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**Supplemental Information**

**Cross-Regulation between TDP-43  
and Paraspeckles Promotes  
Pluripotency-Differentiation Transition**

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**Figure S1. Methods related to Figure 1 - paraspeckle counting and subcellular localization of *NEAT1***

(A) Maximum projection photomicrographs of spontaneously differentiating hESCs demonstrating the analysis of *NEAT1* foci. Two single molecule (sm)FISH probe sets targeting an overlapping region in *NEAT1\_1* (using Q570 and Q670 dyes) confirmed the specificity of *NEAT1\_1* probes (left). *NEAT1\_1* and *NEAT1\_2* probes, which target non-overlapping regions of the transcript, exhibited co-localization in differentiated cells, in accordance with the definition of paraspeckles as foci of full length *NEAT1* (right). A spot detection algorithm was used to detect the foci using arbitrary settings according to (Trcek et al., 2017). Identical analysis was conducted for mESCs, differentiated progeny, and all modified cell lines in this study.

(B,C) Representative maximum projection photomicrographs of *NEAT1\_1, \_2*, *Neat1\_1, 2* foci used for paraspeckle counting in human (B) and mouse ESCs (C) as depicted in Fig. 1A and Fig. 1B. Samples include undifferentiated, spontaneously differentiated (KSR media), BMP4- and CHIR99021-treated hESCs (left), and undifferentiated and 3 d spontaneously differentiated mESCs untreated or treated by doxycycline to induce TDP-43-eGFP expression (scale bars = 10  $\mu$ m. Red: *NEAT1\_1, \_2*, *Neat1\_1, \_2* probes; blue: DAPI - nuclear stain).

(D) RT-qPCR analysis utilizing *NEAT1\_1* and *NEAT1\_2* assays demonstrating that the expression of full length *NEAT1* corresponds to the amount of paraspeckles (Fig. 1A). Samples include undifferentiated, spontaneously differentiated, BMP4- and RA-treated hESCs (n=3 independent replicates, error bars=SD).

(E) A Western blot analysis of predominant proteins in the cytoplasm (ACTB), nucleus (OCT4), nuclear lamina (LMNB1) and chromatin (ser5 phosphorylated RNA PolII CTD) following subcellular fractionation of undifferentiated hESCs (as outlined in Methods section).

(F-H) The enrichment of transcripts in subcellular fractionation-RNA-Seq of hESCs confirmed the locations of *NEAT1* isoforms, *\_1* and *\_2* in the nucleoplasm and chromatin fractions respectively. The nucleoplasmic enrichment of the snoRNA *SCARNA10* and of mature mRNAs (*RPS27*), as well as the enrichment of intronic reads in the chromatin fraction, validates the separation of subnuclear components. These results are in line with previous subcellular fractionation-RNA-Seq results of mouse macrophages (Bhatt et al, 2012, Cell), demonstrating the enrichment of *Neat1* isoforms, *\_1* and *\_2* in the nucleoplasm and chromatin fractions respectively (I,J).

**Figure S2. Methods related to Figure 2 - the genetic editing of *NEAT1* and *Neat1* and to global analysis of RBP-mRNA occupancy**

(A) An illustration of a generic form of human/mouse *NEAT1* where the endogenous pA site (*NEAT1* $\Delta$ pA) and the triple helix region (*Neat1* $\Delta$ TH) were deleted using CRISPR-Cas9 (gRNA oligonucleotides and primers are outlined in Methods section).

(B) RT-qPCR analysis of *NEAT1* isoforms in *NEAT1* $\Delta$ pA and *Neat1* $\Delta$ pA ESC lines. Note the higher mean expression of *NEAT1*\_2 and *Neat1*\_2 in  $\Delta$ pA clones compared to parental lines (n=2 independent replicates/clone, SD=SEM, two sided t-test; P value \*\* < 0.01). The smaller increase of *Neat1*\_1 reflects a higher level of the isoform in undifferentiated mESCs compared to hESCs.

(C) A representative Western blotting of a conditional TDP-43 KO mESCs line (named cTdp-43 KO) harboring floxed alleles of *Tdp-43* and a CAG-ErCreEr cassette (Ling et al., 2015), and following tamoxifen-induced deletion of the gene (3 d). Beta Actin was used as loading control.

(D,E) SDS-PAGE analysis related to the preparation of peptides for LC-MS (**Fig. 2A**), demonstrating the migration of RBPs crosslinked to RNAs from *NEAT1* $\Delta$ pA and parental WT hESC samples. Proteins treated by oligo d(T) magnetic beads remained in gel pockets or migrated following treatment by RNase I, and whole cell lysate samples (input control) showed migration of numerous proteins.

(F) RT-qPCR analysis of *NEAT1*\_2 of samples treated by oligo d(T) magnetic beads, captured and supernatant samples derived from *NEAT1* $\Delta$ pA and parental WT hESCs (n=4, error bars = SD, two sided t-test; P value \*\*\* < 0.001). This analysis confirmed the efficient retention of *NEAT1*\_2 in the oligo d(T) supernatant and is refractory to oligo d(T) mRNA-RBP capture.

(G) Confirmatory Western blot analysis related to **Fig. 2B,C**, showing that mRNA occupancy of paraspeckle RBPs, NONO, SFPQ and of TDP-43 decreased in *NEAT1* $\Delta$ pA hESC clones compared to parental WT cells. The specific enrichment of RBPs is shown by comparing input (left) where Histone H3 signal is clearly visible, to oligo(dT) treated samples (right) where the Histone H3 signal is absent. The RBP CPEB1, which does not localize to paraspeckles, was used as a loading control.

**Figure S3. Results related to Figure 4 - identification of pA sites in ESCs**

(A) A scatter plot displaying transcripts detected by RNA-Seq, samples include undifferentiated hESCs and mesoderm progenitors generated by CHIR99021 treatment (3 d). Differentially expressed genes with an adjusted p-value of  $< 1e-20$  (Fisher's exact test, false discovery rate  $1e-15$ ) were labeled red (n=2 biological replicates per condition). *TARDBP* (gene encoding TDP-43), canonical pluripotency and mesoderm genes are highlighted.

(B) A scatter-plot displaying degrees of lengthening and shortening of transcripts caused by changes in the location of pA sites upon the differentiation of hESCs to mesoderm progenitors, samples as in A. Locations of pA sites were determined by 3' mRNA-Seq (QuantSeq), and pA sites with statistically significant changes (adjusted p-value  $< 0.001$ , Fisher's exact test, explained below) were colored red (n=4 biological replicates per condition).

(C-E) Analyses conducted using a workflow for detecting 3' UTR lengthened or shortened transcripts (direction distal or proximal, respectively) in accordance with (Rot et al., 2017).

(C,D) The positions and the number of pA sites per gene detected in hESCs and mesoderm progenitors (samples corresponding to B) versus sites identified in HEK293 cells (Derti et al, 2012). (E) The nucleotide composition around pA sites that were uniquely identified in hESCs and mesoderm progenitors (samples as in B), or pA sites that overlapped with an existing dataset (Derti et al., 2012). The similar patterns support the *bona fide* classification of novel pA sites in this study.

(F) Representative outlines showing the frequencies of proximal and distal pA sites in transcripts encoding pluripotency factors comparing cTdp-43 KO mESCs treated or untreated by tamoxifen and primitive streak-like progenitors.

**Figure S4. Results supporting the Figure 4 - role of TDP-43 in position-dependent regulation of APA in h/mESCs**

(A) The highest ranked multivalent RNA motifs that were enriched around the pA sites exhibiting significant changes upon differentiation of hESCs or TDP-43 KD (as defined in **Fig. 4A**), or following cTdp-43 KO in mESCs (**Fig. 4B,C**). Fisher exact test and h-index (the motif coverage threshold for cluster formation) of multivalent RNA motifs were calculated as previously described (Rot et al., 2017).

(B-D) The positions of UGU/GUG motif enrichment plotted around enhanced and repressed pA sites, red and blue respectively, corresponding to samples as defined above.

**Figure S5. Methods and results related to Figures 4 and 5 - iCLIP, TDP-43 RNA maps, and regulation of *Neat1* pA site by TDP-43**

(A) Representative SDS-PAGE autoradiographs of <sup>32</sup>P-labelled RNAs from m/hESCs treated by UV-C for crosslinking of RNAs and RBPs, and purified using an anti-TDP-43 antibody. Treatment by high (<sup>+++</sup>) concentration of RNase I indicated the presence of RNAs bound to TDP-43 by location of the radioactive signal. An asterisk marks the position in the autoradiograph corresponding to the size of TDP-43 monomer.

(B,C) Z-scores of pentamer occurrences surrounding (-30 nt to +30 nt) all TDP-43 crosslinked sites in undifferentiated hESCs (B) and mESCs (C) as determined by iCLIP. The sequences of the two highest enriched pentamers are shown. The Pearson's correlation coefficient between the two replicates in hESCs was R=0.91 (B), and these pentamers were also most enriched in mESCs (C) by iCLIP performed using *iTDP-43-eGFP* mESCs and antibodies targeting the endogenous TDP-43 or GFP (fused to TDP-43).

(D) A pie chart depicting the regional distribution of TDP-43 binding sites in mRNAs identified by TDP-43 iCLIP in mESCs (samples as in Fig. 5D,E).

(E-G) "RNA maps" related to Figs. 4 and 5 showing the relationship between the positions of TDP-43 crosslinking (E) or GU-rich motifs of TDP-43 bound genes (F,G) to TDP-43 regulated pA sites. Positive and negative correlations are shown in red and blue respectively. (E, F) Plots that are based on 89 and 119 pA sites that were enriched or depleted respectively in undifferentiated hESCs compared to cells treated by TDP-43 shRNAs. The black lines represent 893 pA sites that did not show a significant change, and thereby were used as a control. Pairs exhibiting highest proximal-distal site fold changes are shown (adjusted p value <0.05). (G) Same analysis as in (F), comparing undifferentiated untreated cTdp-43 KO mESCs with cells following tamoxifen treatment. Plots are based on 316 and 127 pA sites that were enriched or depleted respectively, or 1616 pA sites that did not show a significant change, represented by black lines.

(H) Related to Fig. 5C: A Western blot of TDP-43 and Histone H3, samples: undifferentiated hESCs and following 3 d of differentiation towards mesoderm (CHIR99021) and trophoblast (BMP4) progenitors respectively.

(I) A heat map showing the relative abundance of a selected panel of genes during reprogramming of hiF-T cells, including of pluripotency *LIN28A*, *LIN28B*, *NANOG*, *ZFP42* (*REX1*), epithelial *CDH1* (E-Cadherin), and mesenchymal *CDH2* (N-Cadherin) markers compared to *NEAT1* and *TDP-43* (RNA-Seq dataset from (Cacchiarelli et al., 2015)).

(J) Related to Fig. 5F,G: qPCR analysis of *Neat1\_2* transcripts in *Neat1Δ100nt* and *Neat1* WT *iTDP-43-eGFP* mESCs, treated by doxycycline or untreated (n=4 and 6 independent replicates for *Neat1ΔTDP-43* and *Neat1* WT respectively, error bars = SD, two sided t-test; P value \*\* < 0.01). Analysis shows that *Neat1* isoform switch depends on TDP-43 binding to the

UG-rich conserved region in *Neat1\_1*.

(**K**) Quantification of gated positive cells according to IgG control (red line), samples of WT and *Neat1 $\Delta$ TDP-43* mESCs spontaneously differentiated (2 d) and immunostained for NANOG (error bars = SD, two sided t-test, biological replicates n=3; P value \*\* < 0.001).

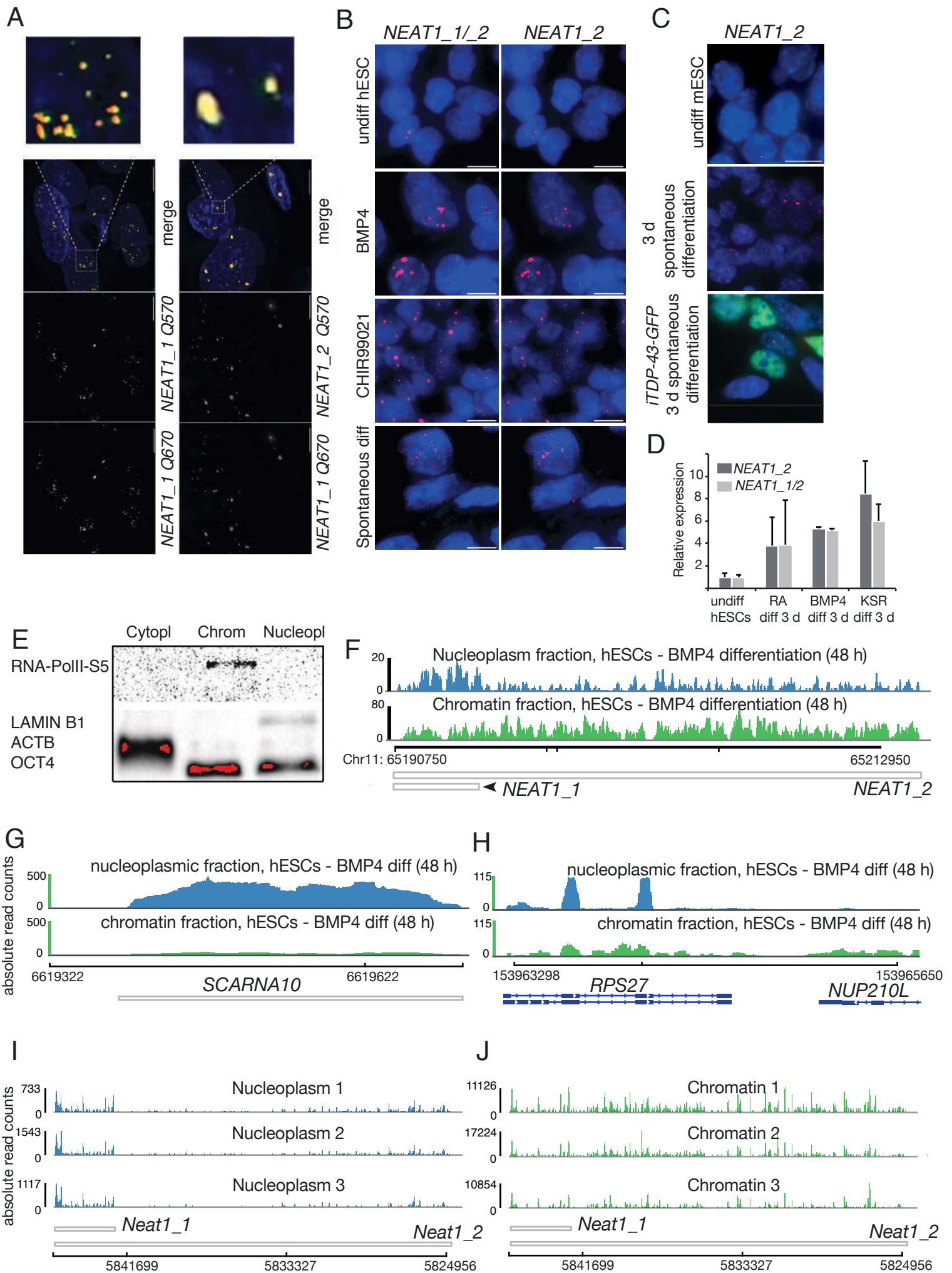
**Figure S6. Results related to Figure 6 - the developmental competence of *Neat1ΔTH* mESCs**

(A) The number of paraspeckles analyzed in 3d spontaneously differentiating WT parental and *Neat1ΔTH* mESC clones. Number of analyzed cells and statistical analysis as in **Fig 1B**.

(B-F) *In vivo* analysis of the developmental potency of mESCs by aggregation with 4n embryos, which together give rise to chimeric embryos (**Fig. 6D**). Embryos constitutively expressing membrane tdTomato were used to distinguish the extraembryonic tissues (visceral endoderm and extra-embryonic ectoderm) which were derived from 4n cells, and embryonic cells that were exclusively derived from mESCs. (B,C) Chimeras produced with *Neat1ΔTH* mESCs, and immunostained using BRACHYURY (B) and FOXA2 (C) antibodies, respectively (5 out of 7 embryos shown). Note the abnormal anatomical characteristics around the node and axial mesoderm during gastrulation in 4n mT ↔ *Neat1ΔTH* mESC chimeras. (D,E) Chimeras produced using *Neat1ΔpA* (D) and the WT parental mESCs (E), and immunostained as above (2 out of 7 embryos shown in D). \* displayed also in main figure **6E,F**. (Blue: DAPI – nuclear stain; Scale bars = 100 μm). A=anterior, P=posterior, p=proximal, d=distal.

(F) qPCR and RNA-seq analysis of pluripotency *SOX2*, *OCT4*, *LEFTY1*, *GDF3* early mesoderm *MESP1*, *T*, *MIXL1*, *EOMES*, *MSX2*, *MYOD*, endoderm *SOX17*, *FOXD3*, *CXCR4*, *NODAL*, *CDH2*, *CER1*, *GSC* markers in *NEAT1ΔpA* versus parental WT hESCs propagated in pluripotency conditions (Error bars: +SD; Mann-Whitney U-test, P value \*\*\* < .001, \*\* < .01, \* < 0.05; n = 2 per clone and 3 of WT hESCs).





**Fig. S1**

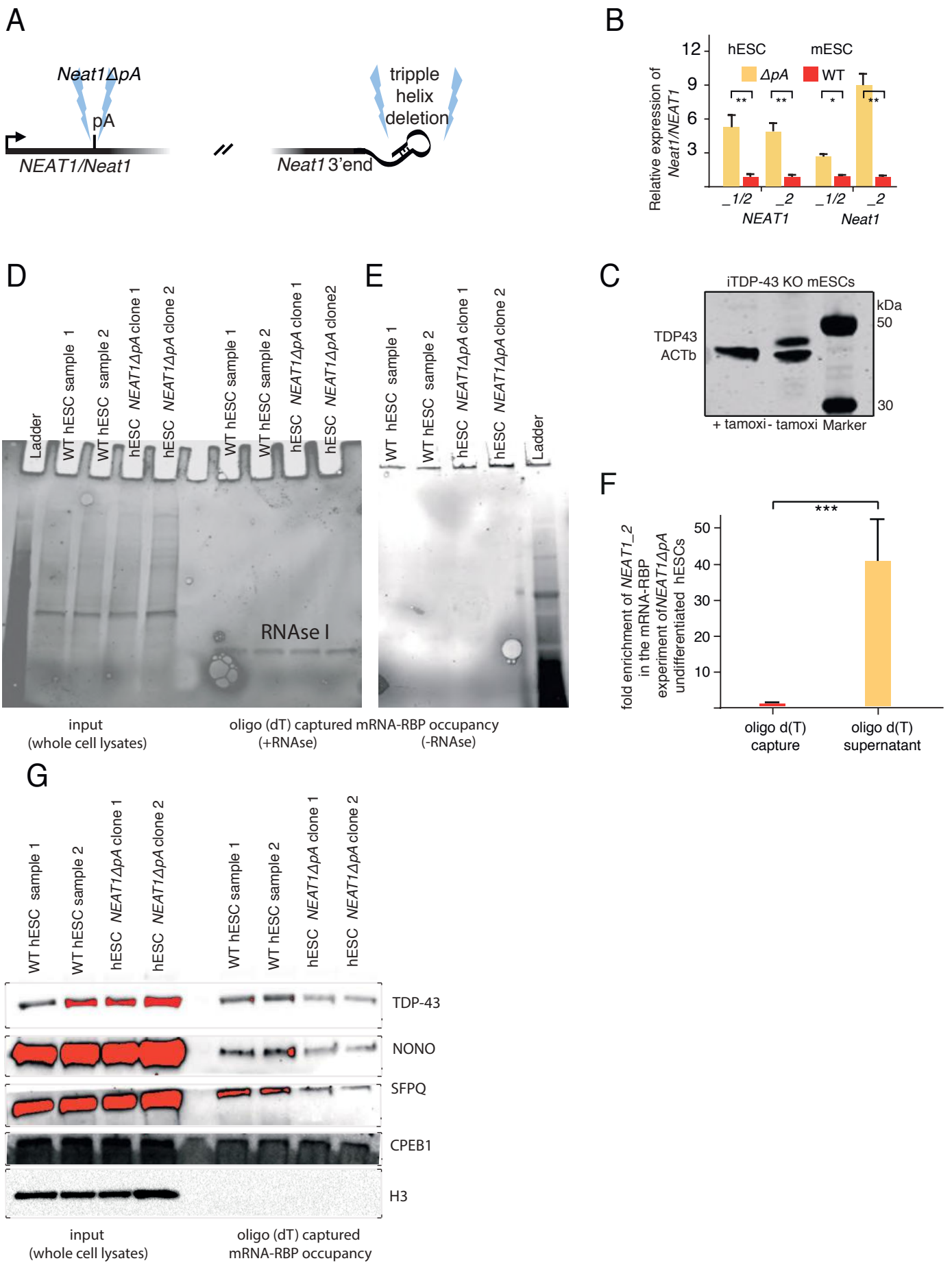
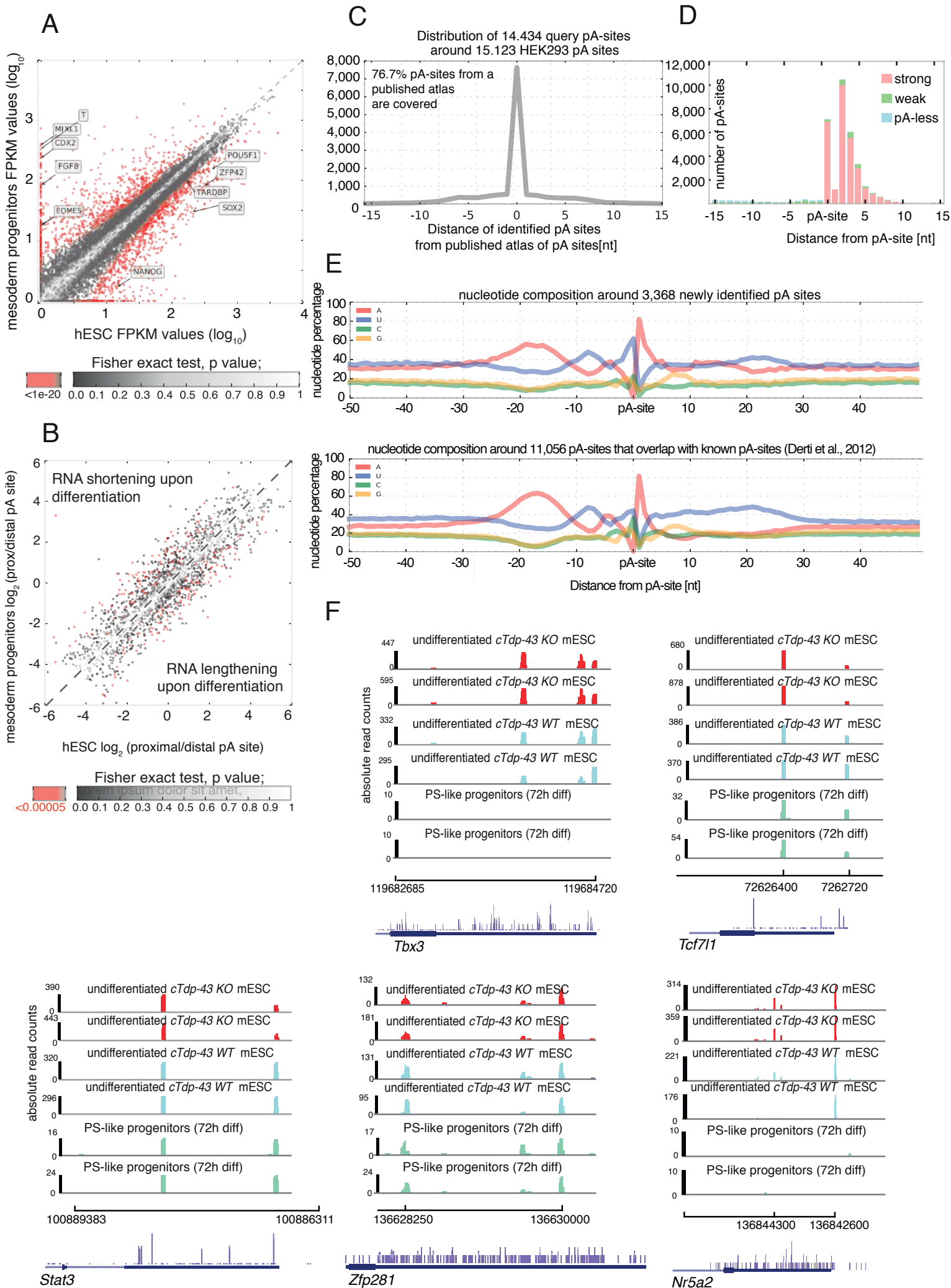


Fig. S2



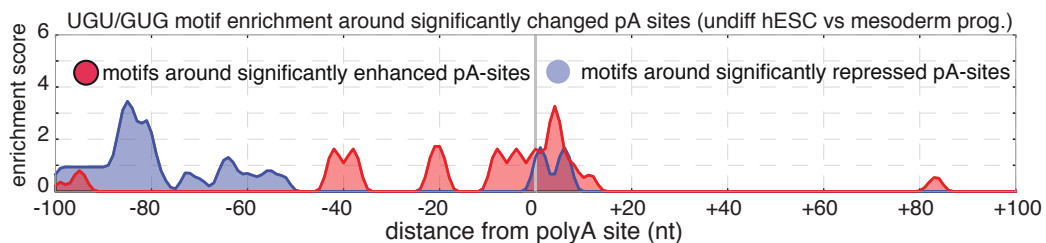
**Fig. S3**

**A**

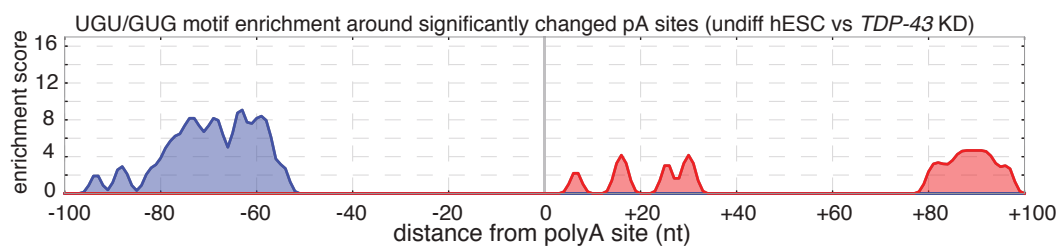
The most enriched multivalent motifs around the regulated APA events:

undiff hESC vs mesoderm progenitors			undiff hESC vs <i>TDP-43</i> KD			undiff mESC vs iTDP-43 KO		
Enriched sequence motif	Fisher		Enriched sequence motif	Fisher		Enriched sequence motif	Fisher	
	valency	fisher		valency	fisher		valency	fisher
GUG	9	0.042	UGU	16	0.0002	GUG	17	0.003
UCAG	5	0.042	AUAU	11	0.0007	GUGU	13	0.008
CUCA	5	0.076	CCCG	4	0.015	UGUG	15	0.010
UUUU	10	0.080	GUGU	9	0.019	UAAC	5	0.014

**B**



**C**



**D**

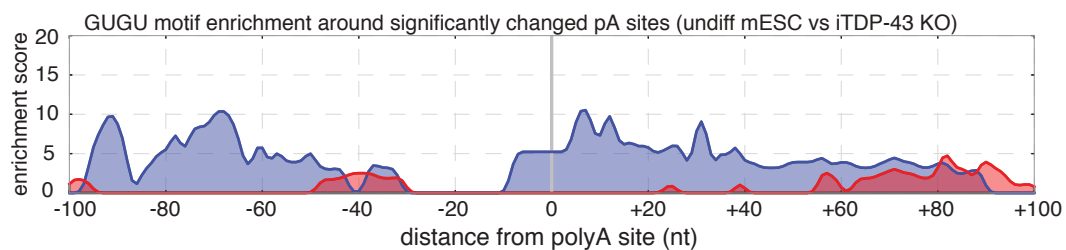


Fig. S4

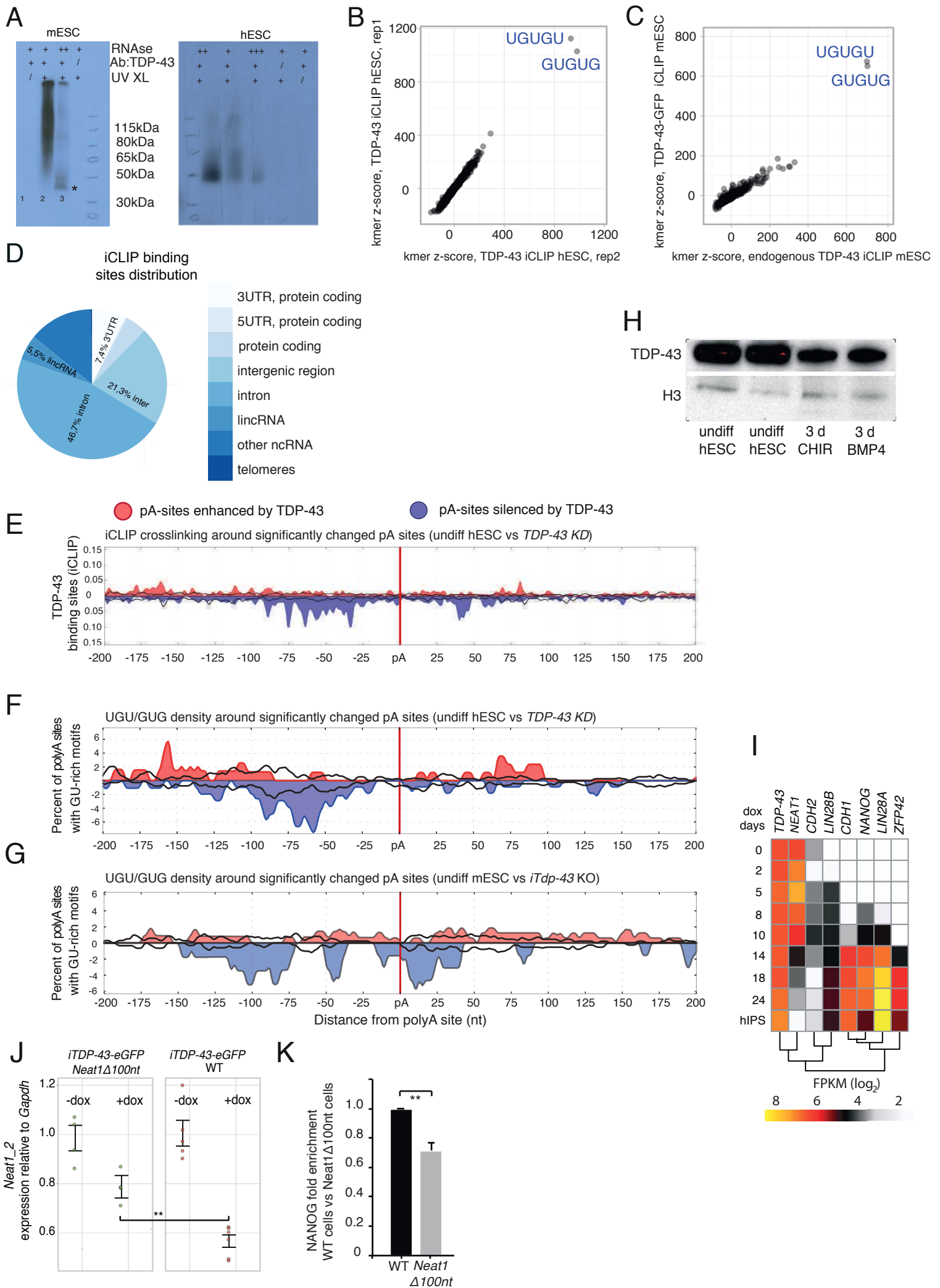


Fig. S5

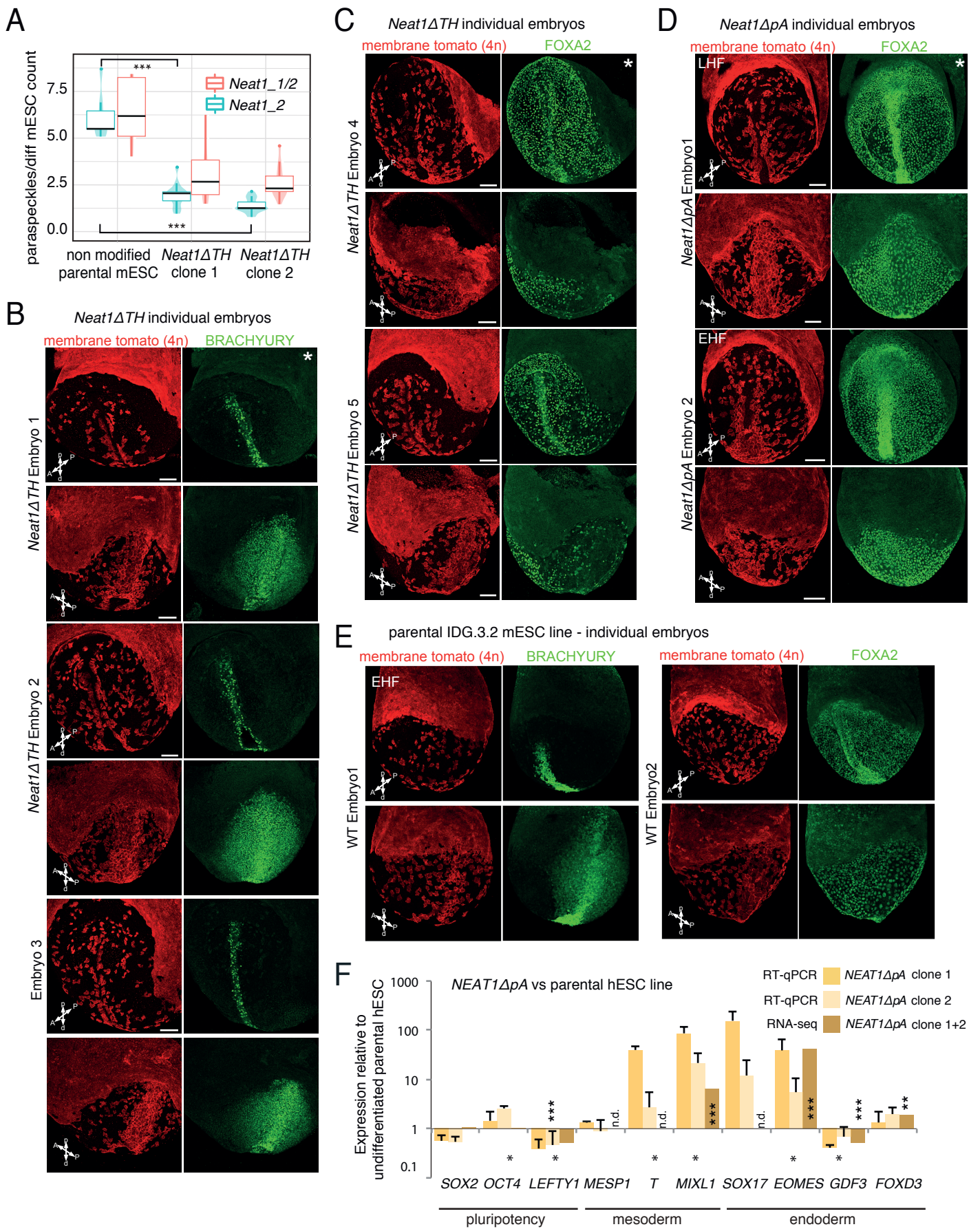


Fig. S6