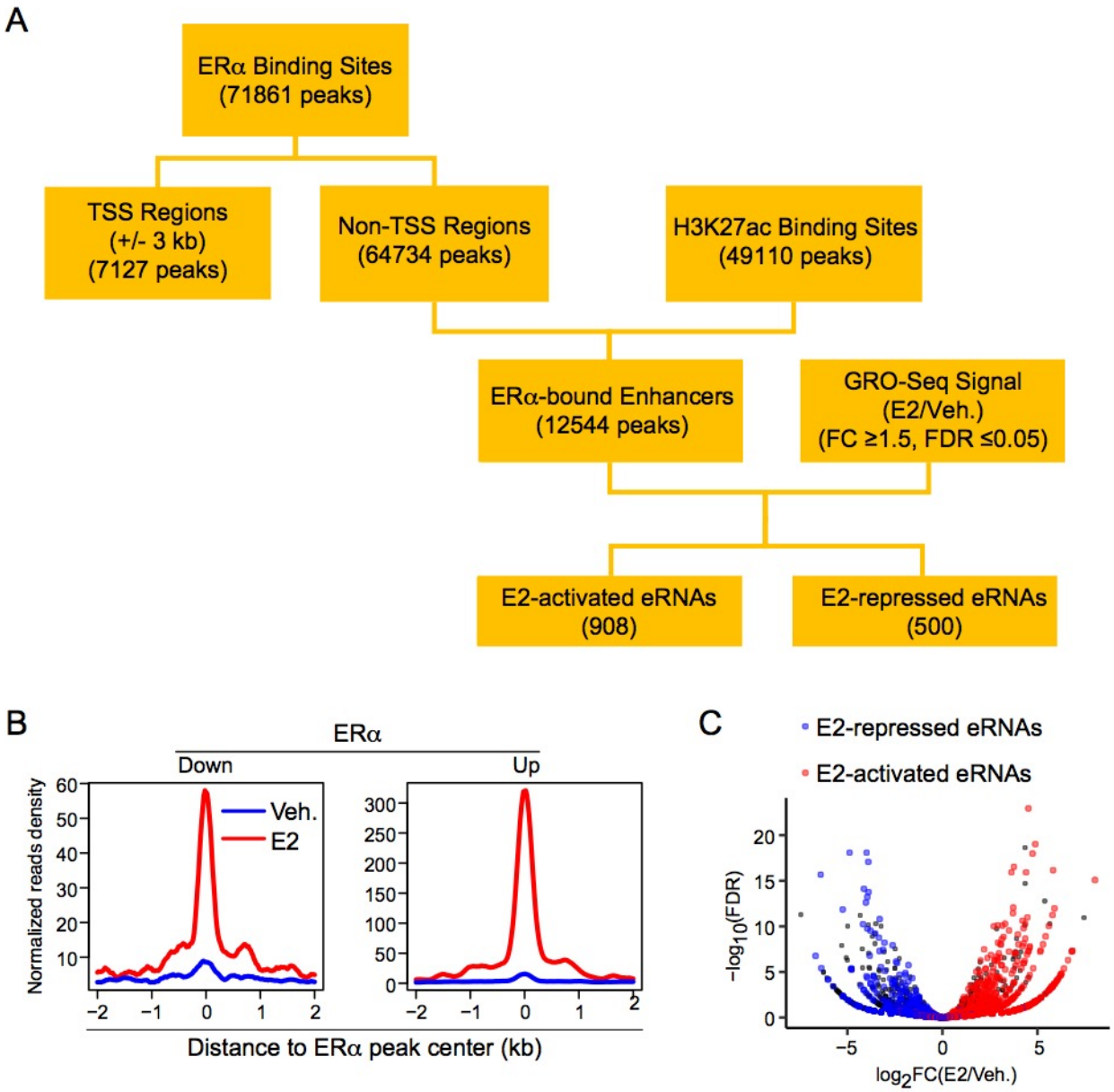


Figure S1. Two groups of ERα-bound enhancers that respond differentially to E2 were confirmed in separate data sets. Related to Figure 1.

(A). Workflow of identifying ERα-bound enhancers that produce eRNAs differentially expressed upon E2 treatment.
(B). ERα binding intensities at E2-downregulated (Down) and E2-upregulated (Up) enhancer regions in the presence of vehicle (Veh.) or E2 using an independent ChIP-Seq data (GSE24166) (Tsai et al., 2010).
(C). Scatter plot showing the $\log_2$[fold change] ($\log_2$FC) of expression of the defined eRNAs under E2 and vehicle treatment conditions (E2/Veh.) in an independent GRO-Seq data (GSE59532) (Franco et al., 2015).

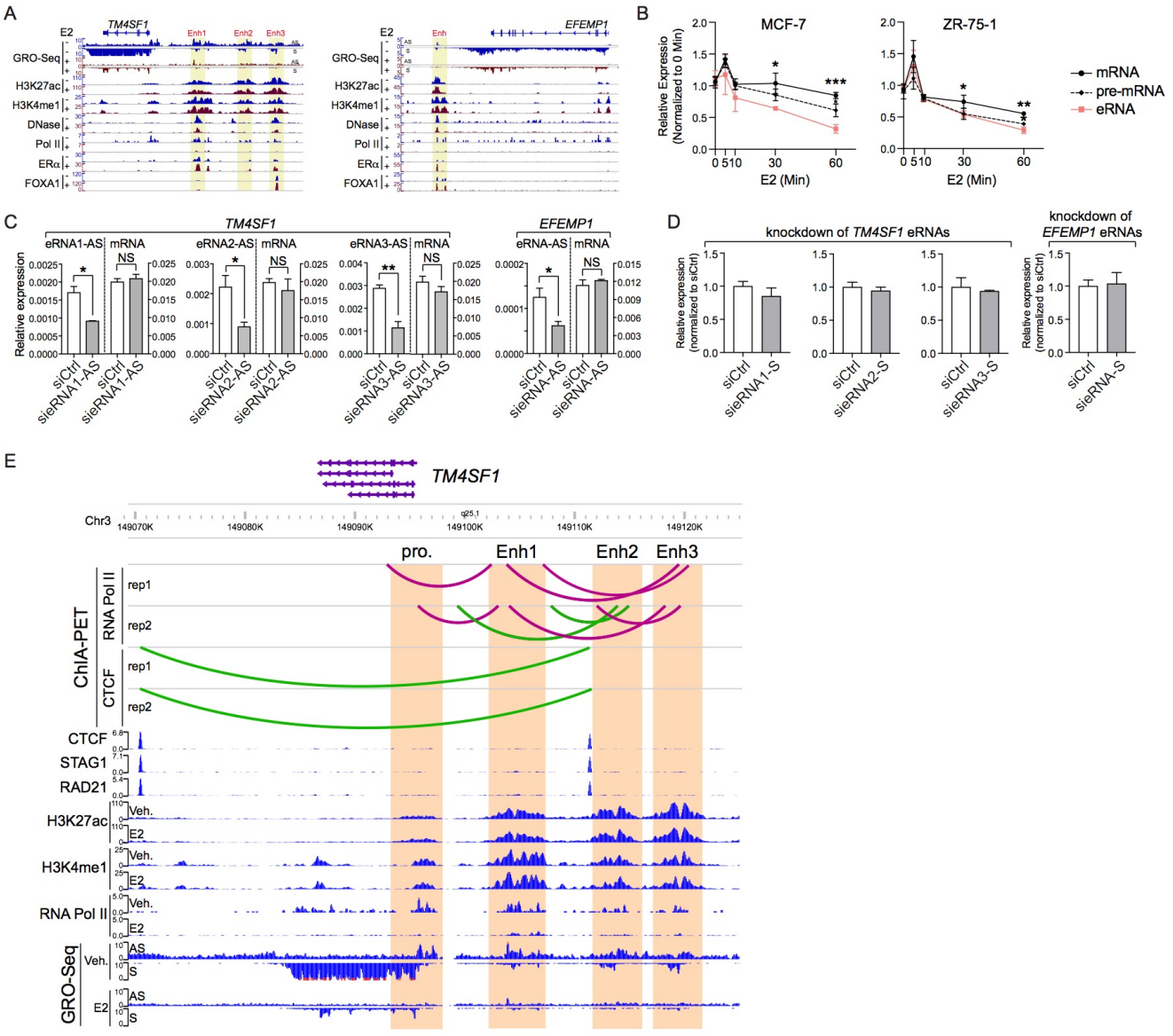


Figure S2. E2-repressed eRNAs control the expression of cognate mRNAs in a specific manner. Related to Figure 2.

(A). The Integrative Genomics Viewer (IGV) of GRO-Seq, ChIP-Seq and DNase-Seq (DNase) at genomic loci of *TM4SF1* and *EFEMP1*. Sense (S)- and antisense (AS)-strand information was indicated. Enhancers of *TM4SF1* (Enh1-3) and *EFEMP1* (Enh) were highlighted. The genome-wide sequencing data sets included in this figure are: GSE45822 (GRO-Seq) (Li et al., 2013), GSE45822 (H3K27ac) (Li et al., 2013), GSE40129 (H3K4me1) (Theodorou et al., 2013), GSE33216 (DNase) (He et al., 2012), GSE45822 (Pol II) (Li et al., 2013), E-TABM-828 (ERα) (Schmidt et al., 2010) and GSE26831 (FOXA1) (Kong et al., 2011).

(B). Expression of mRNA, pre-mRNA and eRNA of *EFEMP1* in MCF-7 and ZR-75-1 cells at different time points upon 100 nM E2 treatment. The forward primer for detecting *EFEMP1* mRNA is aligned across the junction between exon 1 and 2, and the reverse primer targets sequence in exon 3. Both primers for detecting pre-mRNA *EFEMP1* are located in intron 2.

(C). Expression of antisense (AS)-strand eRNA and mRNA of *TM4SF1* and *EFEMP1* in MCF-7 cells after knocking down the specified antisense (AS)-strand eRNAs. Data were normalized to mRNA levels of *GAPDH*.

(D). Expression of *COMMD2* mRNA upon knockdown of sense (S)-strand eRNAs of *TM4SF1* and *EFEMP1*. Data were normalized to conditions with control siRNA (siCtrl) transfection.

Data in (B)-(D) are presented as mean ± SD with three biological and technical replicates. *P*-values in (B) and (C) were calculated by Student's t-test. *, $P < 0.05$; **, $P < 0.001$; ***, $P < 0.005$; NS, not significant.

(E). The chromatin structure around *TM4SF1* gene is specially organized so that the enhancers have distinct functions.

The Integrative Genomics Viewer (IGV) of ChIA-PET, ChIP-Seq and GRO-Seq at genomic locus of *TM4SF1* gene. Sense (S)- and antisense (AS)-strand information was indicated. Data that were generated under vehicle (Veh.) or estradiol (E2) treatment condition were also specified. Promoter (pro.) and enhancers of *TM4SF1* (Enh1-3) were highlighted. Pol II or CTCF-mediated chromatin interactions that involve *TM4SF1* Enh2 were marked in green, otherwise in red. The genome-wide sequencing data sets included in this figure are: GSE33664 (Pol II ChIA-PET) (Li et al., 2012), GSE39495 (CTCF ChIA-PET) (Consortium, 2012), E-TABM-828 (CTCF, STAG1 and RAD21 ChIP-Seq) (Schmidt et al., 2010), GSE45822 (H3K27ac) (Li et al., 2013), GSE40129 (H3K4me1) (Theodorou et al., 2013), GSE45822 (Pol II) (Li et al., 2013), GSE45822 (GRO-Seq) (Li et al., 2013).

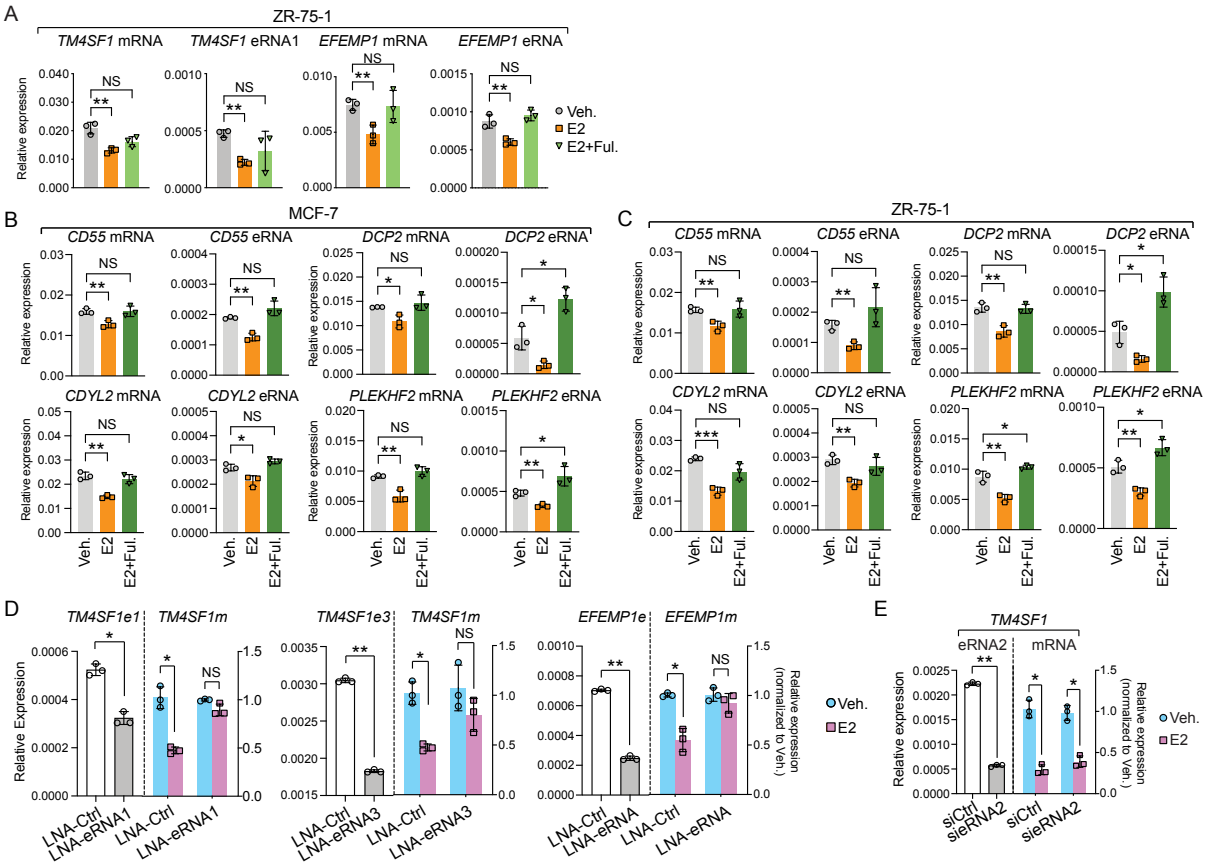


Figure S3. ERα signaling is essential for E2-induced transcriptional silencing of target eRNAs and associated mRNAs. Related to Figure 2.

(A). Expression of mRNA and eRNA of *TM4SF1* and *EFEMP1* in ZR-75-1 cells upon treatment with ethanol (Veh., gray bars), 1 nM estradiol (E2, orange bars) for 3 hrs, or 1 nM estradiol and 1 μM fulvestrant for 3 hrs (E2+Ful., green bars). Data were normalized to mRNA levels of *GAPDH*.

(B and C). Expression of eRNA and mRNA of four extra E2-repressed genes upon the treatment as described in (A) in MCF-7 (B) and ZR-75-1 (C) cells. Data were normalized to mRNA levels of *GAPDH*.

*, $P < 0.05$; **, $P < 0.001$; NS, not significant.

(D and E). E2-repressed eRNAs are required for E2-induced transcriptional silencing. Expression of eRNA (indicated by the white and gray bars) and mRNA (represented by the blue and light pink bars) of *TM4SF1* and *EFEMP1* upon knockdown of specified eRNAs using locked nucleic acid (LNA) probes (D) or siRNA (E) in the absence (Veh.) or presence (E2) of 100 nM estradiol for 3 hrs. Data were normalized to mRNA levels of *GAPDH*. *, $P < 0.01$; **, $P < 0.001$; NS, not significant.

Data are presented as mean ± SD with three biological and technical replicates. Statistical significance was calculated by Student's t-test.

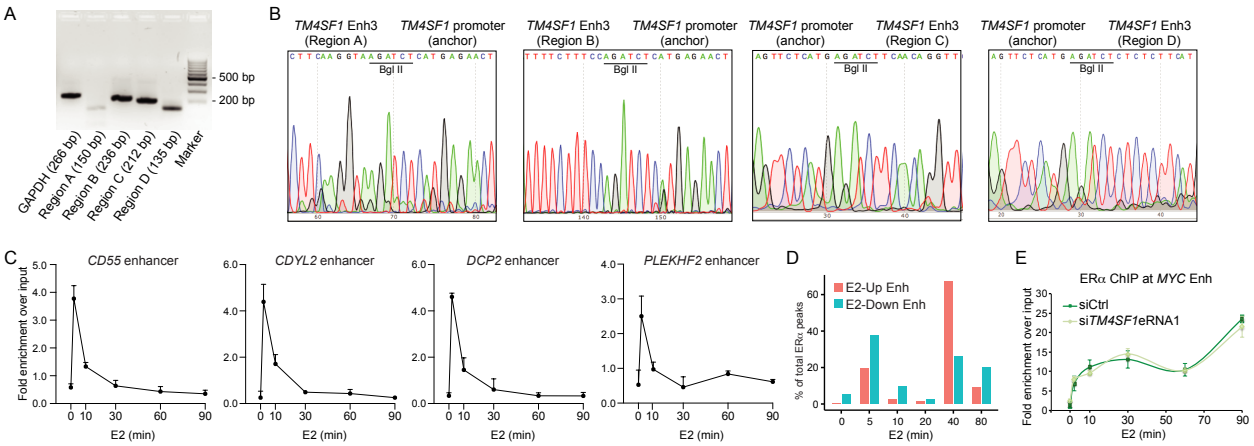


Figure S4. E2-repressed eRNAs play important roles in maintaining functional chromatin environment. Related to Figure 3.

(A). Agarose gel image showing PCR products of 3C ligation assays.
(B). Sanger sequencing results of 3C ligation products between *TM4SF1* promoter and different regions around *TM4SF1* Enh3.
(C). ERα binding at the enhancer regions of indicated genes in MCF-7 cells treated with 100 nM E2 for indicated lengths of time.
(D). Bar plot showing percentages of E2-upregulated (E2-Up Enh) and E2-downregulated enhancers (E2-Down Enh) that show detectable ERα binding intensities at different time points after E2 treatment in a separate ERα ChIP-Seq data (GSE62789) (Honkela et al., 2015).
(E). ERα-targeted ChIP at *MYC* enhancer (*MYC* Enh) after knocking down *TM4SF1* eRNA1 at different time points upon 100 nM E2 treatment in MCF-7 cells.
Data in (C) and (E) are presented as mean ± SD with three biological and technical replicates.

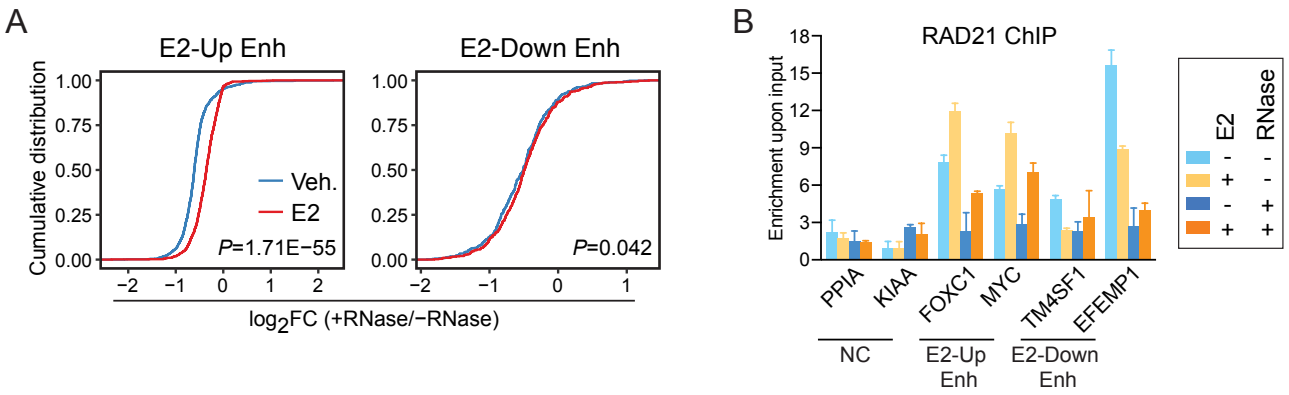


Figure S5. E2-induced ERα binding at E2-downregulated enhancers is particularly dependent on RNA integrity. Related to Figure 4.

(A). Cumulative distribution of ERα binding intensity at E2-upregulated (E2-Up Enh) and E2-downregulated enhancers (E2-Down Enh) before (-) and after (+) RNase treatment in the absence (Veh.) or presence of E2. The fold change of ERα peak intensities was log2-transformed ($log_2FC$).
(B). RAD21-targeted ChIP at E2-upregulated (E2-Up Enh) or E2-downregulated enhancers (E2-Down Enh) in MCF-7 cells. Cells were treated with (+) or without (-) 100 nM E2 for 30 min in the presence or absence of RNase. NC, negative controls using promoters of *PPIA* and *KIAA0066* as binding sites. Data are presented as mean + SD with three biological and technical replicates.

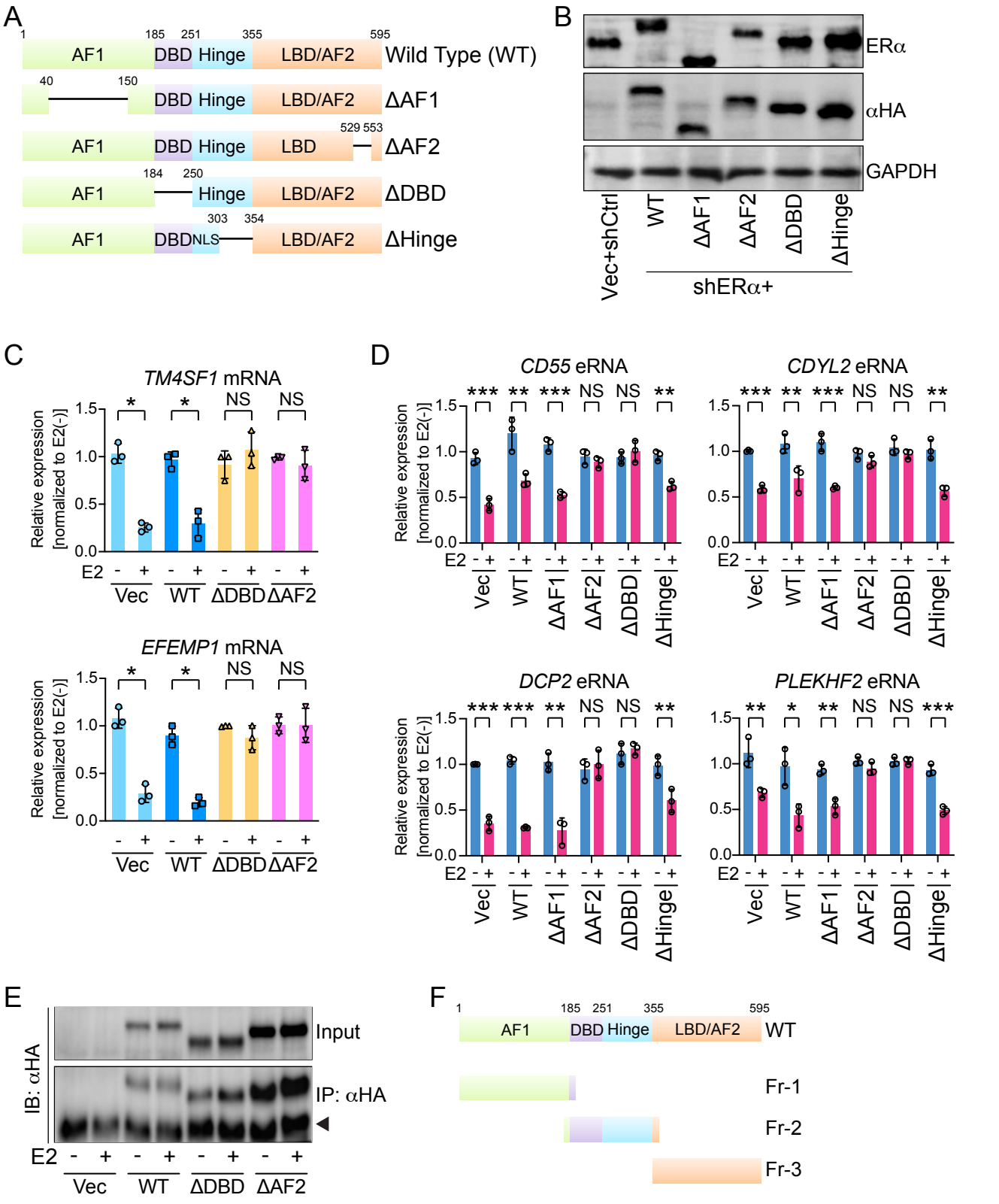


Figure S6. DNA-binding domain (DBD) of ERα plays an essential role in binding with E2-repressed eRNAs. Related to Figure 5.

(A and B). Schematic diagram illustrating the protein structures of wile-type ERα and various truncations (A) and their protein levels after replacing the endogenous ERα in MCF-7 cells (B). ΔAF1, deletion of activation function 1; ΔAF2, deletion of activation function 2; ΔDBD, deletion of DNA-binding domain; ΔHinge, deletion of hinge region; LBD, ligand-binding domain; NLS, nuclear localization signal. The corresponding residues of each domain or deleted parts are numbered.

(C and D). Expression of *TM4SF1* and *EFEMP1* mRNAs (C) or levels of eRNAs of four additional genes (D) in MCF-7 cells expressing empty vector (Vec), wild-type ERα (WT) or its truncated mutants in the absence (-) or presence (+) of 100 nM E2 for 3 hrs. Data were normalized to corresponding vehicle (-E2) condition. p values denoted differences between Veh and E2 (n=3; Student's t-test).

(E). Immunoprecipitation (IP) efficiency of RIP assay using anti-HA beads in MCF-7 cells. The replacement system was the same as illustrated in (A and B), and cells were treated with 100 nM E2 treatment for 5 min. Arrowhead, IgG heavy chain.

(F). Schematic diagram of full-length ERα (WT) and various GST-tagged fragments (Fr-1, -2 and -3). The amino acid numbers of each protein domain were shown.

Data are presented as mean ± SD with three biological and technical replicates. *P*-values were calculated by Student's t-test. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; NS, not significant.

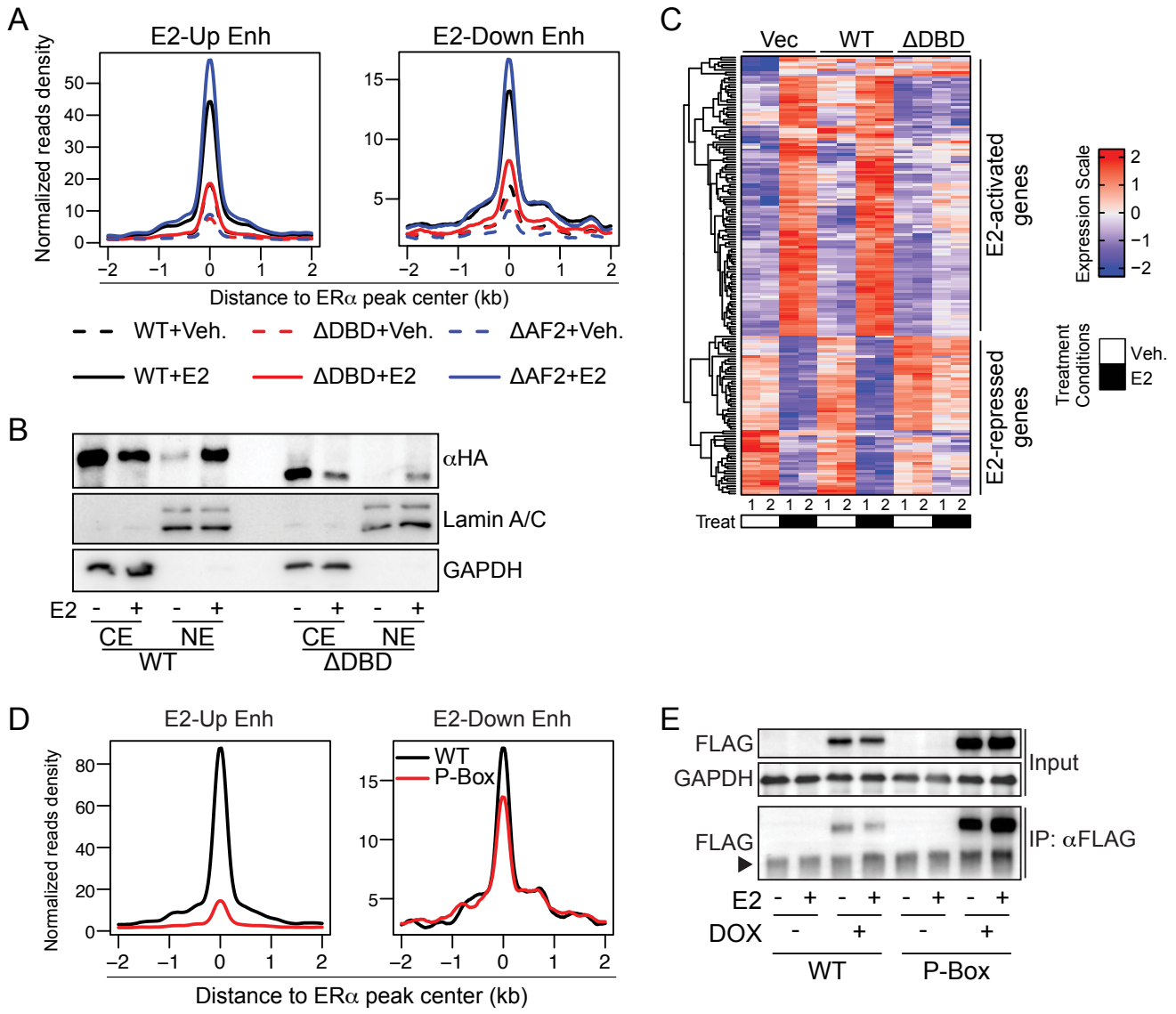


Figure S7. DNA-binding domain (DBD) of ERα is required for indirect chromatin binding of ERα at E2-downregulated enhancers, which is mediated by E2-repressed eRNAs. Related to Figure 5.

(A). Aggregate plots of ERα peak signals at E2-upregulated (E2-Up Enh) or E2-downregulated enhancers (E2-Down Enh) in anti-HA-targeted ChIP-Seq in MCF-7 cells treated with 100 nM E2 for 30 min. WT, wild type; ΔDBD, DNA-binding domain deletion; ΔAF2, activation function 2 deletion.
(B). Cytoplasmic exacts (CE) and nuclear extracts (NE) of MCF-7 cells expressing wild-type ERα (WT) or DBD-deletion mutant (ΔDBD) in the absence (-) or presence (+) of 100 nM E2 for 30 min.
(C). Heat map of E2-dependent expression of E2-activated and E2-repressed coding genes in MCF-7 cells expressing control vector (Vec), wild-type ERα (WT) or DBD-deletion mutant (ΔDBD). Cells were treated with 100 nM E2 for 6 hrs.
(D). Aggregate plot of binding signals of wild-type ERα (WT) or P-Box mutant (P-Box) at E2-upregulated (E2-Up Enh) and E2-downregulated enhancers (E2-Down Enh) in MCF-7 cells that were kept in regular culturing medium.
(E). Immunoprecipitation (IP) efficiency of RIP assay using anti-FLAG antibody in MCF-7 cells expressing inducible wild-type ERα (WT) or P-Box mutant (P-Box). Cells were treated with 100 nM E2 for 5 min and proteins were induced by 2 μg/ml doxycycline (DOX) overnight. Arrowhead, IgG band.

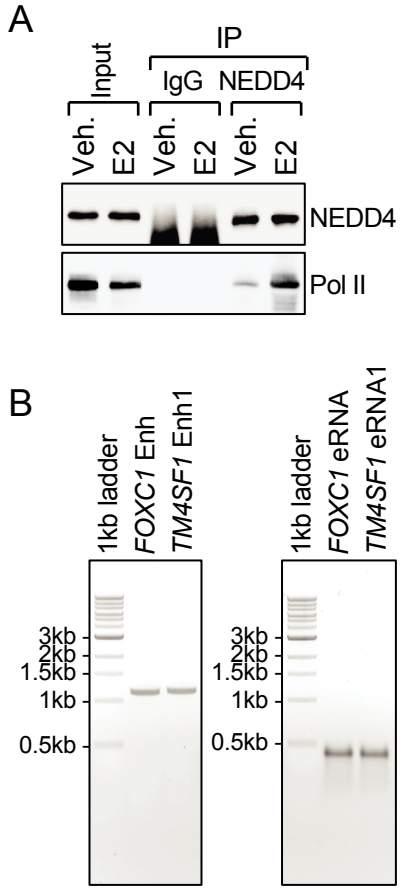


Figure S8. E2-repressed eRNAs assist ERα in its interaction with KDM2A, which leads to association between RNA Pol II and NEDD4. Related to Figure 6.

(A). Immunoprecipitation (IP) of NEDD4 in MCF-7 cells treated with vehicle (Veh.) or 100 nM E2 for 3 hrs.
(B). Agarose gel image showing PCR products that were amplified to contain enhancer regions of *FOXC1* (*FOXC1* Enh) and *TM4SF1* (*TM4SF1* Enh1) (left panel) or *in vitro* transcribed eRNAs of *FOXC1* (*FOXC1* eRNA) and *TM4SF1* (*TM4SF1* eRNA1) (right panel). 1 kb DNA ladder was marked.

Supplemental Tables

Table S1. siRNA and LNA sequences. Related to Figure 2, Figure S2, and Figure S3.

| Names | 5'-3' Sequences |
|---|---|
| siTM4SF1 eRNA1-AS_F | CAGAAAGGGAGUUGAGAUUUU |
| siTM4SF1 eRNA1-AS_R | AAUCUCAACUCCCUUUCUGUU |
| siTM4SF1 eRNA1-S_F | UGAGAGUGCUGAAGUCAUAUU |
| siTM4SF1 eRNA1-S_R | UAUGACUUCAGCACUCUCAUU |
| siTM4SF1 eRNA2-AS_F | GGAGGGGCAUGGAGGUUAAUU |
| siTM4SF1 eRNA2-AS_R | UUAACCUCCAUGCCCCUCCUU |
| siTM4SF1 eRNA2-S_F | UCCCAGAGUCCGCCGUAAAUU |
| siTM4SF1 eRNA2-S_R | UUUACGGCGGACUCUGGGAUU |
| siTM4SF1 eRNA3-AS_F | UGGUAGAAGUCAUGAGAUUUU |
| siTM4SF1 eRNA3-AS_R | AAUCUCAUGACUUCUACCAUU |
| siTM4SF1 eRNA3-S_F | GGUAGGAACUGCAGACUUUUU |
| siTM4SF1 eRNA3-S_R | AAAGUCUGCAGUUCCUACCUU |
| siEFEMP1 eRNA-AS_F | GGGCUUAAUGCCUCCAAAAUU |
| siEFEMP1 eRNA-AS_R | UUUUGGAGGCAUUAAGCCCUU |
| siEFEMP1 eRNA-S_F | GGACAGAGUAGAGGAGAUAUU |
| siEFEMP1 eRNA-S_R | UAUCUCCUCUACUCUGUCCUU |
| LNA-TM4SF1-eRNA1 | AATTAAAAAGTGTCGT |
| LNA-TM4SF1-eRNA3 | CTGACTAGGTAATGCT |
| LNA-EFEMP1-eRNA | TTAGTGGTGTCGAGTG |
| LNA-negative control | AACACGTCTATACGC |

Table S2. Primers for RT-qPCR and RIP-qPCR. Related to Figure 2, Figure 3, Figure 4, Figure 5, Figure 6, Figure S2, Figure S3, and Figure S6.

| Gene Names | 5'-3' Sequences |
|---|---|
| GAPDH_F | TGCACCACCAACTGCTTAGC |
| GAPDH_R | GGCATGGACTGTGGTCATGAG |
| TM4SF1_F | CACAATGTGCTTGGGTTCAG |
| TM4SF1_R | TATGTCTTGATTCCCTCGGC |
| EFEMP1_F | GCCGCACAGGTATTTTTGCT |
| EFEMP1_R | TGTCCTGTGACTTGACCAGC |
| COMMD2_F | TGCTGGTTTAATCTGTTGCCT |
| COMMD2_R | CGATTCTGAGTGAATTGGCA |
| TM4SF1-premRNA_F | TACACCTTTGCCAGCACTGA |
| TM4SF1premRNA_R | AAACACTGGCTAGGTGGGTG |
| EFEMP1-premRNA_F | CCTGGACTCCTACCACATGC |
| EFEMP1-premRNA_R | AGGCCACTTACTTGAGAATGC |
| TM4SF1_eRNA1-S_F | TCTATGACTTCAGCACTCTCAAAGA |
| TM4SF1_eRNA1-S_R | CTTGGAGAATGCTCACACTGC |
| TM4SF1_eRNA1-AS_F | AGTTGTTCACTATGGGAACCC |
| TM4SF1_eRNA1-AS_R | ACAGTCATTTGGCCAGGCTA |
| TM4SF1_eRNA2-S_F | TCTCACTCAACAACAAACTGGC |
| TM4SF1_eRNA2-S_R | ATTTTTACGGCGGACTCTGG |
| TM4SF1_eRNA2-AS_F | CTTAACGCCAAGCTCACAGG |
| TM4SF1_eRNA2-AS_R | CAGACCAGAGATGCACCTCA |
| TM4SF1_eRNA3-S_F | GTCAGGTAGGAACTGCAGACT |
| TM4SF1_eRNA3-S_R | ACCAAAACTATAGCCTCATCCA |
| TM4SF1_eRNA3-AS_F | AGCAGTAGCCAGTTTCAGCA |
| TM4SF1_eRNA3-AS_R | CCTGTTCGGTGTAAAAGGCC |
| EFEMP1_eRNA-S_F | AGGAATTCCCAGCAGCTTCA |
| EFEMP1_eRNA-S_R | CCACCCAGAATCCTGCAGTA |
| EFEMP1_eRNA-AS_F | TGGAGGACTGGGCTTAATGC |
| EFEMP1_eRNA-AS_R | GAGGGAGATGTGGTCACCAA |
| PGLYRP2_eRNA_F | GCATACCGATCACCGAATTGA |
| PGLYRP2_eRNA_R | TCCTGGCAATGATCGTCAAC |
| ZDHHC22_eRNA_F | TGCAGCTCCTTGCATCTT |
| ZDHHC22_eRNA_R | AAGCAGCTTCTGCCTTGA |
| SEMA3G_eRNA_F | CACTCAGGGTGACCTTCTTTC |
| SEMA3G_eRNA_R | CTGTGTATTGTACTAAATGGACTGATG |
| KCNC1_eRNA_F | CAGAGTGAGAGTAGCCTGTAGA |
| KCNC1_eRNA_R | GTAGTGTCCCGTTGGCATAG |
| SYT8_eRNA_F | GAGGATGATCTATGCAGGATGTG |
| SYT8_eRNA_R | CTTGGTGTTCAGGGAGGATTT |

| | |
|---|---|
| PGR_eRNA_F | GCAATTCAGGTCAAGATGTCTAAAT |
| PGR_eRNA_R | TGGTCTCTACAGTCTACAAGGT |
| FOXN1_eRNA_F | AGGGAGTGCTCTGGGAA |
| FOXN1_eRNA_R | AGAGCAGCACTGACATCAC |
| KCNK5_eRNA_F | GTCCTTTGTATCTTTGGGTCTTC |
| KCNK5_eRNA_R | CTGCCTTTCTCCCTCTGAATA |
| ENPP2_eRNA_F | CTGGACTCTCTGGCTTGTTTAG |
| ENPP2_eRNA_R | ATTCCCACAGCAACCCTATG |
| CT62_eRNA_F | CTGGATCAGACCAACGTGAA |
| CT62_eRNA_R | AGGATCTGTTTGCTCTACTAAGAAT |
| SMAD7_eRNA_F | TGGTTCAGTTCAAGTACCTGTT |
| SMAD7_eRNA_R | TTTCCACAGGTGAGCAGAAA |
| MYCB_eRNA_F | GTCAGCACAGCACACTAGAT |
| MYCB_eRNA_R | CTGCTGTTCGTGTTGTCATTT |
| TTC9_eRNA_F | CAGAAAGCCAAGTCAACAGAAG |
| TTC9_eRNA_R | GTAGCATCAGCTTATCAGAAGGA |
| SYDE2_eRNA_F | TTGGGTTTCGAGTGTTACATTTC |
| SYDE2_eRNA_R | TCTTCCACAATCCACCTTCTAC |
| SPRY1_eRNA_F | GTCAGAAGCCTCAGGGAAATAG |
| SPRY1_eRNA_R | GGCAGGGCAAGGGTAATAAA |
| CCNG2_eRNA_F | GTCTGGGCAGCTAATCTATTCC |
| CCNG2_eRNA_R | TTCTCTCCCATTAGGCTCTGA |
| DSCR8_eRNA_F | CAAGGACATGATTTGGGAGTAAGA |
| DSCR8_eRNA_R | GACAGCCTAAGCTACAGAAACC |
| BMF_eRNA_F | CTAGGGACCCATCTCACTCTAT |
| BMF_eRNA_R | TCTGGAACTTAAGCTGGCTAAC |
| KRT7_eRNA_F | CAGTCAGAGCCAATGTGTGA |
| KRT7_eRNA_R | ACCCTGGCACACCTGAG |
| GLCCI1_eRNA_F | GAAGGAGGCCTTCAGTCTATTT |
| GLCCI1_eRNA_R | CCAGGCTTCTTGTAGCCATATTA |
| PAK2_eRNA_F | GTACTGAAGCCTCTTTCACAATAC |
| PAK2_eRNA_R | CCTCCCAAGACCCAACTAAA |
| WEE1_eRNA_F | AGTAATCTGAACGAAGCCAGTT |
| WEE1_eRNA_R | GGGTTAGTGACATACACAGGAAA |
| ARMC9_eRNA_F | GCATGGAGTCCTAGTGACAAATA |
| ARMC9_eRNA_R | AGGCTACTTTGCTGCGTAATA |
| ZNF217_eRNA_F | GGAAGCAGTAAACTCATTTCCAAG |
| ZNF217_eRNA_R | GCAAGAGACAGAGAGAGAGAGA |
| SALL4_eRNA_F | CTGTAACAGAGAGCCACAGAC |
| SALL4_eRNA_R | ATCTACGAGCCAAGGAGAGA |

| | |
|---|---|
| PRLR_eRNA_F | CCCACGTTGCACATTCTCTA |
| PRLR_eRNA_R | AGCAAACTTCTCCATGTCTGT |
| TNFRSF11B_eRNA_F | ACAGACAGACCAAGCCCATT |
| TNFRSF11B_eRNA_R | TTGGAACTTGGAAGGAAGCT |
| ARID5B_eRNA_F | CCCATGGAGTTGGCTATCCT |
| ARID5B_eRNA_R | TGCCTGTTCTACTCTGGTGG |
| LYPD3_eRNA_F | AGCCCTGAAAAAGAGGCTGA |
| LYPD3_eRNA_R | GAGTGAGAGGGTTTAGCCGT |
| TMEM116_eRNA_F | AAGGGTTGCATTGCATTCCC |
| TMEM116_eRNA_R | CAACAGTGCGTGATGTGCTT |
| CDYL2_F | GCCCGTCGGTTGAGAAACT |
| CDYL2_R | GCTTCCGTTTATGGGAGGTCC |
| CDYL2_eRNA_F | GTCTAGAGACACAGGGAGGC |
| CDYL2_eRNA_R | TTCCTGGTTCTGCTCTCTGG |
| CD55_F | AGGCCGTACAAGTTTTCCCG |
| CD55_R | CCTTCTCGCCAGGAATTTTCAC |
| CD55_eRNA_F | GCTCCTCAAGTCTCACACCT |
| CD55_eRNA_R | AGAGATGTGACTGCAGGCAA |
| DCP2_F | AGAACACACCAGGATTACCTCA |
| DCP2_R | AGCAAAAACGGACAATGACTGA |
| DCP2_eRNA_F | TGGAACCAACACCTTCGAAT |
| DCP2_eRNA_R | ACAGACTTGGTGCACAGCTA |
| PLEKHF2_F | CCGTCGGGGCTATTAGTGAAA |
| PLEKHF2_R | TGACCAGCTGCTCCAAAACA |
| PLEKHF2_eRNA_F | ACGTGGTAGGCAAACAGGAT |
| PLEKHF2_eRNA_R | GACAATCTGTTCTGGCAGCC |

Table S3. Primers for 3C-qPCR. Related to Figure 3.

| Names | 5'-3' Sequences |
|---|---|
| Anchor | CTGAATCATGGCAGCAGTTTCCCCCATGC |
| Region A | TGACAGGACACAGAGAGTTAGGTCAGGGCA |
| Region B | AGAGAGTTCAGATGACTTGCCCAGAATCCAG |
| Region C | CACGCTGAGGCTCCACTGACAAGTGCAAG |
| Region D | GCGAGATGTTCTTTAGGTAGGCAGCCAGGGA |
| GAPDH_3C_F | ACAGTCCATGCCATCACTGCC (Hagege et al., 2007) |
| GAPDH_3C_R | GCCTGCTTCACCACCTTCTTG (Hagege et al., 2007) |

Table S4. Primers for ChIP-qPCR. Related to Figure 3, Figure 5, Figure 6, Figure S4, and Figure S5.

| Names | 5'-3' Sequences |
|---|---|
| TM4SF1_Enh1_F | CACCTAGACCTCATGGCCTC |
| TM4SF1_Enh1_R | TGCCATGTTGGACTTTGACA |
| TM4SF1_Enh2_F | TGTGGCTTCTGAAGAGCTGA |
| TM4SF1_Enh2_R | CATGCCCCTCCTTTGTGAAC |
| TM4SF1_Enh3_F | GTCCAAACATACTGCTGCCA |
| TM4SF1_Enh3_R | CCAGTGTGTGTTAGTCAGCC |
| TM4SF1_pro_F | AACTGCCAAGTGTCCGAGAT |
| TM4SF1_pro_R | AGCTCTCAGATTGGAAGCTGT |
| EFEMP1_Enh_F | TGTTCTAAATGCCAGGGCCT |
| EFEMP1_Enh_R | CACAGCTGCAGGGATAGGAA |
| GAPDH_pro_F | TACTAGCGGTTTTACGGGCG (Xu et al., 2012) |
| GAPDH_pro_R | TCGAACAGGAGGAGCAGAGAGCGA (Xu et al., 2012) |
| KIAA0066_F | CTAGGAGGGTGGAGGTAGGG (Varambally et al., 2008) |
| KIAA0066_R | GCCCCAAACAGGAGTAATGA (Varambally et al., 2008) |
| PPIA_F | GCCAGGCTCCTGTTTTAATG |
| PPIA_R | GCAGTCTCCGGTTTTGAGAG |
| MYC_Enh_F | CCAGCTTTCACCAACCACTC |
| MYC_Enh_R | GCAGGTGTCCTAGAGCATGA |
| FOXC1_Enh_F | GCGTCTCAGAATGGACAGGA |
| FOXC1_Enh_R | TAAAGATCGCAGTGGCCCTT |
| CD55_Enh_F | TGAGGCATAGATAGGCACATTAC |
| CD55_Enh_R | CAGGCAACATTCCTCCAGAA |
| CDYL2_Enh_F | GGAGCTAGAATTGGCCACTATG |
| CDYL2_Enh_R | GGACACCACCTACCATCTACT |
| DCP2_Enh_F | TGCCAAGCAGATGGTTAAGT |
| DCP2_Enh_F | CACAGGGAAAGCCTGAAAGA |
| PLEKHF2_Enh_F | CCTACCACGTTGCAGACAAA |
| PLEKHF2_Enh_F | ATGGGTCATCAAAGCACTGG |