Foxp1 Cas9-KO Strategy

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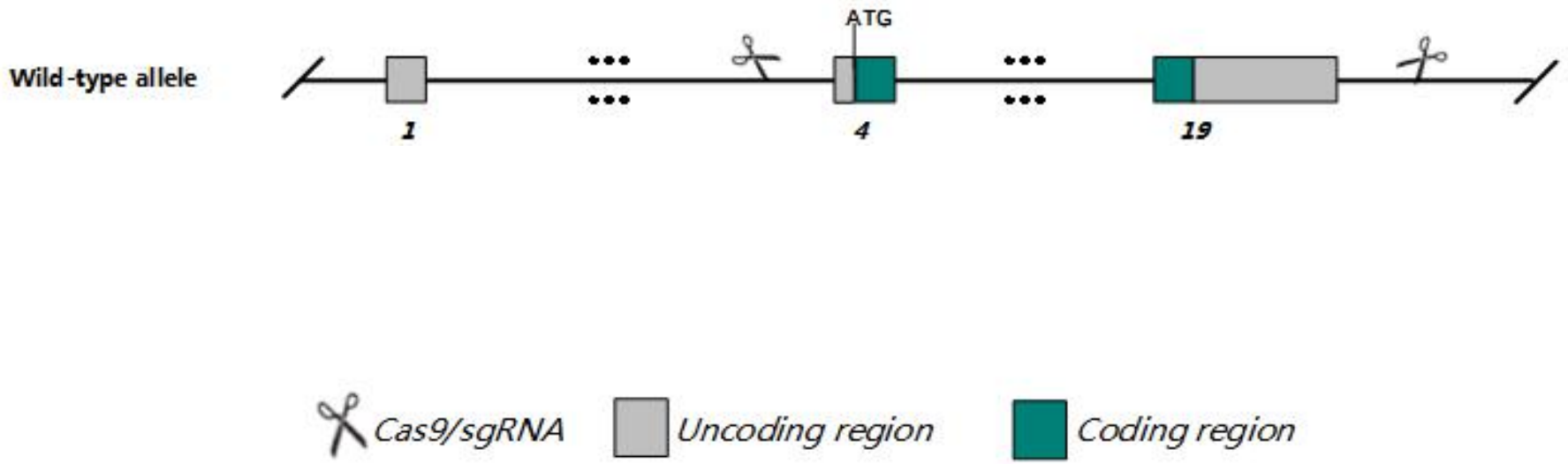
Project Overview

Project Name	***Foxp1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Foxp1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Foxp1* gene has 31 transcripts. According to the structure of *Foxp1* gene, exon4-exon19 of *Foxp1-204* (ENSMUST00000113322.8) 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 *Foxp1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Homozygous null mice display embryonic lethality with abnormal outflow tract septation, ventricular septal defects, abnormal cardiac valve morphology, decreased and irregular heart rate, thin ventricular compact zone, and edema.

- The *Foxp1* gene is located on the Chr6. 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）

集萃药康 GemPharmatech

Foxp1 forkhead box P1 [Mus musculus (house mouse)]

Gene ID: 108655, updated on 2-Apr-2019

Summary

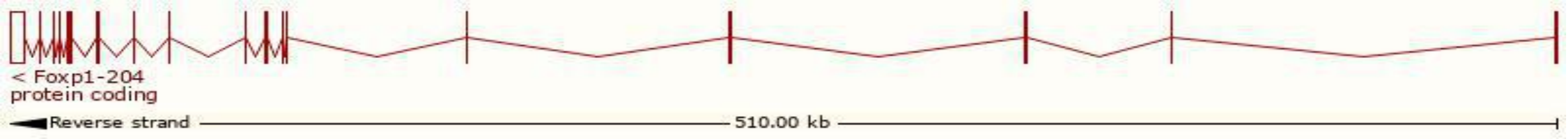
Official Symbol	Foxp1 provided by MGI
Official Full Name	forkhead box P1 provided by MGI
Primary source	MGI:MGI:1914004
See related	Ensembl:ENSMUSG00000030067
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	3110052D19Rik, 4932443N09Rik, AI461938, AW494214
Expression	Ubiquitous expression in spleen adult (RPKM 9.3), lung adult (RPKM 7.6) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

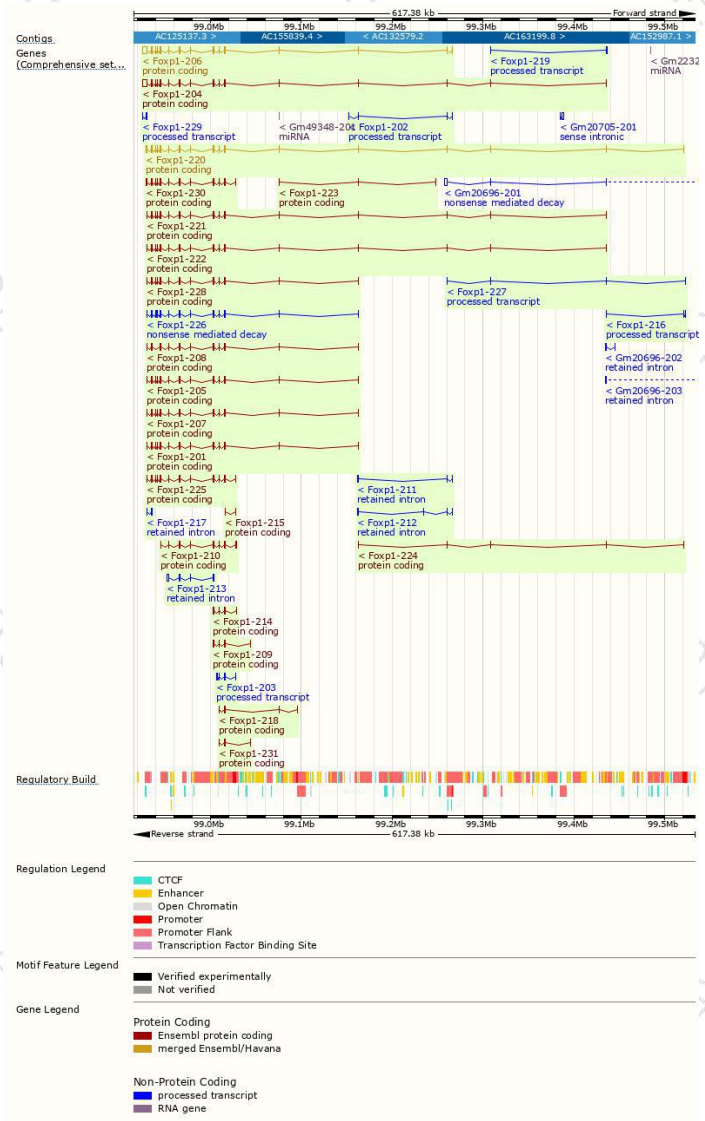
The gene has 31 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Foxp1-204	ENSMUST00000113322.8	7177	705aa	Protein coding	CCDS39578	P58462	TSL:5 GENCODE basic
Foxp1-206	ENSMUST00000113326.8	7029	673aa	Protein coding	CCDS57442	A0A0R4J1H9	TSL:1 GENCODE basic APPRIS P2
Foxp1-220	ENSMUST00000176565.7	3727	705aa	Protein coding	CCDS85105	E2S038	TSL:1 GENCODE basic
Foxp1-230	ENSMUST00000177437.7	2468	576aa	Protein coding	CCDS57441	A0A0R4J282	TSL:1 GENCODE basic
Foxp1-201	ENSMUST00000074346.11	2118	705aa	Protein coding	CCDS39578	P58462	TSL:1 GENCODE basic
Foxp1-222	ENSMUST00000176850.7	2339	675aa	Protein coding	-	H3BJM1	TSL:5 GENCODE basic
Foxp1-221	ENSMUST00000176632.7	2336	674aa	Protein coding	-	H3BL33	TSL:5 GENCODE basic APPRIS ALT1
Foxp1-205	ENSMUST00000113324.8	2121	706aa	Protein coding	-	D3Z6Q4	TSL:5 GENCODE basic
Foxp1-207	ENSMUST00000113328.8	2121	706aa	Protein coding	-	D3Z6Q3	TSL:1 GENCODE basic
Foxp1-228	ENSMUST00000177307.7	2121	706aa	Protein coding	-	H3BLF2	TSL:1 GENCODE basic
Foxp1-208	ENSMUST00000113329.9	1926	641aa	Protein coding	-	P58462	TSL:1 GENCODE basic
Foxp1-225	ENSMUST00000177229.7	1848	577aa	Protein coding	-	H3BJ24	TSL:5 GENCODE basic APPRIS ALT2
Foxp1-210	ENSMUST00000124058.7	1213	348aa	Protein coding	-	D3Z0J5	CDS 3' incomplete TSL:5
Foxp1-224	ENSMUST00000177227.7	967	30aa	Protein coding	-	H3BK30	CDS 3' incomplete TSL:5
Foxp1-214	ENSMUST00000154163.8	853	188aa	Protein coding	-	D3Z2T4	CDS 3' incomplete TSL:5
Foxp1-218	ENSMUST00000175886.7	607	111aa	Protein coding	-	H3BKT4	CDS 3' incomplete TSL:3
Foxp1-209	ENSMUST00000123992.7	525	124aa	Protein coding	-	D3Z454	CDS 3' incomplete TSL:5
Foxp1-231	ENSMUST00000177507.2	456	107aa	Protein coding	-	H3BJ68	CDS 3' incomplete TSL:2
Foxp1-215	ENSMUST00000175670.1	406	32aa	Protein coding	-	H3BK38	CDS 3' incomplete TSL:3
Foxp1-223	ENSMUST00000177208.1	341	86aa	Protein coding	-	H3BJZ5	CDS 3' incomplete TSL:3
Foxp1-226	ENSMUST00000177230.7	2198	564aa	Nonsense mediated decay	-	H3BJR8	TSL:5
Foxp1-203	ENSMUST00000113321.6	1176	No protein	Processed transcript	-	-	TSL:5
Foxp1-202	ENSMUST00000075832.10	791	No protein	Processed transcript	-	-	TSL:1
Foxp1-229	ENSMUST00000177410.1	618	No protein	Processed transcript	-	-	TSL:3
Foxp1-216	ENSMUST00000175838.1	420	No protein	Processed transcript	-	-	TSL:2
Foxp1-227	ENSMUST00000177235.7	392	No protein	Processed transcript	-	-	TSL:5
Foxp1-219	ENSMUST00000176105.1	348	No protein	Processed transcript	-	-	TSL:3
Foxp1-213	ENSMUST00000142164.1	2652	No protein	Retained intron	-	-	TSL:1
Foxp1-212	ENSMUST00000138754.8	1464	No protein	Retained intron	-	-	TSL:1
Foxp1-211	ENSMUST00000131967.7	1351	No protein	Retained intron	-	-	TSL:1
Foxp1-217	ENSMUST00000175880.1	336	No protein	Retained intron	-	-	TSL:2

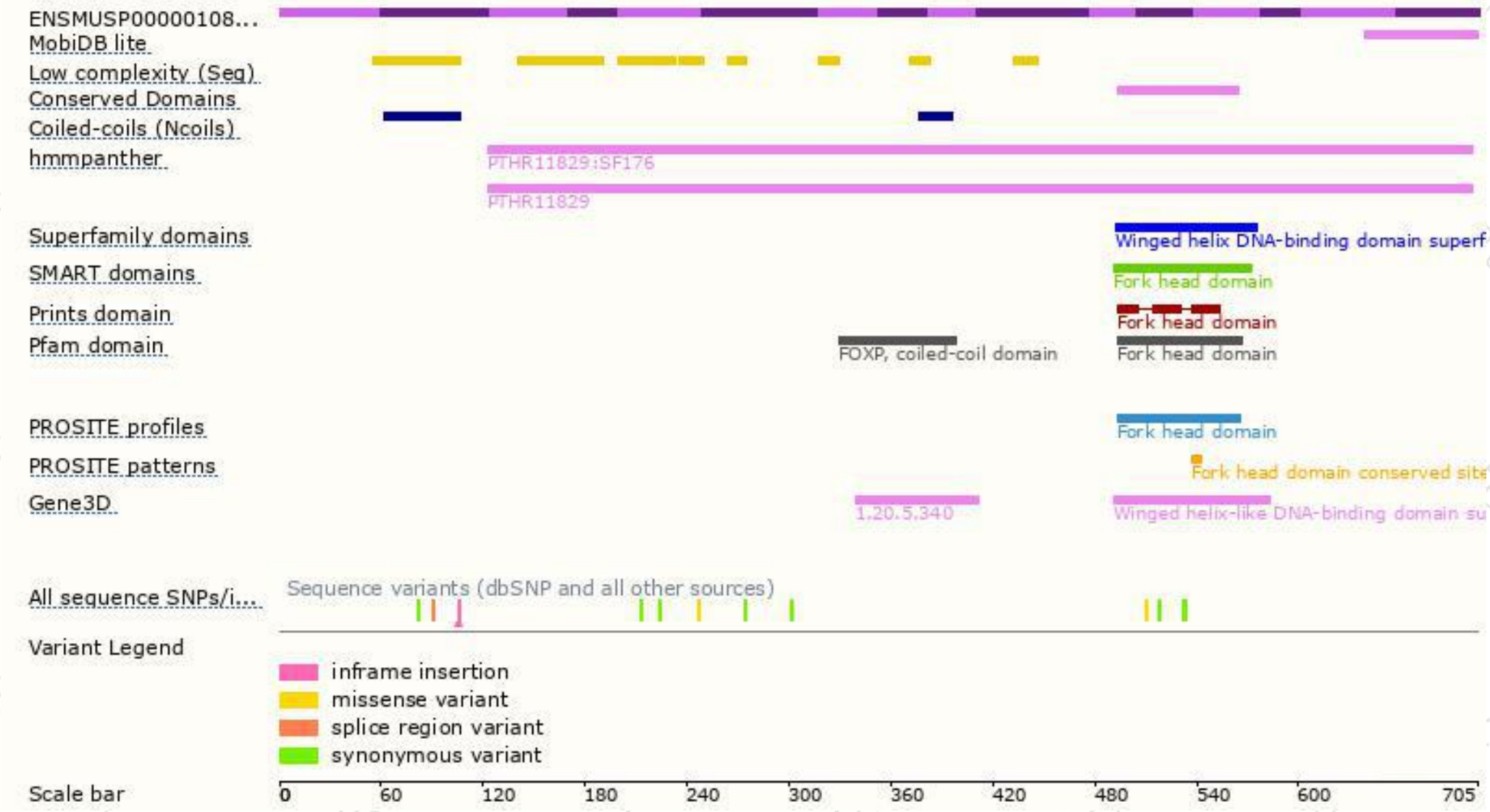
The strategy is based on the design of *Foxp1-204* transcript,The transcription is shown below



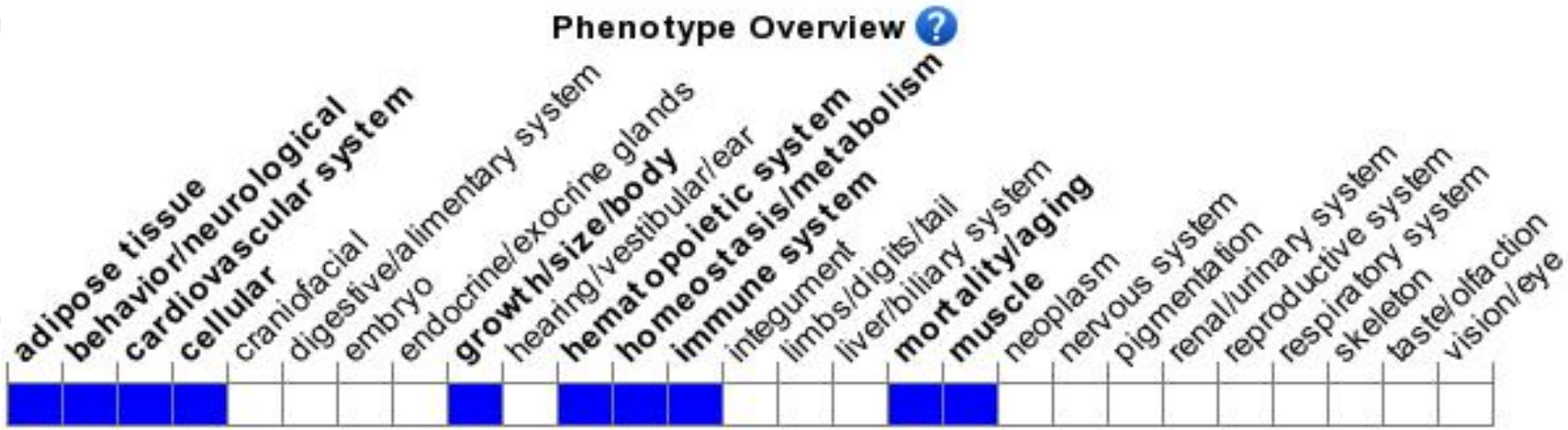
Genomic location distribution



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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