Supplementary Results

Supplementary Table S1. Interfering sequences against MALAT1 and DBC1.

Name	Sequence (5’-3’)
shMALAT1-1	CACCGAAGGCTTAAAGTAG
shMALAT1-2	CAAAGTCAGATCAGTTATG
Scramble sequence	TCCTAAGGTTAAGTCGCCCTC
shDBC1-1	CCCATCTGTGACTTCCTAGAA
siMALAT1_1	CACAGGGAAAGCGAGTGGTTGGTAA
siMALAT1_2	GAG GTGTAAAGGGATTTAT

Supplementary Table S2. Sequences of the DNA primers for DBC1 and its fragments cloning.

Name	Sequence (5’-3’)
DBC_ N1	Forward: CCGGAATTCTCCCAGTTTAAGCGCCAGC Reverse: CCGCTCGAGTAGCCAACTCAGATGCACGGAC
DBC_ N2	Forward: CCGGAATTCTCCCAGTTTAAGCGCCAGC Reverse: CCGCTCGAGGGGCTGGTTGGAGAGCG
DBC_ N3	Forward: CCGGAATTCCAGCGGGTCTTCACTGGTATTG Reverse: CCGCTCGAGGGGCTGGTTGGAGAGCG
DBC_ N4	Forward: CCGGAATTCCCCCTACTGAAGTCCCCAGC Reverse: CCGCTCGAGCCGGCTTGGATGATGGAG
DBC_ C1	Forward: CCGGAATTCCGGATCCAGGTCTCTTCTGAAAAG Reverse: CCGCTCGAGGTTGCTAGGTGCCGGCTCC
Full-length DBC1	Forward: CCGGAATTCGCCACCATGTCCCAGTTTAAGCGCCAG Reverse: AAATATGCGGCCGCGTTGCTAGGTGCCGGCTCC

Supplementary Table S3. Sequences of the DNA primers for qRT-PCR.

Name	Sequence (5’-3’)
MALAT1	Forward: CTCCCCACAAGCAACTTCTC Reverse: TTCAACCCACCAAAGACCTC
NEAT1	Forward:GGCAGGTCTAGTTTGGGCAT Reverse: CCTCATCCCTCCCAGTACCA
DBC1	Forward: TCCAAGAAACGCAAACAGCG Reverse: TAGCCAACTCAGATGCACGG
DBC1-N1	Forward: GCACCTCCTCTTCTGCATGT Reverse: CGCTGTTTGCGTTTCTTGGA
DBC1-N2	Forward: AGCTAAGTGTGGTGAAGGGC Reverse: GAGCGTTTGCACCTTGACAG
DBC1-N3	Forward: AGCTAAGTGTGGTGAAGGGC Reverse: GAGCGTTTGCACCTTGACAG
DBC1-N4	Forward: GCACCTCCTCTTCTGCATGT Reverse: CGCTGTTTGCGTTTCTTGGA
DBC1-C1	Forward: ATCGGAGGCCAAAGGAAAGG Reverse: AAAGCCCATCCTCCTTCAGC
p21	Forward: GGAGACTCTCAGGGTCGAAA Reverse: TTAGGGCTTCCTCTTGGAGA
Bax	Forward: TTGGGACGGCCTCCTCTC Reverse: GCCTCAGCCCATCTTCTTCC
Puma	Forward: GGGCCCAGACTGTGAATCCT Reverse: ACGTGCTCTCTCTAAACCTATGCA

Stat3	Forward: GAGCTGCACCTGATCACCTT Reverse: GGAGATCACCACAACTGGCA
Cyclin D1	Forward: CAGATCATCCGCAAACACGC Reverse: AAGTTGTTGGGGCTCCTCAG
Cyclin E	Forward: ACAGATTGCAGAGCTGTTGG Reverse: AAGGCCGAAGCAGCAAGTAT
18S rRNA	Forward: GCTTAATTTGACTCAACACGGGA Reverse: AGCTATCAATCTGTCAATCCTGTC
FLNA	Forward:TCACCTATACCCCCATGGCA Reverse: GTGGCCTTGGTCAGAGAGTC
LDHB	Forward: TCCGCACGACTGTTACAGAG Reverse: TTGCCTCTTCTTCCGCAACT

Supplementary Table S4. Sequences for in vitro transcription of sense and antisense MALAT1.

Name	Sequence (5’-3’)
sense chain	Forward: taatacgactcactatagggATGCAAGAAACATTCCAAACAAGCAACAG Reverse: AAATATACCGGTCCTGAAGACAGATTAGTAGTCAAAGCA
antisense chain	Forward: taatacgactcactataggg CCTGAAGACAGATTAGTAGTCAAAGCA Reverse: AAATATACCGGTATGCAAGAAACATTCCAAACAAGCAACAG

Supplementary Table 5. List of potential MALAT1 interacting proteins identified by SILAC quantitative proteomics.

Accession #	**Description**	**Coverage (%)**	**Unique Peptides**	**Average ratio$_{c/M}$**	**s.d.**
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	45.2	49	0.41	0.12
P51991	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 - [ROA3_HUMAN]	36.16	26	0.17	0.12
P38159	RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3 - [RBMX_HUMAN]	22.1	24	0.43	0.17
A0AV96	RNA-binding protein 47 OS=Homo sapiens GN=RBM47 PE=1 SV=2 - [RBM47_HUMAN]	20.72	23	0.01	0.00
P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	46.47	22	0.50	0.17
P00966	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN]	17.94	21	0.34	0.05
P82650	28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=1 SV=1 - [RT22_HUMAN]	25.27	21	0.13	0.02
P28288	ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=1 SV=1 - [ABCD3_HUMAN]	19.45	19	0.32	0.11
Q12906	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3 - [ILF3_HUMAN]	7.79	18	0.50	0.03
Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 - [MTCH2_HUMAN]	28.97	18	0.15	0.18
O43427	Acidic fibroblast growth factor intracellular-binding protein OS=Homo sapiens GN=FIBP PE=1 SV=3 - [FIBP_HUMAN]	51.28	17	0.23	0.03
P05166	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	51.28	17	0.32	0.09
O43390	Heterogeneous nuclear ribonucleoprotein R	35.62	15	0.63	0.05

	OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]				
Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2 PE=1 SV=2 - [IF2B2_HUMAN]	23.92	15	0.01	0.00
P11413	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN]	34.91	14	0.03	0.03
P24928	DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2 - [RPB1_HUMAN]	31.76	14	0.20	0.01
Q13867	Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1 - [BLMH_HUMAN]	15.56	14	0.01	0.00
Q9Y285	Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3 - [SYFA_HUMAN]	32.84	14	0.06	0.09
P43686	26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 - [PRS6B_HUMAN]	15.27	13	0.48	0.01
Q9NZB2	Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 - [F120A_HUMAN]	44.44	13	0.41	0.11
Q15393	Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN]	29.25	12	0.01	0.00
Q15428	Splicing factor 3A subunit 2 OS=Homo sapiens GN=SF3A2 PE=1 SV=2 - [SF3A2_HUMAN]	14.63	12	0.22	0.12
Q96QR8	Transcriptional activator protein Pur-beta OS=Homo sapiens GN=PURB PE=1 SV=3 - [PURB_HUMAN]	55.52	12	0.11	0.01
Q13501	Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 - [SQSTM_HUMAN]	28.64	11	0.30	0.20
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	16.84	11	0.22	0.08
Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	38.53	11	0.01	0.00
Q9Y2X3	Nucleolar protein 58 OS=Homo sapiens	26.32	11	0.34	0.06

	GN=NOP58 PE=1 SV=1 - [NOP58_HUMAN]				
P10155	60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=1 SV=2 - [RO60_HUMAN]	14.84	10	0.07	0.12
P52597	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 - [HNRPF_HUMAN]	30	10	0.44	0.08
Q9H5Q4	Dimethyladenosine transferase 2, mitochondrial OS=Homo sapiens GN=TFB2M PE=1 SV=1 - [TFB2M_HUMAN]	26.55	10	0.39	0.11
P0CG48	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]	11.64	9	0.12	0.02
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [PTBP1_HUMAN]	17.22	9	0.29	0.03
Q15717	ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=1 SV=2 - [ELAV1_HUMAN]	25.08	9	0.50	0.19
Q16629	Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=1 SV=1 - [SRSF7_HUMAN]	15.22	9	0.01	0.00
Q8TDD1	ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2 - [DDX54_HUMAN]	19.26	9	0.35	0.15
P82933	28S ribosomal protein S9, mitochondrial OS=Homo sapiens GN=MRPS9 PE=1 SV=2 - [RT09_HUMAN]	26.6	8	0.18	0.09
Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	10.74	8	0.45	0.06
Q15459	Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1 - [SF3A1_HUMAN]	35.14	8	0.13	0.10
Q9H0J9	Poly [ADP-ribose] polymerase 12 OS=Homo sapiens GN=PARP12 PE=1 SV=1 - [PAR12_HUMAN]	10.98	8	0.49	0.00
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	15.8	7	0.01	0.00
Q01081	Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3 - [U2AF1_HUMAN]	13.98	7	0.08	0.06

Q04760	Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4 - [LGUL_HUMAN]	24.58	7	0.02	0.01
Q96I24	Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2 - [FUBP3_HUMAN]	18.03	7	0.09	0.01
Q9BUQ8	Probable ATP-dependent RNA helicase DDX23 OS=Homo sapiens GN=DDX23 PE=1 SV=3 - [DDX23_HUMAN]	17.56	7	0.14	0.01
Q9C0J8	pre-mRNA 3' end processing protein WDR33 OS=Homo sapiens GN=WDR33 PE=1 SV=2 - [WDR33_HUMAN]	18.41	7	0.02	0.02
O75400	Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2 - [PR40A_HUMAN]	26.07	6	0.01	0.00
O75533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	17.17	6	0.42	0.03
P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	17.34	6	0.37	0.19
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4 - [HNRPC_HUMAN]	10.9	6	0.24	0.02
P10599	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 - [THIO_HUMAN]	34.22	6	0.25	0.19
P17980	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3 - [PRS6A_HUMAN]	11.51	6	0.34	0.09
P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1 PE=1 SV=3 - [NDUS1_HUMAN]	21.43	6	0.20	0.15
P55265	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSRAD_HUMAN]	38.03	6	0.01	0.00
P82673	28S ribosomal protein S35, mitochondrial OS=Homo sapiens GN=MRPS35 PE=1 SV=1 - [RT35_HUMAN]	12.56	6	0.37	0.04
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1 - [KHDR1_HUMAN]	23.53	6	0.33	0.12
Q13151	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 - [ROA0_HUMAN]	25.6	6	0.13	0.16

Q15738	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Homo sapiens GN=NSDHL PE=1 SV=2 - [NSDHL_HUMAN]	17.84	6	0.21	0.08
Q96SI9	Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1 - [STRBP_HUMAN]	19.76	6	0.01	0.00
Q9BRZ2	E3 ubiquitin-protein ligase TRIM56 OS=Homo sapiens GN=TRIM56 PE=1 SV=3 - [TRI56_HUMAN]	35.41	6	0.42	0.12
Q9NY93	Probable ATP-dependent RNA helicase DDX56 OS=Homo sapiens GN=DDX56 PE=1 SV=1 - [DDX56_HUMAN]	46.83	6	0.44	0.07
Q9Y2T2	AP-3 complex subunit mu-1 OS=Homo sapiens GN=AP3M1 PE=1 SV=1 - [AP3M1_HUMAN]	10.29	6	0.15	0.18
A6NMY6	Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2 - [AXA2L_HUMAN]	17.94	5	0.15	0.10
O76031	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial OS=Homo sapiens GN=CLPX PE=1 SV=2 - [CLPX_HUMAN]	58.1	5	0.31	0.05
O95433	Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=1 SV=1 - [AHSA1_HUMAN]	6.07	5	0.15	0.06
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	14.75	5	0.50	0.14
Q10570	Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens GN=CPSF1 PE=1 SV=2 - [CPSF1_HUMAN]	18.23	5	0.16	0.03
Q14498	RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2 - [RBM39_HUMAN]	15.03	5	0.15	0.16
Q96DV4	39S ribosomal protein L38, mitochondrial OS=Homo sapiens GN=MRPL38 PE=1 SV=2 - [RM38_HUMAN]	4.88	5	0.01	0.00
Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3 - [H2A1H_HUMAN]	9.09	5	0.35	0.16
Q9NSD9	Phenylalanine--tRNA ligase beta subunit	11.09	5	0.40	0.09

	OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN]				
O94906	Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1 - [PRP6_HUMAN]	10.62	4	0.35	0.03
O95793	Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2 - [STAU1_HUMAN]	3.47	4	0.09	0.01
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]	3.47	4	0.41	0.19
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	27.78	4	0.02	0.02
P26368	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4 - [U2AF2_HUMAN]	15.83	4	0.01	0.00
P33993	DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4 - [MCM7_HUMAN]	17.7	4	0.46	0.14
P43243	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2 - [MATR3_HUMAN]	10.62	4	0.35	0.12
Q12874	Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=1 SV=1 - [SF3A3_HUMAN]	5.42	4	0.35	0.20
Q12905	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2 - [ILF2_HUMAN]	9.69	4	0.46	0.11
Q6UN15	Pre-mRNA 3'-end-processing factor FIP1 OS=Homo sapiens GN=FIP1L1 PE=1 SV=1 - [FIP1_HUMAN]	12.61	4	0.24	0.03
Q8IWZ3	Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 PE=1 SV=1 - [ANKH1_HUMAN]	17.7	4	0.01	0.00
Q92552	28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=1 SV=3 - [RT27_HUMAN]	6.19	4	0.12	0.01
Q9BVI4	Nucleolar complex protein 4 homolog OS=Homo sapiens GN=NOC4L PE=1 SV=1 - [NOC4L_HUMAN]	5.42	4	0.44	0.13
Q9H0D6	5'-3' exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=1 SV=1 - [XRN2_HUMAN]	27.78	4	0.28	0.13

Q9P2I0	Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens GN=CPSF2 PE=1 SV=2 - [CPSF2_HUMAN]	8.86	4	0.01	0.00
Q9Y2P8	RNA 3'-terminal phosphate cyclase-like protein OS=Homo sapiens GN=RCL1 PE=1 SV=3 - [RCL1_HUMAN]	15.83	4	0.24	0.00
O60814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	16.86	3	0.01	0.00
O95400	CD2 antigen cytoplasmic tail-binding protein 2 OS=Homo sapiens GN=CD2BP2 PE=1 SV=1 - [CD2B2_HUMAN]	22.58	3	0.25	0.08
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	11.98	3	0.01	0.00
P31943	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 - [HNRH1_HUMAN]	12.81	3	0.45	0.01
P46777	60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 - [RL5_HUMAN]	1.59	3	0.01	0.00
P51398	28S ribosomal protein S29, mitochondrial OS=Homo sapiens GN=DAP3 PE=1 SV=1 - [RT29_HUMAN]	1.59	3	0.32	0.19
P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 - [HNRPM_HUMAN]	16.86	3	0.50	0.18
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3 - [GBLP_HUMAN]	6.4	3	0.42	0.14
Q08188	Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4 - [TGM3_HUMAN]	16.86	3	0.42	0.12
Q5JTH9	RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 - [RRP12_HUMAN]	8.79	3	0.25	0.07
Q5U7I5	Transthyretin OS=Pan troglodytes GN=TTR PE=2 SV=1 - [TTHY_PANTR]	44.67	3	0.44	0.08
Q8N163	Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2 - [CCAR2_HUMAN]	3.66	3	0.08	0.11
Q92621	Nuclear pore complex protein Nup205	4.22	3	0.01	0.00

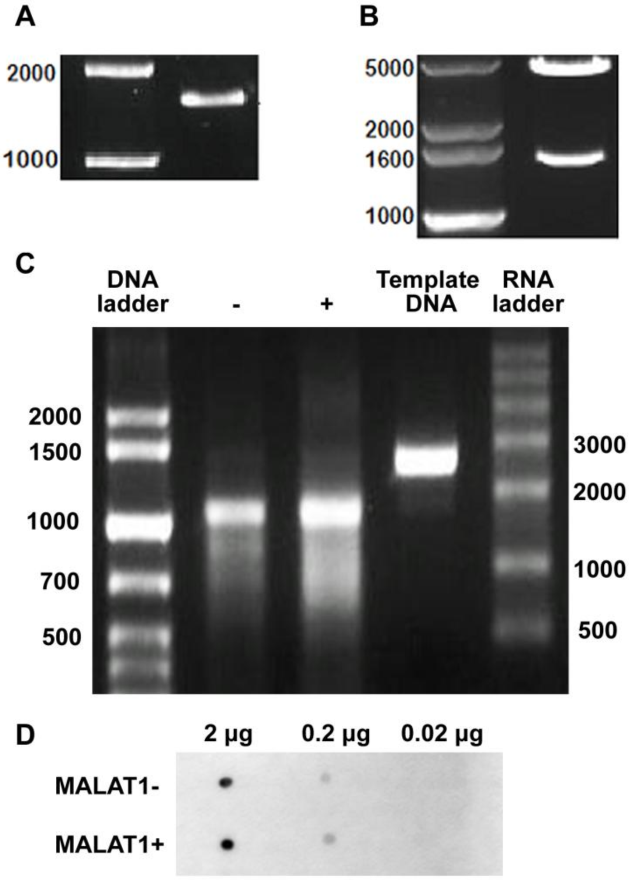
	OS=Homo sapiens GN=NUP205 PE=1 SV=3 - [NU205_HUMAN]				
Q96EY7	Pentatricopeptide repeat domain-containing protein 3, mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=3 - [PTCD3_HUMAN]	6.84	3	0.30	0.01
Q96KR1	Zinc finger RNA-binding protein OS=Homo sapiens GN=ZFR PE=1 SV=2 - [ZFR_HUMAN]	6.57	3	0.16	0.09
Q96P63	Serpin B12 OS=Homo sapiens GN=SERPINB12 PE=1 SV=1 - [SPB12_HUMAN]	3.34	3	0.01	0.00
Q99729	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=1 SV=2 - [ROAA_HUMAN]	7.8	3	0.33	0.19
Q9H0U9	Testis-specific Y-encoded-like protein 1 OS=Homo sapiens GN=TSPYL1 PE=1 SV=3 - [TSYL1_HUMAN]	4.35	3	0.41	0.10
Q9Y4W2	Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 - [LAS1L_HUMAN]	6.57	3	0.09	0.04
Q9Y678	Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 - [COPG1_HUMAN]	27.34	3	0.24	0.20
O00442	RNA 3'-terminal phosphate cyclase OS=Homo sapiens GN=RTCA PE=1 SV=1 - [RTCA_HUMAN]	6.59	2	0.01	0.00
O00635	E3 ubiquitin-protein ligase TRIM38 OS=Homo sapiens GN=TRIM38 PE=1 SV=1 - [TRI38_HUMAN]	7.1	2	0.05	0.04
O60832	H/ACA ribonucleoprotein complex subunit 4 OS=Homo sapiens GN=DKC1 PE=1 SV=3 - [DKC1_HUMAN]	6.83	2	0.01	0.00
P02765	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1 - [FETUA_HUMAN]	3.88	2	0.15	0.17
P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6 - [TRFL_HUMAN]	2.13	2	0.01	0.00
P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	4.29	2	0.33	0.08
P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	9.52	2	0.44	0.13

	OS=Homo sapiens GN=DBT PE=1 SV=3 - [ODB2_HUMAN]				
P13804	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 - [ETFA_HUMAN]	3.54	2	0.12	0.04
P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 - [CAN2_HUMAN]	18.48	2	0.04	0.02
P19387	DNA-directed RNA polymerase II subunit RPB3 OS=Homo sapiens GN=POLR2C PE=1 SV=2 - [RPB3_HUMAN]	10.11	2	0.39	0.14
P31944	Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2 - [CASPE_HUMAN]	3.17	2	0.41	0.06
P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]	6.83	2	0.44	0.08
P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	1.57	2	0.07	0.01
P62195	26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1 - [PRS8_HUMAN]	2.78	2	0.40	0.13
P62995	Transformer-2 protein homolog beta OS=Homo sapiens GN=TRA2B PE=1 SV=1 - [TRA2B_HUMAN]	3.37	2	0.01	0.00
Q00577	Transcriptional activator protein Pur-alpha OS=Homo sapiens GN=PURA PE=1 SV=2 - [PURA_HUMAN]	6.83	2	0.15	0.07
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	7.29	2	0.30	0.08
Q8N1F7	Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 - [NUP93_HUMAN]	2.96	2	0.03	0.03
Q8WVV4	Protein POF1B OS=Homo sapiens GN=POF1B PE=1 SV=3 - [POF1B_HUMAN]	0.28	2	0.35	0.05
Q96RQ3	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=3 - [MCCA_HUMAN]	3.31	2	0.01	0.00
Q9BZE1	39S ribosomal protein L37, mitochondrial	3.57	2	0.39	0.10

	OS=Homo sapiens GN=MRPL37 PE=1 SV=2 - [RM37_HUMAN]

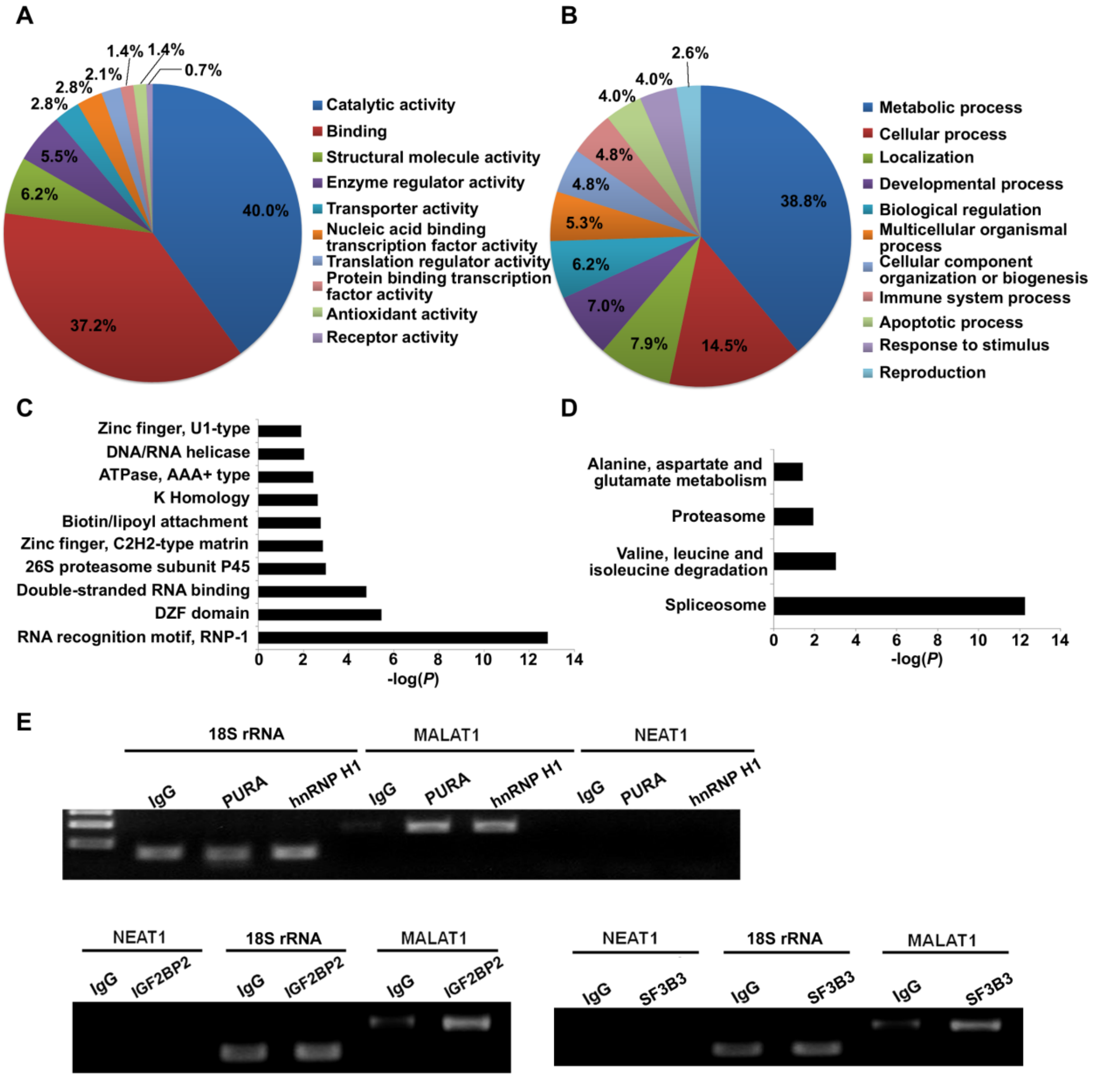
The protein sequence information was obtained from the Uniprot Database.

Supplementary Figure S1.



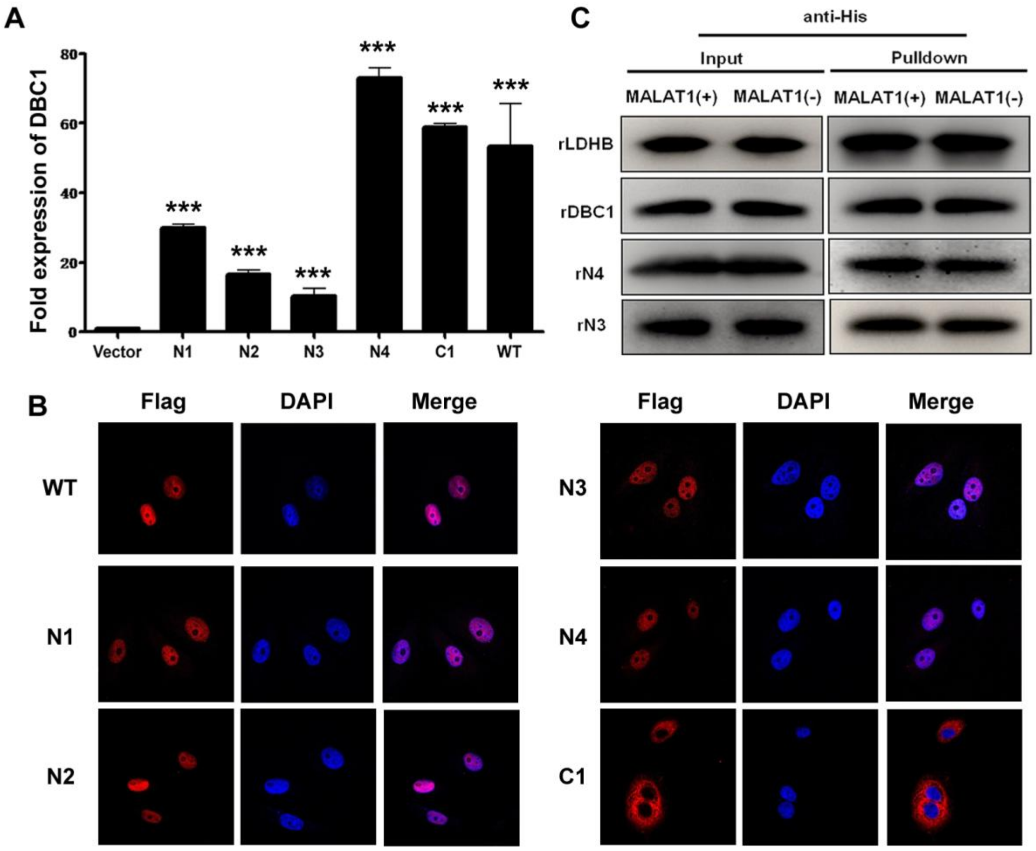
Supplementary Figure S1. *In vitro* transcription of the sense and antisense MALAT1. (**A**) The fragment 6918-8441 nt of MALAT1 gene was amplified by PCR. (**B**) Enzymatic restriction analysis confirmed that the fragment 6918-8441 nt of MALAT1 was inserted into the pcDNA3.1(+) vector correctly. (**C**) Agarose gel electrophoresis separation of the in vitro transcribed sense and antisense MALAT1. The bands of MALAT1 and its DNA template were visualized with EB staining. (**D**) Biotin-HRP dot blot analysis of the sense and antisense MALAT1.

Supplementary Figure S2.



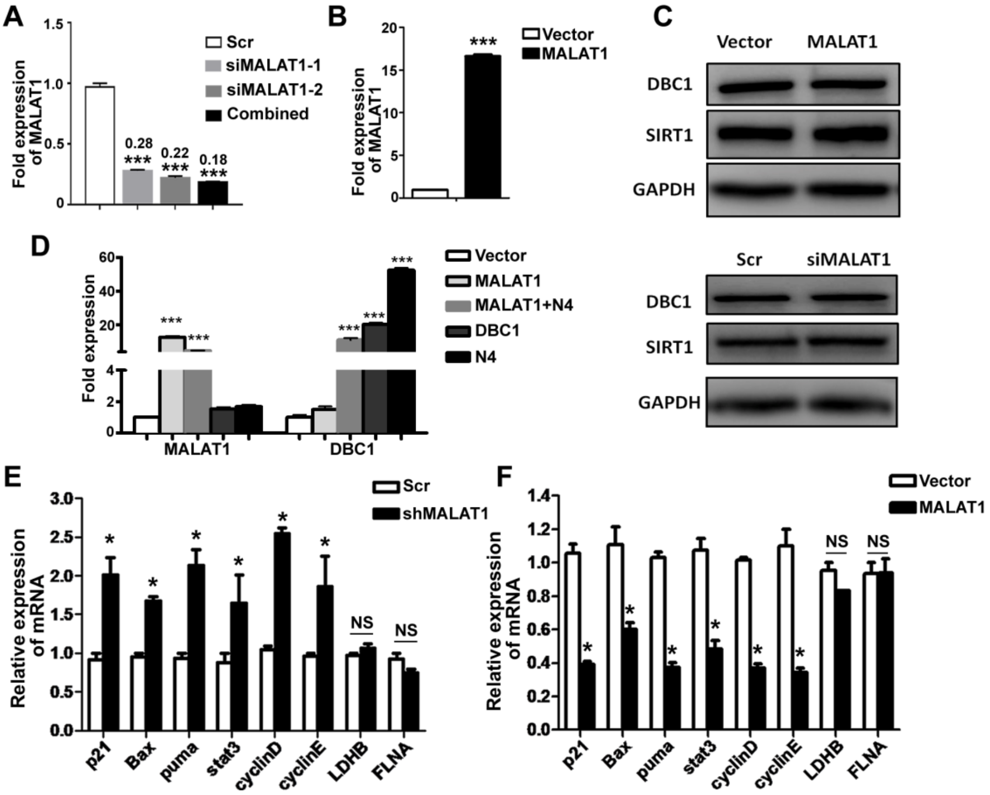
Supplemental Figure S2. Gene ontology analysis of the identified MALAT1-interacting proteins and the validation using RNA immunoprecipitation (RIP). (**A**) Diagram showing the molecular functions of the identified MALAT1-interacting proteins. (**B**) Diagram showing the related biological processes of the identified MALAT1-interacting proteins. The annotation information was acquired through the Panther database (http://www.pantherdb.org). Bar graphs present the *P* values of the enriched protein domains (**C**) and signaling pathways (**D**). The protein domain and pathway analyses were performed using DAVID (https://david.ncifcrf.gov/). (**E**) Agarose gel electrophoresis analysis of the qRT-PCR products of MALAT1, 18S rRNA and NEAT1 in the immunoprecipitates of the selected proteins. IgG was used as negative control.

Supplementary Figure S3



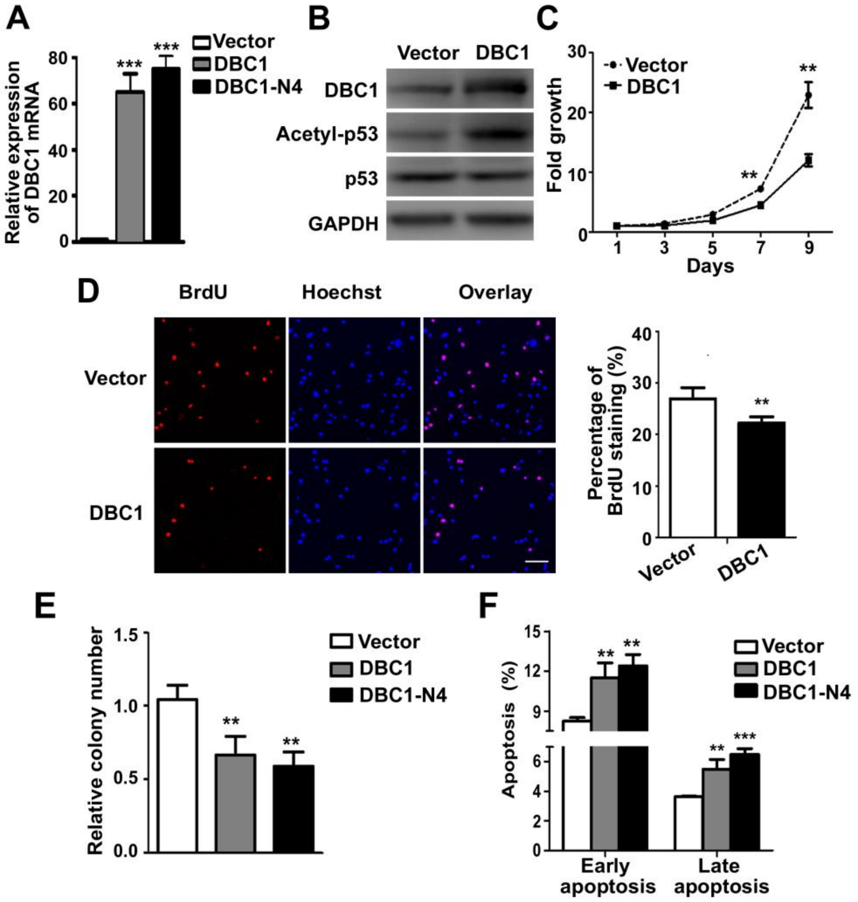
Supplementary Figure S3. Expression and localization of the DBC1 fragment constructs in the HepG2 cells. (**A**) qRT-PCR analysis of the mRNA levels of different DBC1 constructs. Data represent the means ±SD of triplicate independent analyses (***$P < 0.001$, by student's *t*-test). (**B**) Immunofluoresence analysis of the subcellular localization of DBC1 fragments. HepG2 cells transfected with Flag-tagged DBC1 fragments or full-length DBC1 constructs were stained for Flag (red). Cell nuclei were stained with DAPI (blue). Cells were visualized with confocal laser scanning microscopy. (**C**) Western blots of the purified proteins in the input and pulldown samples for the *in vitro* His-tag pulldown assay.

Supplementary Figure S4



Supplementary Figure S4. (**A**) The efficiencies of MALAT1 knockdown using two siRNAs were examined by qRT-PCR. Data represent the means ± SD of triplicate independent analyses (****P* < 0.001, by student's *t*-test). (**B**) The efficiency of MALAT1 overexpression was examined by qRT-PCR. Data represent means ± SD of triplicate independent analyses (****P* < 0.001 , by student's *t*-test). (**C**) Western blot analysis of DBC1 and SIRT1 in HepG2 cells with MALAT1 overexpression or knockdown. GAPDH was used as internal standard. (**D**) qRT-PCR analysis of the MALAT1, DBC1, and DBC1-N4 mRNA levels in the rescue experiments. Data represent the means ± SD of triplicate independent analyses (****P* < 0.001, by one-way ANOVA). The mRNA levels of p53 target genes, lactate dehydrogenase B (LDHB), and filamin A (FLNA) in the HepG2 cells with MALAT1 overexpression (**E**) and knockdown (**F**) were examined using qRT-PCR analysis. Data represent the means ± SD of triplicate independent analyses (**P* < 0.05; NS, not significant; by student's *t*-test).

Supplementary Figure S5



Supplementary Figure S5. DBC1 and DBC1-N4 inhibit cell proliferation and promote apoptosis. (**A**) The overexpression of DBC1 and DBC1-N4 was examined by qRT-PCR. Data represent the means ± SD of triplicate independent analyses (****P* < 0.001, by student's *t*-test). (B) Western blot analysis indicates that DBC1 overexpression increases p53 acetylation. GAPDH expression was used as a control. (C) Growth curve assay using DBC1-overexpressing HepG2 cells. Data represent the means ± SD of triplicate independent analyses (***P* < 0.01, by repeated measures ANVOA). (D) BrdU incorporation analysis using DBC1-overexpressing HepG2 cells. Histogram shows the means ± SD from two independent experiments (***P* < 0.01, by student's *t*-test). (E) Colony-formation assay was performed to study the proliferation of HepG2 cells overexpressing full-length DBC1 or DBC1-N4, and their corresponding control cells. Data represent the means ± SD of two independent analyses (***P* < 0.01, by one-way ANOVA). (F) Apoptosis analysis of HepG2 cells overexpressing full length DBC1 or DBC1-N4. Apoptotic cells were detected by Annexin V/PI staining assay and examined by flow cytometry. Data represent the means ± SD of triplicate independent analyses (***P* < 0.01, ****P* < 0.001, by one-way ANOVA).