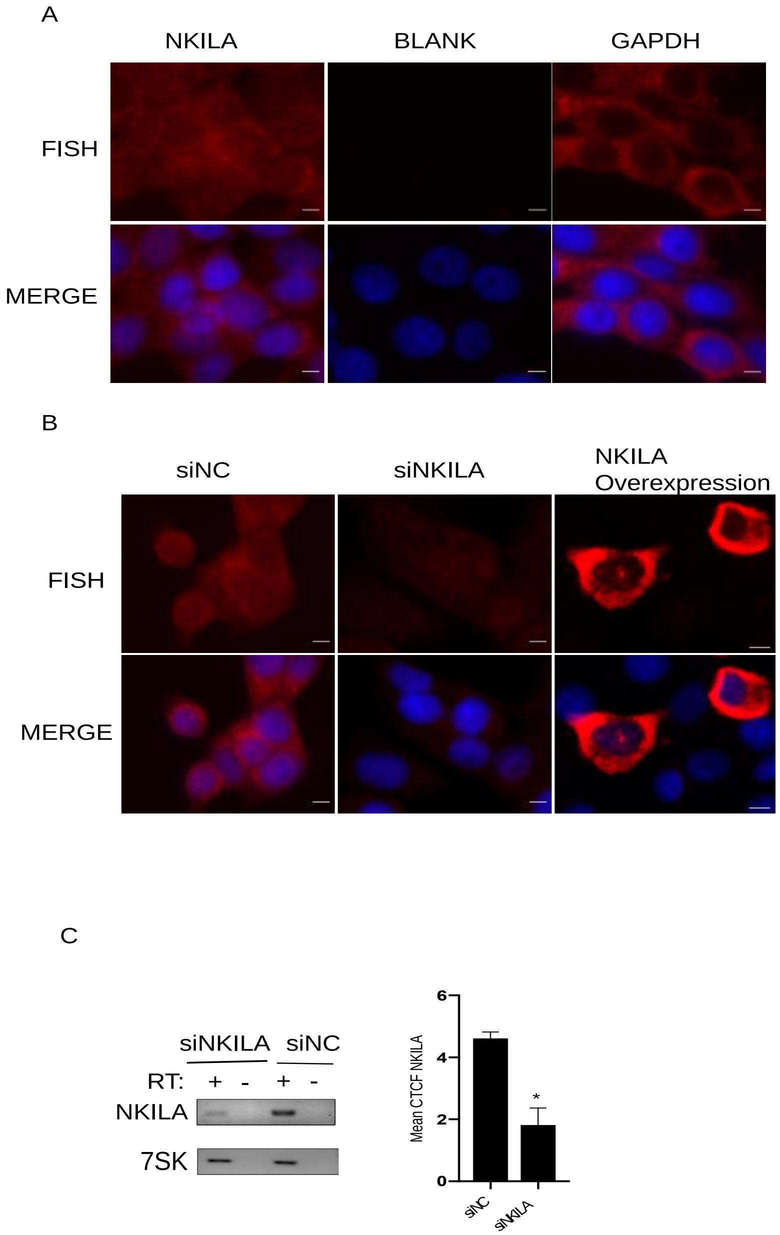
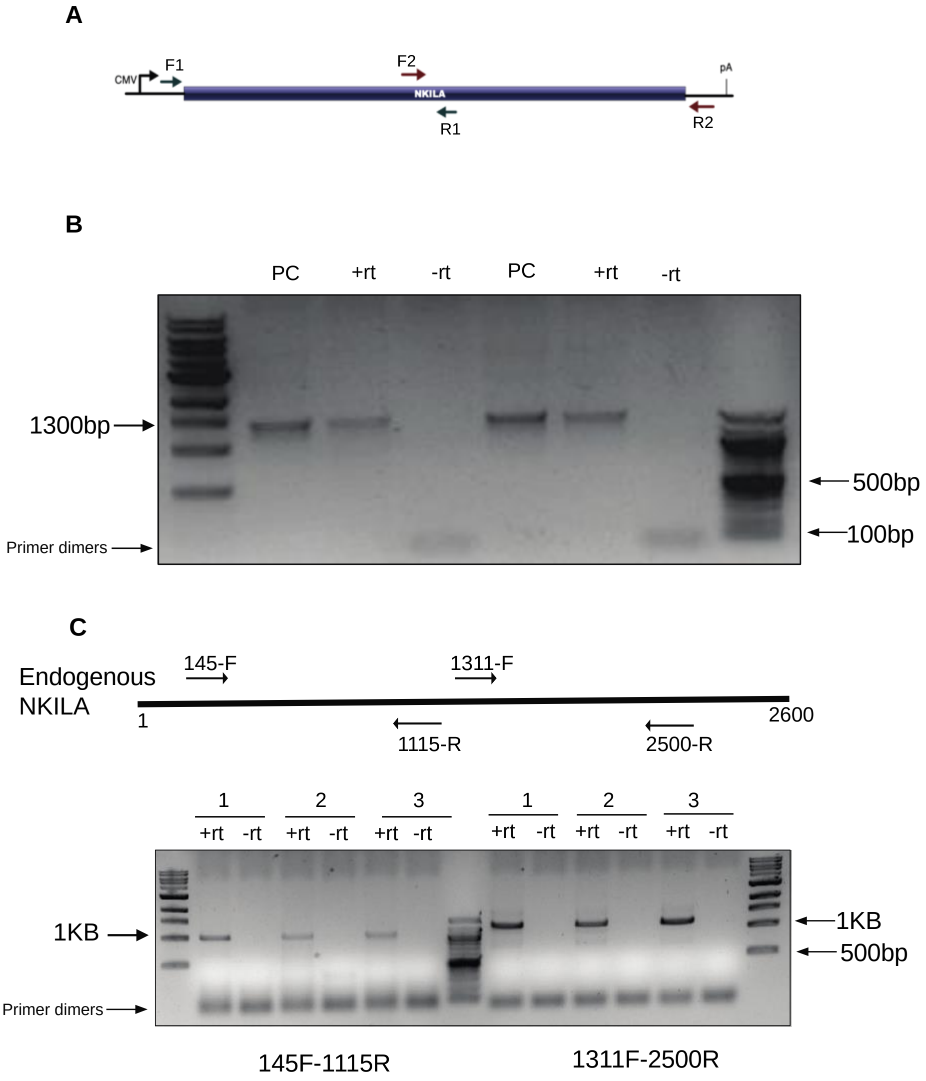
Supplementary Data

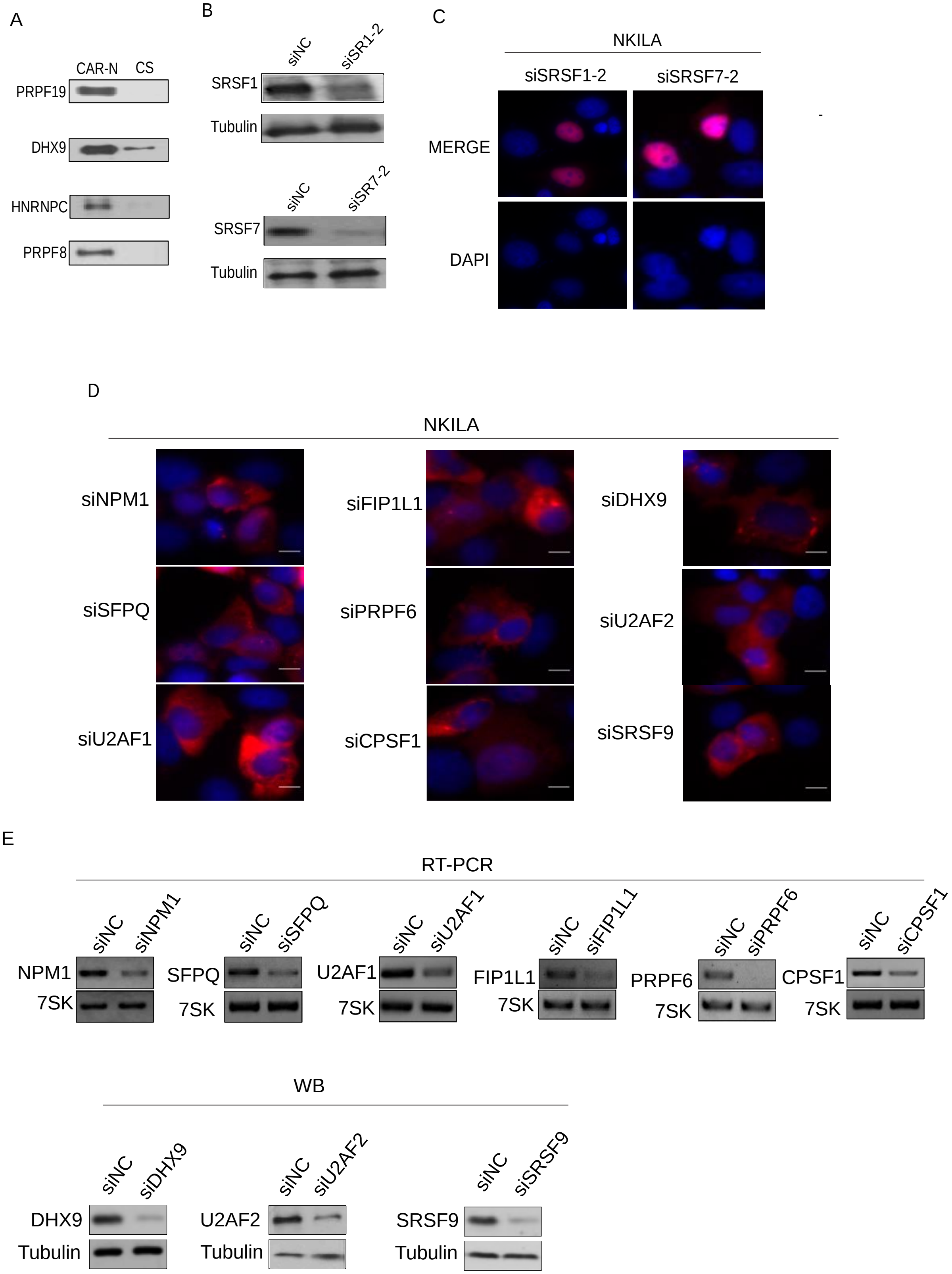
Supplementary Fig. S1



Supplementary Fig. S2



Supplementary Fig. S3



Supplementary Figure Legends

Supplementary Figure S1: Endogenous NKILA is predominately located in the cytoplasm. A) RNA-FISH showing the localization of endogenous NKILA using Stellaris. RNA-FISH of GAPDH mRNA was used as the positive control. Blank sample (without FISH probe) was used as the negative control. Scale bar = 15 μm. B) Comparison of FISH signal for endogenous NKILA in cells transfected with siNC, siNKILA, and after NKILA overexpression. C) RT-PCR to check expression level of NKILA after transfection with siNKILA. +rt: with reverse transcriptase, -rt: negative control without reverse transcriptase. 7SK was used as the loading control for RT-PCR. Right panel showing the corrected total cell fluorescence (CTCF) quantified by ImageJ after two independent experiments. (n=2, approximately 20 cells in each image were quantified. *: $p<0.05$).

Supplementary Figure S2: RT-PCR assay to exclude potential cryptic slicing in NKILA.

A) Schematic to show the NKILA reporter. Arrows indicate the position of primers used in RT PCR. F: forward primer, R: reverse primer. B) RT-PCR after transfection of NKILA reporter showing no cryptic splicing. +rt: with reverse transcriptase, -rt: negative control without reverse transcriptase, PC: positive control with plasmid DNA used as the PCR template. C) RT-PCR of endogenous NKILA. Arrows indicate the position of primers and the digits are nucleotide number of primers. 1, 2, 3 represent three independent experiments.

Supplementary Figure S3: Effect of siRNA treatment targeting CAR-N RNP components on NKILA export.

A) Validation of identified proteins in the RNP by western blot. B) Western blot showing relative protein level after siRNA2 treatment of SRSF1 and SRSF7. C) RNA-FISH showing the localization of NKILA. D) RNA-FISH showing the localization of overexpressed NKILA after treatment with indicated siRNA in MCF-7 cells. Scale bar = 10 µm. E) RT-PCR and western blotting analyses were used to check the knockdown efficiency after siRNA treatment. 7SK and tubulin were used as the loading control for RT-PCR and western blotting, respectively.

Supplementary Table S1,

Primer sequences for cloning or RT-PCR

Target	Fwd Seq (5'-----→3')	Rev Seq (5'-----→3')
NKILA	TTCAGCCACTCCAGACACAG	CAAGCGTTGTGGGTAGGTTT
MEG3-cDNA-Reporter	TATGGTACCAGCCCCTAGCGCAGACG	ATCTCGAGGAGAGCACAGTGGGGTGCG
Truncation (Fig.2A-b)	ATAGGTACCAGACCCGGCACCCGCGCAAC	CATCTCGAGGAGGTCAAGCGTTGTGGGTA
Truncation (Fig.2A-c)	ATAGGTACCAGACCCGGCACCCGCGCAAC	ATACTCGAGCCTCTGGGCTGGGCACGCTT
Truncation (Fig.2A-d)	ATAGGTACCAGACCCGGCACCCGCGCAAC	ATACTCGAGTGCTCATACCCCTTTTGAAC
Truncation (Fig.2A-e)	GGAGGTACCAATTACAGGAGTGCTACAAGAA	AACCTCGAGCCAGTTAAATTGAGATATACTTAC
Truncation (Fig.2A-f)	TTGGGTACCACTCAACCTGACACCGACTC	AACCTCGAGCCAGTTAAATTGAGATATACTTAC
Truncation (Fig.2A-g)	GAAGGTACCCTCGCGTAGACACGCCCGGA	AACCTCGAGCCAGTTAAATTGAGATATACTTAC
Truncation (Fig.2A-h)	TAAGGTACCTCTTCTGAGGAGCACAAGGT	AACCTCGAGCCAGTTAAATTGAGATATACTTAC
Deletion (Fig.2A-i) 1-196	ATAGGTACCAGACCCGGCACCCGCGCAAC	GCACTCCTGTAATTTAGGCTAGCCCCAAGAGCCTGGGTCA
Deletion (Fig.2A-i)	CTTGGGGCTAGCCTAAATTACAGGAGTGCTACAAG	AACCTCGAGCCAGTTAAATTGAGATATACTTAC

601-2597		
Deletion (Fig.2A-j)1-196	ATAGGTACCAGACCCGGCACCCGCGCAAC	GCAGCAGACAATGGTAGGCTAGCCCCAAGAGCCTGGG
Deletion (Fig.2A-j) 501-2597	CTTGGGGCTAGCCTACCATTGTCTGCTGCCCAAGGGGC	AACCTCGAGCCAGTTAAATTGAGATATACTTAC
Deletion (Fig.2A-k) 1-196	ATAGGTACCAGACCCGGCACCCGCGCAAC	CGTGTCTACGCGAGTAGGCTAGCCCCAAGAGCCTGGGT
Deletion (Fig.2A-k) 401-2597	CTTGGGGCTAGCCTACTCGCGTAGACACGCCCGGAAGC	AACCTCGAGCCAGTTAAATTGAGATATACTTAC
Deletion (Fig.2A-l) 1-196	ATAGGTACCAGACCCGGCACCCGCGCAAC	CTGAAGGCGGACAGTAGGCTAGCCCCAAGAGCCTGG
Deletion (Fig.2A-l) 301-2597	TTGGGGCTAGCCTACTGTCCGCCTTCAGTTCTCCAG	AACCTCGAGCCAGTTAAATTGAGATATACTTAC
Deletion (Fig.2A-m) 1-250	ATAGGTACCAGACCCGGCACCCGCGCAAC	CGACAATACACCAGCTTTCTCCAATTTCTCTTCCCT
Deletion (Fig.2A-m450-2597)	AAATTGGAGAAAGCTGGTGTATTGTCGCCGCCCCA	AACCTCGAGCCAGTTAAATTGAGATATACTTAC
NKILA-nt-250-450 (Fig.2N)	CTAGGTACCGGGGGAGGAAGCCCCCAAGA	AGACTCGAGTCCCCGACAGCTATTTACATG

NKILA-nt-1773-1973	AATGGTACCTCAGCCACTCCAGACACAGCCC	ATACTCGAGTGGGAGGTCAAGCGTTGTGGGT
CAR-N-5' ß-globin cDNA (CAR-N)	GGTACCGGGGGAGGAAGCCCCCAAGA	TCAGATGCACCATTCCCCGACAGCTATTTACATG
CAR-N-5' ß -globin cDNA (ß –globin cDNA)	AGCTGTCGGGGAATGGTGCATCTGACTCCTGAGG	CTCGAGTTAGTGATACTTGTGGGCCAGG
CS-5'-ß globin-cDNA (CS)	AATGGTACCTCAGCCACTCCAGACACAGCCC	GATGCACCATTGGGAGGTCAAGCGTTGTGG
CS-5'-ß globin cDNA (ß-globin cDNA)	TGACCTCCCAATGGTGCATCTGACTCCTGA	CTCGAGTTAGTGATACTTGTGGGCCAGG
GAS5cdna-Reporter	CGGGGTACCTTTCGAGGTAGGAGTCGACTCCTGTG	CGCGGATCCAAAATTGGAGACACTGTTTTAATCTTCTTG
CAR-N-5' GAS5 cDNA (CAR-N)	GGTACCGGGGGAGGAAGCCCCCAAGA	TACCTCGAAATCCCCGACAGCTATTTACATGAC
CAR-N-5' GAS5cDNA (GAS5)	AGCTGTCGGGGATTTCGAGGTAGGAGTCGA	GCGCTCGAGAAAATTGGAGACACTGTTTT
CS5'GAS5	AATGGTACCTCAGCCACTCCAG	TACCTCGAAATGGGAGGTCAAGC

cDNA(CS)	ACACAGCCC	GTTGTGGG
CS-5’GAS5 cDNA(GAS)	TGACCTCCCATTTCGAGGTAGGAGTCGAC	GCGCTCGAGAAAATTGGAGACACTGTTTT
5srRNA	GGCCATACCACCCTGAACGC	GGCCATACCACCCTGAACGC
NKILA-Reporter-PCR-1 (Fig.S2)	AATACGACTCACTATAGGG	ATACTCGAGCCTCTGGGCTGGGCACGCTT
NKILA-Reporter-PCR–2 (Fig.S2)	TGCCCAGCCCAGAGGGAGGTTCAG	TAGAAGGCACAGTCGAGG
NPM1	TCCGGATGACTGACCAAGAG	CAAGCAAAGGGTGGAGTTCC
SFPQ	TGCCCTTTCTGTTCGTAATCTT	TCCCTTTGCTGTTTTTCCAT
U2AF1	ATCCCGGGAGCGTCGTTC	CCCCTTATGAACTGGTTTGGTC
FIP1L1	CGTGCATGTGCACAGTGATT	CATACTGTGGTGCTCCCGTT
PRPF6	CCTATGAAAATGCCCGCAAGG	TGTCACATTCCTCGGCATCC
CPSF1	GTACGCCGTGTACAAACAGG	GGGTCTTCAGGTCATGGGTG
GAPDH	CTGAGTACGTCGTGGAGTCC	AGGCAGGGATGATGTTCTGG
7SK	GACATCTGTCACCCCATTGA	GCCTCATTTGGATGTGTCTG
NKILA Endogenous F1	CCCCTCGCCCCCGTCCCTGG	ACTTCCCAAATTCCAGCTTTTCC

NKILA Endogenous F2	TCTTTGGAGGAGTCCAAGCG	GCACACACGAAGCCTCCTA

Supplementary Table S2,

siRNA sequences/IDs

Target	**Sense (5'-----→3')**	**Antisense (5'-----→3')**
siUAP56	GGGCUUGGCUAUCACAUUU	AAAUGUGAUAGCCAAGCCC
siURH49	AAAGGCCUAGCCAUCACUUU	AAAGUGAUGGCUAGGCCUUU
siTAP/NXF1	GCGCCAUUCGCGAACGA	AAUCGUUCGCGAAUGGCGC
siTHOC2	GGUUAUGCCAAGCUGAUUG	CAAUCAGCUUGGCAUAACC
siALYREF	siB09826163427	siB09826163427
siSRSF1	ACGAUUGCCGCAUCUACGU	ACGUAGAUGCGGCAAUCGU
siSRSF1-2	stB0007827A	stB0007827A
siSRSF7	AGGAGAGUUAGAAAGGGCU	AGCCCUUUCUAACUCUCCU
siSRSF7-2	stB0007832A	stB0007832A
siNPM1	CGAAGGCAGUCCAAUUAAA	UUUAAUUGGACUGCCUUCG
siSFPQ	stB0007825C	stB0007825C
siDHX9	GUAAAUGAACGUAUGCUGA	UCAGCAUACGUUCAUUUAC
siSRSF9	stB0008682A	stB0008682A
siU2AF2	GCACGGUGGACUGAUUCGU	ACGAAUCAGUCCACCGUGC
siU2AF1	stB0008214A	stB0008214A
siFIPIL1	StB0013863A	StB0013863A
siPRPF6	GAGAAGAUUGGGCAGCUUA	TAAGCTGCCCAATCTTCTC

siCPSF1	siG13108180752	siG13108180752
siNKILA	GGGCAGUAGGAAAGGAGAA	UUCUCCUUUCCUACUGCCC

Supplementary Table S3

Proteins Identified by Mass Spec in RNP purification

Description	Symbol	# Peptides CAR-N	# Peptides CS	MW [kDa]	CAR-N total Peptides/ MW
Nucleophosmin	NPM1	21	2	32.6	0.645
Splicing factor, proline- and glutamine-rich	SFPQ	30	8	76.1	0.394
Septin 9, isoform CRA_a	Septin9	24	1	63.6	0.377
Serine/arginine-rich splicing factor 1	SRSF1	10	1	27.7	0.360
Probable ATP-dependent RNA helicase DDX17	DDX17	28	9	80.2	0.349
Caprin-1 (Fragment)	CAPRIN1	6		20.2	0.296
SNRPG protein	SNRPG	2		7.1	0.281
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	7		25.2	0.277
X-ray repair cross-complementing protein 6	XRCC6	19	7	69.8	0.272
RPS4X protein (Fragment)	RPS4X	7		27.2	0.256
Replication factor C subunit 5 (Fragment)	RFC5	3		11.9	0.252
ATP-dependent RNA helicase DDX3X	DDX3X	17	5	69.0	0.246
X-ray repair cross-complementing protein 5	XRCC5	20	7	82.7	0.241
ATP-dependent RNA helicase A	DHX9	34	20	140.9	0.241
Lamina-associated polypeptide 2, isoform alpha	TMPO	17		75.4	0.225
Cold-inducible RNA-binding protein (Fragment)	CIRBP	2		8.9	0.224
Small nuclear ribonucleoprotein Sm D2	SNRPD2	3	1	13.5	0.221

Serine/arginine-rich-splicing factor 9	SRSF9	3		13.8	0.217
Polyadenylate-binding protein 1	PABPC1	15		70.6	0.212
FBL protein (Fragment)	FBL	6		28.4	0.211
RPL27/NME2 fusion protein (Fragment)	RPL27	3		14.2	0.210
DNA topoisomerase 1	TOP1	19		90.7	0.209
Nucleolin, isoform CRA_c	NCL	12		58.5	0.205
Receptor of activated protein C kinase 1	RACK1	7	2	35.1	0.199
ELAV-like protein 1	ELAVL1	7	1	36.1	0.194
Septin-2	Septin2	8		41.5	0.192
Cleavage and polyadenylation-specificity factor subunit 6	CPSF6	10		52.2	0.191
RNA-binding motif protein, X chromosome	RBMX	8	4	42.3	0.189
Histone H1.2	HIST1H1C	4		21.4	0.187
Nucleolar RNA helicase 2	DDX21	16		87.3	0.183
Proliferation-associated protein 2G4	PA2G4	8		43.8	0.182
Tropomyosin alpha-3 chain	TPM3	2		11.0	0.181
Histone H1.5	HIST1H1B	4		22.6	0.177
Pre-mRNA-processing factor 19	PRPF19	9		55.1	0.163
Polypyrimidine tract binding protein 1, isoform CRA_b	PTBP1	9	1	56.5	0.159
U2 small nuclear ribonucleoprotein B"	SNRPB2	4	2	25.5	0.157
THO complex subunit 4	ALYREF	4		26.9	0.148
U2 snRNP auxiliary factor large subunit	U2AF2	5		33.9	0.147
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	4	1	27.9	0.143
Splicing factor U2AF 35 kDa subunit	U2AF1	4		27.9	0.143
Poly [ADP-ribose] polymerase 1	PARP1	16		113.0	0.141
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1CA	5		37.5	0.133
Serine/arginine-rich-splicing factor 7	SRSF7	2		15.8	0.126

tRNA-splicing ligase RtcB homolog	RTCB	7		55.2	0.126
Mitotic checkpoint protein BUB3 (Fragment)	BUB3	4		31.7	0.126
ATP-dependent RNA helicase DDX39A	DDX39A	6	4	49.1	0.122
ATP-dependent RNA helicase DDX1	DDX1	9	3	73.9	0.121
Coronin	CORO1C	5		41.6	0.120
H/ACA ribonucleoprotein complex subunit DKC1 (Fragment)	DKC1	3		25.8	0.116
Protein DEK (Fragment)	DEK	2		17.2	0.115
RNA-binding protein 14	RBM14	8		69.4	0.115
Ras GTPase-activating protein-binding protein 1	G3BP1	6		52.1	0.115
Replication factor C (Activator 1) 2, 40kDa, isoform CRA_a	RFC2	4		35.2	0.113
Eukaryotic initiation factor 4A-I (Fragment)	EIF4A1	2		18.0	0.110
Replication factor C subunit 4	RFC4	4		36.9	0.108
Prelamin-A/C	LMNA	8	2	74.1	0.107
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	7		66.5	0.105
Splicing factor 3B subunit 2 (Fragment)	SF3B2	3	1	29.1	0.103
Nucleolar transcription factor 1	UBTF	9		87.4	0.102
RuvB-like helicase (Fragment)	RUVBL1	5	2	50.2	0.099
KRT18 protein (Fragment)	KRT18	4	1	42.1	0.094
DNA topoisomerase 2 (Fragment)	TOP2B	17		180.5	0.094
Coronin-1B	CORO1B	5		54.2	0.092
Poly(U)-binding-splicing factor PUF60 (Fragment)	PUF60	5	1	54.6	0.091
Splicing factor 3A subunit 1	SF3A1	8	2	88.8	0.090
Histone H1x	H1FX	2		22.5	0.088
Matrin-3	MATR3	8	4	94.6	0.084
Heterogeneous nuclear ribonucleoprotein U-like 1, isoform CRA_a	HNRPUL1	7	2	84.7	0.082
Septin 11, isoform CRA_b	Septin11	4		49.0	0.081
Poly(rC)-binding protein 1	PCBP1	3	1	37.5	0.080

Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase, isoform CRA_a	MTHFD1	8		101.5	0.078
RuvB-like 2	RUVBL2	4	1	51.1	0.078
Pre-mRNA-processing factor 6	PRPF6	8		106.9	0.074
DNA-3-methyladenine glycosylase (Fragment)	MPG	2		27.3	0.073
GTPBP4 protein (Fragment)	GTPBP4	5		73.7	0.067
Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	NOP2	6		89.2	0.067
DnaJ homolog subfamily C member 9	DNAJC9	2		29.9	0.066
U4/U6.U5 tri-snRNP-associated protein 2	USP39	4		62.0	0.064
Arginine/serine-rich splicing factor 6 variant (Fragment)		2		31.8	0.062
Cytidine 5'-monophosphate N-acetylneuraminic acid synthetase variant (Fragment)		3		48.3	0.062
RNA-binding protein EWS	EWSR1	4	1	64.9	0.061
Dynamin-2	DNM2	6		98.0	0.061
Septin-8	Septin8	3		49.3	0.060
RNA cytidine acetyltransferase	NAT10	7		115.7	0.060
RCC2 protein (Fragment)	RCC2	3		49.6	0.060
NOP56 protein (Fragment)	NOP56	3		49.7	0.060
Ubiquitin carboxyl-terminal hydrolase 10	USP10	5		87.1	0.057
CD2 antigen cytoplasmic tail-binding protein 2	CD2BP2	2		37.6	0.053
FACT complex subunit SPT16	SUPT16H	6		119.8	0.050
FACT complex subunit SSRP1	SSRP1	4		81.0	0.049
NAT10 protein (Fragment)	NAT10	3		62.3	0.048
Plakophilin-3	PKP3	4		87.0	0.045
DNA topoisomerase 2-alpha	TOP2A	8		174.3	0.045
Fragile X mental retardation autosomal homolog variant p5FK	FXR1	3		67.2	0.044

U4/U6.U5 tri-snRNP-associated protein 1	SART1	4		90.2	0.044
Cleavage stimulation factor subunit 2	CSTF2	2		46.6	0.042
ACTN4 protein (Fragment)	ACTN4	3		73.6	0.040
REST corepressor 1	RCOR1	2		53.3	0.037
Mediator of RNA polymerase II transcription subunit 17	MED17	2		55.9	0.035
60 kDa U4/U6 snRNP-specific spliceosomal protein	PRPF4	2		58.3	0.034
Splicing factor 3B subunit 1	SF3B1	5		145.7	0.034
MRE11A protein (Fragment)	MRE11A	2		59.7	0.033
DNA-dependent protein kinase catalytic subunit	PRKDC	15		468.8	0.031
Coilin	COIL	2		62.6	0.031
Unconventional myosin-Ib	MYO1B	4		128.4	0.031
DNA repair protein XRCC1	XRCC1	2		66.0	0.030
RNA-binding protein 15	RBM15	3		102.1	0.029
Myosin-9	MYH9	6		226.4	0.026
Cleavage and polyadenylation specific factor 1, 160kDa, isoform CRA_a	CPSF1	4		151.9	0.026
Nuclear fragile X mental retardation-interacting protein 2	NUFIP2	2		76.1	0.026
General transcription and DNA repair factor IIH helicase subunit XPD (Fragment)	ERCC2	2		80.5	0.024
E3 ubiquitin-protein ligase UHRF1	UHRF1	2		89.8	0.022
RNA-binding protein 25	RBM25	2		100.1	0.019
DNA mismatch repair protein Msh6	MSH6	3		152.7	0.019
SNRNP200 protein (Fragment)	SNRNP200	4		216.0	0.018
MORC family CW-type zinc finger protein 2	MORC2	2		117.7	0.016
Filamin-A	FLNA	4		245.7	0.016
Pre-mRNA processing splicing factor 8	PRPF8	4		273.4	0.014

Note: Complete list of CAR-N enriched RNP. Proteins with total peptide numbers less than 2 were omitted.

cDNA FLJ Sequences identified by Mass Spec

Description	# Peptides CAR-N	# Peptides CS	MW [kDa]	CAR-N total Peptides/ MW
cDNA FLJ76817, highly similar to Homo sapiens non-POU domain containing, octamer-binding (NONO), mRNA	26	5	54.3	0.479
cDNA FLJ57805, highly similar to Homo sapiens paraspeckle component 1 (PSPC1), transcript variant alpha, mRNA	22	2	52.5	0.418
cDNA FLJ53366, highly similar to Probable ATP-dependent RNA helicase DDX5	25	11	67.7	0.369
cDNA, FLJ93125, highly similar to Homo sapiens cleavage and polyadenylation specific factor 5, 25 kDa(CPSF5), mRNA	7	1	26.2	0.267
cDNA FLJ54551, highly similar to Septin-7	8		47.9	0.167
cDNA, FLJ93365, highly similar to Homo sapiens KH domain containing, RNA binding, signal transduction associated 1 (KHDRBS1), mRNA	8		48.2	0.165
cDNA FLJ59645, highly similar to 116 kDa U5 small nuclear ribonucleoprotein component	16		103.8	0.154
cDNA FLJ53422, highly similar to TATA-binding protein-associated factor 2N	5	1	40.1	0.124
cDNA FLJ57877, highly similar to Cleavage and polyadenylation specificity factor 7	6		51.1	0.117
cDNA, FLJ95131, highly similar to Homo sapiens nucleolar and coiled-body phosphoprotein 1 (NOLC1), mRNA	8		73.6	0.108
cDNA FLJ78677, highly similar to Homo sapiens splicing factor 3b, subunit 3, 130kDa (SF3B3), mRNA	13	3	135.5	0.095
cDNA, FLJ93750, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 6 (DDX6), mRNA	5		53.2	0.094
cDNA FLJ55635, highly similar to pre-mRNA-splicing factorATP-dependent RNA helicase DHX15	8	1	89.5	0.089
cDNA, FLJ94417, highly similar to Homo sapiens WD repeat domain 57 (U5 snRNP specific) (WDR57), mRNA	3		39.2	0.076
cDNA FLJ51295, highly similar to Cell division cycle 5-like protein	6		89.2	0.067

cDNA FLJ13913 fis, clone Y79AA1000231, highly similar to Nucleolar protein NOP5	3		52.3	0.057
cDNA FLJ57893, highly similar to Parafibromin	2		35.9	0.055
cDNA FLJ51688, highly similar to Cleavage stimulation factor 50 kDa subunit	2		46.8	0.042
cDNA FLJ50575, highly similar to U4/U6 small nuclear ribonucleoprotein Prp3	3		72.1	0.041
cDNA FLJ58134, highly similar to Cleavage stimulation factor 77 kDa subunit	3		72.1	0.041
cDNA FLJ58737, highly similar to Splicing factor 3A subunit 3	2		52.4	0.038
cDNA FLJ59523, highly similar to Scaffold attachment factor B	3		91.0	0.032
cDNA FLJ60634, highly similar to Exosome component 10	2		77.7	0.025
cDNA FLJ51771, highly similar to SWI/SNF-related matrix-associatedactin-dependent regulator of chromatin subfamily A member5	3		116.7	0.025
cDNA FLJ59510, highly similar to Homo sapiens tight junction protein 2 (TJP2), transcript variant 2, mRNA	2		115.1	0.017

Supplementary Table S4: Subset of proteins detected by mass spectrometry and categorized by Gene Ontology (GO) as RNA transport/localization/export.

Name	**Symbol**	**Total Peptides CAR-N**	**Total Peptides CS**
Nucleophosmin	NPM1	21	2
Splicing factor, proline- and glutamine-rich	SFPQ	30	8
Serine/arginine-rich splicing factor 1	SRSF1	10	1
ATP-dependent RNA helicase A	DHX9	34	20
Serine/arginine-rich-splicing factor 9	SRSF9	3	-
THO complex subunit 4	ALYREF	4	-
U2 snRNP auxiliary factor large subunit	U2AF2	5	-
Splicing factor U2AF 35 kDa subunit	U2AF1	4	-
Serine/arginine-rich-splicing factor 7	SRSF7	2	-
ATP-dependent RNA helicase DDX39A	DDX39A	6	4
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	7	-
Pre-mRNA-processing factor 6	PRPF6	8	-
Cleavage and polyadenylation specific factor 1	CPSF1	4	-

Subset of proteins detected by mass spectrometry and categorized by gene ontology (GO) in RNA transport/localization/export categories in CAR-N and CS, with the number of peptides.

Supplementary Table S5: Proteins identified by Mass Spec in SRSF1/7-IP

Description	Symbol	# Peptides igG(IP)	# Peptides SRSF1/7 (IP)	MW [kDa]	peptides in SRSF1/7/M.W
Serine/arginine-rich splicing factor 1	SRSF1	2	18	27.7	0.649167603
Serine/arginine-rich-splicing factor 7	SRSF7	1	9	15.8	0.571326369
Alpha-actinin-4	ACTN4	16	50	104.8	0.477151694
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	27	112	284.4	0.39386108
60S ribosomal protein L22 (Fragment)	RPL22		2	5.1	0.393725449
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	1	13	33.1	0.39233617
Serine/arginine-rich-splicing factor 3	SRSF3		4	10.3	0.387823612
X-ray repair cross-complementing protein 6	XRCC6		27	69.8	0.386824708
40S ribosomal protein S3	RPS3	2	10	26.7	0.374933004
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	5	14	37.4	0.374264219
Annexin A2	ANXA2	3	14	38.6	0.362884049
Serine/arginine-rich splicing factor 9	SRSF9	1	9	25.5	0.352575736
Heat shock protein beta-1	HSPB1	5	8	22.8	0.351362721
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1CA	5	13	37.5	0.346779431
cDNA, FLJ93125, highly similar to Homo sapiens cleavage and polyadenylation specific factor 5, 25 kDa(CPSF5), mRNA OS			9	26.2	0.343528437
Major vault protein	MVP		33	99.3	0.332440316
Actin, alpha cardiac muscle 1	ACTC1	9	13	42.0	0.309583643

cDNA FLJ51660, highly similar to Interleukin enhancer-binding factor 2	ILF2	5	12	38.9	0.308593123
Tubulin beta chain	TUBB	9	15	49.6	0.302181913
Serine/threonine-protein phosphatase (Fragment)	PPP1CC	2	10	33.8	0.296280376
Small nuclear ribonucleoprotein-associated protein		2	7	23.6	0.296093631
Spectrin beta chain, non-erythrocytic 2	SPTBN2	20	78	271.2	0.287656092
Coronin	2 SV	3	15	53.2	0.282007915
Mitotic interactor and substrate of PLK1	MISP	6	21	75.3	0.278843897
X-ray repair cross-complementing protein 5	XRCC5		22	82.7	0.266175356
Cell division cycle and apoptosis regulator protein 1	CCAR1		35	132.7	0.263675163
Actin-related protein 2/3 complex subunit 2	ARPC2		9	34.3	0.262302828
RPS4X protein (Fragment)	RPS4X		7	27.2	0.256949379
Vesicle-associated membrane protein-associated protein B/C	VAPB		2	7.8	0.256538944
Actin-related protein 3	ACTR3	1	12	47.3	0.253480158
Alpha-actinin-1	ACTN1	5	26	103.0	0.25244523
U2 small nuclear ribonucleoprotein A'	SNRPA1	5	7	28.4	0.246495062
Tubulin alpha-1C chain	TUBA1C	6	9	36.6	0.245715018
Src substrate cortactin	CTTN		15	61.5	0.243710109
Tubulin beta-4B chain	TUBB4B	8	12	49.8	0.240968673
60S ribosomal protein L9 (Fragment)	RPL9		5	20.8	0.240820666
Spectrin beta chain, non-erythrocytic 1	SPTBN1	14	66	274.4	0.240490866
Neurabin-2	PPP1R9B	6	21	89.1	0.235590544
Ribosomal protein S2	rps2		6	25.6	0.234477667
SmB /B' autoimmune antigene (Fragment)		1	5	22.0	0.227492864

40S ribosomal protein S7	RPS7		5	22.1	0.226108689
40S ribosomal protein S20	RPS20		3	13.4	0.224478495
Epithelial protein lost in neoplasm beta variant (Fragment)			19	85.2	0.223001047
CROP protein (Fragment)	CROP		6	27.0	0.222232327
cDNA FLJ76817, highly similar to Homo sapiens non-POU domain containing, octamer-binding (NONO), mRNA	NONO	6	12	54.3	0.221184422
Poly(U)-binding-splicing factor PUF60 (Fragment)	PUF60	10	12	54.6	0.219812318
Paraspeckle component 1, isoform CRA_b	PSPC1	1	10	45.5	0.219576142
Elongation factor 1-alpha 1	EEF1A1	3	11	50.1	0.219520958
Probable ATP-dependent RNA helicase DDX17	DDX17	7	17	80.2	0.211959332
RPL27/NME2 fusion protein (Fragment)	RPL27		3	14.2	0.210556573
Caspase-6	CASP6		7	33.3	0.210282839
40S ribosomal protein S16	RPS16		3	14.4	0.208189356
cDNA FLJ54552, highly similar to Heterogeneous nuclear ribonucleoprotein K		1	10	48.5	0.206269821
ATP-dependent RNA helicase A	DHX9	6	29	140.9	0.205864855
Splicing factor U2AF 65 kDa subunit	U2AF2	4	11	53.5	0.205733633
Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a	CAPZB		6	29.3	0.204940227
60S ribosomal protein L7	RPL7	1	5	24.4	0.204772108
60S acidic ribosomal protein P0		1	7	34.2	0.2045718

40S ribosomal protein SA (Fragment)	RPSA	1	6	29.4	0.20417918
SFPQ protein (Fragment)	SFPQ	9	14	68.6	0.204117582
40S ribosomal protein S5	RPS5		3	14.8	0.203338374
CSDA protein variant (Fragment)			3	14.8	0.203010649
ATP-dependent RNA helicase DDX5 (Fragment)	DDX5	5	14	69.1	0.20267025
60S ribosomal protein L7a	RPL7A		6	30.0	0.20015328
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	1	5	25.2	0.198089918
X-ray repair complementing defective repair in Chinese hamster cells 4, isoform CRA_a	XRCC4		7	35.3	0.198021432
Unconventional myosin-Ib	MYO1B	1	25	128.4	0.1947041
Tight junction protein ZO-1	TJP1	2	38	195.3	0.194532633
Gelsolin	GSN	1	16	82.5	0.19399976
Ig heavy chain variable region (Fragment)	IgH		2	10.4	0.191990899
Serine/arginine-rich-splicing factor 10	SRSF10		4	20.9	0.1913833
RNA-binding protein 25	RBM25	13	19	100.1	0.189763896
Interleukin enhancer-binding factor 3	ILF3	4	18	95.3	0.188918707
VH6DJ protein (Fragment)	VH6DJ		2	10.6	0.188410157
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	2	13	69.6	0.18689009
LUC7-like (S. cerevisiae), isoform CRA_f	LUC7L	1	6	32.4	0.185025742
Rheumatoid factor RF-IP24 (Fragment)			2	10.8	0.184597735
cDNA FLJ78586, highly similar to Homo sapiens VAMP (vesicle-	VAPA		5	27.3	0.18315036

associated membrane protein)-associated protein A, 33kDa (VAPA), mRNA					
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	4	9	49.2	0.182932737
cDNA FLJ75422, highly similar to Homo sapiens capping protein (actin filament) muscle Z-line, alpha 1, mRNA			6	32.9	0.182435623
Tubulin alpha-4A chain	TUBA4A	5	9	49.9	0.180388298
40S ribosomal protein S13	RPS13		3	16.7	0.179401623
Actin-related protein 2	ACTR2	1	8	44.7	0.178841944
Cofilin 1 (Non-muscle), isoform CRA_a	CFL1	1	3	16.8	0.178562724
60S ribosomal protein L8	RPL8		5	28.0	0.178524947
Elongation factor 1-alpha 2	EEF1A2	3	9	50.4	0.178435797
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	1	7	39.6	0.176899077
Actin-related protein 2/3 complex subunit 5			3	17.0	0.176878551
cDNA FLJ77404, highly similar to Homo sapiens small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen) (SNRP70), transcript variant 1, mRNA	SNRP70	1	9	51.5	0.17487652
cDNA FLJ34725 fis, clone MESAN2005958, highly similar to RNA-binding protein Luc7-like 2		2	7	40.5	0.172981496
Polyadenylate-binding protein	PABPC1	1	10	58.5	0.17094355
cDNA FLJ75556, highly similar to Homo sapiens ribosomal protein L14, mRNA			4	23.6	0.169268361
Cingulin	CGN		23	136.3	0.168740283

U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	13	41	244.4	0.167790296
cDNA FLJ44500 fis, clone UTERU3000828, highly similar to 116 kDa U5 small nuclear ribonucleoprotein component		10	18	108.1	0.16644825
rRNA 2'-O-methyltransferase fibrillarin (Fragment)	FBL		3	18.2	0.164950393
rRNA 2'-O-methyltransferase fibrillarin (Fragment)	FBL		4	24.5	0.16307328
Myosin IC, isoform CRA_a	MYO1C		16	98.9	0.161825114
cDNA, FLJ93681, highly similar to Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA	SNRPA	2	5	31.3	0.159809729
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	1	11	70.9	0.155149734
Aprataxin (Fragment)	APTX		5	32.6	0.153318099
Actin-related protein 2/3 complex subunit 4	ARPC4		2	13.0	0.153267987
cDNA FLJ53573, highly similar to Myosin Ic			18	119.0	0.151282897
SH3-containing Grb-2-like 1 protein			6	39.8	0.150696538
CSNK1A1 protein (Fragment)	CSNK1A1		4	26.7	0.149897108
Splicing factor 3A subunit 1	SF3A1	9	13	88.8	0.146346106
40S ribosomal protein S25	RPS25	2	2	13.7	0.145627187
Cleavage and polyadenylation-specificity factor subunit 7 (Fragment)	CPSF7		6	41.2	0.145487403
ATP-dependent RNA helicase DDX3X	DDX3X	1	10	69.0	0.144917218
cDNA FLJ44468 fis, clone UTERU2026025,		1	2	13.8	0.144872464

moderately similar to SPLICING FACTOR, ARGININE/SERINE-RICH 2					
Casein kinase I isoform alpha	CSNK1A1		4	27.7	0.144284779
Small nuclear ribonucleoprotein Sm D3	SNRPD3	1	2	13.9	0.143809316
Drebrin	DBN1		10	71.4	0.140084585
60S ribosomal protein L24	RPL24		2	14.4	0.13927748
Pre-mRNA-processing-splicing factor 8	PRPF8	7	38	273.4	0.138976983
ELAV-like protein 1	ELAVL1		5	36.1	0.138622611
Nucleolin, isoform CRA_c	NCL		8	58.5	0.136706984
RNA-binding protein 39 (Fragment)	RBM39	2	5	36.6	0.136606512
RAB1B protein	RAB1B		3	22.2	0.135231133
60S ribosomal protein L17 (Fragment)	RPL17		2	14.9	0.134364961
Suppressor of Ty 5 homolog (S. cerevisiae), isoform CRA_a	SUPT5H		14	104.3	0.134205627
DNA damage-binding protein 1	DDB1	12	17	126.9	0.133977129
40S ribosomal protein S3a	RPS3A		4	29.9	0.133664193
40S ribosomal protein S9	RPS9		3	22.6	0.132875315
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	4	6	45.6	0.131455398
DNA topoisomerase 2-beta	TOP2B	1	24	183.2	0.131038371
Pre-mRNA-processing factor 6	PRPF6	5	14	106.9	0.131015237
Filamin A	FLNA	4	36	277.3	0.129808139
Heterogeneous nuclear ribonucleoprotein U-like 1, isoform CRA_a	HNRPUL1	6	11	84.7	0.129807283
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0		4	30.8	0.129778331
E3 ubiquitin-protein ligase TRIM21	TRIM21	6	7	54.1	0.129306064

Heterogeneous nuclear ribonucleoprotein M	HNRNPM	3	10	77.5	0.129001598
40S ribosomal protein S17	RPS17		2	15.5	0.128696894
60S ribosomal protein L18	RPL18		2	15.6	0.127961167
cDNA, FLJ94417, highly similar to Homo sapiens WD repeat domain 57 (U5 snRNP specific) (WDR57), mRNA	WDR57	1	5	39.2	0.127415376
60S ribosomal protein L4	RPL4		6	47.7	0.12587211
Arginine/serine-rich splicing factor 6 variant (Fragment)	SRSF6	2	4	31.8	0.125603886
Heterogeneous nuclear ribonucleoprotein D0 (Fragment)	HNRNPD	1	3	23.9	0.125490575
40S ribosomal protein S14 (Fragment)	RPS14		2	16.1	0.12384323
Splicing factor 3B subunit 1	SF3B1	12	18	145.7	0.123509226
Transformer-2 protein homolog alpha	TRA2A		4	32.7	0.12243999
U4/U6.U5 tri-snRNP-associated protein 2	USP39	1	8	65.3	0.122437051
Archaemetzincins-2, isoform CRA_d	AMZ2	3	5	41.2	0.1212475
Scaffold attachment factor B2	SAFB2	2	13	107.4	0.121033721
60S ribosomal protein L10a	RPL10A		3	24.8	0.120892008
Elongation factor 1-gamma	EEF1G	1	6	50.1	0.119791217
Plakophilin-3 (Fragment)	PKP3		2	16.8	0.119399061
cDNA FLJ46571 fis, clone THYMU3041428, highly similar to Probable ATP-dependent RNA helicase DDX23	ddx23	3	11	93.2	0.118055309
Protein FAM207A	FAM207A		3	25.4	0.117920779

RuvB-like 2	RUVBL2		6	51.1	0.117360431
Parafibromin	CDC73	5	7	60.5	0.115627779
cDNA FLJ54020, highly similar to Heterogeneous nuclear ribonucleoprotein U		3	10	86.8	0.115198935
U1 small nuclear ribonucleoprotein C	SNRPC		2	17.4	0.115066598
Cleavage and polyadenylation-specificity factor subunit 6	CPSF6	3	6	52.2	0.11485938
cDNA FLJ57937, highly similar to DNA-directed RNA polymerase II 33 kDa polypeptide			2	17.5	0.114489804
40S ribosomal protein S18	RPS18		2	17.7	0.112944189
THO complex subunit 4	ALYREF	1	3	26.9	0.111641942
Splicing factor 45	RBM17		5	44.9	0.111274516
60S ribosomal protein L5 (Fragment)	RPL5		3	27.0	0.11099722
SH3KBP1 binding protein 1, isoform CRA_c	SHKBP1	1	8	73.7	0.108604914
Eukaryotic initiation factor 4A-III	EIF4A3	1	5	46.8	0.106743672
Poly(rC)-binding protein 1	PCBP1	2	4	37.5	0.10674083
Testicular tissue protein Li 128			3	28.4	0.105698155
Ladinin-1	LAD1		6	57.1	0.105084615
Transcription elongation regulator 1	TCERG1		13	123.8	0.104988333
Elongation factor 1-delta (Fragment)	EEF1D		3	28.8	0.104153648
KH domain containing, RNA binding, signal transduction associated 1, isoform CRA_b	KHDRBS1		4	38.7	0.103470541
Nucleolar RNA helicase 2	DDX21		9	87.3	0.103104139
60 kDa U4/U6 snRNP-specific spliceosomal protein	PRPF4	2	6	58.3	0.102943601

cDNA FLJ40872 fis, clone TUTER2000283, highly similar to Homo sapiens transformer-2-beta (SFRS10) gene			3	29.2	0.102798808
DNA-dependent protein kinase catalytic subunit	PRKDC	2	48	468.8	0.102391714
Spliceosome RNA helicase DDX39B	DDX39B		5	49.0	0.1021243
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	2	5	49.2	0.101559364
Pre-mRNA-splicing regulator WTAP	WTAP		2	19.9	0.100608641
HCG32740, isoform CRA_b	hCG_32740		12	119.4	0.100515979
cDNA FLJ59523, highly similar to Scaffold attachment factor B		2	9	91.0	0.098868087
cDNA FLJ61545, highly similar to Coatomer subunit beta			3	30.5	0.098331373
Actin-related protein 2/3 complex subunit 3			2	20.5	0.097526135
Nuclear mitotic apparatus protein 1	NUMA1	5	23	236.0	0.097449769
WD repeat-containing protein 61	WDR61	1	2	20.7	0.096475716
Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3	AGAP3		9	95.0	0.094751517
Ran GTPase-activating protein 1	RANGAP1		6	63.5	0.094484756
Fusion (Involved in t(12;16) in malignant liposarcoma) isoform a variant (Fragment)		2	3	32.0	0.093825381
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E		2	21.4	0.093257034
40S ribosomal protein S8	RPS8	1	2	21.9	0.09146614
F-actin-capping protein subunit alpha-2	CAPZA2		3	32.9	0.091106185
Pre-mRNA-processing factor 19	PRPF19	1	5	55.1	0.090667838

Polypyrimidine tract binding protein 1, isoform CRA_b	PTBP1		5	56.5	0.088534204
Actin filament-associated protein 1	AFAP1		7	80.7	0.086768151
cDNA, FLJ96225, highly similar to Homo sapiens heat shock 70kDa protein 1-like (HSPA1L), mRNA		5	6	70.3	0.085309343
cDNA FLJ78246, highly similar to Homo sapiens splicing factor 3a, subunit 3, 60kDa (SF3A3), mRNA	SF3A3	1	5	58.8	0.085100221
FACT complex subunit SPT16	SUPT16H	6	10	119.8	0.083445689
cDNA, FLJ94229, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein L (HNRPL),mRNA	HNRPL	1	5	60.2	0.083041019
Pre-mRNA-processing factor 40 homolog A	PRPF40A	2	9	108.7	0.082768834
Brain-specific angiogenesis inhibitor 1-associated protein 2	BAIAP2		5	60.8	0.082196799
cDNA FLJ53820, highly similar to U4/U6.U5 tri-snRNP-associated protein 1		2	6	73.4	0.081749802
E3 ubiquitin-protein ligase ZNF598	ZNF598		8	98.6	0.081156312
Elongation factor 1-beta	EEF1B2		2	24.7	0.080813751
CD2 antigen cytoplasmic tail-binding protein 2	CD2BP2		3	37.6	0.079737958
cDNA FLJ55635, highly similar to pre-mRNA-splicing factorATP-dependent RNA helicase DHX15	dhx15	4	7	89.5	0.078220549
DNA topoisomerase 1	TOP1	3	7	90.7	0.07720397
CDC2L2 protein (Fragment)	CDC2L2	2	4	52.4	0.076374623

cDNA FLJ53422, highly similar to TATA-binding protein-associated factor 2N		1	3	40.1	0.074898508
Actin-related protein 2/3 complex subunit 1B	ARPC1B		3	40.9	0.073307662
RNA-binding protein 14	RBM14		5	69.4	0.071995372
U2 small nuclear RNA auxillary factor 1 isoform a	U2AF1	1	2	27.9	0.071799319
cDNA FLJ57899, highly similar to Mitotic checkpoint protein BUB3			2	28.2	0.070869513
WD40 repeat-containing protein SMU1	SMU1		4	57.5	0.069556469
TJP3 protein (Fragment)	TJP3		7	101.1	0.069238226
Coronin	CORO1B		2	28.9	0.069130632
Receptor of-activated protein C kinase 1	RACK1		2	29.7	0.067268146
Tight junction protein 2 (Zona occludens 2), isoform CRA_a	TJP2		9	133.9	0.067219209
Serine protease HTRA2, mitochondrial (Fragment)	HTRA2		3	45.1	0.066541029
Taperin	TPRN	1	5	75.5	0.066216678
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	1	2	30.3	0.066041513
DNA-directed RNA polymerase subunit beta	POLR2B		8	121.3	0.065954967
FYVE and coiled-coil domain-containing protein 1	FYCO1		11	166.9	0.065915872
cDNA FLJ57562, highly similar to Cleavage and polyadenylation specificityfactor 73 kDa subunit			3	45.9	0.065360733
DNA ligase	LIG4		6	96.2	0.062400478
Putative oxidoreductase protein	BQ8482_110351		2	32.7	0.061239314
Nuclear receptor subfamily 2 group C member 2	NR2C2		4	65.4	0.061187263

Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	1	4	66.5	0.060162553
Albumin (Fragment)		7	4	66.5	0.060161246
Twinfilin-1 (Fragment)	TWF1		2	33.4	0.059903548
RuvB-like helicase (Fragment)	RUVBL1		3	50.2	0.059779676
Cleavage and polyadenylation specific factor 1, 160kDa, isoform CRA_a	CPSF1		9	151.9	0.059253532
U2 snRNP-associated SURP motif-containing protein	U2SURP	1	7	118.2	0.059212336
RNA-binding protein 15	RBM15		6	102.1	0.058781279
cDNA FLJ38393 fis, clone FEBRA2007212			6	102.9	0.058328432
Protein FAM98A	FAM98A	1	2	34.4	0.058124138
Uncharacterized protein DKFZp686G11190	DKFZp686G11190	2	3	52.0	0.057681245
cDNA FLJ60629, highly similar to Replication factor C subunit 3			2	34.8	0.057454521
Transcription factor ETV6	ETV6		3	53.0	0.056639451
SIPA1L1 protein	SIPA1L1	1	11	199.8	0.055043148
Leucine zipper putative tumor suppressor 2	LZTS2		4	72.7	0.055009357
tRNA-splicing ligase RtcB homolog	RTCB		3	55.2	0.05437259
GTPBP4 protein (Fragment)	GTPBP4		4	73.7	0.054301465
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3		2	36.9	0.054196013
Coatomer subunit delta	ARCN1		3	57.2	0.052471286
Zinc finger protein 185	ZNF185		3	58.3	0.051490911
Cleavage and polyadenylation specificity factor subunit 2		1	4	78.1	0.051188576
cDNA FLJ51017, highly similar to ATP-dependent RNA helicase DDX1 (Fragment)			3	59.2	0.050710704
Coatomer subunit alpha	COPA		7	138.3	0.050630021

Serum paraoxonase/arylesterase 1	PON1		2	39.7	0.05036993
cDNA FLJ61347, highly similar to General transcription factor II-I			3	59.6	0.050349593
cDNA FLJ35376 fis, clone SKMUS2004044, highly similar to Homo sapiens ribosomal protein L3 (RPL3), transcript variant 2, mRNA			2	40.1	0.049850878
cDNA FLJ78217			2	40.3	0.049678431
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2		4	85.1	0.047029957
cDNA, FLJ94450, highly similar to Homo sapiens cyclin-dependent kinase 9 (CDC2-related kinase) (CDK9), mRNA		1	2	42.7	0.046816303
Disks large homolog 5	DLG5		10	213.7	0.046786864
Filamin-B	FLNB		13	278.0	0.04676426
Coatomer subunit beta	COPB1		5	107.1	0.046696784
cDNA FLJ56491, highly similar to DNA-repair protein XRCC1			2	43.2	0.046302457
cDNA FLJ52785, highly similar to Protein cereblon		1	2	43.3	0.046226872
Thyroid hormone receptor-associated protein 3	THRAP3	1	5	108.6	0.046040083
cDNA FLJ55260, highly similar to Exosome complex exonuclease RRP45			2	43.5	0.045941091
Nucleolar transcription factor 1	UBTF	2	4	87.4	0.045776956
WD repeat-containing protein 1	WDR1		3	66.2	0.04535019
cDNA FLJ39996 fis, clone STOMA2002166,		1	2	44.5	0.04498912

highly similar to Splicing factor 3B subunit 4					
cDNA FLJ51295, highly similar to Cell division cycle 5-like protein			4	89.2	0.04485754
DnaJ homolog subfamily A member 1	DNAJA1		2	44.8	0.044603575
Protein FAM83G	FAM83G		4	90.8	0.044063187
Actin-binding LIM protein 1	ABLIM1		2	46.0	0.043438547
Caprin-1	CAPRIN1		3	70.3	0.042668179
Histone-binding protein RBBP7	RBBP7		2	46.9	0.042635933
Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1	MAGI1		7	164.5	0.042558154
Matrin-3	MATR3		4	94.6	0.042299036
Trans-acting T-cell-specific transcription factor GATA-3	GATA3		2	47.9	0.041766434
cDNA FLJ50575, highly similar to U4/U6 small nuclear ribonucleoprotein Prp3			3	72.1	0.041632409
cDNA FLJ60738, highly similar to RNA polymerase-associated protein LEO1			3	72.7	0.041242664
SAFB-like transcription modulator (Fragment)	SLTM		2	48.8	0.040967842
PPP1R9A protein	PPP1R9A		5	122.3	0.040866901
5'-3' exoribonuclease			4	99.9	0.04004482
Splicing factor, arginine/serine-rich 15	SFRS15		5	125.7	0.039789217
Protein unc-45 homolog A	UNC45A		4	103.0	0.038830618
cDNA, FLJ94773, highly similar to Homo sapiens splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA			5	128.8	0.038805652

Anti-RhD monoclonal T125 gamma1 heavy chain		2	2	52.3	0.038219512
Oxysterol-binding protein (Fragment)	OSBPL8		3	79.0	0.037972809
Bcl-2-associated transcription factor 1	BCLAF1		2	52.9	0.037817443
cDNA FLJ35987 fis, clone TESTI2014269, highly similar to D-3-phosphoglycerate dehydrogenase			2	53.0	0.037750509
cDNA FLJ61696, highly similar to Double-stranded RNA-specific adenosine deaminase			4	106.9	0.037401084
cDNA, FLJ79396, highly similar to Phenylalanyl-tRNA synthetase beta chain			2	54.8	0.03650991
Supervillin	SVIL		9	247.6	0.036350035
DNA ligase 3	LIG3		4	112.8	0.035450054
cDNA, FLJ94919, highly similar to Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 12A (PPP1R12A), mRNA			4	115.3	0.034704342
Probable ATP-dependent RNA helicase DDX46	DDX46	1	4	117.3	0.034103647
BTB/POZ domain-containing protein KCTD3	KCTD3		3	88.9	0.033734893
NEDD4-binding protein 3	N4BP3		2	60.4	0.033094651
Nuclear cap-binding protein subunit 1	NCBP1	1	3	91.8	0.032686674
Myosin-9	MYH9		7	226.4	0.030919875
cDNA, FLJ92684, highly similar to Homo sapiens IK cytokine, down-regulator of HLA II (IK), mRNA			2	65.6	0.03049815

HCG1994636, isoform CRA_b	hCG_1994636		3	101.5	0.029549169
Calcium homeostasis endoplasmic reticulum protein	CHERP		3	103.6	0.028947157
Clathrin heavy chain 1	CLTC		2	70.6	0.028325526
Zinc finger CCCH domain-containing protein 18	ZC3H18		3	106.3	0.028217898
Spermatid perinuclear RNA binding protein isoform 2 (Fragment)	STRBP		2	72.1	0.02774456
Endoplasmic reticulum chaperone BiP	HSPA5	5	2	72.3	0.027666941
Complement C4-A	C4A		5	187.6	0.026645933
AKAP8 protein OS	AKAP8	1	2	76.1	0.026274618
KIAA0324 (Fragment)	KIAA0324		5	191.2	0.026151589
RNA cytidine acetyltransferase	NAT10		3	115.7	0.025938856
YLP motif-containing protein 1	YLPM1		6	241.5	0.024845258
cDNA FLJ75071, highly similar to Homo sapiens pinin, desmosome associated protein (PNN), mRNA		1	2	81.5	0.024542002
FN1 protein	FN1		6	246.5	0.024336492
Desmoplakin	DSP	6	8	331.6	0.024127728
DNA-directed RNA polymerase II subunit RPB1	POLR2A		5	217.0	0.023037327
Pleckstrin homology domain-containing family G member 3	PLEKHG3		3	134.3	0.022333183
La-related protein 1 (Fragment)	LARP1		2	90.8	0.022034482
RNA-binding protein 5	RBM5		2	92.1	0.021716242
Kinesin-like protein	KIF23		2	92.6	0.021592517
USP6 N-terminal-like protein	USP6NL		2	94.0	0.02126627
RNA binding motif protein 10 isoform 1 (Fragment)	RBM10		2	94.3	0.021206161

cDNA FLJ45597 fis, clone BRTHA3018409, weakly similar to Mus musculus synaptotagmin-like 4 (Sytl4)			2	95.2	0.021012501
Cyclin-dependent kinase 13 (Fragment)	CDK13		3	143.8	0.020860357
pre-mRNA 3' end processing protein WDR33	WDR33		3	145.8	0.020576231
Coatomer subunit gamma-2	COPG2		2	97.6	0.020500292
cDNA FLJ54557, highly similar to helicase MOV-10			2	106.5	0.018787867
Signal-induced proliferation-associated 1 like 3	SIPA1L3		3	194.5	0.015423881
IQ motif containing GTPase activating protein 1	IQGAP1		2	189.2	0.010572957
Unconventional myosin-Vc	MYO5C		2	202.7	0.009867664
Titin, isoform CRA_b	TTN		2	2991.2	0.000668631

Supplementary Table S6: Proteins identified by Mass Spec in ALYREF-IP

Description	Symbol	# Peptides IgG(IP)	# Peptides ALYREF(IP)	MW [kDa]	peptides ALYREF/MW
RPS4X protein (Fragment)	RPS4X		12	27.2	0.440484649
Histone H4	HIST1H4A		5	11.4	0.440126033
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	5	16	37.4	0.427730536
Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	1	12	33.1	0.362156465
Heat shock protein beta-1	HSPB1	5	8	22.8	0.351362721
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	1	8	25.2	0.316943868
cDNA FLJ51660, highly similar to Interleukin enhancer-binding factor 2	ILF2	5	12	38.9	0.308593123
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	1	11	39.6	0.277984264
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	2	18	69.6	0.258770894
U2 small nuclear ribonucleoprotein A'	SNRPA1	5	7	28.4	0.246495062
Tubulin beta chain	TUBB	9	12	49.6	0.24174553
Actin, alpha cardiac muscle 1	ACTC1	9	10	42.0	0.238141264
Transferrin receptor (P90, CD71), isoform CRA_c	TFRC		18	75.9	0.237102206
THO complex subunit 4	ALYREF	1	6	26.9	0.223283883
Interleukin enhancer-binding factor 3	ILF3	4	21	95.3	0.220405158
Histone H2A type 1-H	HIST1H2AH		3	13.9	0.215860989
Histone H2B			3	14.0	0.214475601
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	1	15	70.9	0.21156782
Tubulin beta-4B chain	TUBB4B	8	10	49.8	0.200807228
Ig heavy chain variable region (Fragment)	IgH		2	10.2	0.195945383

Histone H3	H3F3B	1	2	10.3	0.193651553
Rheumatoid factor RF-ET12 (Fragment)			2	10.5	0.190075289
cDNA FLJ54020, highly similar to Heterogeneous nuclear ribonucleoprotein U		3	16	86.8	0.184318297
Ig heavy chain variable region (Fragment)	IgH		2	11.0	0.182644907
Serine/arginine-rich splicing factor 1	SRSF1	2	5	27.7	0.180324334
Elongation factor 1-alpha 1	EEF1A1	3	9	50.1	0.179608057
IGHV3-72 protein (Fragment)	IGHV3-72		2	11.7	0.171401331
Polyadenylate-binding protein	PABPC1	1	10	58.5	0.17094355
Serine/threonine-protein kinase MRCK gamma	CDC42BPG		29	172.4	0.168260082
Tubulin alpha-1C chain	TUBA1C	6	6	36.6	0.163810012
Alpha-actinin-4	ACTN4	16	17	104.8	0.162231576
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0		5	30.8	0.162222913
Protein SET	SET	1	5	31.1	0.160744503
Tubulin alpha-4A chain	TUBA4A	5	8	49.9	0.160345154
Immunoglobulin heavy variable 3-49	IGHV3-49		2	13.0	0.153285693
cDNA, FLJ93125, highly similar to Homo sapiens cleavage and polyadenylation specific factor 5, 25 kDa(CPSF5), mRNA OS			4	26.2	0.152679305
Spermatid perinuclear RNA binding protein isoform 2 (Fragment)	STRBP		11	72.1	0.152595082
Splicing factor U2AF 65 kDa subunit	U2AF2	4	8	53.5	0.14962446
Poly(U)-binding-splicing factor PUF60 (Fragment)	PUF60	10	8	54.6	0.146541545
GCT-A1 heavy chain variable region (Fragment)			2	13.7	0.145891144

RPS10-NUDT3 readthrough (Fragment)	RPS10-NUDT3		2	14.3	0.14001102
Apolipoprotein E isoform 5 (Fragment)	APOE		2	14.4	0.138779306
SmB /B' autoimmune antigene (Fragment)		1	3	22.0	0.136495718
Junction plakoglobin, isoform CRA_a	JUP		11	81.7	0.134680501
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1CA	5	5	37.5	0.133376704
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	4	6	45.6	0.131455398
ATP-dependent RNA helicase DDX5 (Fragment)	DDX5	5	9	69.1	0.130288018
Serine/arginine-rich-splicing factor 7	SRSF7	1	2	15.8	0.126961415
Small nuclear ribonucleoprotein-associated protein		2	3	23.6	0.12689727
Heterogeneous nuclear ribonucleoprotein D0 (Fragment)	HNRNPD	1	3	23.9	0.125490575
cDNA FLJ54552, highly similar to Heterogeneous nuclear ribonucleoprotein K		1	6	48.5	0.123761892
Spliceosome RNA helicase DDX39B	DDX39B		6	49.0	0.12254916
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	4	6	49.2	0.121955158
Albumin (Fragment)		7	8	66.5	0.120322492
RNA-binding protein 25	RBM25	13	12	100.1	0.119850882
Elongation factor 1-alpha 2	EEF1A2	3	6	50.4	0.118957198
SFPQ protein (Fragment)	SFPQ	9	8	68.6	0.116638618
Splicing factor 3A subunit 1	SF3A1	9	10	88.8	0.112573928
Probable ATP-dependent RNA helicase DDX17	DDX17	7	9	80.2	0.112213764
14-3-3 protein sigma	SFN		3	27.8	0.108082033

U2 small nuclear RNA auxillary factor 1 isoform a	U2AF1	1	3	27.9	0.107698978
Protein arginine N-methyltransferase 1	PRMT1	1	4	37.7	0.106143477
DNA damage-binding protein 1	DDB1	12	13	126.9	0.102453099
cDNA FLJ44500 fis, clone UTERU3000828, highly similar to 116 kDa U5 small nuclear ribonucleoprotein component		10	11	108.1	0.101718375
Receptor of-activated protein C kinase 1	RACK1		3	29.7	0.100902219
Serum paraoxonase/arylesterase 1	PON1		4	39.7	0.100739859
Parafibromin	CDC73	5	6	60.5	0.099109524
Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	1	3	30.3	0.09906227
Ribulose-5-phosphate-3-epimerase, isoform CRA_a	R		2	21.0	0.095427876
cDNA, FLJ96764, highly similar to Homo sapiens sorting nexin 8 (SNX8), mRNA			5	52.6	0.09512191
Mitotic interactor and substrate of PLK1	MISP	6	7	75.3	0.092947966
E3 ubiquitin-protein ligase TRIM21	TRIM21	6	5	54.1	0.092361474
RAB1B protein	RAB1B		2	22.2	0.090154088
Serine/threonine-protein phosphatase (Fragment)	PPP1CC	2	3	33.8	0.088884113
cDNA, FLJ96225, highly similar to Homo sapiens heat shock 70kDa protein 1-like (HSPA1L), mRNA		5	6	70.3	0.085309343
Gelsolin	GSN	1	7	82.5	0.084874895
Heterogeneous nuclear ribonucleoprotein U-like 1, isoform CRA_a	HNRPUL1	6	7	84.7	0.082604635

Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3		3	36.9	0.08129402
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	27	23	284.4	0.080882186
Protein FAM207A	FAM207A		2	25.4	0.078613852
Neurabin-2	PPP1R9B	6	7	89.1	0.078530181
Coronin		3	4	53.2	0.075202111
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	13	18	244.4	0.073664033
Inter-alpha-trypsin inhibitor heavy chain H3	ITIH3		5	75.0	0.066639045
cDNA, FLJ94229, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein L (HNRPL),mRNA	HNRPL	1	4	60.2	0.066432815
POLDIP3 protein (Fragment)	POLDIP3		3	45.6	0.065745771
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	3	5	77.5	0.064500799
cDNA, FLJ93681, highly similar to Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA	SNRPA	2	2	31.3	0.063923892
Fusion (Involved in t(12;16) in malignant liposarcoma) isoform a variant (Fragment)		2	2	32.0	0.062550254
Splicing factor 3B subunit 1	SF3B1	12	9	145.7	0.061754613
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	2	3	49.2	0.060935619
Prothrombin (Fragment)			2	33.6	0.059495512
cDNA FLJ76187			3	51.1	0.058722355
Alpha-actinin-1	ACTN1	5	6	103.0	0.058256592
Uncharacterized protein DKFZp686G11190	DKFZp686G11190	2	3	52.0	0.057681245
Cleavage and polyadenylation-specificity factor subunit 6	CPSF6	3	3	52.2	0.05742969

Anti-RhD monoclonal T125 gamma1 heavy chain		2	3	52.3	0.057329269
Immunoglobulin heavy constant gamma 4	IGHG4	1	2	35.9	0.055682593
ELAV-like protein 1	ELAVL1		2	36.1	0.055449045
Endoplasmic reticulum chaperone BiP	HSPA5	5	4	72.3	0.055333882
cDNA FLJ76817, highly similar to Homo sapiens non-POU domain containing, octamer-binding (NONO), mRNA	NONO	6	3	54.3	0.055296105
La-related protein 1 (Fragment)	LARP1		5	90.8	0.055086206
Pre-mRNA-processing factor 19	PRPF19	1	3	55.1	0.054400703
Desmoplakin	DSP	6	18	331.6	0.054287389
Thrombospondin 1, isoform CRA_a	THBS1		7	129.3	0.054150416
MAP kinase-activated protein kinase 5 (Fragment)	MAPKAPK5		2	37.1	0.053969641
Poly(rC)-binding protein 1	PCBP1	2	2	37.5	0.053370415
Serum paraoxonase/lactonase 3	PON3		2	39.6	0.050527596
cDNA FLJ53422, highly similar to TATA-binding protein-associated factor 2N		1	2	40.1	0.049932339
Plakophilin 1 (Ectodermal dysplasia/skin fragility syndrome), isoform CRA_a	PKP1		4	80.4	0.04972313
Zinc finger transcription factor Trps1	TRPS1		7	141.4	0.049493624
Archaemetzincins-2, isoform CRA_d	AMZ2	3	2	41.2	0.048499
Inter-alpha-trypsin inhibitor heavy chain H2	ITIH2		5	105.2	0.04755108
cDNA: FLJ23531 fis, clone LNG06065			2	46.5	0.043001727

X-ray repair cross-complementing protein 6	XRCC6		3	69.8	0.042980523
Zinc finger RNA binding protein	ZFR		5	116.9	0.042756639
Complement C4-A	C4A		8	187.6	0.042633494
Elongation factor 2	EEF2		4	95.3	0.04198287
Unconventional myosin-Ib	MYO1B	1	5	128.4	0.03894082
CDC2L2 protein (Fragment)	CDC2L2	2	2	52.4	0.038187312
Serpin peptidase inhibitor clade C member 1	SERPINC1		2	52.5	0.038088832
cDNA FLJ35987 fis, clone TESTI2014269, highly similar to D-3-phosphoglycerate dehydrogenase			2	53.0	0.037750509
Complement C5	C5		7	188.2	0.037197213
Uncharacterized protein DKFZp686C06243 (Fragment)	DKFZp686C06243		7	195.5	0.035801124
ATP-dependent RNA helicase A	DHX9	6	5	140.9	0.035493941
Complement C2	C2		2	56.4	0.035441856
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2		3	85.1	0.035272468
Nucleolar RNA helicase 2	DDX21		3	87.3	0.034368046
cDNA FLJ78246, highly similar to Homo sapiens splicing factor 3a, subunit 3, 60kDa (SF3A3), mRNA	SF3A3	1	2	58.8	0.034040089
cDNA, FLJ93914, highly similar to Homo sapiens histidine-rich glycoprotein (HRG), mRNA			2	59.5	0.033627697
cDNA FLJ59523, highly similar to Scaffold attachment factor B		2	3	91.0	0.032956029

cDNA FLJ43122 fis, clone CTONG3003737, highly similar to Leucine-rich repeat-containing protein 15 OS			2	64.4	0.031078468
Alpha-2-macroglobulin	A2M		5	163.2	0.030639527
Spectrin beta chain, non-erythrocytic 1	SPTBN1	14	8	274.4	0.029150408
ATP-dependent RNA helicase DDX3X	DDX3X	1	2	69.0	0.028983444
FN1 protein	FN1		7	246.5	0.028392574
Nuclear cap-binding protein subunit 3	NCBP3		2	70.5	0.028348956
Pre-mRNA-processing factor 6	PRPF6	5	3	106.9	0.028074694
Scaffold attachment factor B2	SAFB2	2	3	107.4	0.027930859
Pre-mRNA-processing-splicing factor 8	PRPF8	7	7	273.4	0.025601023
THO complex subunit 5 homolog	THOC5		2	78.5	0.025491366
cDNA FLJ76877, highly similar to Homo sapiens superkiller viralicidic activity 2-like 2 (SKIV2L2), mRNA		1	3	117.8	0.025461829
FACT complex subunit SPT16	SUPT16H	6	3	119.8	0.025033707
cDNA FLJ57339, highly similar to Complement C3			3	122.5	0.024486736
Uncharacterized protein			3	123.9	0.024205799
X-ray repair cross-complementing protein 5	XRCC5		2	82.7	0.02419776
FAST kinase domain-containing protein 5, mitochondrial	FASTKD5		2	86.5	0.023116409
cDNA FLJ55635, highly similar to pre-mRNA-splicing factorATP-dependent RNA helicase DHX15	dhx15	4	2	89.5	0.022348728

Nuclear cap-binding protein subunit 1	NCBP1	1	2	91.8	0.021791116
Matrin-3	MATR3		2	94.6	0.021149518
Pp100	U11		2	97.1	0.020595118
Myosin IC, isoform CRA_a	MYO1C		2	98.9	0.020228139
5'-3' exoribonuclease			2	99.9	0.02002241
General transcription factor 3C polypeptide 2	GTF3C2		2	100.6	0.0198776
Spectrin beta chain, non-erythrocytic 2	SPTBN2	20	5	271.2	0.018439493
cDNA, FLJ94213, highly similar to Homo sapiens pregnancy-zone protein (PZP), mRNA			3	163.8	0.018318638
Nuclear mitotic apparatus protein 1	NUMA1	5	4	236.0	0.016947786
cDNA FLJ53573, highly similar to Myosin Ic			2	119.0	0.016809211
Filamin A	FLNA	4	4	277.3	0.014423127
Coagulation factor V	F5		3	251.5	0.011926271
DNA topoisomerase 2-beta	TOP2B	1	2	183.2	0.010919864
DNA-dependent protein kinase catalytic subunit	PRKDC	2	4	468.8	0.008532643