



Figure S1. Association between MLV and SIN-MLV integration sites and CpG islands, CNCs, PolIII and histone modifications. Distribution of the distance of SIN-MLV (green bars) and MLV wt (red bars) integrations from the midpoint of CpG islands (A) or CNCs (B) in a 20kb window. In the y axis is plotted the percentage of the total number of CpG islands or CNCs located at ± 50 kb distance from the integrations. The black line indicates the distribution of random control sites. (C) The distribution of epigenetic marks in a 10kb window around vector integration sites (IS) is shown for H3K27me3 (top panels), H2A.Z (middle panels), PolIII (lower panels) with respect to MLV integrations (left panels) or SIN-MLV integrations (right panels). See legend of Figure 1C for explanation of the graphs.