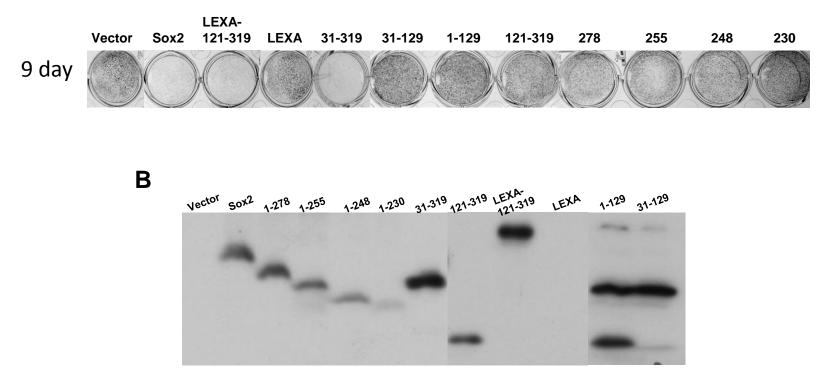
Seo_Supp_Fig1

Α



S 1. Nuclear localized C-terminal domain of Sox2 is sufficient to block osteoblast differentiation.

(A)Differentiation assay with mutants. Primary calvarial osteoblasts were infected with empty vector, Sox2, or indicated mutants respectively and differentiated. Plates are shown at 9 days stained for alkaline phosphatase.
(B) Western analysis. Expression of Sox2 or mutants viral constructs in primary osteoblasts for 48h was verified by immunoblotting with antibodies against C-terminal or HMG region of Sox2.

Seo_Supp_Table1

Gene	Description	Entrez ID	FC FF (72 hr)	p-value	
Arid4b	AT rich interactive domain 4B (RBP1-like)	94246	14.6	1.62E-06	down
Zfp281	zinc finger protein 281	226642	10.19	1.03E-04	down
SmarcaD1	SWI/SNK-related, matrix-associated	13990	9.9	4.41E-07	down
Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase	108155	9.1	5.79E-06	down
SkiL	ski-like	20482	8.77	6.09E-06	down
Rasa1	ras p21 protein activator 1	218397	8.3	5.99E-06	down
Tnr6cA	trinucleotide repeat containing 6a	233833	8	2.18E-06	down
Cbx5	chromobox homolog 5 (Drosophila HP1a)	12419	7.8	1.29E-06	down
Usp25	ubiquitin specific peptidase 25	30940	7.7	5.41E-05	down
Bmi-1	Bmi1 polycomb ring finger oncogene	12151	7.44	5.64E-05	down
Myst3	MYST histone acetyltransferase (monocytic leukemia) 3	244349	7.1	6.52E-06	down
eif4g2	eukaryotic translation initiation factor 4, gamma 2	13690	6.7	1.32E-05	down
Rbm39	RNA binding motif protein 39	170791	6.7	3.58E-05	down
2810474019Rik	RIKEN cDNA 2810474019 gene	67246	6.5	0.001243	down
Bclaf1	BCL2-associated transcription factor 1	72567	6.4	5.80E-05	down
APC	adenomatosis polyposis coli	11789	6.3	1.96E-05	down
FoxP1	forkhead box P1	108655	5.56	4.89E-06	down
Fam76b	family with sequence similarity 76	72826	5.2	1.39E-04	down
Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1	211673	4.98	3.39E-05	down
D730040F13Rik	RIKEN cDNA D730040F13 gene	242474	4.5	1.28E-04	down
Kpna3	karyopherin (importin) alpha 3	16648	4.4	3.39E-05	down
Ubr1	ubiquitin protein ligase E3 component n-recognin 1	22222	4.1	6.67E-05	down
Huwe1	HECT, UBA and WWE domain containing 1	59026	3.9	2.098185	down
Tia1	cytotoxic granule-associated RNA binding protein 1	21841	3.5	3.05E-06	down
Sash1	SAM and SH3 domain containing 1	70097	3.4	2.91E-06	down
Pcf11	cleavage and polyadenylation factor subunit homolog	74737	3.2	3.58E-04	down
Kif11	kinesin family member 11	16551	3.2	1.26E-04	down
Gnai1	guanine nucleotide binding protein (G protein), alpha inhibiting 1	14677	2.8	0.001156	down
Jarid2	jumonji, AT rich interactive domain 2	16468	2.7	0.003223	down
Rif1	Rap1 interacting factor 1 homolog (yeast)	51869	2.5	2.14E-04	down
Zik1	zinc finger protein interacting with K protein 1	22775	2.7	9.10E-05	down
Gsk3b	glycogen synthase kinase 3 beta	56637	2	0.002053	down
Tug1	nc RNA, taurine upregulated gene 1	544752	20.54	8.75E-08	down
Xist	nc RNA, inactive X-specific transcripts	213742	9.15	1.609613	down
Rock1	rho associated colied-coil protein kinase 1	19877	26.92	1.794977	down
suz12	suppressor of zeste 12 homolog (Drosophila)	52615	8.12	2.545952	down
wwp1	WW domain containing E3 ubiquitin protein ligase 1	107568	15.69	5.31034	down
KitL	kit ligand	17311	2.14	0.002737	down
Dcun1d1	DCN1 defective in cullin neddylation 1, domain containing 1	114893	8.13	5.25E-04	down
Dicer1	Dicer, Dcr-1 homolog (Drosophila)	192119	2.96	4.254125	down
CTGF	connective tissue growth factor	14219	3.56	5.66E-06	up
Armc6	armadillo repeat containing 6	76813	3.38	1.19E-05	up
Zfp428	zinc finger protein 428	232969	2.82	4.04E-06	up
CxCl12	chemokine (C-X-C motif) ligand 2	20310	2.32	1.882675	up
	frizzled homolog 2 (Drosophila)	57265	2.04	1.94E-04	up

Table S1. Fold change of genes regulated by Sox2 in Sox2 flox/flox (FF) cells at 72 hours after Cre Infection that are also changed in Sox2 flox/- cell. Genes in bold are defined as direct Sox2 targets by CHIP analysis in embryonic stem cells (9,13)