

Smarca2 Cas9-KO Strategy

Designer:

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Project Overview

Project Name

Smarca2

Project type

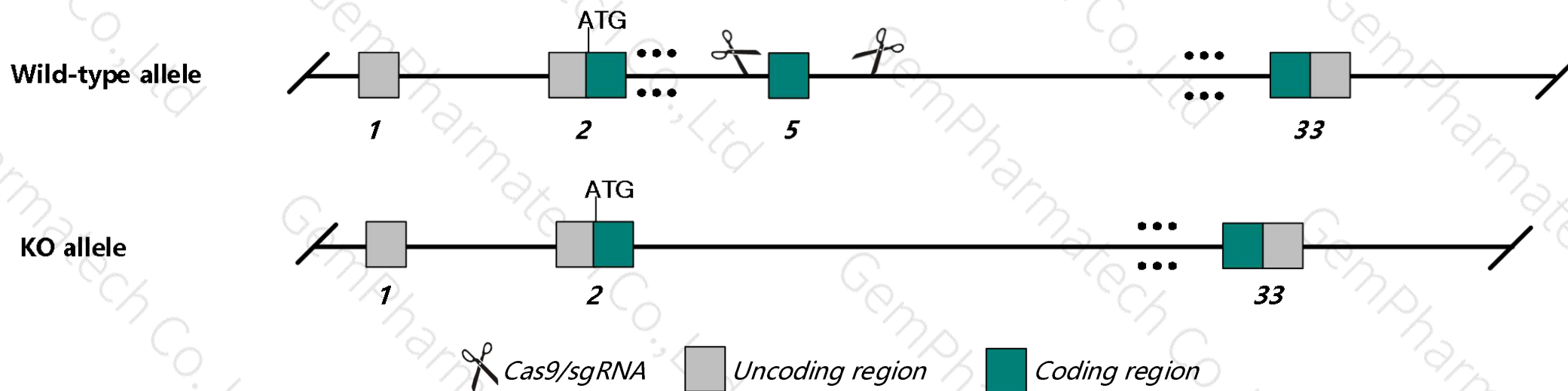
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Smarca2* gene. The schematic diagram is as follows:



- The *Smarca2* gene has 46 transcripts. According to the structure of *Smarca2* gene, exon5 of *Smarca2*-201 transcript is recommended as the knockout region. The region contains 262bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Smarca2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- Transcript *Smarca2*-203,*Smarca2*-242,*Smarca2*-246,*Smarca2*-238,*Smarca2*-210,*Smarca2*-220,*Smarca2*-231,*Smarca2*-213,*Smarca2*-204,*Smarca2*-230,*Smarca2*-221,*Smarca2*-239,*Smarca2*-205,*Smarca2*-227,*Smarca2*-240,*Smarca2*-233,*Smarca2*-228,*Smarca2*-218,*Smarca2*-207,*Smarca2*-235,*Smarca2*-212,*Smarca2*-243,*Smarca2*-241,*Smarca2*-232 may not be affected.
- The *Smarca2* gene is located on the Chr19. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)

Smarca2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 [*Mus musculus* (house mouse)]

Gene ID: 67155, updated on 12-May-2019

Summary

Official Symbol	Smarca2 provided by MGI
Official Full Name	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 provided by MGI
Primary source	MGI:MGI-99603
See related	Ensembl:ENSMUSG00000024921
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	brm; Snf2l2; brahma; SNF2alpha; 2610209L14Rik
Expression	Ubiquitous expression in testis adult (RPKM 20.4), lung adult (RPKM 19.1) and 27 other tissues See more
Orthologs	human all

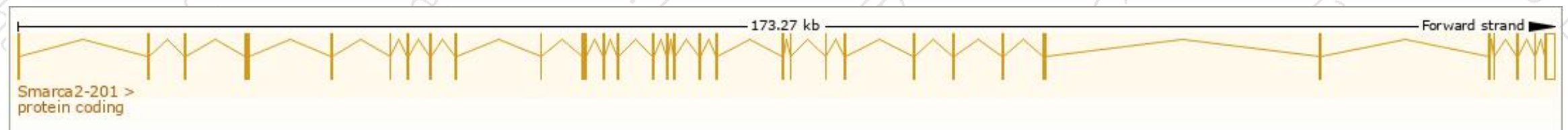
Transcript information (Ensembl)

The gene has 46 transcripts, and all transcripts are shown below :

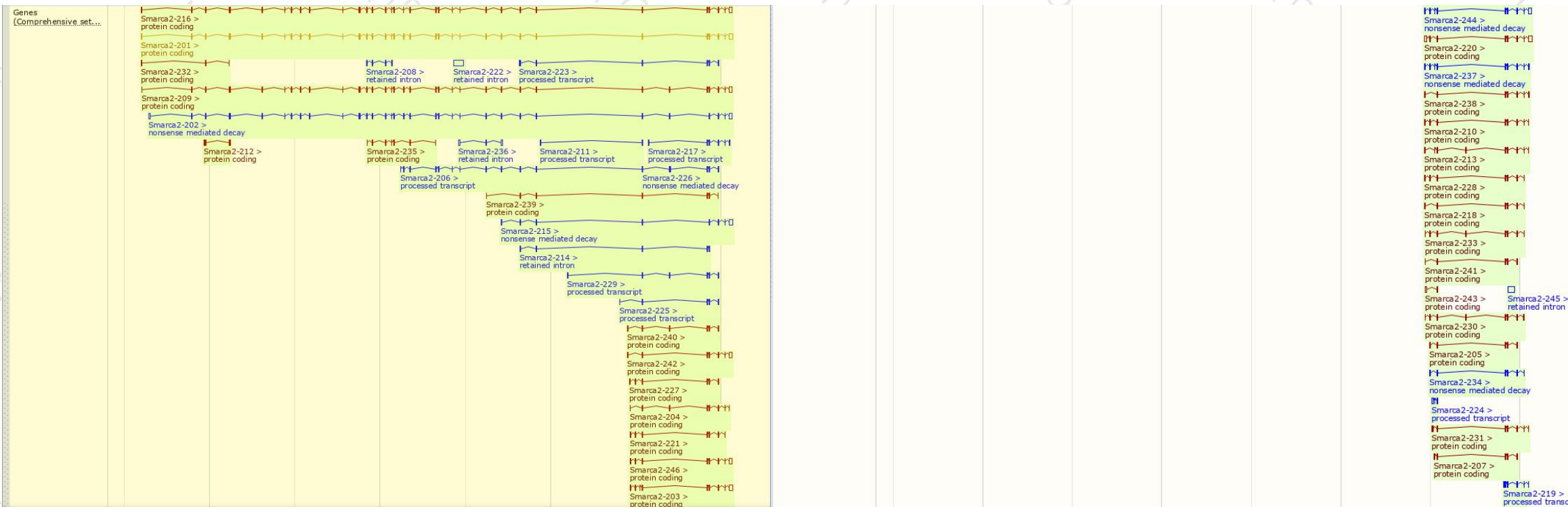
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Smarca2-201	ENSMUST0000025862.14	5921	1583aa	Protein coding	CCDS29720	F2Z4A9	TSL:5 GENCODE basic APPRIS P2
Smarca2-203	ENSMUST00000112637.9	1962	236aa	Protein coding	CCDS37945	Q9D007	TSL:1 GENCODE basic
Smarca2-242	ENSMUST00000208751.1	1846	236aa	Protein coding	CCDS37945	Q9D007	TSL:5 GENCODE basic
Smarca2-246	ENSMUST00000209085.1	1841	276aa	Protein coding	CCDS84428	H3BK47	TSL:5 GENCODE basic
Smarca2-238	ENSMUST00000208589.1	1054	236aa	Protein coding	CCDS37945	Q9D007	TSL:5 GENCODE basic
Smarca2-210	ENSMUST00000176475.8	983	276aa	Protein coding	CCDS84428	H3BK47	TSL:5 GENCODE basic
Smarca2-209	ENSMUST00000176030.7	5862	1601aa	Protein coding	-	H3BLH0	TSL:5 GENCODE basic APPRIS ALT2
Smarca2-216	ENSMUST00000176769.8	5703	1525aa	Protein coding	-	H3BJK2	TSL:5 GENCODE basic
Smarca2-220	ENSMUST00000207054.1	2333	278aa	Protein coding	-	A0A140LHP6	TSL:5 GENCODE basic
Smarca2-231	ENSMUST00000208091.1	1140	260aa	Protein coding	-	A0A140LIM0	TSL:5 GENCODE basic
Smarca2-213	ENSMUST00000176698.8	955	254aa	Protein coding	-	H3BKJ3	TSL:5 GENCODE basic
Smarca2-204	ENSMUST00000175791.8	946	254aa	Protein coding	-	H3BKJ3	TSL:3 GENCODE basic
Smarca2-230	ENSMUST00000208027.1	898	296aa	Protein coding	-	A0A140LHF4	CDS 3' incomplete TSL:5
Smarca2-221	ENSMUST00000207118.1	834	228aa	Protein coding	-	A0A140LHE2	CDS 3' incomplete TSL:3
Smarca2-239	ENSMUST00000208674.1	800	267aa	Protein coding	-	A0A140LID0	CDS 5' and 3' incomplete TSL:5
Smarca2-205	ENSMUST00000175842.3	779	211aa	Protein coding	-	H3BLI4	CDS 3' incomplete TSL:2
Smarca2-227	ENSMUST00000207812.1	756	200aa	Protein coding	-	A0A140LHZ8	CDS 3' incomplete TSL:5
Smarca2-240	ENSMUST00000208705.1	745	170aa	Protein coding	-	A0A140LIV3	CDS 3' incomplete TSL:5
Smarca2-233	ENSMUST00000208185.1	740	244aa	Protein coding	-	A0A140LI14	CDS 3' incomplete TSL:5
Smarca2-228	ENSMUST00000207832.1	712	229aa	Protein coding	-	A0A140LIQ9	CDS 3' incomplete TSL:5
Smarca2-218	ENSMUST00000177252.8	709	201aa	Protein coding	-	H3BJI1	CDS 3' incomplete TSL:5
Smarca2-207	ENSMUST00000175953.2	692	149aa	Protein coding	-	H3BJM2	CDS 3' incomplete TSL:3
Smarca2-235	ENSMUST00000208303.1	683	228aa	Protein coding	-	A0A140LJD7	CDS 5' and 3' incomplete TSL:5
Smarca2-212	ENSMUST00000176584.1	645	173aa	Protein coding	-	H3BKD2	CDS 3' incomplete TSL:3
Smarca2-243	ENSMUST00000208806.1	640	68aa	Protein coding	-	A0A140LHJ8	CDS 3' incomplete TSL:5
Smarca2-241	ENSMUST00000208712.1	630	169aa	Protein coding	-	A0A140LJK1	CDS 3' incomplete TSL:5

Smarca2-232	ENSMUST00000208163.1	421	78aa	Protein coding	-	A0A140LIK7	CDS 3' incomplete TSL:5
Smarca2-202	ENSMUST00000099537.8	5913	1510aa	Nonsense mediated decay	-	E9QAB8	TSL:1
Smarca2-215	ENSMUST00000176731.2	2018	299aa	Nonsense mediated decay	-	H3BKN5	CDS 5' incomplete TSL:5
Smarca2-244	ENSMUST00000208915.1	1914	72aa	Nonsense mediated decay	-	A0A140LI08	TSL:1
Smarca2-237	ENSMUST00000208541.1	1122	72aa	Nonsense mediated decay	-	A0A140LI08	TSL:5
Smarca2-234	ENSMUST00000208226.1	757	45aa	Nonsense mediated decay	-	A0A140LI12	TSL:5
Smarca2-226	ENSMUST00000207535.1	503	93aa	Nonsense mediated decay	-	A0A140LHL7	CDS 5' incomplete TSL:5
Smarca2-206	ENSMUST00000175935.7	1584	No protein	Processed transcript	-	-	TSL:1
Smarca2-217	ENSMUST00000177116.7	968	No protein	Processed transcript	-	-	TSL:3
Smarca2-223	ENSMUST00000207226.1	876	No protein	Processed transcript	-	-	TSL:5
Smarca2-219	ENSMUST00000177484.2	736	No protein	Processed transcript	-	-	TSL:3
Smarca2-229	ENSMUST00000207944.1	681	No protein	Processed transcript	-	-	TSL:5
Smarca2-224	ENSMUST00000207380.1	613	No protein	Processed transcript	-	-	TSL:5
Smarca2-225	ENSMUST00000207418.1	576	No protein	Processed transcript	-	-	TSL:3
Smarca2-211	ENSMUST00000176494.1	426	No protein	Processed transcript	-	-	TSL:3
Smarca2-222	ENSMUST00000207175.1	2838	No protein	Retained intron	-	-	TSL:NA
Smarca2-245	ENSMUST00000208984.1	1924	No protein	Retained intron	-	-	TSL:NA
Smarca2-236	ENSMUST00000208378.1	1133	No protein	Retained intron	-	-	TSL:5
Smarca2-214	ENSMUST00000176700.7	867	No protein	Retained intron	-	-	TSL:3
Smarca2-208	ENSMUST00000176019.1	661	No protein	Retained intron	-	-	TSL:3

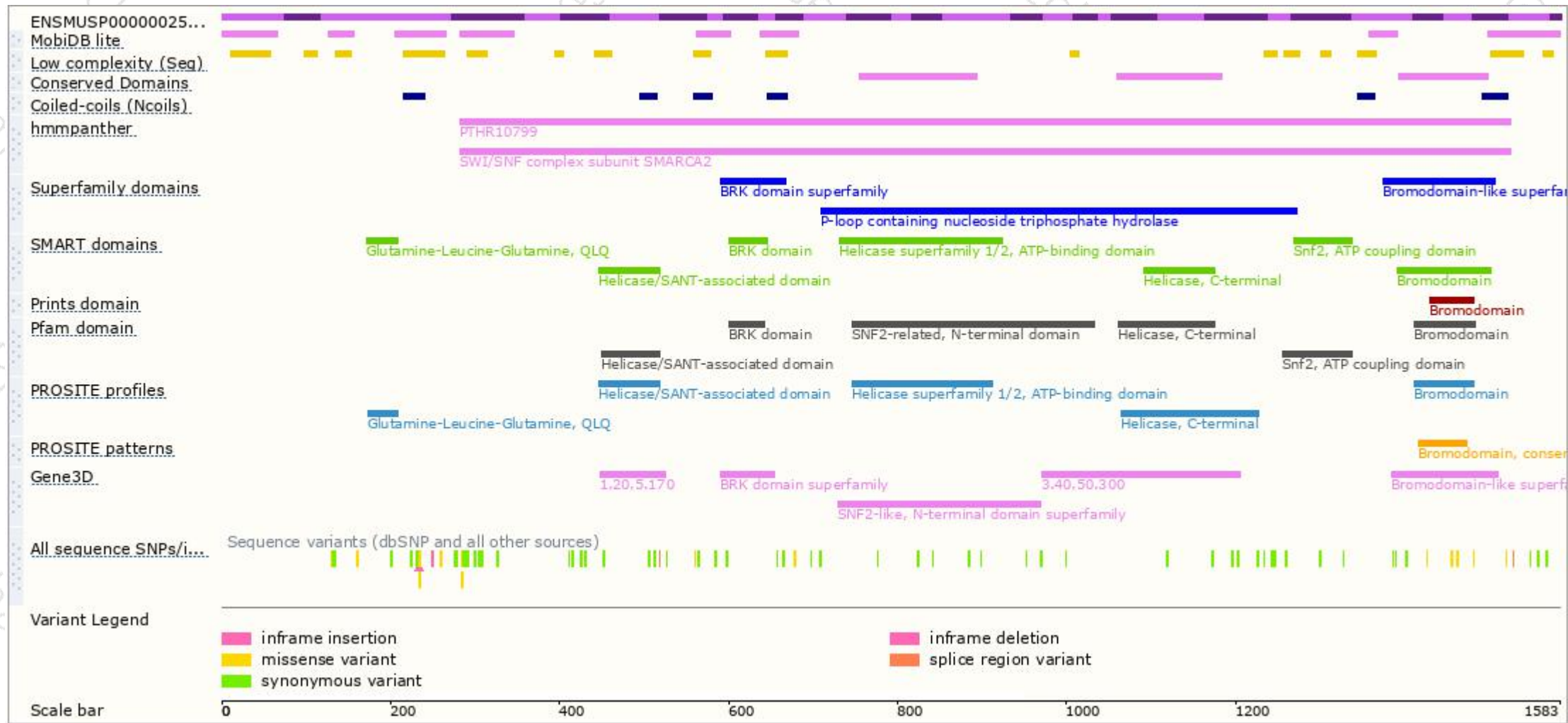
The strategy is based on the design of *Smarca2-201* transcript, The transcription is shown below



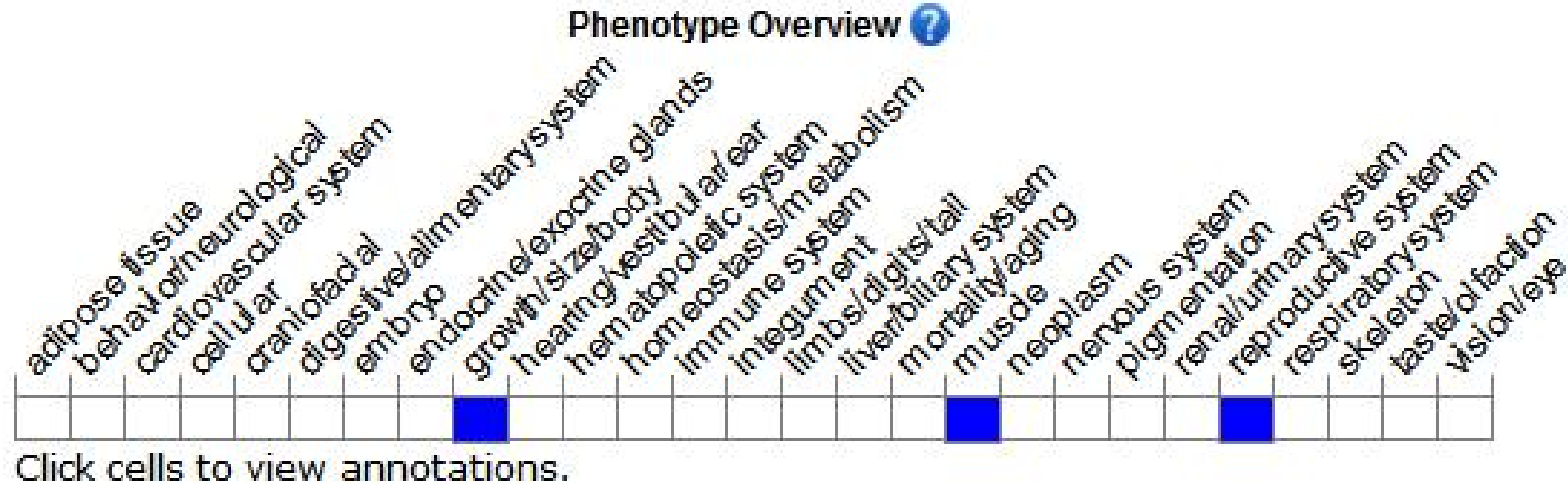
Genomic location (Ensembl)



Protein domain (Ensembl)



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 targeted mutation in this gene may exhibit infertility and a slightly increased body weight in some genetic backgrounds.

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

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