S1 Table. Sources of public data.

Experimental data type	Cell line	GEO/SRA ID(s)	Reference
Pol II ChIP-seq	MCF7	GSM822295	[1]
H2A.Z ChIP-seq	HMEC	GSM1003500	[1]
H3K4me3 ChIP-seq	HMEC	GSM733712	[1]
H3K27ac ChIP-seq	HMEC	GSM733660	[1]
H3K4me1 ChIP-seq	HMEC	GSM733705	[1]
HeK36me3 ChIP-seq	HMEC	GSM733707	[1]
TBP ChIP-seq	GM12878	GSM935277	[1]
GATA3 ChIP-seq	MCF7	GSM1010783	[1]
SP1 ChIP-seq	A549	GSM1010813	[1]
NFIC ChIP-seq	GM12878	GSM1010881	[1]
c-Fos ChIP-seq	K562	GSM935355	[1]
c-Jun ChIP-seq	K562	GSM935411	[1]
p300 ChIP-seq	MCF7	GSM1010800	[1]
CHD1-A ChIP-seq	K562	GSM1003575	[1]
Sap30 ChIP-seq	K562	GSM1003445	[1]
BRG1 ChIP-seq	HeLa	GSM935511	[1]
INI1 ChIP-seq	HeLa	GSM935634	[1]
BAF155 ChIP-seq	HeLa	GSM935637	[1]
BAF170 ChIP-seq	HeLa	GSM935638	[1]
CTCF ChIP-seq	A549	GSM1003606	[1]
FAIRE-seq	T-47D/A1-2	SRA044977	[2]
MNase-seq	MCF7	GSM1856003, GSM1856004, GSM1856005	[3]
Pol II ChIP-seq	GM12878	GSM935386	[1]
Pol II ChIP-seq	K562	GSM935358	[1]
NET-seq	HeLa	GSM1505438, GSM1505439	[4]
NET-seq	HEK239T	GSM1505440, GSM1505441	[4]
GRO-seq	GM12878	GSM1480326	[5]
GRO-seq	K562	GSM1480325	[5]
GRO-cap	GM12878	GSM1480323	[5]
GRO-cap	K562	GSM1480321	[5]
PRO-seq	K562	GSM1480327	[5]
SPT5 ChIP-seq	HeLa	GSM1280295	[6]
NELF-A ChIP-seq	HeLa	GSM1280296	[6]
NELF-E ChIP-seq	K562	GSM935392	[1]
Ccnt2 ChIP-seq	K562	GSM935547	[1]

1. Encode Project Consortium (2012) An integrated encyclopedia of DNA elements in the human genome. Nature 489: 57-74.
2. Burd CJ, Ward JM, Crusselle-Davis VJ, Kissling GE, Phadke D, et al. (2012) Analysis of chromatin dynamics during glucocorticoid receptor activation. Mol Cell Biol 32: 1805-1817.
3. Takaku M, Grimm SA, Shimbo T, Perera L, Menafra R, et al. (2016) GATA3-dependent cellular reprogramming requires activation-domain dependent recruitment of a chromatin remodeler. Genome Biol 17: 36.
4. Mayer A, di Iulio J, Maleri S, Eser U, Vierstra J, et al. (2015) Native elongating transcript sequencing reveals human transcriptional activity at nucleotide resolution. Cell 161: 541-554.
5. Core LJ, Martins AL, Danko CG, Waters CT, Siepel A, et al. (2014) Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. Nat Genet 46: 1311-1320.

6. Liu P, Xiang Y, Fujinaga K, Bartholomeeusen K, Nilson KA, et al. (2014) Release of positive transcription elongation factor b (P-TEFb) from 7SK small nuclear ribonucleoprotein (snRNP) activates hexamethylene bisacetamide-inducible protein (HEXIM1) transcription. J Biol Chem 289: 9918-9925.