**SUPPORTING INFORMATION**

**Figures**

**S1 Fig. Quality control and validation of ZBTB38 ChIP-sequencing profiles and peaks.** (**A**) Percentage of total tag count in ZBTB38 peaks generated by cisgenome with default cutoff and a range of P-values indicated on x-axis. The ratio is on the total mapped tags. (**B**) Plot representing the reproducibility of two biological ZBTB38 ChIP-sequencing replicates. Tag counts per peak (n=3032) is represented. Peaks have been generated by cisgenome, with maximal P-value 10-40 and cutoff at 5. (**C**) Correlation between tag count in 500 base pair windows along chromosome 11 in two ChIP-sequencing replicates and corresponding input samples. (**D**) ChIP-qPCR validation of ZBTB38 binding sites in HeLa-S3-HA-Flag-ZBTB38 cells. (**E**) Genomic distribution of ZBTB38 binding regions determined by transcription factor binding activity. HOT: high occupancy of transcription factors; LOT: low occupancy of transcription factors; PRM: promoter-proximal regulatory module; DRM: gene-distal regulatory module; BAR: binding active regions; BIR: binding inactive regions. (**F**) Genomic distribution of ZBTB38 binding regions determined using HOMER tools. The asterisk indicates a *P*-value <10-3. (**G**)Enrichment of ZBTB38 ChIP-seq tags on a pseudo-genome assembled from a catalog of DNA repeated sequences from the RefBase database.

**S2 Fig. Depletion of *ZBTB38* enhances doxorubicin toxicity.** (**A-C**) Cell survival curve of HeLa-S3 (A), U2OS (B) and HCT-116 (C) cells transfected with *ZBTB38* or control siRNAs and 48 hours later plated in 6-well plate with different concentrations of doxorubicin (n=3).

**S3 Fig.** **Overlap between ZBTB38 and CTCF sites.** (**A**) Venn diagram showing the overlap between ChIP-sequencing peaks from ZBTB38, CTCF, SMC3 and RAD21 datasets.(**B**)ZBTB38, CTCF, RAD21 and SMC3 ChIP-seq peaks and profiles at two representative regions co-bound by the four factors.(**C**) Genomic distribution of ZBTB38 binding regions co-bound by CTCF, RAD21 and SMC3 determined using HOMER tools (LTR: long terminal repeat; CGI: CpG islands; TTS: transcription termination site from -100bp to +1kb; 5’-UTR: 5’-UTR exons; 3’UTR: 3’-UTR exons; DNA: low complexity DNAs).

**Tables**

**S1 Table. Functionnal annotation of ZBTB38 target genes.** In the following analyses only the TOP20 terms are reported according to their P-value. (**A**) KEGG pathway analysis. (**B**) REACTOME analysis. (**C**) GO Biological process analysis. (**D**) GO Molecular funciton analysis

**S2 Table. Analysis of DNA sequences at ZBTB38 binding sites**. (**A**) List of known motifs enriched at the 3032 ZBTB38 binding sites compared to the rest of the genome. (**B**) List of new motifs enriched at the 3032 ZBTB38 binding sites.

**S3 Table. Impact of CpG methylation on the binding of ZNF family factors.** (**A**) Relationship between KAISO and the meC level of its targets in HCT116 cells (ENCODE datasets). (**B**) Relationship between ZNF factors and the meC level at their binding sites in K562 (ENCODE datasets). (**C**) Relationship between 39 GFP-fused ZNF factors and the meC level at their binding sites in 293T (GSE58341). (**D**) Relationship between 190 HA-KRAB-ZNF factors and the meC level at their binding sites in 293T (GSE78099).

**S4 Table. Relationship between transcription factors binding sites and CGI-shores.** The list of genomic sites bound by transcription factors was intersected with the coordinates of CGI-shores and CGI in the human genome (version hg19). (**A**) Overlap between transcription factor binding sites and CGI and CGI-shores in ENCODE datasets (for HeLa-S3 cells). (**B**) Overlap between ZNF binding sites and CGI and CGI-shores in GSE78099.