

## Supplementary figure legends

### **Fig. S1: Relative expression and sequencing analysis of Linc01612.**

(A) Relative expression of Linc01612 in different HCC cells. (B) Relative expression of Linc01612 in transfected Linc01612 or vector HCC cells. (C) Relative expression of Linc01612 in transfected siRNAs or control Hep3B cells. (D) Reactome enrichment analysis of differential expression genes. (E) The top ten differential genes with the most significant *P* value. ATF3 was the most significantly different gene except Linc01612. Values are expressed as the mean  $\pm$  sd, *n* = 3 in A–C. \**p* < 0.05, \*\*\**p* < 0.001.

### **Fig. S2: The correlations among Linc01612, miR-494, and ATF3 levels.**

(A) The expression of ATF3 and YBX1 in subcutaneous tumor tissues. (B) The correlation analysis of the Linc01612 and ATF3 expression. (C) The correlation analysis of the miR-494 and ATF3 expression. (D) The expression of miR-494 in subcutaneous tumor tissues.

### **Fig. S3: Linc01612 exerts tumor suppressor function through upregulation of ATF3.**

(A),(B) Relative expression of ATF3 in transfected siRNAs or siNC HCC cells. (C) Flow cytometric analysis revealed that knockdown ATF3 could partially reverse the Linc01612 mediated increase of apoptotic cells. (D) CCK8 assay revealed that

knockdown of ATF3 could partially reverse the Linc01612 mediated inhibition of HCC cells proliferation. (E) ATF3 was lowly expressed in non-paired HCC samples from TCGA database. Values are expressed as the mean  $\pm$  sd, n = 3 in A, D and E. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001.

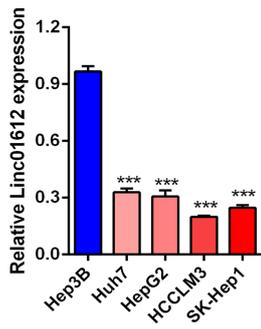
**Fig. S4: Linc01612 exerts tumor suppressor function through down regulation of YBX1.** (A) The predicted secondary structure of Linc01612 from RNA fold Web server (<http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi>). (B) YBX1 was highly expressed in non-paired HCC samples from TCGA database. (C) Kaplan-Meier curves for overall survival in patients with HCC from TCGA database. (D) Immunohistochemical (IHC) analysis indicated that YBX1 was upregulated in HCC tissues. (E) Western blot analysis of p-YBX1 (Ser102) in Linc01612 plasmid transfected HCC cells. (F) Colony formation assay revealed that overexpression of YBX1 could partially reverse the Linc01612 mediated inhibition of HCC cells proliferation. (G) Transwell assay showed that overexpression of YBX1 could partially reverse the Linc01612 mediated inhibition of HCC cells invasion. Values are expressed as the mean  $\pm$  sd, n = 3 in A and B. \*\*\*p < 0.001.

**Fig. S5: Linc01612 is differentially expressed in a variety of cancers.**

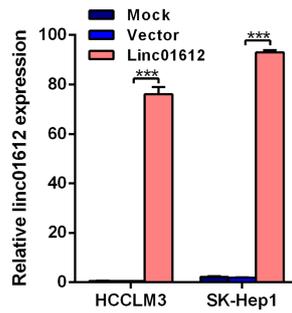
(A) Linc01612 was downregulated in non-paired CHOL samples from TCGA database. (B) Linc01612 was downregulated in many cancers from TCGA database. (C) Linc01612 was downregulated in CHOL tissues compared with the paired adjacent tissues (n=8); tested by RT-qPCR. \*p < 0.05.

Fig. S1

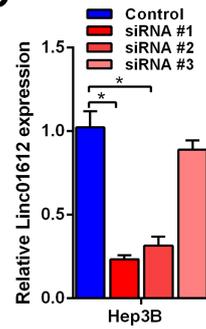
**A**



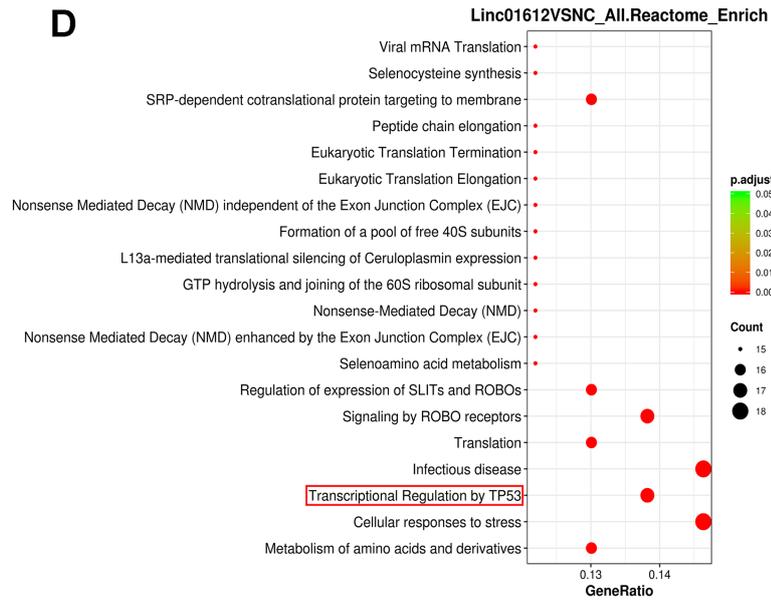
**B**



**C**



**D**



**E**

	A	B	C	D	E	F	G	H	I	J
1	GeneName	log2FC	Pvalue	padj	Linc01612	Linc01612	Linc01612	NC_1	NC_2	NC_3
2	LINC01612	16.04114	5.39E-42	8.22E-38	23371	29658	22901	0	1	0
3	ATF3	1.158676	3.98E-23	3.04E-19	1027	1364	930	484	495	435
4	PPP1R15A	0.951647	9.14E-23	4.65E-19	2168	2620	1965	1068	1104	1159
5	NR1D1	1.187133	3.94E-19	1.50E-15	1997	2296	1706	697	945	872
6	PER1	1.618831	1.10E-18	3.37E-15	1017	1157	839	220	376	339
7	FOSB	1.37663	2.16E-15	5.49E-12	609	605	457	169	230	217
8	JUN	0.874802	3.79E-14	8.27E-11	1867	2246	1763	900	1049	1111
9	ZNF699	1.852539	2.94E-11	5.61E-08	116	163	106	31	30	40
10	HIST1H1C	0.755616	1.63E-10	2.76E-07	856	1120	896	535	512	577
11	HLF	2.388653	2.01E-09	3.07E-06	61	80	57	11	14	11

Fig. S2

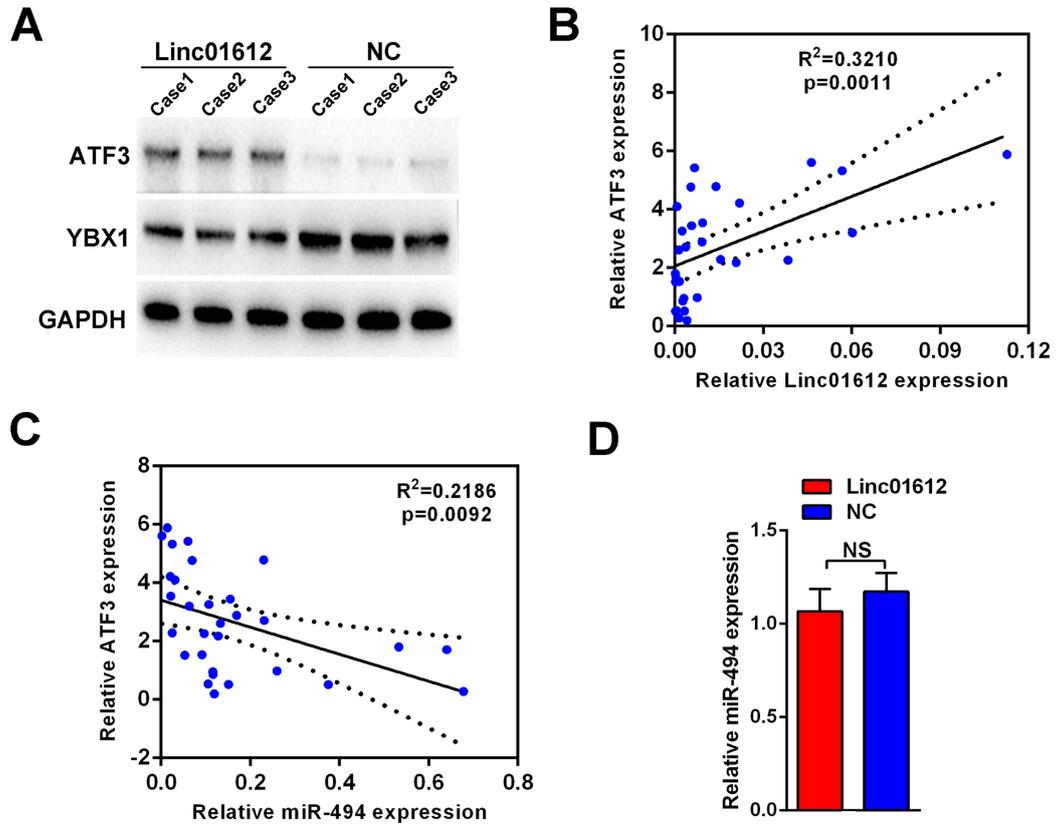


Fig. S3

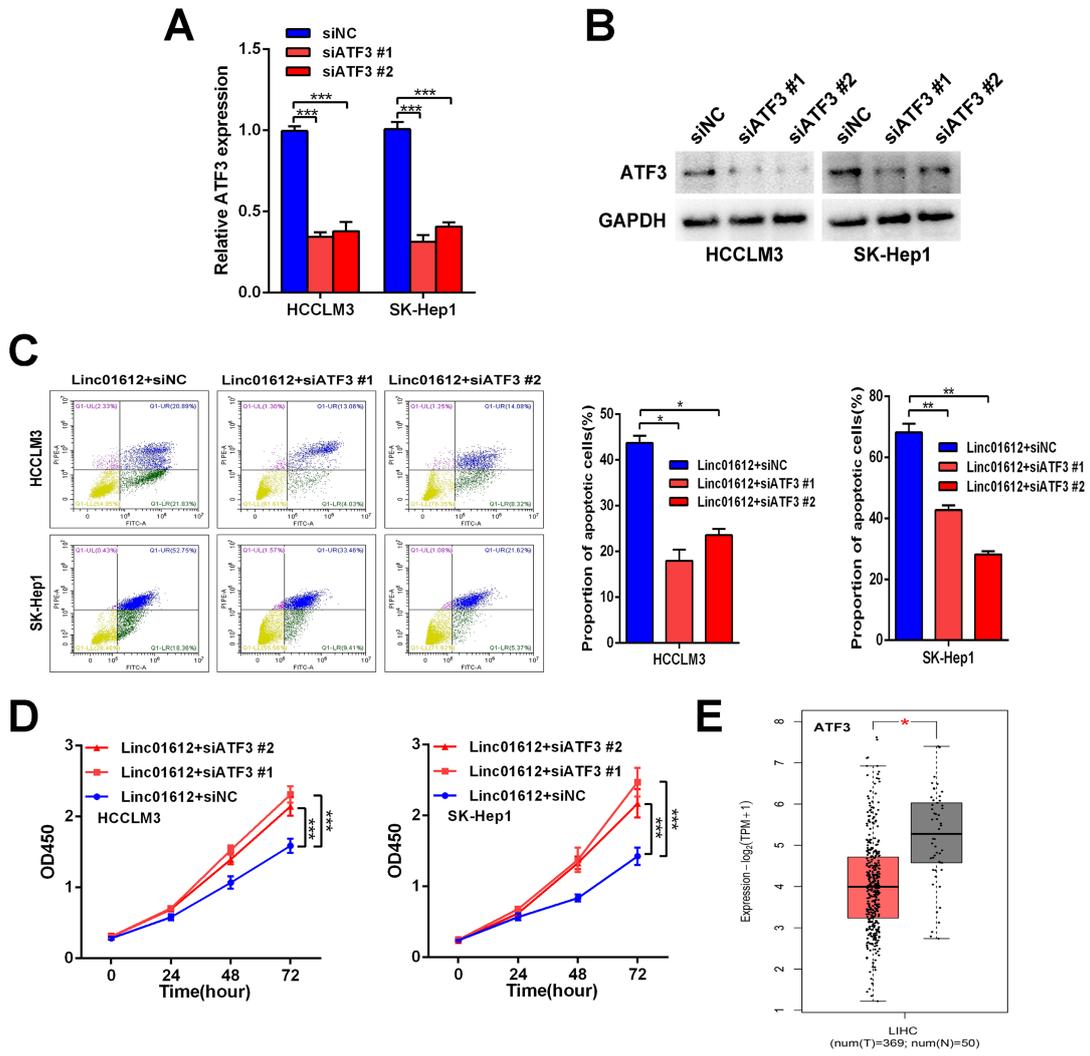


Fig. S4

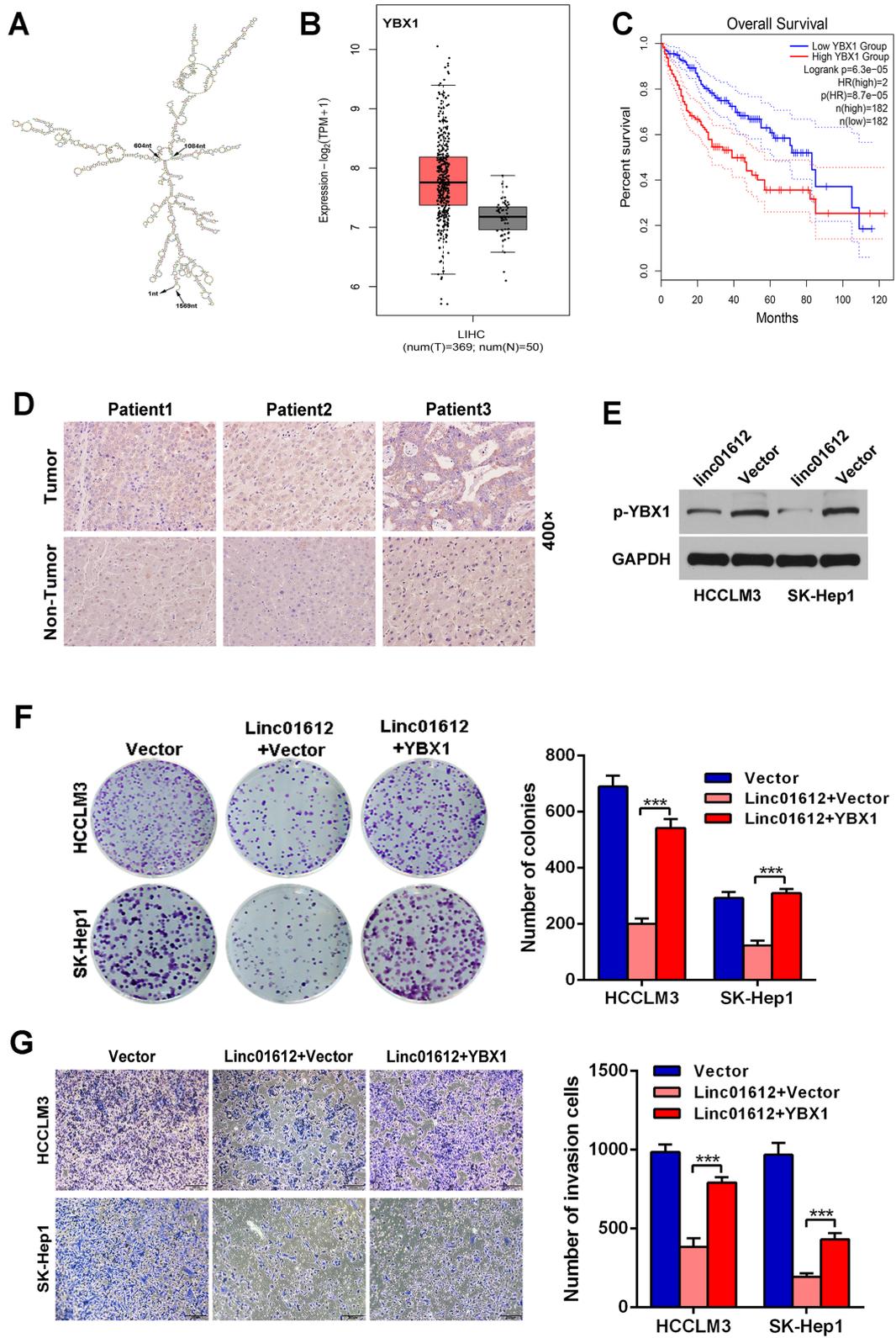


Fig. S5

