Asap1 Cas9-CKO Strategy

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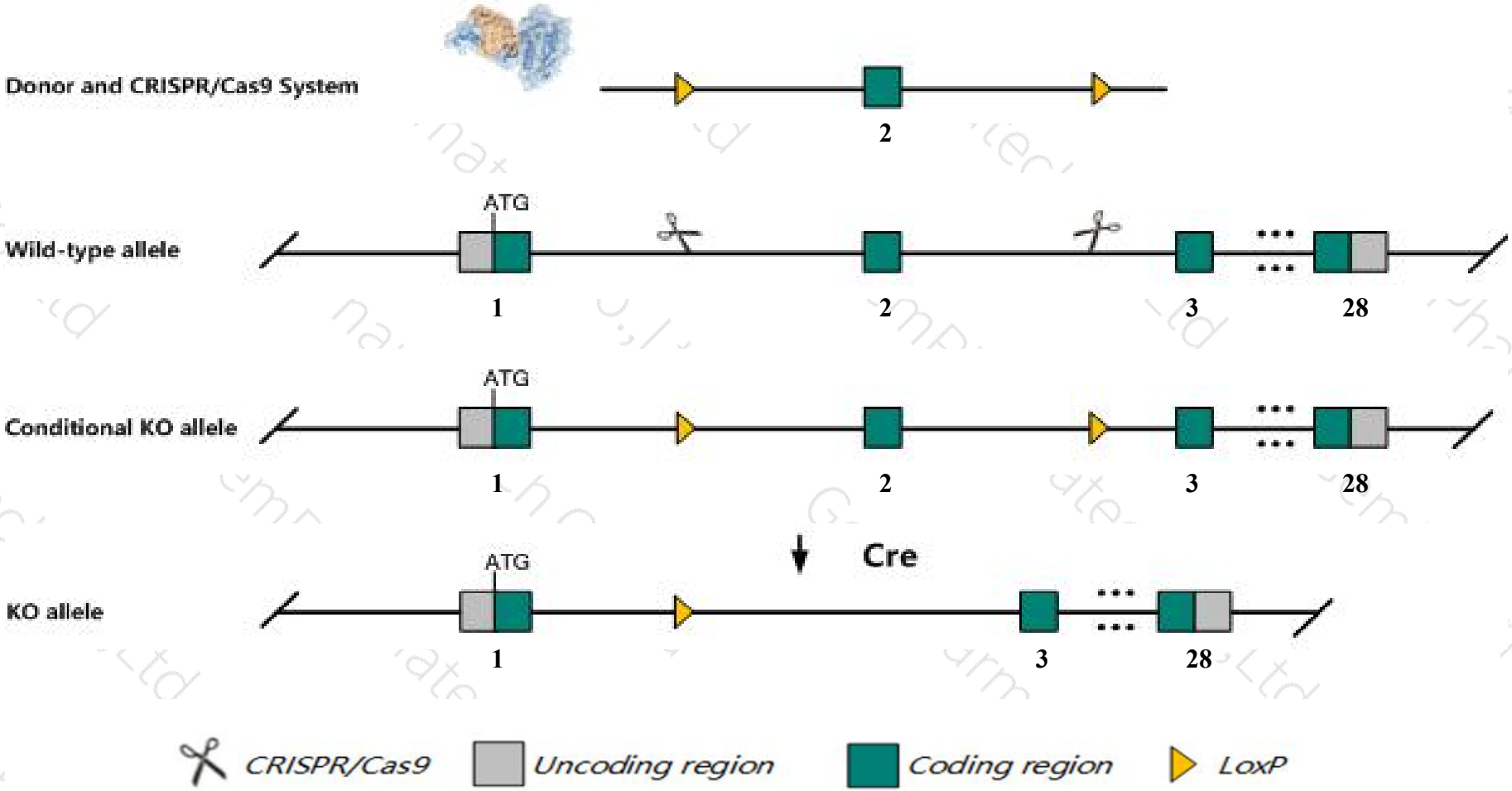
Project Overview

Project Name	***Asap1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Asap1* gene. The schematic diagram is as follows:



Technical routes

- The *Asap1* gene has 19 transcripts. According to the structure of *Asap1* gene, exon2 of *Asap1-217* (ENSMUST00000177371.7) transcript is recommended as the knockout region.The region contains 73bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Asap1* 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

➢ The *Asap1* gene is located on the Chr15. 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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Asap1 ArfGAP with SH3 domain, ankyrin repeat and PH domain1 [Mus musculus (house mouse)]

Gene ID: 13196, updated on 7-Apr-2019

Summary

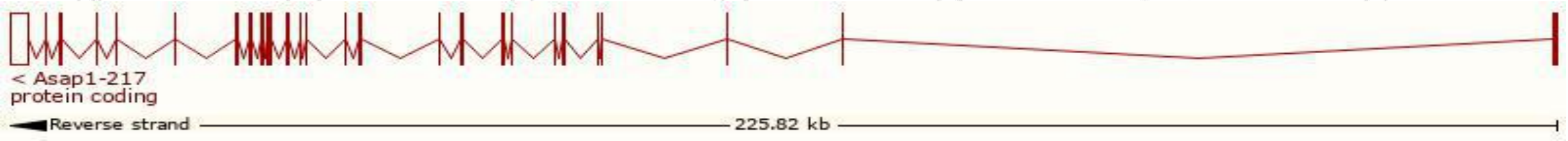
Official Symbol	Asap1 provided by MGI
Official Full Name	ArfGAP with SH3 domain, ankyrin repeat and PH domain1 provided by MGI
Primary source	MGI:MGI:1342335
See related	Ensembl:ENSMUSG00000022377
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AV239055, DEF-1, Ddef1, PAP, mKIAA1249, s19
Expression	Ubiquitous expression in testis adult (RPKM 21.3), cortex adult (RPKM 15.3) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

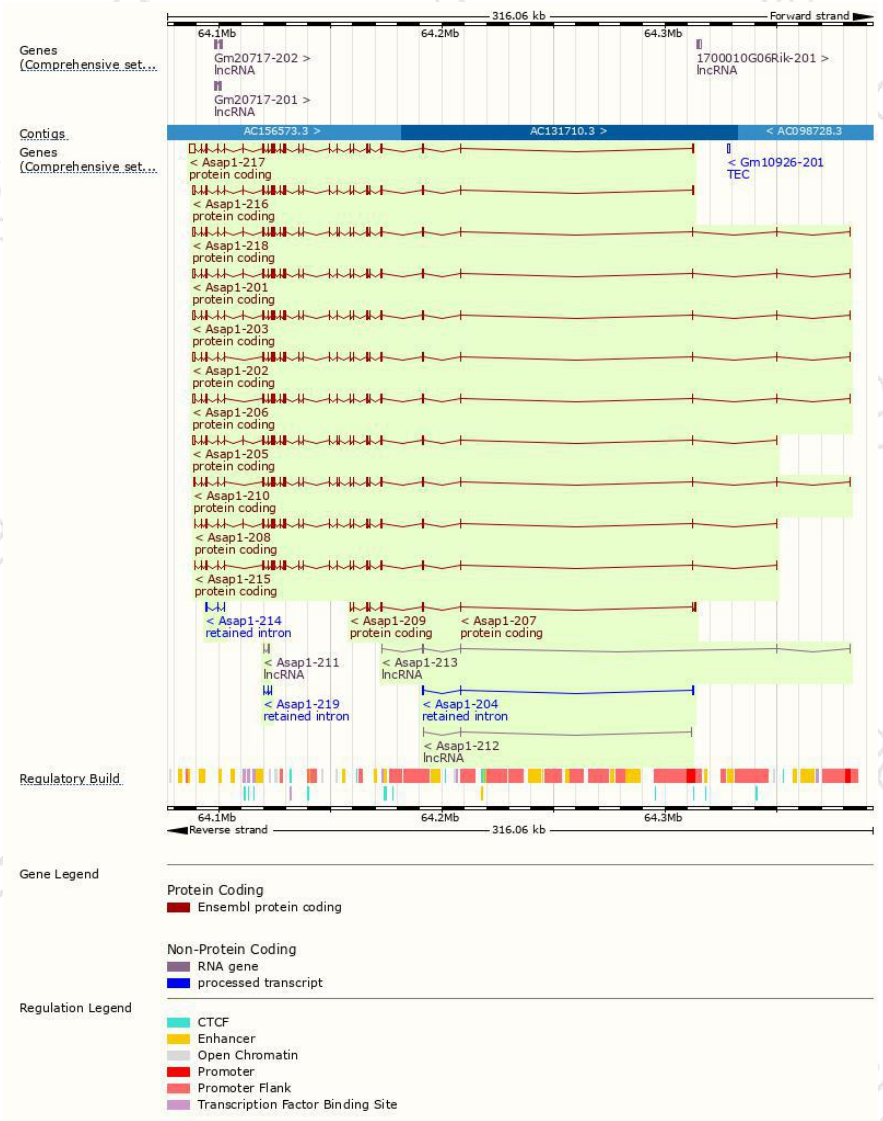
The gene has 19 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Asap1-217	ENSMUST00000177371.7	6164	1124aa	Protein coding	CCDS70631	H3BL41	TSL:1 GENCODE basic APPRIS ALT2
Asap1-218	ENSMUST00000177374.7	4582	1147aa	Protein coding	CCDS56986	Q9QWY8	TSL:1 GENCODE basic APPRIS P3
Asap1-216	ENSMUST00000177083.7	4415	1112aa	Protein coding	CCDS70632	E9QMJ1	TSL:1 GENCODE basic APPRIS ALT2
Asap1-206	ENSMUST00000175799.7	4237	1087aa	Protein coding	CCDS70633	H3BKE6	TSL:5 GENCODE basic APPRIS ALT2
Asap1-210	ENSMUST00000176384.7	4149	1090aa	Protein coding	CCDS70634	Q9QWY8	TSL:1 GENCODE basic APPRIS ALT2
Asap1-201	ENSMUST00000023008.15	4580	1147aa	Protein coding	-	E9QN63	TSL:5 GENCODE basic APPRIS ALT2
Asap1-203	ENSMUST00000110115.8	4535	1132aa	Protein coding	-	Q9QWY8	TSL:5 GENCODE basic APPRIS ALT2
Asap1-202	ENSMUST00000110114.9	4409	1090aa	Protein coding	-	E9QMI7	TSL:5 GENCODE basic APPRIS ALT2
Asap1-205	ENSMUST00000175793.7	4314	1135aa	Protein coding	-	Q9QWY8	TSL:5 GENCODE basic APPRIS ALT2
Asap1-208	ENSMUST00000176014.7	3435	1144aa	Protein coding	-	H3BJY2	TSL:5 GENCODE basic APPRIS ALT2
Asap1-215	ENSMUST00000177035.7	3228	1075aa	Protein coding	-	H3BKD4	TSL:5 GENCODE basic APPRIS ALT2
Asap1-209	ENSMUST00000176358.1	631	211aa	Protein coding	-	H3BK40	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Asap1-207	ENSMUST00000175963.1	466	98aa	Protein coding	-	H3BJM7	CDS 3' incomplete TSL:2
Asap1-204	ENSMUST00000175710.7	985	No protein	Retained intron	-	-	TSL:1
Asap1-214	ENSMUST00000176909.1	474	No protein	Retained intron	-	-	TSL:3
Asap1-219	ENSMUST00000177475.1	339	No protein	Retained intron	-	-	TSL:3
Asap1-213	ENSMUST00000176821.7	396	No protein	lncRNA	-	-	TSL:5
Asap1-211	ENSMUST00000176427.7	339	No protein	lncRNA	-	-	TSL:5
Asap1-212	ENSMUST00000176516.1	238	No protein	lncRNA	-	-	TSL:3

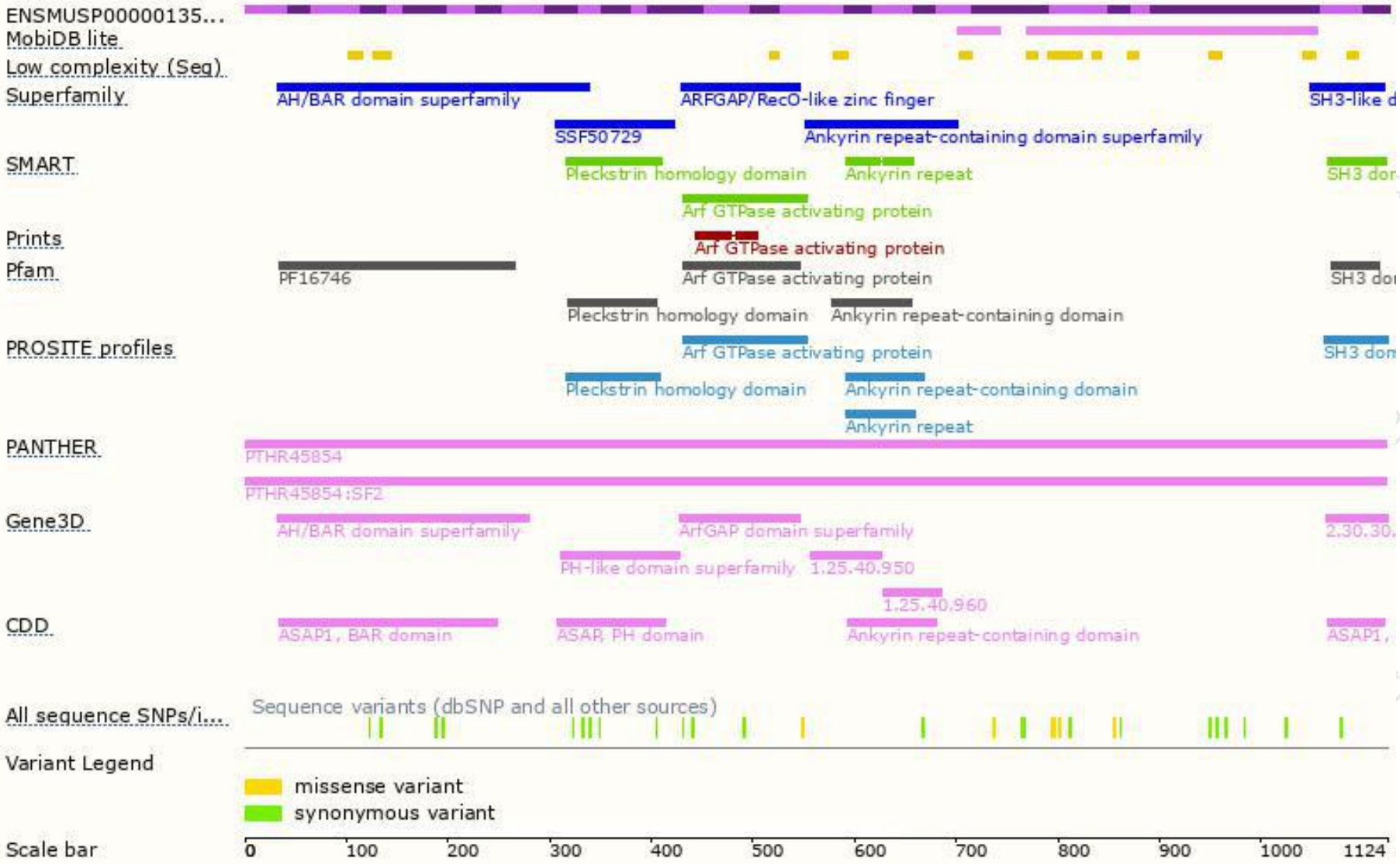
The strategy is based on the design of *Asap1-217* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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