#### Supplemental Figure Legend

## Supplementary Figure 1. BRWD2/PHIP CRISPR knockout and antibody validation A. Design of BRWD2/PHIP CRISPR-Cas9 gene knockout strategy. CRISPR sgRNA guides were designed flanking the BRWD2/PHIP promoter and first 4 exons (region highlighted in pink). H3K4me3 and H3K27ac ChIP-seq are shown to identify the BRWD2/PHIP promoter. B. RNA-sequencing track example at the BRWD2/PHIP locus in wildtype HCT-116 and 2 independent BRWD2/PHIP knockout (\DRWD2/PHIP) clones. BRWD2/PHIP transcripts are undetectable in $\Delta$ BRWD2/PHIP clones whereas transcript levels of neighboring gene (HMGN3) are not altered. C. Western blotting for BRWD2/PHIP in HCT-116 wildtype and $\Delta$ BRWD2/PHIP cells. BRWD2/PHIP is undetectable in ΔBRWD2/PHIP cells using antibodies #833 (ab#833) and #834 (ab#834). Arrow to the right of the ab #834 panel indicates the specific BRWD2/PHIP band, whereas the asterisk indicates a non-specific band that migrates above BRWD2/PHIP. D. Example UCSC genome browser track of BRWD2/PHIP and H3K4me1 ChIP-seq in wildtype and $\Delta BRWD2/PHIP$ HCT-116 cells. BRWD2/PHIP ChIP-signal with both antibodies is markedly reduced in ABRWD2/PHIP mutant HCT-116 cells, whereas H3K4me1 signal is unchanged. E. Genome wide occupancy plot of BRWD2/PHIP and H3K4me1 ChIP-seq signal in HCT-116 wildtype and $\Delta$ BRWD2/PHIP mutant cells. F. Venn diagram of BRWD2/PHIP ChIP-seq peaks detected in HCT-116 wildtype and △BRWD2/PHIP cells. For antibodies #833 and #834 respectively, 31,515 and 37,972 BRWD2/PHIP peaks are detected in wildtype HCT-116 cells. In $\Delta$ BRWD2/PHIP mutant cells 29,380 (93%) and 36,557 (96%) of wildtype peaks are lost.

## Supplementary Figure 2. Analysis of BRWD2/PHIP protein-protein interactions by tandem mass spectrometry

A. Table of selected MS results from the representative purification in Figure 2A. Spectral counts for two control replicates and two Flag-BRWD2/PHIP replicates are shown. Interacting proteins are broken down into six categories: CUL4-DDB1 (CRL4), COP9 Signalosome (CSN), Nedd8-binding, histones, chromatin remodelers and other proteins. Note that spectral counts for CRL4 components, in particular DDB1, are highly abundant in Flag-BRWD2/PHIP purifications suggesting a strong interaction. B. MS results from purifications of Flag-BRWD2/PHIP after treatment with combinations of MLN4924 and MG132. In the presence of MLN4924, spectral counts for Nedd8 are dramatically diminished. In addition association of CSN and the Nedd8-binding protein UBXN7 are dramatically reduced. C. Western blot of MLN4924 and MG132 treated inputs and Flag-BRWD2/PHIP immunoprecipitations. Treatment with MLN4924 converts the majority of CUL4A to the unmodified (Unmod.) non-Neddylated state. Neither inhibitor strongly diminishes BRWD2/PHIP interaction with DDB1, however, CUL4A interaction appears slightly diminished in the presence of MLN4924.

## Supplementary Figure 3. BRWD2/PHIP CryptoTudor domain analysis using PHYRE2 and HHPRED secondary structure prediction

A. Diagram depicting BRWD2/PHIP domain structure (top) and a sequence alignment of the human and *Drosophila* CryptoTudor-Bromodomain module (bottom). WD repeats: green boxes, CryptoTudor domain: blue box, Bromodomains: pink boxes. B. Analysis of BRWD2/PHIP CryptoTudor domain using PHYRE2. Alignment of BRWD2/PHIP

CryptoTudor (Query sequence) and PHF20 Tudor (Template sequence) domains indicating similarity in predicted secondary structure. As indicated by the blue arrows (extended beta sheets), the BRWD2/PHIP CryptoTudor domain is predicted to adopt a 3 strand beta-barrel type conformation similar to the Tudor fold. C. Analysis of BRWD2/PHIP CryptoTudor domain using HHPRED. Sequence alignments of the BRWD2/PHIP CryptoTudor domain with the Tudor domains of PHF20, Lamin B Receptor (LBR), PHD Finger Protein 1 (PHF1) and Polycomb-Like (PCL). In all instances, BRWD2/PHIP is predicted to adopt a 3 beta-strand conformation. Blue "E"s represent regions predicted to be extended beta sheets, red "H"s represent predicted alpha-helixes.

## Supplemental figure 4. BRWD2/PHIP ChIP-seq in Mammalian Cells additional track examples

A. UCSC genome browser track example in HCT116 cells displaying a region upstream of the NTF3 gene where MLL1 knockout (MLL1-KO) results in increased H3K4me1 and BRWD2/PHIP occupancy (indicated by grey boxes). Some sites that gain H3K4me1 and BRWD2/PHIP in MLL1-KO cells lose occupancy of these factors in cells lacking MLL4 enzymatic activity (indicated by light blue boxes). B. Track example in v6.5 embryonic stem cells (ESCs) displaying a region near the Ier5 and Mr1 genes at which H4K4me1 and BRWD2/PHIP occupancy is dependent on MLL4 methyltransferase activity (indicated by grey boxes).

# Supplemental figure 5. BRWD2/PHIP ChIP-seq in *Drosophila* additional track examples

A. UCSC genome browser track example in *Drosophila* S2 cells displaying occupancy of dBRWD3, H3K4me1, H3K4me3, H3K27ac in control and dBRWD3 RNAi treated cells. Blue highlight boxes indicate regions that lose H3K27ac signal in dBRWD3 knockdown cells. Red highlight box indicates a region where H3K27ac signal spreads in dBRWD3 RNAi treated cells. B. A. UCSC genome browser track example in *Drosophila* S2 cells displaying occupancy of dBRWD3, H3K4me1, H3K4me3, H3K27ac in control and dBRWD3 RNAi treated cells. Red highlight boxes indicate cells. Red highlight boxes indicate cells.

## Supplementary Figure 1.



BRWD2 peaks (ab #833)

BRWD2 peaks (ab #834)

### Supplementary Figure 2.

#### **Spectral Counts**

С

Protein     Control rep1     Control rep2     Flag-BRWD2 rep1     Flad-CorP3 rep3     Flag-BRWD2 rep1	Δ			Spe		115
CUL4-DDB1     BRWD2/PH-interacting protein 1 (DDB1)     0     0     185     316       CUL4-DDB1     Interacting protein 1 (DDB1)     0     0     54     99       CCP4     Culin-4A (CUL4A)     0     0     54     99       Colins-4A (CUL4A)     0     0     9     9       COP9     Signalosome complex subunit 1 (GPS1)     0     0     9     9       COP9 signalosome complex subunit 3 (COPS2)     0     0     10     12       COP9 signalosome complex subunit 3 (COPS3)     0     0     8     14       COP9 signalosome complex subunit 3 (COPS6)     0     0     4     8       COP9 signalosome complex subunit 7 (COPS6)     0     4     8     10       COP9 signalosome complex subunit 7 (COPS6)     0     4     8     10       COP9 signalosome complex subunit 8 (COPS6)     0     4     5     13       Myeloma-overexpressed gene 2 protein (MYEOV2)     0     4     5     13       Myeloma-overexpressed gene 2 protein (MYEOV2)     0     4     5     14<	~	Protein	Control rep1	Control rep2	Flag-BRWD2 rep1	Flag-BRWD2 rep2
CUL4-DDB1     DNA damage-binding protein 1 (DDB1)     0     0     183     366       (CRL4)     Isoform 2 of Cullin-4B (CUL4B)     0     0     0     39     52       NEDD8 (NEDD8)     0     0     9     9     9       COP9 signalosome complex subunit 1 (GPS1)     0     0     9     9       COP9 signalosome complex subunit 2 (COPS2)     0     0     10     12       COP9 signalosome complex subunit 3 (COPS4)     0     211     22       COP9 signalosome complex subunit 4 (COPS4)     0     211     22       COP9 signalosome complex subunit 5 (COPS5)     0     0     4     8       COP9 signalosome complex subunit 7a (COPS6)     0     4     10     10       COP9 signalosome complex subunit 7a (COPS6)     0     4     10     10       COP9 signalosome complex subunit 7a (COPS6)     0     4     10     10       COP9 signalosome complex subunit 7a (COPS7A)     0     0     4     10       COP9 signalosome complex subunit 7a (COPS6)     0     39     54		BRWD2/PH-interacting protein (PHIP)	0	0	185	316
CUL4-DDB1 (CRL4)     Isoform 2 of Cullin-4B (CUL4B)     0     0     54     99       Cullin-4A (CUL4A)     0     0     39     52       COP9 signalosome complex subunit 1 (GPS1)     0     9     9       COP9 signalosome complex subunit 2 (COPS2)     0     0     10     12       COP9 signalosome complex subunit 3 (COPS3)     0     8     14       COP9 signalosome complex subunit 4 (COPS4)     0     211     22       COP9 signalosome complex subunit 5 (COPS6)     0     6     9       COP9 signalosome complex subunit 6 (COPS6)     0     4     8       COP9 signalosome complex subunit 7a (COPS7A)     0     4     10       COP9 signalosome complex subunit 7a (COPS7A)     0     4     7       Wedd8-binding     UBX domain-containing protein 7 (UBXN7)     0     4     5       Histone H2A     0     0     31     38       Histone H2A     0     0     18     22       Histone H3.2     0     0     12     8       FACT complex subunit SCPT16)     0		DNA damage-binding protein 1 (DDB1)	0	0	183	366
CCRL4)     Cullin-4A (CUL4A)     0     0     39     52       NEDD8 (NEDD8)     0     0     9     9       COP9 signalosome complex subunit 1 (GPS1)     0     0     9     9       COP9 signalosome complex subunit 2 (COPS2)     0     0     10     12       COP9 signalosome complex subunit 2 (COPS4)     0     21     22       COP9 signalosome complex subunit 4 (COPS4)     0     21     22       COP9 signalosome complex subunit 6 (COPS6)     0     4     8       COP9 signalosome complex subunit 6 (COPS7A)     0     4     10       COP9 signalosome complex subunit 78 (COPS7A)     0     4     7       OP signalosome complex subunit 74 (COPS7A)     0     4     7       COP9 signalosome complex subunit 74 (COPS7A)     0     4     7       Vedd8-binding     UBX domain-containing protein 7 (UBXN7)     0     4     5       Histone H2A     0     0     31     38       Histone H2A     0     0     18     22       Histone H2A.Z     0     12	CUL4-DDB1	Isoform 2 of Cullin-4B (CUL4B)	0	0	54	99
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COP9 Signalosome (CSN)     COP3 signalosome complex subunit 2 (COPS2)     0     0     10     12       COP3 signalosome complex subunit 3 (COPS3)     0     0     10     12       COP3 signalosome complex subunit 3 (COPS3)     0     0     11     22       COP3 signalosome complex subunit 5 (COPS5)     0     0     6     9       COP3 signalosome complex subunit 6 (COPS6)     0     0     4     8       COP3 signalosome complex subunit 6 (COPS6)     0     0     4     8       COP9 signalosome complex subunit 6 (COPS6)     0     0     4     7       Veld8-binding     UBX domain-containing protein 7 (UBXN7)     0     0     4     5       Histone H2B     0     0     31     38     1     38       Histone H2B     0     0     18     22     1     31       Histone H2A     0     0     18     22     18     18       Histone H2B     0     0     7     20     20     20     20       Fistone H2A <td< td=""><td></td><td></td><td></td><td></td><td></td><td></td></td<>						
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Histones     Histone H3.3     0     0     20     25       Histone H3.2     0     0     18     22       Histone H3.2     0     0     18     22       Histone H4     8     7     77     129       Histone H2A.Z     4     2     41     31       PHD finger protein 6 (PHF6)     0     0     7     20       Remodeling and spacing factor 1 (RSF1)     0     0     12     18       FACT complex subunit SSRP1 (SSRP1)     0     0     12     8       FACT complex subunit SPT16 (SUPT16H)     0     0     9     22       SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 50     0     7     12       (SMARCA5)     Chromodomain-helicase-DNA-binding protein 1 (CHD1)     0     0     1     3       Chrem domain-helicase-DNA-binding protein 1 (NOLC1)     0     0     1     3     3       Other     Nucleolar and colied-body phosphoprotein 1 (NOLC1)     0     5     2     2       Ubiquitin carboxyl-ter		Historie H2B	0	0	39	29
Histones     Initial PR-3.3     0     0     20     23       Histone H3.2     0     0     18     22       Histone H3.2     0     0     18     22       Histone H4     8     7     77     129       Histone H2A.Z     4     2     41     31       PHD finger protein 6 (PHF6)     0     0     7     20       Remodeling and spacing factor 1 (RSF1)     0     0     12     18       FACT complex subunit SSRP1 (SSRP1)     0     0     12     8       FACT complex subunit SPT16 (SUPT16H)     0     0     9     22       SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 50     0     7     12       (SMARCA5)     Chromodomain-helicase-DNA-binding protein 1 (CHD1)     0     0     1     3       Other     Spectrin beta chain, non-erythrocytic 1 (SPTBN1)     0     0     11     8       Nucleolar and colied-body phosphoprotein 1 (NOLC1)     0     0     3     2       Ubiquitin carboxyl-terminal hydrolase (US		Historie H2A	0	0	31	30
Chromatin Remodellers     Inistone H2A.Z     0     0     16     22       Histone H4     8     7     77     129       Histone H2A.Z     4     2     41     31       PHD finger protein 6 (PHF6)     0     0     7     20       Remodeling and spacing factor 1 (RSF1)     0     0     12     18       FACT complex subunit SSRP1 (SSRP1)     0     0     12     8       SWI/SNNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5     0     7     12       Chromodomain-helicase-DNA-binding protein 1 (CHD1)     0     0     1     3       Spectrin beta chain, non-erythrocytic 1 (SPTBN1)     0     0     1     8       Other proteins     X-ray repair cross-complementing protein 5 (XRCC5)     0     3     2	Histones	Histone H3.3	0	0	20	25
Chromatin     PACT complex subunit SSRP1 (SSRP1)     0     0     7     129       Chromatin     FACT complex subunit SSRP1 (SSRP1)     0     0     7     20       Remodellers     FACT complex subunit SSRP1 (SSRP1)     0     0     12     18       FACT complex subunit SSRP1 (SSRP1)     0     0     12     8       SWI/SINF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5     0     0     7     12       Chromodomain-helicase-DNA-binding protein 1 (CHD1)     0     0     1     3       Other     Spectrin beta chain, non-erythrocytic 1 (SPTBN1)     0     0     11     8       Nucleolar and coiled-body phosphoprotein 1 (NOLC1)     0     5     2     2       Other     X-ray repair cross-complementing protein 5 (XRCC5)     0     3     2       Ubiquitin carboxyl-terminal hydrolase (USP7)     0     0     1     3		Historie H3.2	0	0	18	22
Chromatin Remodellers     FACT complex subunit SSRP1 (SSRP1)     0     0     7     20       Remodellers     FACT complex subunit SSRP1 (SSRP1)     0     0     12     18       FACT complex subunit SSRP1 (SSRP1)     0     0     12     8       FACT complex subunit SSRP1 (SSRP1)     0     0     9     22       SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5     0     0     7     12       Chromodomain-helicase-DNA-binding protein 1 (CHD1)     0     0     6     11       Chromodomain-helicase-DNA-binding protein 1 (NDLC1)     0     0     1     3       Other     Spectrin beta chain, non-erythrocytic 1 (SPTBN1)     0     0     11     8       Vucleolar and coiled-body phosphoprotein 1 (NOLC1)     0     0     5     2     2       Ubiquitin carboxyl-terminal hydrolase (USP7)     0     0     1     3     3			8	/	//	129
PHD finger protein 6 (PHF6)     0     0     7     20       Remodeling and spacing factor 1 (RSF1)     0     0     12     18       FACT complex subunit SSRP1 (SSRP1)     0     0     12     8       FACT complex subunit SSRP1 (SSRP1)     0     0     9     22       SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5     0     7     12       Chromodomain-helicase-DNA-binding protein 1 (CHD1)     0     0     6     11       Chromodomain-helicase-DNA-binding protein 1 (NOLC1)     0     0     1     3       Other     Nucleolar and coiled-body phosphoprotein 1 (NOLC1)     0     0     5     2       Proteins     X-ray repair cross-complementing protein 5 (XRCC5)     0     0     3     2		Histone H2A.2	4	2	41	31
Chromatin     PHD Inger protein 5 (rHP6)     0     0     0     1     20       Remodeling and spacing factor 1 (RSF1)     0     0     12     18       FACT complex subunit SSRP1 (SSRP1)     0     0     12     8       FACT complex subunit SSRP1 (SUPT16H)     0     0     9     22       SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5     0     7     12       Chromodomain-helicase-DNA-binding protein 1 (CHD1)     0     0     6     11       Chromodomain-helicase-DNA-binding protein 4 (CHD4)     0     1     3       Spectrin beta chain, non-erythrocytic 1 (SPTBN1)     0     11     8       Other proteins     Vucleolar and colled-body phosphoprotein 1 (NOLC1)     0     5     2       Vary repair cross-complementing protein 5 (XRC5)     0     3     2     1		PLID fin non mateix () (PLIE()	0	0	7	00
Chromatin   FACT complex subunit SSRP1 (SSRP1)   0   0   12   18     FACT complex subunit SSRP1 (SSRP1)   0   0   12   8     FACT complex subunit SPT16 (SUPT16H)   0   0   9   22     SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 50   0   7   12     Chromodomain-helicase-DNA-binding protein 1 (CHD1)   0   0   6   11     Chromodomain-helicase-DNA-binding protein 1 (CHD4)   0   0   1   3     Spectrin beta chain, non-erythrocytic 1 (SPTBN1)   0   0   11   8     Other   Nucleolar and coiled-body phosphoprotein 1 (NOLC1)   0   0   5   2     proteins   X-ray repair cross-complementing protein 5 (XRCC5)   0   0   3   2		PHD finger protein 6 (PHF6)	0	0	/	20
Chromatin Remodellers FACT complex subunit SSHP1 (SSHP1) 0 0 12 8   FACT complex subunit SSHP16 (SUPT16H) 0 0 9 22   SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 0 0 7 12   Chromodomain-helicase-DNA-binding protein 1 (CHD1) 0 0 6 11   Chromodomain-helicase-DNA-binding protein 4 (CHD4) 0 0 1 3   Spectrin beta chain, non-erythrocytic 1 (SPTBN1) 0 0 11 8   Other proteins Vucleolar and coiled-body phosphoprotein 1 (NOLC1) 0 0 3 2   Ubiquitin carboxyl-terminal hydrolase (USP7) 0 0 1 3		Remodeling and spacing factor 1 (RSF1)	0	0	12	18
Action Complex suburits P116 (S0P116H) 0 0 0 9 22   Remodellers SWV/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 0 0 7 12   (SMARCA5) Chromodomain-helicase-DNA-binding protein 1 (CHD1) 0 0 6 11   Chromodomain-helicase-DNA-binding protein 4 (CHD4) 0 0 1 3   Spectrin beta chain, non-erythrocytic 1 (SPTBN1) 0 0 11 8   Other Nucleolar and coiled-body phosphoprotein 1 (NOLC1) 0 0 5 2   proteins X-ray repair cross-complementing protein 5 (XRCC5) 0 0 3 2	Chromatin	FACT complex subunit SSRP1 (SSRP1)	0	0	12	8
Other of the original relative associated active performance of the original relative associated active astressociated active associated active assoc	Remodellers	FACT complex subunit SPT16 (SUPT16H)	0	0	9	22
Other   Chromodomain-helicase-DNA-binding protein 1 (CHD1)   0   0   6   11     Chromodomain-helicase-DNA-binding protein 4 (CHD4)   0   0   1   3     Spectrin beta chain, non-erythrocytic 1 (SPTBN1)   0   0   11   8     Other   Nucleolar and coiled-body phosphoprotein 1 (NOLC1)   0   5   2     Proteins   X-ray repair cross-complementing protein 5 (XRCC5)   0   0   1   3	Hernodellord	regulator of chromatin subfamily A member 5 (SMARCA5)	0	0	7	12
Chromodomain-helicase-DNA-binding protein 4 (CHD4)     0     0     1     3       Spectrin beta chain, non-erythrocytic 1 (SPTBN1)     0     0     11     8       Other     Nucleolar and coiled-body phosphoprotein 1 (NOLC1)     0     0     5     2       Proteins     X-ray repair cross-complementing protein 5 (XRCC5)     0     0     3     2       Ubiquitin carboxyl-terminal hydrolase (USP7)     0     0     1     3		Chromodomain-helicase-DNA-binding protein 1 (CHD1)	0	0	6	11
Spectrin beta chain, non-erythrocytic 1 (SPTBN1)     0     0     11     8       Other     Nucleolar and colled-body phosphoprotein 1 (NOLC1)     0     0     5     2       proteins     X-ray repair cross-complementing protein 5 (XRCC5)     0     3     2       Ubiquitin carboxyl-terminal hydrolase (USP7)     0     0     1     3		Chromodomain-helicase-DNA-binding protein 4 (CHD4)	0	0	1	3
Spectrin beta chain, non-erythrocytic 1 (SPTBN1)     0     0     11     8       Other     Nucleolar and coiled-body phosphoprotein 1 (NOLC1)     0     0     5     2       proteins     X-ray repair cross-complementing protein 5 (XRCC5)     0     0     3     2       Ubiquitin carboxyl-terminal hydrolase (USP7)     0     0     1     3						
Other     Nucleolar and coiled-body phosphoprotein 1 (NOLC1)     0     0     5     2       proteins     X-ray repair cross-complementing protein 5 (XRCC5)     0     0     3     2       Ubiquitin carboxyl-terminal hydrolase (USP7)     0     0     1     3		Spectrin beta chain, non-erythrocytic 1 (SPTBN1)	0	0	11	8
proteins X-ray repair cross-complementing protein 5 (XRCC5) 0 0 3 2 Ubiquitin carboxyl-terminal hydrolase (USP7) 0 0 1 3	Other	Nucleolar and coiled-body phosphoprotein 1 (NOLC1)	0	0	5	2
Ubiquitin carboxyl-terminal hydrolase (USP7) 0 0 1 3	proteins	X-ray repair cross-complementing protein 5 (XRCC5)	0	0	3	2
		Ubiquitin carboxyl-terminal hydrolase (USP7)	0	0	1	3

В

#### **Spectral Counts**

	Protein	DMSO	MLN4924	MG132	MLN4924 + MG132
	BRWD2/PH-interacting protein (PHIP)	160	182	252	169
	DNA damage-binding protein 1 (DDB1)	103	138	177	124
CUL4-DDB1	Isoform 2 of Cullin-4B (CUL4B)	90	52	100	41
(CRL4)	Cullin-4A (CUL4A)	62	51	76	37
	NEDD8 (NEDD8)	23	2	19	1
	COP9 signalosome complex subunit 1 (GPS1)	3	0	3	0
	COP9 signalosome complex subunit 2 (COPS2)	5	0	6	0
	COP9 signalosome complex subunit 3 (COPS3)	3	0	7	0
COP9	COP9 signalosome complex subunit 4 (COPS4)	7	0	7	0
Signalosome	COP9 signalosome complex subunit 5 (COPS5)	6	0	5	0
(CSN)	COP9 signalosome complex subunit 6 (COPS6)	1	0	0	0
	COP9 signalosome complex subunit 7a (COPS7A)	5	0	5	0
	COP9 signalosome complex subunit 7b (COPS7B)	1	0	1	0
	COP9 signalosome complex subunit 8 (COPS8)	5	0	3	0
	Myeloma-overexpressed gene 2 protein (MYEOV2)	1	0	2	0
Nedd8-binding	UBX domain-containing protein 7 (UBXN7)	10	0	14	1
	Histone H4	38	32	42	40
	Histone H2B	23	17	28	35
Histones	Histone H2A	20	21	32	16
	Histone H3.3	8	5	7	7
	Histone H3.2	8	5	8	7
	Histone H2A.Z	6	4	5	2
Chromatin Remodellers					
	PHD finger protein 6 (PHF6)	15	17	17	10
	Chromodomain-helicase-DNA-binding protein 4 (CHD4)	59	70	70	59
	Transcription activator BRG1 (SMARCA4)	17	14	13	6
	Chromodomain-helicase-DNA-binding protein 5 (CHD5)	16	16	16	9
	Protein polybromo-1 (PBRM1)	15	8	11	5
	Remodeling and spacing factor 1 (RSF1)	19	20	19	12
	FACT complex subunit SPT16 (SUPT16H)	13	18	14	12
	FACT complex subunit SSRP1 (SSRP1)	12	14	11	5



### Supplementary Figure 3



В

#### PHYRE2 BRWD2-CryptoTudor x PHF20 tudor



С

#### HHPRED

PHF20	ZLDM_A Uncharacterized protein; PHF20, Tudor domain, Epigenetics, methylated; NMR {Homo sapiens}       Probability: 94.35     E-value: 0.12     Score: 36.12     Aligned Cols: 53     Identities: 9%     Similarity: 0.23		Template alignment   Template 3D structure   PDBe 2M00_A PHD finger protein 1, H3X36me3; Tudor Domain, H3K36me3 binding, PEPTIDE; NMR {Homo sapiens} Probability: 93.47 E-value: 0.31 Score: 34.53 Aligned Cols: 52 Identities: 15% Similarity: 0.115
	Q     ss_pred     CCCCCCCCEEEEe-CCCCEEEEEEEECCCCCCCCCCCCC	86 (224) 86 (224) 8 (81) 8 (81)	Q     ss_pred     CCCCCCCEEEEE-CCCEEEEEEEEEEEEEEEEEEEEEE
LBR	Template alignment   Template 3D structure   PDBe 2L8D_A Lamin-B receptor; DNA BINDING PROTEIN; NMR {Gallus gallus} Probability: 93.55 E-value: 0.34 Score: 31.93 Aligned Cols: 54 Identities: 15% Similarity: 0.225	PCL	Template alignment   Template 3D structure   PDBe 2XK0_A POLYCOMB PROTEIN PCL; TRANSCRIPTION, AROMATIC CAGE; NMR {DROSOPHILA MELANOGASTER} Probability: 91.44 E-value: 1.5 Score: 30.1 Aligned Cols: 55 Identities: 15% Similarity: 0.236
	Q     ss_pred     CCCCCCCCEEEEECCEEEEEEEEEEEEEECCCCCCCC	86 (224) 886 (224) 83 (66) 83 (66)	Q     ss_pred     CCCCCCCCEEEEE-CCCCEEEEEEECCCCCCCCCCCCC
	T ss_pred cCCCCCEEEEEEEEEEEEEEEECCCCEEEEEEECCCCEEEEeHHHeeeCCc		I ss_prea cccccctttttttttttttttcccEEEEEECCCCEEEeCHHHcEECCCCCC

## Supplementary Figure 4





## Supplementary Figure 5.

