Supplementary information for

DDX49 is an RNA helicase that affects translation by regulating mRNA export and the levels of pre-ribosomal RNA

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			10S	20L	30L	40R	50S		
DDX49/1-483	1	MAGFAELGL	SSWL VE	EQCROLGLKO	труоцяст	PAILEGROCLO	GCAKTGSGKTAAF	VLPIL 60	C
DDX47/1-455	1	MAAFKDLG	/ T D V L C E	ACDQL <mark>G</mark> WTK	TKIQIEAI	PLALQGRDIIC	GL <mark>AETG</mark> S <mark>GKT</mark> GAF.	ALPIL 82	2
DDX23/1-820	1	MAGWKDSSL	PPHILE	EVIDKC <mark>GYKE</mark>	PTPIQRQAI	PIGLONRDIIC	G V A E T G S G K T A A F	LIPLL 44	19
DDX27/1-796	1	MVLFQDMNL	SRPLLK	(AITAMGFKQ)	PTPIQKACI	PVGLLGKDIC	AC AATGTGKTAAF.	ALPVL 27	76
DD19A/1-478	1	MATEELRL	. KPOLLC	QG V Y AMG FNR	SKIQENAL	PMML APQNL I	AQSQSGTGKTAAF	VLAML 15	51
DD19B/1-4/9	1	MATELLAL	KPQLLC		SKIQENAL	PLML APQNLI	AQSQSGIGKTAAF	VLAML 15	52
DDX25/1-483	1	MASPEELKL	KEELLK		SKIQEMAL		AQSQSGIGKTAAF		57 54
DDX0/1-403	1	MATEDTAGI			SALOOBAL	KOLLKGBDVL	AOSOSGIGKTATE		34
DDX2B/1-407	1	MSGEDDMNI	KESLIB	GIYAYGEEKI	SALOORAL	IPCIKGYDVI	AQ AQ SG TGKTATE		1
DDX2A/1-406	1	MS - FDDMNL	SESLLR	GIYAYGFEK	SALQQRAI	LPCIKGYDVI	AQAQSGTGKTATE	AISIL 90)
DX39B/1-428	1	MAEFRDFLL	KPELLE	AIVDCGFEHF	SEVQHECI	PQAILGMDVLC	CQAKSGMGKTAVF	VLATL 10)3
DX39A/1-427	1	MAEFRDFLL	KPELLR	≀AIVDC <mark>GFE</mark> HF	SEVQHECI	PQAILGMDVLO	CQ <mark>A</mark> KS <mark>G</mark> M <mark>GKT</mark> AVF	VLATL 10)2
DDX20/1-824	1	MAAFESLLL	SRPVLE	EG L R A A <mark>G F E</mark> R <mark>F</mark>	PSPVQLKAI	PLGRCGLDLI	VQ A K S G T G K T C V F	STIAL 12	20
DDX59/1-619	1	MFVFEHCSL	PEVLNH	INLKKSGYEV	PTPIQMQMI	PVGLLGRDIL	ASADTGSGKTAAF	LLPVI 26	51
DDX3Y/1-660	1	MSHFSDIDA	IGELIMG	IN LELTRYTR	PTPVQKHAI	PIIKGKRDLM	ACAQTGSGKTAAF	LLPIL 23	36
DDX3X/1-662	1	MSHESDVEN			TRVOKHAL		AC AQIGSGKTAAF		16
DDX4/1-724 DDX46/1-1031	1		SMKILN				AC AQTOSOKTAAF	LLPIL 34	+0 20
DDX40/1-1031	1	MNWFAHEGE		OLBKSEYTO	TPLOCOGV	PVAL SGRDMIC	GLAKTGSGKTAAF		11
DDX17/1-729	1	MPTEHHANE	POYVMD		TPIOCOGE	PLALSGRDMV	GLAQTGSGKTLAY	LLPAI 22	29
DDX5/1-614	1	MSGFYEANF	PANVMD	VIARQNFTE	TAIQAQGW	PVALSGLDMV	AQTGSGKTLSY	LLPAI 15	52
DDX43/1-648	1	MSHFDDAQC	YPEVME	EN I KKA <mark>GFOK</mark>	PTPIQ SQAW	PIVLOGIDLIC	A V A Q T G T G K T L C Y	LM <mark>P</mark> GF 30	00
DDX53/1-631	1	MSHFKDAQC	YPDLLK	(SIIRV <mark>G</mark> IVK	PTPIQ SQAW	PIILOGIDLIV	V V A Q T G T G K T L S Y	LMPGF 28	30
DDX41/1-622	1	MEEFKEMKF	PAAILE	IGLKKK <mark>G</mark> IHH	PTPIQIQGI	PTILSGRDMIC	AFTGSGKTLVF	TLPVI 23	39
DDX54/1-881	1	MAAFQSMGL	SYPVER	GIMKKGYKV	PTPIQRKTI	PVILDGKDVV/	AMARTGSGKTACE	LLPMF 15	54
DDX56/1-54/	1			AVIDLGWSRI			ARARIGSGKIAAY.		2
DDX52/1-599	1		SEETIK				ADTOTOKTESE		23 17
DDX50/1-737	1	MPGESNE - I	SEETIK		FPIOVKTE	GPVYFGKDLL	AQABTGTGKTESE	AIPLI 19	75
DDX24/1-859	1	MKLWKDL - F	VPRVLB	ALSFLGFSA	TPIQALTL	APAIRKLDILO	BAAETGSGKTLAF	AIPMI 25	51
DDX28/1-540	1	MALFADLGL	EPRVLH	IALQEAAPEQ	TTVQSSTI	PSLLRGRHVVC	CAAETGSGKTLSY	LLPLL 18	36
DDX31/1-851	1	MAPFHELGL	HPHLIS	STINTVLKMSN	M T S V <mark>Q</mark> K Q S I	PVLLEGRDAL	VR SQ TG SG KT L A Y	CIPVV 28	39
DDX51/1-666	1	MALIEDID	/HPDLQK	(QLRAH <mark>G</mark> ISS)	(FPVQAAVI	PALLEPSDLCV	/ S A P T G S G K T L A F	VIPVV 27	70
DDX10/1-875	1	MGKFSDF-L	SKKTLK	GLQEAQYRL	TEIQKQTI	G L A L Q G K D V L C	GAAKTGSGKTLAF	LVPVL 12	27
DDX55/1-600	1	M WESL-L		ALRELGERYN	ATPVQSATI		AEAVIGSGKILAF	VIPIL 67	7
DDX10/1-0/0	1						KESKNCKDLGLAF		20
BBXIII 140	'			arbiti <mark>ar</mark> gai					_0
							GYCKT		
							GXGKT		
			700	00 B	005	1001/	GXGKT		
			70G	80R	90F	100K	110M		
DDX49/1-483	61	LQKLSEDP	70G YGIFCL	80R VLT <mark>PTRELA</mark> Y	90F QIAEQFRVL	100K .G <mark>K</mark> PLGL KDC I	110M I VGGMDMVAQALE	LSRK 12	0
DDX49/1-483 DDX47/1-455	61 83	LOKL SED P LNALLETP	70G YGIFCL QRLFAL	80R VLT <mark>PTRELA</mark> Y VLTPTRELAF	90F I A EQ FR V L Q I S EQ F E A L	100K I I I I I I I I I I I I I I I I I I	110M I VGGMDMVAQALE I VGGIDSMSQSLA	LSRK 12 LAKK 14	0
DDX49/1-483 DDX47/1-455 DDX23/1-820	61 83 450	LOKLSEDP LNALLETP LDRIEESD	70G YGIFCL QRLFAL QGPYAI	80R VLTPTRELAY VLTPTRELAF ILAPTRELAQ	90F I Q I A EQ FR V L Q I S EQ F E A L Q I E E E T I K F	100K GKPLGLKDCI GSSIGVQSAV GKPLGIRTVA	110M I VGGMD WAQALE I VGGID SMSQSLA VIGGI SREDQGFR	LSRK 12 LAKK 14 LRMG 51	028
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD100/14770	61 83 450 277	LOKLSEDP LNALLETP LDRIESD LERLIYKP	70G YGIFCL QRLFAL QGPYAI RGTRVL	80R VLTPTRELAY VLTPTRELAF ILAPTRELAQ VLVPTRELGI	90F I A EQ FR VL Q I S EQ F E A L Q I E E E T I K F Q V H S V T RQ L	100K GKPLGLKDCI GSSIGVQSAV GKPLGIRTVA AQFCNITTCL	110M I VGG MD WAQALE I VGG I D SMSQSLA VI GG I SR EDQG FR A VGGLD VKSQEAA	LSRK 12 LAKK 14 LRMG 51 LRAA 31	02891
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD19A/1-478 DD198/1-478	61 83 450 277 152	LOKLSEDP LNALLETP LDRIEESD LERLIYKP LSRVEPSD	70G QRLFAL QRLFAL QGPYAI RQTRVL RQTRVL RYPQCL	80R VLTPTRELAY VLTPTRELAG ILAPTRELAG VLVPTRELGI CLSPTYELAL	90F QIAEQFRVL QISEQFEAL QIEETIKF QVHSVTRQL QTGKVIEQM	100K GKPLGLKDCI GSSIGVQSAV GKPLGIRTVA AQFCNITTCL IGKFYELKLAY	110M I VGG MD W AQ A L E I VGG I D SMSQS L A VI GG I SR EDQG FR AVGG LD VKSQE AA AVGG LD VKSQE AA AVGO KL ERGQK I	L SR K 12 L AKK 14 L RMG 51 L R A A 33 SEQ - 21	028912
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD19A/1-478 DD19B/1-479 DDX25/1-483	61 83 450 277 152 153 158	LQKLSEDP LNALLETP LDRIEESD LERLIYKP LSRVEPSD LSQVEPAN LSRVALF	70G YGIFCL QRLFAL QGPYAI RGTRVL RYPQCL KYPQCL LEPQCL	80R VLTPTRELAY VLTPTRELAF ILAPTRELAO VLVPTRELGI CLSPTYELAL CLSPTYELAL CLSPTYELAL	90F QIAEQFRVL QISEQFEAL QIEETIKF QVHSVTRQL QTGKVIEQM QTGKVIEQM QTGRVVFOM	100K GKPLGLKDCI GSSIGVQSAV GKPLGIRTVA AQFCNITTCL IGKFYELKLAY IGKFYELKLAY	110M I VGG MD V AQ A L E I VGG I D SMSQ S L A VIGG I SR EDQG FR AVGG L D VKSQ E AA AVR GN KL ERGQ K I AVR GN KL ERGQ K I A UR GN KL ERGQ T L	L SR K 12 L AKK 14 L RMG 51 L R A 33 SEQ - 21 SEQ - 21 SEQ - 21	0289127
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD19A/1-478 DD19B/1-479 DDX25/1-483 DDX6/1-483	61 83 450 277 152 153 158 155	UQKLSEDP UQXALLETP UDERLIYKP USRVEPSD USRVEPA USRVEPA USRVEPA USRVEPA USRVEPA USRVEPA USRVES USRVES USRVES USRVES USRVES USRVES USRVES USRVES USRVES USRVES USPVES	70G YGIFCL QRLFAL QGPYAI RQTRVL RYPQCL KYPQCL LFPQCL DNIQAM	80R VLTPTRELAY VLTPTRELAF ILAPTRELAQ VLVPTRELGI CLSPTYELAL CLSPTYELAL CLAPTYELAL VIVPTRELAL	90F QIAEQFEVL QISEQFEAL QIEETIKF QVHSVTRQL QTGKVIEQM QTGKVIEQM QTGRVVEQM QVSQICIQV	100K GKPLGLKDCI GSSIGVQSAV GKPLGIRTVA AQFCNITTCL IGKFYELKLAY IGKFYELKLAY IGKFYELKLAY IGKFYELKLAY	110M I VGG MD V AQALE I VGG I D SMSQSLA VIGG I SREDQGFR AVGG LD VKSQEAA AVGG N KLERGQKI AVRGN KLERGQKI AIRGNR I PRGTD I MTGG TN LRDD IMR	LSRK 12 LAKK 14 LRMG 51 LRAA 33 SEQ - 21 SEQ - 21 SEQ - 21 TKQ - 21 LDDT 21	02891275
DDX49/1-483 DDX47/1-455 DDX23/1-820 DD192/1-796 DD194/1-478 DD19B/1-479 DDX25/1-483 DDX6/1-483 DDX48/1-411	61 83 450 277 152 153 158 155 97	UNALLETP UNALLETP UNALLETP UNALLETP USRELISP USRELISP USRELL USRELD UCCUN UCCUN UCCUN UCCUN UCCUN	70G YGIFCL QRLFAL QRYAI RQTRVL RYPQCL KYPQCL LFPQCL DNIQAM RETQAL	80R VLTPTRELAY VLTPTRELAF ILAPTRELAQ VLVPTRELGI CLSPTYELAL CLSPTYELAL CLAPTYELAL VIVPTRELAV	90F I A EQ F F V L Q I S EQ F E A L Q I S EQ F E A L Q I S E E T I K F Q VH S V T R Q L Q T G K V I E Q M Q T G K V I E Q M Q T G K V I E Q M Q V S Q I C I Q V Q I Q K G L L A L	100K GKPLGLKDCI GSSIGVQSAV GKPLGIRTVA AQFCNITTCL IGKFYELKLAY IGKFYELKLAY IGKFCDVQVMY SKHMGAKVMA GDYMNVQCHA	110M I VGG MD VAQALE I VGG I D SMSQSLA VIGG I SREDQG FR AVGG LD VKSQEAA AVRGN KLERGQKI AVRGN KLERGQKI AIRGNR I PRGTD I M CIGG TN VGED I RK	L SR K 12 L AKK 14 L RMG 51 L RAA 33 SEQ - 21 SEQ - 21 SEQ - 21 T KQ - 21 L D YG 15	028912756
DDX49/1-483 DDX47/1-455 DDX23/1-820 DD194/1-478 DD194/1-479 DDX25/1-483 DDX46/1-481 DDX48/1-411 DDX48/1-411	61 83 450 277 152 153 158 155 97 92	LOKLSED VALLETP LORIESD LSRVEPAN LSRVEPAN LSRVALE LSRLDLKV LOCLSV LQLEI F	70G YGIFCL QRLFAL QGPYAI RQTRVL RYPQCL KYPQCL LFPQCL DNIQAM RETQAL KETQAL	80R VLTPTRELAY VLTPTRELAF ILAPTRELAQ VLVPTRELGI CLSPTYELAL CLSPTYELAL CLAPTYELAL VIVPTRELAV VLAPTRELAQ	90F 1 A EQ F R VL 0 I SEQ F EAL 1 E EET I K F 0 VH SV TR QL 0 TG K V I EQM 0 TG K V EQM 0 VSQ I C I QV 0 VSQ I C I QV 0 QKG LL AL 0 QK V I LAL	100K GKPLGLKDCI GSSIGVQSAV GKPLGIRTVA AQFCNITTCL IGKFYELKLAY IGKFCDVQVMY /SKHMGAKVMA GDYMQGATCHA	110M I VGG MD W AQ A L E I VGG I D SMSQS L A VIGG I SR EDQG FR AVGG L D VK SQ E AA A VR GN K L ERGQK I A VR GN K L ERGQK I A I RG NR I PRGTD I T TGG TN LRDD I MR C I GG TN VGED I RK C I GG TN VR NEMQK	L SR K 12 L AKK 14 LRMG 51 LRAA 33 SEQ 21 TKQ 21 TKQ 21 LDDT 21 LDYG 15 LQAA 15	0289127562
DDX49/1-483 DDX27/1-455 DDX23/1-820 DDX27/1-796 DD19A/1-478 DD192/1-478 DDX25/1-483 DDX6/1-483 DDX8/1-413 DDX28/1-407 DDX22/1-406	61 83 450 277 152 153 158 155 97 92 91	LUERSON LEDI	70G YGIFCL QGPYAI RGTRVL RYPQCL LFPQCL DNIQAM RETQAL KETQAL KETQAL	80R VLTPTRELAY VLTPTRELAF ILAPTRELAG VLVPTRELAL CLSPTYELAL CLSPTYELAL VIVPTRELAL VIVPTRELAV VLAPTRELAQ VLAPTRELAQ	90F I A EQ F EAL I SEQ F EAL VH SVTRQL TGKVI EQM TGRVV EQM VSQICIQV I QKGLLAL QIQKVI ALL QIQKVVMAL	100K GKPLGLKDCI GSSIGVQSAV GKPLGIRTVA AQFCNITTCL IGKFYELKLAY IGKFYELKLAY IGKFCDVQVMY VSKHMGAKVMA GDYMQATCHA GDYMGASCHA	110M I VGG MD V AQ A L E I VGG I D SMSQS L A VI GG I SR EDQG FR AVGG L D VKSQE AA A VR GN K L ERGQK I A VR GN K L ERGQK I A VR GN K L ERGQT D I T T GG TN VR DD I I MR C I GG TN VR AE VQ K C I GG TN VR AE VQ K	L SR K 12 L AKK 14 L RMG 51 L RAA 33 SEQ - 21 SEQ - 21 T KQ - 21 T KQ - 21 L D YG 15 L Q AA 15 L Q AA 15	02891275621
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD19A/1-478 DD19A/1-478 DDX25/1-483 DDX6/1-483 DDX48/1-411 DDX2B/1-407 DDX24/1-406 DX39B/1-428	61 83 450 277 152 153 158 155 97 92 91 104	UNALLETP UNALLETP UNALLETP UNALLETS UNALLETS USROVEPANE USROVEPANE USROVEPANE USROVEPANE USROVEPANE USROVEPANE USROVEPANE USROVEPANE	70G YGIFCL QRLFAL QRPYAI ROTRVL RYPQCL LFPQCL LFPQCL DNIQAM RETQAL KETQAL KETQAL KATQAL GQVSVL	80R VLTPTRELAY VLTPTRELAF ILAPTRELAF ILSPTYELAL CLSPTYELAL CLSPTYELAL VIVPTRELAL VIVPTRELAV VLAPTRELAQ VMCHTRELAF	90F	100K G K P L G L K D C I G S S I G V Q S A V G K P L G I R T V A AQ F C N I T T C L IG K F Y E L K L A Y IG K F Y E L K L A Y IG K F Y E L K L A Y S K H M G A K V M A G D Y M G A S C H A G D Y M G A S C H A S K Y M Q A V V A V	110M I VGG MD V AQ A L E I VGG I D SMSQSL A VIGG I SR EDQG FR AVGQ L D VKSQE AA AVG C N KL ERGQK I AVR C N KL ERGQK I A VR C N KL ERGQK I TGG TN L RDD I MR C I GG TN VG D I MR C I GG TN VR AE VQK F GG L S I KKD E E V	L SR K 12 L A K K 14 L R A 33 S EQ - 21 S EQ - 21 T K Q - 21 L D Y G 15 L Q A 15 L Q A 15 L C A A 15	0289127562151
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD19A/1-478 DD19E/1-478 DDX25/1-483 DDX48/1-411 DDX28/1-407 DDX24/1-406 DX39B/1-428 DX39A/1-427	61 83 450 277 152 153 158 155 97 92 91 104 103 121	ULNER LIES QNALLEES ULNER LIES VEP AL LISS OF R LIOU LISS OF R LIOU LISS OF R LIOU LOU LISS OF R LIOU LOU LOU LOU LOU LOU LOU LOU LOU LOU L	70G YGIFCL QRLFAL QGPYAI RYPQCLC KYPQCLC LFPQCLC RETQAL KETQAL KETQAL KETQAL KETQAL KETQAL SQVTVL	80R VLTPTRELAY VLTPTRELAF ILAPTRELAQ VLVPTRELGI CLSPTYELAL CLSPTYELAL VIVPTRELAL VIVPTRELAV VLAPTRELAQ VMCHTRELAF VMCHTRELAF	90F I A EQ F E VL I S EQ F E AL I S EQ F E AL I S EQ F E AL I S E V I EQM I G K V I C I Q V I Q K G L L AL I Q K V I L AL I S K E Y ER F I S K E Y ER F I S K E Y ER F	100K GKPLGLKDCI GSSIGVQSAV GKPLGIRTVA AQFCNITTCL IGKFYELKLAY IGKFYELKLAY IGKFYELKLAY IGKFQOVQVMY SKHMGAKVMA GDYMQATCHA GDYMQATCHA SKYMNVKVAV SKYMSVKVSV	110M I VGG MD V AQALE I VGG I D SMSQSLA VIGG I SREDQGFR AVGG LD VKSQEAA AVGG N KLERGQKI AVRGN KLERGQKI AIRGNR I PRGTD I TGG TN VRDINR CIGG TN VRDINR CIGG TN VRDEN KCIGG TN VRDEN KDEEV FGGLSI KKDEEV FFGGLSI KKDEEV	L SR K 12 L A K K 14 L RMG 51 L R AA 33 SEQ - 21 SEQ - 21 SEQ - 21 L D YG 15 L Q AA 15 L Q AA 15 L Q AA 15 L Q AA 15 L C MA 15	02891275621540
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD198/1-479 DDX25/1-483 DDX48/1-483 DDX48/1-411 DDX28/1-407 DDX28/1-407 DDX28/1-407 DDX28/1-407 DDX28/1-428 DX39A/1-427 DDX39/1-428 DX39A/1-427	61 83 450 277 152 153 158 155 97 91 104 103 121 262	CONTRACTOR OF POLICY STATES ST	70G YGIFCL QRLFAL QRPYAI ROTRVL RYPQCL KYPQCL LFPQCL KYPQCL KTQAL KETQAL KETQAL KETQAL GQTVVL LSTPSAL	80R VLTPTRELAY VLTPTRELAG VLVPTRELAG CLSPTYELAL CLSPTYELAL CLSPTYELAL VIVPTRELAU VIVPTRELAU VIVPTRELAV VLAPTRELAQ VMCHTRELAF VMCHTRELAF ILAPTRELAY	90F 1 A EQ F R VL 0 I SEQ F E AL 1 E EE T I K F 0 VH S VT R QL 0 T G K V I E QM 0 I G K QL AL 0 I G K V I L AL 0 I G K V I L AL 0 I S K E Y E R F 0 I S K E Y E R F	100K GKPLGLKDCI GSSIGVQSAV GKPLGIRTVA AQFCNITTCL IGKFYELKLAY IGKFYELKLAY IGKFCDVQVMY SKHMGAKVMA GDYMGATCHA GDYMGATCHA GDYMGASCHA SKYMNVKVAV SKYMSVKVSV GIKMGLECHV	110M I VGG MD W AQ A L E I VGG I D SMSQS L A VI GG I SR EDQG FR AVGG L D VKSQE AA AVGG L D VKSQE AA AVGG K L ERGQK I AVG N K L ERGQK I A GT N L RDD I MR C I GG TN VG ED I R K C I GG TN VR NEMQK C I GG TN VR NEMQK C I GG TN VR AE VQK F FGG L SI KKD EE V F FGG L SI KKD EE V F FGG L SI KKD EE V F I GG T PL SQD KTR VGG T PL SQD KTR VGG L P PPOI VR	L SR K 12 L AKK 14 LRMG 51 LRAA 33 SEQ - 21 TKQ - 21 LDDYG 15 LQAA 15 LQMA 15 LCMA 15 LKKC 16 LKKC 16 LKKC 18	028912756215402
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD192/1-796 DD192/1-479 DDX25/1-483 DDX6/1-483 DDX6/1-483 DDX26/1-483 DDX28/1-407 DDX28/1-407 DDX28/1-407 DDX28/1-427 DDX29/1-620 DX39/1-660	61 83 450 277 152 153 158 155 97 92 91 104 103 121 262 237	CALLESSON SETTON NALLESSON CALLESSON CALLESSON SSETCLDEL CONSTRUCTION	70G YGIFCL YGRFYAL YGRFYAL GGTFYAL RYYPQCCL LNTIQAL KYPQCAA KYPQCAA LNTIQAL GGVYQIL KKOVSVL GGVYQIL KKOVSVL GGVYQIL KFPSAL KFPSAL	80R VLTPTRELAY VLTPTRELAF ILAPTRELAG VLVPTRELAL CLSPTYELAL CLSPTYELAL VIVPTRELAV VLAPTRELAV VLAPTRELAG VMCHTRELAF VMCHTRELAF ILAPTREIAV	90F 1 A EQ F F VL 0 I SEQ F EAL 0 I E EET I KF 0 VH SV TR QL 0 TG KVI EQM 0 TG KVI EQM 0 TG RVV EQM 0 VSQ I C I QV 0 I QKGL LAL 0 I QKUVMAL 0 I QKEYER F 0 I H SVI TAI 0 I FEQ AKEL 0 I YEEAR KF	100K GKPLGLKDCI GSSLGVQSAV GKPLGIRTVA AQFCNITTCL IGKFYELKLAY IGKFYELKLAY IGKFKUKLAY IGKFCDVQVMY VSKHMGAKVMA GDYMGATCHA GDYMGASCHA GDYMGASCHA SKYMSVKVSV GIKMGLECHV MSGLRMKTVL	110M I VGG MD VAQALE I VGG I D SMSQSLA VIGG I SREDQGFR AVGG LD VKSQEAA AVGG NKLERGQKI AVRGNKLERGQKI AVRGNKLERGQKI TTGG TN VRDD IMR CIGG TN VRDD IMR CIGG TN VRDD IMR CIGG TN VRAEVQK FFGGLSIKKDEEV FFGGLSIKKDEEV FIGG TPLSQDKTR LVGGLPLPPQLYR	L SR K 12 L A K K 14 L R A S 1 SEQ - 21 SEQ - 21 L D D T 21 L D D T 21 L D V G 15 L Q A 15 L Q A 15 L Q A 15 L K K C 16 L K K - 18 L Q C H 32 L C K G 31	0289127562154024
DDX49/1-483 DDX23/1-820 DDX27/1-455 DDX27/1-796 DD19A/1-478 DDX25/1-483 DDX6/1-483 DDX6/1-483 DDX28/1-400 DX28/1-400 DX28/1-400 DX39A/1-427 DDX29/1-619 DDX39/1-660 DDX39/1-660 DDX39/1-660	61 83 450 277 152 153 158 155 97 92 91 104 103 121 262 237 239	ULUE SEDEN S	70G IFCL QRLFAL QQFYAI RYPQCL DNIQAM KYPQCL DNIQAM KFPQCL DNIQAM KFPQCL DNIQAL KFPQCL LNIQAL KFPQCL LNIQAL KTPSAL ENPISL	80R VLTPTRELAY VLTPTRELAF ILAPTRELAF ILSPTYELAL CLSPTYELAL CLSPTYELAL CLAPTYELAL VIVPTRELAV VLAPTRELAQ VMCHTRELAF VMCHTRELAF VMCHTRELAF VMCHTRELAF VMCHTRELAY VLAPTRELAV VLAPTRELAV	90F I A EQ FR VL I SEQ FEAL I SEQ FEAL I SEQ FEAL I SEQ FEAL I SEQ FEAL I SE VIEQM I GKVIEQM I GKVVEQM I GKVVEQM I GKVIEAL I SKEYER F I SKEYER F I SKEYER F I SKEYER F I SEQ AKEL I YEEAR KF	100K GKPLGLKDCI GSSIGVQSAV GKPLGIRTVA AQFCNITTCL IGKFYELKLAY IGKFYELKLAY IGKFCDVQVMY VSKHMGAKVMA GDYMGASCHA GDYMGASCHA SSKYMSVKVSV GIKMGLECHV MSGLRMKTVL SYRSRVRPCV SYRSRVRPCV	110M I VGG MD VAQALE I VGG I D SMSQSLA VIGG I SREDQGFR AVGG LD VKSQEAA AVGG LD VKSQEAA AVRGN KLERGQKI AVRGN KLERGQKI AVRGN KLERGQKI TTGG TN VGD I IMR CIGG TN VGD I IMR CIGG TN VGD I IMR CIGG TN VGAD I SQU FFGG LSIKKD EEV FFGG LSIKKD EEV FFGG LSIKKD EEV FFGG LSIKKD EUV FFGG LSIKKD EUV FFGG LSIKKD EUV FGG LSIKKD EUV VGG AD I GQQ I RD	L SR K 12 L A KK 14 L R AG 51 S EQ - 21 S EQ - 21 T KQ - 21 L D D T 21 L D D T 21 L D D T 15 L C A 15	02891275621540246
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD19A/1-478 DD19B/1-479 DDX25/1-483 DDX6/1-483 DDX48/1-411 DDX28/1-407 DDX24/1-406 DX39B/1-428 DX39A/1-427 DDX24/1-619 DDX29/1-619 DDX31/1-662 DDX31/1-724	61 83 450 277 152 153 158 155 97 92 91 104 103 121 262 237 239 347	ULUES PPO SET SPO SET	70G I F C L QG L F A L QG L F A L QG P Y A I R Y P Q C L R Y P Q C L C L F A L C L F A L C L F A L C L F A L R Y P Q C L C L F A L C L	80R VLTPTRELAY VLTPTRELAF ILAPTRELAQ VLVPTRELAL CLSPTYELAL CLSPTYELAL VIVPTRELAL VIVPTRELAV VLAPTRELAQ VMCHTRELAF VMCHTRELAF VMCHTRELAF VMCHTRELAY VLAPTRELAV VLAPTRELAV VLAPTRELAV VLAPTRELAV	90F I A EQ F E AL I SEQ F E AL I SE V E QM I GK V I EQM I GK V I EQM I GK V I CAL I QK V I AL I SKEYER F I YEEAR KF I YEEAR KF I YEEAR KF	100K G K P L G L K D C I G S S I G VQ S A V G K P L G I R T V A AQ F C'N I T T C L IG K F Y E L K L A Y IG K F Y E L K K Y E Y IG K F Y E Y E Y E Y IG K F Y E Y E Y E Y E Y E Y IG K F Y E Y E Y E Y E Y E Y E Y E Y E Y E Y	110M I VGG MD VAQALE I VGG I D SMSQSLA VIGG I SREDQGFR AVGCLD VKSQEAA AVGCNKLERGQKI AVRGNKLERGQKI AVRGNKLERGQKI I GG TN VGD I MR CIGG TN VGD I MR CIGG TN VGD I MR CIGG TN VR AE VQK FFGGLSIKKDEEV FFGGLSIKKDEEV FFGGLSIKKDEEV FFGGLSIKKDEU VGGLPLPQLYR VYGGAD I GQQ I RD VYGGAD I GQQ I RD VYGGAD I GQQ I RD VYGGAD I GQQ I RD	L SRK 12 L AKK 14 L RMG 51 SEQ - 21 SEQ - 21 SEQ - 21 L D YG 15 L CAA 15 L	028912756215402465
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DDX49/1-483 DDX23/1-820 DDX23/1-820 DDX27/1-796 DD198/1-479 DDX25/1-483 DDX6/1-483 DDX48/1-411 DDX28/1-407 DDX29/1-427 DDX29/1-427 DDX39/1-620 DDX39/1-660 DDX31/1-660 DDX31/1-662 DDX46/1-1031 DDX42/1-938	61 83 450 277 152 153 158 155 97 92 91 104 103 121 262 237 239 347 431 312		70G YGIFFAL YGRUFYAI GGGTFQQCCL CANCELE CAN	80R VLTPTRELAY VLTPTRELAF ILAPTRELAG VLVPTRELAL CLSPTYELAL CLSPTYELAL VIVPTRELAV VIVPTRELAV VLAPTRELAQ VMCHTRELAF VMCHTRELAF VMCHTRELAF VMCHTRELAF VMCHTRELAF VMCHTRELAF VMCHTRELAV VMCHTRELAF VMCHTRELAV VMCHTRELAV VMCHTRELAV VMCHTRELAV VMCHTRELAV VMCHTRELAV	90F	100K GKPLGLKDCI GSSIGVQSAV GKPLGIRTVA AQFCNITTCL IGKFYELKLAY IGKFYELKLAY IGKFYELKLAY IGKFCDVQVMY VSKHMGAKVMA GDYMGASCHA GDYMGASCHA GDYMGASCHA SKYMSVKVSV GIKMGLECHV SSYRSRVRPCV SSYRSRVRPCV SSFTLGLRVVC GKAYNLRSVA	110M I VGG MD WAQALE I VGG I D SMSQSLA VIGG I SREDQG FR VGG LD VKSQEAA AVGC LD VKSQEAA AVGC NKLERGQKI AVGC NKLERGQKI AVGC NKLERGQKI AVGC NKLERGQKI CIGG TN VGED I RK CIGG TN VGED I RK FGG LSI KKDEEV FIGG TPLSQDKTR LVGG LPLPPQLYR VGG AD I GQQ I RD VGG G CLGHSI RQ VGG G SMWEQAKA	L SR K 12 L A KK 14 L R AA 51 L R AA 51 SEQ - 21 SEQ - 21 L D D T 21 L D D T 21 L D D T 21 L D V G 15 L C MA 15 L C MA 15 L KKC 16 L KKC 16 L KKC 16 L KKC 16 L KKC 16 L KKC 31 L C R G 31 L C R G 31 L C R G 49 L C G 27 L K K G 49 L K K G 49 L K K G 49 L C G 27 L K K G 49 L K K K K K K K K K K K K K K K K K K K	02891275621540246556
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DDX49/1-483 DDX49/1-483 DDX27/1-796 DD198/1-479 DD198/1-479 DDX25/1-483 DDX48/1-483 DDX48/1-483 DDX48/1-483 DX39A/1-427 DDX29/1-629 DDX39/1-629 DDX39/1-660 DDX39/1-660 DDX39/1-660 DDX41/1-724 DDX46/1-1031 DDX41/1-724 DDX46/1-1031 DDX41/1-729 DDX51/1-614 DDX51/1-614 DDX52/1-599 DDX52/1-599 DDX52/1-599 DDX52/1-599 DDX52/1-783 DDX52/1-783 DDX52/1-7859 DDX52/1-7859 DDX24/1-851 DDX51/1-666 DDX10/1-875 DDX51/1-666 DDX10/1-875	61 83 450 2777 152 158 155 97 92 91 104 103 121 239 347 431 215 301 155 224 240 155 224 240 252 2187 2290 271 128 240 252 2187 200 271 2290 271 2290 271 2290 271 2290 221 2290 221 2290 221 2290 221 2290 221 2290 221 2290 221 2290 221 2290 221 2290 2297 2297 2297 2297 2297 2297 2297	P.P.D. PALEKY SET SP.D. S.	70G YGL FAL YGL FAL	80R VL T PTR EL A Y VL T PTR EL A F I L A P TR EL A G VL V PTR EL A CL S PT Y EL A L CL S PT Y EL A L CL S PT Y EL A L VI V P TR EL A G VI V P TR EL A G VI V P TR EL A G VI A P TR E	90F 1 A EQF F A L 1 SEQF F A L 1 E E F T I K F 2 VH S V T R Q L 2 T G K V I E Q M 2 T G K V I C M 2 T G K V I	100K GKPLGLKDCI GKPLGLRTVA AGFCNITTCL IGKFYELKLAY IGKFYELKLAY IGKFYELKLAY IGKFCDVQVMY GSKHMGAKVMA GDYMGATCHA GDYMGATCHA GDYMGASCHA SSYMSVKVSV GIKMGLECHV SSGTWSVKVSV GIKMGLECHV SSGTWSVKVSV GIKMGLECHV SSGTWSVKVSV GIKMGLECHV SSGTWSVKVSV GIKMGLECHV SSGTGA GKCSGLKSTC CCRACRLKSTC CCRACRLKSTC CCRACRLKSTC CCRACRLKSTC CCRLLLRCAL GKCSGLKSTC CCRLLLRCAL GKCSGLKSTC CCRLLLRCAL GKCSGLKSTC CCRLLLRCAL GKCSGLKSTC CCRLLLRCAL GKTGLKSVC CCRLLLRCAL GKCSGLKSTC CCRLLLRCAL GKCSGLKSTC CCRLLLRCAL GKCSGLKSTC CCRLLLRCAL GKCSGLKSTC CCRLLLRCAL GKSTGLKSTC CCRLLLRCAL GKSTGLKSTC CCRLLLRCAL GKSTGLKSTC CCRLLLRCAL GKSTGLKSTC CCRLLLRCAL GKSTGLKSTC CCRLLLRCAL GKSTGLKSTC CCRLLLRCAL GKSTGLKSTC CCRLLLRCAL GKSTGLKSTC CCRLLLRCAL GKSTGLKSTC CCRLLL GKSTGLKSTC CCRLLL GKSTGLKSTC CCRLLL GKSTGLKSTC CCRLL GKSTGLKSTC CCRLL GKSTGLKSTC CCRL GKSTGLKSTC CCRLL GKSTGLKSTC CCRL GKSTGLKSTC CCRL GKSTGLKSTC CCRL GKSTGLKSTC CCRL GKSTGLKSTC CCRL CCRL CCRL CCRL CCRL CCRL CCRL CC	110M I VGG MDW AQALE I VGG I D SMSQSLA VIGG I SR EDQG FR AVGG LD VKSQEAA AVGG LD VKSQEAA AVGG KLERGQKI AVGG NKLERGQKI AVGG NKLERGQKI GG TN VRNEMQK CIGG TN VRNEMQK CIGG TN VRNEMQK CIGG TN VRNEMQK CIGG TN VRNEMQK FFGG LSIKKDEEV FFGG LSIKKDEEV FFGG LSIKKDEV FFGG LSIKKDEV FFGG LSIKKDEV FGG LSIKKDEV FGG LSIKKDEV FGG LSIKKDEV FGG LSIKKDEV FGG AD IGQQIRD VYGG AD IGQQIRD VYGG AD IGQQIRD VYGG TGISEQIAE VYGG SMWEQAKA VGG SMKEQAI I YGG APKGPQIRD I YGG APKGPQIRD I YGG APKGPQIRD I YGG TSYGQGF R VSAAEDSVSQRAV IHKAAVAAKKFGP FYGG TSYGSQINH LVGG MSTQKQQRW LEGGHGMRRIRLO VGG KKSEKAR VTGQKSLAKEQES I IGG KDLKHEAER	L SRKK 12 LAKK 14 LRMG 51 LRMG 51 LRMG 21 SEQ - 21 TKDT 21 LDQAA 15 LQAA 15 LQAA 15 LQAA 15 LKKC 16 LXKC 16 LKKC 16 LK	028912756215402465556475536458975690410

PTRELAxQ

			130R	140T	150V	160Q	170E		
DDX49/1-483 DDX3/1-820 DDX23/1-820 DD19A/1-478 DD19B/1-479 DDX25/1-483 DDX6/1-483 DDX48/1-411 DDX28/1-406 DX39B/1-428 DX39A/1-427 DDX20/1-824 DDX39/1-619 DDX39/1-619 DDX39/1-619 DDX39/1-619 DDX39/1-662 DDX4/1-724 DDX46/1-1031 DDX4/1-729 DDX5/1-614 DDX43/1-648 DDX5/1-614 DDX5/1-6148 DDX5/1-6148 DDX52/1-599 DDX21/1-789 DDX21/1-789 DDX21/1-785 DDX21/1-875 DDX25/1-600 DDX31/1-875 DDX55/1-600 DDX31/1-875 DDX55/1-600 DDX11/1-740	121 143 519 340 212 213 218 157 153 216 165 165 315 317 496 377 2218 366 314 217 295 218 3646 314 217 295 218 3646 314 217 295 286 309 260 314 215 215 317 215 215 317 215 317 215 317 215 317 215 317 215 317 215 317 215 317 215 317 215 317 215 317 215 317 215 317 215 317 215 317 215 317 215 317 215 317 215 317 317 317 317 315 317 317 317 317 325 317 317 317 325 317 317 325 317 317 325 317 317 325 317 317 325 317 317 325 317 317 325 317 317 325 317 317 325 317 315 327 315 317 315 327 317 325 317 325 317 325 317 317 325 325 317 326 317 325 325 327 327 327 327 327 327 327 327 327 327	PH V V I AT PG PH I I I AT PG C E I V I AT PG C E I V I AT PG PD I L I AT PG PD I L I AT PG PH I V GT PG PH I V VG TPG PH I VVG TPG PH I VVG TPG PH I VVG TPG CH L VAT PG CH L VAT PG VE C I AT PG VE C I AT PG VE I V V T PG I I L V T PG VE I V V T PG		NTFSIRK SNTFSIRK SNTFSIRK SNTFSIR SNTF		DR LL EQGC T DR ILL EQGC T DR ILD N DR MID N DR MID N DVMIAT C DVMIAT C D	TO F T VD L E A TO F T VD L E A TO F E T VD K MG F E PD VOK GG H QDQS I R QG H QDQS I R QG F SDH S I R QG F SDH S I R MG F KEQ I YD V QG F KEQ I YD V QG F KEQ I YD V QG F KDQ I YE I DMR RD VQE DMR RD VQE DMR RD VQE I DMR RD V	L A A'V P AR R L K V I PR DR R L K V I PR DR R GR ML PR NCC QR AL P SK QR AL P SK C QR AL P SK F F N S I PN C VE OK S S I PN C VE OK VE OK	180 199 600 396 267 268 271 212 208 271 237 271 237 378 374 376 374 376 273 421 369 272 191 347 369 320 192 241 347 369 320 193 241 347 349 247 241 241 241 241 241 241 241 241
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SAT

		250S	260T	270K	280S	290A	
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD19B/1-479 DDX57/1-483 DDX67/1-483 DDX48/1-479 DDX26/1-483 DDX48/1-479 DDX28/1-470 DDX28/1-427 DDX28/1-427 DDX39/1-610 DDX39/1-610 DDX37/1-610 DDX37/1-610 DDX47/1-724 DDX47/1-724 DDX57/1-614 DDX37/1-614 DDX37/1-614 DDX57/1-614 DDX57/1-614 DDX57/1-614 DDX57/1-614 DDX57/1-614 DDX57/1-614 DDX57/1-615 DDX57/1-615 DDX57/1-615 DDX57/1-635 DDX57/1-737 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-859 DDX57/1-800 DDX57/1-800	241 260 661 460 329 330 235 331 274 270 289 283 306 435 437 557 515 494 435 437 537 515 494 435 433 335 437 435 433 433 537 433 537 435 433 537 435 537 537 537 537 537 537 537 537 537 5	R FQD EH EDWSIII ELAGN SFMI QGP PII AITIA - QAMI AITIA - QAMI SITIG - QAII RLGIN - QAMI TLTIA - QAMI TLTIT - QAVI RIGDE - QVI ATGSDS - LTLV ATGKDS - LTLV ATGSDS - LTLV ATGSDS - LTLV ATGSDS - SVIL EIMKEN - KTIV SMSSTD - KVIN KTP - PVL NVPQD - KVIN KGF - NPPVL VYSHQG - RTII QYP - RSLV HRDRTGPSGTVLV VSHQG - RVIN QYP - RSLV QKCEDQ - KWVV EMQFS - RVLO SHLKK - KSLV KNRKK - KLLW KNRKK - KLWV	F TN TC KTC Q I LCM F CSTCNNTQR TAL F VNQKKGCD VLAK F VNQKKGCD VLAK F QTKKQAHRMH I F CH TR KTASWLAA F CH TR KTASWLAA F CH TR KTASWLAA F CH TR KTOWLTE F LN TRR KVDWLTE F LN TRR KVDWLTE F LN TRR KVDWLTE F VKS VQRC I ALAQ F VK SVQRC I ALAQ F V SVG I ADDL SS F A KK AD VD A I HE F VA T KHA A S I SC I KR LSG F CN SS T VNWLGY F SSC CL VE F HYS F NS R SN SHR L F L F SSC KE VQ Y LYR F SSC KS VK Y HYE F CR TK I DCDN LEQ	MLR KFSFPT LLRNLGFTA SLEKMG YNGLGVI ELSKEGHQV ELSKEGHQV ELSKEGHQV ELSKEGHQV KISQLGYSC KMR FANFTV KMH ARDFTV KMH ARDFTV KMH ARDFTV LVEQNFPA AVQKTGFPA AVQKTGFPA AVQKTGFPA AVQKTGFPA AVQKTGFPA AVQKTGFPA AVQKTGFPA AVQKTGFPA LVEQNFPA LVEQNFPA AVQKTGFPA AVQKTGFPA AVQKTGFPA AVQKTGFPA AVQKTGFPA AVQKTGFPA LVEQNFPA LVEQNFPA AVQKTG	VALHSMMKOKE IPLHGOMSOSK CTLHGGKGOEO GELHGNLSOTO ALLSGEMVEO SLSGETVEO SLSGETVEO SSHGDMPOKE SAHGDMDOKE SAHGDMDOKE SAHGDMDOKE IAIHRGMPOEE IAIHRGMAOEE ECISGNMNONO ISIHSEKSOIE TSIHGDRSORD TSIHGDRSORD TSIHGDRSORD TSIHGDRSORD TSIHGDRSORD TSIHGDRSORD SLHGDREORE MGIHGDKSOPE MGIHGCKSOPE MGIHGDKSOPE MGIHGCKSOPE MGIH	A A L A K F K SS I Y R A L G S L N K F K K A K A R S A F A L S N K K A K A R S A F A L S N L K A G A K O A A V I E R F R E G K E K A A V I E R F R E G K E K A A V I E R F R E G K E K A A V I E R F R E G K E K A A V I E R F R E G K E K A A V I E R F R E G K E K A A V I E R F R E G K E K A A V I E R F R G S S R C V I M R E F R S G S S R C V I M R E F R S G S S R C V I M R E F R S G S S R C V I M R E F R S G S S R C V I M R E F R S G S S R C V I M R E F R S G S S R C V I M R E F R S G S S R C V I M R E F R S G S S R C V I M R E F R S G S S R C V I M R E F R S G S S R C V I M R E F R S G S S R C S I M C S C S C S R C S I M C S C S C S C S C S C S C S C S C S C	300 315 515 515 384 385 329 329 325 324 339 325 324 497 493 3592 550 470 303 539 544 493 339 494 493 339 497 497 497 497 497 497 497 49
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD19A/1-478 DD19B/1-479 DDX6/1-479 DDX6/1-483 DDX48/1-411 DDX28/1-406 DX39B/1-428 DDX48/1-406 DDX29/1-619 DDX29/1-619 DDX59/1-619 DDX59/1-619 DDX59/1-619 DDX59/1-619 DDX37/1-620 DDX37/1-620 DDX37/1-620 DDX37/1-631 DDX42/1-938 DDX17/1-729 DDX56/1-547 DDX56/1-547 DDX56/1-547 DDX56/1-547 DDX56/1-547 DDX56/1-783 DDX21/1-783 DDX21/1-785 DDX51/1-650 DDX31/1-855 DDX51/1-670 DDX10/1-740	301 717 516 385 385 330 326 330 326 340 339 492 494 494 494 494 494 551 311 485 540 551 311 4450 551 311 4450 558 321 478 568 321 478	I L I ATD VA SRG LD I L LA TD VA SRG LD I L LA TD VA SRG LD I L VATD VA ARG D VL VT TN VC ARG I D VL VT TN VC ARG I D VL VT TN VC ARG I D VL I TTD VC ARG D VL I TTD VA ARG D VL I STD VWARG LD VL I STD VWARG LD VL I STD L'L ARG I D I L VA TN L'FGRG MD I L VA TN L'FGRG MD VL I STD L'L SRG D VL VS TG VLGRG LD VL V STG VLGRG LD VL VA TN VA ARG LD VL VA TN VA ARG LD VL VA TN VA ARG LD VL VA TA VA ARG LD I L VA TA VA ARG LD I L VA TA VA ARG LD VL VA TO VA SKG LD I L I ATD VA SKG LD I L I ATD VA SKG LD I L I ATD VA SKG LD VL VA TN VA ARG LD VL LC TD I ASRG LD VL LC TD I ASRG LD VL LC TD I ASRG LD VL LC TD VA ARG LD FL I CTD VA ARG LD FL CTD VA ARG LD FL CTD VA ARG LD	I PT VQ VV I NHNT P I PH VQ VVN FDI P I QD VSMV VN YDMA I EG VKT V IN FTMP VEQ VSV IN FDL P VEQ VSV IN FDL P VEQ VSL I IN YDL P VQQ VSL VIN FDL P VQQ VSL VIN FDL P VQQ VSL VIN YDL P I ER VN I AFN YDMP I SN VKH VIN FDL P VQQ VSL VIN YDL P I SN VKH VIN FDL P I SN VKH VIN FDL P I SN VKH VIN FDL P VKH VIN YDF P I SN VKH VIN YDF P FHA VSA VLN FDL P FKG VL VIN YDF P FHH VSA VLN FDL P FKG VL VIN YDF P FKG VL VIN YDF P I PE VDL VIQ SSPP I PE VDL	GLPKIYIHR GLPKIYIHR KNIEDYIHR KNIEDYIHR KNIEDYIHR KNIEDYIHR PDNETYLHR PDNETYLHR PDNETYLHR FDNETYLHR SDIEEYVHR SDIEEYVHR SDIEEYVHR SSIEDYUHR SSIEVYHR SSIEDYVHR SSIEDYVHR RNIEVYHR RNIEVYHR RNIEVYHR RNIEVYHR SSIEVYHR	VGR T AR AGR GG VGR T AR AGR GG VGR T AR AGR GG I GR TGR AG KSG I GR TGR FG KRG I GR TGR FG KRG I GR TGR FG KKG I GR GGR FGR KG I GR GGR FGR KG I GR GGR FGR KG VAR AGR FG T KG I GR GGR FGR KG VAR AGR FG T KG I GR TGR VGN LG I GR TGR VGN LG I GR TGR VGN LG I GR TGR VGN LG I GR TGR CGN TG AGR TGR AGN KG I GR TGR AGN KG I GR TGR AG KG I G I G TGR AG KG I G I G I G I G I G I G I G I G I G I	A I T L V T Q YD I H L V KA I T F L T KED SAVF VA I T F L T KED SAVF I S V S L VG EDDER KM L L A V M VD S K SMN I L L A V M VD S K SMN I L L A T M I E VD EL P SL L A I N F V T EED KR I L VA I N F V T EED KR I L VA I N F V T EED KR I L VA I N F V T EED KR I L VA I N F V T EED KR I L VA I N F V T EED KR I L L A I T F V S END A KI L L A I T F V S END A KI L L A I T F V S END A KI L L A I T F V S END A KI L L A I T F V S END A KI L L A I T F V S END A KI L L A I T F V S END A KI L L A I T F V S END A KI L L A I T F T F N E K N N I T S A I S F F E E S D N H L A Y A YT F I T ED Q A R Y A Y A YT F I T ED Q A R Y A T A YT F F T P O'N I K Q A Y A YT F I T ED Q S KA A I A T F F T P O'N I K Q A Y A YT F I T ED D K P L V A I T F T F D K A D E S V L I V I T F V L P T E O F H L K A I T F F T P O'N I K Q A Y C I C F Y O'P H KE E Y Q L I S L I T F V T P WD V S L V S S L I L A P S E A E Y V Q A F I L L V Y E K AM V S A L V F L L P M E E S Y I H A L L I L P E E L G F L L A I S L V A E K E M Q L	360 375 375 451 452 456 389 385 440 399 945 557 551 553 653 653 653 653 397 545 307 545 307 545 307 545 307 545 307 545 307 545 307 545 307 545 307 545 307 545 307 545 307 545 307 545 307 545 307 545 307 545 307 545 307 397 545 307 397 397 545 307 397 545 307 397 545 307 397 545 307 397 545 307 397 545 300 397 397 545 300 397 545 300 397 397 545 300 397 545 300 397 397 545 300 397 397 545 300 397 397 307 397 307 397 307 397 307 397 307 397 307 397 307 397 307 397 307 397 307 397 307 397 307 397 307 397 307 397 307 397 307 397 307 397 307 397 307 307 307 307 307 307 307 307 307 30

			370K	380E	390V	400E	4101
DDX49/1-483 DDX27/1-455 DDX23/1-820 DDX27/1-796 DD198/1-479 DDX55/1-483 DDX48/1-479 DDX25/1-483 DDX48/1-407 DDX25/1-483 DDX48/1-411 DDX28/1-407 DDX28/1-407 DDX29/1-428 DX39A/1-427 DDX20/1-824 DDX39/1-619 DDX37/1-669 DDX37/1-669 DDX47/1-724 DDX46/1-1031 DDX47/1-729 DDX57/1-614 DDX33/1-638 DDX53/1-631 DDX54/1-881 DDX56/1-547 DDX52/1-599 DDX2/1-778	361 376 777 452 453 385 401 400 423 385 554 401 400 423 555 611 531 558 611 531 558 614 558 614 451 388 556 451 451 631 536 536 536 536 536 536 536 536 536 536	HAIEHQA AIEHQA AIEHQA KNR KALAQDHG KARANKA QODG KARANKA QODG KARANKA KADIEQA KARANKA KADIEQA KANKA KADIEQA KANKA KADILLIK KAN KADILLIK KAN KADILLIK KAN KADILLIK KAN KADILLIK KAN KADILLIK KAN KADILLIK KAN KADILLIK KAN KADILLIK KAN KADILLIK KAN KADILLIK KAN KADILLIK KAN KAN KAN KAN KAN KAN KAN KAN KAN KA	370K 1 KKKLEFS 1 GKKLPGFP 1 KKKLEFS 1 GKKLPGFP 1 GKKLPGFP 1 FNKKIERLD 1 FNKKIERLD 1 FNKKIERLD 1 FNKKIERLD 1 FNKSIKQLN 2 GYNTTVEEMP 2 YNTTVEEMP 2 YNT	380E VEEAEVLQILT TQDDEVMMLTE PELANHPC DKIEKMEKEEK TDDLDEI AEDMDEI AEDMDEI MNVADLI MNVADLI MNVADLI BEIDISSY SGLMEECVLKK PQLLSSY SGLMEECVLKK SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYYKG SWLENMAYKG FLUQVLHC PKLMQLVD PKLMQLVD SYQFRMEEIMRS EYIKGFQKALSK	390V 2 VN V VRR ECEIK 3 VAEAOR FARME MOQSEANTAKR EMOQSEANTAKR 6 CONSEANTAKR 6 CONSEANTAKR	400E L L A AH FD E K K LR EHG E K K R S LL E KG K E AR K VAE YH SE P VAE YH SE P F SGG FG AR RQ I PG F SG ST RG F SGG FG AR RQ I PG F SG ST RG S SG F SG KG R K F KGG KG K K R E GGGGGG S SG SG SG SG SG I DG SG SG SG SG SG SG SG F SG KG R K I DG SG R SG SG SG F SG KG R K I DG SG R SG SG SG F SG KG R K I DG SG R SG S	4101 RED AGDN 431 RED AGDN 431 KEKIAKALQLRG 677 473 478 423 423 423 423 423
DDX21/1-783 DDX50/1-737	550 501	VQVEQK RYVEQK	(A G	SATEIIKALDS STMDLVKSLAS	/ P P T A I SQ S A E K / S Y A A V D P S A Q R	LIEEKGAVSG LIEEKGAVSG	ATSVDQRSLILQ 642 ASSFEPRSLTLE 593
DDX24/1-859 DDX28/1-540	700 513	KKIYKT QKIELA	LKKDED PVQ	TKYMDVVKARQ SSVKEPLP	IEKSEYR	EQ	AAAALEIELYKG 770 537
DDX31/1-851 DDX51/1-666	641 619	RMLTEA	GAPELQELS	SKLLQPLV			RATVLQTVFVHS 703
DDX10/1-875 DDX55/1-600	428 381	NFLAIN		PKLKSMALFVS	VQAYAKNLIFRI		KQFPDFVPVFKD 488
DDX18/1-8/0 DDX1/1-740	660	SELEEH		PDIKVPVDFDG	VTYGQK		AGG 698
			430K	440N	450T	460G	470S 480Q
DDX49/1-483 DDX47/1-455	421 432	KD PD L E	430K AKRKAELAK	440N IKQKNBRFKEK	450T ZEETLKRQKAGR	460G Aghkgrpprt	470S 480Q PSGSHSGPVPSQGLV 48
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX23/1-790	421 432 801	KD PD L E	430K A K R K A E L A K T E G A I G H K P G T I E R S G E F A E R	440N I KQKNRRFKEK VRNKV LTKKR	450T / EETLKRQKAGR AGGKMKK REETLFA REETLFA	460G AGHKGRPPRT	470S 480Q PSGSHSGPVPSQGLV 48
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD19A/1-478	421 432 801 678 474	KD PD L E	430K A KR K A E L A K T E G A I G H K P G T I K E R S Q F E A E R	440N I KQKNRRFKEK VRNKV LTKKR L AKRNRKKQKQ 	450T VEETLKRQKAGR AGGKMKK REETIFA AKKSVFD E IAN	460G AĞHKGRPPRT 	470S 480Q PSGSHSGPVPSQGLV 48
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD19A/1-478 DD19B/1-479 DDX25/1-483	421 432 801 678 474 475 479	KD PD L E	430K AKRKAELAK TEGAIQ HKPGTI ERSQFEAER	440N I KQKNRRFKEK VRNKV LTKKR L AKRNRKKQKO EK EK	450T VEETLKRQKAGR AGGKMKK RETIFA AKSVFDE IAN	460G AĠHKGRPPRT	470S 480Q PSGSHSGPVPSQGLV 48
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD19A/1-478 DD19B/1-479 DDX25/1-483 DDX6/1-483	421 432 801 678 474 475 479 478	KD PD L E	430K A K R K A E L A K T E G A I G H K P G T I E R S G F E A E R 	440N I KQKNRRFKEK VRNKV VRNKKQKQ I AKRNRKKQKQ EK EK VEDEK	450T VEETLKRQKAGR AGGKMKK REETIFA AN	460G AĞHKGRPPRT	470S 480Q PSGSHSGPVPSQGLV 46
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD19A/1-478 DD19B/1-479 DDX25/1-483 DDX6/1-483 DDX6/1-483 DDX6/1-407	421 432 801 678 474 475 479 478	KD PD L E	430K AKRKAELAK TEGAIG HKPGTI ERSQFEAER	440N I KQKNRRFKEK VRNKV L AKRNRKKQKQ EK EK 	450T V E E T L KRQ KAGR AGGKMKK	460G AĠHKGRPPRT LTNTSKK	470S 480Q PSGSHSGPVPSQGLV 46
DDX49/1-483 DDX27/1-455 DDX23/1-820 DDX27/1-796 DD19B/1-479 DDX25/1-483 DDX6/1-483 DDX6/1-483 DDX8/1-407 DDX22/1-406	421 432 801 678 474 475 479 478	KD PD L E	430K A K R K A E L A K T E G A I G H K PG T I E R SQ F E A E R 	440N I KQKNRR F KE K VRN KV L AKRNR KKQKQ EK EK 	450T V E E T L KRQ KAGR AGGKMKK	460G AĠHKGRPPRT LTNTSKK	470S 480Q PSGSHSGPVPSQGLV 45
DDX49/1-483 DDX47/1-455 DDX23/1-820 DDX27/1-796 DD198/1-479 DDX25/1-483 DDX6/1-483 DDX48/1-411 DDX28/1-407 DDX28/1-407 DX28/1-427	421 432 801 678 474 475 479 478 424 423	KD PD L E	430K A KR K A E L A K T E G A I G H K PG T I E R SQ F E A E R E R SQ F E A E R	440N I KQKNRR F KEK VRNKV LTKKR L AKRNRKKQKQ EK 	450T V E E T L KRQ KAGR AGGKMKK E E T I F A E I KKS V F D E I AN	460G AĠHKGRPPRT LTNTSKK	470S 480Q PSGSHSGPVPSQGLV 45 AGPSFEERKQ
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DDX49/1-483 DDX47/1-455 DDX27/1-796 DD198/1-479 DD198/1-479 DDX25/1-483 DDX48/1-411 DDX25/1-483 DDX48/1-411 DDX25/1-407 DDX28/1-407 DDX28/1-407 DDX28/1-427 DDX29/1-624 DDX39/1-660	421 432 801 678 474 475 479 478 424 423 540 608 612	KD PD L E	430K A KR K A E L A K T E G A I G - H K PG T I - E R SQ F E A E R C R SQ F E A E R C R S S S -	440N I KQ KNRR F KE K VRNKV LT KKRI L AKRNR KKQKQ EK EK EK EK 	450T VEETLKRQKAGR AGGKMKK EETIFA AKSVFD AN AN D Y O SGDSESDSDSDSYS SGDSESDSDSYS KSNSQK	460G AĠHKGRPPRT LTNTSKK SRTSSQSPRR	470S 480Q PSGSHSGPVPSQGLV 48
DDX49/1-483 DDX47/1-455 DDX27/1-796 DD198/1-479 DDX25/1-479 DDX25/1-483 DDX48/1-471 DDX25/1-483 DDX48/1-407 DDX28/1-407 DDX28/1-407 DDX28/1-428 DX394/1-427 DDX20/1-824 DDX59/1-619 DDX3/1-660 DDX3/1-724	421 432 801 678 474 475 479 478 424 423 540 608 612 612 612 612	KKKRK	430K TEGAIG- HKPGTI CERSQFEAER VKEALPAEL SRGSSS SRASSS BKGKST	440N I KQ KNRR F KE K VRNKV LTKKRI L AKRNR KKQKQ EK EK EK 	450T / EE [†] L KRQ KAGR AGGKMKK EET I FA AKS VFD AN D Y 	460G AĠHKGRPPRT LTNTSKK SRTSSQSPRR	470S 480Q PSGSHSGPVPSQGLV 48
DDX49/1-483 DDX47/1-455 DDX23/1-820 DD19A/1-478 DD19A/1-478 DD19A/1-478 DDX25/1-483 DDX46/1-483 DDX46/1-483 DDX46/1-483 DDX26/1-497 DDX22/1-400 DX39A/1-427 DDX29/1-610 DDX37/1-660 DDX37/1-660 DDX37/1-620 DDX46/1-1031	421 432 801 678 474 475 479 478 478 424 423 540 608 612 614 697 824	KD PD L E	430K TEGAIG- HKPGTI CERSQFEAER VKEALPAEL SRGSSS SRASSS RKGKST	440N I KQ KNRR F KE K VRNKV LTKKRI L AKRNR KKQKQ EK EK EK 	450T / EE [†] L KRQ KAGR AGGKMKK EET I FA AKS VFD AN D Y 	460G AĠHKGRPPRT LTNTSKK SRTSSQSPRR	470S 480Q PSGSHSGPVPSQGLV 48
DDX49/1-483 DDX47/1-455 DDX23/1-820 DD139/1-478 DD139/1-478 DDX5/1-483 DDX6/1-483 DDX46/1-483 DDX46/1-483 DDX26/1-483 DDX26/1-483 DDX26/1-483 DDX26/1-483 DDX26/1-483 DDX26/1-483 DDX26/1-483 DDX37/1-660 DDX37/1-660 DDX37/1-660 DDX37/1-660 DDX37/1-660 DDX37/1-600 DDX37/1-600 DDX37/1-600 DDX37/1-600 DDX37/1-600 DDX37/1-600 DDX46/1-1031 DDX42/1-338	421 432 801 678 474 475 479 478 424 423 540 608 612 614 697 824 697 824	KD PD L E	430K TEGAIG- HKPGTI CERSQFEAER VKEALPAEL SRGSSS SRASSS RKGKST	440N I KQ KNRR F KE K VRNKV LTKKRI L AKRNR KKQKQ EK EK EK 	450T / EE [†] L KRQ KAGR AGGKMKK EET I FA KKS VFD AN AN D Y CONSUME AN CONSUME CONSU	460G AGHKGRPPRT SRTSSQSPRR SRTSSQSPRR KQEEERQPQT SAAKGIPGET	470S 480Q PSG SH SG P V P SQ G L V 48
DDX49/1-483 DDX47/1-455 DDX23/1-820 DD139/1-478 DD139/1-479 DDX25/1-483 DDX6/1-483 DDX46/1-483 DDX46/1-483 DDX26/1-483 DDX28/1-406 DX38/1-427 DDX20/1-824 DDX20/1-824 DDX39/1-600 DDX3/1-600 DDX3/1-604	421 432 801 678 474 475 479 478 424 423 540 608 612 612 614 697 824 697 824 992	KD PD L E	430K TEGAIG- HKPGTI CERSQFEAER SQFEAER SRGSSS	440N I KQ KNRR F KE K VRNKV EK EK EK EK 	450T / EE [†] L KRQ KAGR AGGKMKK EET I FA KKS VFD AN AN D Y CONSUME	460G AGHKGRPPRT SRTSSQSPRR SRTSSQSPRR KQEEERQPQT SAAKGIPGET QGTYG- GVYS	470S 4800 P SG SH SG P V P S G L V 48
DDX49/1-483 DDX47/1-455 DDX23/1-820 DD13A/1-478 DD13A/1-478 DD13B/1-479 DDX55/1-483 DDX6/1-483 DDX46/1-483 DDX26/1-483 DDX28/1-406 DDX24/1-406 DDX24/1-406 DDX34/1-662 DDX34/1-662 DDX34/1-729 DDX46/1-1031 DDX42/1-538 DDX17/1-729 DDX57/1-614 DDX33/1-614 DDX33/1-614	421 432 801 474 475 479 478 423 540 608 612 614 697 824 685 582 492 636	KD PD L E	430K TEGAIG- HKPGTI CERSQFEAER SQFEAER SRGSSS	440N I KQ KN R R F K E K	450T / EE [†] L KRQ KAGR AGGKMKK EET I FA KKS VFD AKS VFD AN D Y CONSUME CONS	460G AGHKGRPPRT SRTSSQSPRR SRTSSQSPRR KQEEERQPQT SAAKGIPGET QGTYG - GVYS	470S 4800 PSGSHSGPVPSQGLV 48
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Supplementary Figure S1. Multiple sequence alignment of human DExD box helicases

Amino acid sequences of 38 human DExD box helicases (Supplementary Table S1) were obtained from Uniprot database. Multiple sequence alignment (MSA) was generated using MAFFT (1) from EMBL-EBI server. In the MSA provided, DDX49

was set as the reference sequence and all insertions are masked. The positions of insertions are shown by vertical dotted red lines. Conserved residue columns with sequence identity > 40% are highlighted in blue color, with darker color indicating higher conservation. The grey numbers indicate the start and end of the specific DExD box helicase for a given section of MSA. The number followed by amino acid at the top of the alignment corresponds to the residue position in the reference, DDX49. Sequence motifs, predicted based on conservation profiles, are provided at the bottom of the MSA with a brown line.



Supplementary Figure S2. Chromatin preparation from HEK293 cells

The sheared chromatin was run on 1% agarose gel and stained with ethidium bromide. The gel shows the presence of mononucleosomes, dinucleosomes, trinucleosomes and higher molecular weight chromatin.



Supplementary Figure S3. The helicase activity of DDX49 is RNA independent

RNA helicase activity of DDX49 was determined in the presence and absence of R13 RNA oligo (**A**) or Total RNA (**B**).



Supplementary Figure S4. Relative quantification of endogenous DDX39B and DDX49 transcript levels

Quantitative RT-PCR analysis of DDX39B and DDX49 levels in HEK293 cells. The levels of DDX39B and DDX49 were normalized to GAPDH expression and are presented relative to the DDX49 expression. Data are represented as mean of three independent experiments, with error bars representing standard deviation.



Supplementary Figure S5. Efficiency of siRNA mediated knockdown of DDX39B and DDX49

Efficiency of siRNA mediated knockdown of DDX39B or DDX49 transcripts was tested using quantitative RT-PCR analysis in HeLa cells. Cells were transfected with control siRNA, DDX39B siRNA (left panel) or DDX49 siRNA (right panel). The transcript levels of DDX39B and DDX49 were normalized to GAPDH expression and are presented relative to the control sample. Data are represented as mean of three independent experiments, with error bars representing standard deviation.



Supplementary Figure S6. DDX49 is essential for efficient poly (A)⁺ RNA export

HeLa cells treated with control, DDX39B or DDX49 siRNA were fixed and poly (A)⁺ RNAs were labelled with ATTO 550 dye (red in merge; inverted grey image in monochrome channel). Subsequently, cells were washed with SSC buffer and DNA stained with DAPI (blue) and embedded in Mowiol. Images were acquired using fluorescence microscope (Nikon-Eclipse 80i) with 100X oil immersion objective. Scale bar is depicted.



T: Total cell extract C: Cytoplasmic extract

Supplementary Figure S7. The purity of the cytoplasmic extract used for the quantification of mRNA export (Corresponds to Figure 2C)

Western blot analysis of total (T) and cytoplasmic (C) extracts prepared from HeLa cells, which were transfected with control siRNA, DDX39B siRNA or DDX49 siRNA. The immunoblotting was performed with histone 3 antibody (nuclear protein) or beta actin antibody. The absence of histone 3 signal in cytoplasmic extracts indicates the absence of nuclear leakage in the cytoplasmic fractions.



Supplementary Figure S8. Subcellular localization of DDX49 and DDX39B in different cell types

DDX49 is localized in the nucleolus. Representative images depicting the colocalization of DDX49 and fibrillarin in (**A**) HeLa cells and (**B**) U251MG cells. Cells were transfected with pEGFP-DDX49 or pEGFP-DDX39B (green), immunostained with fibrillarin antibody (red), which stains the nucleolus. DAPI is shown in blue. Representative image depicting the colocalization of DDX49 and fibrillarin and the absence of colocalization of DDX39B with fibrillarin. The white arrows indicate the nucleolus. Insets show the magnified images of the regions outlined by the dotted white squares. Scale bar is depicted.



Supplementary Figure S9. Effect of DDX49 perturbation on cell proliferation

(A) Depletion of DDX49 (siDDX49) inhibits cell proliferation. HeLa cells were transfected with control siRNA or DDX49 siRNA and the cell numbers were counted at 48, 72 and 96 hours post transfection. The dots represent the mean of triplicates, with error bars representing standard deviation. (B) Overexpression of DDX49 (DDX49OE) promotes cell proliferation. HeLa cells were transfected with pEGFP-C1 vector or pEGFP-DDX49 and the cell numbers were counted 48, 72 and 96 hours post transfection. The dots represent the mean of triplicates, with error bars representing standard deviation. (C) HeLa cells were transfected with the control or DDX49 siRNAs or treated with 0.5 µg of MG-132 (left panel) or pEGFP-DDX49 (right panel). After 72 hours of transfection or drug treatment, MTT assay was performed. MG-132 is a potent proteosomal inhibitor known to induce apoptosis (2,3) was used as positive control for the assay. Data are represented as mean of three independent experiments, with error bars representing standard deviation. Statistical significance was estimated using two-tailed T-test. * indicates P<0.05 and ** indicates P<0.01.







Supplementary Figure S10. DDX49 is a distinct DExD box RNA helicase

(A) Pairwise sequence identity of DDX49 with the other DExD box RNA helicases. (B) Protein-protein interaction landscape of DDX49. The bar plot on the left shows the extent of overlap of interaction partners between DDX49 and other DExD box RNA helicases, quantified using Jaccard Similarity Index (JSI). The legend at the bottom provides a schematic representation of how JSI was calculated. The numbers in the parenthesis represent the number of protein interactors identified so far for the corresponding DExD box helicase. The network on the right, drawn using Cytoscape, shows the interaction of DDX49 interactors with diverse DExD box RNA helicases. DDX49 (green color node) and its interaction partners (grey nodes) are connected by green color links. Golden yellow nodes represent the other DExD box RNA helicases and the grey links show their connections with the interaction partners of DDX49. The table below the network provides a brief description of the proteins interacting with DDX49.

Uniprot accession	Ensembl gene	Entrez gene	Gene name(s)	Protein length	DExD Motif type	DExD Motif position
Q9H8H2	ENSG00000125485	64794	DDX31	851	DEAD	388-391
015523	ENSG0000067048	8653	DDX3Y, DBY	660	DEAD	345-348
Q9NUU7	ENSG00000168872	55308	DDX19A, DDX19L	478	DEAD	241-244
Q9UMR2	ENSG00000157349	11269	DDX19B, DBP5, DDX19, TDBP	479	DEAD	242-245
Q92499	ENSG0000079785	1653	DDX1	740	DEAD	370-373
Q7L014	ENSG00000145833	9879	DDX46, KIAA0801	1031	DEAD	529-532
Q9Y6V7	ENSG00000105671	54555	DDX49	483	DEAD	152-155
Q13838	ENSG00000198563	7919	DDX39B, BAT1, UAP56	428	DECD	196-199
Q13206	ENSG00000178105	1662	DDX10	875	DEAD	222-225
Q9NVP1	ENSG0000088205	8886	DDX18, cPERP-D	670	DEAD	333-336
Q9GZR7	ENSG0000089737	57062	DDX24	859	DEAD	471-474
Q96GQ7	ENSG00000124228	55661	DDX27, cPERP-F, RHLP, HSPC259, PP3241	796	DEAD	371-374
O00571	ENSG00000215301	1654	DDX3X, DBX, DDX3	662	DEAD	347-350
Q9NXZ2	ENSG0000080007	55510	DDX43, HAGE	648	DEAD	396-399
Q86TM3	ENSG00000184735	168400	DDX53, CAGE	631	DEAD	376-379
Q8NHQ9	ENSG00000111364	57696	DDX55, KIAA1595	600	DEAD	171-174
Q5T1V6	ENSG00000118197	83479	DDX59, ZNHIT5	619	DEAD	353-356
Q9NR30	ENSG00000165732	9188	DDX21	783	DEVD	339-342
Q9UHL0	ENSG00000109832	29118	DDX25, GRTH	483	DEAD	247-250
Q9UJV9	ENSG00000183258	51428	DDX41, ABS	622	DEAD	344-347
Q9Y2R4	ENSG00000278053	11056	DDX52, ROK1, HUSSY-19	599	DESD	318-321
Q9UHI6	ENSG0000064703	11218	DDX20, DP103, GEMIN3	824	DEAD	211-214

Supplementary Table S1. Members of human DExD family of RNA helicases

Uniprot accession	Ensembl gene	Entrez gene	Gene name(s)	Protein length	DExD Motif type	DExD Motif position
Q9NUL7	ENSG00000182810	55794	DDX28, MDDX28	540	DEAD	286-289
Q9H0S4	ENSG00000213782	51202	DDX47	455	DEAD	174-177
Q9NQI0	ENSG00000152670	54514	DDX4, VASA	724	DEAD	446-449
Q9BQ39	ENSG00000107625	79009	DDX50	737	DEVD	290-293
Q8TDD1	ENSG00000123064	79039	DDX54	881	DEAD	247-250
P26196	ENSG00000110367	1656	DDX6, HLR2, RCK	483	DEAD	246-249
Q86XP3	ENSG00000198231	11325	DDX42	938	DEAD	407-410
Q8N8A6	ENSG00000185163	317781	DDX51	666	DEAD	371-374
Q92841	ENSG00000100201	10521	DDX17	729	DEAD	325-328
Q9BUQ8	ENSG00000174243	9416	DDX23	820	DEAD	549-552
Q9NY93	ENSG00000136271	54606	DDX56, DDX21, NOH61	547	DEAD	166-169
P17844	ENSG00000108654	1655	DDX5, G17P1, HELR, HLR1	614	DEAD	248-251
O00148	ENSG00000123136	10212	DDX39A, DDX39	427	DECD	195-198
P38919	ENSG00000141543	9775	EIF4A3, DDX48, KIAA0111	411	DEAD	187-190
Q14240	ENSG00000156976	1974	EIF4A2, DDX2B, EIF4F	407	DEAD	183-186
P60842	ENSG00000161960	1973	EIF4A1, DDX2A, EIF4A	406	DEAD	182-185

Supplementary Table S2. List of the siRNAs used in various experiments

siRNA	Sequence (5' to 3') (Sense strand)
siControl	AUCCGCGCGAUAGUACGUA
siDDX49	GAGAGUGUGAGAUCAAACU
siDDX39B	GUGCUACCUUGAGCAAAGA

Supplementary Table S3. List of the primers used in qPCR for various investigations

Gene Name	Sequence (5' to 3')	Investigation
U1 snRNA-FP	ACCTGGCAGGGGGAGATACCA	mRNA Export
U1 snRNA-RP	GGGGAAAGCGCGAACGCAGT	mRNA Export
Egr1-FP	GACCCGTTCGGATCCTTTCC	mRNA Export
Egr1-RP	GCCACAAGGTGTTGCCACTG	mRNA Export
GAPDH-FP	TCACCAGGGCTGCTTTTAAC	mRNA Export
GAPDH-RP	TGACGGTGCCATGGAATTTG	mRNA Export
YY2-FP	TATAGCGGCTGCGAAAAGAT	mRNA Export
YY2-RP	CTTTGCCACATTCTGCACAT	mRNA Export
47S rRNA-FP	CTGTCCTCTGGCGACCTG	47S rRNA level
47S rRNA-RP	GAGAGAACAGCAGGCCCG	47S rRNA level
DDX39B-FP	GAGCAAAGAGATCCGTCCAG	DDX39B Expression
DDX39B-RP	TTCCGGTTCTTCTCGTTGTC	DDX39B Expression
DDX49-FP	CTTCTTCTGGGAAGCACAGG	DDX49 Expression
DDX49-RP	TTCATCATGGAGTGCAGAGC	DDX49 Expression
H42-FP	GCACCGTTTGTGTGGGGGTTGG	ChIP
H42-RP	CGAGACAGATCCGGCTGGCAG	ChIP
H0-FP	GGAGGTATATCTTTCGCTCCGAG	ChIP
H0-RP	GACGACAGGTCGCCAGAGGA	ChIP
H13-FP	ACCTGGCGCTAAACCATTCGT	ChIP
H13-RP	GGACAAACCCTTGTGTCGAGG	ChIP
H18-FP	GTTGACGTACAGGGTGGACTG	ChIP
H18-RP	GGAAGTTGTCTTCACGCCTGA	ChIP

Supplementary References

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