

HNF4 α is a target of the Wnt/ β -catenin pathway and regulates colorectal carcinogenesis

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Abstract

Hepatocyte nuclear factor 4 α (HNF4 α) is a transcription factor involved in liver function. Dysregulation of HNF4 α leads to hepatocarcinogenesis. However, the role and mechanism of HNF4 α in colorectal cancer is still unknown. Here we demonstrate that HNF4 α is upregulated in colorectal cancers. and HNF4 α upregulation promotes colorectal tumorigenesis. Notably, expression levels of HNF4 α are positively correlated with the Wnt/ β -catenin signaling pathway in colorectal cancer patients. Further, we showed that HNF4 α is transcriptionally activated by Wnt/ β -catenin/TCF3 and is at least partially responsible for the oncogenesis activity of the Wnt signaling in colorectal cancer. Our findings indicate that HNF4 α is a direct target of that Wnt/ β -catenin pathway and could play an important role in colorectal carcinogenesis.

Author Summary

Here we demonstrate that HNF4 α is upregulated in colorectal cancers and HNF4 α upregulation promotes colorectal tumorigenesis. Notably, expression level of HNF4 α are positively correlated with the Wnt/ β -catenin pathway in colorectal cancer patients. Further, we showed that HNF4 α is transcriptionally activated by Wnt/ β -catenin/TCF3 and is at least partially responsible for the oncogenesis activity of the Wnt signaling pathway in colorectal cancer.

Key words : Colorectal cancer; HNF4 α ; Wnt/ β -catenin; TCF3

Introduction:

Colorectal cancer (CRC) is graded as one of the most common cancers and accounts for the second leading cause of cancer deaths worldwide. Despite an overall decreasing incidence of the disease, early-onset colorectal cancer is a growing concern and rapidly rising in those under the age of 50 over the last two decades[1-3]. While a number of major targets have been identified during the course of CRC development such as Ras[4], Tp53[5], and APC/ β -catenin[6], the pathogenesis of CRC still remains elusive. Identification of new molecules that are involved in CRC could lead to early detection, prevention and therapeutic intervention.

Hepatocyte Nuclear Factor 4 Alpha (HNF4 α), a master transcription factor, is predominantly expressed in the liver, kidney, intestine and endocrine pancreas, and is necessary for liver development and function[7, 8]. However, accumulating evidence shows its inhibitory role in the liver cancer. The HNF4 α mutations at G79C, F83C and M125I (Zn-finger DNA-binding domain region) were detected in liver cancer and were believed to trigger liver tumorigenesis[9]. Previous studies revealed the contradictory role of HNF4 α in colorectal carcinogenesis[10]. The regulation of HNF4 α in CRC is largely unknown. Further investigation of the role and the specific regulation mechanism of HNF4 α in the development and progression of CRC is of great significance for establishing HNF4 α as a diagnostic/prognostic marker and therapeutic target in CRC.

The Wnt/ β -catenin signaling pathway is a recognized driver of colorectal carcinogenesis and the defect of this cascade occurs in 70–80% of CRC [11, 12]. Activation of the Wnt pathway induces β -catenin translocation into the nucleus where it functions as a transcriptional coactivator of TCF /LEF family factors[13]. While several molecules that regulate this cascade have been identified including APC, GSK3 β and AXIN, the role and regulation of Wnt/ β -catenin activation in CRC is still not completely understood.

Here, we demonstrated that HNF4 α was upregulated in CRC and promoted

colorectal tumorigenesis. HNF4 α levels were positively correlated with and directly regulated by the Wnt/ β -catenin-TCF3 signaling pathway. We further showed that HNF4 α is a positive regulator of the Wnt/ β -catenin and that HNF4 α overexpression promotes β -catenin nuclear localization. Our results suggested that HNF4 α is a potential prognostic marker for the Wnt/ β -catenin-related CRC and that HNF4 α forms a feedback loop with Wnt/ β -catenin to control colorectal tumorigenesis.

Results

1. HNF4 α promotes colorectal carcinogenesis

Recently, we found that the loss of *nhr-14* gene in *C. elegans* resulted in the dysregulation of DNA damage-induced response [14], which usually leads to cancer development [15-18]. Thus, we examined HNF4 α expression levels in different cancers and matched paired normal tissues. TCGA database analysis revealed upregulation of HNF4 α in Colon adenocarcinoma (COAD), Rectum adenocarcinoma (READ) and Pancreatic adenocarcinoma (PAAD), suggesting that HNF4 α may play an important role in gastrointestinal tumorigenesis, especially in colorectal carcinogenesis (Figure 1A). We further analyzed the HNF4 α protein levels in 59 paired colon cancer and normal tissues and found significant increase of HNF4 α in 43 tumors (Figure 1B and 1C). Immunohistochemical staining of CRC microarray also revealed remarkable upregulation of HNF4 α in cancer tissues (n=244) when compared to normal colon tissues (n=99) (Figure 1D). These results indicate that overexpression of HNF4 α is a recurrent event in CRC and could play a significant role in this malignancy.

Previous studies have shown that HNF4 α could behave as either a tumor suppressor or an oncogene largely depending on the tumor type and organ [10, 18, 19]. Thus, we next investigated the function of HNF4 α in CRC by stable transfection of HNF4 α into SW480 and SW620 colon cancer cell lines. We found that ectopic expression of HNF4 α significantly increased colony formation (Figure 1E). Xenograft mouse experiments also showed that overexpression of HNF4 α considerably promoted the tumor growth and increased the tumor volume and weight (Figure F-H). These findings suggest that

HNF4 α acts as an oncogene and could be a driver in CRC.

2. HNF4 α is positively correlated with and is regulated by the Wnt/ β -catenin signaling pathway

To examine the mechanism by which HNF4 α is upregulated in CRC, we downloaded the COAD and READ data from TCGA database and performed GESA analysis. Among the enriched HNF4 α -correlated signaling pathway, oncogenic Wnt/ β -catenin and MYC pathways were significantly and positively associated with HNF4 α expression (Figure 2A). It has been reported that the WNT/ β -catenin transcriptionally induces c-Myc expression to promote colorectal tumorigenesis [20]. Thus, we primarily focused on the relationship between HNF4 α and the Wnt/ β -catenin pathway. We also analyzed the correlation between β -catenin and HNF4 α , and the result indicated that β -catenin positively associated with HNF4 α expression levels in TCGA database (Figure 2B). Then we transfected SW480 cells with shRNA-HNF4 α and control shRNA and found no expression change of CTNB1 at mRNA or protein levels between HNF4 α -knockdown and control cells (data not shown). Conversely, SW480 cells after transfection with shRNA-CTNB1 expressed significant low levels of HNF4 α mRNA when compared to the cells treated with control shRNA (Figure 2C). Moreover, we transfected shRNA-CTNB1 into other 2 (SW620 and DLD1) colon cancer cell lines. Western blot analysis showed that knockdown of β -catenin significantly reduced the protein level of HNF4 α in SW480, SW620 and DLD1 cell lines (Figure 2D). These results suggest that HNF4 α is regulated by the WNT / β -catenin pathway at the transcription level.

To further support this conclusion, we treated colon cancer cells with SKL2001, an activator of the Wnt/ β -catenin pathway by disrupting Axin/ β -catenin interaction, at different doses for 12h. Western blot analysis of cellular fractionation revealed significant nuclear accumulation of β -catenin and increased expression of HNF4 α following SKL2001 treatment (Figure 2E-F). In addition, we treated SW480 and SW620 cells with Chir-99021, another β -catenin activator by selectively inhibiting

GSK-3 α/β , and found upregulation of HNF4 α in both cell lines after Chir-99021 treatment (Figure 2F). These results further confirmed that β -catenin is an activator of HNF4 α .

3. Ectopic expression of HNF4 α rescues β -catenin knockdown in tumor growth

As HNF4 α is a downstream target of the Wnt/ β -catenin pathway, we next investigated whether HNF4 α mediates the role of the Wnt/ β -catenin axis in colon carcinogenesis. SW620 cells were stably transfected with β -catenin shRNA or β -catenin shRNA and HNF4 α overexpression, respectively. The cells treated with vector alone were used as control (Figure 3A). These cells were subcutaneously injected to nude mice. As expected, knockdown of β -catenin inhibited tumor growth and reduced tumor volume and weight (Figure 3B-E). Notably, ectopic expression of HNF4 α largely overrode these phenotypes caused by β -catenin knockdown (Figure 3B-E). These findings further indicate that HNF4 α is a major target of β -catenin in colon cancer.

4. TCF3 (TCF7L1) promotes HNF4 α expression

β -catenin is a transcription co-activator of TCF/LEF transcription factor (TF) family. To further understand the molecular mechanisms by which wnt/ β -catenin induces HNF4 α transcription, we first analyzed the expression relationship between HNF4 α and TCF7(TCF-1), LEF1, TCF7L1(TCF-3), TCF7L2(TCF-4), which are TCF/LEF family members, in CRC through the TCGA database. We found that HNF4 α had the highest correlation with TCF1 and TCF3, but not LEF1 and TCF4 (Figure 4A-4D). Meanwhile, we individually knocked down these transcription factors in SW480 (Figure 4E-F). Western blot analysis showed that HNF4 α was reduced in TCF3 knockdown cells but not in shRNA-TCF1, shRNA-TCF4 or shRNA-LEF1 treated cells (Figure 4E). We further confirmed the result in two different CRC cell lines, LS174T and DLD1. Similarly, TCF3 knockdown decreased HNF4 α expression (Figure 4G). Moreover, ectopic expression of TCF3 induced HNF4 α level, but ectopic expression of TCF3 in β -catenin shRNA cells can't rescue HNF4 α level (Figure 4H-I). These results suggest that TCF3 is a major transcriptional factor that mediates the action of Wnt/ β -catenin in

induction of HNF4 α in CRC.

5. TCF3 directly binds to the -90--80bp region of the HNF4 α promoter

To investigate whether TCF3 can directly bind to the HNF4 α promoter to regulate HNF4 α transcription, we first examined the TCF3 consensus binding motif “CACCTGC” in the HNF4 α promoter region through the website (<https://jaspar.genereg.net/>). As shown in Figure 5A, there are 10 TCF3 putative binding sites within a 2.0-kb HNF4 α promoter. To determine which binding site(s) is required for TCF3-mediated HNF4 α transcription, we constructed deletion mutants of the HNF4 α promoter including pGL3-P_{HNF4 α} 1700bp, pGL3-P_{HNF4 α} 800bp and pGL3-P_{HNF4 α} 300bp, which contain 10, 7 and 3 TCF3 putative binding sites, respectively (Figure 5A). Luciferase reporter assays revealed that knockdown of TCF3 significantly reduced the basal promoter activity in three HNF4 α deletion promoter mutants (Figure 5B), suggesting that pGL3-P_{HNF4 α} 300bp contains major TCF3 response motifs (Figure 5A). Since there are 3 TCF3 putative binding sites in pGL3-P_{HNF4 α} 300bp, we next mutated each site in this promoter region (Figure 5C). Interestingly, mutations of the 90 to 80-bp motif, which is the closest to transcription start site of HNF4 α gene, completely abrogated the pGL3-P_{HNF4 α} 300bp promoter activity, whereas mutation of the rest two sites had no significant effect on the promoter activity (Figure 5D). These findings suggest that TCF3 transcriptionally activates HNF4 α primarily through binding to the first motif of the HNF4 α promoter.

6. Overexpression of HNF4 α activates WNT and promotes β -catenin nuclear localization

We next performed RNA sequencing analysis between SW480-vector and SW480-HNF4 α cells in an attempt to investigate the mechanism of HNF4 α in colorectal tumorigenesis. The signals enriched by HNF4 α overexpression were involved in cardiac system diseases, neurological diseases, tumor progression and other features, among which the most tumor-related signaling pathways were the MAPK, Hippo and Wnt signaling cascades (Figure 6A). Notably, Wnt1, Wnt4, Wnt7b and Wnt11 were up-regulated in SW480-HNF4 α cells when compared to SW480-vector control cells (Figure 6B), which were further confirmed by qPCR assay (Figure 6C). However, we

did not observe expression level changes of β -catenin in the cells ectopically expressing HNF4 α (Figure 6D). As HNF4 α induces expression levels of several Wnt family members, we hypothesized that HNF4 α could promote β -catenin translocation from the cytoplasm to the nucleus. Cell fractionations were obtained from SW480-vector and SW480-HNF4 α cells. Immunoblotting analysis revealed that the nuclear fraction of β -catenin was significantly enriched in the HNF4 α overexpressing cells (Figure 6E). Collectively, our findings indicate that HNF4 α and Wnt/ β -catenin regulated each other and form a feedback regulation loop to contribute to colorectal carcinogenesis.

7. The β -catenin/TCF3-HNF4 α axis correlates with colorectal tumorigenesis

To evaluate the clinical significance of β -catenin/TCF3-HNF4 α in colorectal cancer, we performed IHC analysis and examined the HNF4 α and β -catenin/TCF3 expression level in a colon cancer tissue array and investigated the correlation of β -catenin/TCF3 with HNF4 α in colorectal cancer. The results showed that the tumor tissue with high levels of β -catenin/TCF3 usually express high levels of HNF4 α , and the tumor tissue with low levels of β -catenin/TCF3 usually have low levels of HNF4 α (Figure 7A). The correlation analysis indicated that HNF4 α was significantly correlated with β -catenin and TCF3 (Figure 7B and 7C). Taken together, these results indicated that HNF4 was correlated with the WNT/ β -catenin pathway and involved in colorectal tumorigenesis.

To further test our hypothesis, we employed AOM/DSS Model of Colitis-Associated colorectal Cancer model[21], and AOM/DSS treatment can not only induce intestinal inflammation and colorectal cancer, but also induce highly express β -Catenin and HNF4 in the intestinal tissues of treated mice (Figure 7D). The result implied that the β -catenin/TCF3-HNF4 α axis plays an important role in colorectal cancer (Figure 7E).

In conclusion, our results show that HNF4 α acts as a WNT/ β -catenin downstream factor and affected by direct regulation of β -catenin/TCF3 to regulate the occurrence of colorectal cancer. Overexpression of HNF4 α can activate the expression of wnt family members and promote β -catenin nuclear localization and promotes wnt/ β -catenin signal pathway. The Wnt/ β -catenin-TCF3-HNF4 α feedback loop promotes

colorectal tumorigenesis. This study can provide strategies for the treatment and prevention of colorectal cancer.

Discussion

CRC is a highly heterogeneous disease, the roles of HNF4 α in colorectal tumorigenesis have been reported are contradictory, Single-cell chromatin accessibility analysis reveals that HNF4 α is key iCMS-specific transcription factors in colorectal malignant tumor cells, suggesting that HNF4 α may play important roles in colorectal tumorigenesis and progression[22]. However, the role and regulatory mechanism of HNF4 α in colorectal cancer are still largely unknown.

Wnt/ β -catenin activation is a recognized driver of colorectal carcinogenesis, however, the regulation of wnt/ β -catenin in colorectal cancer is still largely unknown. HNF4 α is necessary for liver development and function and is a negative regulator for liver cancer. Previous research reports have shown that HNF4 α expression was negatively regulated by Wnt- β -catenin signaling in hepatocellular carcinoma[23]. The regulatory relationship between Wnt/ β -catenin and HNF4 α in colorectal cancer is rarely reported.

Here we showed that HNF4 α promotes the development of colon cancer. HNF4 α is a Wnt/ β -catenin effector and is directly regulated by Wnt/ β -catenin signaling. HNF4 α overexpression further affects Wnt/ β -catenin signaling pathway activation and promotes the colorectal cancer. There are four transcription factors (TCF1, LEF1, TCF3 and TCF4) in the wnt/ β -catenin signaling pathway and they exhibit significant differences in regulating target genes[24]. Compared to the other three transcription factors, TCF-3 was the least reported in tumors. The mutual regulatory relationship between TCF3 and HNF4 α has not been reported. Our study indicates that β -catenin activates TCF3, which directly binds to the HNF4 α promoter region and regulates HNF4 α expression and colorectal tumorigenesis.

In conclusion, our study demonstrated that the Wnt/ β -catenin-TCF3-HNF4 α feedback loop confers colorectal tumorigenesis. Our result also suggested that HNF4 α is a new target of Wnt/ β -catenin-TCF3(TCF7L1) and HNF4 α overexpression feedback

regulates WNT expression and promotes β -catenin nuclear localization. Further investigation of the role and the specific mechanism of HNF4 α in the development and progression of CRC is of great significance for establishing HNF4 α as a therapeutic target in CRC. Our study will provide strategies for the treatment and prevention of colorectal cancer.

Materials and Methods:

Cell culture and activator treatment

Colon cancer cell line SW480, SW620 and DLD-1 were cultured in RPMI1640 medium supplemented with 10% fetal bovine serum (FBS) and 1% penicillin/streptomycin. For the inhibitor and activator treatment, cells (5×10^5) were seeded in 6 well plates and treated with 2 μ M or 5 μ M SKL2001 and CHIR99021 for 12 h, 24 h, and 36 h after the cells attached to the dish.

RNA interference

RNA interference was performed using the plko.1 vector. To efficiently knockdown β -catenin and TCF family, the shRNAs targeting to different genes were synthesized and inserted to plko.1 vector between Age I and EcoR I. The target sequences were as follows:

TTGTTATCAGAGGACTAAATA (β -catenin shRNA) ;

GCACCTACCTGCAGATGAAAT (TCF3 shRNA);

CAACTCTCTCTCTACGAACAT (TCF1 shRNA);

CCATCAGATGTCAACTCCAAA (LEF1 shRNA);

CCTTTCACCTCCCTCCGATTAC (TCF4 shRNA);

Western blotting

Cells were lysed in RIPA buffer (20 mM Tris-HCl pH 7.5, 100 mM NaCl, 0.1% SDS, 0.5% sodium deoxycholate, and 1 mM PMSF) containing Complete Protease Inhibitor Cocktail (Roche). Cell lysates were spun down at 12,000 rpm for 10 min, and 50 μ g supernatants were resolved on SDS-PAGE and blotted with the indicated antibodies. The amount of GAPDH was used as the loading control. The results were detected by an ECL-plus Western blotting detection system (Tanon-5200Multi). The primary

antibodies used in this study were as follows:

HNF4 α , Rabbit #3113 CST WB: 1:1000

TCF3, Rabbit #PA5-40327 Thermo Fisher Tech. WB: 1:1000

TCF1, MOUSE #sc-271453 Santa cruz bio. WB: 1:1000

β -catenin, Rabbit # A117811 GeneScript WB: 1:1000

Actin, Rabbit #4970 CST WB: 1:1000

GAPDH, mouse#sc-166574 Santa cruz bio. WB: 1:1000

Quantitative reverse transcription–polymerase chain reaction (qPCR)

Total RNA was extracted using Trizol (Invitrogen) and chloroform. 2 μ g of RNA was used as template to generate cDNAs using the ImProm-II Reverse Transcription system (Promega, Madison, Wisconsin, USA). qPCR reactions were carried out on an MX3000P system (Agilent Technologies, Santa Clara, CA).

Mouse Xenograft

All the mice were obtained from the Animal Research and Resource Center, Yunnan University. {Certification NO. SCXK(Dian)K2021-0001}. All animal experiments were performed according to protocols approved by the Animal Care Committee of the Yunnan University (Kunming, China).

For the Subcutaneous tumor models, 1×10^6 SW620 cells were re-suspended in 100 μ l 0.25 mg/ml Matrigel (Corning) with PBS buffer, then injected into the flanks of the nude mouse. The tumor volumes were measured from day 3 to 11 after injection. At 11 days after the injection, tumors were dissected. Tumors were then imaged and weighted.

GESA analysis and correlation analysis

The mRNA sequencing data of COAD READ BRCA LIHC LUAD LUSC PAAD SKCM were download from TCGA database (<https://portal.gdc.cancer.gov/repository>) respectively, and the merge normal tissues UCSC Xena (<https://xenabrowser.net>) mRNA Sequencing data was downloaded as control. the Pearson correlation coefficient R value and the correlation curve were calculated and draw by Using the ggplot2 function in R 4.2.0 software. the boxplot was drawn using the simplevis package after processing the TPM as log2 (TPM+1). The genes that significantly ($p < 0.01$, $r \geq 0.3$ or r

≤ -0.3) related to HNF4 α were screened by FPKM value of COAD READ and used for GSEA and KEGG enrichment analysis[25].

Luciferase Assay

the Dual Luciferase Assay were performed according to a previously reported protocol with minor modification [2013 Jianwei sun JBC]. The HNF4 α promoter luciferase reporter constructs were generated by inserting 1.7K, 800bp or 300bp human HNF4 α promoter into pGL3 basic vector (Promega) between XhoI and HindIII. To perform dual luciferase reporter assay, 2,0000 SW480 cells were seeded in 12-well plates and cultured overnight. Cells were transfected with 1 g/well HNF4 α promoter reporter together with 100 ng/well Renilla luciferase construct (pRL-TK) using Lipofectamine 2000. 24h after transfection, the cells were lysed and Cell lysates were subjected to dual reporter luciferase assays according to the manufacturer's instructions (Promega).

Tissue microarray and immunohistochemistry

Tissue microarrays (TMAs) were constructed using a manual tissue microarray instrument (Beecher Instruments) equipped with a 2.0 mm punch needle, as we previously described. An immunohistochemical (IHC) study of rabbit anti-human β -catenin, rabbit anti-human TCF3/TCF7L1 antibody, rabbit anti-human HNF4 α antibody was carried out on formalin-fixed paraffin, with a 4- μ m-thick serial section of tissue, according to the manufacturer's recommended protocol. The levels of β -catenin, TCF3/TCF7L1 and HNF4 α were assessed via the average of 5 count fields per patient in the original magnification of X200 on light microscopy. The positive cells for HNF4 α were defined as those with brown staining. The expression of β -catenin, TCF3/TCF7L1 and HNF4 α was scored based on staining intensity. Staining intensity was subclassified as follows: 0, negative; 1, weak; 2, moderate; and 3, strong.

The primary antibodies used in this study were as follows:

HNF4 α , Rabbit #3113 CST IHC: 1:200

TCF3, Rabbit #PA5-40327 Thermo Fisher Tech. IHC: 5 μ g/mL

β -catenin, Rabbit # ZA-0646 Zhongshan Golden Bridge Biotech. IHC: ready to use

Statistics analysis

Data were analyzed with Prism (GraphPad software). Statistical analyses were performed using *t*-tests or ANOVA. * $P < 0.05$ was considered statistically significant. ** $P < 0.01$ was considered significant. *** $P < 0.001$ was considered extremely significant. $P > 0.05$ was considered not significant (ns)

Conflict of Interest

The authors declare that they have no conflicts of interest with the contents of this article.

Acknowledgments

We thank Dr. Jing Li for their helpful suggestion and comments on the manuscript. This work was supported by the National Natural Science Foundation of China (NSFC) fund (82273460 and 32260167), the Yunnan Applied Basic Research Projects (202101AV070002 and 202301AS070117), and grants (Grant No. 2023Y0222, KC-23234451, KC-23233927 and 202310673059) from Yunnan University.

Authors' Contributions

LS, WB, CL and RD: Experiments and data analysis. QH, YZ, XY, and RS: Vector construction and dual-luciferase assay. XL, MM and JY: Cell culture and Western blot. JS, YS and JS: Experiments design, data analysis, manuscript writing. All authors read and approved the final manuscript.

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Figure 1 HNF4 α is frequently upregulated in CRC and plays an oncogenic role during colorectal tumorigenesis.

- A. TCGA database analysis of HNF4 α expression in different tumor types.
 - B. Western blot analysis of HNF4 α protein level in CRC tumor (T) and corresponding adjacent normal (N) tissues.
 - C. Schematic diagram of HNF4 α expression in 59 pairs of CRC tumor and normal tissues.
 - D. Immunohistochemical staining of CRC tissue microarray (TMA) with an antibody against HNF4 α and statistical analysis of HNF4 α expression levels in the CRC TMA.
 - E. Effects of ectopic expression of HNF4 α on colony formation in SW480 cells.
 - F. Tumor volume of mouse xenografts established with parental (6 mice) and HNF4 α overexpressing (6 mice) SW480.
 - G. Growth curve reflects the effect HNF4 α overexpression on tumor growth in xenograft mouse model.
 - H. Effects HNF4 α overexpression on tumor weight.
- * P<0.05, ** P<0.01 and *** P<0.001.

Figure 2 HNF4 α is a target of Wnt/ β -catenin

- A. GESA analysis of HNF4 α in TCGA database, * indicates the significant correlation of HNF4 α with Wnt and Myc pathways.
 - B. Correlations analysis between HNF4 α and β -catenin mRNA level in TCGA database.
 - C. Q-PCR analysis of the effect of β -catenin knockdown on HNF4 α mRNA level.
 - D. Western blotting analysis of the effect of β -catenin knockdown on HNF4 α protein expression in 3 different colon cancer cell lines.
 - E. Western blotting analysis of the effect of SKL2001 on subcellular location and expression of β -catenin and HNF4 α .
 - F. Western blotting analysis of the effect of SKL2001 and Chir-99021, 2 activators of WNT/ β -catenin signaling, on HNF4 α expression in SW480 and SW620 cell lines.
- ***p<0.001.

Figure 3 HNF4 α mediates Wnt/ β -catenin function in colon tumorigenesis

- A. Western blotting analysis of β -catenin and HNF4 α expression in SW620 cells transfected with β -catenin shRNA, β -catenin shRNA/HNF4 α .
 - B. Effect of β -catenin knockdown, β -catenin shRNA/HNF4 α on tumor growth.
 - C. Representative images of the effects of β -catenin shRNA, β -catenin shRNA/HNF4 α on tumor growth.
 - D. Effect of β -catenin shRNA, β -catenin shRNA/HNF4 α on tumor size.
 - E. Effect of β -catenin shRNA, β -catenin shRNA/HNF4 α on tumor weight.
- * p < 0.05, ** p < 0.01, ***p < 0.001.

Figure 4 TCF-3 is a major transcription factor to induce HNF4 α expression.

- A-D. Correlation analysis of mRNA levels between HNF4 α & TCF/LEF family

members using TCGA database.

E. Western blotting analysis of the effects of TCF/LEF members on HNF4 α expression.

F. Q-PCR analysis of the shRNA efficiency on LEF1 and TCF4

G. Western blot analysis of the effect of TCF3 knockdown on HNF4 α levels in DLD1 and LS174T cell lines.

H. Western blotting analysis of the effect of β -catenin knockdown and TCF3 overexpression on HNF4 α expression.

I. Western blotting analysis of the effect of TCF3 overexpression in β -catenin knockdown cells on HNF4 α expression.

Figure 5 TCF3 directly binds to the HNF4 α promoter and regulates its transcription.

A. JASPAR (<https://jaspar.genereg.net/>) analysis of 1.7-kb HNF4 α promoter for putative TCF3 transcription factor binding motif(s). Graphical representation of predicted binding sites and TCF3 binding sequence motifs shown on the top left.

B. Luciferase activity of HNF4 α promoters.

C. Mutation of each TCF3 binding motif in the pGL3-HNF4 α /300bp promoter region.

D. Luciferase activity of three mutants of pGL3-HNF4 α /300bp promoter.

***p<0.001.

Fig 6 HNF4 α induces expression of Wnt family members and β -catenin translocation from the cytoplasm to the nucleus.

A. KEGG pathway analysis by RNA sequencing data obtained from SW480-vector control and SW480-HNF4 α cells.

B. A heat map showing expression levels of the genes involved in WNT, MAPK, Hippo signaling pathways that are regulated by HNF4 α .

C. q-PCR analysis of HNF4 α overexpression on Wnt family members level.

D. Western blot analysis of the effect of HNF4 α overexpression on β -catenin level

E. Western blot analysis of the effect of HNF4 α overexpression on β -catenin nuclear localization.

Fig7 β -catenin/TCF3-HNF4 α axis correlate with colorectal tumorigenesis

A. Representative images of β -catenin, TCF3 and HNF4 α immunohistochemical staining in colorectal cancer tissue

B. Correlation analysis between TCF3 and HNF4 α level

C. Correlation analysis between β -catenin and HNF4 α level

D. Western blot analysis of β -catenin, TCF3 and HNF4 α level in colon tissue of AOM-DSS mouse colon cancer model

E. Model of β -catenin/TCF3-HNF4 α regulation in colorectal tumorigenesis

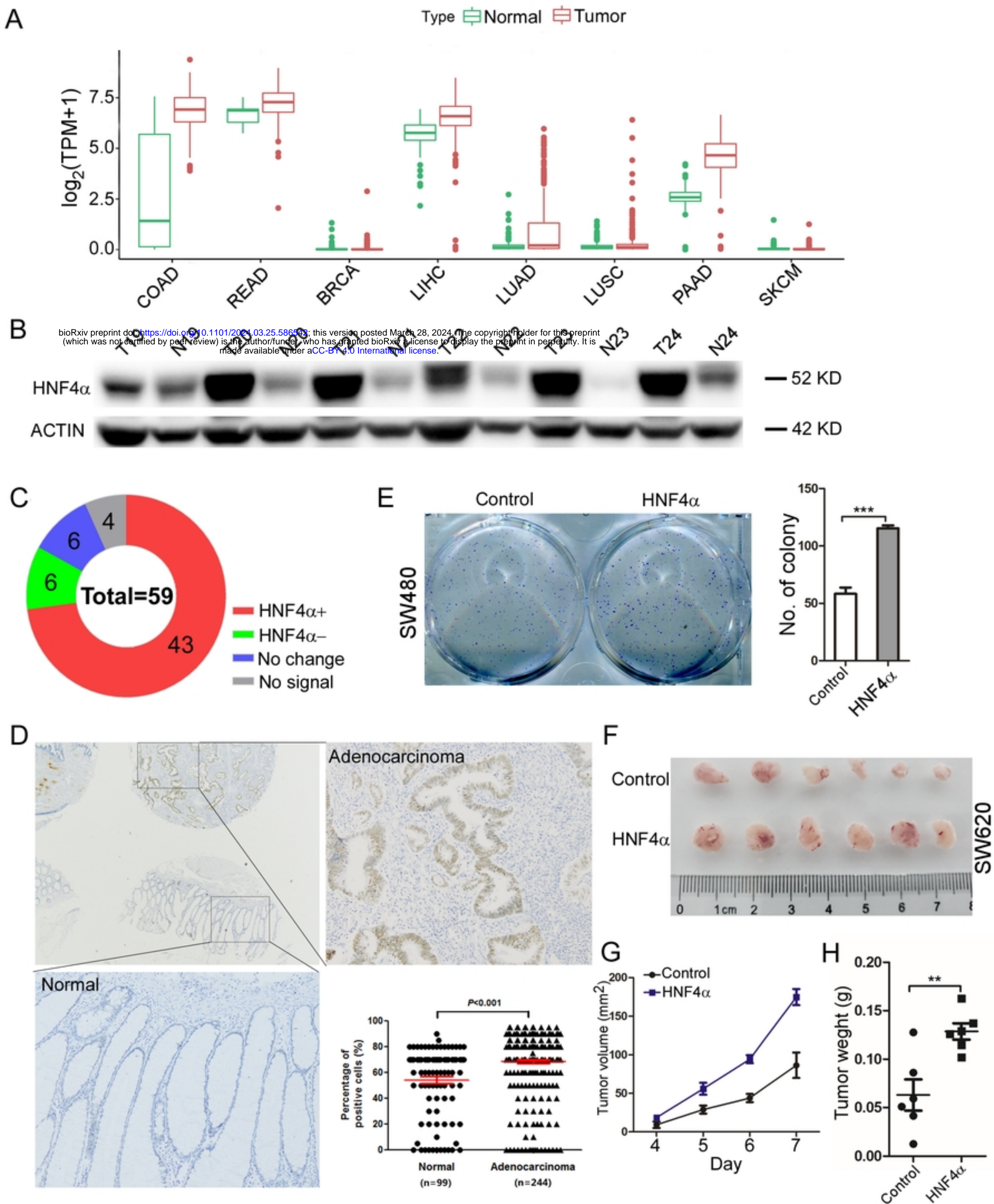
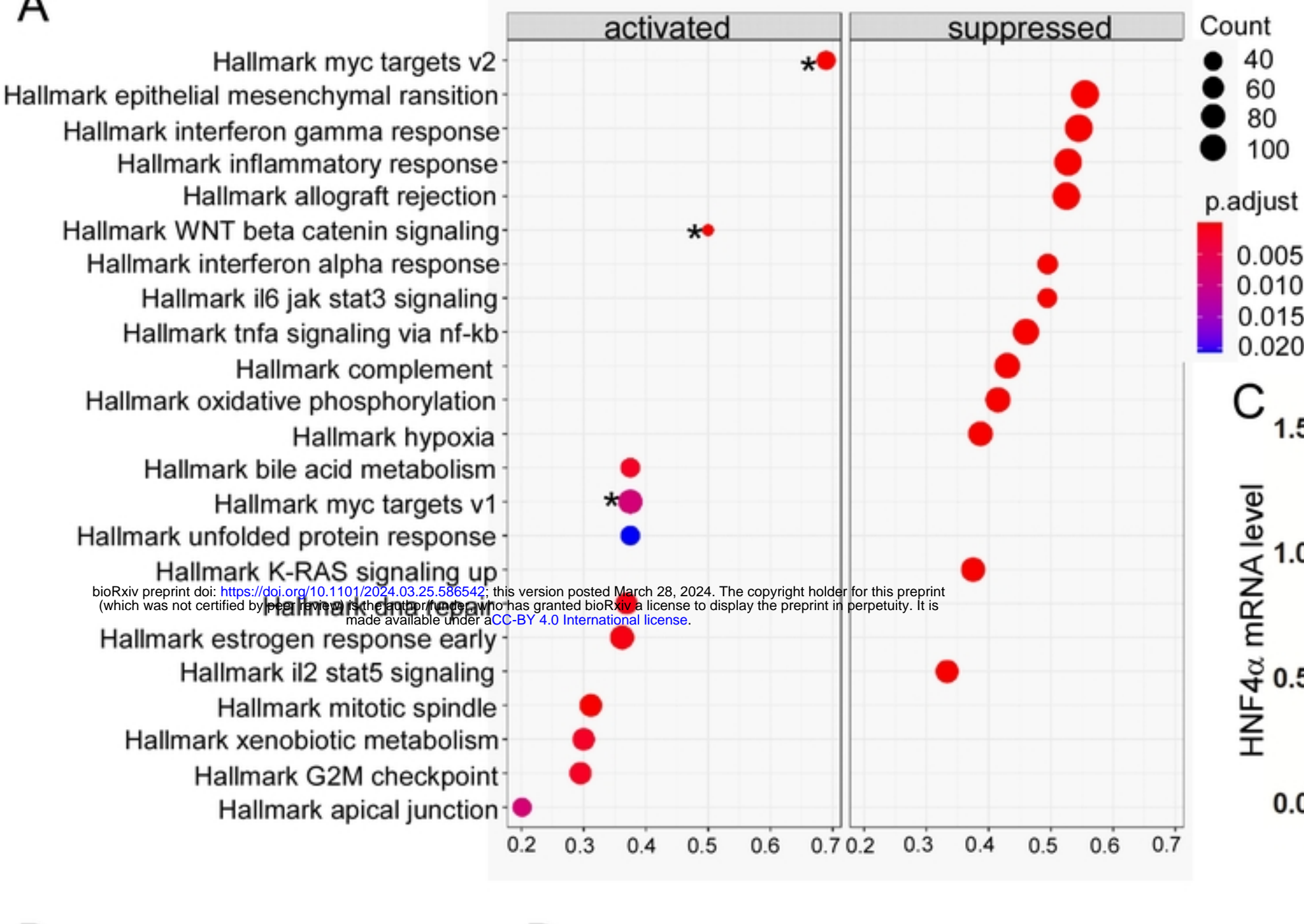
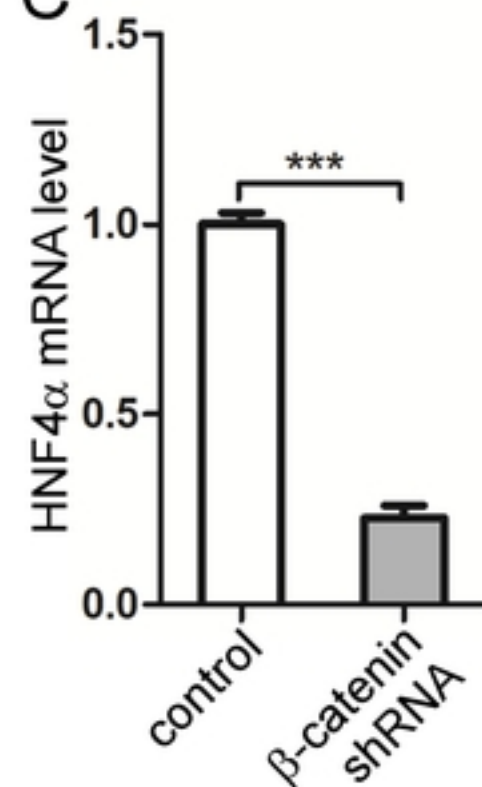


Figure1

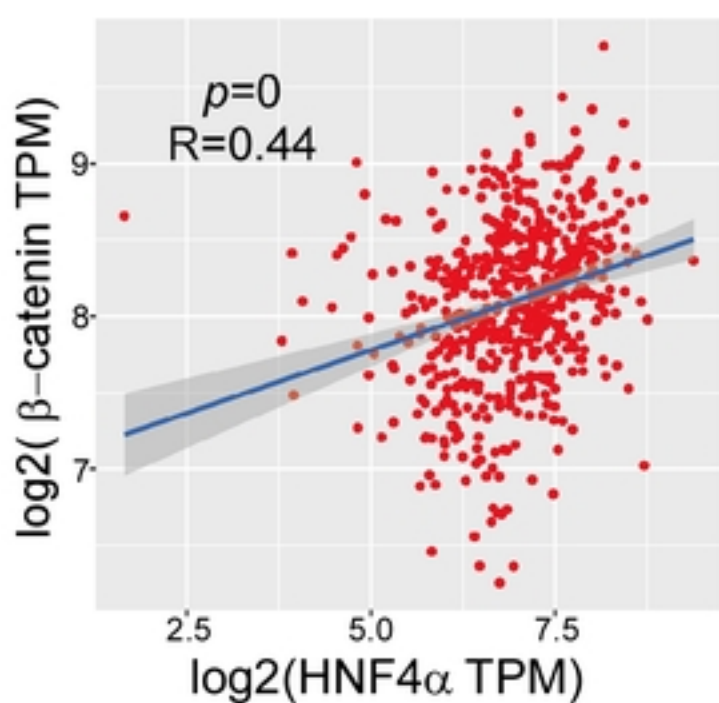
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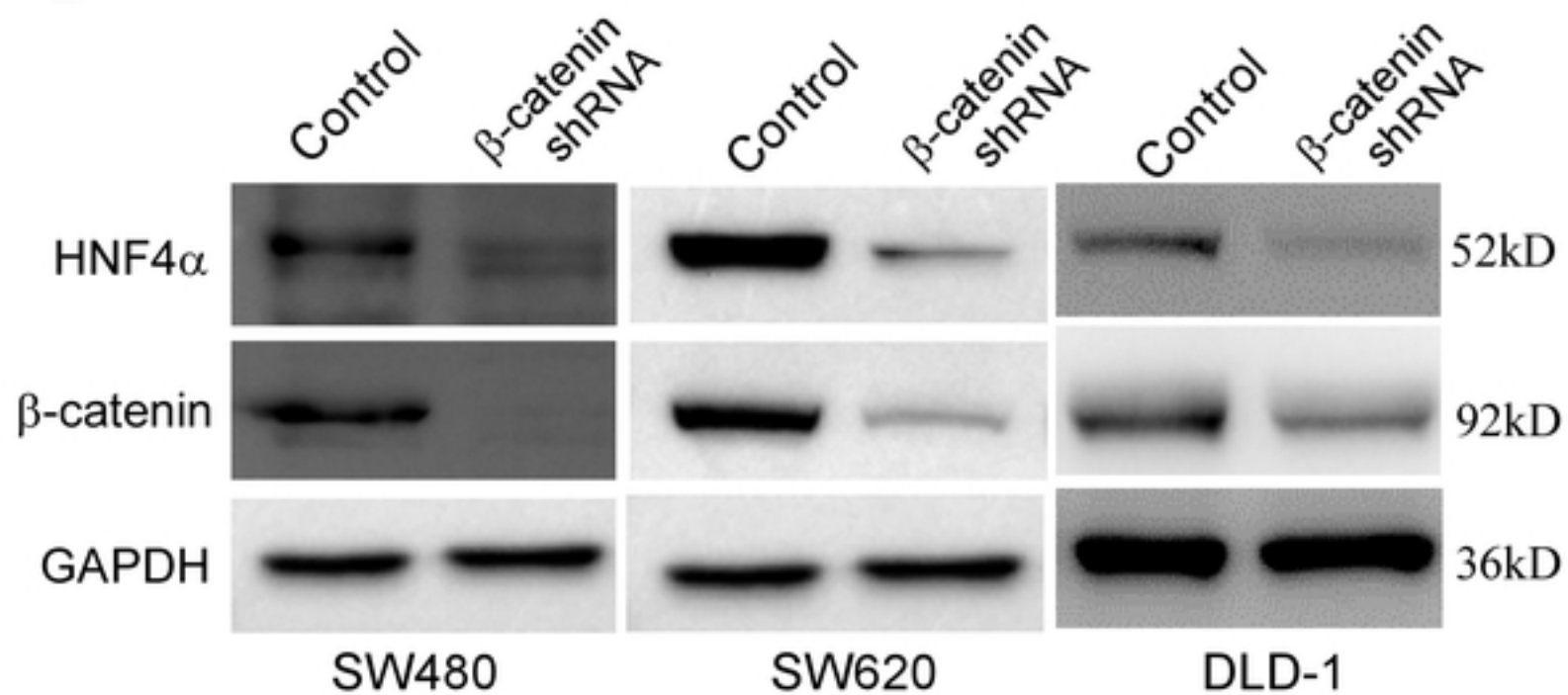
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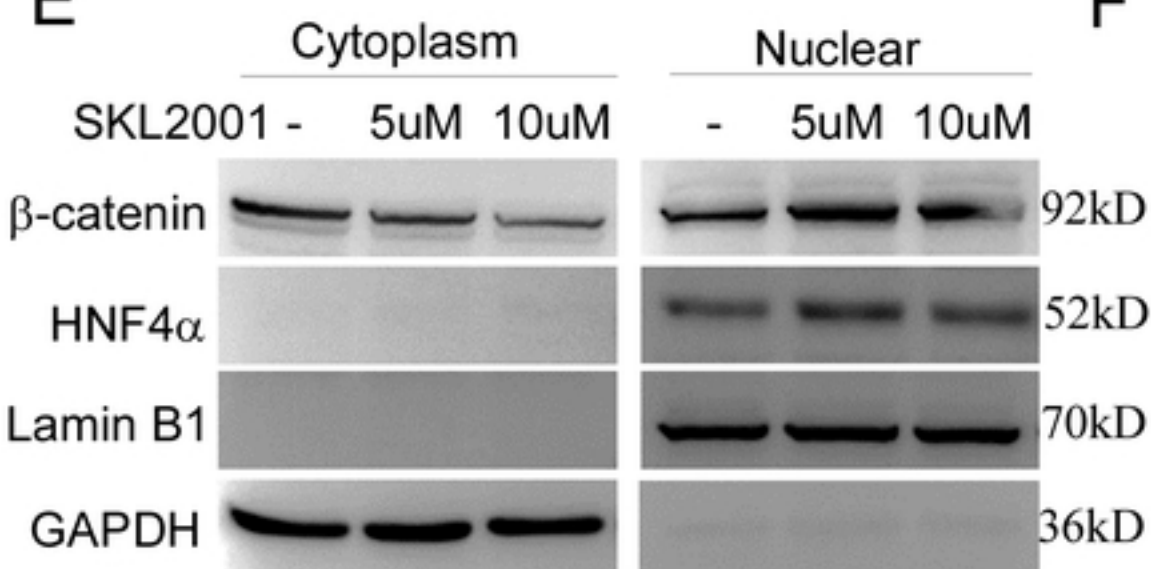
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D



E



F

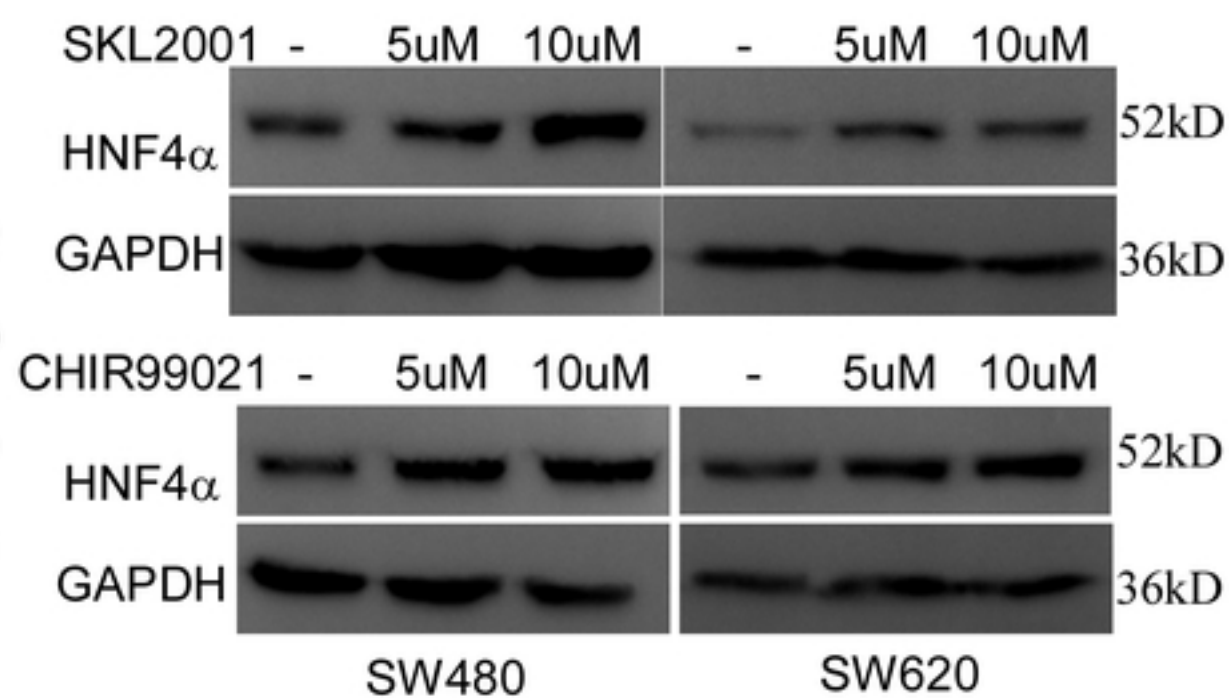


Figure2

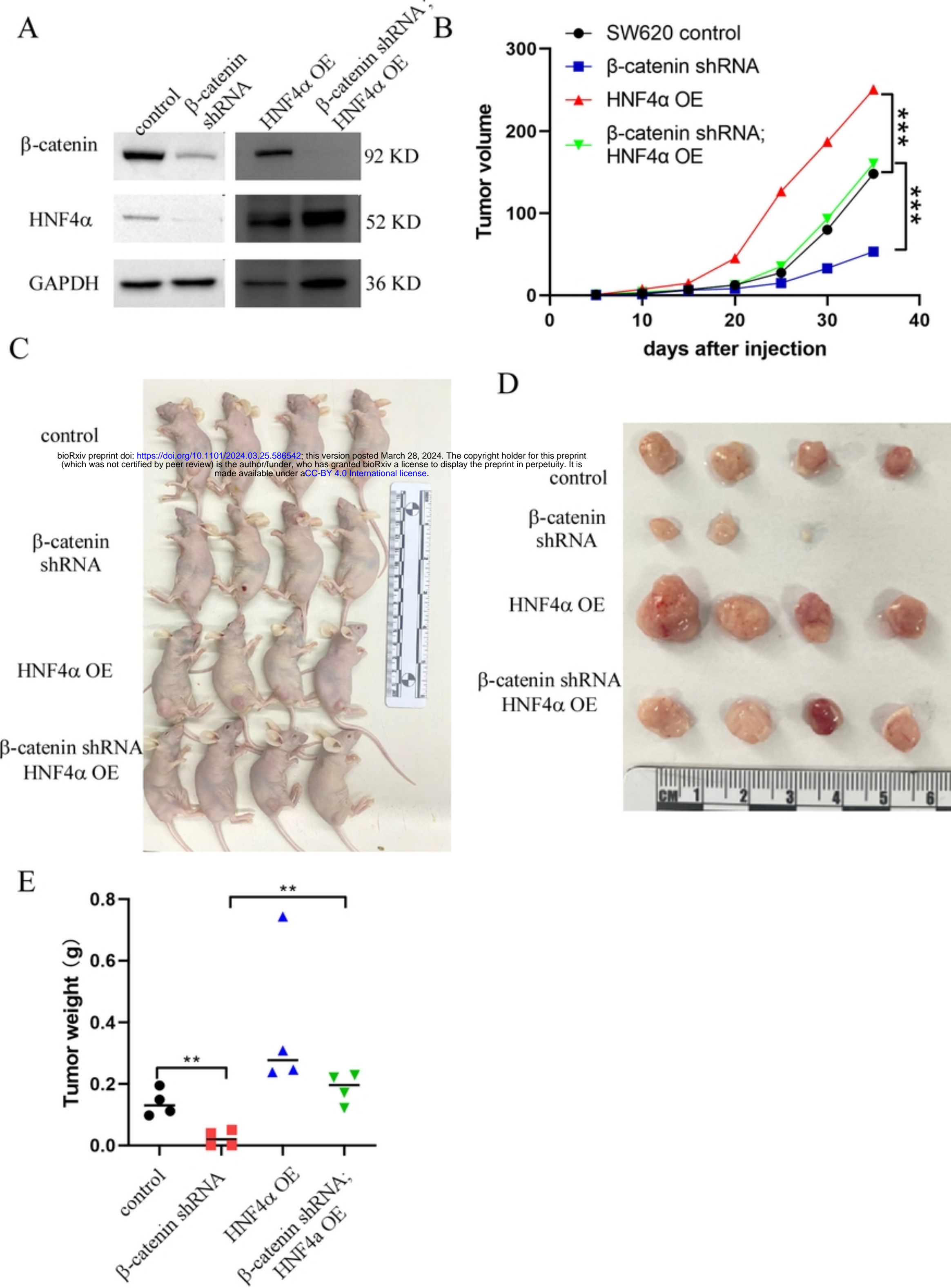


Figure3

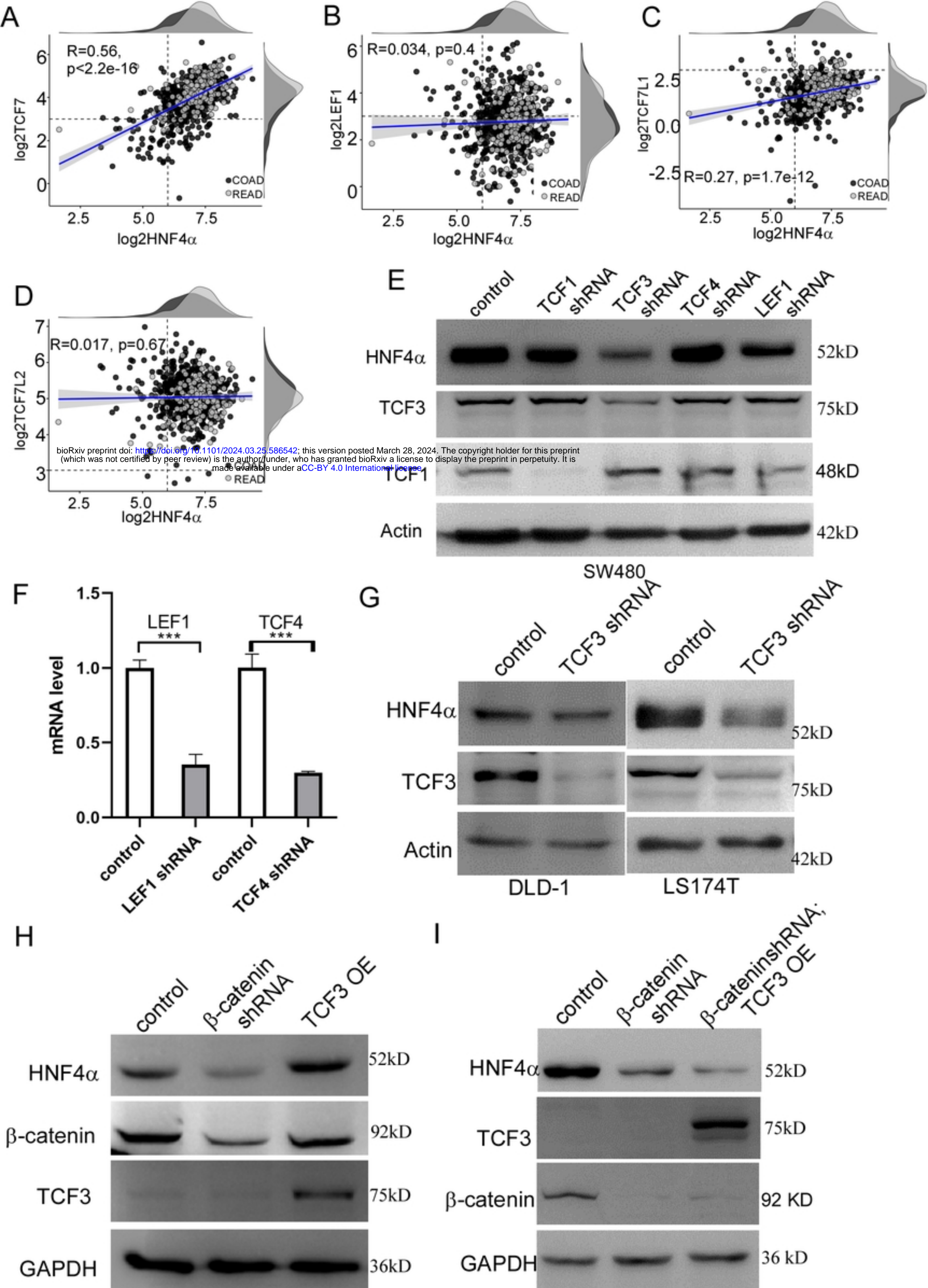
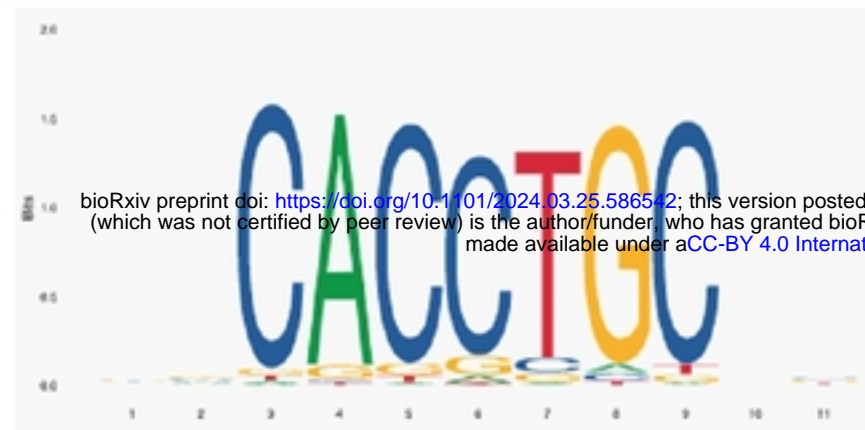


Figure4

A



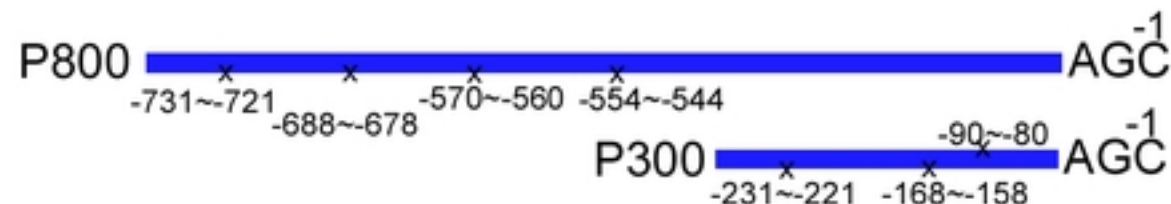
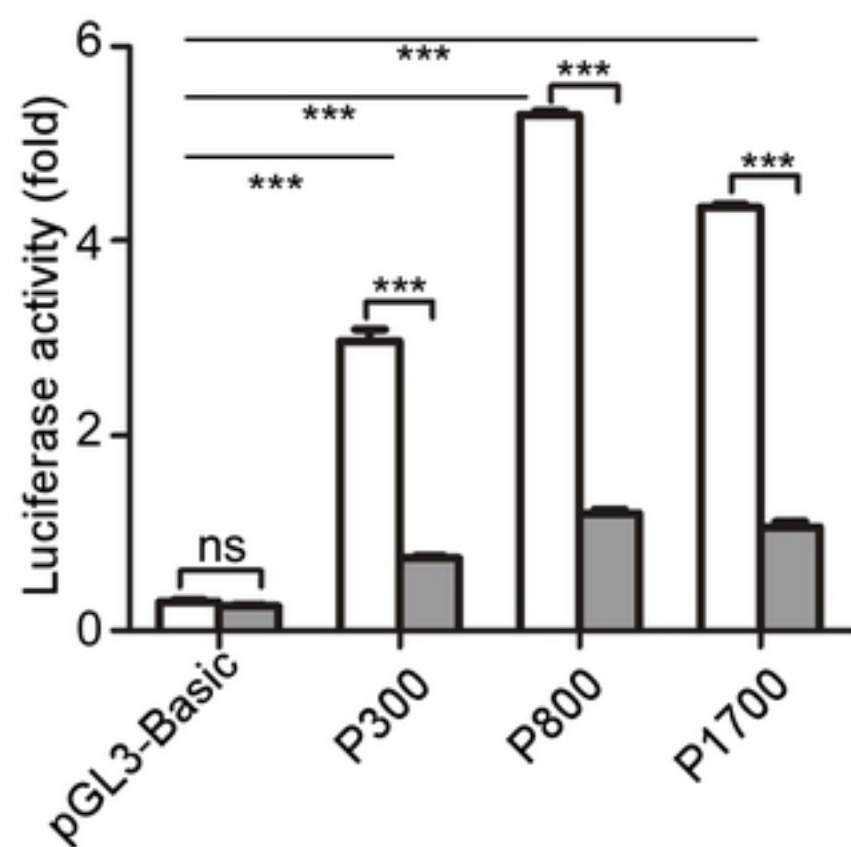
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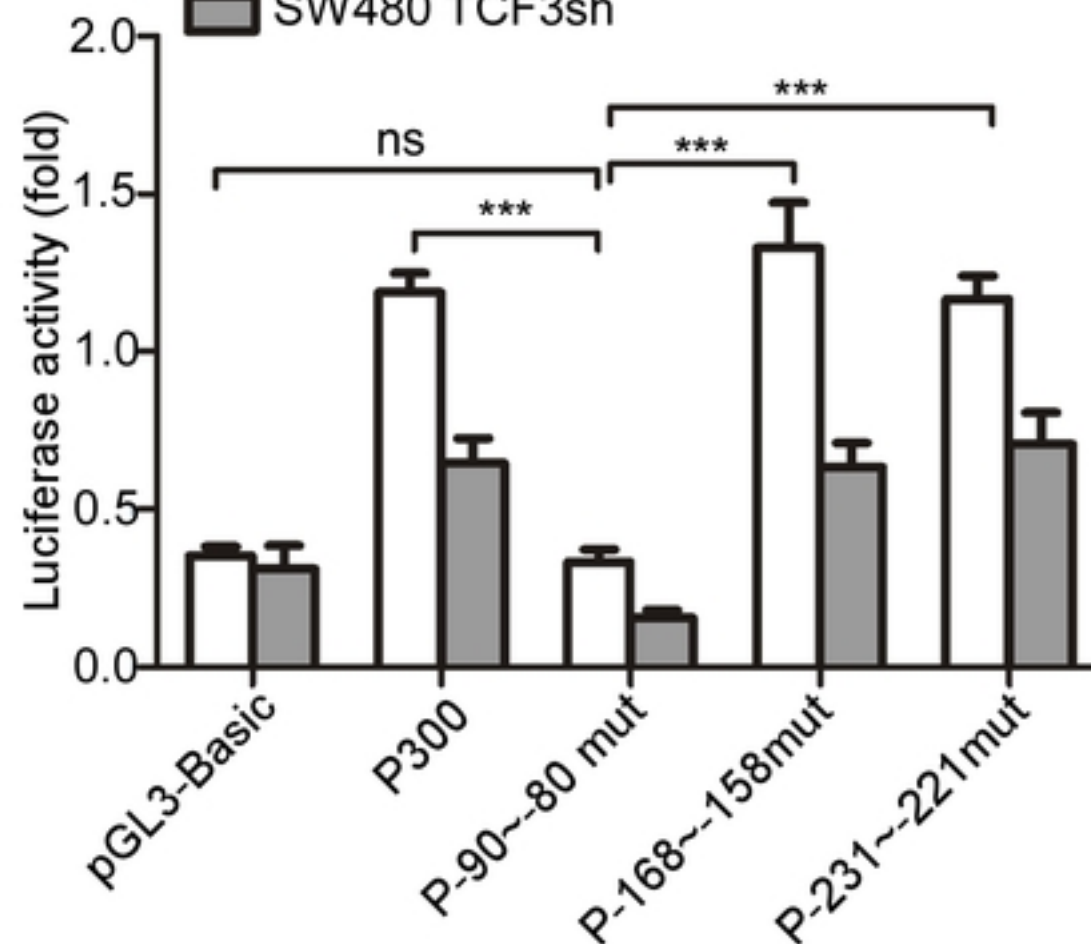
B

SW480 Control
 SW480 TCF3sh



D

SW480 Control
 SW480 TCF3sh



C

Mutation binding site

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	↓		
-90~-80 mut	tcacaattagg		
	↓		
-: -168~-158	tacaactgctg	-: -231~-221	ctcacggggcac
	↓		↓
-168~-158mut	taaccagtatg	-231~-221 mut	ctacattaac

Figure5

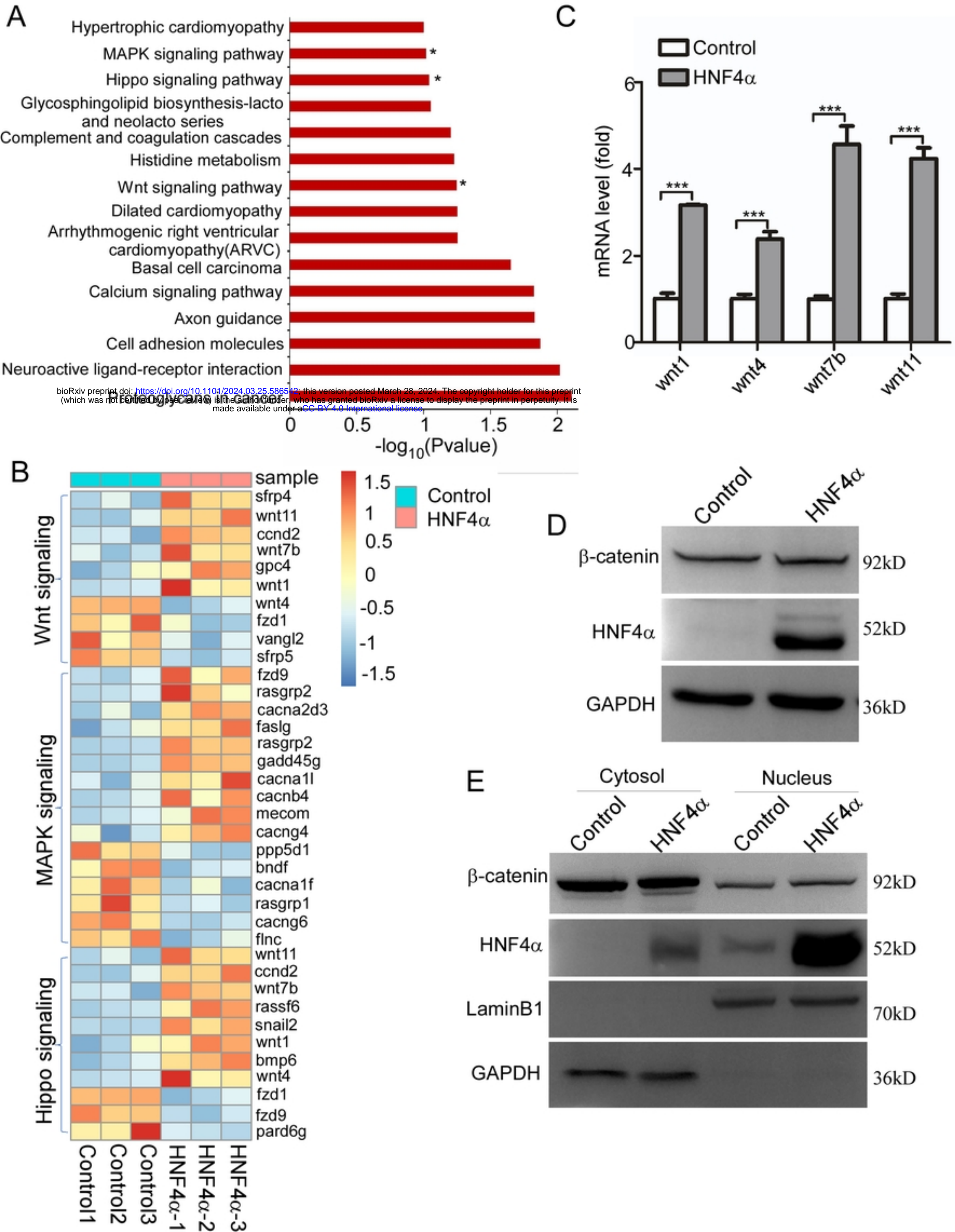


Figure6

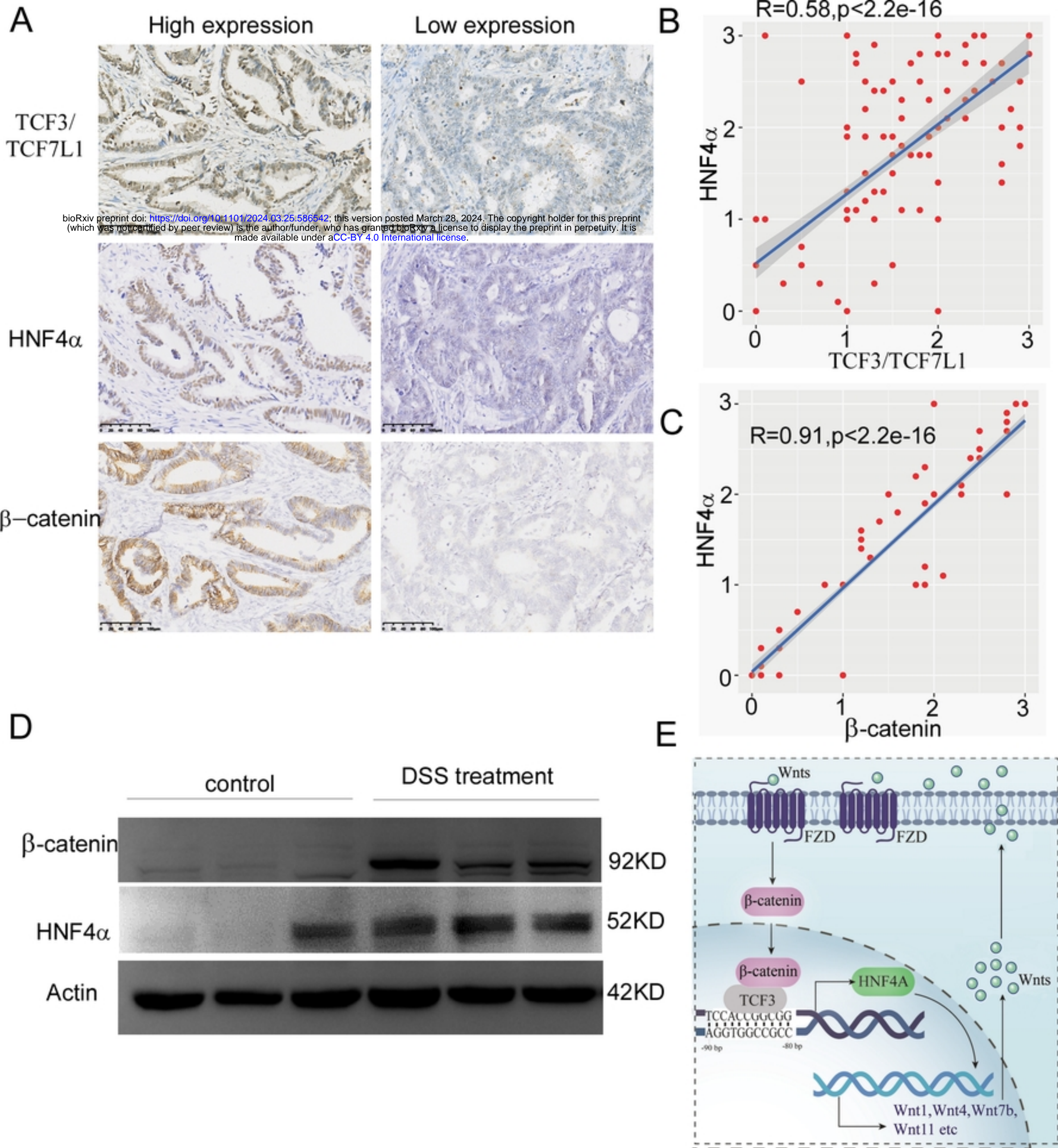


Figure7