Electronic supplementary material

ESM Fig. 4  Identification of enriched regions with Global Identifier of Target Regions (GLITR). This procedure accurately identifies enriched regions in target data by calculating a fold-change based on random samples of control (input chromatin) data. It uses a classification method to identify regions in ChIP data that have a peak height and fold-change that do not resemble regions in an input sample. Stack height and fold-change (relative to a pool of human input sequence) of regions identified in (a) input material and (b) TCF7L2 ChIP material from HCT116 cells are indicated by red dots. Black points stand for an equal number of reads sampled from the human input pool. Green dots indicate regions that are significantly different (with a false discovery rate =1%) from the distribution of pooled input regions. Significant regions in the TCF7L2 ChIP were then removed if they overlapped with a region from the HCT116 input sample. Encircled data-points represent distinct signals over background. Diagonal crosses, pseudo-ChIP