Sstr2 Cas9-CKO *Strategy*

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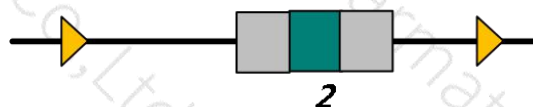|	
Project Name	*Sstr2*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

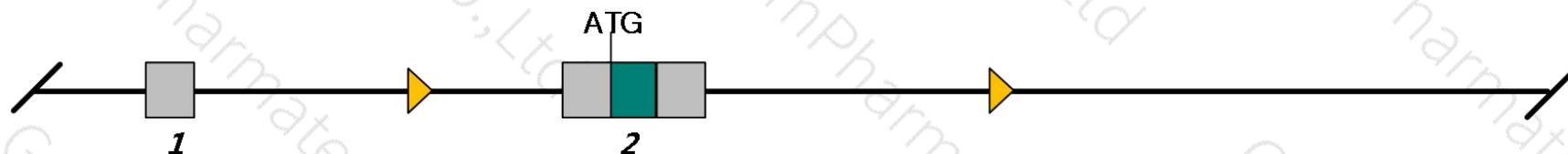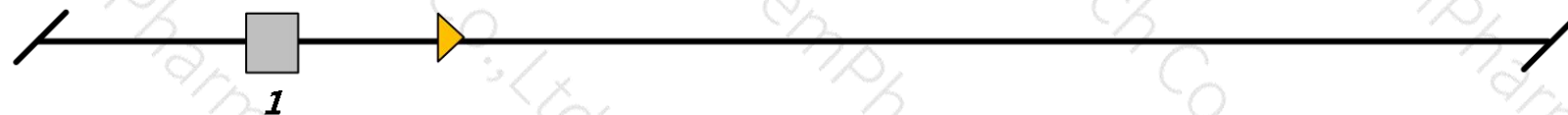This model will use CRISPR/Cas9 technology to edit the *Sstr2* gene. The schematic diagram is as follows:

Technical routes

➤ The *Sstr2* gene has 3 transcript.According to the structure of *Sstr2* gene, exon2 of *Sstr2*-203 transcript is recommended as the knockout region.The region contains all coding sequence.Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Sstr2* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed.Cas9, gRNA 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 or cell types.

Notice

➢ According to the existing MGI data，homozygotes for a null allele show elevated anxiety and locomotor and exploratory deficits. Homozygotes for a reporter allele show altered motor coordination, somatostatin-induced dopamine and glutamate release, retinal rod bipolar cells and EEG patterns, and reduced infarction after focal ischemia.

➢ The KO region is in the intron of *Slc39a11* gene.Knockout the region may affect the function of *Slc39a11* gene.

➢ The *Sstr2* gene is located on the Chr11. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

Sstr2 somatostatin receptor 2 [*Mus musculus* (house mouse)]

Gene ID: 20606, updated on 8-Dec-2018

Summary

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Official Symbol	Sstr2 provided by MGI
Official Full Name	somatostatin receptor 2 provided by MGI
Primary source	MGI:MGI:98328
See related	Ensembl:ENSMUSG00000047904
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	SS2R; sst2; SRIF-1; SSTR-2; Smstr2; Smstr-2
Summary	The protein encoded by this gene is a receptor for somatostatin, which acts at many sites to inhibit the release of several hormones and other secretory proteins. The encoded protein is a member of the superfamily of receptors having seven transmembrane segments and is involved in many processes, including adenylyl cyclase inhibition, phosphotyrosine phosphatase stimulation, and inhibition of calcium entry and cell growth. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Sep 2015]
Expression	Biased expression in whole brain E14.5 (RPKM 13.8), CNS E14 (RPKM 13.2) and 13 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 3 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
Sstr2-203	ENSMUST00000146390.2	2143	369aa	Protein coding	CCDS59571	P30875	NM_001042606 NP_001036071	TSL:5 GENCODE basic APPRIS P1
Sstr2-202	ENSMUST00000106630.1	1537	346aa	Protein coding	CCDS25598	P30875	NM_009217 NP_033243	TSL:1 GENCODE basic
Sstr2-201	ENSMUST00000067591.2	1041	346aa	Protein coding	CCDS25598	P30875	-	TSL:2 GENCODE basic

The strategy is based on the design of *Sstr2*-203 transcript,The transcription is shown below

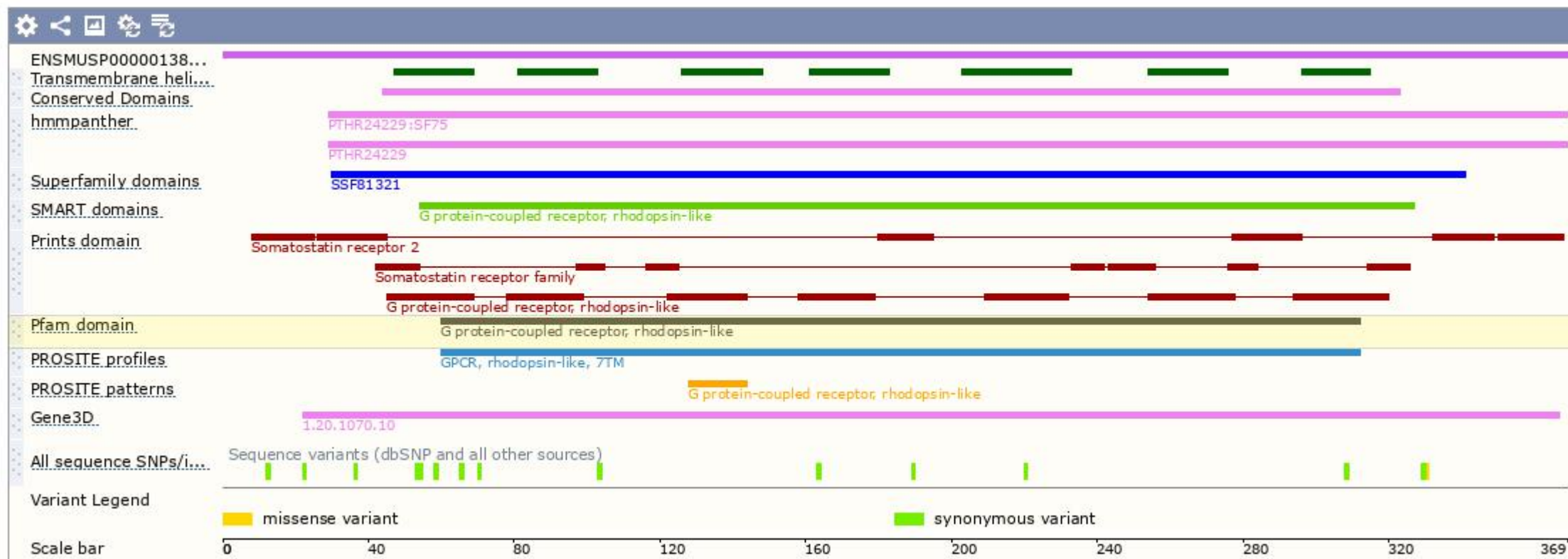

Sstr2-203 >
protein coding
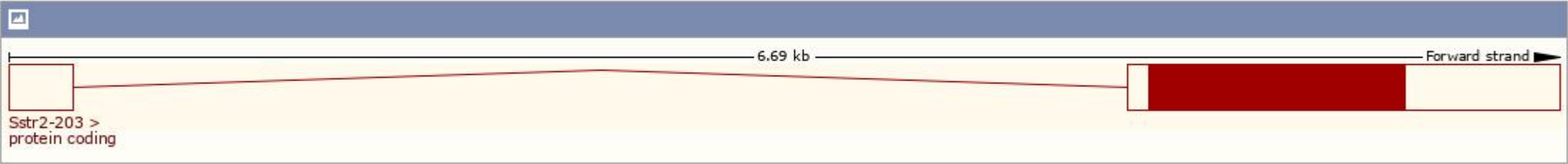
Genomic location distribution
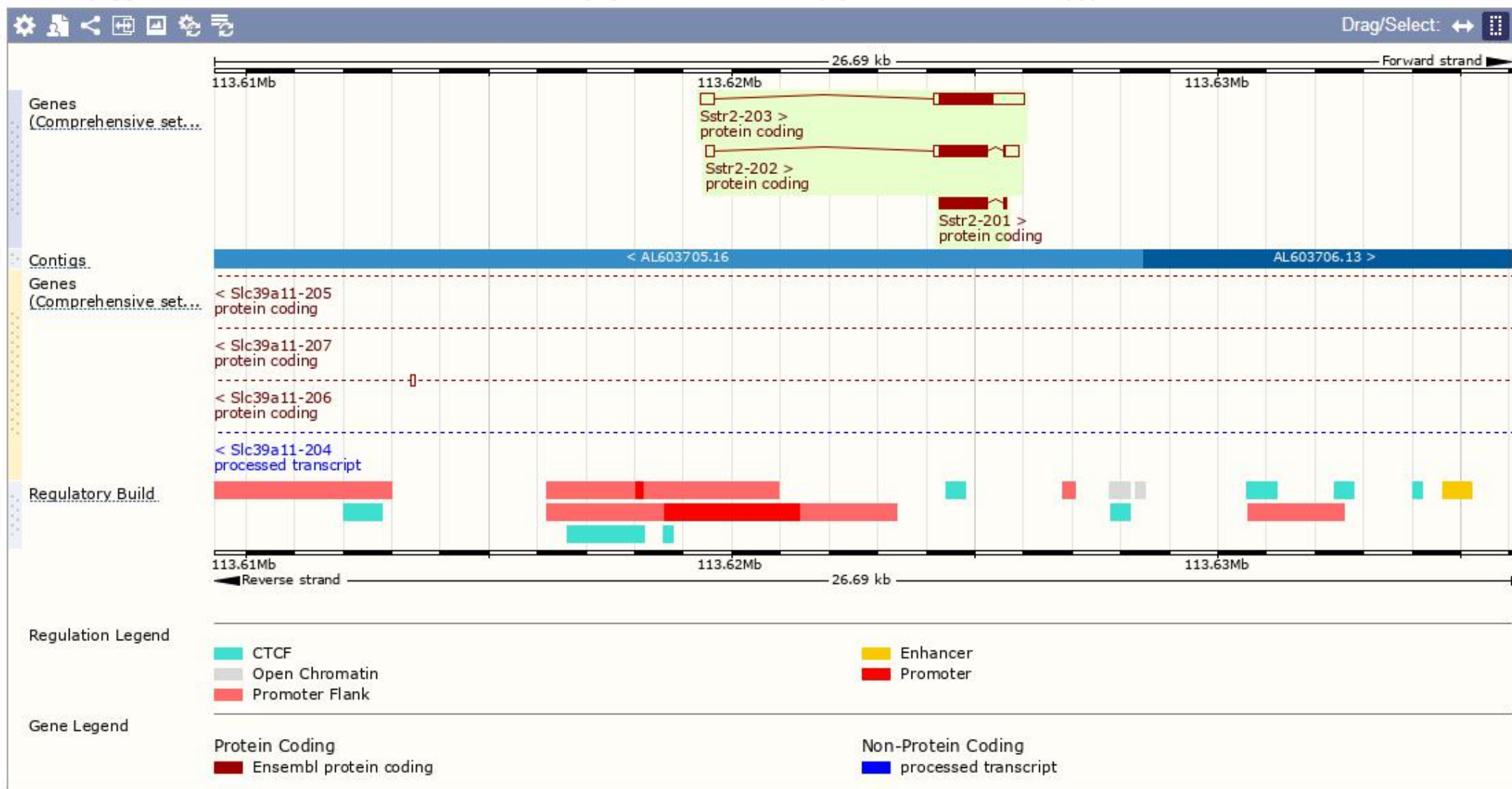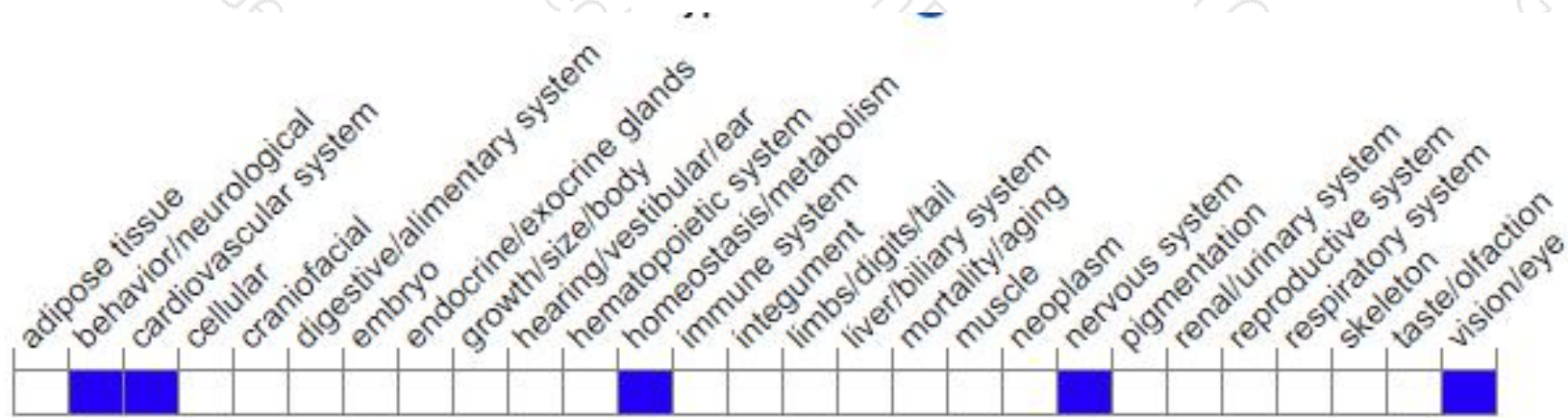
Protein domain

Mouse phenotype description(MGI)

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

Homozygotes for a null allele show elevated anxiety and locomotor and exploratory deficits. Homozygotes for a reporter allele show altered motor coordination, somatostatin-induced dopamine and glutamate release, retinal rod bipolar cells and EEG patterns, and reduced infarction after focal ischemia.

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