## SUPPLEMENTARY FIGURES AND LEGENDS

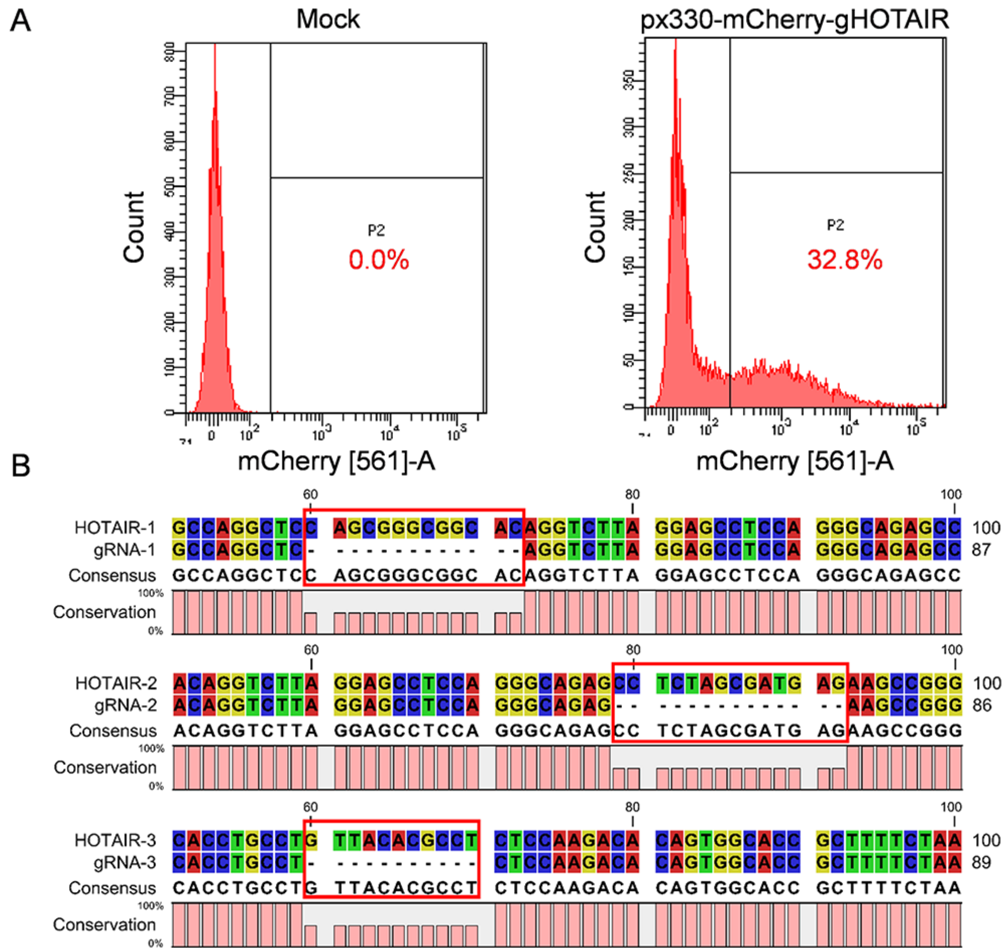


**Figure S1. CRISPRi-mediated knockdown of HOTAIR in HeLa cells.**

(A) Flow cytometry sorting showed 0.0% mCherry fluorescence intensity of the negative control (mock) and 32.8% mCherry fluorescence intensity of the px330-mCherry-gHOTAIR. (B) Sequence alignment shows the positions of the absence area of nucleotides in the three different transfected HeLa cell lines.

A

| | siHOTAIR-1 | siHOTAIR-2 | siHOTAIR-3 | siNC-1 | siNC-2 | siNC-3 |
|---|---|---|---|---|---|---|
| siHOTAIR-1 | 1.000 | 0.994 | 0.993 | | | |
| siHOTAIR-2 | 0.994 | 1.000 | 0.979 | | | |
| siHOTAIR-3 | 0.993 | 0.979 | 1.000 | | | |
| siNC-1 | | | | 1.000 | 0.912 | 0.996 |
| siNC-2 | | | | 0.912 | 1.000 | 0.911 |
| siNC-3 | | | | 0.996 | 0.911 | 1.000 |

B

| | siHOTAIR-1 (115) | siHOTAIR-2 (117) | siNC-1 (114) | siNC-2 (116) |
|---|---|---|---|---|
| siHOTAIR-1 (115) | 1.000 | 0.990 | | |
| siHOTAIR-2 (117) | 0.990 | 1.000 | | |
| siNC-1 (114) | | | 1.000 | 0.980 |
| siNC-2 (116) | | | 0.980 | 1.000 |

**Figure S2. Repeatability of the transcriptomic and quantitative proteomic data.**

(A) Correlation analysis of the RPKM of different biological replicates of transcriptomic data.

(B) Correlation analysis of the ion intensities of two biological replicates. Correlation analysis show good repeatability of both transcriptomic and proteomic data.

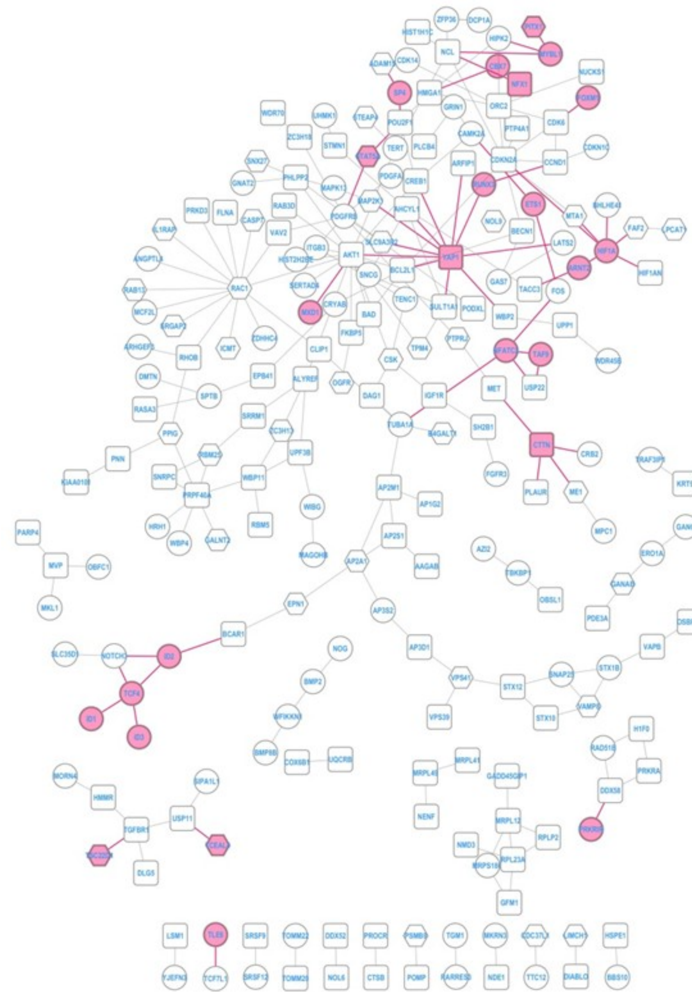

**Figure S3 The Protein-protein interaction network of the DEPs and DEGs.** The PPI network was constructed by searching against the STRING v10.0 and visualized by Cytoscape 3.4.0, organism was set to "human", and interaction source was set to "experiments". 137 DEPs and 115 DEGs are involved in the PPI network. Round nodes denote DEGs that don't have protein expression information. Round rectangle nodes denote DEPs which are unchanged in transcription levels or haven't been detected in transcriptomic data. Hexagon nodes denote genes which were dysregulated at both mRNA and protein levels. Red nodes denote transcriptional factors.

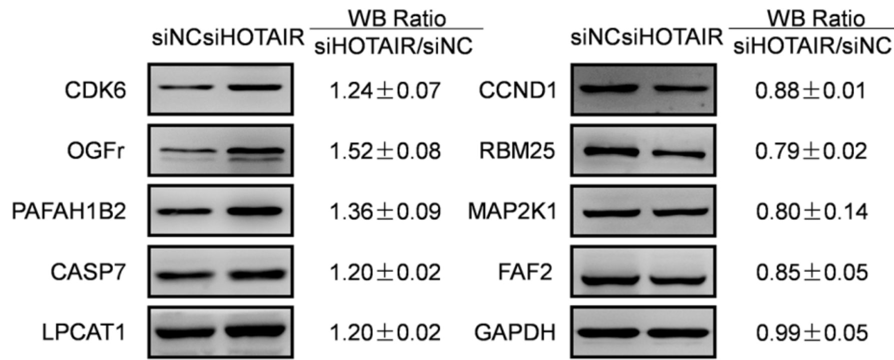


**Figure S4. Validation of the DEPs in Huh-7 cells.** Western blot analysis of the expression levels of ten DEPs in another HCC cell line, Huh-7. Fold changes of protein levels were determined using Image J software and GAPDH was used as an internal control.

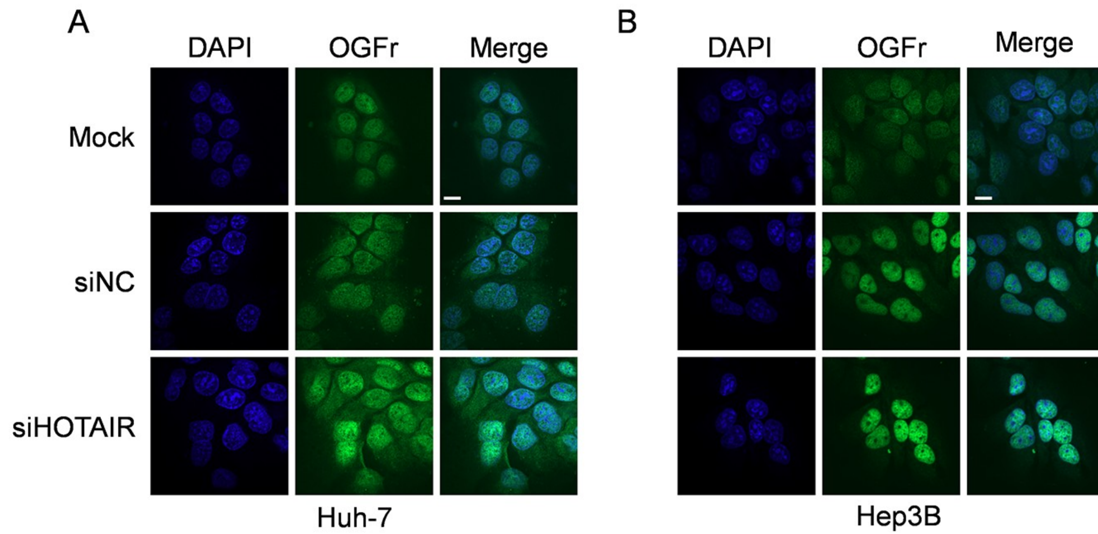


**Figure S5. Inhibition of HOTAIR affects the expression level of OGFr in Huh-7 and Hep3B cells.** (A) Representative confocal microscopy images showing the location of OGFr in Huh-7 cells and the expression level of OGFr in Huh-7 cells was up-regulated after HOTAIR knockdown. (B) Representative confocal microscopy images showing the location of OGFR in Hep3B cells and the expression level of OGFr in Hep3B cells was up-regulated after HOTAIR knockdown. The nucleus was stained with DAPI. The images were acquired by fluorescence microscopy under a 60 × objective lens (scale bar, 11 μm).

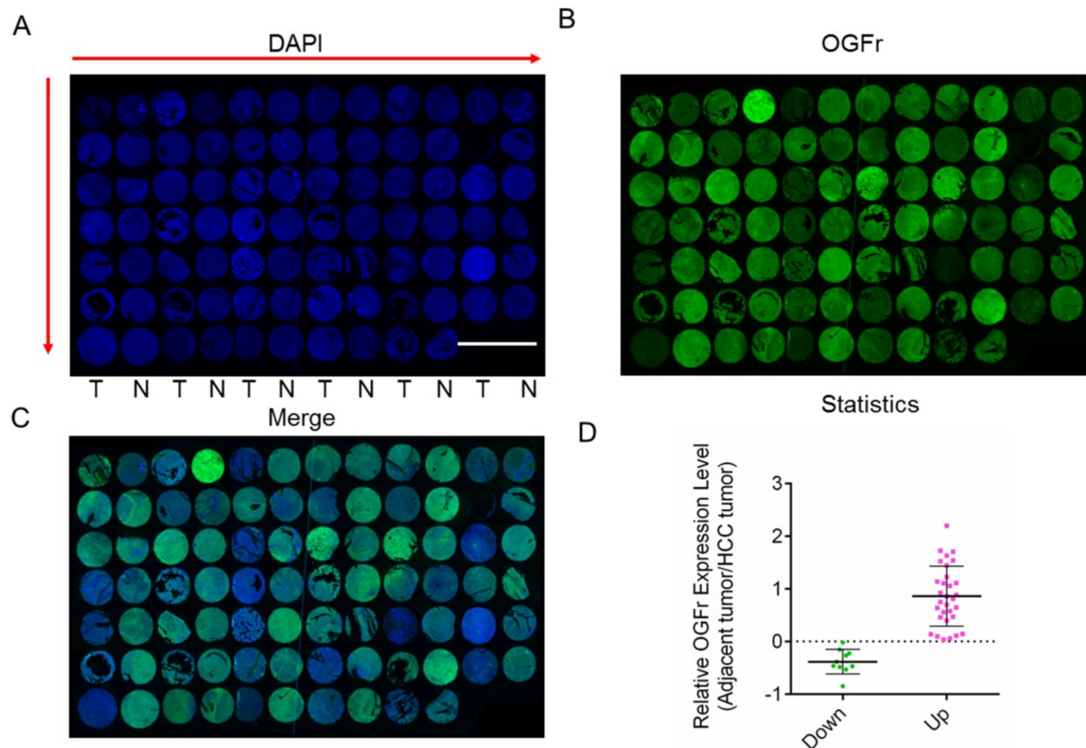


**Figure S6. HCC tissue microarray analysis** (A) HCC tissue microarray were mounted in ProLong Gold antifade reagent with 4’6-diamidino-2- phenylindole (DAPI) for nucleic labeling. (B) Digital microscopy scanner images showing the expression level of OGFr in HCC tissue microarray. (C) Merged picture of the DAPI fluorescence and FITC fluorescence. (D) Statistics showing that the relative OGFr expression level in 41 matched pairs of HCC samples and their corresponding adjacent liver tissues. Results showed in 31 out of the 41 pairs of samples, the OGFr expression in HCC tissue was significantly lower than that in the corresponding adjacent liver tissues. The fold changes of protein expression levels were determined using Image J software. The images were acquired by Pannoramic MIDI with a 20 × microscope objective (scale bar, 5000 μm).

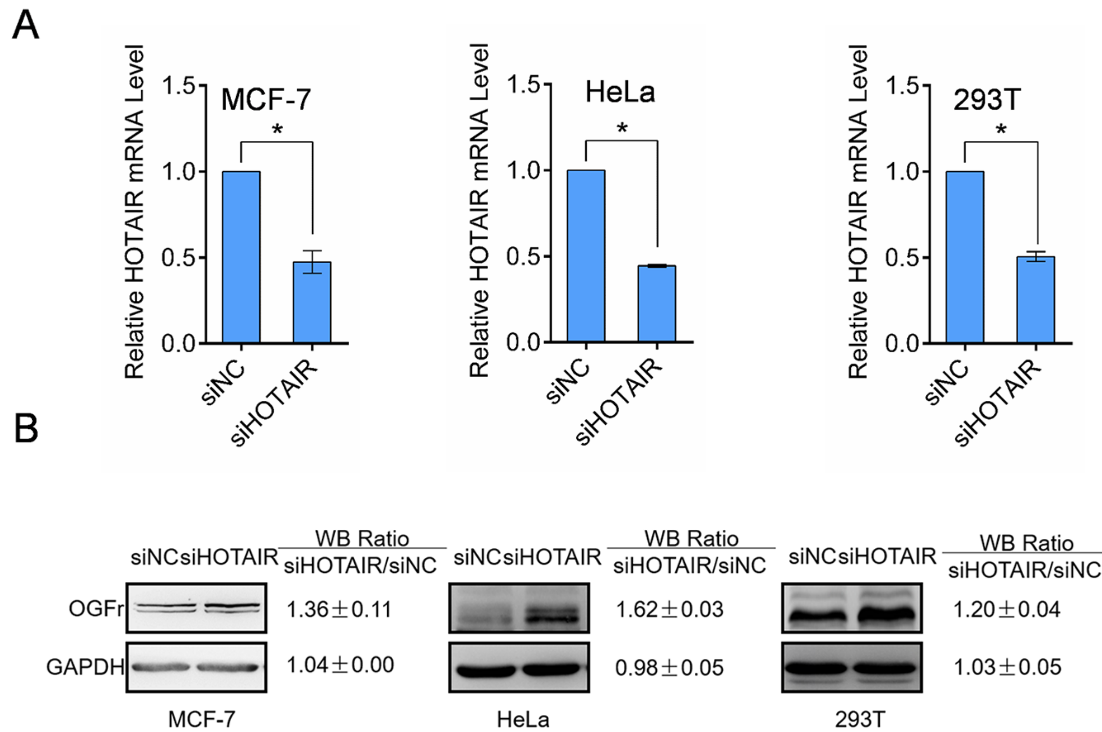


**Figure S7. Expression of OGFr in different cancer cell lines after HOTAIR inhibition.** (A) The knockdown efficiency of HOTAIR in different cell lines when transfected with siHOTAIR for 48 hr. HOTAIR expression was determined by qPCR. The HOTAIR expression level was normalized to GAPDH. Data are presented as means ± S.D. and represent results from three independent experiments. (B) Western blotting analysis of OGFr expression in different transfected cell lines after transfected with siHOTAIR or siNC for 48 hr. GAPDH was used as an internal control and fold changes of protein levels were determined using Image J software. Statistically significant differences are indicated: *$P < 0.05$.