Chromatin binding profiles for BRD1-S and BRD1-L in relation to identified epigenetic marks in HEK293 cell lines. ChIP-seq data (fastq files), from HEK293 cell lines and cell line derivatives, was obtained from the ENCODE project and mapped to hg19 (for further details see Materials and Methods). An in house histone H3K9ac ChIP-seq dataset was also included in the analysis. The minimum distance from (A) BRD1-S or (B) BRD1-L ChIP-seq peak to transcription factor binding site or histone mark was identified for all 2205 and 1722 peaks, respectively. The results were summarized as histograms with a +/- 30 kb window from BRD1 binding (distance from BRD1 peaks). The number of peaks within each of the summed bins (columns) can be read on the y-axis (Number of peaks). Random ChIP-seq peak regions (Random), with the same composition of chromosomes and peak region sizes, were generated to evaluate if the results could be explained by chance.