Supplemental Figure 4

A. Genome H3K4me3 density for WT, Ehmt1^-/-, and Ehmt2^-/- cells, showing increased density in the de novo group.

B. Heatmaps of RT RNAseq + strand and RNAseq - strand for WT, Ehmt1^-/-, and Ehmt2^-/- cells, highlighting genes affected by EHMT1 and EHMT2 deletion.

C. Density plot of H3K36me3 showing differences between WT, Ehmt1^-/-, and Ehmt2^-/- cells.

D. Graphs showing the number of H3K4me3 marks in the genome, gained, and de novo categories.

E. Boxplots of distance to RT boundary for all, gained, and de novo groups, indicating statistical significance.

F. Circular genome view depicting the distribution of SINE, LINE, LTR, and TSS elements.

G. Heatmaps of H3K4me3 and RT RNAseq for WT, Ehmt1^-/-, and Ehmt2^-/- cells, showing trends and patterns.