A predominant enhancer co-amplified with the *SOX2* oncogene is necessary and sufficient for its expression in squamous cancer

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Supplementary Information

The Supplementary Information contains 10 Supplementary Figures (including figure legends) and 2 Supplementary Tables.



Supplementary Figure 1:

a. GISTIC results from TCGA glioma and squamous cancer samples

b. Profiles of the averaged copy number score (log2(copy number/2)) for copy number alterations from all squamous cancer samples or focal amplifications (<10 Mb) from samples that are associated with *SOX2* amplifications (log2(copy number/2) > 0.1).

c. Upper: distribution of GISTIC score in a ~5Mb windown centered at the *SOX2* gene. Middle: averaged ATAC-seq signal for TCGA glioma and squamous cancer samples. Bottom: copy number profiles of focal amplifications (<10 Mb) from samples that are associated with *SOX2* amplifications (log2(copy number/2) > 0.1).



Supplementary Figure 2:

Expression levels of *SOX2* and *SOX2-OT* in TCGA samples with both RNA-seq and copy number data available. Upper: squamous cancers with *SOX2* focal amplifications (n=122 biologically independent samples), with *SOX2* non-focal amplifications (n=998 biologically independent samples), or without *SOX2* amplifications (n=258 biologically independent samples). Bottom: gliomas with *SOX2* focal amplifications (n=21), with *SOX2* non-focal amplifications (n=71), or without *SOX2* amplifications (n=563). Boxplots: middle bar, median; lower and upper box limits, the first and third quartiles, respectively; whiskers, the first quartile minus 1.5 times the interquartile range (IQR) and the third quartile plus 1.5 times the IQR, respectively. P values are derived from two-sided t-tests.



Supplementary Figure 3:

a. The CTCF ChIP-seq profile surrounding the *SOX2* promoter region. Underneath presented are motifs and their orientations of chromatin looping factors CTCF, ZNF143, and YY1.

b. Expression level (CCLE RNA-seq: log2(TPM+1)) and copy number score (CCLE log2(copy number/2)) of the SOX2 region in squamous cancer cell lines.

c. The squamous cancer-specific enhancers and super-enhancer of *SOX2* (converted to mm9 genome) is distinct from the Sox2 super-enhancer reported for mouse ESC cells. Note: the enhancer e8 listed in Figure 2B has no corresponding region in the mouse mm9 genome (based on the liftOver tool).

d. H3K27ac HiChIP loops that are connected to the *SOX2* promoter in the squamous cancer cell line KYSE70. HiChIP anchors are defined by the union of H3K27ac peaks identified from the *SOX2*-high squamous cancer cell lines listed in Figure 2B. The color intensity corresponds to the number of PETs supporting each of the loops.



Supplementary Figure 4:

a. Cas9 ChIP-qPCR results showing enrichment of the dCas9-MeCP2-KRAB complex at each of the enhancers that are targeted by sgRNAs. For each region, ChIP-qPCR signal is normalized to sonicated genomic DNA. NCR: negative control region. n=2 biologically independent experiments.

b. Doxycycline-induced SOX2 expression in KYSE140 cells rescues the proliferation-inhibitory phenotype caused by e1 repression (six days post seeding the same number of cells with and without e1 repression). n=3 biologically independent experiments. P values are derived from a two-tailed t-test. The immunoblotting experiment was repeated once independently with similar results.

c. Immunoblots of SOX2 and ACTIN in KYSE140 cells with and without SOX2 knockouts (three days post selection). KYSE140 cells with all the conditions, except sgSOX2#1, were processed with RNA-seq to identify SOX2-regulated genes. The immunoblotting experiment was repeated once independently with similar results.



a. Number of PETs that connecting promoter regions of the candidate genes and the four HiChIP enhancer anchors. Note: The *SOX2-OT* gene has three alternative promoters - only the P3 promoter is connected to the enhancer anchors in two of the cell lines. N.S.: no significant loops.

b. Expression change (%) of each of the candidate genes in KYSE140 cells after individual repression of e1-e8. Expression level is normalized to the negative control (sg-NC#1). n=3 biologically independent experiments.

c. Expression change (%) of the endogenous *SOX2* and *SOX2-OT* after e1 repression in KYSE140 cells with and without ectopic expression of *SOX2*. Primers targeting the *SOX2* 3'UTR region were used to distinguish the endogenous and ectopic *SOX2*. n=3 biologically independent experiments. P value is derived from two-sided t-test.

d. SOX2 ChIP-seq profile at the SOX2-OT (P3 promoter isoform) locus.

b а Duplication Deletion • Translocation • Tail-tail inversion Head-head inversion • WGS Squamous cancer GISTIC SOX2 e1-e8 SA525054 1p34.2 1q21.2 SA503701 SOX2 2p16.1 ~2q11.2 SA301678 2q31.2 e1-e8 SA503918 chr3:181124634-183609829 3q26.33 4q12 SA315264 **SNP-array GISTIC** 5p12 SA534431 6q12 SA307934 7p11.2 7q11.21 SA306844 8p11.22 8q24.21 SA503919 9p13.3 SA310500 11p11.12 - 11q13.3 SA317863 . 11q22.2 SA503211 14q13.3 SA306087 15a26.3 WGS GISTIC 17q12 SA305520 19q13.2 SA503473 20q11.21 22q11.21 SA298231 0.25 10⁻⁴ 10-20 10-30 10⁻² 10⁻⁸ 179264844 179964844 180664844 181364844 182064844 182764844 183464844 q value SOX2 e1-e8 SNP-array **CN** segments (n=6)

Supplementary Figure 6:

a. GISTIC result from squamous cancer WGS data.

b. Upper: Structural variants identified by WGS analysis at the *SOX2*-e1 locus in squamous cancers. Bottom: SNP-array-based copy number data showing squamous cancer samples that have amplifications of the enhancer region alone.



Supplementary Figure 7:

a. H3K27ac HiChIP contact heatmap showing the interaction between e1 and the other enhancers in the squamous cancer enhancer cluster in KYSE140 cells.

b. ChIP-seq of BRD4 and SOX2 signal at the e1-e8 locus. *: based on peak calling, e8 has no significant enrichment of BRD4 in KYSE140 cells. BRD4 ChIP-seq data was from KYSE140 sg-NC#1.

c. BRD4 ChIP-qPCR results showing the % change of BRD4 binding at e1-e7 after e1 repression in KYSE140 cells with and without Doxycycline-induced ectopic expression of *SOX2*. n=3 biologically independent experiments. P values are derived from two-sided t-tests.



cuttable SOX motifs

Supplementary Figure 8:

a. List of motifs that are disrupted by CRISPR cutting.

b. Left: SOX2 ChIP-qPCR at the e1 enhancer in KYSE140 cells with and without CRISPR-mediated disruption of the 2nd SOX2 motif found in e1. Right: FOSL1 ChIP-qPCR at the e1 enhancer in KYSE140 cells with and without CRISPR-mediated disruption of the AP-1 motif found in e1. ChIP enrichment was normalized to DNA concentration of each sample (measured by Qubit) and then to sonicated genomic input. n=2 biologically independent experiments.

c. Expression of *SOX2* in KYSE140 cells with cutting of SOX motifs in e2-e8 and *SOX2* promoter. The expression levels are normalized to the AAVS1 negative control. The 2nd SOX motif in e1 serves as a positive control for the experiment. n=3 biologically independent experiments. P values are derived from two-sided t-tests.



Supplementary Figure 9:

a. Immunoblots of BRD4 and ACTIN in KYSE140 cells treated with two hours of DMSO or 0.5 µM ARV-771. The immunoblotting experiment was repeated once independently with similar results.
b. Cell proliferation assays of KYSE140 and LK2 cells treated with 48 hours of DMSO or ARV-771. Cell numbers were normalized to the DMSO controls. n=2 biologically independent experiments. Source data are provided as a Source Data file.



Supplementary Figure 10:

Expression fold change of *FXR1*, *SOX2-OT* (P3 promoter isoform), *SOX2*, *LINC01206*, and *ATP11B* in SKMES1 cells after CRISPR-mediated activation of e1-e8. The expression levels are normalized to the sg-NC#1 negative control. n=3 biologically independent experiments.

Table S1: KEGG pathway analysis for e1-activated genes

Collection(s):	CP:KEGG
# overlaps shown:	20
# genesets in collections:	186
# genes in comparison (n):	1526
# genes in universe (N):	40071

Gene Set Name	# Genes in Gene Set (K)	Descri
KEGG_AXON_GUIDANCE	129	Axon g
KEGG_LYSOSOME	121	Lysos
KEGG_MAPK_SIGNALING_PATHWAY	267	MAPK
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	44	Valine
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	213	Regula
KEGG_PATHWAYS_IN_CANCER	325	Pathw
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	31	Glycin
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	115	Vascu
KEGG_BASAL_CELL_CARCINOMA	55	Basal
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	126	Neuro
KEGG_MELANOGENESIS	101	Melan
KEGG_BUTANOATE_METABOLISM	34	Butan
KEGG_GAP_JUNCTION	90	Gap ju
KEGG_HEDGEHOG_SIGNALING_PATHWAY	56	Hedge
KEGG_CALCIUM_SIGNALING_PATHWAY	178	Calciu
KEGG_ENDOCYTOSIS	181	Endoc
KEGG_TGF_BETA_SIGNALING_PATHWAY	86	TGF-b
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	74	Arrhyti
KEGG_CHEMOKINE_SIGNALING_PATHWAY	189	Chem
KEGG GNRH SIGNALING PATHWAY	101	GnRH

Gene Set (K)	Description	# Genes in Overlap (k)	k/K	p-value	FDR q-value
	Axon guidance	22	0.1705	3.76E-09	5.68E-07
	Lysosome	21	0.1736	6.11E-09	5.68E-07
	MAPK signaling pathway	32	0.1199	1.20E-08	7.46E-07
	Valine, leucine and isoleucine degradation	11	0.25	5.68E-07	2.53E-05
	Regulation of actin cytoskeleton	25	0.1174	6.81E-07	2.53E-05
	Pathways in cancer	32	0.0985	1.11E-06	3.44E-05
	Glycine, serine and threonine metabolism	9	0.2903	1.55E-06	4.06E-05
	Vascular smooth muscle contraction	17	0.1478	1.74E-06	4.06E-05
	Basal cell carcinoma	11	0.2	6.03E-06	1.25E-04
	Neurotrophin signaling pathway	16	0.127	2.50E-05	4.65E-04
	Melanogenesis	14	0.1386	2.95E-05	4.99E-04
	Butanoate metabolism	8	0.2353	3.25E-05	5.04E-04
	Gap junction	13	0.1444	3.62E-05	5.18E-04
	Hedgehog signaling pathway	10	0.1786	4.49E-05	5.96E-04
	Calcium signaling pathway	19	0.1067	5.39E-05	6.68E-04
	Endocytosis	19	0.105	6.77E-05	7.86E-04
	TGF-beta signaling pathway	12	0.1395	1.01E-04	1.10E-03
	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	11	0.1486	1.09E-04	1.12E-03
	Chemokine signaling pathway	19	0.1005	1.21E-04	1.14E-03
	GnRH signaling pathway	13	0.1287	1.22E-04	1.14E-03

Table S2: Primers used in the study

sgRNAs for CRISPRi and CRIS	PRa	PLAT regions (hg10)	Notes
sg_NC1_F	CACCGATCGTTTCCGCTTAACGGCG	N/A	Notes Negative control
sg_NC1_R	AAACCGCCGTTAAGCGGAAACGATC	N/A	Negative control
sg_NC2_R	AAACAACTTTTATTTTTCACTCAGC	N/A	Negative control
sg_Prom_F	CACCGCCCCCTTTCATGCAAAACC	chr3:181429603-181429622	
sg_e1_1_F	CACCGGCAAACCTTGAAACGGGGGC	chr3:181625876-181625895	Also used for cutting the 2nd SOX motif at e1
sg_e1_1_R	AAACGCTTTGTTTCAAGGTTTGCC		
sg_e1_2_F sg_e1_2_R	AAACGTGGGAACGTTCATCTTGAGC	0113:161625972-161625991	
sg_e1_3_F	CACCGTCAGAAAACCTGCACCTGTG	chr3:181626079-181626098	Also used for cutting the SNAIL motif at e1
sg_e2_F	CACCGATGTCTTCACATATGACTGG	chr3:181631224-181631243	
sg_e2_R	AAACCCAGTCATATGTGAAGACATC	abr0-101633517 101633536	
sg_e3_F sg_e3_R	AAACGCAGTTGGAGTTGGTATTAGC	CH13:161633517-161633536	
sg_e4_F	CACCGTAAATCTTAGCGTTGGTAA	chr3:181659352-181659371	
sg_e4_K sg_e5_F	CACCGCATGCTCTAAGACCCTAAGG	chr3:181661141-181661160	
sg_e5_R	AAACCCTTAGGGTCTTAGAGCATGC	abr2:191660171 191660100	
sg_e6_R	AAACAGTATCTCATTACGTCAGGAC	0113.101003171-101003130	
sg_e7_F	CACCGTTATGTCCCATCCTTTCACA	chr3:181671025-181671044	
sg_e8_F	CACCGGTACACCCAGACAGAGTGA	chr3:181674059-181674078	
sg_e8_R	AAACTCACTCTGTCTGGGTGTACC		
sgRNAs for CRISPR-mediated	motif cutting within the e1 enhancer	and the ONAL media	
sg_e1_1 was used to cut the 2 Names	Sequences Sequences	BLAT regions (hg19)	Notes
sg_e1_1stSOX_F	CACCGCTTGTGTGTGATTTGCATTGTT	chr3:181625525-181625544	1st SOX motif
sg_e1_1stSTAT_F	CACCGCTGCTAGAAGCCAGCATTCT	chr3:181625563-181625582	1st STAT motif
sg_e1_1stSTAT_R	AAACAGAATGCTGGCTTCTAGCAGC		
sg_e1_1stEHF_R	AAACGATTTGTTGCTTTGTTTAAC	CH13:161625637-161625656	Ist EAF Motil
sg_e1_2ndEHF_F	CACCGTTTAAGAGACATTTCCTCT	chr3:181625651-181625670	2nd EHF motif
sg_e1_ZNF148_F	CACCGAATAAAAGGAACGTGGTGGA	chr3:181625851-181625870	ZNF148 motif
sg_e1_ZNF148_R	AAACTCCACCACGTTCCTTTATTC	chr3-181625023-191625042	AP1 motif
sg_e1_AP1_R	AAACGAGTCAGAACCTCCACCACC	0110.101020923-101020942	A THOU
sg_e1_RUNX_F	CACCGCTGTGGGGAACGTTCATCTTG	chr3:181625974-181625993	RUNX motif
sg_e1_RUNX_R sg_e1_2ndSTAT_F	CACCGAGCAGGCAGCTTTGTTTCTC	chr3:181626001-181626020	2nd STAT motif
sg_e1_2ndSTAT_R	AAACGAGAAACAAAGCTGCCTGCTC	chr3-181626026 191626055	PELA motif
sg_e1_RELA_R	AAACGAATTCCCAAGGTGAATGTTC	0113.101020030-101020055	NEEA IIIOUI
sg_e1_ZNF263_F	CACCGTTCCGGCAGCACCGGGGAGG	chr3:181626053-181626072	ZNF263 motif
sg_e1_TCF_F	CACCGGAGTTGCCAGAGTTCAAAG	chr3:181626110-181626129	TCF motif
sg_e1_TCF_R	AAACCTTTGAACTCTGGCAACTCC		
sgRNAs for CRISPR-mediated	cutting of SOX motifs outside of e1		
prom SOX 1st F	Sequences CACCGAATCTTTACGTCGGGACAAT	BLAT regions (hg19) chr3:181428321-181428340	Notes
prom_SOX_1st_R	AAACATTGTCCCGACGTAAAGATTC		
prom_SOX_2nd_F prom_SOX_2nd_R	AAACTTGTGGTGGCCGCAAAGCCC	chr3:181428571-181428590	
e3_SOX_F	CACCGTCCTGATACTTAGGGAACAA	chr3:181633327-181633346	
e3_SOX_R e4 SOX F	CACCGTTCTGTTCTTTGCATACAAT	chr3:181659264-181659283	
e4_SOX_R	AAACATTGTATGCAAAGAACAGAAC		
e5_50X_F	CACCGAAAGCTTCAAGCGAACAATG	CIII3:101001244-101001203	
e5 SOX R	AAACCATIGTICGCTIGAAGCTITC		
e5_SOX_R e6_SOX_F	AAACCATIGIICGCIIGAAGCIIIC CACCGTCACTATGCAGAAGAAACAA	chr3:181669056-181669075	
e5_SOX_R e6_SOX_F e6_SOX_R e7_SOX_F	AAACCATTGTTCGCTTGAAGAAACAA CACCGTCACTATGCAGAAGAAACAA AAACTTGTTTCTTCTGCATAGTGAC CACCGACTGAAAAACTTAAACACAA	chr3:181669056-181669075 chr3:181671304-181671323	
e5_SOX_R e6_SOX_F e6_SOX_R e7_SOX_F e7_SOX_F e7_SOX_F	AAACCATIGTICGCTIGAAGCATIC CACCGTCACTATGCAGAAGAAACAA AAACTTGTTTCTTCGCATAGTGAC CACCGACTGAAAAACTTAAACACAA AAACTTGTGTTTAAGTTTTCAGTC	chr3:181669056-181669075 chr3:181671304-181671323	
eb_SOX_R e6_SOX_F e6_SOX_R e7_SOX_F e7_SOX_F e8_SOX_F e8_SOX_F e8_SOX_R	AAACCATIGTICGCTIGAAGGACTITC CACCGTCACTATGCAGAAGAAACAA AAACTTGTTTCTTCTCGCATAGTGAC CACCGACTGGAAAACTTTAAACACAA AAACTTGTGTTTAAGTTTTTCAGTC CACCGTGGGAAACATTCACAACAAA AAACTTGTTGTGGAAATGTTCCCAC	chr3:181669056-181669075 chr3:181671304-181671323 chr3:181674027-181674046	
e5_S0X_R e6_S0X_F e6_S0X_R e7_S0X_F e7_S0X_F e8_S0X_F e8_S0X_F sgRNA for CRISPR-mediated S	AAACCCATTGTICAGAGCTTCC CACCGTCACTATGCAGAGAACAA AAACTTGTTTCTTCTCGCATAGTGAC CACCGACTGAAAACTTAAACACAA AAACTTGTGTAAAGTTTTCAGTC CACCGGTGGGAACATTCACAACAAA AAACTTGTGTGAAATGTTCCCAC	chr3:181669056-181669075 chr3:181671304-181671323 chr3:181674027-181674046	
eb_S0X_R e6_S0X_F e6_S0X_R e7_S0X_F e7_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_R sgRNA for CRISPR-mediated S Names to AN/01_E	AAALCATIGTIOSCI ISAAGUITIC CACCGTCACTATGCAGAAGAAACAA AAACTIGTITCTTCTGCAGAAGACAA CACCGACGAAAACTTAAAAACTAAAAACAA AAACTIGTGTITAGTTTTCAGTC CACCGTGGGAACATTCACACAAA AAACTTTGTGGAATGTTCCCAC OX2 knockout Sequences	chr3:181669056-181669075 chr3:181671304-181671323 chr3:181674027-181674046 BLAT regiones (hg19)	Notes
e5_S0X_R e6_S0X_F e7_S0X_F e7_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F sgRAVST_F sg_AAVS1_F sg_AAVS1_R	AAACAGGCAATTGTTGTGAAACAA AAACTTGTTGTTGCAAAAGAAACAA AAACTTGTTGTTCTCTGCAAAGCAAA	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181674027-181674046 BLAT regions (hg19) chr19:55627180-55627199	Notes Negative control
e5_S0X_R e6_S0X_F e6_S0X_F e7_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_R sg_AAVS1_F sg_AAVS1_R sg_AAVS1_R sg_AAV2_F sg_AAV2_F sg_AAV2_F	AAACCATIGTICSCITIGAAGCITIC CACCGTCACTATGCAGAAGAAACAA AAACTIGTICTICTICGCATAGTGAC CACCGACGAAAACCTAAAAACCTAAAAACAA AAACTIGTIGTITAAGTICTICAGTC CACCGTGGAAACATTCAACACAAA AAACTIGTIGTIGAATGTICCCAC OX2 knockout Sequences CACCGAGCCACATTAACCGGCCCT CACCGAGCCACATTAACCGGCCCT CACCGAGTGGCGTTAATGTGGCCC CACCGGTGGCGTAGGAGCAGTG	chr3:181669056-181669075 chr3:181671304-181671323 chr3:181674027-181674046 BLAT regions (hg19) chr19:55627180-55627199 chr2:151131560-151131579	Notes Negative control Negative control
e5_S0X_R e6_S0X_F e6_S0X_F e7_S0X_F e7_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F sg_AAVS1_F	AAACCATIGTICSCITIGAAGCITIC CACCGTCACTATGCAGAAGAAACAA AAACTTGTTTCTTCTGCATAGTGAC CACCGACTGAAAACCTAAAAACAA AAACTTGTGTTTAAGTTTTCAGTC CACCGTGGGAACATTCAACACAAA AAACTTGTTGTGAATGTTCCCAC OX2 knockout Sequences CACCGAGCCAACATTAACCGGCCCT AAACAGGCCCGATTAAACCGGCCCT CACCGAGCGCTATGAAGCAGTG AAACCACTGCTTCATAGGCACAGTG AAACCACTGCTTCATAGGCACAC	chr3:181669056-181669075 chr3:181671304-181671323 chr3:181674027-181674046 BLAT regions (hg19) chr19:55627180-55627199 chr2:151131560-151131579 chr3:181430550-181430569	Notes Negative control Negative control
e5_S0X_R e6_S0X_R e7_S0X_F e7_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_R sg_RAA for CRISPR-mediated S Mames g_AAVS1_F sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AC2_1_F sg_S0X2_1_R	AAACCASTIGTICSCIIGAASCITIC CACCGTCACTTATGCASAASCAA AAACTIGTITCTTCTGCATASTGAC CACCGACGAAAACTTAAACACAA AAACTIGTGTTTAGTTTTCASTC CACCGTGGAACATTCAACACAA AAACTTGTGTGTAATGTTCCCAC OX2 knockout Sequences CACCGGGCGACATTCAACCGGCCCT CACCGGGGGCGGCATTAACTGGCTC CACCGGGTGGGCATTGAACCACC CACCGGTGGGCATTGAACCACC CACCGGTGGCGCATTGAACCACC CACCGGTGTGCGCATGGCACC	chr3:181669056-181669075 chr3:181671304-181671323 chr3:181674027-181674046 BLAT regions (hg19) chr19:55627180-55627199 chr2:151131560-151131579 chr3:181430550-181430569 chr3:181430550-181430569	Notes Negative control Negative control
e5_S0X_R e6_S0X_F e6_S0X_F e7_S0X_F e7_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_R 9g_AAVS1_F 9g_AAVS1_F 9g_AAVS1_R 9g_cht22_F 9g_S0X2_1_F 9g_S0X2_1_F 9g_S0X2_2_F 9g_S0X2_2_R	AAACCAGTGCATTGCAAAAGAAACAA AAACTTGCTTGTTCAGAAAGAAACAA AAACTTGTTGTTCTCTCGCATAGTGAC CACCGACGAAAACTTAAAAACTAAAACAAA AAACTTGTGTTTAAGTTCTCAGTC CACCGTGGAAACATTAAACACAAA AAACTTGTGTTAAGTTCCCAC X2 knockout Sequences CACCGGAGCCACATTAACGGGCCCT CACCGGGTGGCAATTGCAACGGCAC CACCGGTGGCCATTGCAACACAGCAGCA AAACCAGGCGCAATACATGGCACC CACCGGTGGCCATGCACACCCGCACC CACCGGCGCATAGCACGGCAAC CACCGAAGCCCCACTGGCGCAC	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181674027-181674046 BLAT regions (hg19) chr/9:55627180-55627199 ch/2:151131560-151131579 ch/3:181430550-181430569 ch/3:181430373-181430392	Notes Negative control Negative control
e5_S0X_R e6_S0X_F e6_S0X_F e7_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_R sg_RAA for CRISPR-mediated S Names sg_AAVS1_F sg_chr22_F sg_chr22_R sg_chr22_R sg_S0X2_1_F sg_S0X2_1_R sg_S0X2_1_R sg_S0X2_2_R sg_S0X2_2_R sg_S0X2_2_R sg_S0X2_2_R sg_S0X2_2_R sg_S0X2_2_R sg_S0X2_3_R sg_S0X_3_R	AAACCATIGITICSCITIGAAGCITIC CACCGTCACTATGCAAAAGAAAACAA AAACTIGITICTICTGCATAGTGAC CACCGACGAAAACTTAAACACAA AAACTIGITITIAGTTICAGTC CACCGTGGAAAACTTAAACACAAA AAACTIGIGAAAGTTCACACAAA AAACTIGIGAAACTTCACACACAA AAACCATGGAAACTTCACACACAA AAACCAGCGCGATAATGACACACA AAACCAGCGCGATTAACTGGGCCC CACCGGTGGCCATGCACACACCAC CACCGGTGGCCATGCACACCC CACCGGCGATGACAACTTIC CACCGGCGCGATGACAACTTIC CACCGGCCGCGATGGCCCGAC	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181674027-181674046 BLAT regions (hg19) chr19:55627180-55627199 ch/2:151131560-151131579 ch/3:181430550-181430569 ch/3:181430373-181430392 ch/3:181430363-181430382	Notes Negative control Negative control
e5_S0X_R e6_S0X_R e6_S0X_R e7_S0X_F e7_S0X_F e8_S0X_F e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e9_ANVS1_F e9_ANVS1_F e9_ANVS1_R e9_ANVS1_R e9_ANVS1_R e9_ANVS1_R e9_ANVS1_R e9_S0X2_1.F e9_S0X2_1.F e9_S0X2_2.F e9_S0X2_2.F e9_S0X2_2.F e9_S0X2_2.R e9_S0X2_3.F e9_S0X2_3.F e9_S0X2_4.F	AAALCATIGTICSCI IGAAGCITIC CACCGTCACTATGCAAAAGAAACAA AAACTIGTITCTTCTGCAATAGTGAC CACCGACGAAAACTAAAAACTAAAACAAA AAACTIGTGTITAGTTTTCAGTC CACCGACGGACACTTCAAACACAA AAACTTGTGTTAAGTTCCCAC OZX hockout Sequences CACCGAGGCCACATTAAACGGCCCCT AAACAGGGCCGCATTAAACGGCCCC CACCGGAGCCAACTTCAATGGCCAC CACCGAGGCCCATGCATAGCGCCCC AAACGGGCCCCAGGCCACGAAAACTTCC CACCGGAGGCCCAGGGCAACTTCAACGGCCCC AAACGGGCCCCGGGCGAAAACTTCC CACCGGGCGCCCAGGCCCGGAG AAACTCGGCGCCCGAGGCCCGAG AAACTCGGCGCCCGAGGCCCTGCC	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181671304-181671323 ch/3:181674027-181674046 BLAT regions (hg19) ch/19:55627180-55627199 ch/2:151131560-151131579 ch/3:181430550-181430569 ch/3:181430373-181430392 ch/3:181430363-181430382 ch/3:181430241-181430260	Notes Negative control Negative control
e5_S0X_R e6_S0X_R e6_S0X_R e7_S0X_F e7_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e9_ANVS1_R e9_ANVS1_R e9_ANVS1_R e9_ANVS1_R e9_ANVS1_R e9_S0X2_1_F e9_S0X2_1_R e9_S0X2_1_R e9_S0X2_2_R e9_S0X2_2_R e9_S0X2_3_R e9_S0X2_4_R e9_S0X2_4_R e9_S0X2_4_R	AAALCATIGTICSCI IGAAGCITIC CACCGTCATTGTCAGAAACAA AAACTIGTITCTTCTGCATAGTGAC CACCGACGTAGAAAACTAAAACAA AAACTIGTGTTTTCTTCTGCATAGTGAC CACCGTGGGAAAAACTTAAACAAAAAACAAA AAACTIGTGTTTAAGTTCCCAC OX2 knockout Bequencs CACCGTGGGACACATTAAACGGGCCC CACCGTGGGCCGGATAATGTGGCCAC CACCGACGGCCGGGAATAACGGCCGAC AAACGGCGGCGCAATGGACACAC CACCGACGCCATGCATGGCCGC AAACGGCGGCCAATGGACACCC CACCGACGCCCGGCCAAACGGCCCC AAACGGCGCCGAGGCAACTTGCACGCCCC AAACGGCGCCCAGGCCCCGAG AAACCTCGGCCCCGAGGCCCT AAACGGCCGCCAGGCCCCGAG AAACCTCGGCCCCGAGGCCCT	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181674027-181674046 BLAT regions (hg19) chr/19:5527180-56627199 ch/3:181430550-181130569 ch/3:181430373-181430392 ch/3:181430373-181430382 ch/3:181430241-181430260	Notes Negative control Negative control
e5_S0X_R e6_S0X_R e6_S0X_R e7_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R sgRNA for CRISPR-mediated S mames sg_AAVS1_R sgcht22_R sgcht22_R sgS0X2_1_R sgS0X2_1_R sgS0X2_1_R sgS0X2_2_R sgS0X2_2_R sgS0X2_2_R sgS0X2_3_R sgS0X2_4_R RT-qPCR	AAACCATIGITICSCIIGAASCITIC CACCGTACATTATGCAAAACAAAACAA AAACTTGITTCITTCTGCAAAGAAAACAA AAACTTGITGITTCITCTGCAAAGAAACAA AAACTTGIGITTAAGTTCICCAC CACCGTGGGAACATTCACACAAA AAACTTGIGAACATTCACACAAA AAACTTGIGAACATTCACACAAA AAACTTGIGAACATTAACCGGCCCT CACCGGGGGGCAATAAACTGGCACA CACCGGGCGGTTAATGIGGCCC CACCGGTGGCCAATGACAACTGCCAA AAACCAGGCCGATTGAAACAGGCAA AAACCGCGCGAATGACAACTTGCCAC CACCGGCGGCAATACACTGGCCCC CACCGGAAGCCAATGACAACTTGC CACCGCGAAGCCAATGACAACTTGC CACCGCAAGCCCAGGCCCAAACAACTGCCAA AAACGCGCCGCGGGCCCAGGCCCCA AAACGCGCCCGAGTGGAACATGCCAA AAACCGCGCCCAGGCCCCAGCCCAAACTTGC CACCGCACGCCCAGGCCCCAGCCCAAACTTGCCCCC CACCGCACGCCCAGGCCCCAGCCCAAACTTGCCCCCC CACCGCCGCCCGAGCGCCAACCTTGC CACCGCCCGCCCGGCCCCAGCCCAAACTTGCCCCCCCCCC	chr3:181669056-181669075 chr3:181671304-181671323 chr3:181674027-181674046 BLAT regions (hg19) chr19:55627180-55627199 chr2:151131560-151131579 chr3:181430569 chr3:18143050-181430569 chr3:181430373-181430382 chr3:181430363-181430382 chr3:181430241-181430260	Notes Negative control Negative control
e5_S0X_R e6_S0X_F e6_S0X_F e7_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_R 9AAVS1_F 9AAVS1_F 9Ch/22_F 9S0X2_1_F 9S0X2_1_F 9S0X2_1_R 9S0X2_2_R 9S0X2_2_R 9S0X2_3_F 9S0X2_4_F 9S0X2_4_R RT_QPCR Names RT ACTB F	AAACCATIGTTGCTGAAAACAA AAACTTGTTGTTCTGCTGAAAACAA AAACTTGTTGTTCTGCTGAAAACAA AAACTTGTGTTGTTCAGAAAACTAA AAACTTGTGTTTAAGTGC CACCGTGGAAAAACTTAAACACAA AAACTTGTGTTTAAGTTCCAC X2 knockout Bequences CACCGGGGAAACATTCAACACAAA AAACAGGCGGGTAATGGGCC CACCGGGGGACACATTAACGGCCC CACCGGGGGAATGACACAGGCAA AAACCAGGCGCCAAGCACAGCAAACTTC CACCGGCGGCAAACACTGGCCC CACCGGCGGCAAACACTGGCCC CACCGCGGCAAACACTGGCCC CACCGCGGCAAACACTGGCCC CACCGCGGCAAACACTGGCCC CACCGCGGCAAACACTGGCCC CACCGCGGCAAACACTGGCCC CACCGCGGCAAACACTGGCCC CACCGCGGCAAACACTGGCCC CACCGCGGCAAACACTGGCCC CACCGCGGCAAACACTGGCCC CACCGCGCGCAACACAAAAACCGC CACCGCGCGCAACACACAAAAACCGC CACCGCGGCAACACACCC	ch3:181669056-181669075 ch3:181671304-181671323 ch3:181671027-181674046 BLAT regions (hg19) chr19:55627180-55627199 ch/2:151131560-151131579 ch/3:181430550-181430569 ch/3:181430373-181430392 ch/3:181430363-181430382 ch/3:181430241-181430260 Target genes ACTB	Notes Negative control Negative control
e5_S0X_R e6_S0X_F e6_S0X_F e7_S0X_F e7_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_R sg_AAVS1_F sg_AAVS1_F sg_AAVS1_R	AAACCATIGTITCHCTIGAAGCHTC CACCGTACATTATGAGAAGAAACAA AAACTTGTTTCHTCTGCATAGTGAC CACCGACGAAAACTTAAACACAA AAACTTGTGTTTTAAGTTCACCAC CACCGTGGAAAACTTAAACACAAA AAACTTGTGTTTAAGTTCCACC 022 knockout 3squences CACCGAGCCACATTAACCGGCCCT CACCGGGGGACACTTAAACGGCCC CACCGGGGCAATGACACACAC CACCGGCGGCATAGCACACCC CACCGGCGCAAGACACACACCC CACCGGCGCAAGACACCCCACCCCCC CACCGGCGCAACACAAAAACACGCC AAACCGCGGCAAGAGCCCCCCCC	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181674027-181674046 BLAT regions (hg19) chr/19:55627180-55627199 ch/2:151131560-151131579 ch/3:181430550-181430569 ch/3:181430373-181430392 ch/3:181430343-181430382 ch/3:181430241-181430260 Target genes ACTB	Notes Negative control Negative control
e5_S0X_R e6_S0X_R e6_S0X_R e7_S0X_F e7_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e9_AAVS1_R e9_AAVS1_R e9_AAVS1_R e9_AAVS1_R e9_AAVS1_R e9_S0X2_1,F e9_S0X2_1,F e9_S0X2_1,F e9_S0X2_1,F e9_S0X2_2,F e9_S0X2_2,F e9_S0X2_2,F e9_S0X2_2,F e9_S0X2_3,F e9_S0X2_3,F e9_S0X2_4,	AAALCATIGTICSCI IGAAGCITIC CACCGTCATTGTCAGAAACAA AAACTIGTITCTTCTGCATAGTGAC CACCGTCATTGTCAGAAACAA AAACTIGTIGTITTAGTTCACTC CACCGTCGAGAAAACTTAAACACAA AAACTIGTIGTITTAGTTTTCAGTC CACCGTGGGACACATTCAACACAA AAACTIGTIGTIGAATGTTCCCAC OX2 knockou Sequences CACCGTGGCACAATTAACCGGCCCCT AAACGGCCGCAATGTAATCGGCCC CACCGAGGCCCAGTGCATAGCACGC AAACGGCCGCAATGCATGGCCCC AAACGGCCGCAATGCATGGCCCC AAACGGCCGCAATGCATGGCCCC AAACGGCCGCAATGCATGGCCCC CACCGACGCCAGTGCATGGCCCC AAACGGCCGCAATGCATGGCCCC AAACGGCCGCAATGCATGGCCCC AAACGGCCGCAATGCATGGCCCC AAACGGCCGCAATGCATGGCCCC AAACGGCCGCAACGCAA	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:1816713027-181674046 BLAT regions (hg19) chr/9:55627180-56627199 ch/3:181430550-181131579 ch/3:181430373-181430359 ch/3:181430373-181430392 ch/3:181430341-181430260 Target genes ACTB HPRT1	Notes Negative control Negative control
eb_SOX_R eb_SOX_F eb_SOX_F eb_SOX_F eb_SOX_F eb_SOX_F eb_SOX_F sgRNA for CRISPR-mediated S mames sg_AAVS1_F sg_AAVS1_R sg_dr122_F sg_SOX2_1_R sg_SOX2_1_F sg_SOX2_1_F sg_SOX2_1_R sg_SOX2_2_R sg_SOX2_2_R sg_SOX2_2_R sg_SOX2_2_R sg_SOX2_2_R sg_SOX2_2_R sg_SOX2_4_R RT_qPCR Names RT_ACTB_F RT_ACTB_F RT_HPRT1_F RT_HPRT	AAACCATIGITICSCI IGAAGCITIC CACCGTACATATGACAAAACAA AAACTIGITICTICTICGATAGTGAC CACCGTAGTAAAACTTAAACACAA AAACTIGITITICTICTICGATAGTGAC CACCGTAGGAAAACTTAAACACAAA AAACTIGIGITIAAGTITICCAC CACCGTAGGAACATTCACACAAA AAACTIGIGAACTACACACACAA AAACAGGCCGGTTAATGTCGCCC CACCGTGGCAACATTAACGGGCCCT CACCGGTGGCCAATGACAACTGCCA CACCGGCGGCAATAGACAGGCAA AAACCAGGCCGATTGAAACAGGCCA CACCGGCGGCAATAGCACGCCA CACCGGCGCAATGACAACTGCCAA AAACGCGCGCGATGACAACTGCCAA CAACGGCGCCGATGACAACTGCCAA CAACGGCGCCGATGACAACTGCCC CACCGCGCAAGCACTCCGGCCCC CACCGGCGCCAAGCACTGCCCAACGCCCAACGGCAACTTCCCACCGCCAAGCAACTGCCCAACGCCCAGGCCCAGGCCCAACGCCCA CACCGCCGCGAGGAAAACTTCC CACCGCCGCGCAGGAAAACTTCC CACCGCCGCGCAGGAAAACTTCC CACCGCCGCGAGGAAACTTCC CACCGCCGCGAGGAAACTTCC CACCGCCGCGAGGAAACTTCC CACCGCCGCGAGGAAACTTCC CACCGCCCGCGCCGAGGCCCAACCTTCC CACCGCCGCGAGAAAACTGCCCC AACCGCCCGCGCCAGGCCCAGCCAACTTCC CACCGCCGCGAGAAAGCTGACC AGCCTTGAAACGCACGCCAAGCTACC CCTGCACACGGGAAACGTACCA AGCCCTCCAAAGGGAAAGCCAAG	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181671304-181671323 ch/3:181674027-181674046 BLAT regions (hg19) chr/9:55627189-55627199 ch/2:151131560-151131579 ch/3:181430569 ch/3:181430550-181430569 ch/3:181430373-181430382 ch/3:181430343-181430382 ch/3:181430241-181430260 Target genes ACTB HPRT1 GAPDH	Notes Negative control Negative control
e5_S0X_R e6_S0X_F e6_S0X_F e7_S0X_F e7_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_1R e9_S0X2_1	AAACCATIGITIGATIGAAACAA AAACTIGITIGTITCITCIGAAAACAA AAACTIGITIGTITCITCIGAAAACAA AAACTIGIGAAAACTIAAAAACAAA AAACTIGIGAAAACTIAAACAAA AAACTIGIGAAAACTIAAACAAA AAACTIGIGAAACTICAACAAA AAACTIGIGAAACTICAACAAA AAACAGAGCAACATICAACAAA AAACAGAGCACGATAAATIGACCC CACCGGGAACCACATIAACAGCAACA AAACAGAGCACCATAATIGAACCIGACA CACCGGCGCAATACACAGCAAACTIC CACCGGCGCAATACACAGCAACTIC CACCGCGGCAAACACTACACGCAAC AAACCAGCGCCCAGGCAAAACTIC CACCGCGGCAAACCTCACGCCC CACCGCGGCAAACCTCACGCCC CACCGCGGCAAACCTCACGCCC CACCGCGGCAAACCTCGGCCCCA CACCGCGCGCCAGGCCAAACTIC CACCGCGCGCAAGCCCGAGCCTAAC CACCGCGCGGCAACGCCCGAGCCTAC CACCGCGCGGAAACATCACC CACCGCGGCGAAGCACCCCCCA AAACGCCCCGGGCCAGCCCAACCTIC CACCGCGGCGAACACTCC CACCGCGGCGAACACCTACC AACCGCCCGGGCAACGCCCAACCC CACCGCGGCAACGCCCACCGCCGACCAACTIC CACCGCGGCGAACCACCCCCCAAACTIC CCTACCAACGGGAACACTACC AGCCACTCACACAGGGAACCTACC AGCCACTCACACAGGGAACCTACC AGCCACTCACACGGGAACCTACC	ch3:181669056-181669075 ch3:181671304-181671323 ch3:181671304-181671323 ch3:181674027-181674046 BLAT regions (hg19) chr19:55627180-55627199 ch2:151131560-151131579 ch3:181430550-181430569 ch3:181430550-181430382 ch3:18143033-181430382 ch3:181430241-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon)	Notes Negative control Negative control
eb_SUX_R eb_SUX_R eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_1F eb_SUX_1F eb_SUX_2F eb	AAALCATIGTIGECI IGAAGUITIC CACCGTCATTATGCAAAAGAAAACAA AAACTIGTITTCTTCTEGATAGTGAC CACCGACGAAAAACTAAAAACAA AAACTIGTGTTTAGTGATAGTGAC CACCGACGAAAAACTAAAAACAA AAACTIGTGTTTAGTGATGTCCCAC W2X hockout Sequences CACCGAGCCACATTAATCGGGCCCT AAACAGGCCGCGATTAATCGGGCCC CACCGAGCGCATGCATAGGCCAC CACCGAGCCACATTCATGGGCAC CACCGAGCGCATGCATAGCGCCCC AAACGGGCGCCATGCATAGCGCCCC CACCGAGCGCATGCATAGCCGCCC AAACGGGCGCCATGCATAGCCGCCC AAACGGGCGCCATGCATAGCCGCCC AAACGGGCGCCAGGCAACTGCAC CACCGGCGGCAATGCATAGCCGCCC AAACGGGCGCCAGGCAAACAGCC CACCGGCGGCACAGGCAAACAGCC AAACGGCGGCCAAGGAACATGCC CACCGCGGAGCACCGAAAACAGCC AAACGGCGGAAAGATGACC CACCGCGGAGAAGAATGACC CACCGCGGAGAAGAATGACC CACCGCGGAGAAGAATGACC CACCGCGGAGAAGAATGACC CACCGCGGAGAAGAATGACC CACCGCGGGAAAGAATGACC CACCGCGGAGAAGAATGACC CACCGCGGAGAAGAATGACC CACCGCGGAGAAGAATGACC CACCGCGGAGAAGAATGACC CACCGCGGAGAAGAATGACC CAACGGCGGAAAGCATGACC AACGGCGGAAAGCACCCAAAG GGAGCGGAAAGCACCCAAAG	ch3:181669056-181669075 ch3:181671304-181671323 ch3:181674027-181674046 BLAT regions (hg19) chr19:55627180-55627199 ch/2:151131560-151131579 ch/3:181430550-181430569 ch/3:181430373-181430392 ch/3:181430341-181430382 ch/3:181430241-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (exon)	Notes
eb_SUX_R eb_SUX_R eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_1F eb_SUX_2F eb	AAALCAATIGTICSCIIGAAGCITIC CACCGTCACTATGCAAAAGAAAACAA AAACTIGTITCTTCTGCAATAGTGAC CACCGACGAAAAACTAAAACAA AAACTIGTIGTITTAGTCACACAAA AAACTIGTIGTITTAGTTCACTC CACCGTGGGAAAAACTTAAACAAAA AAACTIGTIGTITTAGTTCACTC CACCGAGGAAAAACTTAAACAAAA AAACTIGTIGTIAATGTGCCAC CACCGAGGACACATTAAACGGGCCCT CACCGAGGACACATTAAACGGGCCCT CACCGAGGACACATTAATGTGGCAC CACCGAGGACACATTAATGTGGCAC CACCGAGGACACATTAACGAGGCCC AAACGGCGGCAATGAATGGCCAC CACCGAGGACCATGTAATGGGCCC CACCGAGGACCATGTAATGGGCCC CACCGAGGACCATGCATGGCCGCC AAACGGCGGCAATGGATGGCCCC CACCGAGGCCCAGGCCCGGAG AAACGGCGGCAACGAAGAACGGCC CACCGCAGGACCCAAGGCCCTGCC CACCGCAGGACCCAAGGCCCTGCC CACCGCAGGCACCAAGGCCCGGGCC AAACGGCGGCAACGAAAAAACGGC AAACGGCGGAACAATGACC CACCGCGAGAACGAAGAACGCC CACCGCAGGACACGAAAAAAACGGC AAACGGCGGAACGAAGAACGCC CACCGCGAGAAGAAGGAAACGACA GGCTGGTGAGAAAGCAAAG GGACGGAGCGGCACTGCAAGGGGCAAGGTTG GCACGAGGAGGAGAAGGTTG	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181671304-181671323 ch/3:181674027-181674046 ELAT regions (hg19) ch/3:155627180-56527199 ch/3:151131560-151131579 ch/3:181430550-181430569 ch/3:181430373-181430392 ch/3:181430373-181430392 ch/3:181430341-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (sUTR)	Notes Negative control Negative control
eb_S0X_R eb_S0X_F eb_S0X_F eb_S0X_F eb_S0X_F eb_S0X_F eb_S0X_F eb_S0X_F sgRNA for CRISPR-mediated S mames sg_AAVS1_F sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AX2_T sg_S0X2_1_R sg_S0X2_1_R sg_S0X2_2_R sg_S0X2_2_R sg_S0X2_2_R sg_S0X2_2_R sg_S0X2_2_R sg_S0X2_4_R RT_qPCR Names RT_ACTB_F RT_ACTB_F RT_ACTB_F RT_ACTB_F RT_ACTB_F RT_ACTB_F RT_ACTB_R RT_GAPDH_F RT_GAPDH_F RT_S0X2_1_F RT_S0X2_1_F RT_S0X2_2_F RT_S0X2_F RT_S0X2_F RT_S0X2_F RT_S0X2_F RT_S0X2_F RT_S0X2_F RT_S0X2_F RT_S0X2_F RT_S0X	AAACCATIGITICSCI IGAAGCITIC CACCGTACTATGICAGAAGAAAACAA AAACTIGITTICTICTICGATAGTGAC CACCGTAGAAAACTTAAACACAA AAACTIGITITICTICTICGATAGTGAC CACCGTAGGAAAATCTAAACACAA AAACTIGIGITITAAGTICTICCAC OX2 knockout Sequences CACCGTGGCAACATTAAACCGGCCCT AAACAGGGCCGGTTAATGIGGCTC CACCGGTGGCGATTAGTGACACAC CACCGGTGGCGATTAATGIGGCTC CACCGGTGGCGATTGAAACAGGCAC CACCGGTGGCGATTGAAACAGGCCC AAACGAGGCCGATTGAAACAGGCCA CACCGGCGGCAATAGCACGCC CACCGGCGGCAATAGCACGCCC CACCGGCGGCAATAGCACGCCC CACCGGCGGCAATAGCACGCCC CACCGGCGGCAATAGCACGCCC CACCGCGCGAGGAAAACTTGCCACC CACCGCGCGAGGCAATAGCCACC CACCGCCGCAGGCAAACTGCCCA AAACGGCGCCGAGTGAAACTTGC CACCGCCGCGAGGCAAACTTGCCCC CACCGCCGCAGGCAACTGCCCC CACCGCGCGCAGGCCCAAGCCCCC CACCGCGCGCCAGGCCCAAGCCCCC CACCGCGCGCAGGCCCAAGCCCCC CACCGCGCGCAGGCCCAAGCCCCC CACCGCGCGCAGGCACACCCCCCCAACGGCCCAA GCCTGGATAGCAACGTACA GGCGTGTGCACACGGCAACTTG CCTGACAAGGGAACGCACAG CCGGCCAAGCCCCCCGAAGCAACTTG CCTGACAAGGGAACGCCCA GGCCAGCCCCGCGGGCCCAAGCCCCCC CACCGCGCGCG	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181671304-181671323 ch/3:181674027-181674046 BLAT regions (hg19) chr/9:55627189-55627199 ch/2:151131560-151131579 ch/3:181430550-181430569 ch/3:181430373-181430382 ch/3:181430343-181430382 ch/3:181430341-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (3'UTR) FXR1	Notes Negative control Negative control
eb_SUX_R eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F sg_AAVS1_F sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AVS1_R sg_AVS1_R sg_AVS1_R sg_SUX2_1_F sg_SUX2_1_F sg_SUX2_1_R sg_SUX2_2_R sg_SUX2_2_R sg_SUX2_2_R sg_SUX2_4F sg_SUX2_4	AAACCATIGITIGATIGAARCHTIC CACCGTACATATGACAAAACTAA AAACTIGTITTICTICTIGAATAGTAAC CACCGTAGAAAACTTAAAAACTAAAAACAAA AAACTIGTITTICTICTIGAATAGTAC CACCGTAGAAAACTTAAAACAAA AAACTIGTIGTITAAGTITICCAC OX2 knockout Sequences CACCGAGCCAACATTAACCAGCACT AAACAAGGCCGCTATATGTGGCTC CACCGGGGACCACATTAACCGGCCCT AAACCAGCGCGATAGACATGGCAC CACCGGGGCAATAGCACTGGCAC CACCGGCGCAATAGCACTGGCCAC CACCGGCGCAATAGCACTGGCCAC CACCGCGGCAATAGCACTGGCCAC CACCGCGGCAATAGCACTGGCCAC CACCGCGCGCAATAGCACTGGCCAC CACCGCGCGCAATAGCACTGGCCC CACCGCGCGCAATAGCACTGGCCCAA AAACGCACGCCGCAGTGGCACACTGGCCCAA CAACCGCCGCGCAATGGCCCAA CACCGCCGCGCAATGGCCCAA CACCGCCGCGCAATGGCCCAA CACCGCCGCGCAATGGCCCCAA CCCTGGATAGCAACCGTCAC CACCGCCGGGAACACTTCC CACCGCCGGGAACACTGCCCCAA CGCCTGGATAGCAACCGTAC AGCCAGTCACACAGGGAACTTC CTGACCAAGGGAAGCATG CCTGGATAGCAACCGTACA AGCCGTGGTAGCAACCGTACA CCGCGCGAGACACACGTACA CCGCGCGCAACGCGCAAGCACTG CCTGGATACCACGGGAGCAT CCTGACAAGGGAAGCAACG GGACCTGCCTCTCAAAAT GGCCTGCTTGGTAGCACGTACA CGGCCAATCCTCCCACACA	ch3:181669056-181669075 ch3:181671304-181671323 ch3:181671304-181671323 ch3:181674027-181674046 BLAT regions (hg19) chr19:55627180-55627199 ch2:151131560-151131579 ch3:181430550-181430569 ch3:181430373-181430382 ch3:181430341-181430382 ch3:181430241-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (s0UTR) FXR1 ATP11B	Notes Negative control Negative control
eb_SUX_R eb_SUX_R eb_SUX_R eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_1F eb_SUX_2F eb	AAALCATIGITIGEI IIGAAGUITIC CACCGTCATTATGCAAAAGAAAACAA AAACTIGITTICTICTIGCAATAGTGAC CACCGACGAAAAACTTAAAAACAA AAACTIGITITICTICTIGCAATAGTGAC CACCGACGAAAAACTTAAAAACAAA AAACTIGIGITITAAGTICTICCAC OX2X hackad Sequences CACCGAGGCACATTAAACGGGCCCT AAACAGGCCGCGATTAAACGGGCACCT CACCGAGGCCACATTAATGTGGCTC CACCGAGGCCACATTAATGTGGCTC CACCGAGGCCACATTAATGTGGCTC CACCGAGGCCACATTAATGTGGCTC CACCGAGGCCACATTAATGTGGCTC CACCGAGGCCACATTAATGTGGCTC CACCGAGGCCACATTAATGTGGCTC CACCGAGGCCCATGTAATGCGGCCC AAACGGGCGCCATGTAATGCGGCCC CACCGAGGCCACTGCATTGGCGCC CACCGAGGCCCATGCATTGGCGCC CACCGAGGCCCATGCATTGGCGCC CACCGAGGCCCATGCATTGGCGCCC AAACGGGCGCCAGGCACGGCAAACGTC CACCGCGGGGAACGAGTGGAAACTTC CACCGCGGGGAACGAGTGGAAACGACC AAACGGCGGAACGACGAAAACGGCC AAACGGCGGAACGACGAAAACGGCC AAACGGCGGAACGACGAAAACGGCC AAACGGCGGAAGAGATGACC CGGCACGAGAAGGAAGGACA GGCGGGAATGCCTCCCAAAT GGCGGGAAGCAGCTACA GGCAGGAAGCCTCCCTGAA TGGAGTGGGAAGGAAAGGTA GGAAGTGGCCTGCCTGAAGGTA GGAAGTGGCCACGACGAAAGGTA GGAAGCTGGCACGAGGAAGGTA GGAAGTGGCCTGCTGCTGAA	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181671302-181674046 BLAT regions (hg19) chr19:55627180-55627199 ch/2:151131560-151131579 ch/3:181430550-181430569 ch/3:181430373-181430392 ch/3:181430363-181430382 ch/3:181430241-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (soun) SOX2 (soun) SOX2 (soun) SOX2 (soun) SOX2 (soun)	Notes Negative control Negative control
e5_S0X_R e6_S0X_R e6_S0X_R e7_S0X_F e7_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e9_AAVS1_R e9_AAVS1_R e9_AAVS1_R e9_AAVS1_R e9_S0X2_1,F e9_S0X2_1,F e9_S0X2_1,F e9_S0X2_1,F e9_S0X2_2,F e9_S0X2_2,F e9_S0X2_2,F e9_S0X2_2,F e9_S0X2_2,F e9_S0X2_4,F e9_S0X	AAALCATIGTICSCIIGAAGCITIC CACCGTCATATGCAAAACAAAACAA AAACTIGTITCTTCTGCAATAGTGAC CACCGTCATGTGTCATGCAATAGTGAC CACCGTCGACAAAACCTTAAACACAA AAACTIGTGTTTATGTGATAGTGAC CACCGTGGAAAAACTTAAACAAAA AAACTIGTGTTTAATGTGCCAC OX2 knockau Sequences CACCGTGGCACAATTAACCGGCCCCT AAACGGCGCGCATGTAATGGGCAC CACCGTGGCCAATGTAATGGGCAC CACCGTGGCCCATGCTATGGCCAC CACCGTGGCCCATGCTATGGCCAC CACCGTGGCCCATGCTATGGCCGCC AAACGGCCGCGCATGGATAGCAGCGCG AAACGGCCGCATGGCATG	ch3:181669056-181669075 ch3:181671304-181671323 ch3:181671304-181671323 ch3:181674027-181674046 ELAT regions (hg19) ch7:155627180-56627199 ch3:181430550-181130569 ch3:181430373-181430392 ch3:181430373-181430392 ch3:181430341-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (exon) SOX2 (soUR) FXR1 ATP11B SOX20T (P3)	Notes Negative control Negative control
eb_SUX_R eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_F eb_SUX_1R eb_L122_F eb_SUX_2R eb_	AAADCACTIGTITOSCI IGAAGCI TIC CACCGTCACTATIGTCAGAAGAAACAA AAACTIGTITTICTICTIGCATAGTGAC CACCGTAGAAAACTTAAACAGAAACAA AAACTIGTIGTITTICTICTIGCATAGTGAC CACCGTAGGAAAACTTAAACACAA AAACTIGTIGTITTIAGTC CACCGTAGGAAACATTAAACACAA AAACTIGTIGTITTIGTIGATTCCAC OX2 knockout Bequences CACCGTAGGCAACTTAAACCGGGCCCT CACCGGGGGGCAACTACATGAGCAC CACCGGGGGGCAATGACTATTIGCGCCC CACCGGGGGGCAATGACTATTIGCGCCC CACCGGGGGGCAATGACACCG CACCGGGGGGCAATGACACCG CACCGGGGGGCAATGACCACCG CACCGGGGGCAATGACCACCG CACCGGGGGCAATGACCACCG CACCGGGGGCAATGACCACCG CACCGGGGGCAATGACCACCG CACCGGGGGCAATGACCACCG CACCGGGGGCAATGACCACCG CACCGGGGGCAATGACCCGGGCCCA AAACGGCGGGAATCACTGGGGCCCAG CACCGGGGGCAACGACAAAAACAGCC CACCGGGGGCAACGACGGGCTGC CACCGGGGGCAACGACGGGCTGC CACCGGGGGAACGCAGGGGCACG GGCGGTGTCTTAACGAGGCACCA GGCGGGGATGCCTCCAAATG GGCGGGGATGCCTCCAAATG GGCGGGATGCCTCCCAAATG GGCGGGATGCCTCCCAAATG GGCGGGATCCCTCCCAAATG GGCGGGATCCCTCCCAAATG GGCGGGATCCCTCCCAAATG GGCGGGATCCCTCCCAAATG GGCGGGATCCCTCCCAAATG GGCAGAATCCCCCTTCAATG GGCAGAATCCCCCTTCAATG GGCAGAATCCCCCTTCAATG GGCAGAATCCCCCTTCCATG TTGAAGTGGGGCAGGGGAACGTA GGCAGGAACCCCCTGCTGAA TGGAGGGGCAGGCGGGGGGTG CAACGAGCGAGGCTTGCT CAACGCGGGAGGCAGGTAGCTAATG GGCAGAATCCCCCTTCCAAATG GGCAGAATCCCCCTTCCAAAGGTA GGCAGAATCCCCCTTCCATGA TTGAAGTGGGCAGGGCA	ch3:181669056-181669075 ch3:181671304-181671323 ch3:181671304-181671323 ch3:181674027-181674046 BLAT regions (hg19) chr19:55827180-55627199 ch2:151131560-151131579 ch3:181430550-181430569 ch3:181430373-181430382 ch3:181430373-181430382 ch3:181430363-181430382 ch3:181430241-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (soun) SOX2	Notes Negative control Negative control
eb_S0X_R eb_S0X_F eb_S0X_F eb_S0X_F eb_S0X_F eb_S0X_F eb_S0X_F eb_S0X_F sgRNA for CRISPR-mediated S Mames sg_AAVS1_F sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AVX_1R sg_AVX_1R sg_AVX_1R sg_AVX_1R sg_AVX_1R sg_AVX_1R sg_AVX_2R sg_S0X_2,R sg_S0	AAACCATIGITICSCIIGAAGCITIC CACCGTCATTGITCATAGCAAAACAA AAACTIGITTGITTCITCTGCATAGTGAC CACCGACGTAGAAAACTTAAACACAA AAACTIGIGITTAAGTTGCATAGTGAC CACCGTGGAACATTCACACACAA AAACTIGIGITTAAGTGICCCAC CACCGTGGAACATTCACACACAA AAACTIGIGITTGIGATAGTGCCC CACCGTGGCCAGTTAATGIGGCTC CACCGGGGGCGCATTGACACAG AAACCAGGCCGGTTAATGIGGCTC CACCGGGGGCCATTGCACCACC CACCGGGGGCCATTGACACACG CACCGGGGCCATGCACATGGCGCC CACCGGGGCCATGCACATGGCGCC CACCGGCGGCAATGCACATGGCGCC CACCGGCGGCAATGCACATGGCGCC CACCGGCGCAATGCCACC CACCGGCGCAGACACACGCCC CACCGCGCGCAGGCACACGCCC CACCGCGCGCAGACACACGCCC CACCGCGCGCAGACGCCAACTGCCCAC CACCGCGCGCGCAGCACACGCCC CACCGCGCGCAGACGCCGCGGCCCA CACCGGCGCCAGGCCCAGCCCACC CACCGCGCGGCCAGCGCCAGCCCACC CACCGCGCGCG	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181671304-181671323 ch/3:181674027-181674046 BLAT regions (hg19) chr/9:55627180-55627199 ch/2:151131560-151131579 ch/3:181430550-181430369 ch/3:181430373-181430382 ch/3:181430343-181430382 ch/3:181430241-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (sxon) SOX2 (3'UTR) FXR1 ATP11B SOX20T (P3) LINC01206	Notes Negative control Negative control
e5_S0X_R e5_S0X_R e5_S0X_F e5_S0X_F e7_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_F e8_S0X_1F e9_AVS1_F e9_AVS1_F e9_AVS1_F e9_S0X2_1F e9_S0X2_1F e9_S0X2_1F e9_S0X2_1F e9_S0X2_1F e9_S0X2_1F e9_S0X2_1F e9_S0X2_1F e9_S0X2_1F e9_S0X2_1F e9_S0X2_1F e9_S0X2_1F e9_S0X2_1F e9_S0X2_1F e9_S0X2_4F e9_S0X2_4F e9_S0X2_4F e9_S0X2_4F e9_S0X2_4F e9_S0X2_4F e9_S0X2_1F e1_S0X2_1F	AAADCATIGTICGCIIGAAGCITIC CACCGTCATTGTCAGAAGAACAA AAACTIGTITGTTCTGCGAAAGCAAACAA AAACTIGTITGTTCTGCGACAGAACAA AAACTIGTGTTTAGTGAAACCAA AAACTIGTGTTTAGTGAAACAA AAACTIGTGTTTAAGTGCCACACAA AAACTIGTGTTTAAGTGTCCCAC OZ2 MacCaA Bequences CACCGAGCCACATTAACCGGCCCCT AAACAGGCCCGGTTAATGTGGCTC CACCGAGCGCACATTAATGTGGCTC CACCGAGCGCACATTAATGTGGCTC CACCGAGCCACATTAATGTGGCTC CACCGGCGGCCATGCATTGGCGCG CACCGAGCCACATTCAATGGCGCCC CACCGAGCGCCATGCATTGGCGCCC CACCGAGCGCCATGCATTGGCCGCC AAACGGCGCCCAGTGGAAACAGCC CACCGAGCGCCAGCATGGCAACC CACCGGCGGCCAAGCGCGGCCGAA AACGGCGGCCCAGGCCGGCC	ch3:181669056-181669075 ch3:181671304-181671323 ch3:181671304-181671323 ch3:181674027-181674046 BLAT regions (hg19) chr19:55627180-55627199 ch2:151131560-151131579 ch3:18143050-181430369 ch3:181430373-181430382 ch3:181430341-181430382 ch3:181430241-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (exon) SOX2 (aUTR) FXR1 ATP11B SOX207 (P3) LINC01206 Amplified regions (hg19)	Notes Notes
eb_SUX_R eb_SUX_R eb_SUX_R eb_SUX_F eb_SUX	AAADCATIGTICSCIIGAAGCITIC CACCGTCATTATGCAGAAGAAACAA AAACTIGTITTICTICTICGATAGTGAC CACCGTCATTATGCAGAAGAAACAA AAACTIGTIGTITTICTICTICGATAGTGAC CACCGTGGAGAAAACTTAAACACAA AAACTIGTIGTITTICTICTICGATAGTGAC CACCGTGGAGCAAATTCAACACAA AAACTIGTIGTITTICTICTICAGTC CACCGTGGCGACAATTAACCGGGCCCT CACCGTGGCGCAATTAATCGGGCCC CACCGGCGGCAATTAATCGGGCAC CACCGGCGGCAATTAATCGGGCAC CACCGGCGGCAATGCATTGGGCGCC CACCGGCGGCAATGCATTGGGCGCC CACCGGCGGCAATGCATGGGCGCC CACCGGCGGCAATGCATGGGCGCC CACCGGCGGCCATGGATGGCGCC CACCGGCGCAAGCATGCACGGCGCC CACCGGCGCCAAGCGCGGCGCCGGAC CACCGGCGCCAAGCGCGGCGCGGCC CACCGGCGCCCAGGCCGCGGCCCGAC CACCGGCGCCCAGGCCCGGGCCCGAC CACCGCGGCCCCAGGCCCTTGC CACCGCGGCCCCAGGCCCTTGC CACCGCGGCCCCAGGCCCTTGC CACCGCGGCCCCAGGCCCCGGCC CACCGCGGCCCCAGGCCCTTGC CACCGCGGCCCCAGGCCCCTGCC CACCGCGGCCCCAGGCCCTGCC CACCGCGGCCCCAGGCCCTTGC CACCGCGGCCCCAGGCCCCGAC CACCGCGGCCCCAGGCCCCGGCC CACCGCGGCCCCAGGCCCCGGCC CACCGCGGCCCCAGGCCCCGCGGCCCGAC CACCGCGGCCCCAGGCCCCGAC CACCGCGGCCCCAGGCCCCGGCC CACCGCGGCCCCAGGCCCCGGCCCGAC CACCGCGCGCCCGGCCCGAGCCCGCGCGCCGCGCGCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGGCCCGCG	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181671304-181671323 ch/3:181674027-181674046 ELAT regions (hg19) ch/2:151131560-151131579 ch/3:181430550-181430569 ch/3:181430373-181430392 ch/3:181430373-181430392 ch/3:181430341-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (gx0n) SOX2	Notes Negative control Negative control Notes Notes Notes
e5_S0X_R e6_S0X_R e6_S0X_R e7_S0X_F e7_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e8_S0X_R e9_AVX9_R e9_AVX9_R e9_AVX9_R e9_AVX9_R e9_AVX9_R e9_AVX9_R e9_AVX9_R e9_S0X2_1,F e9_S0X2_1,F e9_S0X2_1,F e9_S0X2_2,F e9_S0X2_2,F e9_S0X2_2,F e9_S0X2_4,F e9_S0X	AAADCASTIGTICSCI IGAAGCI TIC CACCGTCATTGTCAGAAGAAACAA AAACTIGTITTCTTCTGCATAGTGAC CACCGTAGAAAACTTAAACACAA AAACTIGTITTGTTCTTCTGCATAGTGAC CACCGTAGGAAAACTTAAACACAA AAACTIGTGTTTAAGTTCCCAC OX2 knockout Bequences CACCGTAGGCAACTTCAACACAAA AAACTIGTGTTTGTGATGCCCC CACCGTAGGCAACTTCAACGGGCCCT AAACAGGGCGGCATTAACCGGGCCCT CACCGTAGGCACGTCAATTGAACCACGG CACCGTAGGCCGCATGTAACCGGGCCC CACCGGTAGTTCAATTGGCCCC CACCGGCAGTTCAATTGCCCCCC CACCGGCAGCTCCATTGCCCCCC CACCGGCAGCTCCATTGCCCCCCC CACCGGCAGCTCCATTGCCCCCCC CACCGGCAGCTCCATTGCCCCCCCCCC	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181671304-181671323 ch/3:181674027-181674046 BLAT regions (hg19) ch/7:955627180-55627199 ch/3:181430560-151131579 ch/3:181430550-181430569 ch/3:181430373-181430382 ch/3:181430373-181430382 ch/3:181430341-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (exon) SOX2 (gxUTR) FXR1 ATP11B SOX20T (P3) LINC01206 Amplified regions (hg19) ch/3:129250980-129250952 ch/11:112964712-112964844	Notes Notes Notes Notes Notes Notes Negative control region Negative control region
eb_SOX_R eb_SOX_F eb_SOX_F eb_SOX_F eb_SOX_F eb_SOX_F eb_SOX_F eb_SOX_F sgRNA for CRISPR-mediated S Names sg_AAVS1_F sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AAVS1_R sg_AX2_1 sg_SOX2_1_F sg_SOX2_1_F sg_SOX2_1_F sg_SOX2_1_F sg_SOX2_2_R sg_SOX2_2_R sg_SOX2_2_R sg_SOX2_2_R sg_SOX2_2_R sg_SOX2_4_R RT_QPCR Names RT_ACTB_R RT_ACTB	AAADCAATIGITICSCITIGAAGCITIC CACCGTACTATIGTCAGAAGAAACAA AAACTIGTITICTICTIGCATAGTGAC CACCGTAGAAAACTTAAAACACAA AAACTIGTIGTITIAGTTCACACAAA AAACTIGTIGTITIAGTTCACACAAA AAACTIGTIGTITIAGTCTCCACA CACCGTGGAACATTCAAACACAAA AAACTIGTIGTITIAGTCTCCCAC V2 knockout Sequences CACCGGAGCAACATTCAAACGGGCCCT CACCGGGGGCGGTTAATGTGGCCC CACCGGGGGCGGTTAATGTGGCCC CACCGGTGGGCATGGCTTATIGCGCGC CACCGGGGGGCAATGACACACC CACCGGGGGCGATTGAACACCC CACCGGGGGCGATTGAAGCACC CACCGGGGGCGATTGAACACCC CACCGGCGGCATGGCCCAGGCAACC CACCGGCGGCGAGTGAACTTCC CACCGGCGGAGCAAGACACC CACCGGCGGAGCAAGACACC CACCGGCGGAGCAAGACACC CACCGCGGAGCAAGACACC CACCGCGGAGCAAGACACC CACCGCGGAGCAAGACACC CACCGCGGAGCAAGACACC CACCGCGGAGCACAGGCACAC CACCGCGGAGCACAGGCCCAG CACCGCGGAGCACAGGCACA CCTGGATGCCCAGGGCCCAGGCCCAA CCTGGATGCCCAGGGCCCAGGCCCGAG GGCGCCAGGCCCAGGGCCCGAG CCGCGGAGCACCGCGAGGCACC CCGCGGGAGCACGGCCAGGCCCGAG GGCCCGGGCCGGGGCCCGGGCCCGAG CCGCGCGGGCCGGGGCCCGGGCCCGAG CCGCCGGGAGCACGGCCGGGCCCGAG CCGCGCGGGCCGGGGCCGGGCCGGAG CCGCCGGGGCCGGGGCCGGGCCGGAG CCGCGCGGGCCGGGGCCGGCGGCGC	ch/3:181669056-181669075 ch/3:181671304-181671323 ch/3:181671304-181671323 ch/3:181674027-181674046 BLAT regions (hg19) chr/9:55627180-55627199 ch/3:18143056-181131579 ch/3:18143056-181430569 ch/3:18143037-181430382 ch/3:18143033-181430382 ch/3:18143034-181430382 ch/3:18143034-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (exon) SOX2 (exon) SOX2 (exon) SOX2 (exon) SOX2 (g0TR) FXR1 ATP11B SOX207 (P3) LINC01206 Amplified regions (hg19) ch/3:129250860-129250952 ch/11:112964712-112964844	Notes Negative control Notes Notes Negative control region Negative control region
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eb_SOX_R eb_SOX_F eb_SOX_F eb_SOX_F eb_SOX_F eb_SOX_F eb_SOX_F eb_SOX_F sgRNA for CRISPR-mediated S Names sg_AAVS1_F sg_AAVS1_R	AAACCATIGITICSCI IGAAGCITIC CACCGTCATATIGCAAAAGAAACAA AAACTIGITITICTICTICGATAGTGAC CACCGTAGAAAACTTAAACACAA AAACTIGITITITICTICTICGATAGTGAC CACCGTAGGAAAACTTAAACACAA AAACTIGIGITITAGTITICCAC CACCGTAGGAACATTAAACCACAAA AAACTIGIGATTGAAAACTTAAACACAA AAACTIGIGATTGAGAACTTAAACCAGGCCC CACCGTGAGCAACATTAAACCGGCCCC CACCGTGGGTGGGTATAGTGAGCAC CACCGGGGGGGCATTAATGTGGCTC CACCGGGGGGGCATTGAAGCAGC CACCGGGGGGGCATTGAAGCAGC CACCGGGGGGCATTGATGAGCACC CACCGGGGGGCAATGACCACG CACCGGGGGACATGACTGAGCAAC CACCGGGGGGAATGCACGGGCCC AACCGGGGGACATGACCC CACCGGGGGAACATCACGGGCCC AACCGGGGGAACTTGGGCCC CACCGGGGAACCACGGGCCAGGGCCAA CACCGGGGGCAAGCAGCGGCCGAG CACCGGGGGCAGGGCCAGGGGCCAG CACCGGGGGAACCACGGGCCAGGGCCAA CACCGGGGGAACCACGGGCCAGAGAAAACAGCC CACCGGGGAACCGCGGGGGCCAAC CACCGGGGAACCACGGAAAAACAGCC CACCGGGGAACCACGGCCAGGGGCCAAC CACCGGGGAACCACGGAAAAACAGCC CACCGGGGAACCACGGAACAAACA	ch3:181669056-181669075 ch3:181671304-181671323 ch3:181671027-181674046 BLAT regions (hg19) chr19:55627180-55627199 chr2:151131560-151131579 chr3:18143059 chr3:18143059 chr3:181430373-181430382 chr3:181430363-181430382 chr3:181430341-181430260 Target genes ACTB HPRT1 GAPDH SOX2 (exon) SOX2 (exon) SOX2 (axon) SOX2 (ax	Notes Notes Notes Notes Notes
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Uncropped immunoblots included in supplementary figures



The above two images are from the same membrane that was scanned with two separate channels in LI-COR.



The above two images are from the same set of membranes that were scanned with two separate channels in LI-COR.