

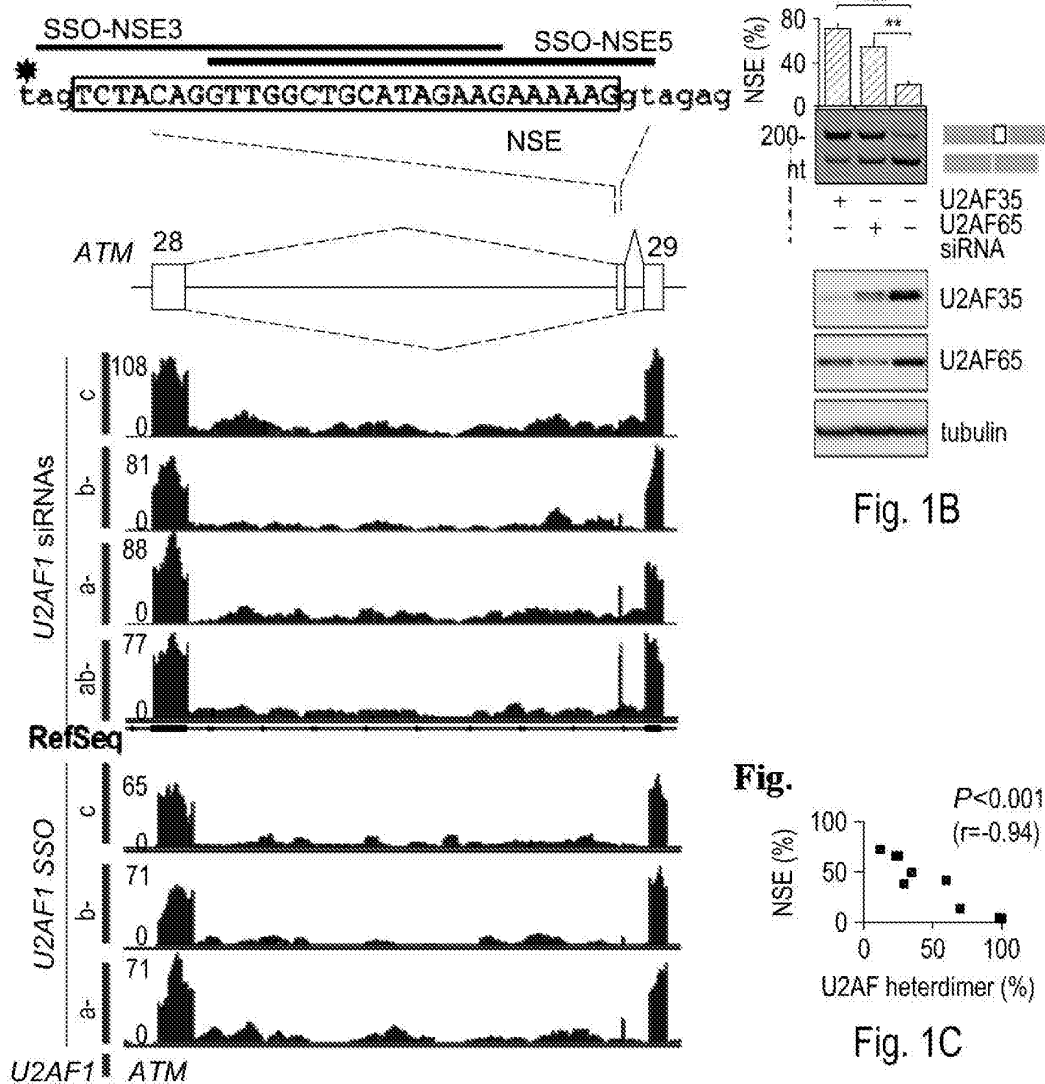


Fig. 1A

Fig. 1B

Fig.

$P < 0.001$

$(r = -0.94)$

NSE (%)

100

50

0

0

50

100

U2AF heterodimer (%)

Fig. 1C

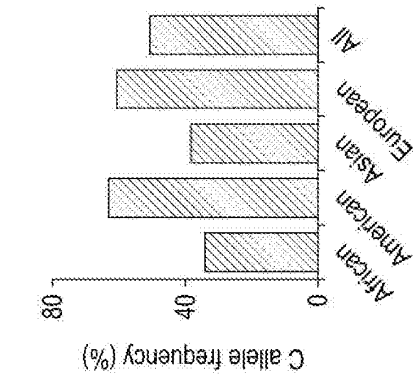


Fig. 2A

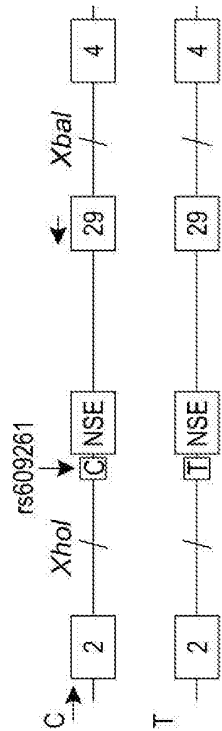


Fig. 2B

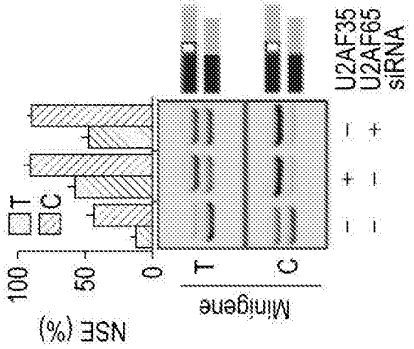
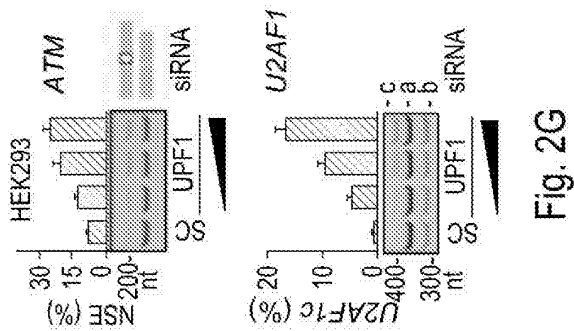
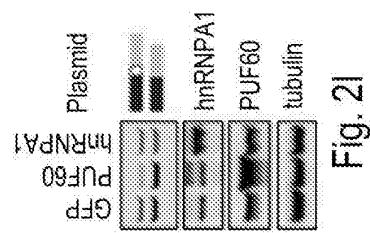
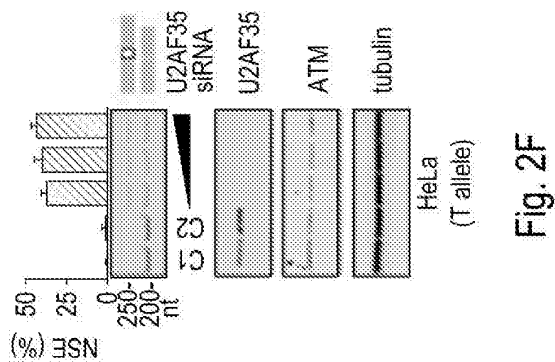
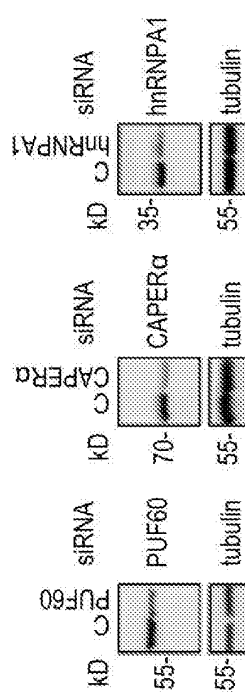
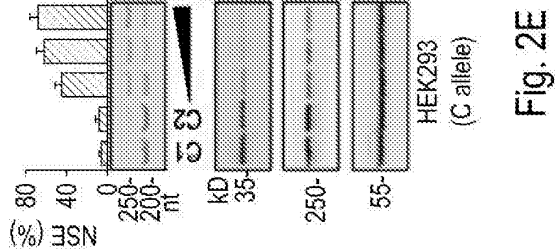
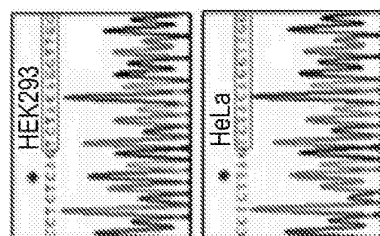
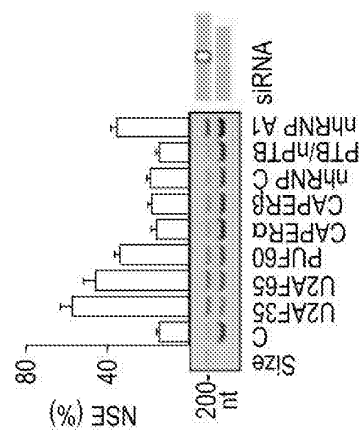


Fig. 2C



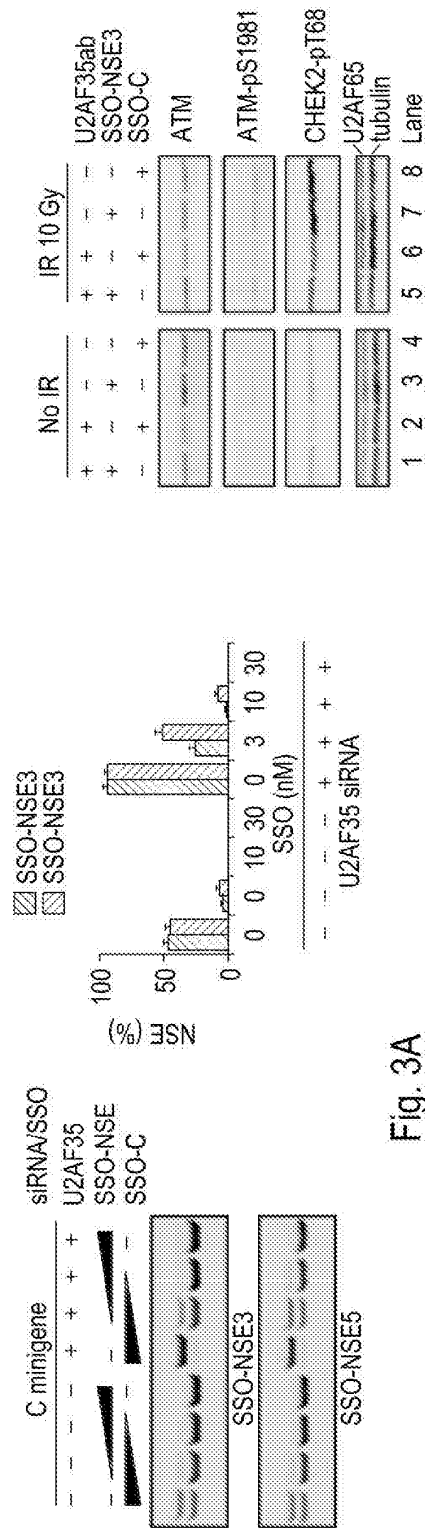


Fig. 3A

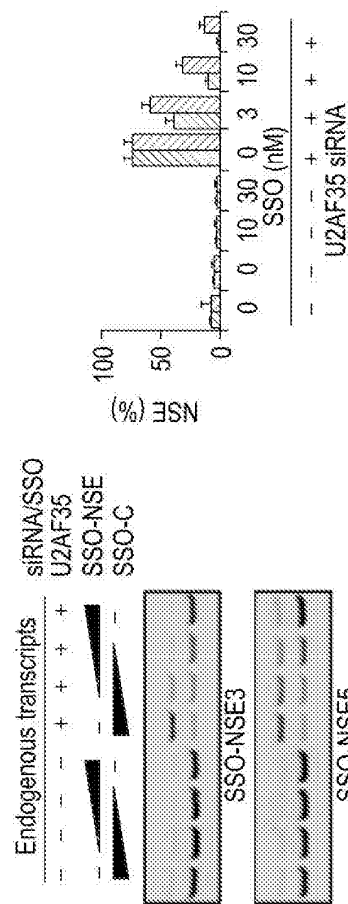


Fig. 3B

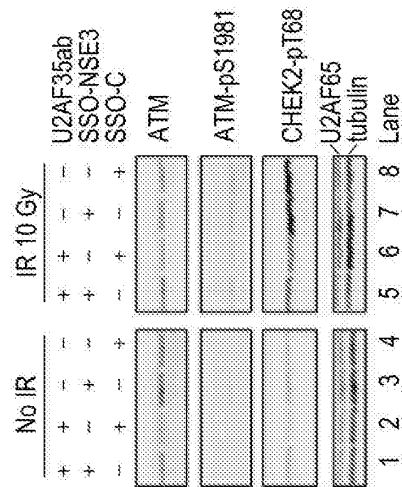


Fig. 3C

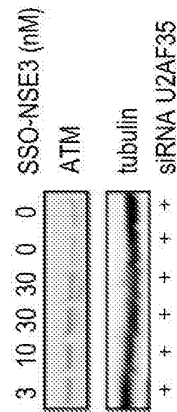


Fig. 3D

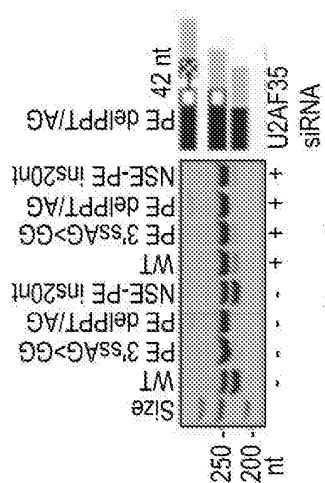


Fig. 4B

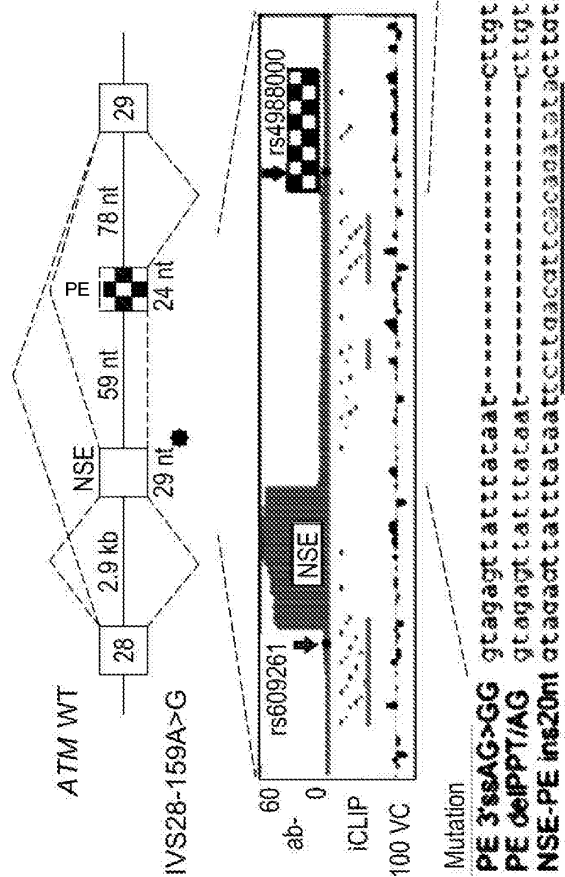
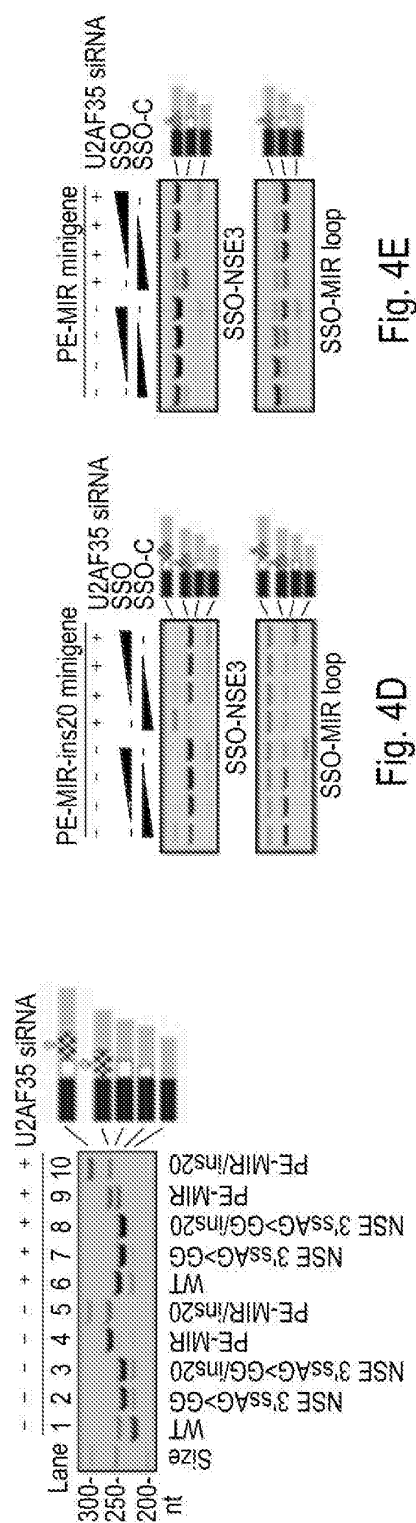
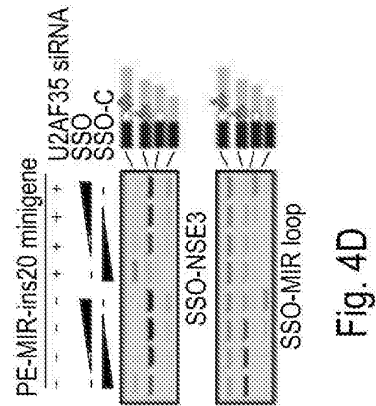
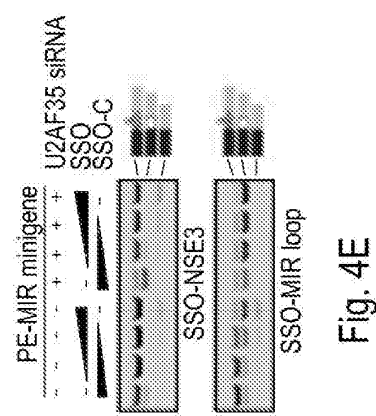
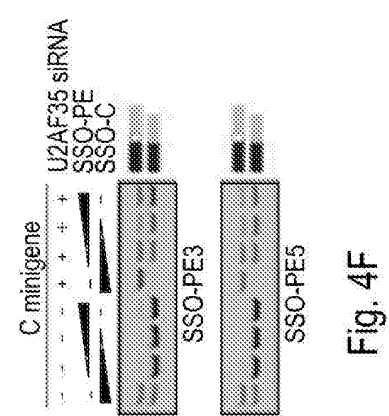
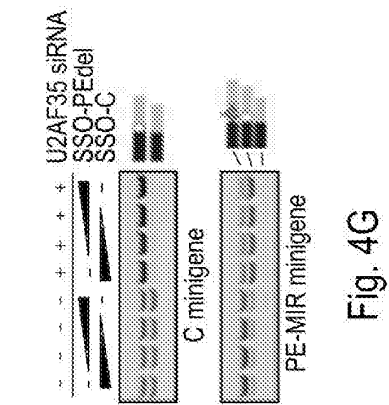
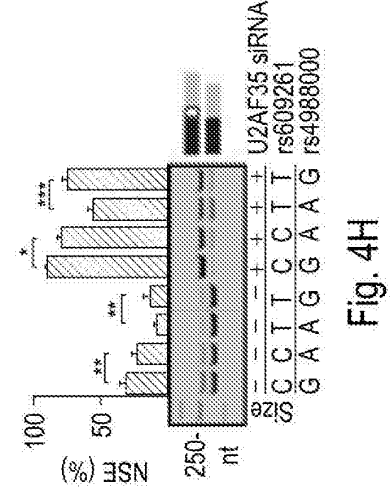


Fig. 4A



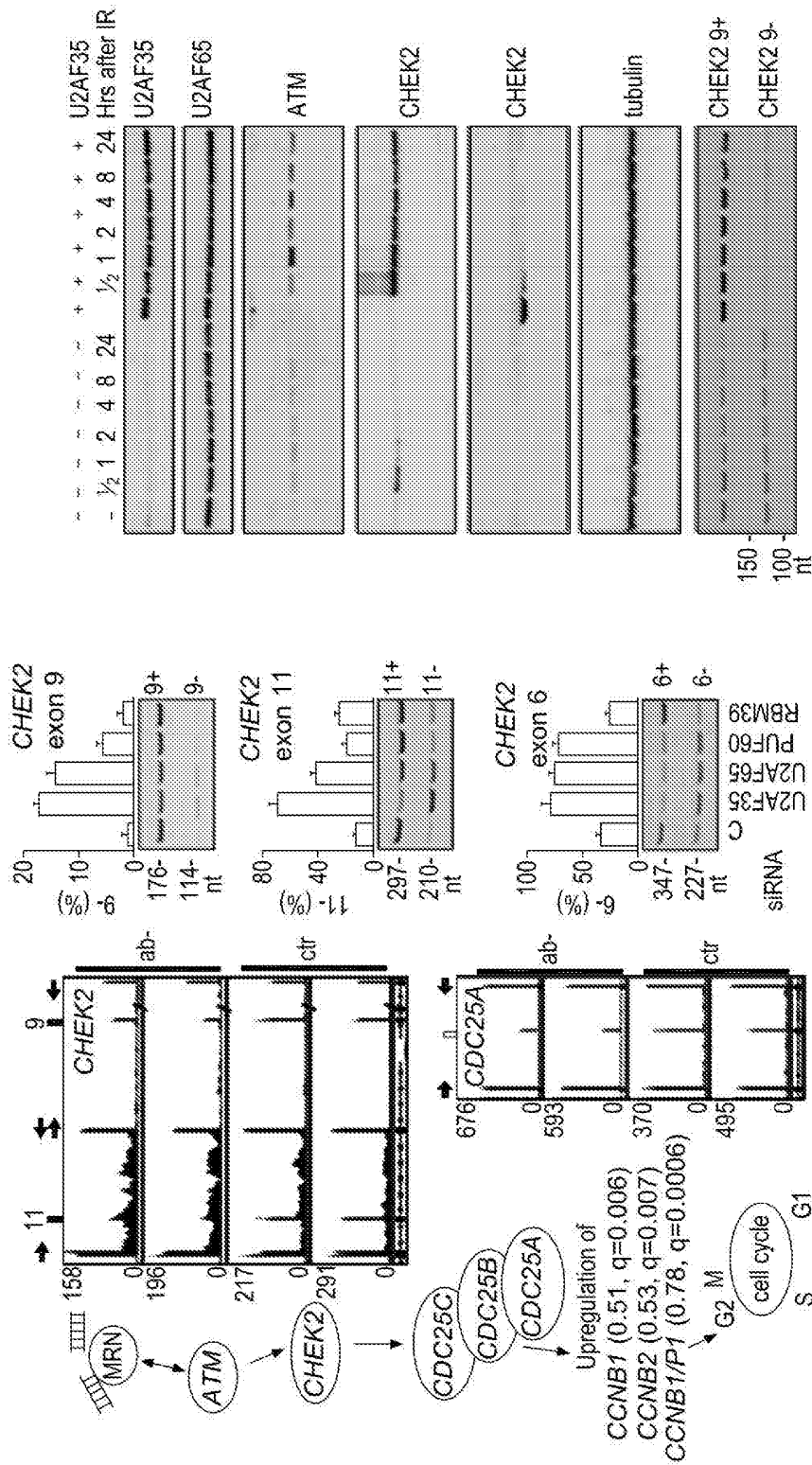
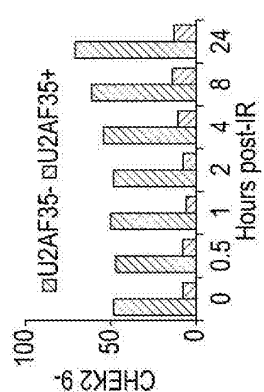
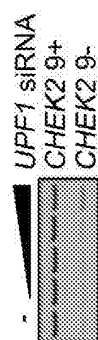
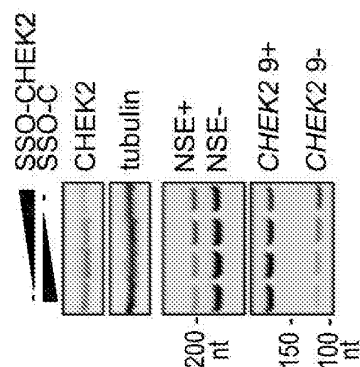
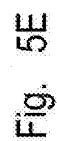
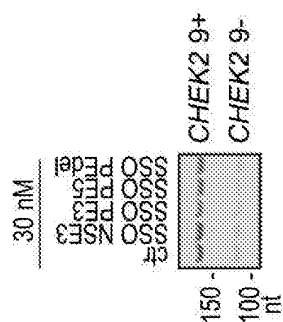
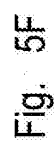
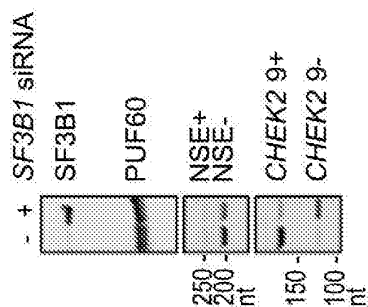


Fig. 5B

Fig. 5A



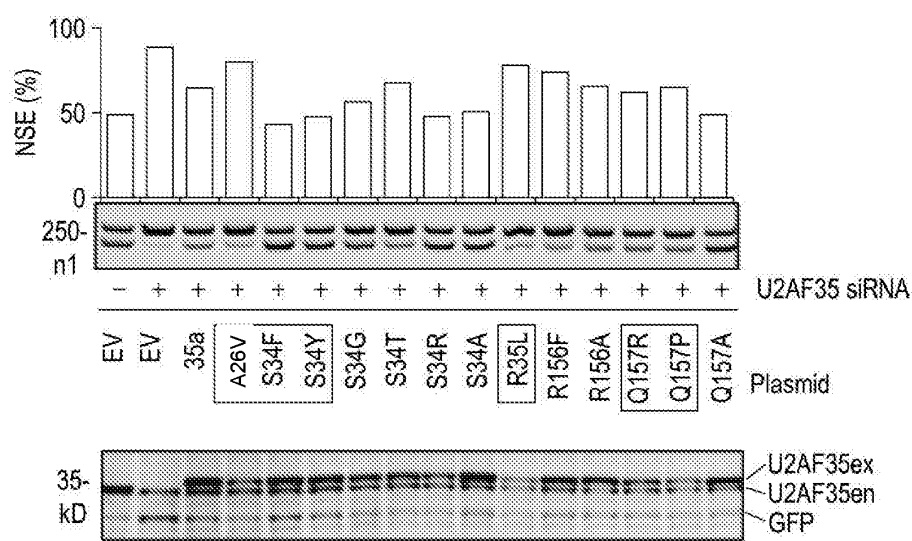


Fig. 6

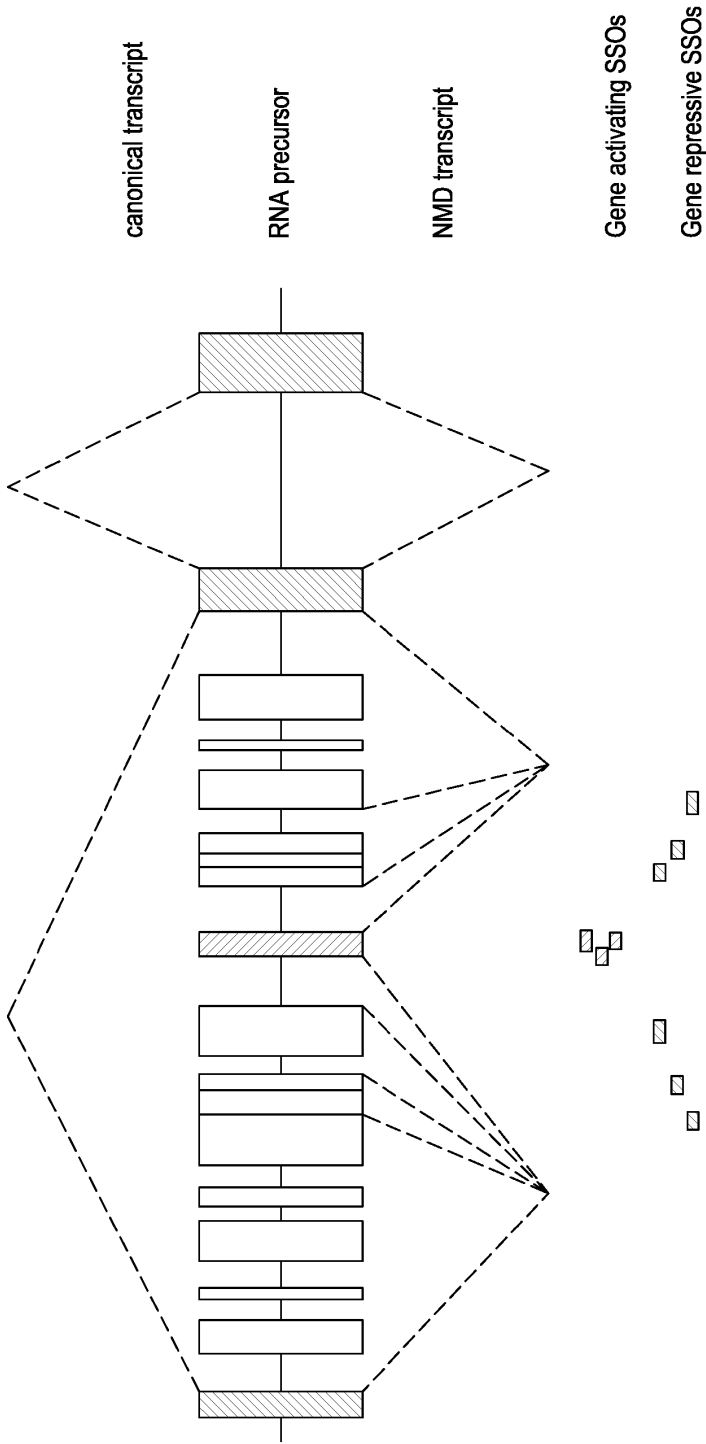
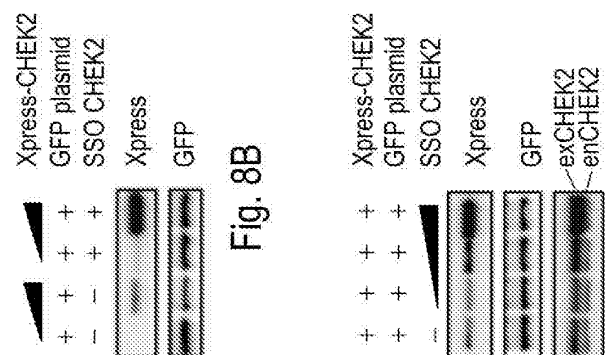
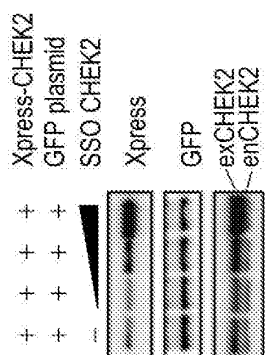
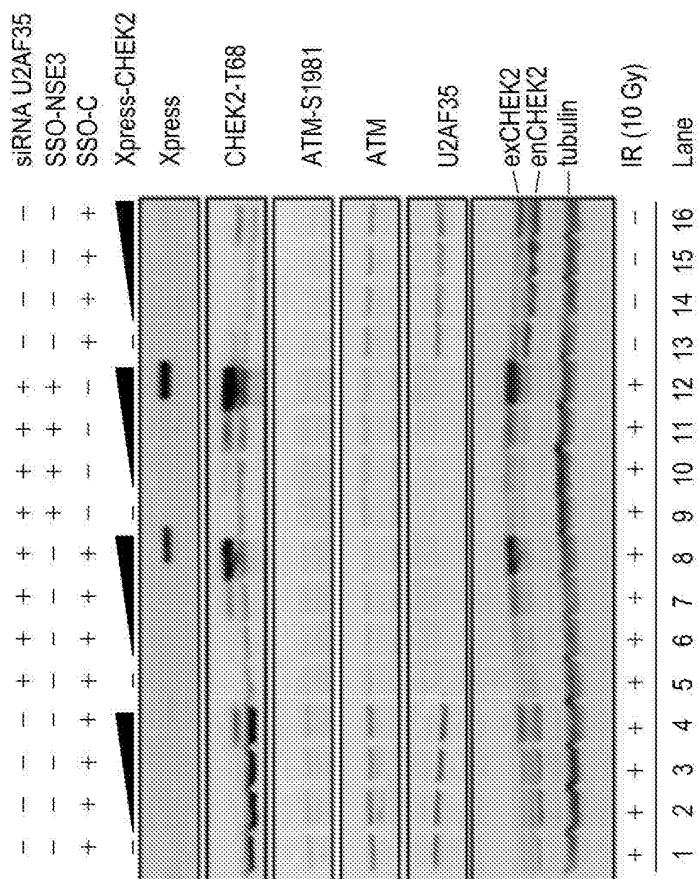


Fig. 7



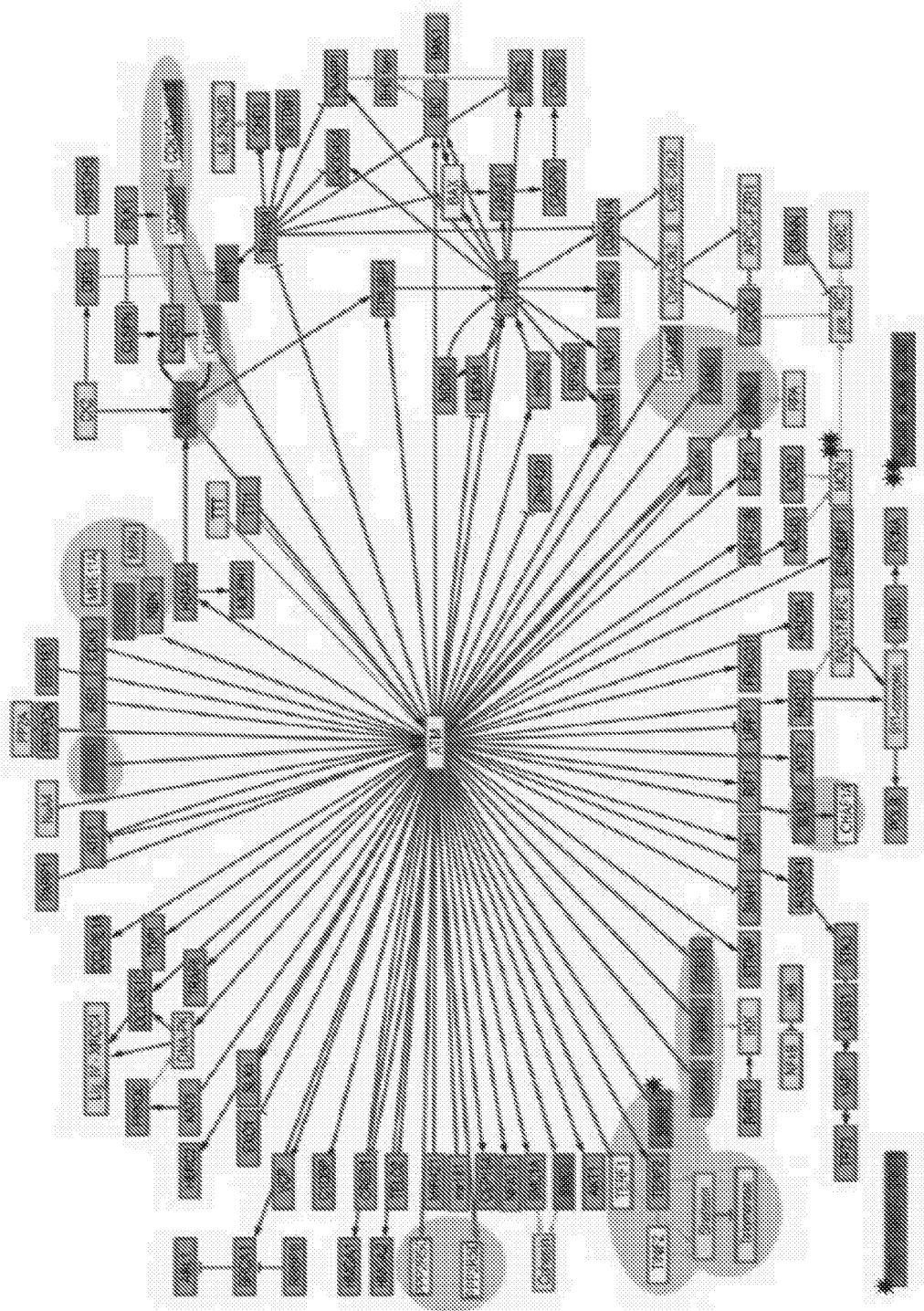


Fig. 9

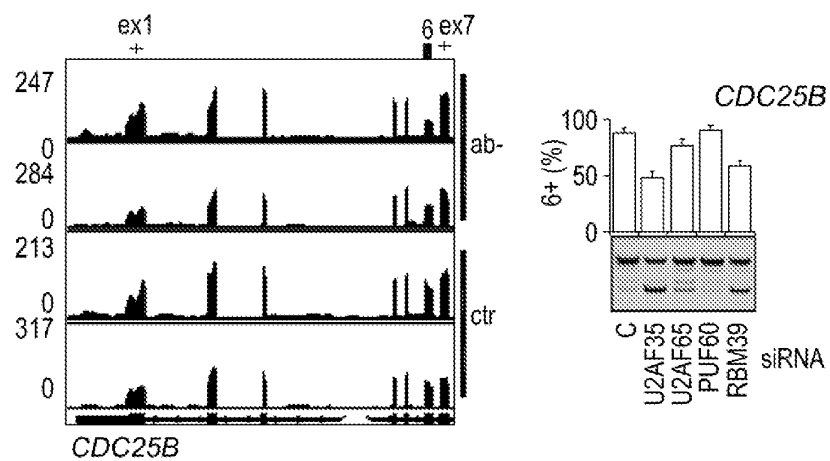


Fig. 10A

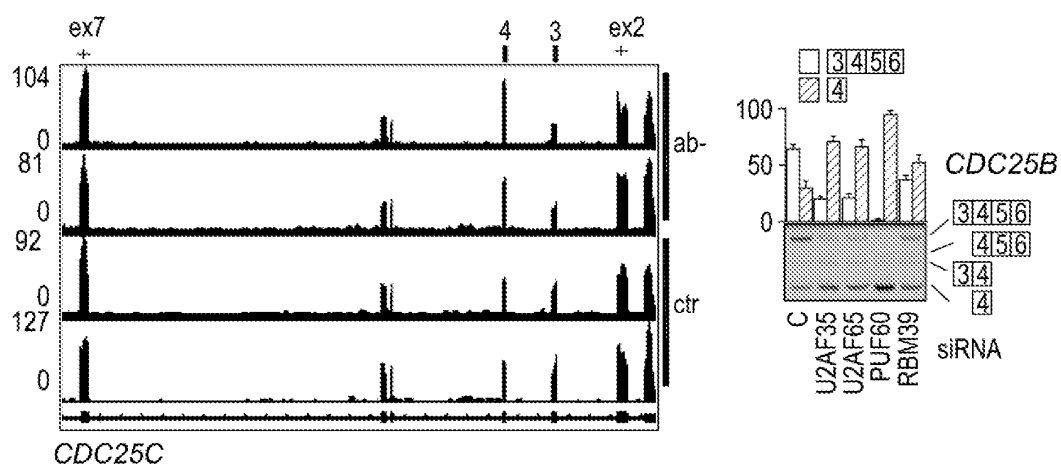


Fig. 10B

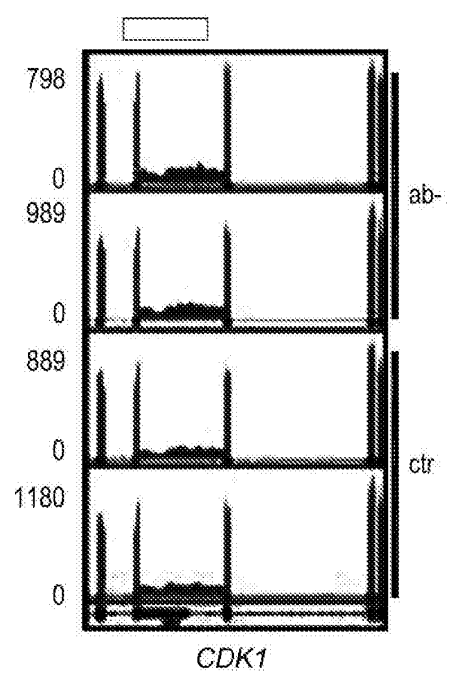


Fig. 11C

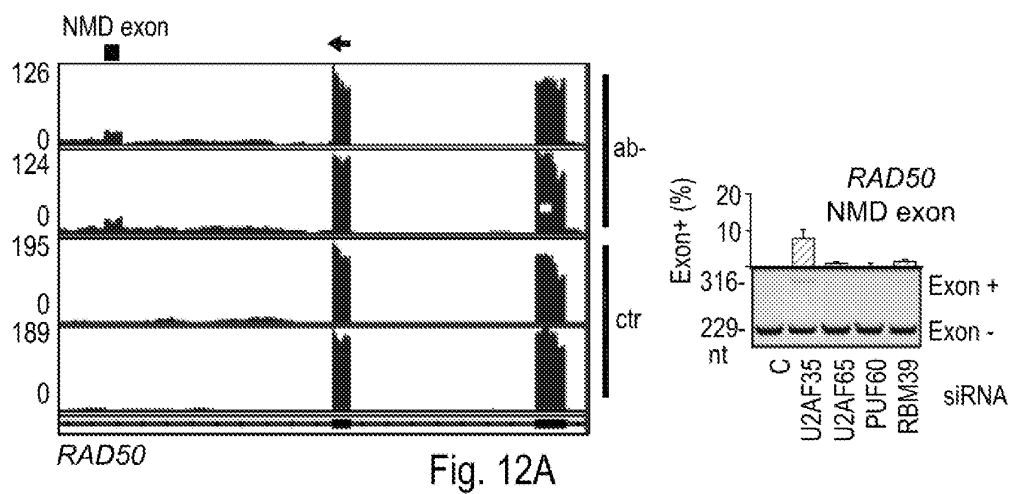


Fig. 12A

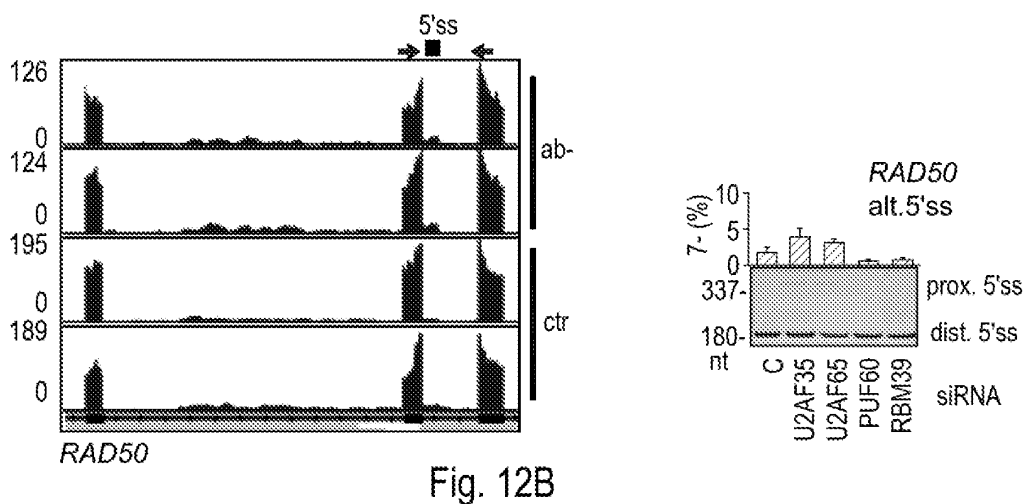


Fig. 12B

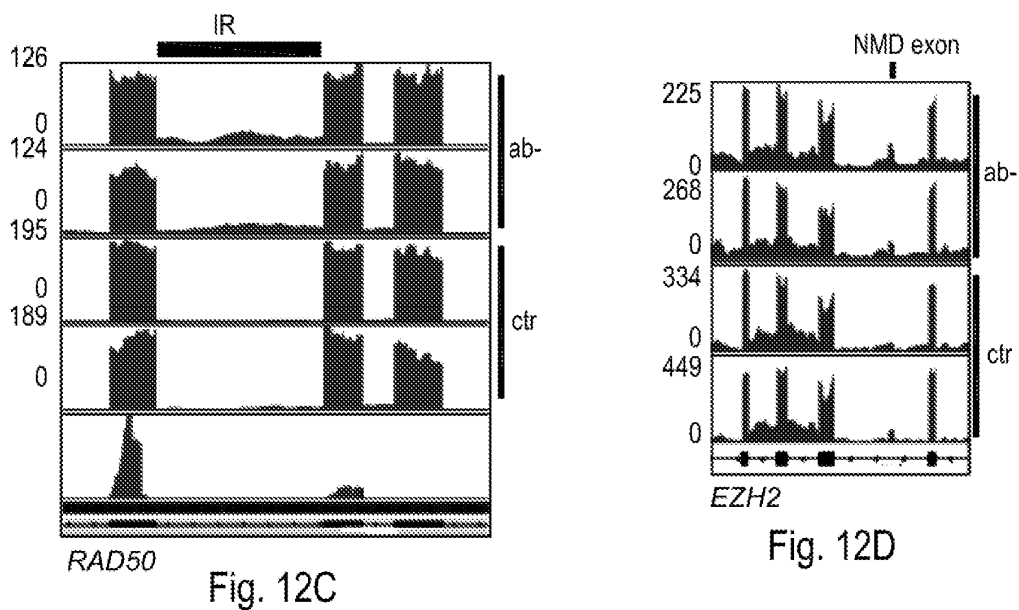


Fig. 12C

Fig. 12D

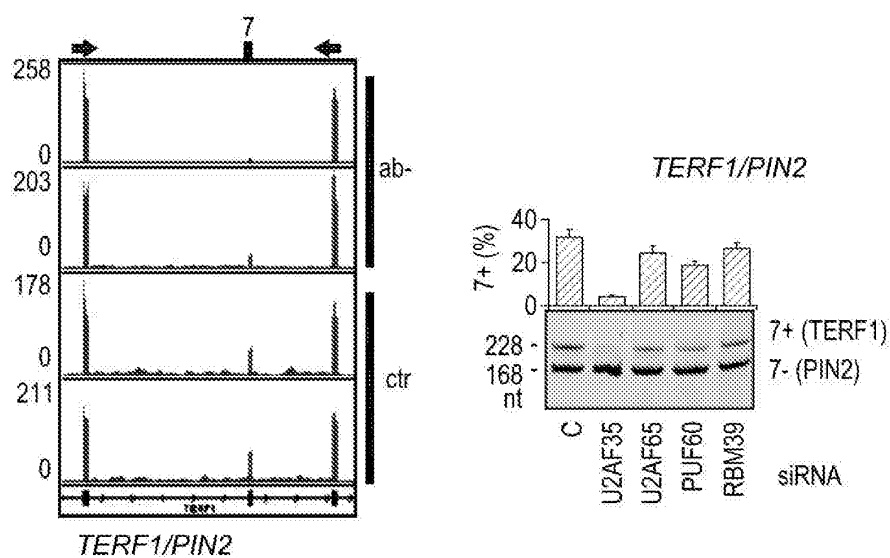


Fig. 13A

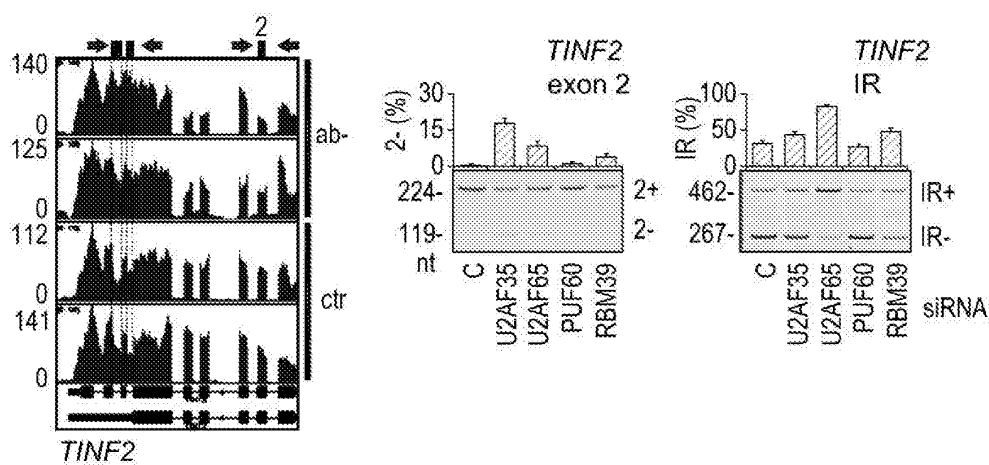


Fig. 13B

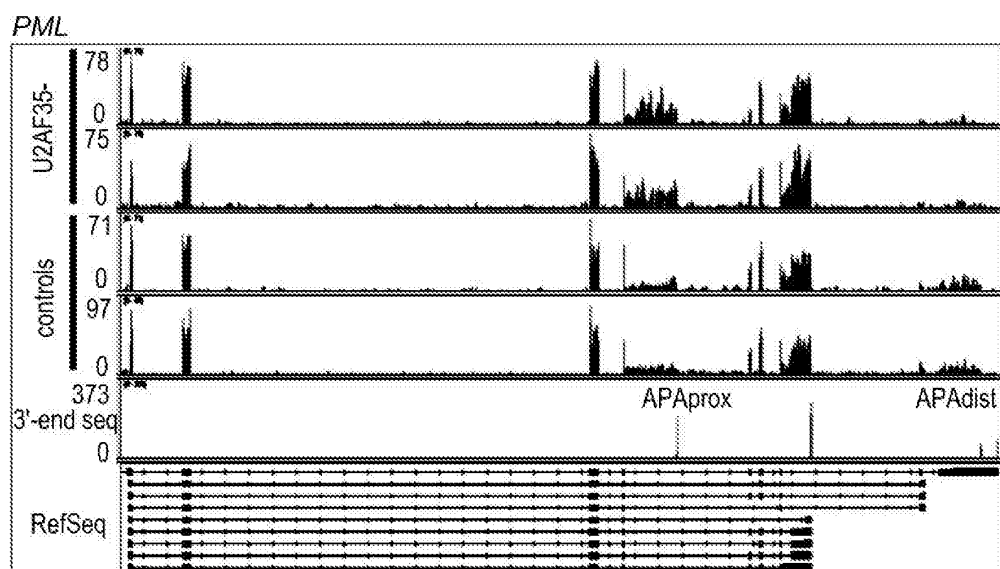


Fig. 14A

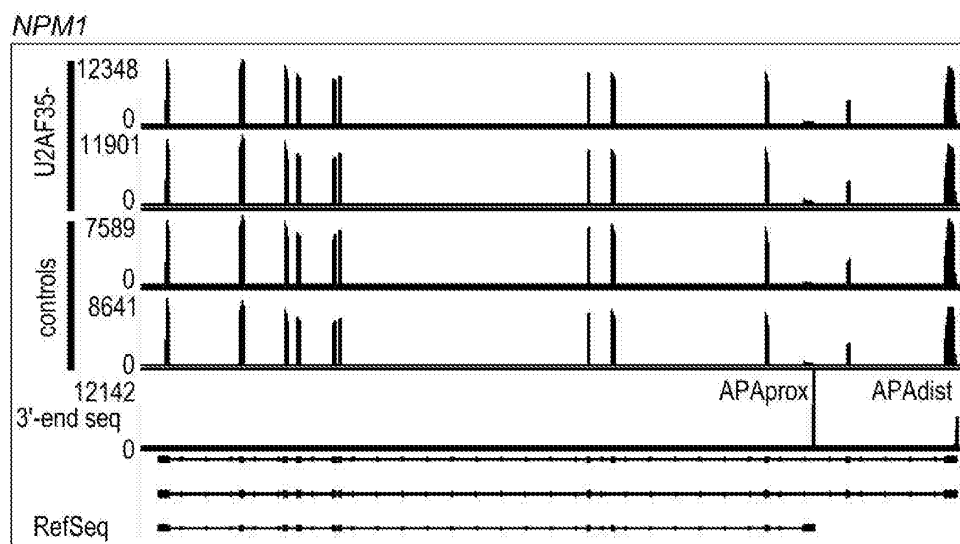


Fig. 14B

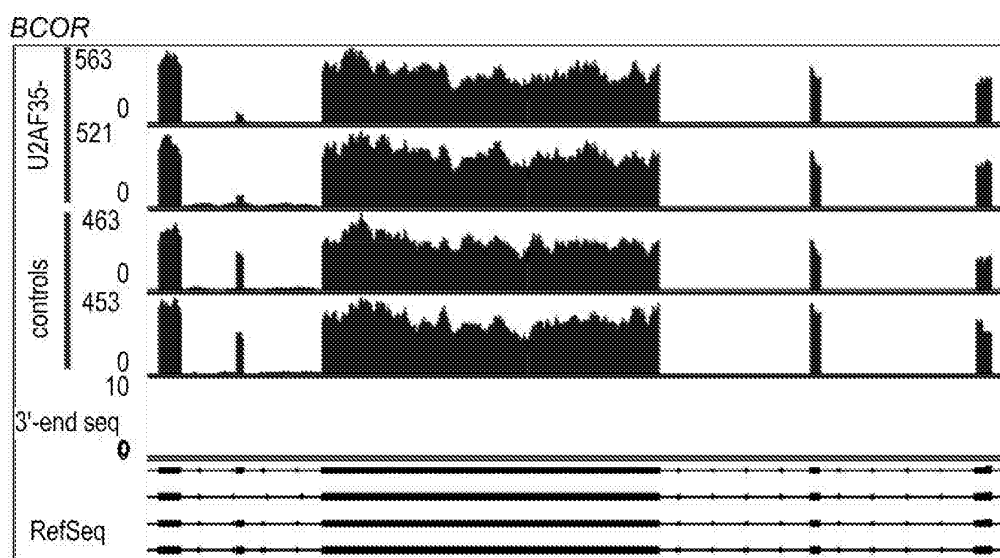


Fig. 14C

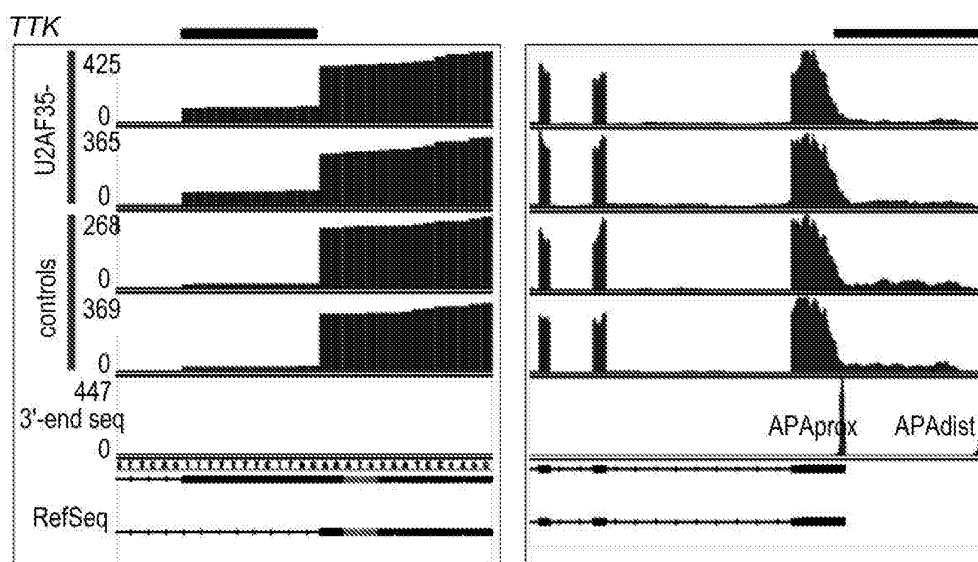
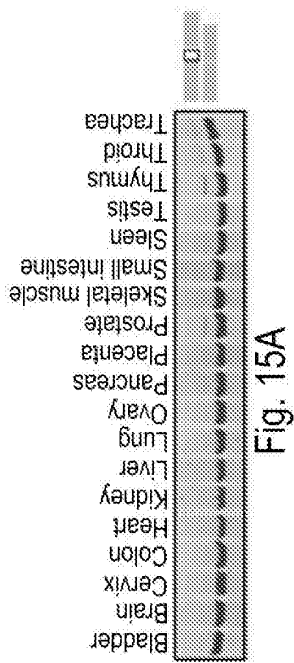
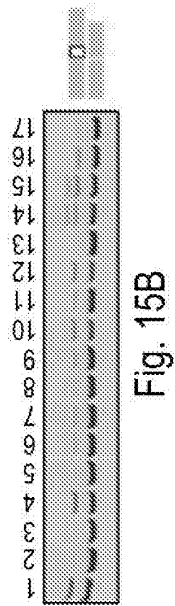
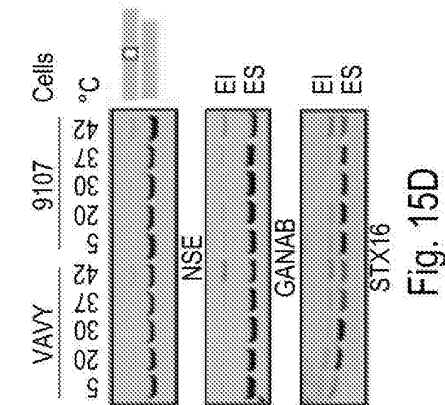
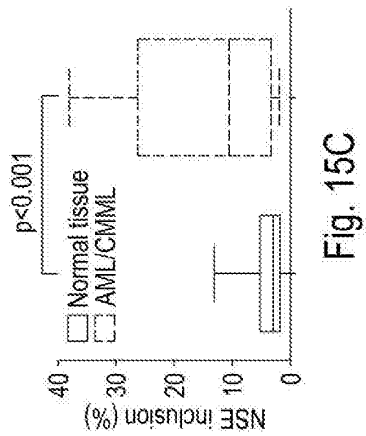
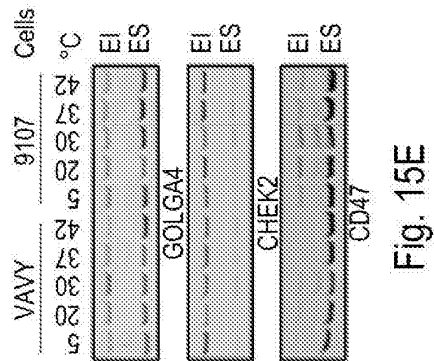


Fig. 14D



ACCESSION NUMBER
Accession number for RNA-Seq data is E-MTAB-2682 (ArrayExpress).



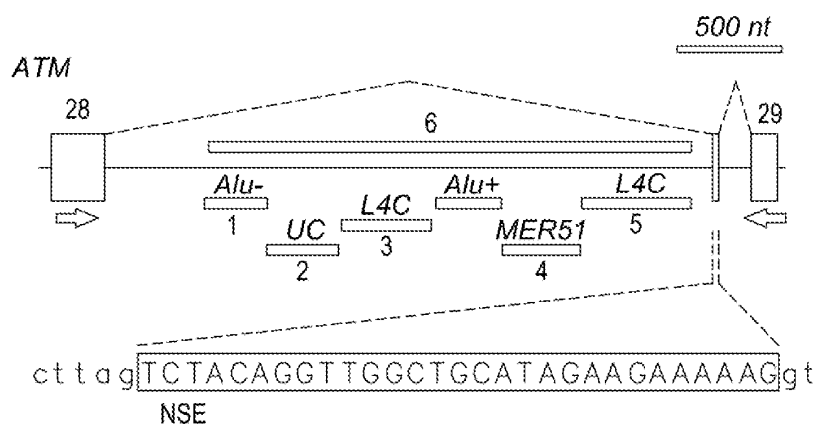


Fig. 16A

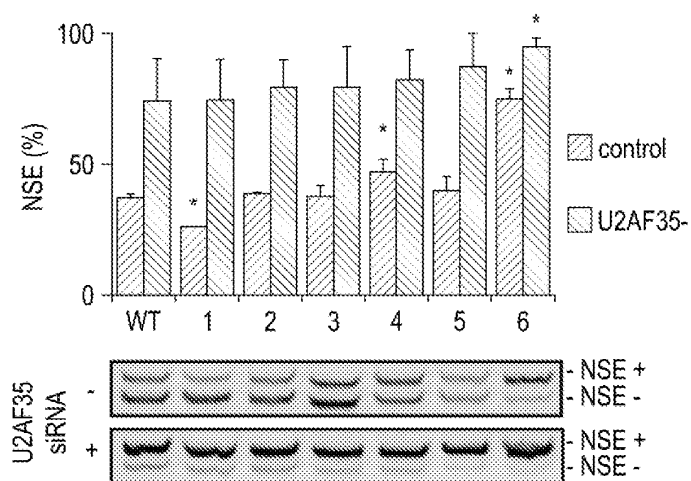


Fig. 16B

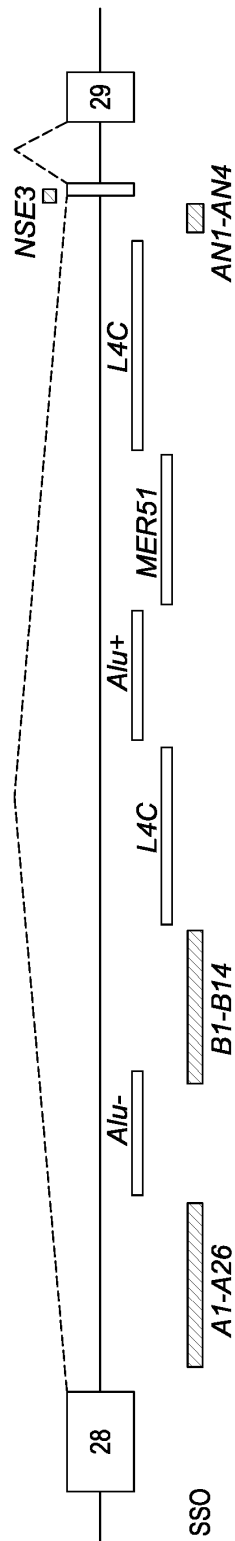


Fig. 17A

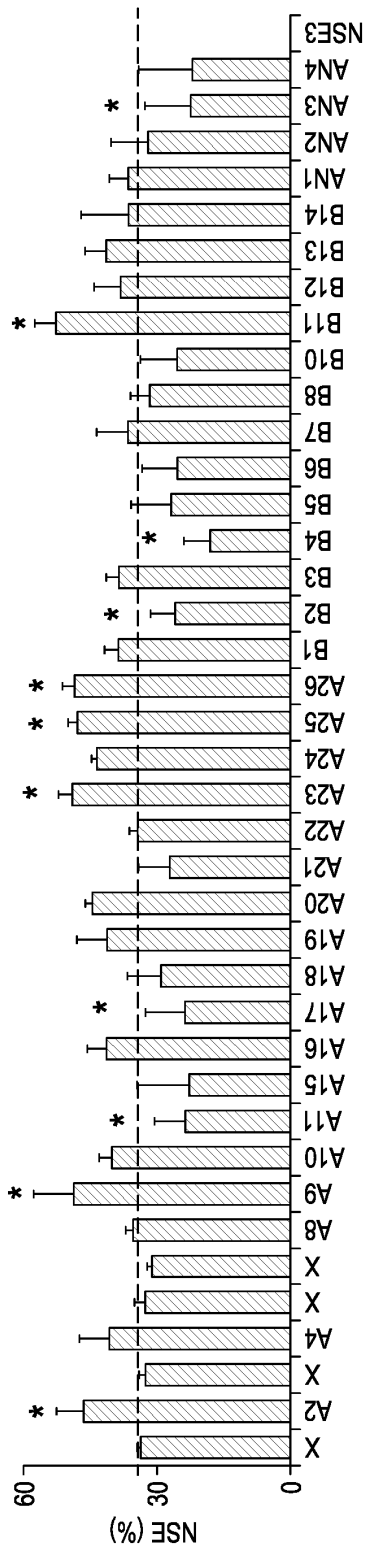


Fig. 17B

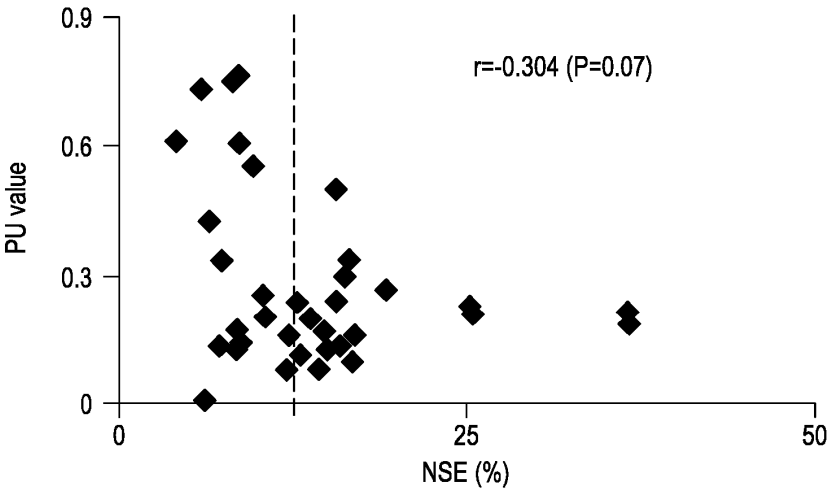


Fig. 17C

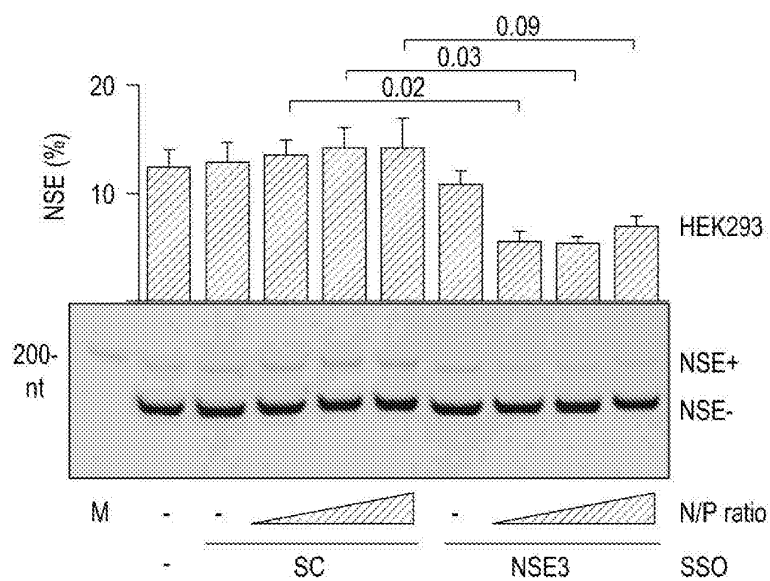


Fig. 18A

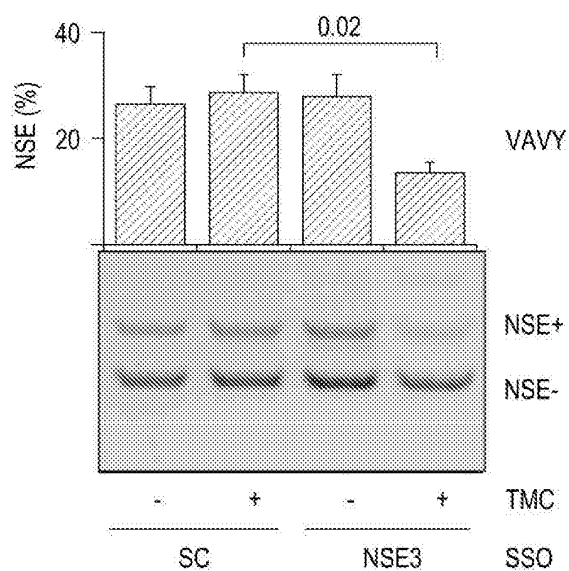


Fig. 18B

ATM intron 28	UUGUAUAAAACACACAAAACAAAGCAAGGAAAGAAUGAAGCAACAAAGCCA
MERS1A#LTR/ER	UUGGACAAAACSCACAAAACAAAGCAAGGAAAGAAUGAAGCAACAAAAGCCA
ATM intron 28	GAGAUUUACUGAAAUGAAAUAUUAUACUCCACAGAGUGGGAGUC
MERS1A#LTR/ER	GAGAUUUUAUUGAAAACGAAAGUACACUCCACAGGGUGGGAGCGGGCCG-G
ATM intron 28	AAGUG
MERS1A#LTR/ER	AGCAAGCGGCUCACAGGGCCCGGUUACAGAAUUUUCUGGGGUUAAAUAACC
ATM intron 28	CUUCAGAGGUUUUCCAUGGGUUAUUGGUUAUACACCCUAUGUAAAUGAAG
MERS1A#LTR/ER	CUCUAGAGGUUUCGCAUUGGUUAUUGGUUAUACACCCUAUGUAAAUGAAG
ATM intron 28	UAGUG
MERS1A#LTR/ER	UAGUGGCCCGCAAUACAGUCUGUUGGUUGCGGAAAGCGACCAAUACAGAGG
ATM intron 28	UACAC-CCUAUGUAAAUGAAGUAGUGGUCUGUAAUACAGUCUUAUUGGUUA
MERS1A#LTR/ER	UACACUCCUAUGCAAAUGAAGACUUGGCCCGGACACAGUCUGAUUGGUUG
ATM intron 28	UUCAAUUUCUUAUCUGCCA--CAGUAAAAGGG
MERS1A#LTR/ER	UUCAAUUUCCCAUUCUGCCAACACAG-AAAAGGUGGGGGGUUCCAAAGGGAG
ATM intron 28	GUCCUUUUGUUAUUGAGCAUGGAAAGUUGGGGUUUUCCUU
MERS1A#LTR/ER	UAGCCUCUGGUCCUUUUGUUAUUGGGCGUGGAAAGUUGGGGUUUUCCUU
ATM intron 28	UUGAUUUUGUUCUAGGAGGUCAGCAUGGAUUGACCUUAGGUUCCCUGCCU
MERS1A#LTR/ER	UCGAUUUAGUUCUAGGAAGUCAGCGUGAAUCGGCCUUAGGUUCCCUGCCU
ATM intron 28	CCAGACCUUAUUGCCCUCCUCA
MERS1A#LTR/ER	CCAGACCUUAUUCUCCCUCCUCA

Fig. 19

RT-PCR primers	Sequence (5'-3')	Reference
ATM-F	GAGGGTACCAGAGACAGTGGGATGGC	This study
ATM-R	GGCTCATGTAACGTCATCAAT	This study
PL3	GGGAGACCCAAGCTGGCTA	[1]
CHEK2-E9-F	AGACCCAGCTCTCAATGTTG	This study
CHEK2-E9-R	TAGCTTCTTTAGGCGTTTA	This study
CHEK2-E11F1	AGTGGTGGGGAATAAACG	This study
CHEK2-E11R	CAGCAGTCCACAGCACGGT	This study
CDC25B-F	CTCAGTCCAGCAGGCGTGTG	This study
CDC25B-R	GGTCTCTGGGCAAAGGCTTC	This study
CDC25A-F	CAGAAGCTGTTGGGATGTAG	This study
CDC25A-R	TCTCCATCGAGAAGGTCCAC	This study
CDC25C-F	TGGCTCAGGACCCAGTTTTA	[2]
CDC25C-R	TCTTCTGCCTGGTCTTCTCC	[2]
TIN2-F1	CCTGGCTTGGTTCGCTACC	This study
TIN2-R3	TGCTTCACCTGCTGGTAAAA	This study
TIN2-F6	GAAGAACATGCGATATACACA	This study
TIN2-R8	GTCTAAAACCAAGTCCCCTAT	This study
PIN1-F	GAGGGAAGATGGCGGACGAG	This study
PIN1-R	TCCTCCTTGGTCCGGGTGAT	This study
TERF1-F	GCAGCGGCAAAAGTAGTAGA	This study
TERF1-R	GTCTGTTGCTGGGTTCCA	This study
RAD50-cr5-F	AAAATCATCAAAACAGCGAG	This study
RAD50-cr5-R	TGGAGCAAGTCGCAGTTTAG	This study
RAD50-E-F	GGCGACAGAAAGGTTATGAA	This study
RAD50-E-R	CGCCACAGGTCACGTATAAT	This study
Cloning primers		
ATM-XhoI	ATAGAATTCTCGAGGGGAGGGTTTATTCTACTA	This study
ATM-XbaI	ATAGGGCCCTCTAGACTGTGGGAGACTATGGTAA	This study
CHEK2-EcoRI	ATTAGAATTCTCTCGGGAGTCGGATGTTG	This study
CHEK2-NotI	ATTAGCGGCCGCGGTACATTTCTTTCGTGTTCA	This study
Modified antisense oligonucleotides		
SSO-NSE3	CUUCUAUGCAGCCAACCUUGAGACU	This study
SSO-NSE5	ACCUUUUUCUUCUAUGCAGCCAAC	This study
SSO-PE3	AUUUCCAAAAGUAUUCGAUGACUG	This study
SSO-PE5	UAUAUUACCUUAUUUCCAAAAGUA	This study
SSO-PEBP	CUGUAAAAGAAAAUAGAUGACUCAA	This study
SSO-PEdel	CUGUAAAAGAAAAUAGA	This study
SSO-CHEK2-ex9	ACUUACAAUCCAAAACAAUUAUAAU	This study
SSO-C	AGGUGCUUCGCGGGUGG	[3]
SSO-MIR loop	AGUUGCUUCAUCU	[4]
siRNA		
U2AF35ab	GGCUGUGAUUGACUUGAAU	[5]
U2AF65	GCAAGUACGGGCUUGUCA	[6]
RBM39	GGAUUUAUUGUUAUUGUA	[7]
PUF60	GCAGUAGAACUCGGUGAUG	[6]
UPF1	AAGAUGCAGUUCGCUCCAUU	[8]

Fig. 20

[illegible]

Fig. 21

Pseudoxon	Allel e	FAS-ESS ¹	PES S ¹	PES E ¹	RESCUE-ESE ¹	SF2/ASF ESE ¹	EIE density ¹
NSE	C	3.45	3.45	5	6	9.3	975.4
NSE	T	3.45	3.45	5	6	9.3	975.4
PE	G	4.17	0	0	3	0	403.8
PE	A	4.17	0	0	5	0	334.2
Reference	[9]	[10]	[11]	[11]	[12]	[13]	[14]

Legend: ¹Densities of the indicated enhancers and silencers predicted in NSE and PE were computed as described [15]. Support vector machine scores for the best predicted BPS of NSE and PE [16] were 1.3 and 0.5.

Fig. 22

Transcript	Levels in depleted cells
<i>UPF3A</i>	Down (q=0.002)
<i>UPF3B</i> ¹	Down (q=0.0006), skipping of a 39-nt exon
<i>SMG7</i>	Up (q=0.0002)
<i>SMG8</i>	Up (q=0.001)
<i>DHX34</i>	Up (q=0.002)
<i>CASC3</i>	Up (q=0.004)
<i>RNPS1</i>	Up (q=0.003) through putative intronic alternative polyadenylation site
<i>RBFOX2</i>	Up (q=0.007)

¹*UPF3B* was implicated as exhibiting a distinct level of exon inclusion in patients with myeloid neoplasms [17].

Fig. 23