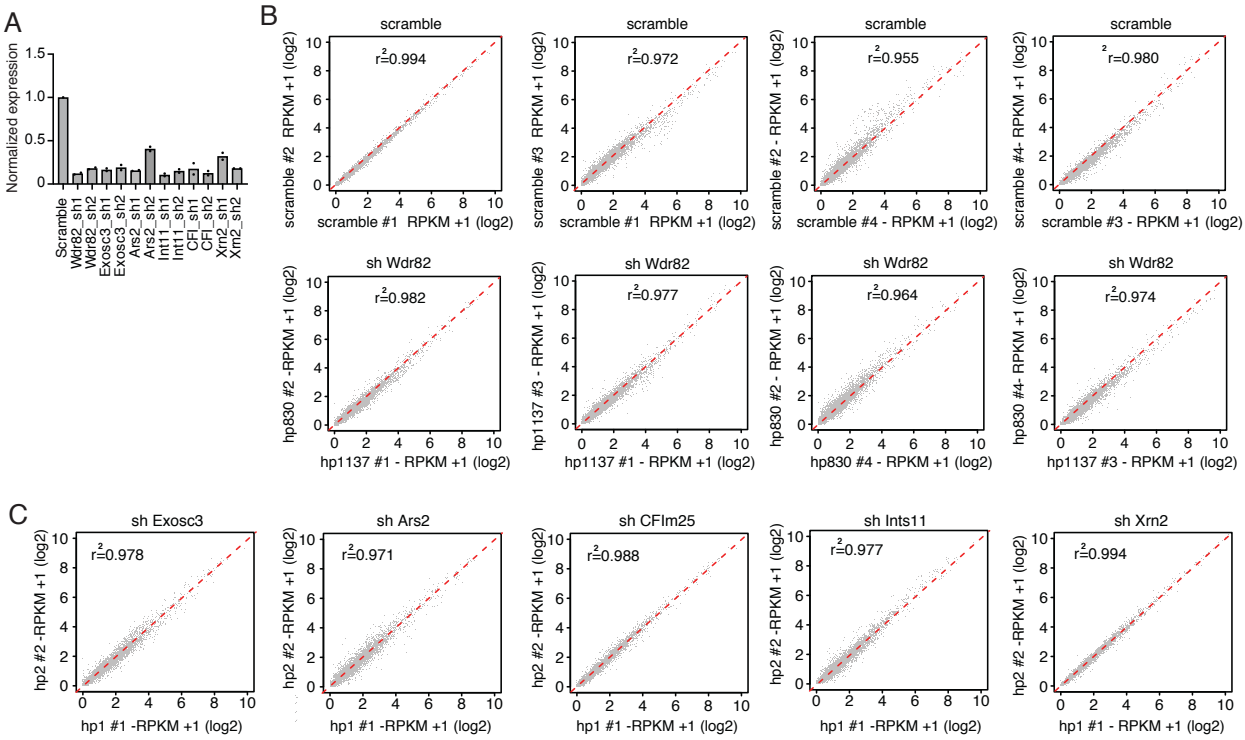
SUPPLEMENTARY FIGURES

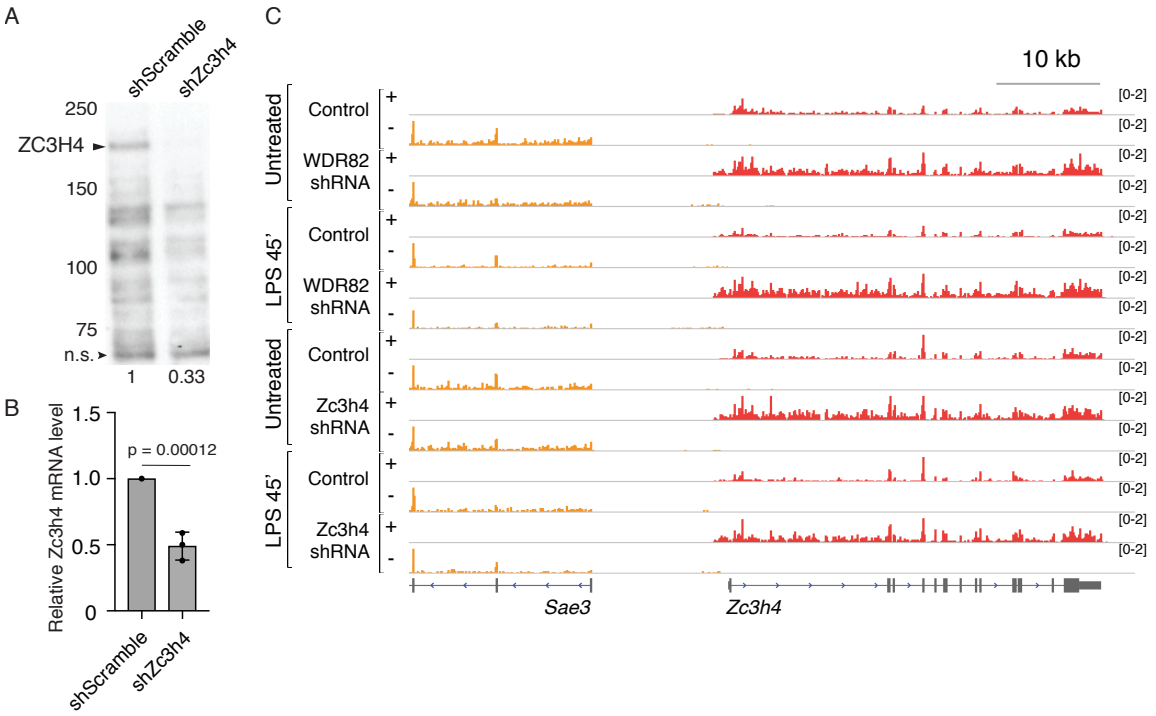


Supplementary Figure 1. *Depletion of transcription termination factors in primary mouse bone marrow-derived macrophages*.

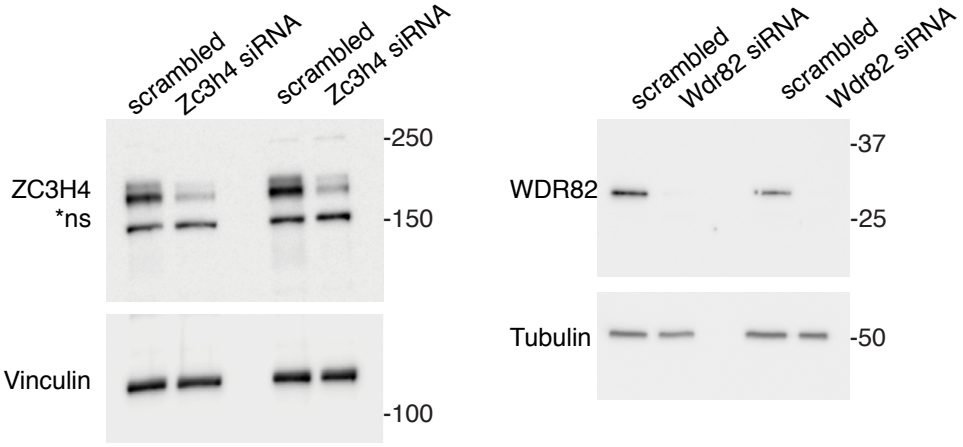
A) Depletion efficiency for the indicated termination factors in mouse macrophages transduced with shRNA retroviral expression vectors. The plot shows two sample points from one representative experiment. A total of at least 3 experiments for each hairpin were done with similar results. The data were normalized on the housekeeping gene *Tbp.*

B) Intensity of RNA-seq signals in experiments of shRNA-mediated depletion of WDR82. Pearson's correlations are shown. Two shRNAs targeting WDR82 (hp830 and hp1137) were used in n=4 biological replicates. Representative comparisons are shown.

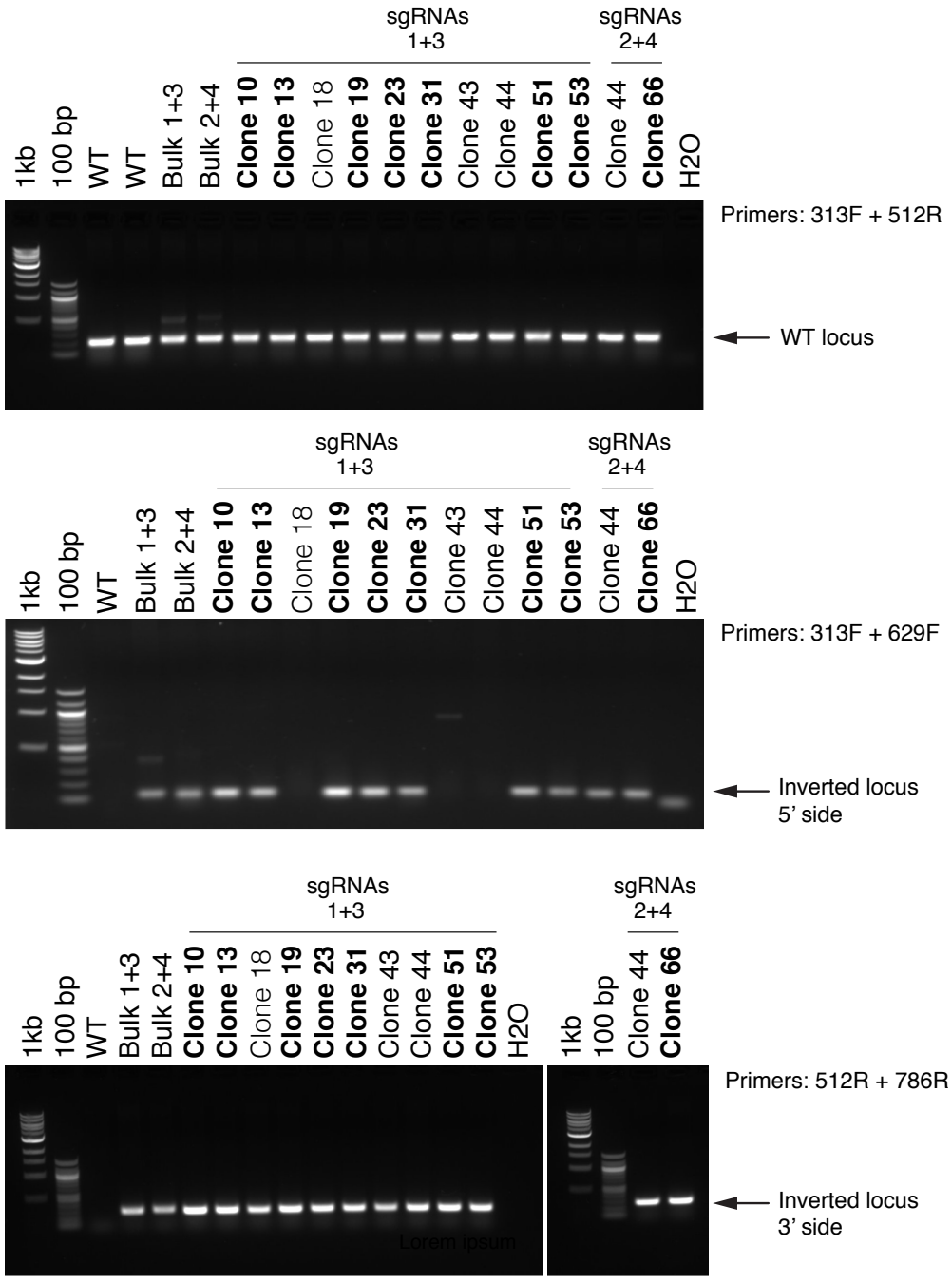
C) Intensity of RNA-seq signals in biological replicates from experiments of shRNA-mediated depletion of different termination factors.



Supplementary Figure 2. *Effects of ZC3H4 depletion on Zc3h4 gene transcription*.
A) ZC3H4 protein depletion in macrophages. The ZC3H4 band was quantified in control and depleted cells using the non-specific (n.s.) band at the bottom of the gel for normalization. M.W. markers (kDa) are shown on the left.
B) ZC3H4 mRNA depletion. The plot show the mean +/- s.d. of n=3 independent experiments. *P* = 0.00012, by two tailed t-test. The data were normalized on the housekeeping gene Tbp.
C) 4sU-seq snapshot showing *Zc3h4* gene transcription in control and WDR82- or ZC3H4-depleted macrophages. Data in untreated and LPS-stimulated cells are shown. The adjacent gene (*Sae3*) is shown for comparison.

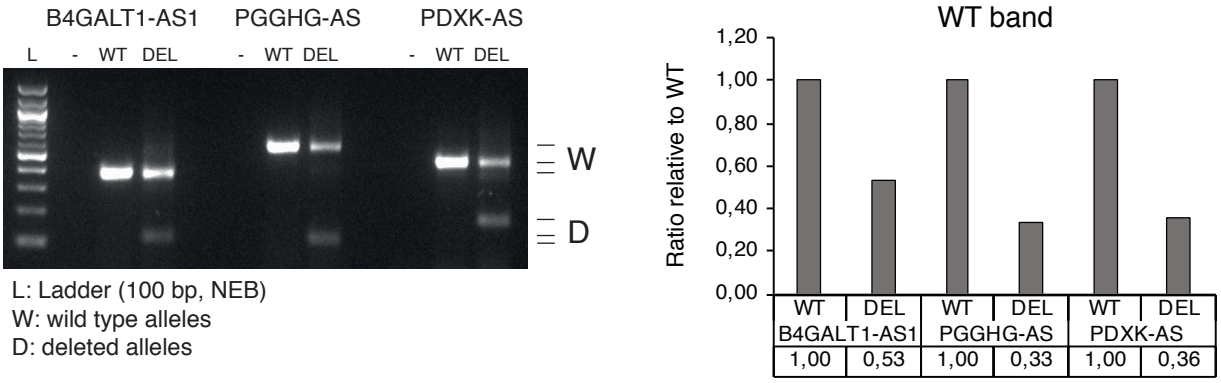


Supplementary Figure 3. *Depletion of WDR82 and ZC3H4 in HeLa cells*.
Western blots with the indicated antibodies are shown. n.s.: non-specific band. Vinculin and Tubulin are shown as loading controls. Data from n=2 representative experiments out of n>5 repeats are shown.



Supplementary Figure 4. *Inversion of the promoter/TSS of the MARCH6 coding/non-coding transcriptional unit in Hela cells*.

Genomic PCRs with different primers sets were used to identify junctions specifically generated upon inversion. of the locus. Arrows indicate the wild type (WT), the deleted (DEL) and the inverted (left and right, respectively) bands.



Supplementary Figure 5. *Genomic PCRs showing the deletion efficiency of 1st exons of lncRNAs.*
WT and deleted alleles were identified by genomic DNA PCR (left) and measured by densitometry (right).