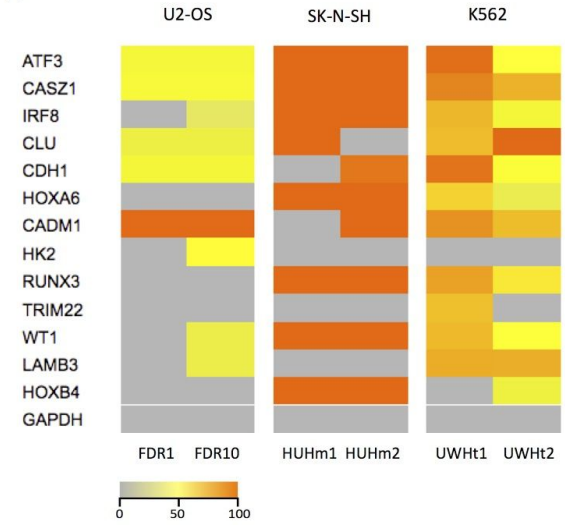
SUPPLEMENTAL FIGURES AND TABLES

A



B

Gene	U2-OS		SK-N-SH		K562	
	H3K27me3	qRT-PCR	H3K27me3	qRT-PCR	H3K27me3	qRT-PCR
ATF3	yes	up	yes	up	yes	up
CASZ1	yes	up	yes	up	yes	up
IRF8	yes	up	yes	up	yes	up
CLU	yes	up	yes	no	yes	up
CDH1	yes	up	yes	up	yes	no
HOXA6	no	no	yes	up	yes	up
CADM1	yes	up	yes	no	yes	no
HK2	yes	up	no	no	no	no
RUNX3	no	no	yes	up	yes	no
TRIM22	no	no	no	no	yes	up
WT1	no	no	yes	no	yes	up
LAMB3	no	up	no	up	yes	no
HOXB4	no	up	yes	no	yes	no
GAPDH	no	no	no	no	no	no

Figure S1. H3K27me3 enrichment at known Polycomb-regulated genes in U-2 OS, SK-N-SH, and K562. (A) H3K27me3 ChIP enrichment data for 13 known Polycomb-repressed genes and one active housekeeping-gene control. For each gene, we determined the highest ChIP signal within 1000 bp upstream of the TSS and along the gene body. These values were scaled to the maximum value within each set of data displayed here. For SK-N-SH and K562, we assessed the level of histone H3K27 trimethylation using shared and public data. SK-N-SH signals were determined using the Homer algorithm[1] for two replicate experiments (HUHm1 and HUHm2). SK-N-SH data was provided by B. Bernstein prior to submission to UCSC ENCODE database. K562 signals were determined using the Hotspots algorithm (UCSC Accession wgEncodeEH000923) for two replicate experiments (UWHt1 and UWHt2). For U-2 OS Hotspot values, FDR1 = a false discovery rate of 1%, FDR10 = a false discovery rate of 10%. (B) Comparison of H3K27me3 and response to PcTF expression (determined by qRT-PCR, see Fig. 1b) for each gene shown in A.

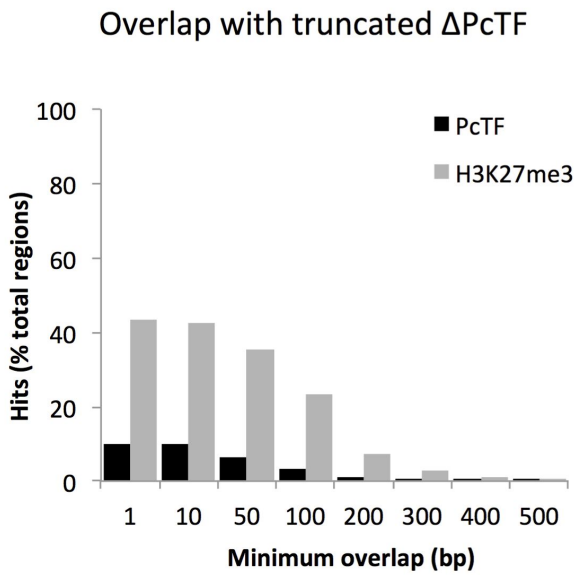


Figure S2. Overlap of PcTF and H3K27me3 ChIP-seq signal regions (Hotspots, FDR 1%) with signal regions from ChIP-seq for a cell line that expresses a truncated version of PcTF that lacks the PCD (histone-binding domain). The doxycycline-inducible delta-PcTF cell line was generated as described for PcTF. ChIP data was obtained as described for PcTF.

Gene Symbol	Transcript	Forward Primer	Reverse Primer	LNA probe
ATF3	NM_001030287	aaggattttcagcaccttgc	gatggcagaagcactcacttc	13
CADM1	NM_001098517	gcgcatgtcattagcatctc	ctcggcagcactacactcg	16
CASZ1	NM_001079843	caacaacaacctggtgaacg	ttcggaactcgcagtgct	54
CDH1	NM_004360	ggtctgtcatggaaggtgct	gatggcggcattgtaggt	5
CLU	NM_001831	gggaccagacggtctcag	cgtacttacttccctgattggac	1
HK2	NM_000189	tccttccctgaacctttcc	cagatttcaagagacatgacattagc	22
HOXA6	NM_024014	gcagcggatgaactcctg	ggttgaagtggaactccttctc	47
HOXB4	NM_024015	ctggatgcgcaaagttcac	agcggttgtagtgaaattcctt	62
IRF8	NM_002163	gaggtggtccaggtcttcg	cggccctggctgttatag	20
LAMB3	NM_001017402	cccagtttgctttgctgtg	gggcaaaacacaagaggaag	41
RUNX3	NM_004350	ggcctctccatgccttct	aggagggaagaaactacaaggac	38
TRIM22	NM_006074	tcacttctgagaatttaactttcgtt	ggctggtctccacaaatga	17
WT1	NM_001198551	agggctctgaggattgtgc	cgaaggtgaccgtgctgta	37

Table S1. Primers and probes were designed to analyze, via real time quantitative PCR, the expression of genes that were predicted as targets of the synthetic chromatin protein. The HUGO Gene Symbol and RNA transcript ID is shown for each gene. The Roche Assay Design Center tool (http://www.roche-applied-science.com/sis/rtpcr/upl/index.jsp?id=UP030000) was used to choose each forward primer, reverse primer, and Locked nucleic acid (LNA) probe from the Roche

Universal Probe Library (UPL).

SUPPLEMENTAL REFERENCES

1. Heinz S, Benner C, Spann N, Bertolino E, Lin YC, Laslo P, Cheng JX, Murre C, Singh H, Glass CK. (2010) Simple combinations of lineage-determining transcription factors prime cis-regulatory elements required for macrophage and B cell identities. Mol Cell. 38:576-89.