Figure S2 – FAIRE fold change for H3K9me2 nucleation sites as compared to the whole genome.

The increase in chromatin accessibility as measured by the log of the fold change of the FAIRE signal for UNC0638 over DMSO for all H3K9me2 nucleation sites (H3K9me2) as compared to the log of the fold change for FAIRE (UNC0638/DMSO) for all 1kb windows across the genome tiled in 50bp increments (Background).