

Supplementary Table S1. ChIP and FAIRE sequencing statistics, Related to Figures 1 and 2.

Library	raw reads		total aligned		total non-aligned		aligned to multiple places		unique alignments		PCR duplicates	
	reads	%	reads	%	reads	%	reads	%	reads	%	reads	%
HIRA ChIP	27,524,520	100	19,959,130	73	7,565,390	27	2,088,010	8	10,565,008	38	7,306,112	27
UBN1 ChIP	34,344,609	100	32,462,304	95	1,882,305	5	3,329,300	10	22,305,171	65	6,827,833	20
ASF1a ChIP	32,183,402	100	28,649,667	89	3,533,735	11	3,052,060	9	19,452,448	60	6,145,159	19
input	34,217,500	100	32,683,344	96	1,534,156	4	3,561,466	10	26,424,527	77	2,697,351	8
HA-H3.3 ChIP	35,698,648	100	31,252,271	88	4,446,377	12	3,004,809	8	24,279,974	68	3,967,488	11
FAIRE	35,762,737	100	25,623,173	72	10,139,564	28	4,468,770	12	18,098,502	51	3,055,901	9
input	37,319,035	100	33,905,676	91	3,413,359	9	4,237,570	11	28,758,882	77	909,224	2

Supplementary Table S2. Genomic locations probed by ChIP-PCR and corresponding primer sequences, Related to Figures 1, 2, S2.

	Related to figure	Genomic location (hg18)	Size	Forward primer sequence (primer ID)	Reverse primer sequence (primer ID)
1	Fig 1B, -10kb region	chr20 : 46234383 - 46234494	112bp	CGTGTGACTTTTGCTTCTCG (1257)	TCAGACATTGCACCAAGCTC (1258)
2	Fig 1B, -5kb region	chr20 : 46238499 - 46238594	96bp	TGCCTTCTCTTGCAGTGTG (1259)	GCCGACTTTGACATTTACCG (1260)
3	Fig 1B, -2kb region	chr20 : 46241060 - 46241145	86bp	TGAAGCTCTTGCCATGTGTC (1263)	CTGAATAAAGGGGACTGAGTGG (1264)
4	Fig 1B, 0kb region	chr20 : 46242773 - 46242889	117bp	TGAACAATGAGGCCACCATA (1128)	AAATTTCCACTGTGCTTCAACA (1132)
5	Fig 1B, +1kb region	chr20 : 46243817 - 46243898	82bp	AGGCCGATACCTGAGAATTG (1267)	TCCCATGACCACAGTGATTG (1268)
6	Fig 1B, +5kb region	chr20 : 46247073 - 46247166	94bp	GCCAAAAATGGACCTCAGTG (1273)	AAGGAGCACGAACGCTTATC (1274)
7	Fig 1B, +10kb region	chr20 : 46253138 - 46253240	103bp	GCAACGAGAACAATGAGGAAG (1275)	TGCCATGGGAGAAGTTAAGC (1276)
8	Fig 1C	chr20 : 46242773 - 46242889	117bp	TGAACAATGAGGCCACCATA (1128)	AAATTTCCACTGTGCTTCAACA (1132)
9	Fig S1A	chr20 : 46242773 - 46242889	117bp	TGAACAATGAGGCCACCATA (1128)	AAATTTCCACTGTGCTTCAACA (1132)
10	Fig 1E, top left	chr9 : 132711743 - 132711936	194bp	CTGAACCGTCTCCAAGAACC (1067)	CCCAGTACCGGCTACTTCAC (1068)
11	Fig 1E, top centre	chr11 : 47836056 - 47836221	166bp	CTCATTTTGCCTGCCAAGTT (1069)	GAAAAGCATTGGCCTCTGAC (1070)
12	Fig 1E, top right	chr20 : 46242773 - 46242999	227bp	TGAACAATGAGGCCACCATA (1071)	CGCCAATCCAAATTTTTCTG (1072)
13	Fig 1E, middle left	chr9 : 112340732 - 112340931	200bp	ATAGCTGGAGCTTTGGCTCA (1075)	AGCAGTTGCAGCTGTTCTGA (1076)
14	Fig 1E, middle centre	chr1 : 78071247 - 78071411	165bp	TGGCAGAGCATAGGAAAAGC (1077)	TGGGGCTGACATTTGATGTA (1078)
15	Fig 1E, middle right	chr9 : 129376242 - 129376399	158bp	TCCCTTTTCTTGGCTCAGG (1079)	CAGGACCTGTAGGTGGCATT (1080)
16	Fig 1E, bottom left	chr10 : 30752037 - 30752199	163bp	AGTGTGGCCTGGAAGACTG (1183)	GCTGAGGAAGTTCTGGATGG (1184)
17	Fig 1E, bottom centre	chr10 : 73601138 - 73601260	123bp	CAATCTCCACTTTAATCGTCACC (1185)	TGGTATCTTGCCATTGTACTION (1186)
18	Fig 1E, bottom right	chr17 : 22897979 - 22898139	161bp	ACGGTTGTGAGCTTCATGC (1187)	CTGATCCCCTGACATTCCTG (1188)
19	Fig 2C, Cluster1 left	chr2 : 145133621 - 145133710	90bp	CGAGCTGGGCTTAAAATTCA (1871)	GGCACCACGAAGAAAACATT (1872)
20	Fig 2C, Cluster1 right	chr5 : 32804652 - 32804742	91bp	CGATGGGACAGTTATTTGG (1875)	CCCTCTGGCATACTTCTTGC (1876)
21	Fig 2C, Cluster2 left	chr5 : 39461077 - 39461153	77bp	GGGTGCAAATAAGGACAGGA (1531)	ACGGATCTGTGAAACGAAGC (1532)
22	Fig 2C, Cluster2 right	chr1 : 29381316 - 29381406	91bp	GAGCTGGAGCTTTGGAATCA (1851)	AAAGGAGGGTCCGAGACATC (1852)
23	Fig 2C, Cluster3 left	chr1 : 194643811 - 194643938	128bp	GCCACTTGCCAATGTTTCTC (1355)	TGGCCCCATGTAGTGAAAAG (1356)
24	Fig 2C, Cluster3 right	chr4 : 119906101 - 119906177	77bp	TGGCAAAGATCTGGAAGTCAT (1841)	GGCCATATTTGTCCAAGTGC (1842)
25	Fig S2B, Cluster1	chr16 : 84106170 - 84106251	82bp	ATGCCTATGGATGTGTGTGC (1473)	ACACTGGGAGCAGCAAGATT (1474)
26	Fig S2B, Cluster2 left	chr1 : 151784191 - 151784268	78bp	TTTTTCCACCCCTCACTCAG (1337)	GGAGGGAAAAGAATGGCAAG (1338)
27	Fig S2B, Cluster2 right	chr3 : 14419070 - 14419144	75bp	CCGAGCTGGTATTTTTCCAC (1509)	ACCTCGCGTGTCTGTTGTCT (1510)

Supplementary Table S3. Overlap between HIRA/UBN1/ASF1a and chromatin proteins characterized by the ENCODE project, Related to Figure 4A.

Protein	% overlap with HIRA/UBN1/ASF1a
TFAP2A	20
TFAP2C	25
BAF155	57
BAF170	41
INI1	41
BRG1	36
c-MYC	35
MAX	42
JUND	50
c-FOS	31
c-JUN	37
RNA POL II	27
E2F1	10
E2F4	6
E2F6	8
NRF1	12
RPC155	4
TFIIIC	8
BDP1	2
BRF1	1
BRF2	0
TR4	2
p300	68