



**Figure S1. Comparison of H3K36me2/3, H3K27me1/2/3 and DNAm distribution across different conditions.** A) Aggregate plots (normalized by read depth and MS ratios) across the genome, centered on active genes ( $n = 15850$ ), inactive genes ( $n = 12759$ ) and intergenic regions ( $n = 11629$ ), in WT vs *Nsd1*-KO, for Replicate 1. B) Similar aggregate plots were also made for Replicate 2, confirming the changes shown in Replicate 1. C) Signal intensity plot (normalized by input and MS ratios) of H3K27me3 (Replicate 2), centred on transcription start sites (TSS) of inactive genes ( $n = 12759$ ), confirming the nearly uniform spread of H3K27me3 in *Nsd1*-KO. D) Heatmap clustering of histone modifications from different replicates, showing the similarity of the same mark among replicates. Data used in this figure are generated in this study.