Chen et al., figure S2

Figure S2. Comparison of H3K27me3 in WT, *Dnmt*-TKO and *Nsd1*-KO, using replicates. A) Aggregate plots of H3K27me1/2/3 (normalized by read depth and MS ratios) around active genes (n = 15850) in WT vs *Dnmt*-TKO, showing the limited changes of these marks especially H3K27me1/2 between the two conditions. B) Signal intensity plot (normalized by input and MS ratios) of H3K27me3 (Replicate 2) centred on CGIs overlapping SUZ12 peaks (n = 4543), confirming limited and localized H3K27me3 spread in *Dnmt*-TKO and full spread in *Nsd1*-KO. The "dip" in the centre appears in all four samples, is due to technical artifact, most likely a GC bias in the library preparation for this batch of samples (Replicate 2). C) Peakiness score of H3K27me3, using replicates in-house and from public sources. The in-house replicates confirm the spreading (i.e. lower peakiness) of H3K27me3 in *Nsd1*-KO. The replicates from public sources confirm a certain spread of H3K27me3 in *Dnmt*-TKO. ChIP-seq data used in (A) and (B) as well parts of (C) are generated in this study; (C) also includes data from Brinkman et al. 2012 and Hagarman et al. 2013.