**Additional material**

Additional file 1 .xls Table S1: **H1T2 ChIP-seq data: MACS 1.4.2 output file with annotations.** H1T2 ChIP peaks MACS 1.4.2 with p-value cutoff of 1e-05. A total of 11570 peaks were identified as overlapping peaks between the two replicates and the H1T2 peaks were annotated using HOMER v4.7.

Additional file 2 .xls Table S2: **Chromosome-wise distribution of H1T2 peaks.** Representative excel file of the number of H1T2 peaks across different chromosomes.

Additional file 3A Figure S1, **Chromosome wise peak length distribution of H1T2 ChIP peaks.** Box plot representing the H1T2 associated average peak length (*y*-axis) across different chromosomes (*x*-axis); Additional file 3B .xls Table S3: Representative excel file of the peak length of H1T2 peaks across the chromosomes.

Additional file 4A Figure S2, **Fold enrichment of H1T2 peaks.** Box plot showing the fold enrichment of H1T2 peaks (*y*-axis) across different rat chromosomes; Additional file 4B .xls Table S4: Representative excel file of the fold enrichment of H1T2 peaks across chromosomes.

Additional file 5 .xls Table S5: **Repeat elements associated with H1T2.** Excel file representing the different classes of repeat elements associated with H1T2.

Additional file 6 .xls Table S6: **LINE elements subclasses associated with H1T2.** Representative excel file of the subclasses of LINE repeats associated with H1T2.

Additional file 7 .xls Table S7: **Motif identification.** Table represents the significant motifs identified from the overlapping peak summits using MEME analysis.

Additional file 8 .xls Table S8: **GO enrichment analysis of the genes whose promoter TSS is occupied by H1T2**. Excel file related to Figure 4B: GO analysis\_DAVID\_Biological processes.

Additional file 9 .xls Table S9: **GO enrichment analysis of the genes whose promoter TSS is occupied by H1T2.** Excel file related to Figure 4C: GO analysis\_DAVID\_Molecular function.

Additional file 10 .xls Table S10: **H1T2 IP/MS analysis.** List of H1T2 associated protein identified by mass spectrometric analysis (≥4 number of unique peptides).

Additional file 11 .xls Table S11: **GO enrichment analysis of the H1T2 IP/MS identified proteins.** Excel file related to Figure 6C: GO analysis\_DAVID\_ Molecular function.

Additional file 12 .xls Table S12: **GO enrichment analysis of the H1T2 IP/MS identified proteins.** Excel file related to Figure 6C: GO analysis\_DAVID\_ Biological processes.

Additional file 13 .xls Table S13: **GO enrichment analysis of the H1T2 IP/MS identified proteins.** Excel file related to Figure 6C: GO analysis\_DAVID\_ Sperm related functions.

Additional file 14 .xls Table S14: List of primers used for H1T2 ChIP-PCR analysis.