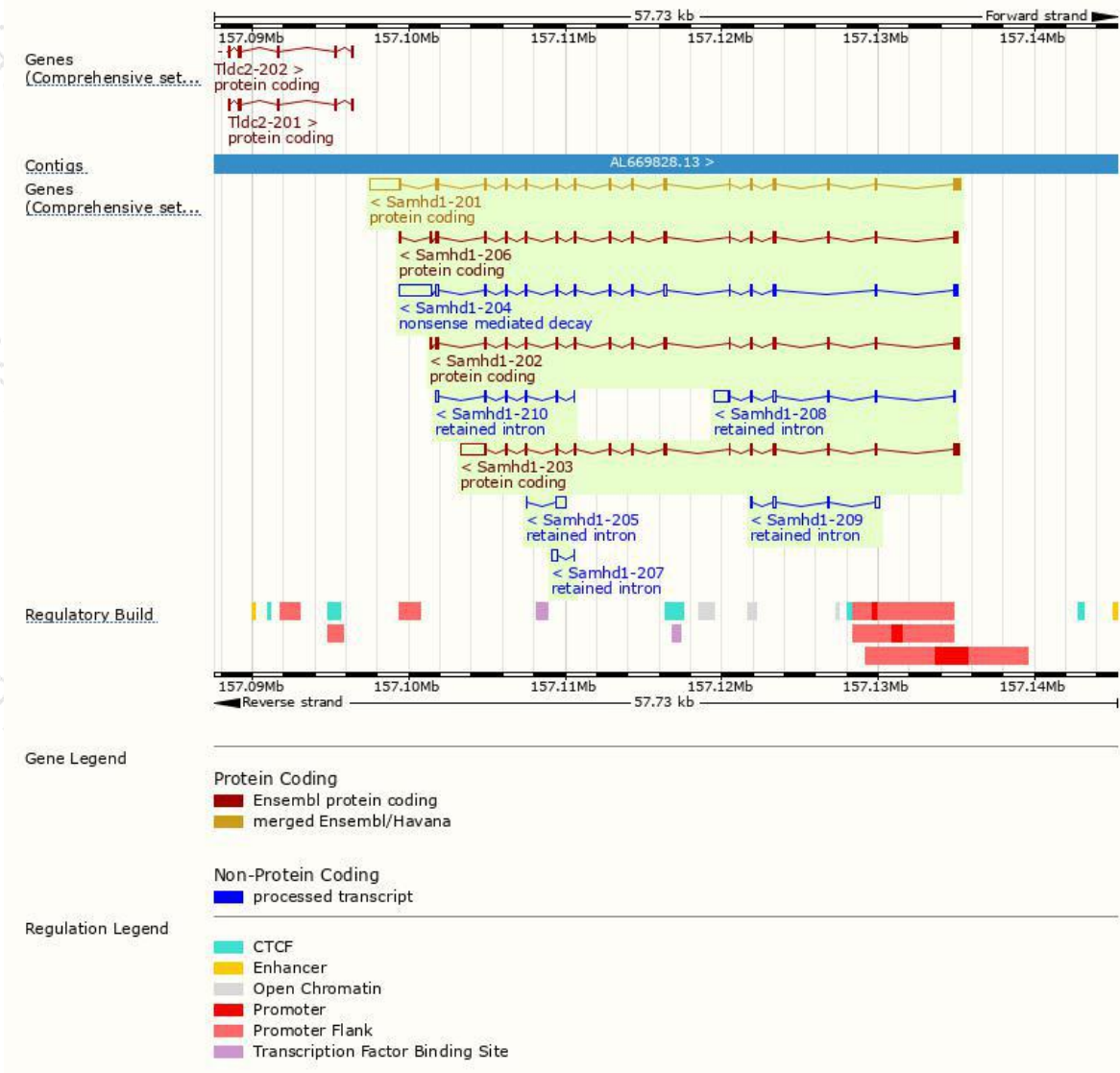
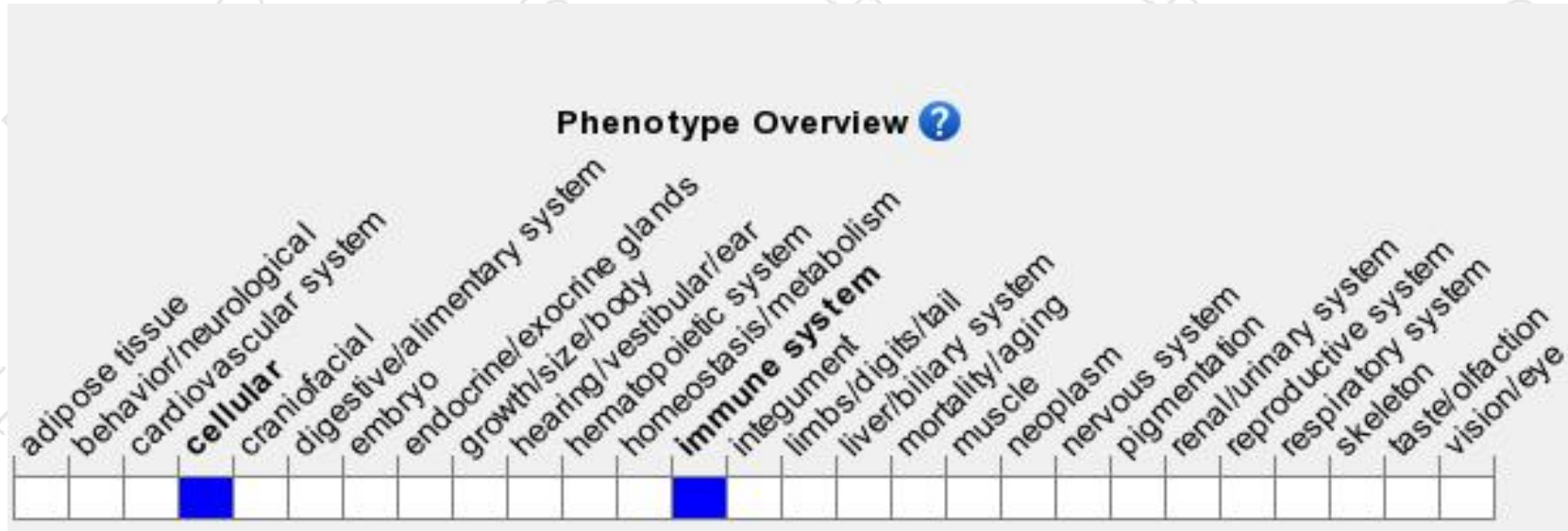# Protein domain

Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data,Mice homozygous for a knock-out allele exhibit increased susceptibility to infection with pseudotyped HIV-1.

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