

ESM Figure 1. Chromatin modifications at HCT-116 and U2OS regulatory elements.

Enrichment of chromatin marks in HCT-116 colorectal carcinoma cells (a) and U2OS osteosarcoma cells (b) are shown. The average fold enrichment of immunoprecipiated chromatin (IP) compared to input for both H3K27ac and H3K4me3 (denoted below graph) at regions 5, 7, 14, 22 and 25 are displayed. Results for control regions C1 (negative control, representing a *TCF7L2* intronic sequence without enhancer activity) and C2 (positive control, representing the constitutively active promoter of human *beta-tubulin* gene) are also given. Numbers near the top of region C2 H3K4me3 bars represent the final enrichment levels. Significant enrichments ($P < 0.05$) in H3K27ac levels between each region and the negative control interval (C1) are marked by asterisks. Regions 14 ($p = 0.059$) and 22 ($p = 0.15$) exhibited trends for H3K27ac enrichment in HCT-116 cells while regions 5 ($p = 0.13$) and 14 ($p = 0.067$) displayed similar trends in U2OS cells.

