

Overexpression of *DDx49* promotes cell proliferation and associated with poor prognosis in liver cancer: *In silico* analysis

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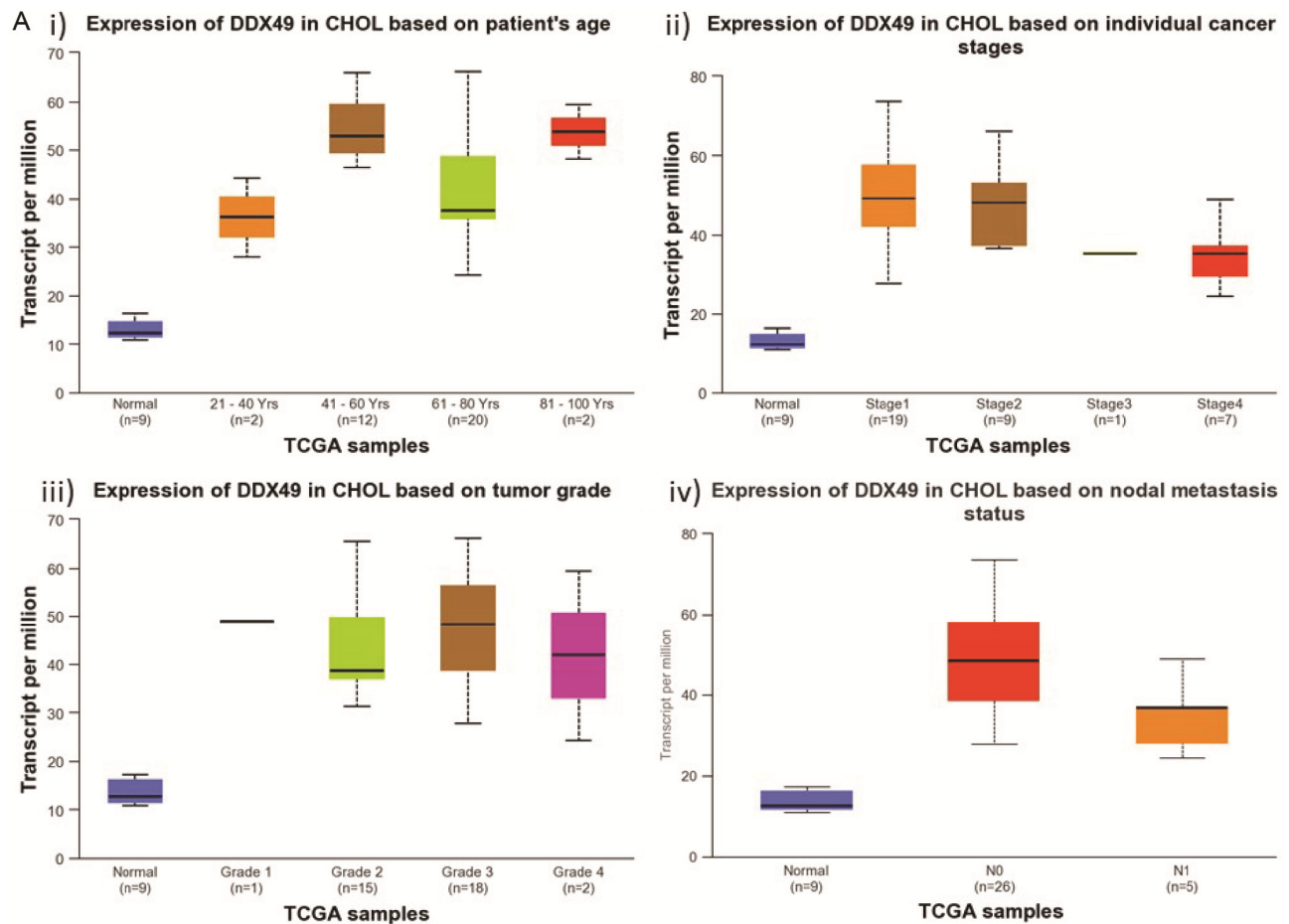
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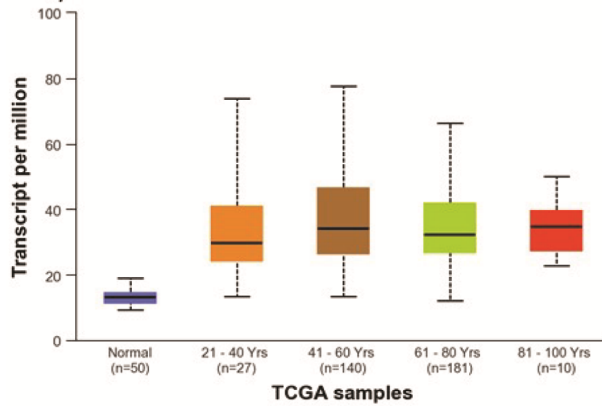
Supplementary Data



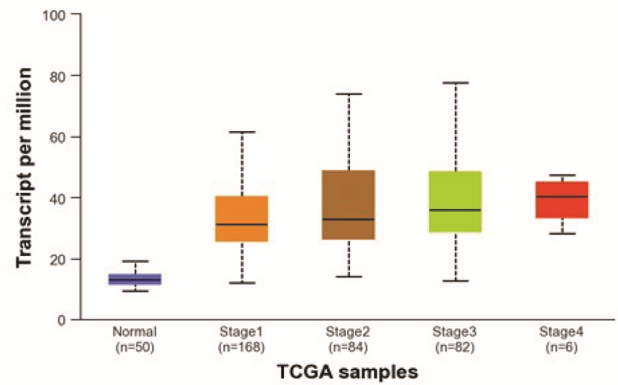
Suppl. Fig. 1 — Expression of *DDx49* in different clinical characters in (A) CHOL (Cholangiocarcinoma); and (B) LIHC (Liver hepatocellular carcinoma); The table shows the p value of each figure (*Contd.*)

Characters	CHOL p-value	LIHC p-value
i) Patient's age		
21-40	2.15E-01	1.83E-05
41-60	2.06E-09	1.62E-12
61-80	1.17E-09	<1E-12
81-100	8.86E-02	2.44E-05
ii) Individual cancer stages		
1	3.19E-11	1.62E-12
2	4.82E-06	<1E-12
3	N/A	<1E-12
4	2.83E-03	5.22E-04
iii) Tumor grade		
Grade 1	N/A	2.70E-12
Grade 2	6.83E-01	<1E-12
Grade 3	5.56E-01	<1E-12
Grade 4	1.00E-01	6.18E-05
iv) nodal metastasis status		
N0	4.10E-15	<1E-12
N1	7.74E-03	3.84E-02

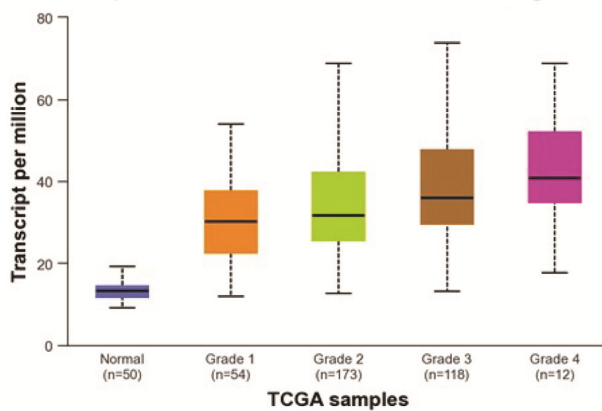
B i) Expression of DDX49 in LIHC based on patient's age



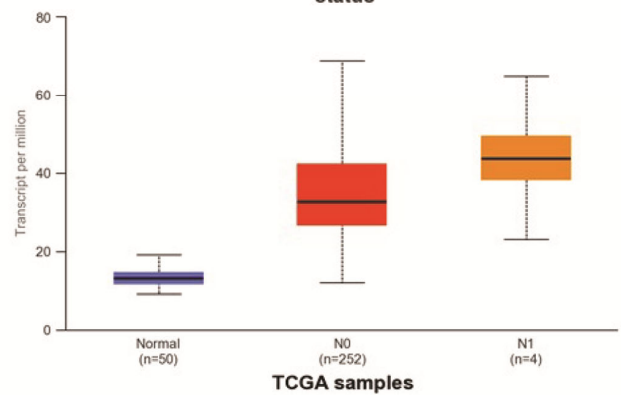
ii) Expression of DDX49 in LIHC based on individual cancer stages



iii) Expression of DDX49 in LIHC based on tumor grade



iv) Expression of DDX49 in LIHC based on nodal metastasis status



Suppl. Fig. 1 — Expression of *DDx49* in different clinical characters in (A) CHOL (Cholangiocarcinoma); and (B) LIHC (Liver hepatocellular carcinoma); The table shows the p value of each figure

Suppl. Table 1 — Demographic and clinical parameter of Cholangiocarcinoma (TCGA-LIHC) and liver hepatocellular carcinoma (TCGA-CHOL) cohort dataset

Characteristics	Cholangiocarcinoma Total(N)	Liver hepatocellular carcinoma Total(N)
Normal	9	50
Tumor	36	371
Pathologic stage		
1	19 (52.78%)	168 (45.28%)
2	9 (25)	84 (22.64%)
3	1 (2.78%)	82 (22.10%)
4	7 (19.44%)	6 (1.61%)
Gender		
Male	16 (44.44%)	245 (66.03%)
Female	20 (55.55%)	117 (31.53%)
Race		
Caucasian	31 (86.11%)	117 (31.53%)
African-American	2 (5.55%)	17 (4.58%)
Asian	3 (8.33%)	157 (42.31%)
Age		
21-40	2 (5.55%)	27 (7.28%)
41-60	12 (33.33%)	140 (37.73%)
61-80	20 (55.55%)	181 (48.79%)
81-100	2 (5.55%)	10 (2.69%)
Histologic grade		
Grade 1	1 (2.78%)	54 (14.55%)
Grade 2	15 (41.65%)	173 (46.63%)
Grade 3	18 (50%)	118 (31.80%)
Grade 4	2 (5.55%)	12 (3.23%)
N Stage		
N0	26 (72.22%)	252 (67.92%)
N1	5 (13.89%)	4 (1.07%)

Suppl. Table 2 — GO and KEGG Biological pathways datasets for *DDx49* interacting proteins found from STRING database

Category	term ID	term description	observed gene count	false discovery rate	matching proteins in your network (labels)
GO Process	GO:0006364	rRNA processing	28	8.62E-47	DIMT1, UTP18, KRR1, BYSL, RRP9, MPHOSPH10, <i>DDX49</i> , UTP3, NAT10, IMP4, UTP20, UTP6, NOP58, NOB1, ABT1, RIOK2, PWP2, UTP15, DCAF13, NOL6, TSR1, WDR3, DHX37, PDCD11, WDR46, UTP25, EMG1, DDX52
GO Process	GO:0042274	Ribosomal small subunit biogenesis	19	6.39E-34	BYSL, MPHOSPH10, UTP3, NAT10, IMP4, UTP20, UTP6, NOB1, 1, RIOK2, PWP2, DCAF13, TSR1, WDR3, DHX37, WDR46, UTP25, EMG1, DDX52
GO Process	GO:0030490	Maturation of SSU-rRNA	18	6.75E-34	BYSL, MPHOSPH10, UTP3, NAT10, IMP4, UTP20, UTP6, NOB1, ABT1, RIOK2, PWP2, DCAF13, TSR1, WDR3, DHX37, WDR46, UTP25, DDX52
GO Process	GO:0000462	Maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	11	8.35E-19	BYSL, UTP3, UTP20, UTP6, ABT1, PWP2, DCAF13, TSR1, DHX37, WDR46, UTP25

(Contd.)

Suppl. Table 2 — GO and KEGG Biological pathways datasets for *DDx49* interacting proteins found from STRING database (*Contd.*)

Category	term ID	term description	observed gene count	false discovery rate	matching proteins in your network (labels)
GO Process	GO:0000469	Cleavage involved in rRNA processing	4	0.0001	UTP20, NOB1, ABT1, TSR1
GO Process	GO:2000234	Positive regulation of rRNA processing	3	0.00056	DIMT1, RIOK2, UTP15
GO Process	GO:0000479	Endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3	0.0018	UTP20, ABT1, TSR1
GO Process	GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	4	0.0045	UTP20, NOB1, ABT1, TSR1
GO Process	GO:0000154	rRNA modification	3	0.0147	DIMT1, NAT10, EMG1
GO Process	GO:0000472	Endonucleolytic cleavage to generate mature 5-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2	0.023	UTP20, ABT1
GO Process	GO:0000480	Endonucleolytic cleavage in 5-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2	0.044	UTP20, ABT1
KEGG	hsa03008	Ribosome biogenesis in eukaryotes	13	9.71E-21	UTP18, MPHOSPH10, NAT10, IMP4, UTP6, NOP58, NOB1, RIOK2, PWP2, UTP15, NOL6, WDR3, EMG1

Suppl. Table 3 — *DDx49* interacting genes from GeneMANIA

S. No	Symbol	Description	Weight
1	OR2B3	Olfactory Receptor Family 2 Subfamily B Member 3	0.01605
2	RTL3	Retrotransposon Gag like 3	0.00865
3	CDC23	Cell division cycle 23	0.008
4	HSD17B8	Hydroxysteroid 17-Beta Dehydrogenase 8	0.00701
5	SSR2	Signal sequence receptor subunit 2	0.00665
6	WNT8B	Wnt family member 8B	0.00643
7	EMID1	EMI domain containing 1	0.00619
8	GAS2L2	Growth arrest specific 2 like 2	0.00608
9	EHMT2	Euchromatic Histone Lysine Methyltransferase 2	0.00564
10	TREM2	Triggering receptor expressed on myeloid cells 2	0.00546
11	KRT79	Keratin 79	0.00544
12	IL13	Interleukin 13	0.00538
13	TIMM22	Translocase of Inner Mitochondrial Membrane 22	0.00533
14	IER3	Immediate Early Response 3	0.00526
15	NRARP	NOTCH regulated ankyrin repeat protein	0.00507
16	LATS1	Large tumor suppressor kinase 1	0.00499
17	IFITM1	Interferon induced transmembrane protein 1	0.00473
18	FAM234B	Family with sequence similarity 234 member B	0.00468
19	TMEM179	Transmembrane Protein 179	0.00467
20	MYO1C	Myosin IC	0.00445