Figure S1. *UBE3A* protein expression after siRNA knockdown. A. Western blot against *UBE3A* under siRNA control and knockdown conditions in biological triplicates each for SH(15M) and SH-SY5Y cell lines. Average knockdown efficiency in SH(15M) (72%) and SH-SY5Y (90%) was calculated by band intensity. **B.** Western blot against *GAPDH* under siRNA control and knockdown conditions in biological triplicates each for SH(15M) and SH-SY5Y cell lines used as protein level controls.

Figure S2. Epigenomic profile of *UBE3A* knockdown in SH-SH5Y and SH(15M). Circos plots containing each genomic data set for all four UBE3A level comparison groups. Layers from out to in: chromosomes, DMR heatmap (mean differential methylation level), DE genes heatmap (log10 fold-change), H3K4me3 differential peaks, and H2A.Z differential peaks.

Figure S3. PCA plots for DMRs identified in each comparison group. Principle component analysis on differentially methylated regions identified for each comparison group. Analysis compared variance between the two sample groups used to create the comparison group.

Figure S4. PCA plots for DE genes read counts identified in each comparison group. Principle component analysis on read counts measured from differentially expressed genes for each comparison group. Analysis compared variance between the two sample groups used to create the comparison group.

Figure S5. Genome browser image of genomic datasets at *DLK1* for KDSH comparison group. UCSC Genome Browser snap shot at imprinted gene *DLK1* showing tracks for genomic datasets used in the study: DMRs, RNA expression, H3K4me3 ChIP peak levels, and H2A.Z ChIP peak levels. DMR track shows regions of differential DNA methylation for hypermethylated regions (red) and hypomethylated regions (blue). RNA track shows RNA expression levels of the KDSH samples (red), the control samples (blue), and their overlap (black). K4me3 track shows ChIP peaks for H3K4me3 of the KDSH samples (red), the control samples (blue), and their overlap (black). H2AZ track shows ChIP peaks for H2A.Z of the KDSH samples (red), the control samples (blue), and their overlap (black).

Figure S6. Genome browser image of genomic datasets at *EEF2* for KDSH comparison group. UCSC Genome Browser snap shot at non-imprinted *EEF2* showing tracks for genomic datasets used in the study: DMRs, RNA expression, H3K4me3 ChIP peak levels, and H2A.Z ChIP peak levels. DMR track shows regions of differential DNA methylation for hypermethylated regions (red) and hypomethylated regions (blue). RNA track shows RNA expression levels of the KDSH samples (red), the control samples (blue), and their overlap (black). K4me3 track shows ChIP peaks for H3K4me3 of the KDSH samples (red), the control samples (blue), and their overlap (black). H2AZ track shows ChIP peaks for H2A.Z of the KDSH samples (red), the control samples (blue), and their overlap (black).

Figure S7. Genome browser image of genomic datasets at *GNAS* for KDSH comparison group. UCSC Genome Browser snap shot at imprinted gene *GNAS* showing tracks for genomic datasets used in the study: DMRs, RNA expression, H3K4me3 ChIP peak levels, and H2A.Z ChIP peak levels. DMR track shows regions of differential DNA methylation for hypermethylated regions (red) and hypomethylated regions (blue). RNA track shows RNA expression levels of the KDSH samples (red), the control samples (blue), and their overlap (black). K4me3 track shows ChIP peaks for H3K4me3 of the KDSH samples (red), the control samples (blue), and their overlap (black). H2AZ track shows ChIP peaks for H2A.Z of the KDSH samples (red), the control samples (blue), and their overlap (black).

Figure S8. Genome browser image of genomic datasets at *RTL1* for KDSH comparison group. UCSC Genome Browser snap shot at imprinted gene *RTL1* showing tracks for genomic datasets used in the study: DMRs, RNA expression, H3K4me3 ChIP peak levels, and H2A.Z ChIP peak levels. DMR track shows regions of differential DNA methylation for hypermethylated regions (red) and hypomethylated regions (blue). RNA track shows RNA expression levels of the KDSH samples (red), the control samples (blue), and their overlap (black). K4me3 track shows ChIP peaks for H3K4me3 of the KDSH samples (red), the control samples (blue), and their overlap (black). H2AZ track shows ChIP peaks for H2A.Z of the KDSH samples (red), the control samples (blue), and their overlap (black).

Figure S9. H2A.Z promoter vs gene body levels for each cell type and knockdown condition. H2A.Z ChIP-seq levels for all genes plotted to compare promoter (y-axes) versus gene body (x-axes) levels. Quadrants were created using input values where all input levels were contained to quadrant 3 (lower left). Plots show all genes (black), genes previously identified to contain differential H2A.Z levels in all comparison groups (red), and four imprinted genes *DLK1, GNAS, IGF2, and RTL1,* as well as *EEF2* (green). Percent of genes in each quadrant are indicated for total genes (black) and the differential H2A.Z subset (red).

Figure S10. Percent methylation vs H2A.Z gene body levels for each cell type and knockdown condition. Percent DNA methylation from WGBS (y-axes) plotted against H2A.Z ChIP-seq levels across gene body (x-axes) for all genes. Quadrants were created using H2A.Z ChIP-seq input values where all input levels were to the left, and the average DNA methylation for all samples. Plots show all genes (black), genes previously identified to contain differential H2A.Z levels in all comparison groups (red), and four imprinted genes *DLK1, GNAS, IGF2, and RTL1,* as well as *EEF2* (green). Percent of genes in each quadrant are indicated for total genes (black) and the differential H2A.Z subset (red).

Figure S11. Percent methylation vs H2A.Z promoter levels for each cell type and knockdown condition. Percent DNA methylation from WGBS (y-axes) plotted against H2A.Z ChIP-seq levels (x-axes) at promoters for all genes. Quadrants were created using H2A.Z ChIP-seq input values where all input levels were to the left, and the average DNA methylation for all samples. Plots show all genes (black), genes previously identified to contain differential H2A.Z levels in all comparison groups (red), and four imprinted genes *DLK1, GNAS, IGF2, and RTL1,* as well as *EEF2* (green). Percent of genes in each quadrant are indicated for total genes (black) and the differential H2A.Z subset (red).