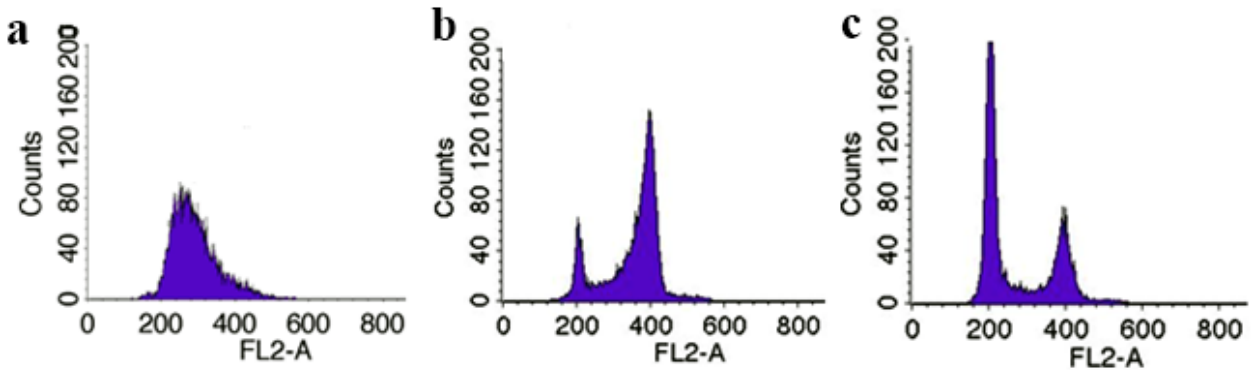

Figure S1: Different phase synchronized the cells. a, Double thymidine treated G1/S phase synchronized cells. b, Thymidine and nocodazole treated G2/M phase synchronized cells. c, G1 phase synchronized cells collected 8h after release from G2/M.

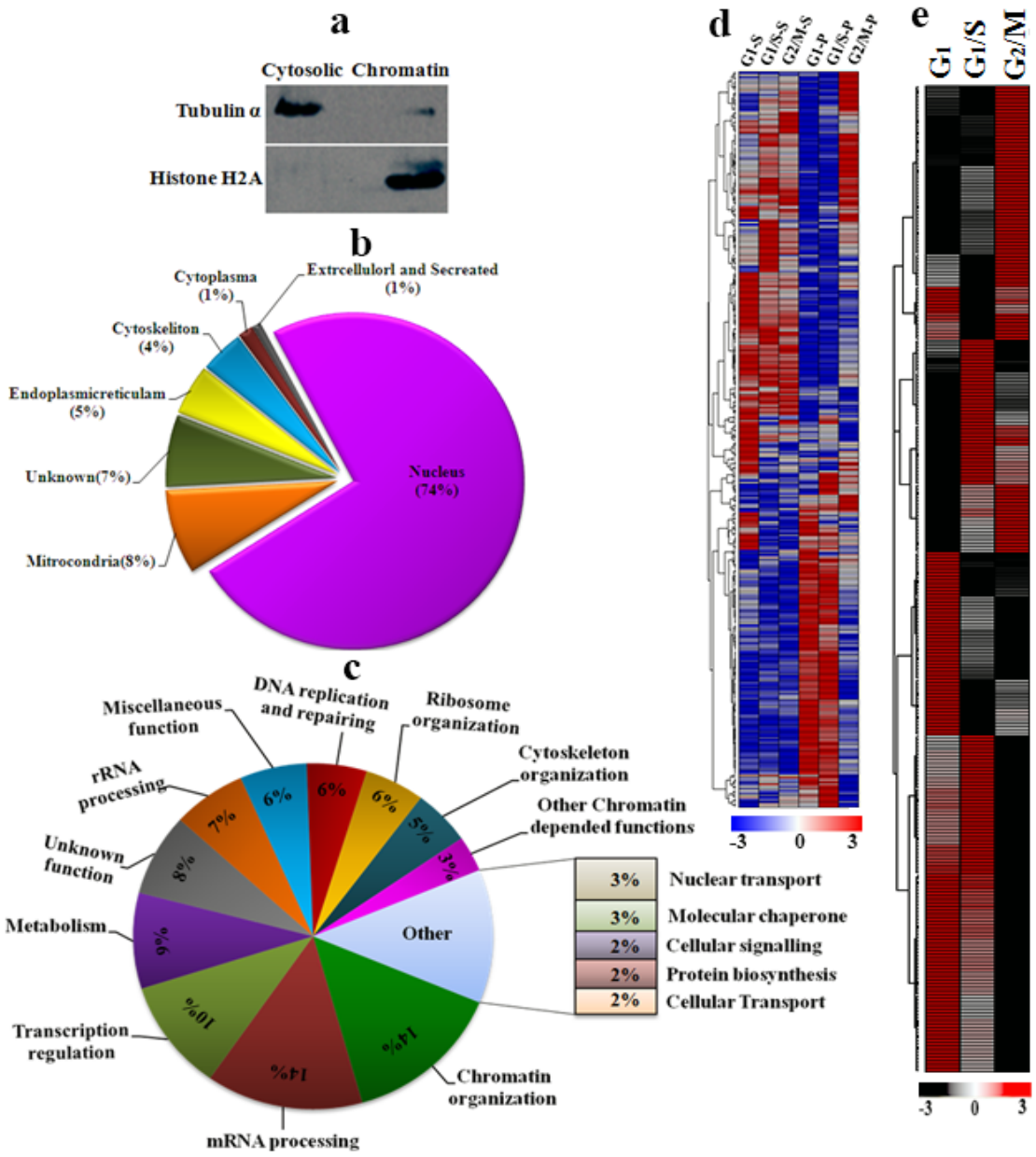

Figure S2: Characterization of identified proteins. a, western blot of tubulin α and histone H2A in cytosolic and chromatin fraction indicating enrichment of chromatin. b, Classification of identified proteins according to their subcellular localization. c, Functional classification of identified proteins. d, Differential release patterns of chromatome from different interphase chromatins upon partial MNase digestion. Heat map represent the relative protein abundance in the different interphase chromatin digests. The clustering was performed using the iTRAQ ration of different chromatin digests. e: A global view of dynamic chromatin binding levels of chromatome during interphase progression. Heat map represent the relative protein binding levels with different interphase chromatin. The combined iTRAQ ratios of matching pellet and supernatant fractions were used for the clustered analysis. During hierarchical clustering the values of individual protein were normalized in a -3 to 3 color scale.

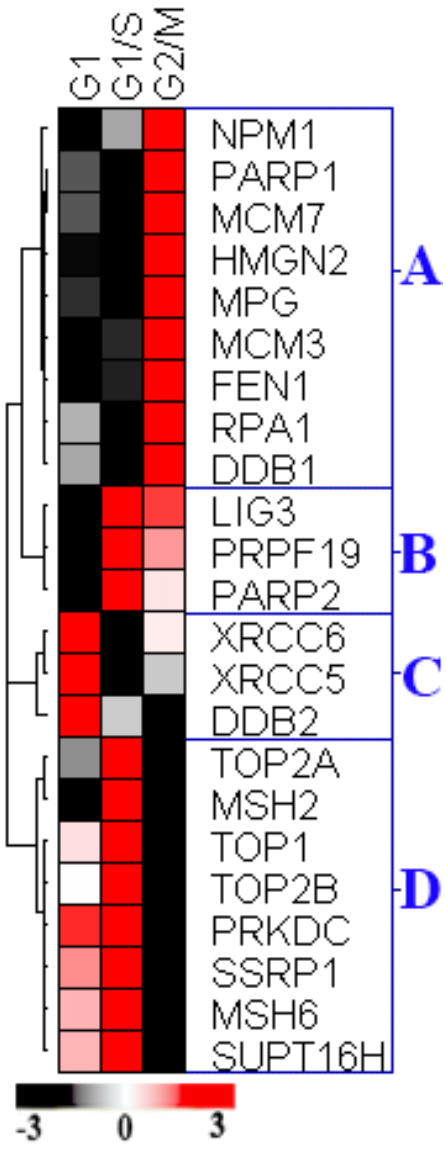

Figure S3: Chromatin association dynamics of DNA repair proteins during interphase progression. The combined iTRAQ ratios of matching pellet and supernatant fractions were used for the clustered analysis and the color code reflect the relative binding levels of the proteins. Proteins are cluster in to four distinct clusters. 'Cluster A', proteins association was comparatively increase within G2/M phase chromatin; 'cluster B', proteins association was comparatively increase in G1/S phase chromatin but decrease greatly during early G1 phase ; proteins association was comparatively increase within G2/M phase chromatin; 'cluster C', proteins association was comparatively increase within early G1 phase chromatin; 'cluster D', proteins association was comparatively increase within late G1 phase (G1/S) chromatin but greatly decrease during early G2/M phase.

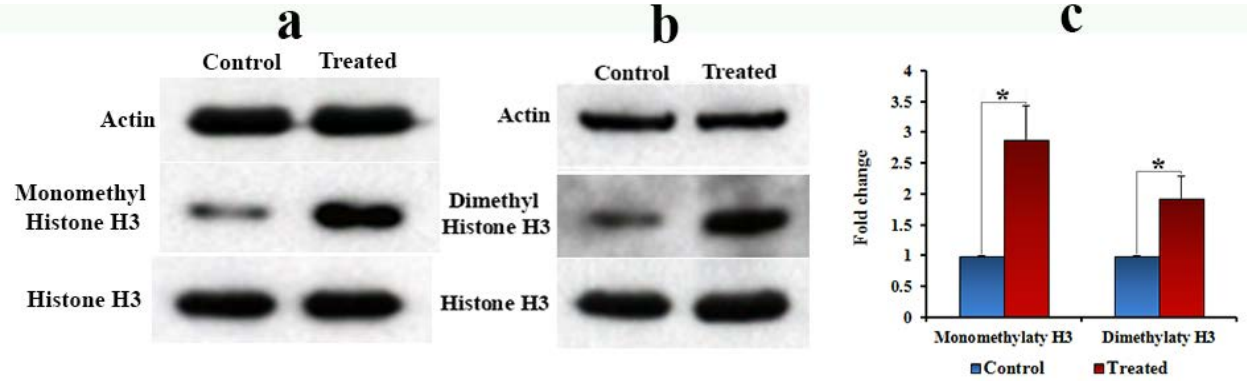

Figure S4: Effect of KDM1 blocking upon histone methylation. a-b, Expression level of monomethylated and dimethylated histone H3 in 2PCPA treated cells. c, Histone methylation level after KDM1 inhibition. Cells were treated with 100μM 2PCPA for 24h to inhibit KDM1 and PBS was used as vehicle control. N=6 experimental replicates were used for this study, *P value <0.05.

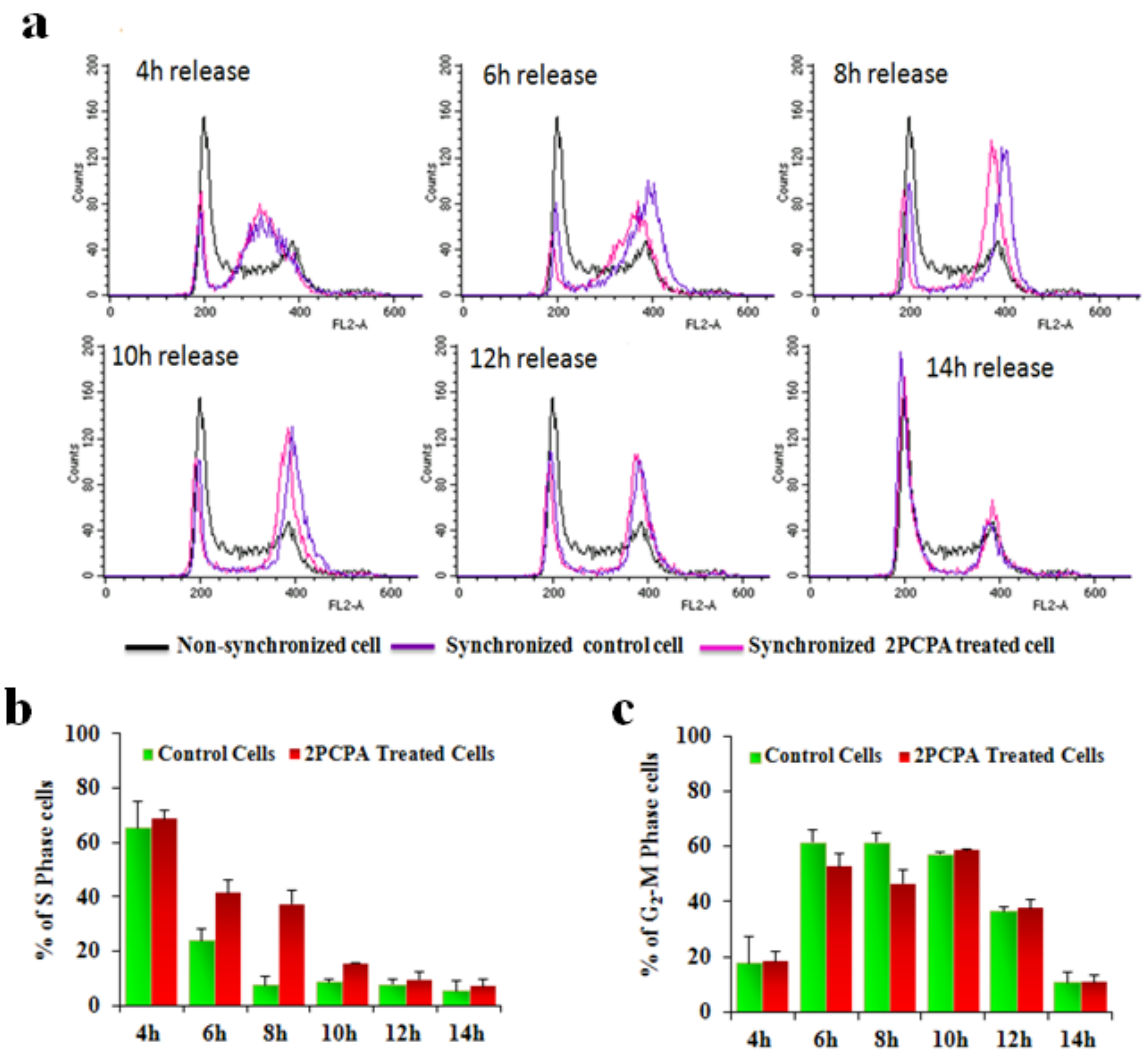

Figure S5: Effect of KDM1 blocking in cell cycle progression. a, Histograms representation the cell cycle progression within 4-14 h time period after release from double thymidine block. b-c, % of S phase and G_2-M phase cells present into the total population of cells during 4-14h time period after release from double thymidine block.

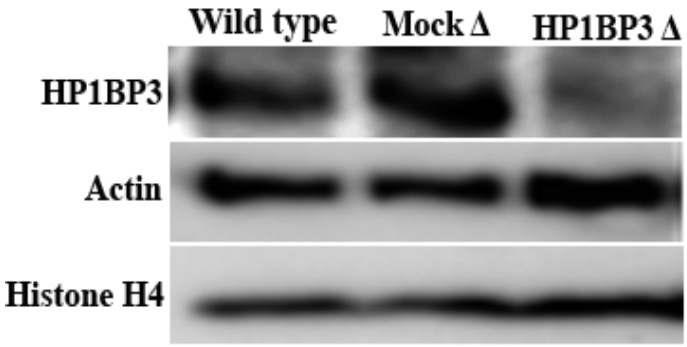

Figure S6: Conformation of HP1BP3 knockdown. Western blot showed the HP1BP3 expression level in wild type, mock depleted, and HP1BP3 depleted 293T stable cell line.

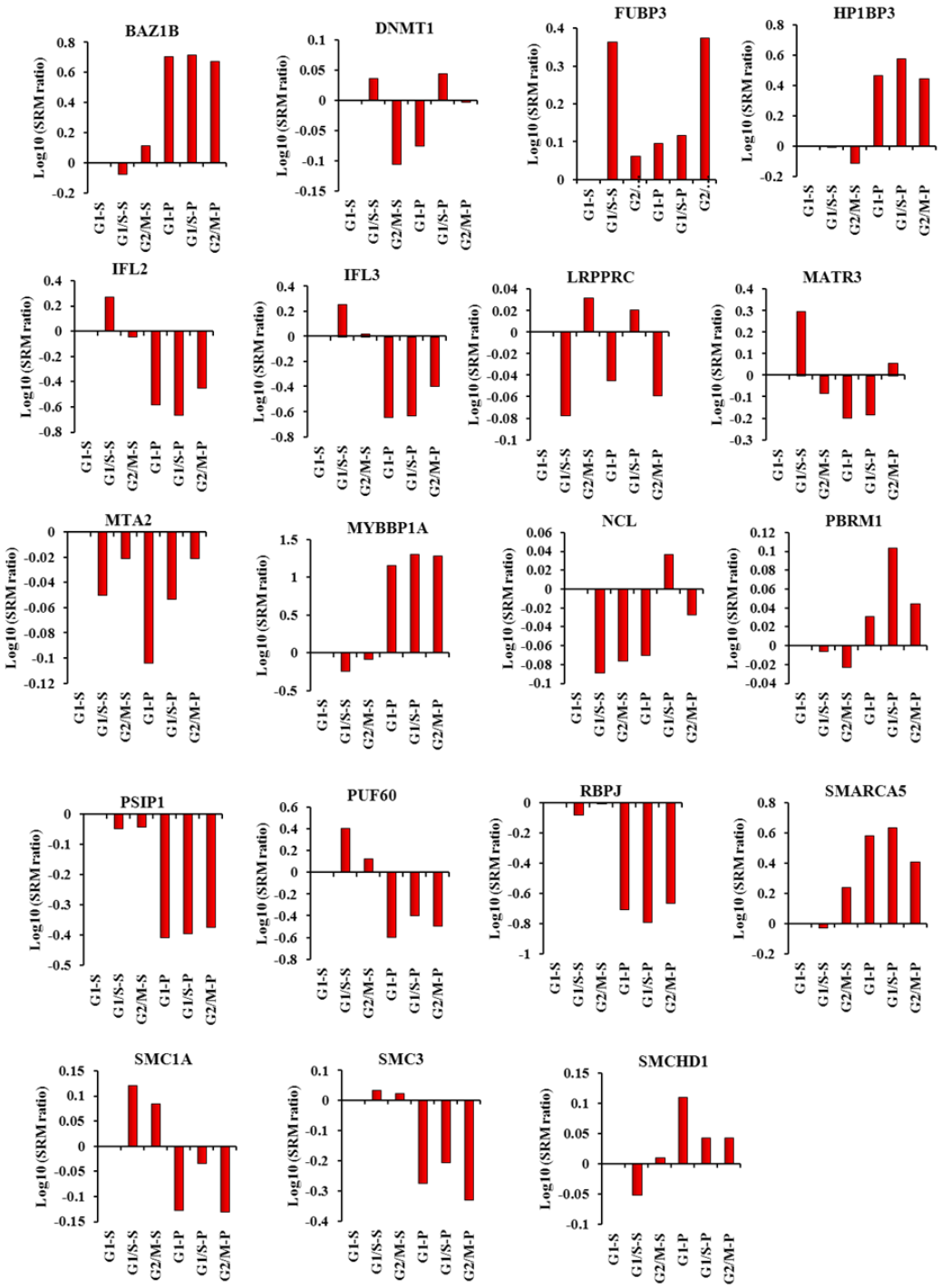

Figure S7: Validation of quantitative result by SRM based quantification. Graphical representation of Log_{10}(SRM ratio) of selective proteins. Chromatins from different conditions were partially digested by MNase and proteins were quantified by SRM based proteomic approach. SRM ratios are indicating the relative abundance of proteins in the different chromatin fractions. Supernatant fractions G1-S, G1/S-S and G2/M-S, and pellet fractions G1-P, G1/S-P and G2/M-P were obtained by partial MNase digestion.