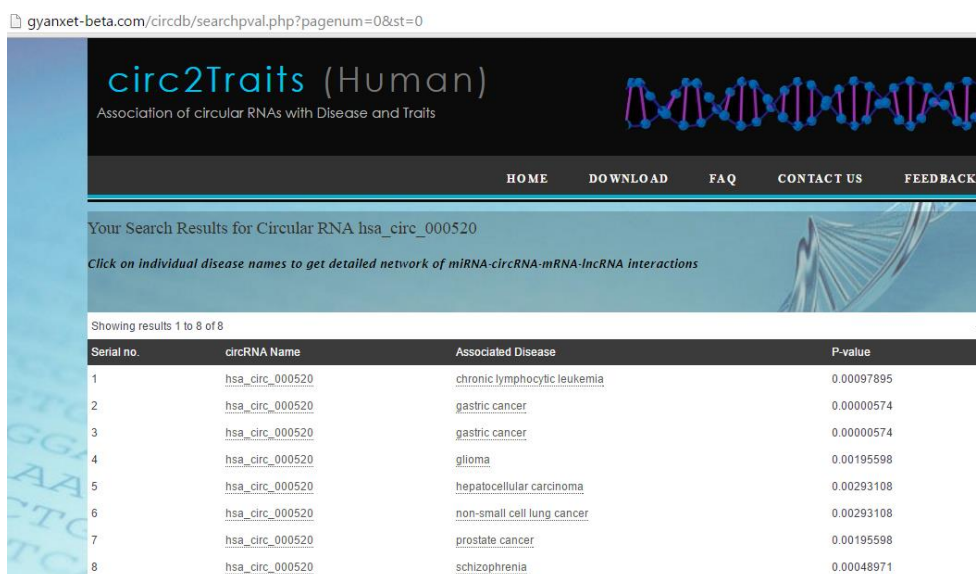


Supplementary Materials: Impact of circ-0000221 in the Pathogenesis of Hepatocellular via Modulation of miR-661–PTPN11 mRNA Axis

Marwa Matboli, Mohmed K. Hassan, Mahmoud A. Ali, Mohamed Tarek Mansour, Waheba Elsayed, Reham Atteya, Hebatallah Said Aly, Mahmoud El Meteini, Hesham Elghazaly, Sherif El-Khamisy and Sara H.A. Agwa

Figure S1. Print screen Shot fot hsa_circ_000022 predicted by Circ 2 trait : <http://gyanxet-beta.com/circdb/>, accessed on 10. November 2021.

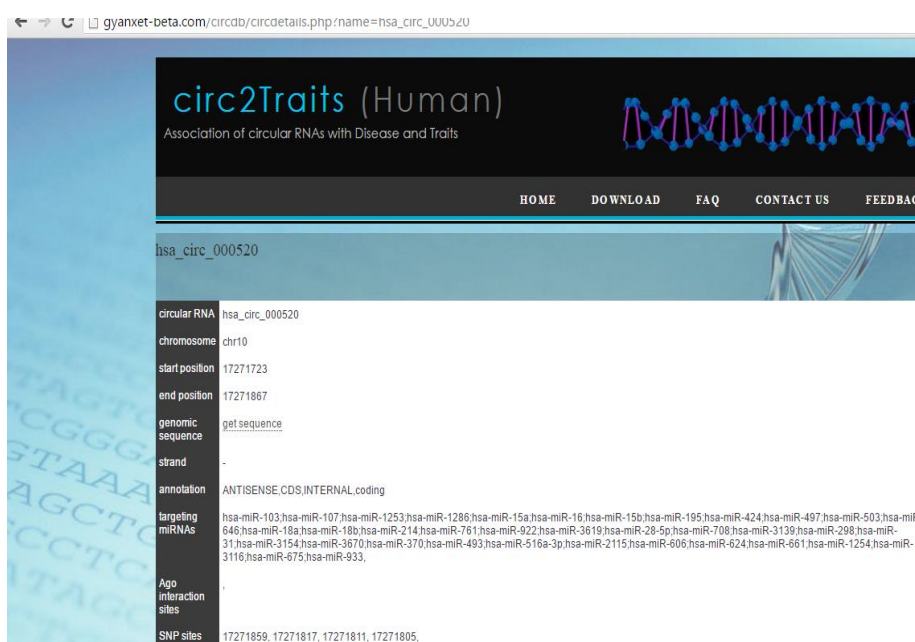
gyanxet-beta.com/circdb/searchpval.php?pagenum=0&st=0



Serial no.	circRNA Name	Associated Disease	P-value
1	hsa_circ_000520	chronic lymphocytic leukemia	0.00097895
2	hsa_circ_000520	gastric cancer	0.00000574
3	hsa_circ_000520	gastric cancer	0.00000574
4	hsa_circ_000520	glioma	0.00195598
5	hsa_circ_000520	hepatocellular carcinoma	0.00293108
6	hsa_circ_000520	non-small cell lung cancer	0.00293108
7	hsa_circ_000520	prostate cancer	0.00195598
8	hsa_circ_000520	schizophrenia	0.00048971

Figure S2. Print screen Shot fot hsa_circ_000022 & miR-661 predicted by Circ 2 trait : <http://gyanxet-beta.com/circdb/>, accessed on 10. November 2021.

gyanxet-beta.com/circdb/circdetails.php?name=hsa_circ_000520



circular RNA	hsa_circ_000520
chromosome	chr10
start position	17271723
end position	17271867
genomic sequence	get sequence
strand	-
annotation	ANTISENSE,CDS,INTERNAL coding
targeting miRNAs	hsa-miR-103,hsa-miR-107,hsa-miR-1253,hsa-miR-1286,hsa-miR-15a,hsa-miR-16,hsa-miR-15b,hsa-miR-195,hsa-miR-424,hsa-miR-497,hsa-miR-503,hsa-miR-646,hsa-miR-18a,hsa-miR-18b,hsa-miR-214,hsa-miR-761,hsa-miR-922,hsa-miR-3619,hsa-miR-28-5p,hsa-miR-708,hsa-miR-3139,hsa-miR-298,hsa-miR-31,hsa-miR-3154,hsa-miR-3670,hsa-miR-370,hsa-miR-493,hsa-miR-516a-3p,hsa-miR-2115,hsa-miR-606,hsa-miR-624,hsa-miR-661,hsa-miR-1254,hsa-miR-3116,hsa-miR-675,hsa-miR-933,
Ago interaction sites	-
SNP sites	17271859, 17271817, 17271811, 17271805,

Figure S3. Print screen Shot for miR-661 & PTPN-11 predicted by Target scan; Available at http://amp.pharm.mssm.edu/Harmonizome/gene_set/hsa-miR-661/TargetScan+Predicted+Conserved+microRNA+Targets accessed on 10. November 2021.

← → ↺ amp.pharm.mssm.edu/Harmonizome/gene_set/hsa-miR-661/TargetScan+Predicted+Conserved+microRNA+Targets		
FAM214B	family with sequence similarity 214, member B	1.45615
PTPN3	protein tyrosine phosphatase, non-receptor type 3	1.45615
STYX	serine/threonine/tyrosine interacting protein	1.45615
NAA25	N(alpha)-acetyltransferase 25, NatB auxiliary subunit	1.45615
GALE	UDP-galactose-4-epimerase	1.45615
PAXBP1	PAX3 and PAX7 binding protein 1	1.45615
PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	1.45615
NHP2	NHP2 ribonucleoprotein	1.45615
GJC1	gap junction protein, gamma 1, 45kDa	1.45615
FUZ	fuzzy planar cell polarity protein	1.45615
KCTD15	potassium channel tetramerization domain containing 15	1.26663
DTX1	deltex 1, E3 ubiquitin ligase	1.26663
MAP3K3	mitogen-activated protein kinase kinase kinase 3	1.26663
SIM2	single-minded family bHLH transcription factor 2	1.26663
EPHB2	EPH receptor B2	1.26663
CHRM1	cholinergic receptor, muscarinic 1	1.26663
PRPF38A	pre-mRNA processing factor 38A	1.26663
ECE1	endothelin converting enzyme 1	1.26663
CALCOCO2	calcium binding and coiled-coil domain 2	1.26663

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Figure S4. Exogenous expression of hsa_circ_000022 significantly reduced the colony-forming ability of the SNU449 and HepG2 cells.

