

## **SHH signaling directed by two oral epithelium-specific enhancers controls tooth and oral development**

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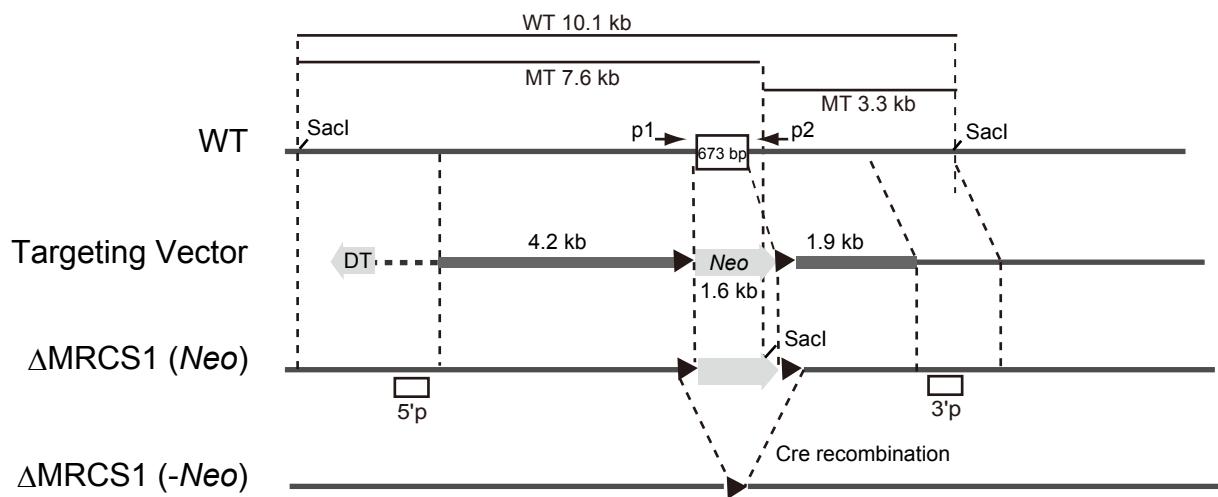
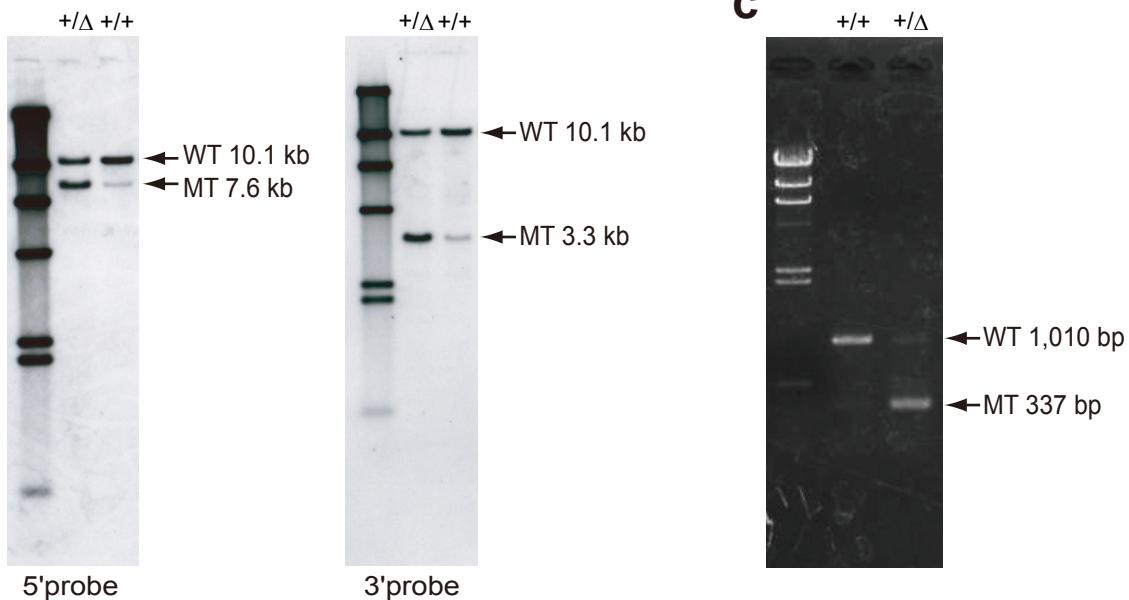
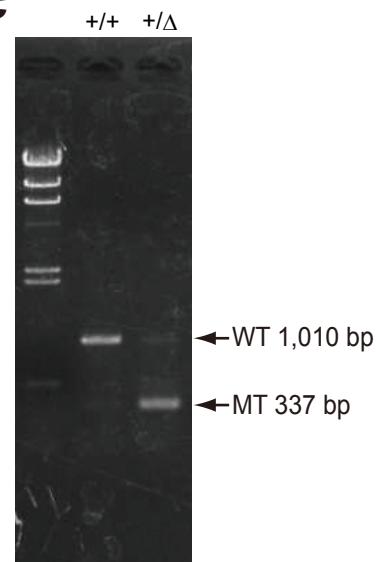
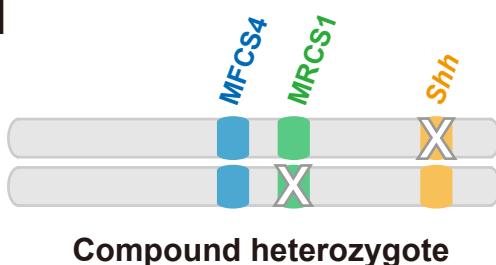
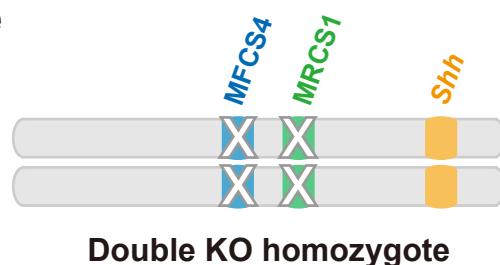
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#These two authors contributed equally to this study.

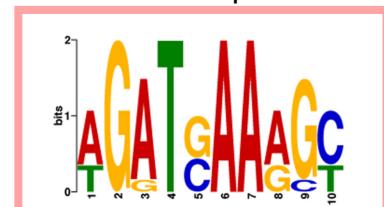
\*Author for correspondence: Toshihiko Shiroishi

**a****b****c****d****e**

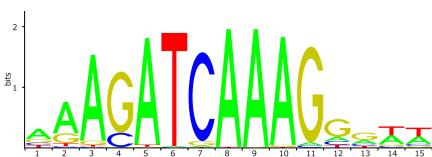
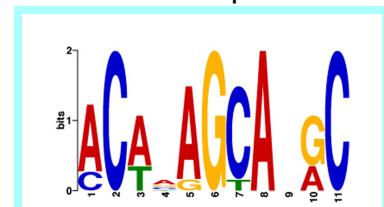
**Supplementary Fig. 1. Generation of mutant mice in this study.** (a) Schematic diagram of the ES cell targeting of MRCS1. (b) Southern blot analysis was carried out for Sacl-digested genomic DNAs. The 5' probe (5' p in (a)) detected fragments of 10.1 kb in the wild type allele (WT) and 7.6 kb in the mutant allele (MT). The 3' probe (3' p in (a)) detected fragments of 10.1 kb in WT and 3.3 kb in MT. (c) PCR amplification of the WT allele (1,010 bp) and the MT allele (337 bp) with primer pairs p1-p2. The left lanes are  $\lambda$ /HindIII marker. Schematic diagram of the mouse chromosome 5 illustrating composition of mutant alleles in the compound heterozygote of the MRCS1 KO and the Shh coding sequence KO alleles (d), and the homozygote of the double KO mouse of MRCS1 and MFCS4 (e).

**a**

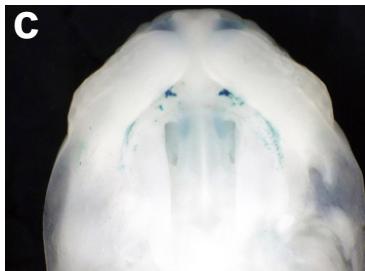
shared sequence 1



shared sequence 2



LEF1

**b****d**

KB021656:129180776-129180914 (xenTro7)

CATGGGATTCTTCGTGGGC TGATGAAAGT CATTCTTGTTGCCG  
 motif1

TGTCA AACAAAGCA TGCTTATTGTCACATTGTGGTTGTATCTT  
 motif2

TTTAGAAGCTTC GCTTTGATCT CGATCAAGATCCAGCGAGTAA  
 motif3

**Supplementary Fig. 2. Sequences shared between MRCS1 and MFCS4.** (a) Shared short sequences in MRCS1 and MFCS4 of mouse and opossum were identified by MEME (red and blue boxes). Position weight matrix of the two shared sequences and LEF1 binding sites are shown. (b) The *LacZ* reporter transgene construct with three tandem repeats. (c) The maxillary occlusal view of the E13.5 mouse embryo. The *LacZ* expression driven by the three tandem copies of the core sequence of mouse MRCS1 was observed in the incisor and molar rudiments but not in the palatal rugae. (d) The three shared motifs in the core sequence of *Xenopus* MFCS4.

**Supplementary Table1 Incidence of the supernumerary tooth**

Genotype	Mice with Maxillary sn		Mice with Mandibular sn		Incidence
	Right	Left	Right	Left	
wild type	0	0	0	0	0/20 (0%)
$\Delta$ MRCS1/+	0	0	0	0	0/12 (0%)
<i>ShhKO</i> /+	0	0	0	0	0/12 (0%)
$\Delta$ MRCS1/ $\Delta$ MRCS1	0	1	1	1	1/21 (4.7%)
$\Delta$ MRCS1/ <i>ShhKO</i>	8	6	10	12	15/19 (78.9%)
$\Delta$ MFCS4/ $\Delta$ MFCS4	0	0	0	0	0/15 (0%)
DKO/DKO	4	3	6	5	8/12 (66.7%)

sn, supernumerary tooth. Incidence is indicated as affected mice/observed mice.

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$\Delta$ MRCS1/ $\Delta$ MRCS1	0	1	1	1	1/21 (4.7%)
$\Delta$ MRCS1/ <i>Shh</i> KO	8	6	10	12	15/19 (78.9%)
$\Delta$ MFCS4/ $\Delta$ MFCS4	0	0	0	0	0/15 (0%)
DKO/DKO	4	3	6	5	8/12 (66.7%)

sn, supernumerary tooth. Incidence is indicated as affected mice/observed mice.

**Supplementary Table 2 Primers and oligonucleotides used in this study**

<b>For ESC targeting</b>		
Long arm	F	AGGAACCTTCAGTCTCACTGGG
	R	AATCTCGAGCTTGTGGGTTGTCTCCTTG
Short arm	F	TAAGGATCCCAGAGAGTGAUTGCCAAATG
	R	TTACCCGGGTATGCTCTTGAGCCTAGG
<b>Probes for Southern blotting</b>		
5' probe	F	TGCCTTATTAGATCTTGATC
	R	CTATGCTCTCCTGCACTGTT
3' probe	F	AGGCCAGAGCCCAGAACCTA
	R	GATGAGGTCAAGAGGATGACT
<b>For genotyping</b>		
P1	F	CATTGCCACAGAGCAGAAGT
P2	R	TGTGCACCTCTATGTGTGCC
<b>For cloning enhancers</b>		
Mouse whole MRCS1	F	AGGAGACAAACCCACAAGAG
	R	CATTGGCAGTCACTCTCTG
Mouse core MRCS1	F	AAGGCTTCACCTGCTTTGC
	R	CCTTTAACCGGTCTGAG
<i>Xenopus</i> whole MFCS4	F	TGTGTATCAGGAAGCAGAGC
	R	AAGACAGAACATGGGCATGG
<i>Xenopus</i> core MFCS4	F	CCTGCAGACAACACAATTAG
	R	GTGACAATATACTCCCTGG
Mouse whole MFCS4	F	AGCAGGTTAACCGCAGTTC
	R	TCCATCCCAGCTTCTAATGC
Mouse core MFCS4	F	TAATCAGGCTGATGAAAGTC
	R	TTTAGATCAAAGCGAAAAC
<b>For deletion constructs</b>		
del1	F	CTGCCAACAAACAAAGCTT
	R	CATTGGCAGTCACTCTCTG
del2	F	AGGAGACAAACCCACAAGAG

	R	CCTCTGGTTTCCTTGCT
del3	F	AGGAGACAAACCCACAAGAG
	R	AAGGCTTCACCTGCTTTGC
del4	F	AGGAGACAAACCCACAAGAG
	R	CTCAGGACCGGTATTAAAGG
Δmo1 (inverse PCR)	F	CTTGAGACAAAGCAGGCT
	R	CCGGGCAAAAGCAGGTGAAG
Δmo2 (inverse PCR)	F	GGCTGGGTTGGGCCTTGATC
	R	TGCAAAGATGAAAGCCGGC
Δmo3 (inverse PCR)	F	AGGGCGTGCTCAGGACCGGT
	R	GCCCAACCCAGCCTGCTTG
mut mo1 (inverse PCR)	F	TGCATCTTGCAGACAAAGCAGGCTGGTTG
	R	CGCCGGGCAAAAGCAGGTGAAGCCTTTTG
<b>Oligonucleotides for EMSA</b>		
MRCS1-motif1-WT	S	CCTGCTTTGCCCGGCTTCATCTTGAGACAAAGC
	A	GCCTGCTTGTCTGAAAGATGAAAGCCGGGCAAAAG
MRCS1-motif1-mut	S	CCTGCTTTGCCGGCgTgCATCTTGAGACAAAGC
	A	GCCTGCTTGTCTGAAAGATGcAcGCCGGGCAAAAG
MFCS4-motif1-WT	S	ATTCTTAATCAGGCTGATGAAAGTCATTATTGTTG
	A	ACAGCAAACAATAAATGACTTCATCAGCCTGATTAA
MFCS4-motif1-mut	S	ATTCTTAATCAGGCTGATGcAcGTCATTATTGTTG
	A	ACAGCAAACAATAAATGACgTgCATCAGCCTGATTAA

\* F, forward primer; R, reverse primer; S, sense oligonucleotide; A, antisense oligonucleotide.