Sost-CreERT2 Cas9-KI Strategy

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Design Date:

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Project Overview





Knockin strategy



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





- The Sost gene has 1 transcript. According to the structure of Sost gene, Sost-201(ENSMUST00000001534.7) is selected for presentation of the recommended strategy.
- Sost-201 gene has 2 exons, with the ATG start codon in exon1 and TAG stop codon in exon2. The sequence of CreERT2-P2A will insert near to the start codon(ATG) of Sost gene.
- In this project we use CRISPR/Cas9 technology to modify *Sost* 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.

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- According to the existing MGI data, in mild form, mice homozygous for a null allele exhibit an increase in trabecular and cortical bone volume, mineral density, and formation.
- The P2A-linked gene drives expression in the same promoter and is cleaved at the translational level. The gene expression levels are consistent, and the before of P2A expressing gene carries the P2A-translated polypeptide.
- ▶ Insertion of CreERT2-P2A may affect the regulation of the 5' end of the *Sost* gene.
- There may be 1 to 2 amino acid synonymous mutation in exon1 of *Sost* gene in this strategy.
- There may be base mutations in the modeling process because of the repetitive sequences(PolyC&PolyG) upstream and downstream of the insertion site.
- > The insertion site is near to the N-terminal of *Gm20659* gene, the strategy may influence the functionN-terminal of *Gm20659* gene.
- The Sost gene is located on the Chr11. If the knockin 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.

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Notice

Gene information (NCBI)



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Sost sclerostin [Mus musculus (house mouse)] L Download Datasets Gene ID: 74499, updated on 1-Oct-2021 Summary Official Symbol Sost provided by MGI Official Full Name sclerostin provided by MGI Primary source MGI:MGI:1921749 See related Ensembl:ENSMUSG0000001494 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 5430411E23Rik Expression Biased expression in genital fat pad adult (RPKM 4.4), testis adult (RPKM 2.5) and 7 other tissues See more Orthologs human all Try the new Gene table NEW Try the new Transcript table

Genomic context					≈ ?
.ocation: 11; 11 D				See Sost in Genome I)ata Viewer
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Annotation release	Status	Assembly	Chr	Location	
109	current	GRCm39 (GCF_000001635.27)	11	NC_000077.7 (101853284101857841, complement)	
108.20200622	previous assembly	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (101962458101967015, complement)	
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (101823772101828329, complement)	
\leq	31			12. V	"Ge
		Chromosome 11 - NC 00	0077.7		
	[101830285	•		[101883090]>	
	Rp127-p	s2 4930417022Rik Dusp3 - Dusp3 -	Cfap97o	a S	

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Transcript information (Ensembl)



The gene has 1 transcript, and the transcript is shown below :

Name 🖕	Transcript ID 🍦	bp 🍦	Protein 🖕	Biotype 🍦	CCDS 🍦	UniProt Match 🖕	Flags 🍦			
Sost-201	ENSMUST0000001534.7	2066	<u>211aa</u>	Protein coding	<u>CCDS25481</u> &	<u>Q99P68</u> &	GENCODE basic	APPRIS P1	TSL:1	

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





Genomic location distribution



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Protein domain



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ENSMUSP00000001 Low complexity (Seg) All sequence SNPs/i	Sequence	variants (dbSNP a	nd all other sources)					-		
Variant Legend	missense variant					synonymous variant				
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Mouse phenotype description(MGI)



Phenotype Overview 🕜 endocrine/exocrine glands cardiovascular system heating/vestibularleat hematopoietic system nomeostasisimetabolis digestive/alimentarys behaviorneurologic respiratory system innune system iverbilary syste adiposetissue . limbs/digits/tail motality/aging tastelofaction reproductive pignentation renallurinary nervoussyst integument visionleye neoplasm

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/marker/MGI:1921749).

Mice homozygous for a null allele exhibit an increase in trabecular and cortical bone volume, mineral density, and formation.

Click cells to view annotations.

If you have any questions, you are welcome to inquire. Tel: 400-966 0890



