Supplementary tables

Table S1. Classification of Chromatin Regulatory Factors.

Gene name(a)	Description	Function(b)
Polycomb Repressive Complex 2		
*EZH2**	Catalytic subunit	H3K27me1/me2/me3 HMT. Major role in stem cell identity maintenance. Also methylates GATA4. Interacts with DNMTs.
SUZ12	EZH2 coenzyme	Required for PRC2 H3K27 HMT activity (1). Interacts with SIRT1.
EED		Different isoforms determine PRC3 or PRC4 PRC2 variants.
*RBBP4 (RBAP46)**		Required for the association of PRC2 to the histone tail (2). Binds Rb to regulate cell proliferation.
*RBBP7 (RBAP48)**		Interacts with BRCA1 and may regulate cell proliferation and differentiation.
PHF1 (PCL1)		Mediates PRC2 intrusion into active H3K36 chromatin regions (3).
PHF19 (PCL3)		Mediates interaction of PRC2 with H3K36me3, essential for full PRC2 activity (4).
ASXL1		Associates with PRC2 to promote gene repression (5).
MTF2 (PCL2)		Required for PRC2-mediated Hox repression (6).
*JARID2 (JMJ)**		Essential in embryonic development, inhibits H3K27me3 by PRC2.
*YY1**		Interacts with PRC2, and it is required for EZH2-mediated H3K27me3 (7). Also part of chromatin remodelling INO80 complex.
*SIRT1**	Class III HDAC	Transiently interacts with PRC2. Histone and protein deacetylase activity.
Polycomb Repressive Complex 1		
EZH1	Catalytic subunit	H3K27me1/me2/me3 HMT. Less critical for H3K27me3 formation than *EZH2*.
BAP1		Catalytic component of the PR-DUB complex, that specifically deubiquitinates H2AK119ub1.
BMI1		Maintenance of transcriptional repression of key genes during development. H2AK119ub.
RING1		H2AK119ub.
RNF2 (RING1B)		H2AK119ub. Acts as the main ub ligase in PRC1.
CBX2		
CBX3		Part of PRC1-like complex 4 (8). Binds the nuclear lamina through lamin B receptor.
CBX4		
CBX6		
CBX7		Promotes H3K9me3. Regulates cellular lifespan by repressing CDKN2A.
CBX8		
PCGF1 (NSPC1)	BCOR complex	Represses CDKN1A expression in a RARE-dependent manner.
PCGF2 (MEL18)		
PCGF6 (MBLR)		
PHC1		
PHC2		
PHC3		
AEBP2		
L3MBTL1		Specifically recognizes me1 and me2 lysines.
Histone deacetylases		
*HDAC1**	Class I	Controls embryonic stem cell differentiation (but not HDAC2) (9). Modulation of cell growth and apoptosis by down-regulation of p53. Also part of NuRD/Mi-2 ATP-dependent chromatin remodelling complex.
*HDAC2**		Relevant role in haematopoiesis. Also part of NuRD/Mi-2 ATP-dependent chromatin remodelling complex.
HDAC3		Modulation of cell growth and apoptosis by down-regulation of p53.
HDAC8		
HDAC4	Class Iia	Protects neurons from apoptosis.
HDAC9		
HDAC5		
HDAC7		
HDAC6	Class Iib	
HDAC10		
*SIRT1**	Class III, NAD-dependent	Interacts with PRC2, non-histone deacetylase activity. Involved in normal ageing through resistance to cellular stress. Deacetylates p53. Located in nucleus and cytoplasm (10).
SIRT2		Deacetylates alpha-tubulin. Located in the cytoplasm (10).
SIRT3		Located in the mitochondria (10).
SIRT4		

SIRT5		
SIRT6		Located in the nucleus (10). H3K9 and H3K56 deacetylase activity.
SIRT7		Located in the nucleus (10).
HDAC11	Class IV	
ARID4A		Bridging molecule to recruit HDACs.
TBL1XR1		Associates with HDAC3 (11).
NCOR1		Forms complex with HDAC1.
*TRIM28 (KAP1)**		Proposed to be a transcriptional repressor. Mediates apoptosis. through degradation of p53 (12).
Histone acetyltransferases		
EP300	Type A, CBP/P300 family	Acetylates all four core histones, and non-histone proteins like p53 and MyoD (13).
CREBBP (CBP)		Critical role in embryonic development, acetylates both histone and non-histone proteins.
NCOA3		HAT activity not studied in detail.
BRPF1 (TAF250)	Type A	
ATF2		Specifically acetylates H2B and H4 *in vitro*.
KAT6A (MOZ)	Type A, MYST family	Component of the MOZ/MORF complex, which has a histone H3 acetyltransferase activity.
KAT6B (MORF)		
KAT5 (TIP60)		
KAT8 (MOF)		
KAT7 (HBO1)		Responsible for the bulk of histone H4 acetylation *in vivo*.
KAT2A (GCN5)	Type A, GNAT family	
KAT2B (PCAF)		
HAT1	Type B	
ING4		Facilitates targeting of HBO1-mediated acetylation to H3K4me3 sites (14).
SET	HAT inhibitor	Promotes apoptosis. Inhibits p300/CBP and PCAF-mediated acetyltransferase.
Histone methyltransferases		
ASH1L (ASH1)		H3K36 HMT.
ASH2L		H3K4 HMT. Complex with MLL
*ATF7IP (MCAF)**		Required to stimulate SETDB1 activity, couples H3K9me3 with DNA methylation.
DOT1L (KMT4)		H3K79 HMT.
EHMT2 (G9a)		H3K9me1/me2, H3K27me HMT.
EHMT1		H3K9me1/me2 HMT.
*EZH2**		H3K27me1/me2/me3 HMT. Major role in stem cell identity maintenance. Also methylates GATA4. Catalytic subunit of PRC2 complex.
MEN1		H3K4 HMT. Essential component of a MLL/SET1 HMT complex. Represses telomerase expression. Role in TGFB1-mediated inhibition of cell-proliferation.
MLL		H3K4 HMT. Key regulator of development and haematopoiesis.
MLL2		H3K4 HMT.
MLL3		
MLL4		H3K4 HMT. Required to control the bulk of H3K4me3 during oocyte growth and preimplantation.
MLL5		H3K4me1/me2 HMT. Key regulator of haematopoiesis.
NSD1 (KMT3B)		H3K36, H4K20 HMT. May influence transcription positively or negatively.
PRDM2 (RIZ1)		H3K9 HMT.
PRDM9		H3K4me3 HMT. Essential for meiotic progression.
RBBP5		Complex with MLL.
RTF1		Required for H3K4me3 HMT on stem cell pluripotency genes.
SETD1A (SET1A)		H3K4 HMT.
SETD1B (SET1B)		H3K4 HMT.
SETD2 (KMT3A)		H3K36 HMT.
SETD7 (SET7)		H3K4 HMT.
SETD8 (KMT5A)		Trimethylates H4K20 (15).
SETDB1 (ESET)		H3K9 HMT.
SETDB2		H3K9 HMT.
SMYD1		H3K4 HMT (16).
SMYD2 (KMT3C)		H3K4me, H3K36me2 HMT. Also methylates TP53 and RB1.
SMYD3		H3K4me2/me3 HMT.
SUV39H1 (KMT1A)		H3K9me3 HMT, uses H3K9me1 as substrate.
SUV39H2 (KMT1B)		
SUV420H1 (KMT5B)		H4K20me3 HMT. Key in constitutive heterochromatin formation at pericentormeric regions.
SUV420H2 (KMT5C)		
*TRIM28 (KAP1)**		Mediates silencing by recruiting SET1 H3K9me3 HMT and HDAC NuRD complex. Mediates apoptosis through degradation of p53 (12).

WDR5		Complex with MLL.
Histone demethylases		
*KDM1A (LSD1)**		H3K4me2/me1, H3K9 HDM, also demethylates and stabilizes DNMT1.
*KDM1B (LSD2)**		H3K4me2/me1 HDM. Required for *de novo* DNA methylation of a subset of imprinted genes during oogenesis.
KDM2A		H3K36me2 HDM. Required to maintain heterochromatic state at centromeres.
KDM2B		H3K4me3, H3K36me2 HDM. Represses rRNA genes.
KDM3A		H3K9me2/me1 HDM.
KDM3B		H3K9 HDM.
KDM4A		H3K9me3, H3K36me3 HDM.
KDM4B		H3K9me3 HDM.
KDM4C		H3K9me3, H3K36me3 HDM.
KDM4D		H3K9me3/me2 HDM.
KDM5A (RBP2)		H3K4me2/me3 HDM. Prominent role in cell differentiation and senescence (17).
KDM5B (PLU1)		H3K4me3/me2/me1 HDM.
KDM5C (SMCX)		H3K4me3/me2 HDM. Participates in the repression of neuronal genes.
KDM5D (SMCY)		H3K4me3/me2 HDM.
KDM6A (UTX) *KDM6B (JMJD3)*		H3K27me2/me3 HDM. Regulation of HOX gene expression.
JHDM1D (KDM7A)		H3K9me2, H3K27me2, H4K20me1 HDM. Required for brain development.
KDM8 (JMJD5)		H3K36me2 HDM. Required for G2/M cell cycle progression.
JMJD1C (TRIP8)		H3K9 HDM.
JMJD6		H3R2, H4R3 HDM. Key regulator of haematopoietic differentiation.
PHF2		H3K9me2 HDM.
PHF8		H3K9me1/me2, H3K27me2, H4K20me1 HDM. Key role in cell cycle progression.
UTY		H3K27me3/me2/me1 HDM (18).
*JARID2 (JMJ)**		Essential role in embryonic development, inhibits PRC2 trimethylation of H3K27 (19).
DNA methyltransferases		
DNMT1		Maintainins methylation patterns established in development.
DNMT3A *DNMT3B*		Genome-wide *de novo* methylation, essential for the establishment of DNA methylation patterns during development.
DNMT3L		Catalytically inactive, but essential for DNMT3A and DNMT3B function.
MECP2 *MBD1* *MBD2** *MBD4*		Essential for embryonic development. Specifically bind methylated DNA and repress transcription at methylated promoters.
*ATF7IP (MCAF)**		Mediates MBD1 transcriptional repression, couples H3K9me3 with DNA methylation.
*KDM1A (LSD1)**		HDM, also demethylates and stabilizes DNMT1.
*KDM1B (LSD2)**		HDM, required for *de novo* DNA methylation of a subset of imprinted genes during oogenesis.
DNA demethylases		
TET1 *TET2*	Converts 5mC to 5hmC	Putative role in DNA demethylation (20).
AICDA (AID)		May play a role in DNA demethylation.
TDG		Essential for DNA demethylation (21).
ATP-dependent chromatin remodelling		
SMARCA2 (BRM)	SWI/SNF complex is required for transcriptional activation of genes normally repressed by chromatin (22).	Catalytic component of SWI/SNIF complex (23).
SMARCA4 (BRG1)		Essential for the maintenance of multipotent neural stem cells.
SMARCB1 (BAF47) *SMARCC1* *SMARCC2* *SMARCD1* *SMARCD2* *SMARCD3* *SMARCE1 (BAF57)* *ARID1A* *ARID1B (BAF250B)*		
ARID2 (BAF200)		Required for the stability of the SWI/SNF chromatin remodelling complex SWI/SNF-B.
ACTL6A (BAF53A)		Required for maximal SMARCA4 activity and for the association of the SWI/SNF complex with chromatin.
ACTL6B (BAF53B) *DPF1 (BAF45B)* *DPF2 (BAF45D)*		

DPF3 (BAF45C)		
EP400		Regulates nucleosome stability during DNA repair (24).
PBRM1		Regulator of cell proliferation.
PHF10 (BAF45A)		Required for the proliferation of neural progenitors.
MTA1	NuRD/Mi-2 complex has ATP-dependent chromatin remodelling activity and HDAC activity	
MTA2		
MTA3		Maintenance of the normal epithelial architecture through the repression of SNAI1 transcription in a HDAC-dependent manner.
CHD3 (Mi-2α)		
CHD4 (Mi-2β)		Main component of the NuRD/Mi-2 complex.
GATAD2A		
GATAD2B		
*HDAC1**		
*HDAC2**		
*MBD2**		Essential for embryonic development. Also bind methylated DNA.
*RBBP4 (RBAP46)**		Also part of PRC2 complex.
*RBBP7 (RBAP48)**		
INO80	INO80 complex has DNA- and nucleosome-activated ATPase activity and catalyzes ATP-dependent nucleosome sliding (25).	
TFPT		Putative regulatory component of the INO80 complex
*YY1**		Also interacts with PRC2 and is required for EZH2-mediated H3K27me3 (7).
SMARCA1 (SNF2L)	ISWI complex mobilizes mononucleosomes away from DNA ends without changing the arrangement of DNA on the surface of the histone octamer (22).	
SMARCA5 (SNF2H)		Required for replication of pericentric heterochromatin in S-phase specifically in conjunction with BAZ1A.
BAZ1A (ACF1)		
BAZ1B (WSTF)		Acts as a mark that distinguishes between apoptotic and repair responses to genotoxic stress. Maintenance of chromatin structures during DNA replication processes.
BAZ2A (TIP5)		
BPTF		Binds H3K4me3.
CHRAC1		
POLE3		
RSF1		
*RBBP4 (RBAP46)**		Also part of PRC2 complex.
*RBBP7 (RBAP48)**		
CHD1		Required for the maintenance of open chromatin and pluripotency in ESC.
CHD2		SNF2-related helicase/ATPase domains.
HNF1A		Possible regulation of transcription through chromatin remodelling (26).
*IKZF1**		Targets NuRD/Mi-2 and SWI/SNF complexes in a single complex.
Global chromatin regulators		
LMNA	lamin A/C	Global heterochromatic changes induced by lamin perturbation are often mirrored by altered levels of chromatin-associated epigenetic histone marks (27).
LMNB1	lamin B1	
LMNB2	lamin B2	
Other chromatin regulators		
BAG6	Complex EP300	p300-mediated p53 acetylation upon DNA damage. May mediate H3K4me2.
ATRX	ATRX-DAXX complex	Thought to regulate deposition of H3.3 at heterochromatic regions of the genome, including telomeres (28).
DAXX		
MUM1		Opens chromatin to facilitate DNA damage repair (29).

*Genes with more than one function in chromatin remodelling appear more than once in the table.

(a) HGNC HUGO gene names. In parenthesis, common alternative gene names.

(b) Gene function provided by Uniprot, unless otherwise stated.(30)

Table S2. Described oncogenic alterations in Chromatin Regulatory Factors. This is an exhaustive compilation of alterations(*) reported in CRFs not included in Table 1. Gene names correspond to HUGO HGNC approved symbols. In bold typeface, genes included in the Cancer Gene Census (CGC) (31). ALL: Acute Lymphocytic Leukaemia; AML: Acute Myeloid Leukaemia; B-ALL: B Acute Lymphoblastic Leukaemia; B-NHL: B-cell non-Hodgkin Lymphoma; CLL: Chronic Lymphocytic Leukaemia; ccOC: Clear Cell Ovarian Carcinoma; ccRCC: clear-cell Renal Cell Carcinoma; CMML: Chronic Myelomonocytic leukaemia; ESCC: Oesophageal Squamous Cell Carcinoma; FL: Follicular Lymphoma; HCC: Hepatocellular Carcinoma; HL: Hodgkin Lymphoma; HNSCC: Head and Neck Squamous Cell Carcinoma; MCL: Mantle cell Lymphoma; MDS: Myelodysplastic Syndrome; MSI: Microsatellite instability; NMSC: Non-Melanoma Skin Cancer; NSCLC: Non-Small Cell Lung Carcinoma; OSCC: Oral Squamous Cell Carcinoma; RCC: Renal Cell Carcinoma; T-ALL: T Acute Lymphoblastic Leukaemia.

*Evidence based solely on cancer cell lines is excluded from this table. Only evidence in human samples have been used. Effects of pharmacological inhibition are not included. Germline polymorphisms are excluded.

Gene	Literature evidence
AEBP2	Deleted in AML (32).
ATF2	Over-expressed in melanoma (33).
BAZ1A	Amplified in ESCC (34). Deleted in papillary type 2 RCC (35).
BMI1	Over-expressed in B-NHL, leukaemia, MCL, medulloblastoma, neuroblastoma, NSCLC (36) and prostate tumours (37).
CBX2	Over-expressed in breast cancer (38).
CBX3	Over-expressed in osteosarcoma (39), myxoid liposarcoma, colon, breast, esophageal, cervical, and lung tumours (40).
CBX7	Over-expressed in lymphoma (41). Down-regulated in bladder (42), and aggressive gastric (43), pancreatic (44) and thyroid cancer (45).
CHD1	Mutated in high MSI gastric and colorectal cancers (46). Deleted in prostate cancer (47).
CREBBP	Mutated in AML, ALL, DLBCL, N-NHL (CGC), bladder (48), medulloblastoma (49) and SCLC (50). LOH in lung (51).
DAXX	Mutated in paediatric glioblastoma and neuroendocrine pancreatic tumours (CGC). Over-expressed in prostate cancer (52).
DNMT1	Over-expressed in AML (53), gliomas (54) and pancreatic tumours (55).
DNMT3B	Over-expressed in breast (56), colorectal and stomach (57), prostate cancer (58), advanced stages of DLBCL (59).
DNMT3L	Over-expressed in testicular embryonal carcinoma (60). Loss of methylation and consequent over-expression in cervical cancer (61).
EHMT2	Over-expressed in bladder (62), resistant cervical (63) and aggressive lung tumours (64).
EPC1	Mutated in pancreatic cancer (65).
EZH1	Over-expressed and amplified in myeloproliferative neoplasms (66).
EZH2	Mutated in DLBCL (CGC), MDS (67). Over-expressed in bladder, breast, colon, liver, melanoma and prostate tumours; DLBCL, HL and MCL (36).
GATAD2B	Deleted in OSCC (68).
HDAC1	Over-expressed in HCC (69). Down-regulated in aggressive breast tumours (70).
HDAC2	Mutated in colon cancer with microsatellite instability (71). Over-expressed in gastrointestinal tumours (72), prostate (73), aggressive HCC (74), lung (75), cervical (76), ovarian and endometrial endometrioid carcinomas (77).

HDAC3	Over-expressed in gastrointestinal tumours (72), b-cell lymphomas (78) and CLL (79).
HDAC4	Mutated in melanoma (80) and breast cancer (81). Over-expressed in T-ALL (82) and treatment-resistant ovarian tumours (83).
HDAC5	Over-expressed in B-ALL (82) and aggressive medulloblastoma (84).
HDAC6	Over-expressed in HCC (85), cisplatin-resistant NSCLC (86) and breast tumours with good prognosis (87). Down-regulated in CLL (79).
HDAC7	Over-expressed in pancreatic adenocarcinoma (88) and aggressive childhood ALL (82).
HDAC8	Over-expressed in aggressive neuroblastoma (89).
HDAC9	Over-expressed in high grade medulloblastoma (84) and childhood ALL with poor prognosis (82). Amplified in OSCC (68).
HDAC10	Down-regulated in adrenocortical tumours (90), CLL (91) and aggressive NSCLC (92).
HNF1A	Mutated in neuroendocrine tumours (93), endometrial cancer (94), high MSI CRC (95) and hepatocellular adenoma (96). Down-regulated in aggressive HCC (97).
IKZF1	Mutated in ALL, DLBCL (CGC). Deleted in aggressive paediatric B-ALL (98).
ING4	Down-regulated in HNSCC (99), melanoma (100), gastric adenocarcinoma (101), lung tumours (102) and colorectal cancer (103). Deleted in HNSCC (99) and breast tumours (104).
JARID2	Mutated in NSCLC (105). Deleted in AML (32).
JMJD1C	Over-expressed in pancreatic ductal adenocarcinoma (106).
JMJD6	Over-expressed in aggressive breast tumours (107).
KAT5	Down-regulated in gastric cancer (108), aggressive melanoma (109) and advanced colorectal carcinoma (110).
KAT6A	Translocated in AML (111).
KAT6B	Translocated in AML (111) and benign uterine tumours (112).
KAT7	Over-expressed in testicular, breast, ovarian, bladder, oral and oesophageal carcinomas (113).
KAT8	Down-regulated in breast carcinoma and medulloblastoma (114).
KDM1A	Over-expressed in NSCLC (115), highly malignant sarcomas (116), bladder (117) and aggressive prostate tumours (118). Down-regulated in breast carcinoma (119).
KDM2A	Down-regulated in prostate cancer (120).
KDM2B	Over-expressed in ALL, AML (121) and pancreatic ductal adenocarcinoma (106).
KDM3A	Over-expressed in prostate cancer (122) and RCC (123).
KDM3B	Over-expressed in ALL (124) and prostate cancer (122).
KDM4A	Over-expressed in breast (125) and prostate cancer (122). Down-regulated in bladder tumours (126).
KDM4B	Over-expressed in gastric cancer (127).
KDM4C	Over-expressed and amplified in breast cancer (128).
KDM5A	Mutated in AML (CGC). Down-regulated in melanoma (129). Over-expressed in breast tumours with good prognosis (130) and in pancreatic ductal adenocarcinoma (106).
KDM5B	Over-expressed in breast tumours, prostate cancer (122) and uveal melanoma (131).
KDM6B	Over-expressed in HL (132) and pancreatic ductal adenocarcinoma (106).
LMNA	Over-expressed in aggressive colorectal cancer (133). Down-regulated in DLBCL (134), ALL and NHL (135).
LMNB1	Over-expressed in HCC (136) and colorectal tumours (137).
MBD4	Mutated in sporadic colon cancer (138) and HNPCC with MSI (139).

MECP2	Over-expressed in breast tumours (140).
MEN1	Mutated in pancreas, parathyroid (CGC) and in lung carcinoids (141). MLL-fusion partner in leukaemias (142).
MLL5	Down-regulated in poor prognosis AML (143).
MTA1	Over-expressed in OSCC, ESCC, early NSCLC, HCC, osteosarcoma, and colorectal, pancreatic, endometrial, ovarian, prostate, breast and gastric cancers. It is one of the most commonly over-expressed genes in human tumours (144).
MTA2	Over-expressed in NSCLC (145), aggressive HCC (146) and epithelial ovarian cancer (147).
MUM1	Over-expressed in aggressive PCLBCL (148) and CLL (149), DLBCL and HL (150).
NCOA3	Over-expressed in HCC, breast (151), urothelial carcinoma of the bladder (152), NSCLC (153) and prostate tumours (154). Amplified in breast cancer (155). Fusion partner of KAT6A in AML (156).
PCGF2	Over-expressed in aggressive medulloblastoma (157). Down-regulated in breast tumours (158) and high-grade prostate cancer (159).
PHC1	Over-expressed in ALL (36).
PHF8	Over-expressed in prostate cancer (122).
PHF19	Over-expressed in colon, skin, lung, rectal, cervical, uterine and hepatic tumours (36).
PRDM2	Mutated in endometrial, gastrointestinal (160) and colon tumours with MSI (161), melanoma (162). Over-expressed in ALL (163). Down-regulated in ESCC (164), neuroblastoma (165), HCC (166), epithelial ovarian carcinoma (167), thyroid carcinoma (168) and AML (163). Deleted in parathyroid tumours (169).
RBBP4	Over-expressed in HPV-positive oropharyngeal tumours (170). Down-regulated in mucoepidermoid carcinoma (171).
RBBP5	Amplified in glioblastomas (172).
RBBP7	Over-expressed in NSCLC (173) and breast tumours (174).
RING1	Over-expressed in prostate tumours (37).
RSF1	Over-expressed in NSCLC (175), urinary bladder (176), colon (177), gallbladder (178), nasopharyngeal (179) and ovarian aggressive carcinomas (180). Amplified in aggressive ovarian carcinoma (181).
SET	Mutated in AML (CGC). Over-expressed in colorectal adenocarcinoma (182) and paediatric B-ALL and T-ALL (183).
SET8	Over-expressed in aggressive breast tumours (184).
SETDB2	Deleted in CLL (185).
SIRT1	Over-expressed in leukaemia, prostate, skin and colon cancers (186) Down-regulated in breast tumours and HCC (187).
SIRT2	Down-regulated in gliomas (188).
SIRT3	Down-regulated in HCC (189).
SIRT6	Down-regulated in pancreas and colorectal cancer (190). Deleted in colorectal cancer (190).
SIRT7	Over-expressed in breast (191) and thyroid carcinoma (192).
SMARCB1	Mutated in malignant rhabdoid tumours (CGC).
SMARCC1	Over-expressed in prostate cancer (193) and precancerous cervical lesions (194). High expression correlates with good prognosis in colorectal cancer (195).
SMARCD1	Mutated in breast tumours (196).
SMARCD3	Over-expressed in advanced neuroblastoma (197).
SMARCE1	Over-expressed in aggressive endometrial carcinoma (198).
SMYD2	Over-expressed in ESCC (199).
SMYD3	Over-expressed in colorectal cancer (200).
SUZ12	Mutated in endometrial stromal tumours (CGC). Over-expressed in breast, colon, liver (36) and ovarian tumours (201).

	Amplified in MCL (202).
TBL1XR1	Over-expressed in SCC (203). Deleted in ALL (204) and PCNSL (205).
TET1	Mutated in T-ALL (206). Down-regulated in prostate and breast tumours (207).
TFPT	Mutated in pre-B ALL (CGC).
TRIM28	Over-expressed in colorectal tumours (208), gastric cancer cell lines (209), NSCLC and breast (210). Over-expression predicts better survival in early lung tumours (210). High expression indicates good prognosis in gastric cancer (209).
YY1	Over-expressed in prostate, colon, ovary, breast, bone, liver, lung, bladder, cervix, skin and blood (DLBCL, AML, CML, ALL, HL, BL, MCL, CLL and FL) cancers (211). Down-regulated in melanomas, paediatric osteosarcomas and urothelial carcinomas (211). There are contradictory results on the prognostic significance of YY1 in cancer (211).

Table S3. Mutually exclusivity test for mutations in genes coding proteins that act in the same complex.

Protein complex	Site	Gene 1	Gene 2	*P* value Fisher Test
SWISNF	Bladder	ARID2	ARID1A	0.02
ISWI	Bladder	BAZ2A	BPTF	0.03
NURDMI2	Bladder	CHD3	CHD4	$P < 10^{-16}$
SWISNF	Breast	ARID2	ARID1A	0.01
SWISNF	Breast	SMARCA2	ARID1A	0.01
SWISNF	Breast	SMARCA4	ARID1A	$P < 10^{-16}$
ISWI	Breast	BAZ2A	BPTF	$1.08*10^{-5}$
NURDMI2	Breast	CHD3	CHD4	$1.13*10^{-6}$
PRC1	Breast	BAP1	PHC3	$P < 10^{-16}$
SWISNF	Head & Neck	ARID2	SMARCA4	0.05
NURDMI2	Head & Neck	CHD3	CHD4	$1.98*10^{-5}$
PRC1	Head & Neck	BAP1	PHC3	0.01
SWISNF	Lung	SMARCA2	SMARCA4	0.04
SWISNF	Lung	SMARCA2	ARID1A	0.04
ISWI	Lung	BAZ2A	BPTF	$P < 10^{-16}$
NURDMI2	Lung	CHD3	CHD4	$8.35*10^{-9}$
PRC1	Lung	BAP1	PHC3	0
SWISNF	Ovary	ARID2	SMARCA4	0.05
SWISNF	Uteri	PBRM1	ARID1A	0.02
SWISNF	Uteri	SMARCA4	ARID1A	0
ISWI	Uteri	BAZ2A	BPTF	0
NURDMI2	Uteri	CHD3	CHD4	$5.29*10^{-8}$

Table S4. Gene regulatory modules collected for the analysis.

Group	Name	Cell type	Nº of genes	Source
EP300	EP300 ES	ES	1191	Lister *et al*. 2009 (212)
	EP300 CD4	CD4	3792	Wang *et al*. 2009 (213)
Activating histone marks	H3K4me3 ES	ES	12312	ENCODE (214)
	H3K4me3 CD4	CD4	11423	Barski *et al*. 2007 (215)
	H3K4me3 gm12878	gm12878	11771	ENCODE (214)
	H3K9ac ES	ES	10489	ENCODE (214)
	H3K9ac CD4	CD4	6906	Wang *et al*. 2009 (213)
	H3K9ac gm12878	gm12878	9918	ENCODE (214)
Repressive histone marks	H3K27me3 ES	ES	6665	ENCODE (214)
	H3K27me3 CD4	CD4	5207	Wang *et al*. 2009 (213)
	H3K27me3 gm12878	gm12878	6099	ENCODE (214)
Replication Timing	Late RT ES	ES	918	Hansen *et al*. 2010 (216)
	Late RT lymphoid	lymphoid	260	Hansen *et al*. 2010 (216)

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