## Genome-wide binding of transcription factor ZEB1 in triple-negative breast cancer cells

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## **Supporting information**

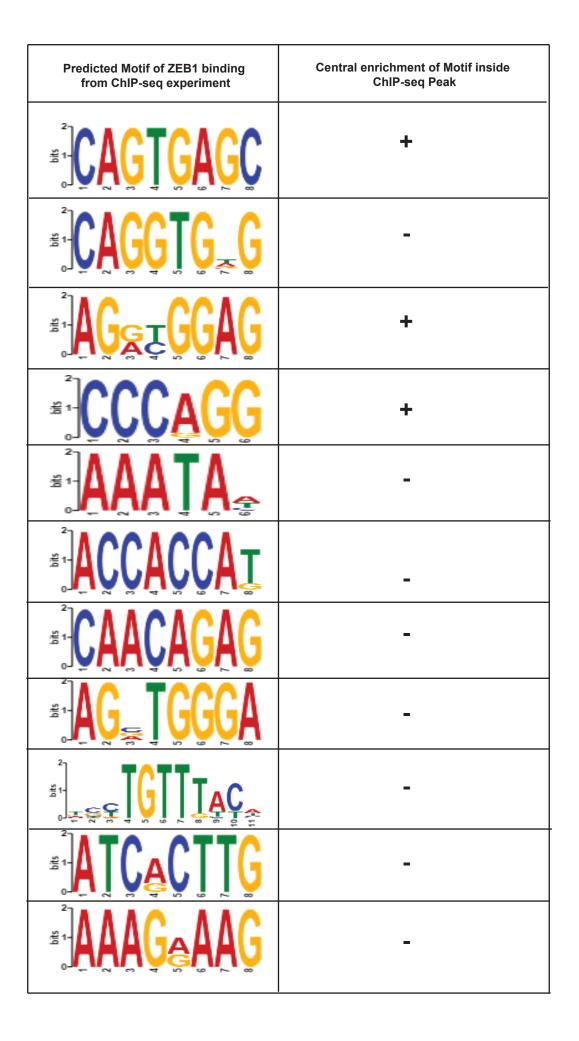
**Supplementary Table S1.** An Excel file including primary data from the ChIP-Seq analysis. This file tabulates in an organized manner the raw data deposited in Array Express under accession number E-MTAB-5241. The data are organized as: chromosome number, peak start, peak end, MACS, peak score, gene start, gene end, gene name, gene annotation, transcribed strand and distance from the gene start.

**Supplementary Table S2.** An Excel file presenting the primary data from the AmpliSeq analysis. This file tabulates in an organized manner the raw data deposited in Array Express under accession number E-MTAB-5243. The data are organized as: Gene name, Target ID, ENTREZ\_GENE\_ID, normalized expression values in triplicate samples of the mock C3 clone (up\_242\_1, up\_242\_2, up\_242\_3) and the ZEB1 KO CZ1 clone (up\_242\_7, up\_242\_8, up\_242\_9), mean of the mock C3 clone expression (meanCtrl), mean of the ZEB1 KO CZ1 clone expression (mean ZEB1), fold-change in expression between ZEB1 KO CZ1 and control C3 cells (absMeanFC), p-value (pval), adjusted p-value (padj), differentially expressed gene (DEG) and coincidence with the ChIP-Seq peaks (chipSeqPeak).

**Supplementary Table S3.** An Excel file presenting a short list of genes generated by the combination of ChIP-Seq and AmpliSeq analysis. The data are organized as: Gene name, mean expression values in the mock C3 clone (meanCntrl), mean expression values in the ZEB1 KO CZ1 clone (mean ZEB1 KO), fold-change in mean expression between ZEB1 KO CZ1 and control C3 cells (Mean fold-change), p-value (pval), adjusted p-value (padj), The top table (red) shows genes that are down-regulated when ZEB1 is lost, i.e. transcriptionally induced in the presence of ZEB1, and the bottom table (green) shows genes that are up-regulated when ZEB1 is lost, i.e. transcriptionally repressed in the presence of ZEB1.

## Supplementary Figure S1. DNA motifs enriched in the ZEB1 ChIP-Seq experiment.

Visualization of statistically significant, centrally-enriched or not DNA motifs, derived from the ZEB1 binding site sequences in Hs578T cells using the TOMTOM motif comparison tool. Sequence position is graphed on the x-axis versus probability of frequency (bits) on the y-axis.



Maturi\_Sup.Fig1.