

Supplementary Table S1. Chromatin Remodelers/Modulators differentially expressed during cell transformation. The Table describes their reported function and involvement in cancer, and provides the corresponding references. Abbreviations: TDRD – Tudor domain, HMT – histone methyltransferase, BRD – bromodomain, CHD – chromodomain, HAT – histone acetyltransferases. Supplementary data references are in the Additional file 6 of this manuscript.

CRM (Alternative symbol) NCBI gene ID gene name			co-path	CR class	Functional group / Function	Involvement in cancer
<i>HELLS</i> (<i>LSH</i>)	3070	helicase, lymphoid-specific	i	remodeler	SNF2-like protein/ transcriptional repressor ^{1,2,3}	Overexpressed in prostate cancer; drives retinoblastoma tumor progression ^{4,5}
<i>LBR</i>	3930	lamin B receptor	i	reader	TDRD containing protein/ bind H4K20me2/ Represses transcription ⁶	Unknown
<i>SCML2</i>	10389	sex comb on midleg-like 2	i	-	Polycomb group (PcG) gene, part of PRC1 complex/ binds and modulates CDK/CYCLIN/p21 complexes ⁷	Overexpressed in AML patients ^{8,9}
<i>SUV39H2</i> (<i>KMT1B</i>)	79723	suppressor of variegation 3-9 homolog 2 (Drosophila)	i	writer	HMT/ Trimethylates 'Lys-9' of histone H3/ maintains heterochromatin, ensures genome stability ^{10,11}	Overexpressed in human lung, bladder cancers, multiple myeloma; suggested as a novel target of anticancer therapy ¹²
<i>MTF2</i> (<i>PCL2</i>)	22823	metal response element binding transcription factor 2	i	-	PcG gene, associates with the PRC2 complex and promotes H3K27me3 at target genes ¹³	Unknown
<i>SP110</i> (<i>IFI45</i>)	3431	SP110 nuclear body protein	ii	reader	BRD containing protein, known to recognize acetyl- lysine residues/ potentially involved in chromatin remodeling ¹⁴	Unknown
<i>KDM4D</i> (<i>JMJD2D</i>)	55693	lysine (K)-specific demethylase 4D	ii	eraser	Histone demethylase/ demethylase both H3K9me2 and H3K9me3 ¹⁵	Both pro-oncogenic function and activation of p53-dependent gene expression are reported ¹⁶
<i>TDRD7</i>	23424	tudor domain containing 7	iii	reader	TDRD containing protein/ preferentially binds H3K9me2/3 ¹⁷	Unknown
<i>CHD7</i>	55636	chromodomain helicase DNA binding protein 7	iv	reader	CHD enzyme of SNF2 family/ bind to methylated H3K4/ positive regulator of rRNA biogenesis ^{18,19}	Dysregulated in 13-35% of pancreatic adenocarcinoma; low CHD7 expression predicts higher survival outcomes in patients with pancreatic cancer ^{20,21}
<i>AKAP1</i> (<i>TDRD17</i>)	8165	A kinase (PRKA) anchor protein 1	iv	reader	Protein, containing TDRD, known to bind di- and trimethylated lysine and dimethylated arginine ²²	Unknown
<i>CHD1</i>	1105	chromodomain helicase DNA binding protein 1	iv	reader	CHD, containing protein/ Bind trimethylated lysine with sequence specificity via tandem chromodomain ²³	Tumor suppressor required for ERG rearrangement in prostate cancer ²⁴
<i>PRMT6</i>	55170	protein arginine methyltransferase 6	iv	writer	Methyltransferase/ Generates monomethylarginine and asymmetric dimethylarginine ^{25,26}	Knockdown of PRMT6 in osteosarcoma cells led to the up- regulation of THBS1, natural inhibitor of angiogenesis and cell migration ²⁷

CRM (Alternative symbol) NCBI gene ID gene name		co-path	CR class	Functional group / Function	Involvement in cancer	
<i>GTF3C4</i> (<i>KAT12</i>)	9329	general transcription factor IIIC, polypeptide 4, 90kDa	iv	writer	HAT/ has substrate specificity for H3 ²⁸	Unknown
<i>PRMT5</i>	10419	protein arginine methyltransferase 5	iv	writer	Generates mono- and dimethylarginin, dimethylates histones H3 and H4 and nonchromatin proteins ^{29,30}	Overexpressed in ovarian cancer and glioblastoma, candidate therapeutic target in glioblastoma ^{31,32}
<i>PRMT3</i>	10196	protein arginine methyltransferase 3	iv	writer	Generates monomethylarginine and asymmetric dimethylarginine ³³	Unknown
<i>MINA</i> (<i>MDIG</i>)	84864	MYC induced nuclear antigen	iv	eraser	Histone demethylase/ demethylase of H3K9me3 ^{34,35}	Overexpressed in colon cancer, associated with lung cancer, potential prognostic factor for esophageal squamous cell carcinoma; marker of adenocarcinoma ³⁶⁻³⁹
<i>KAT2A</i> (<i>GCN5</i>)	2648	K(Lysine) acetyltransferase 2A	iv	writer	HAT/ belongs to SAGA and ATAC complexes ^{40,41}	Promote transcription of TNFRSF10A/10B in lung cancer cells ⁴²
<i>SHPRH</i>	257218	SNF2 histone linker PHD RING helicase	iv	reader?	PhD containing protein, but doesn't recognize H3K4/ Poly-Ubiquitinate PCNA ⁴³	Possible candidate for the tumor suppressor gene ⁴⁴
<i>KDM1A</i> (<i>KDM1A</i>)	23028	lysine (K)-specific demethylase 1	iv	eraser	HMT/ Demethylate both H3K4me1/me2 and H3K9me1/me2, thus acting as coactivator or a corepressor ^{45,46}	Overexpressed in bladder, colorectal, gastric, lung, ER-negative breast cancers, chondrosarcoma, osteosarcoma ⁴⁷⁻⁴⁹
<i>UHRF1</i>	29128	ubiquitin-like with PHD and RING finger domains 1	iv	reader	TDRD and PHD containing protein/ Binds to H3K9me3 and unmodified H3 ^{50,51}	Drive retinoblastoma tumor progression; upregulated and associated with cellular proliferation on colorectal cancer; overexpressed in hepatocellular carcinoma ^{5,52,53}
<i>SMARCA2</i> (<i>HBRM</i>)	6595	SWI/SNF related, matrix associated, actin dep-t regulator of chromatin A2	v	reader	BRD containing protein/ stabilize the interaction between DNA and histones ⁵⁴	Loss of SMARCA2 confer a proliferative advantage in prostate cancer ⁵⁵
<i>MBD5</i>	55777	methyl-CpG binding domain protein 5	v	reader	Binds to heterochromatin, but does not interact with methylated or unmethylated DNA ⁵⁶	Unknown
<i>PRDM1</i>	639	positive regulatory domain-containing protein 1	vii	writer	Methyltransferase/ potential nucleator for H3K27me3 accumulation and spread ^{22,57}	Tumor suppressor in diffuse large B-cell lymphomas, in aggressive natural killer cell lymphomas and anaplastic large-cell lymphoma ⁵⁸⁻⁶⁰
<i>HDAC5</i>	10014	histone deacetylase 5	vii	eraser	Deacetylase/ required for maintenance of pericentric heterochromatin and long telomeres ^{61,62}	Downregulated in glioblastoma ⁶³