

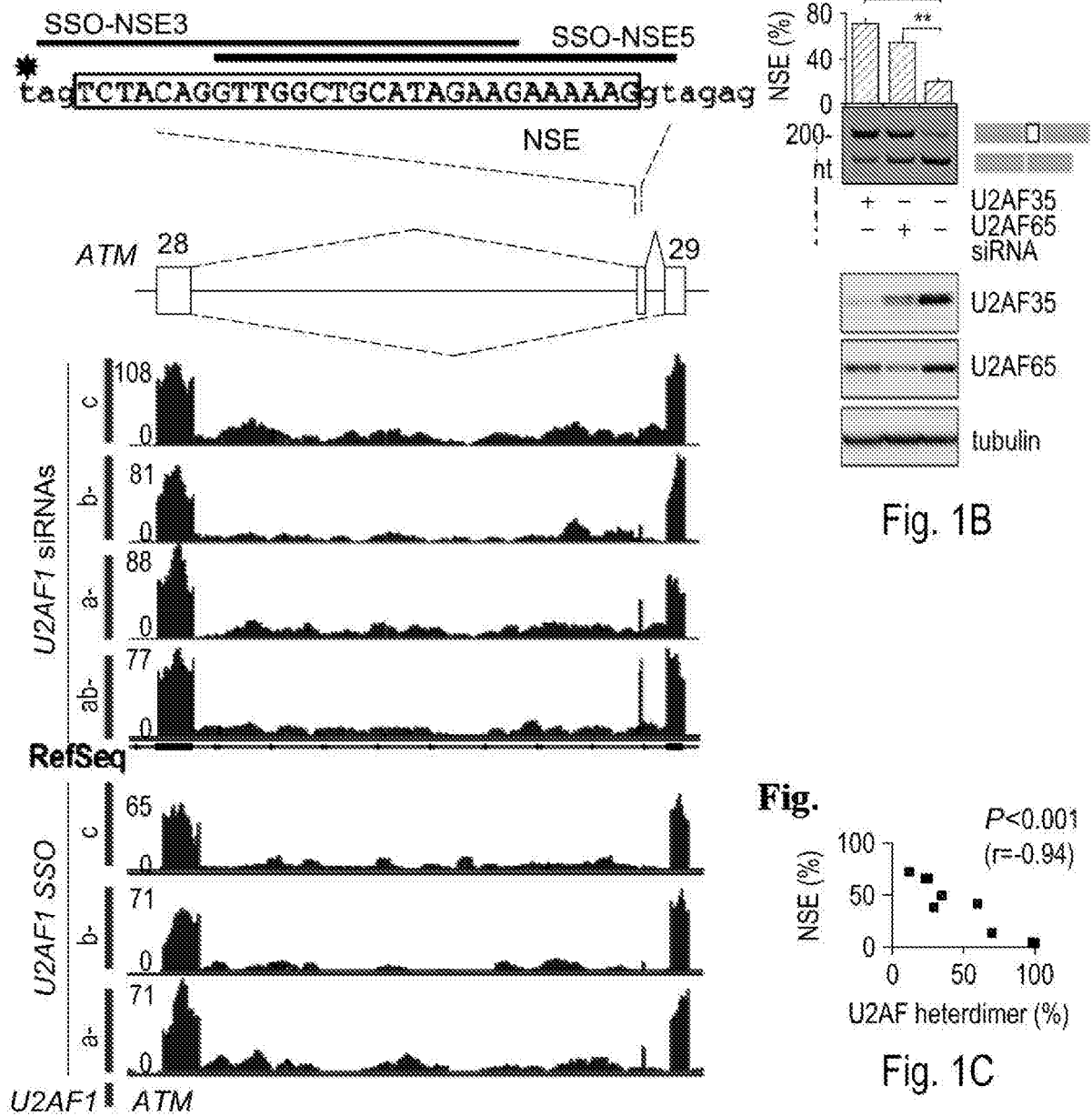


Fig. 1A

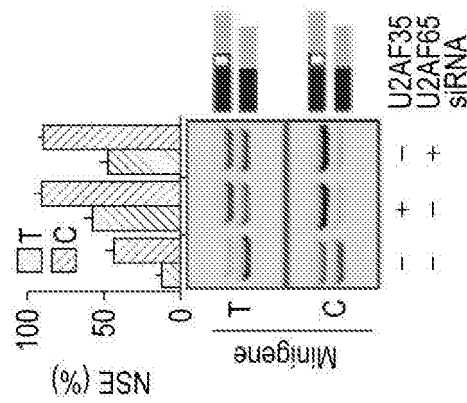


Fig. 2C

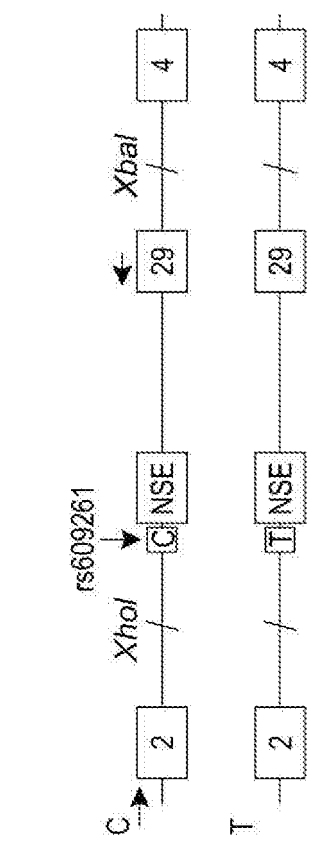


Fig. 2B

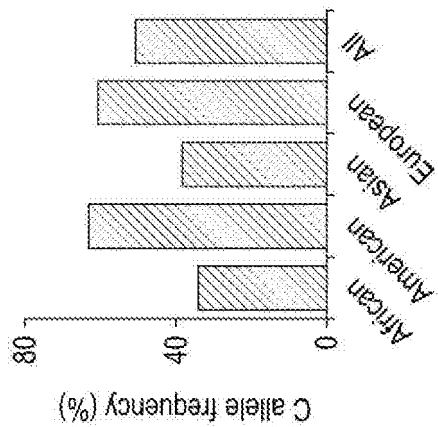
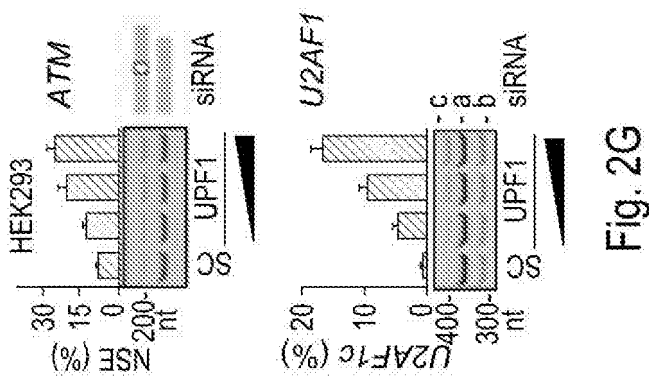
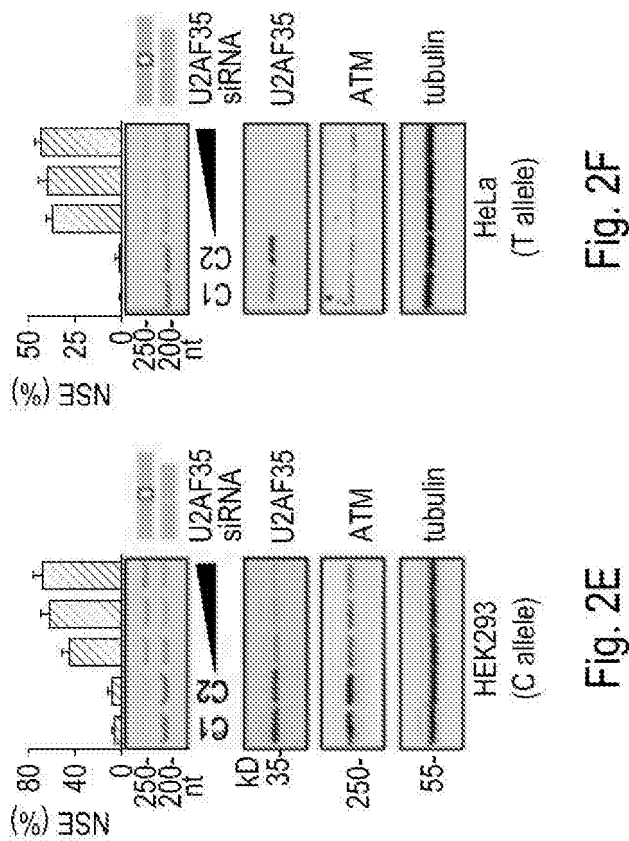
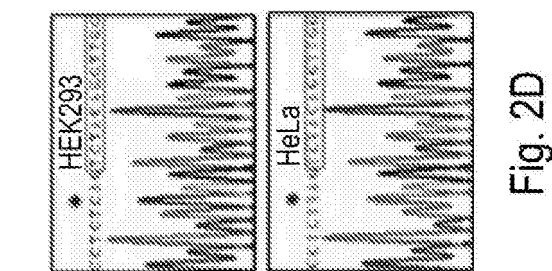
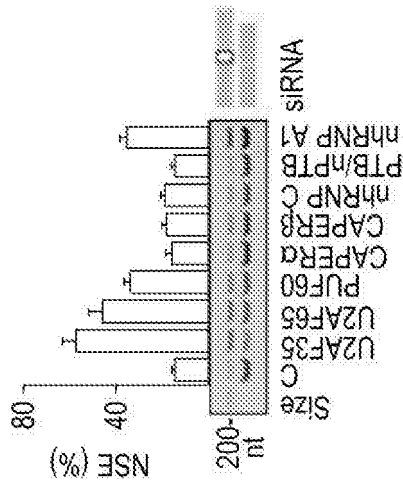
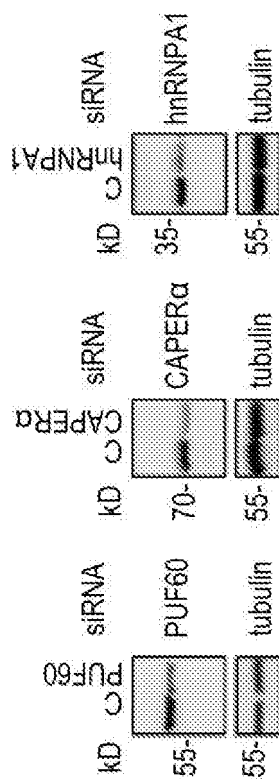
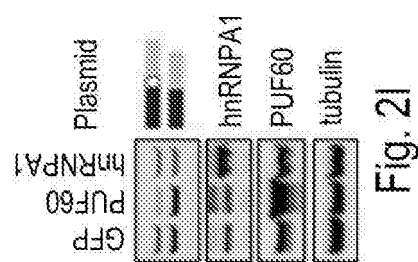


Fig. 2A



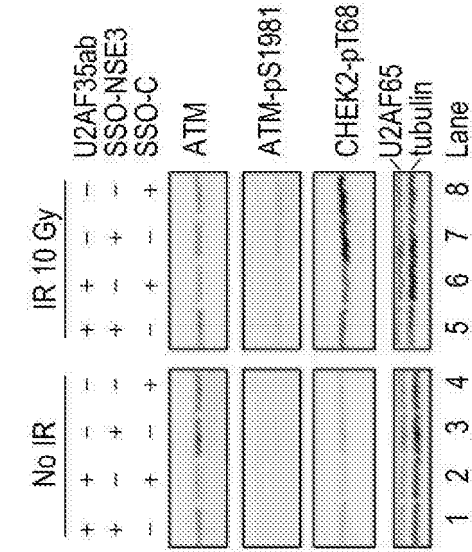


Fig. 3C

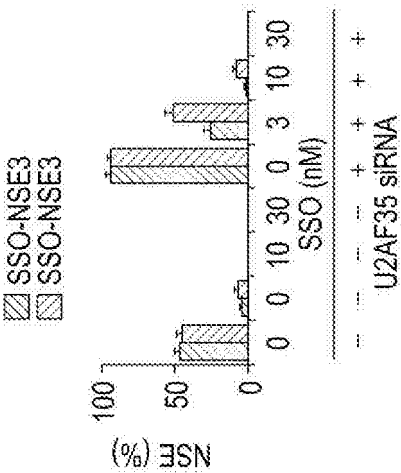


Fig. 3A

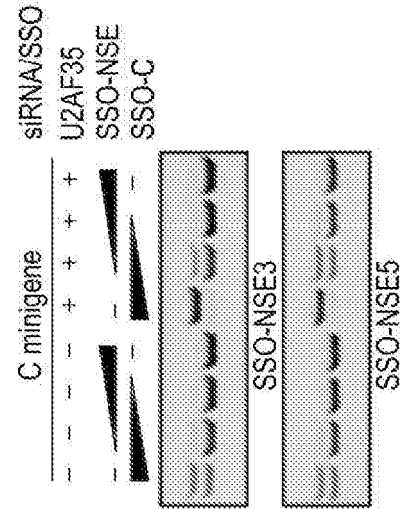
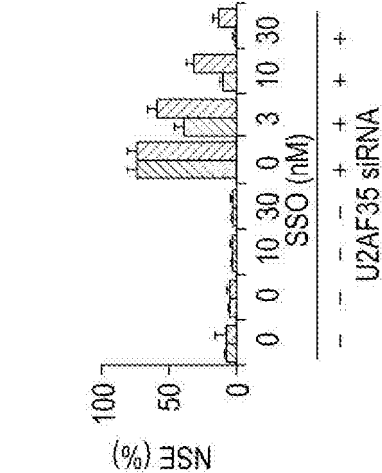


Fig. 3B

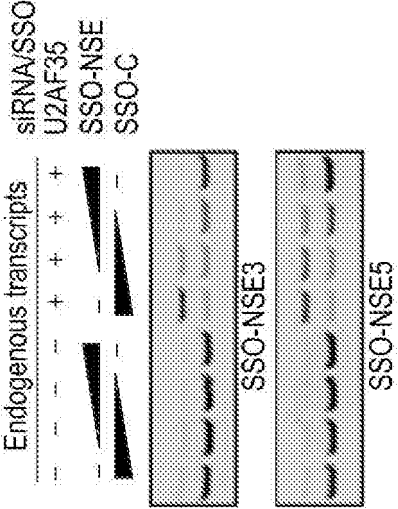
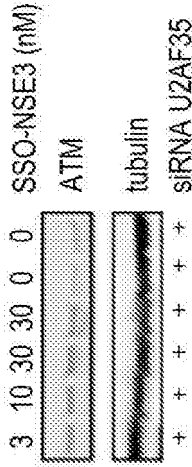


Fig. 3D



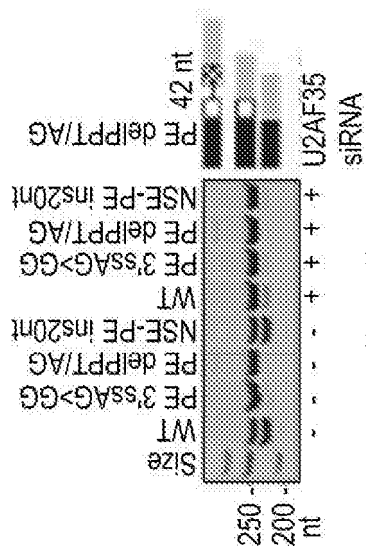


Fig. 4B

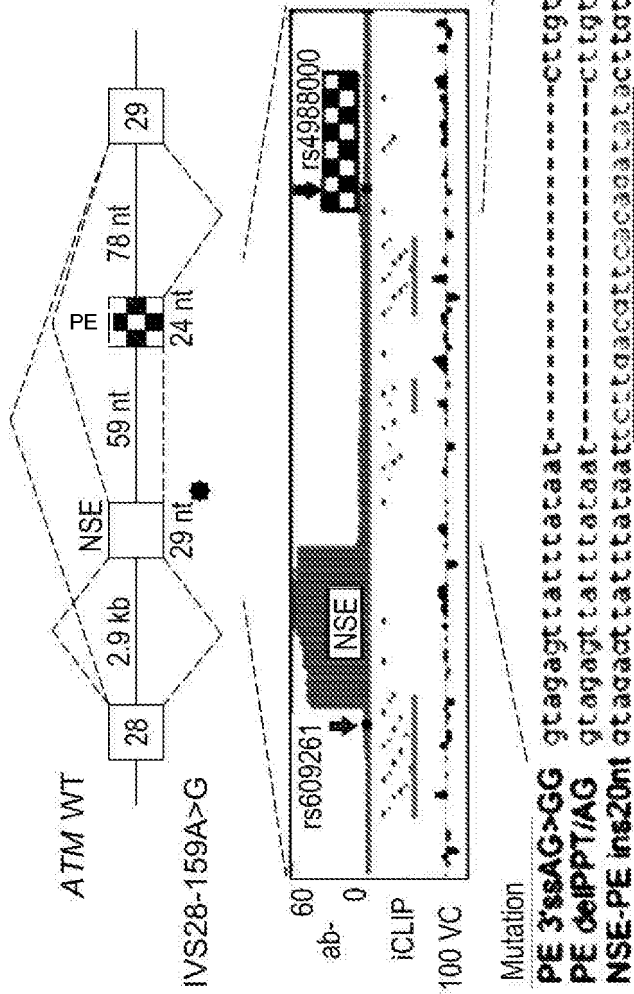


Fig. 4A

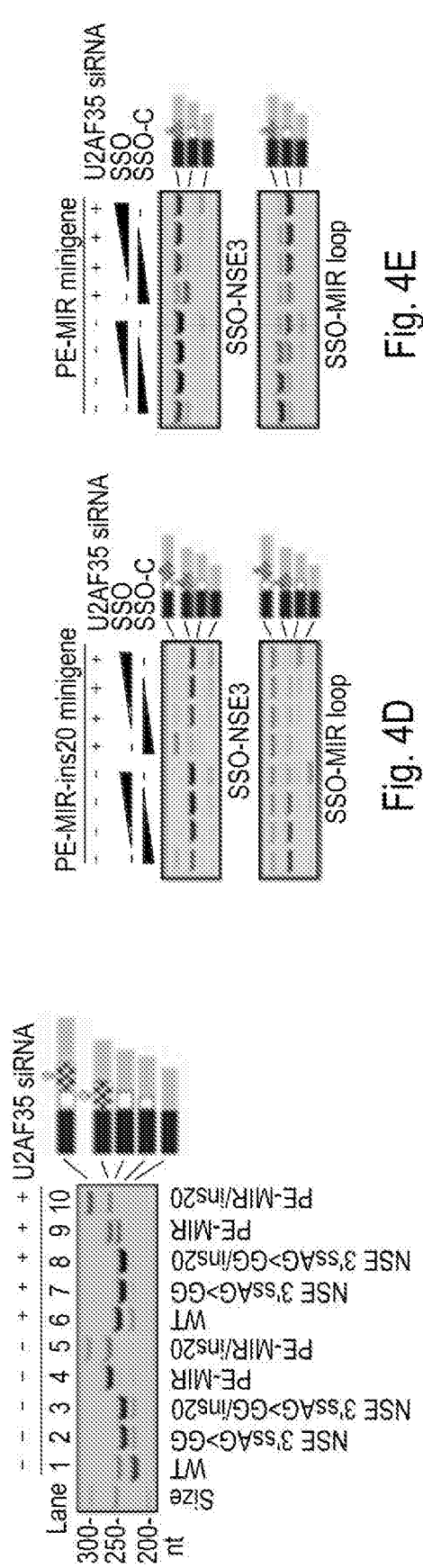


Fig. 4C

Fig. 4D

Fig. 4E

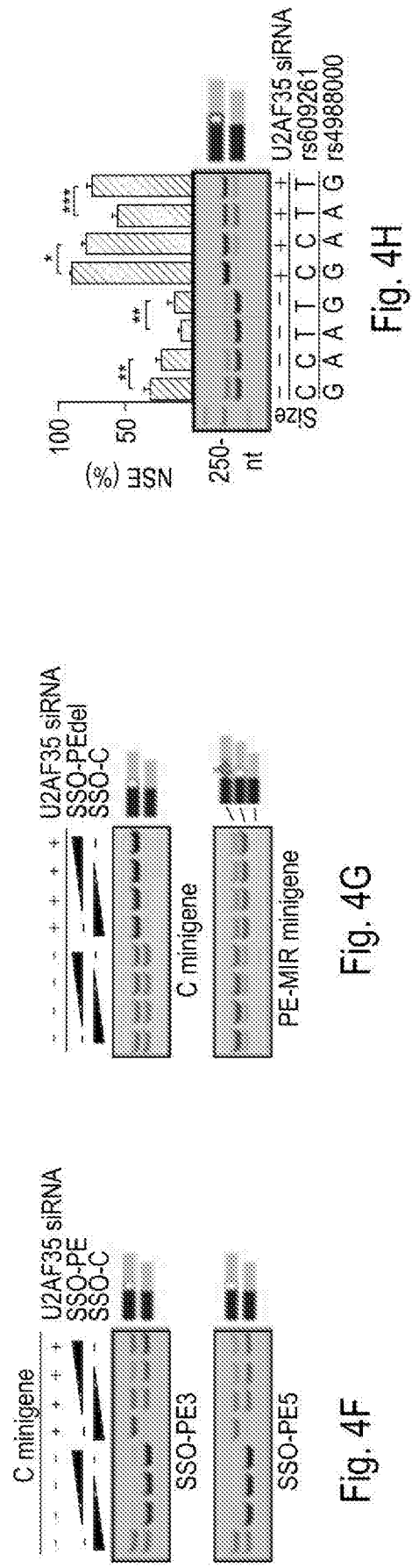


Fig. 4F

Fig. 4G

Fig. 4H

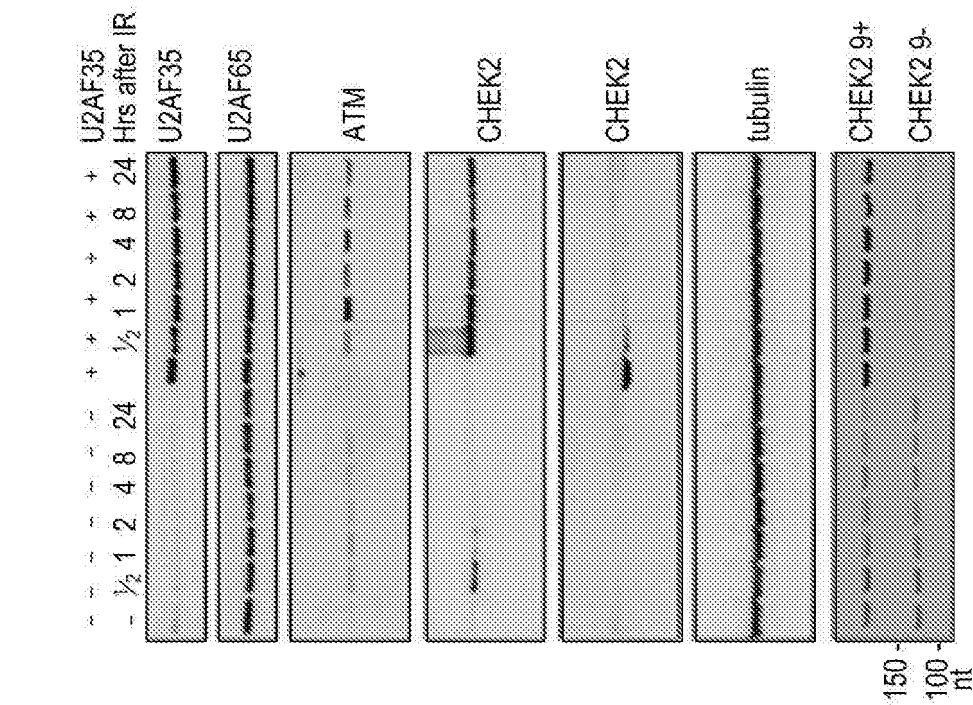


Fig. 5B

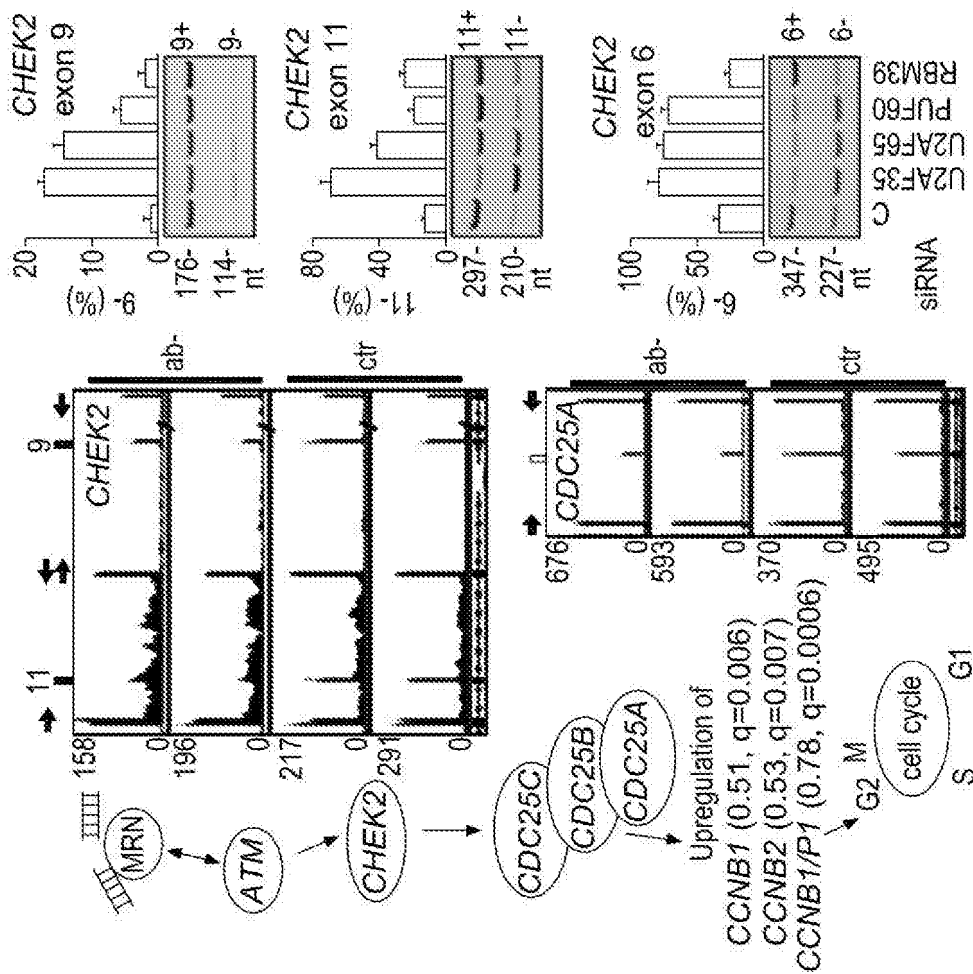


Fig. 5A

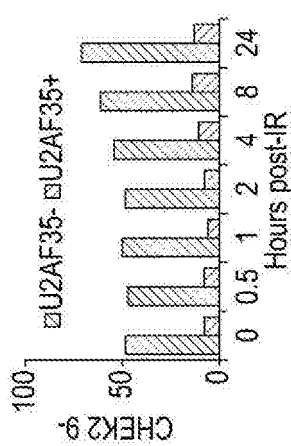


Fig. 5C

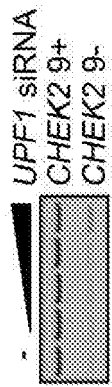


Fig. 5D

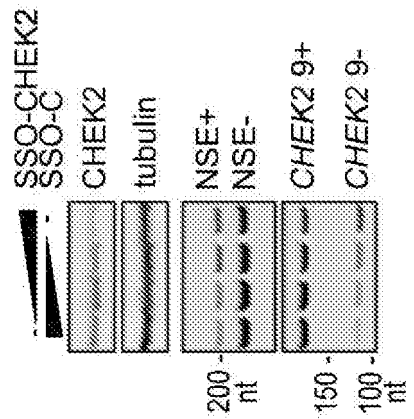


Fig. 5E

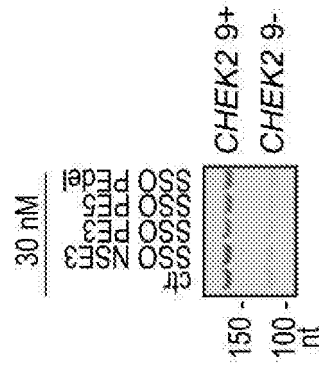


Fig. 5F

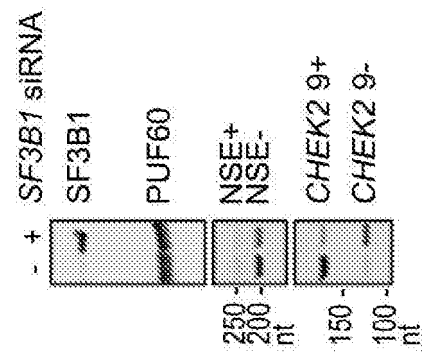


Fig. 5G

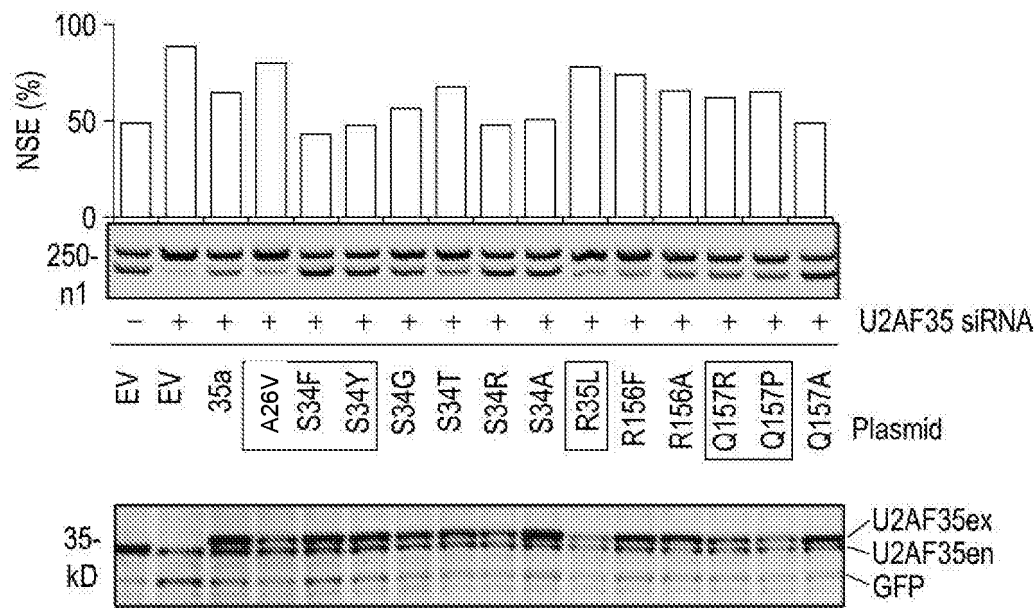


Fig. 6

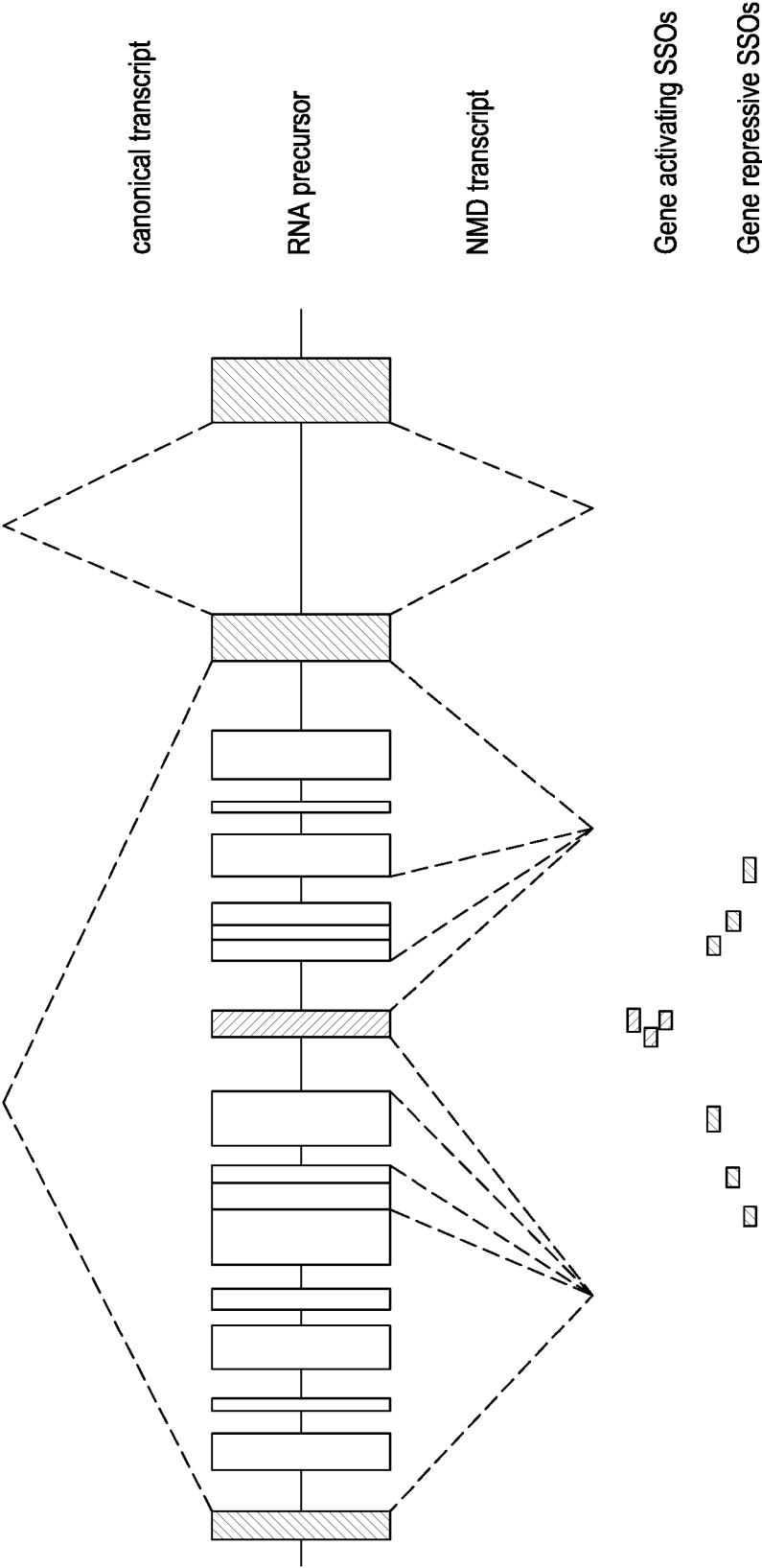
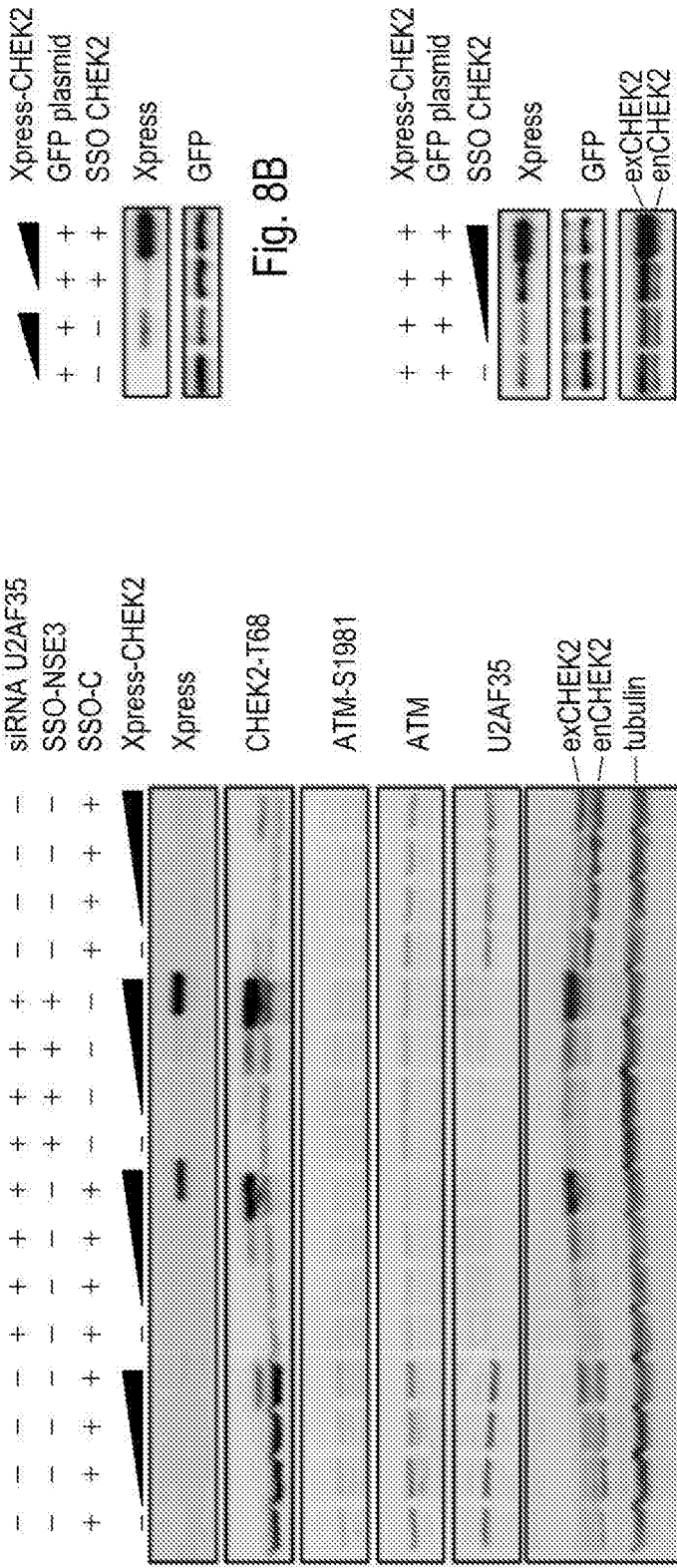


Fig. 7



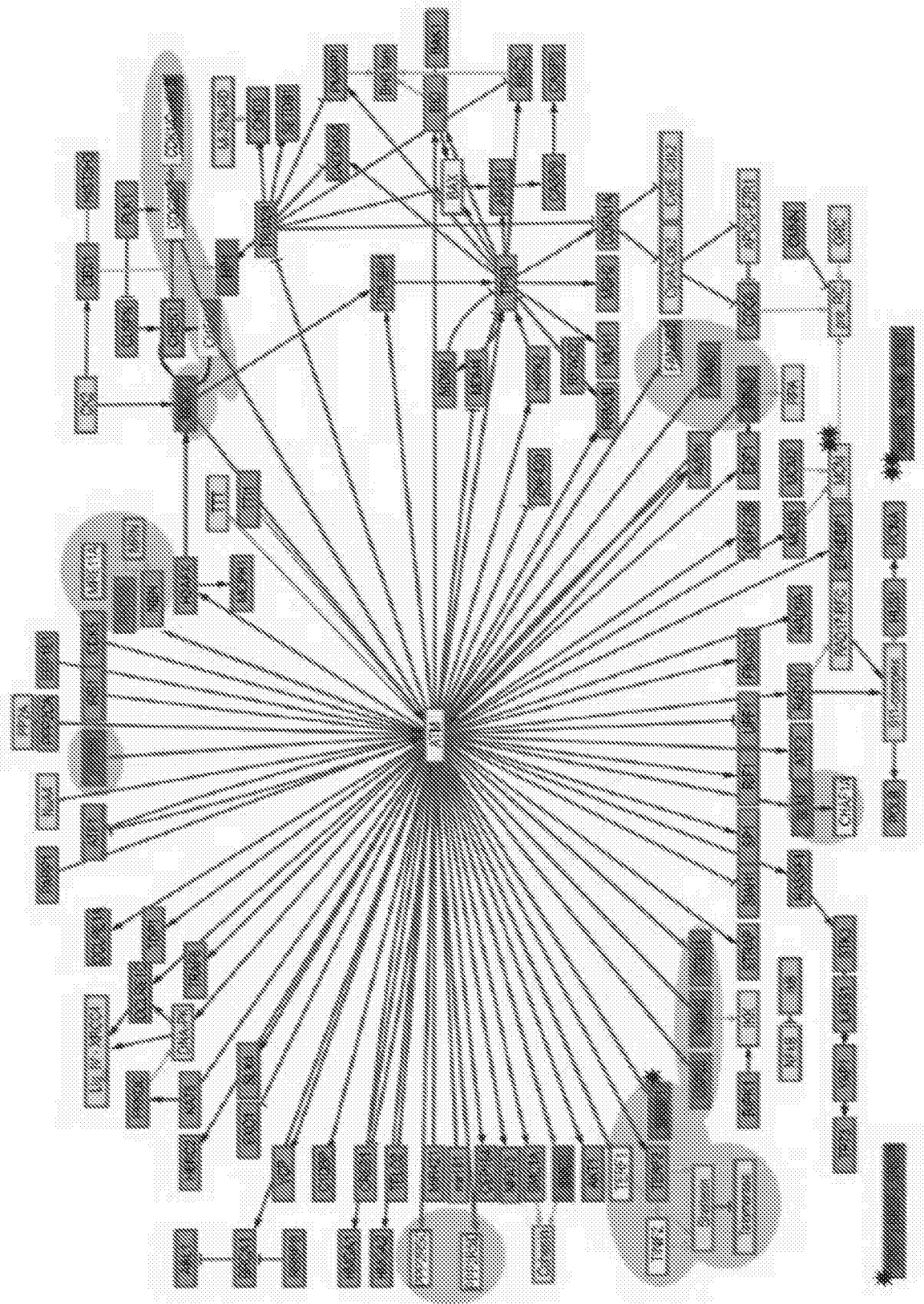


Fig. 9

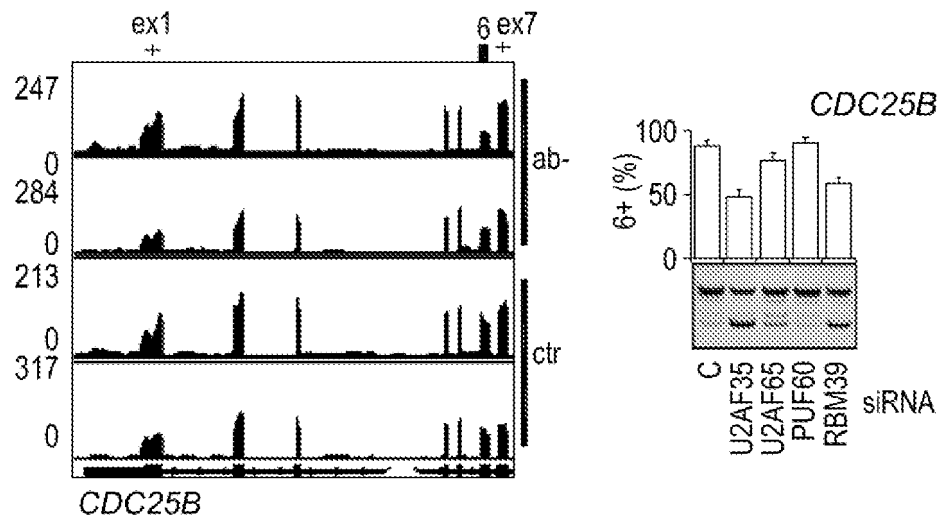


Fig. 10A

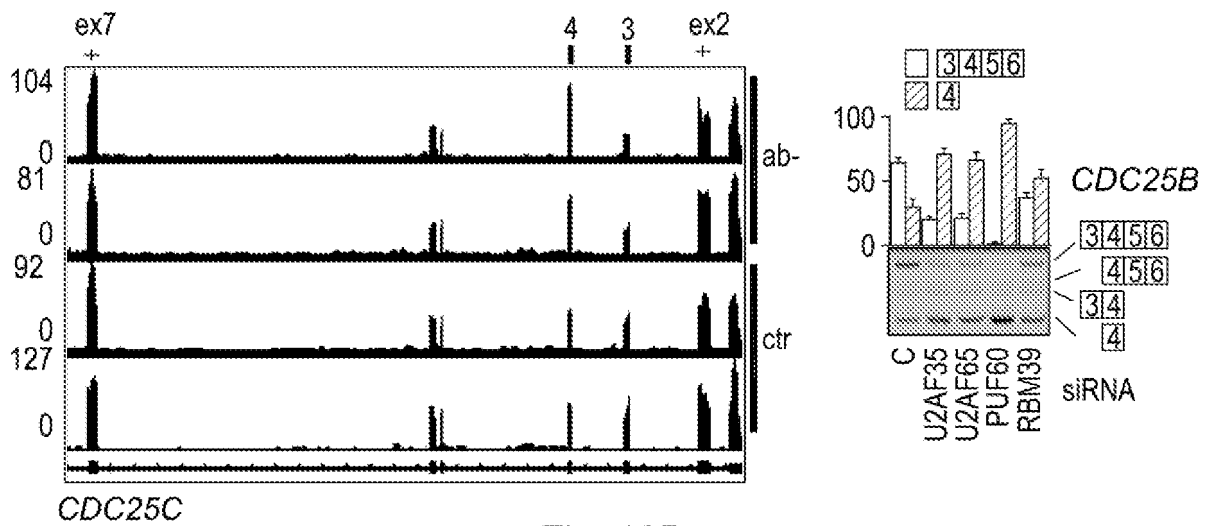


Fig. 10B

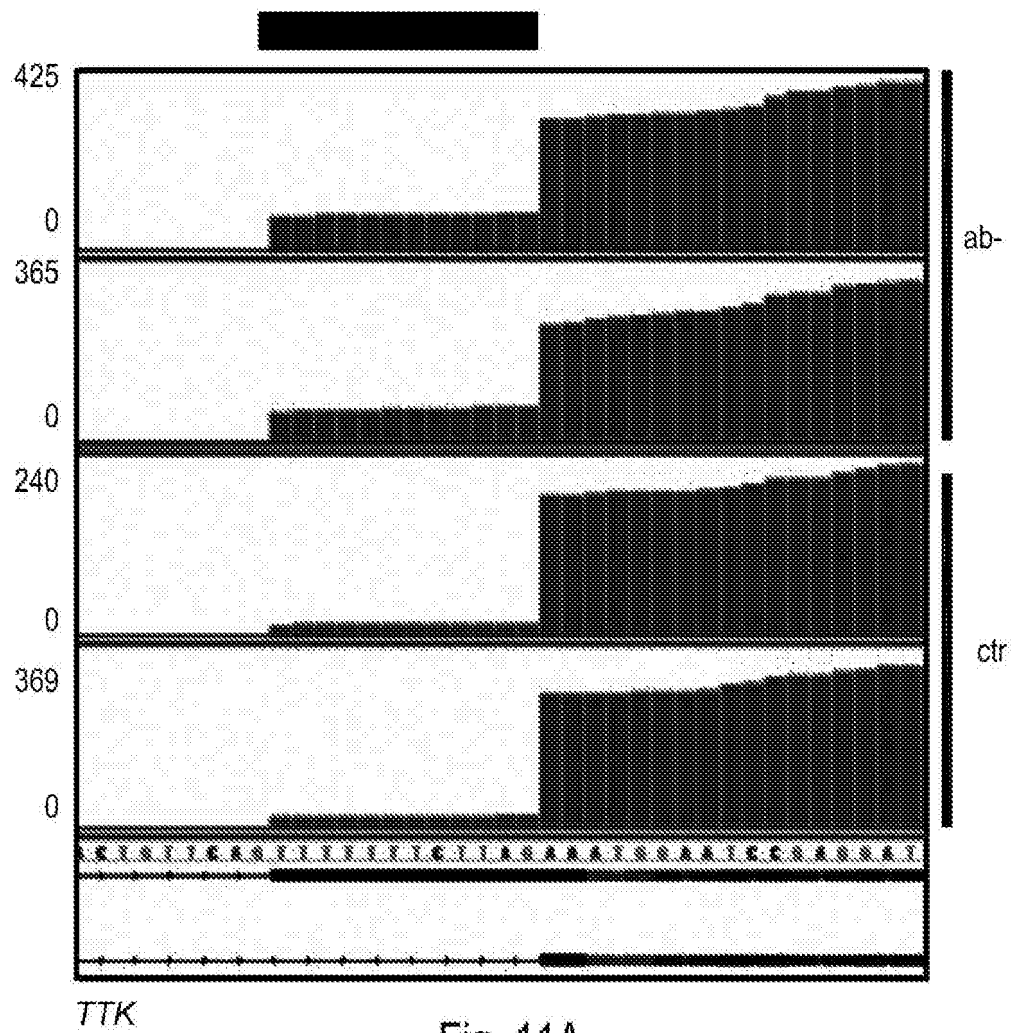


Fig. 11A

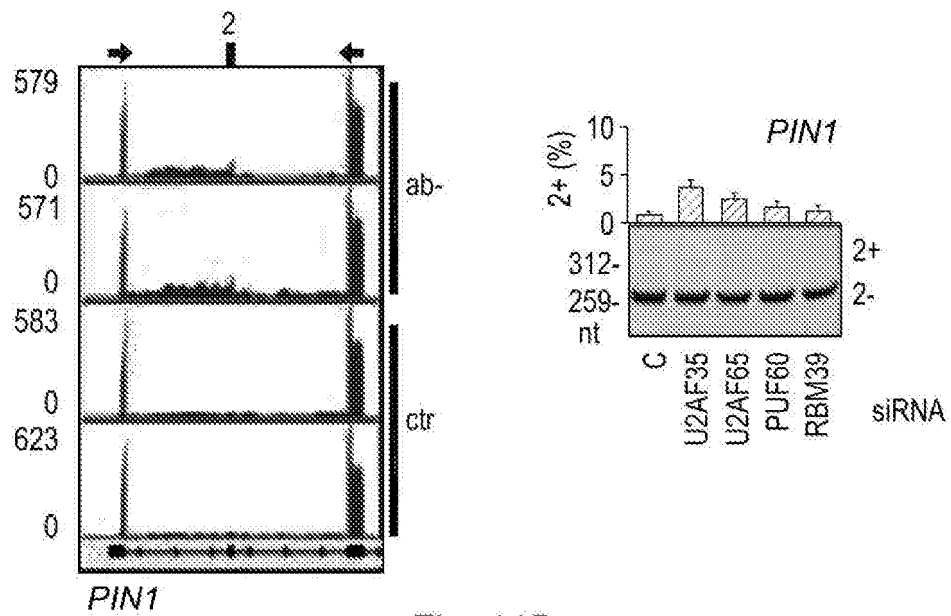


Fig. 11B

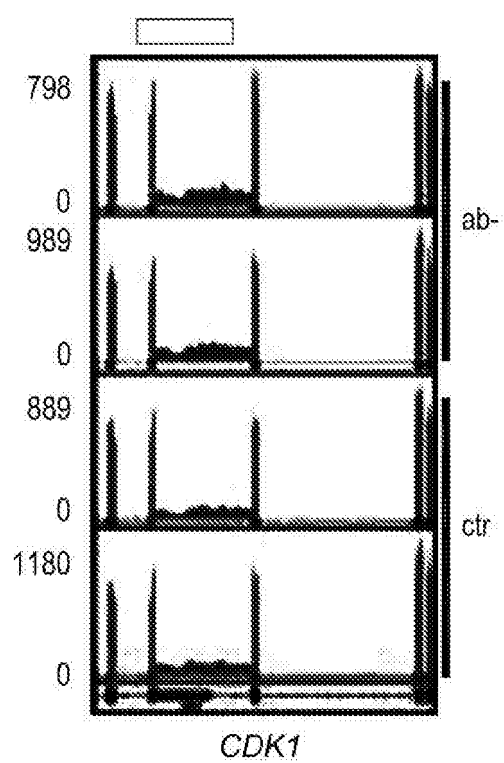


Fig. 11C

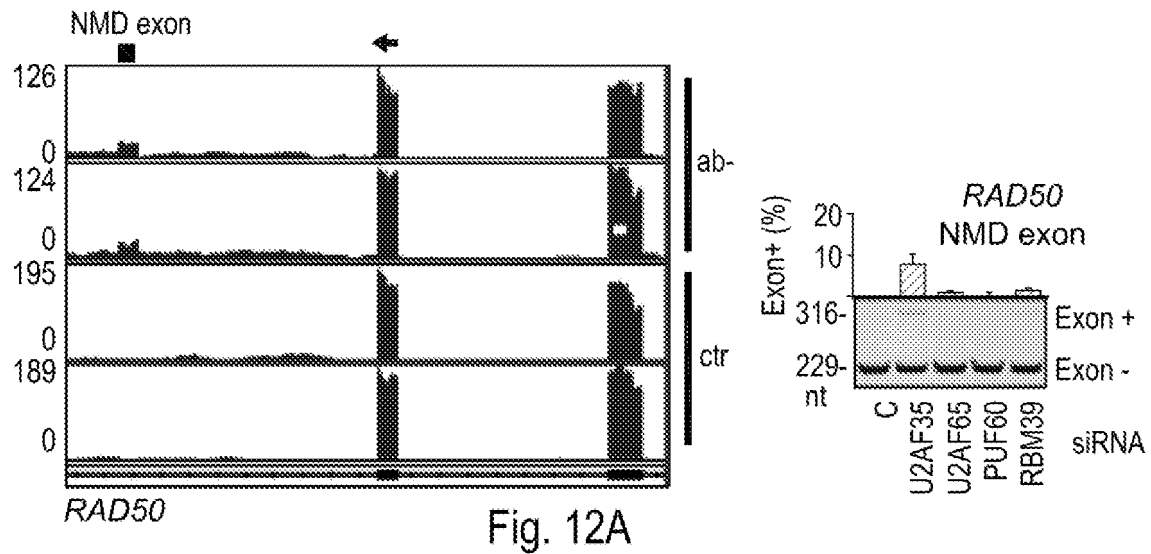


Fig. 12A

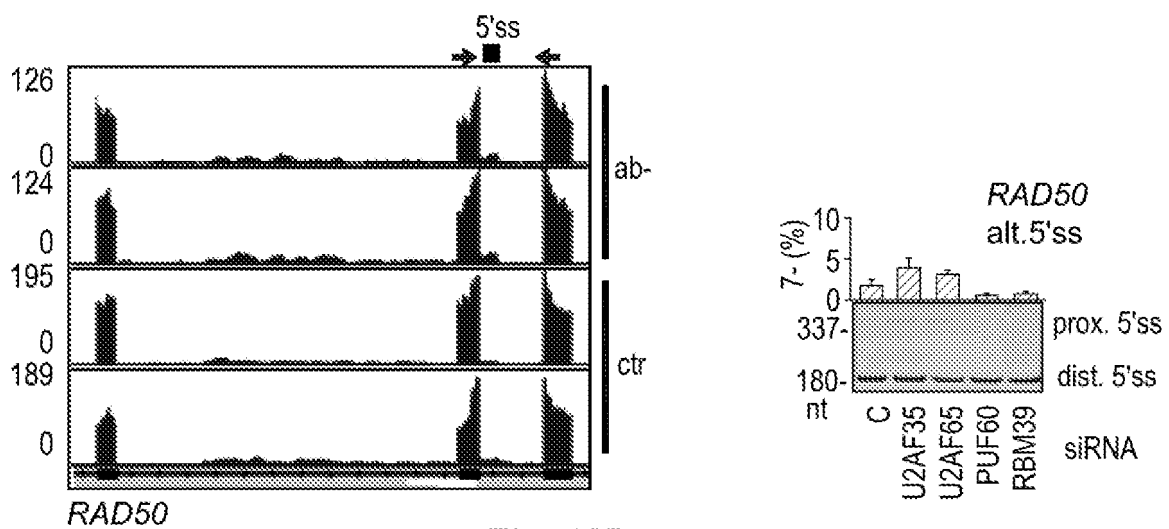


Fig. 12B

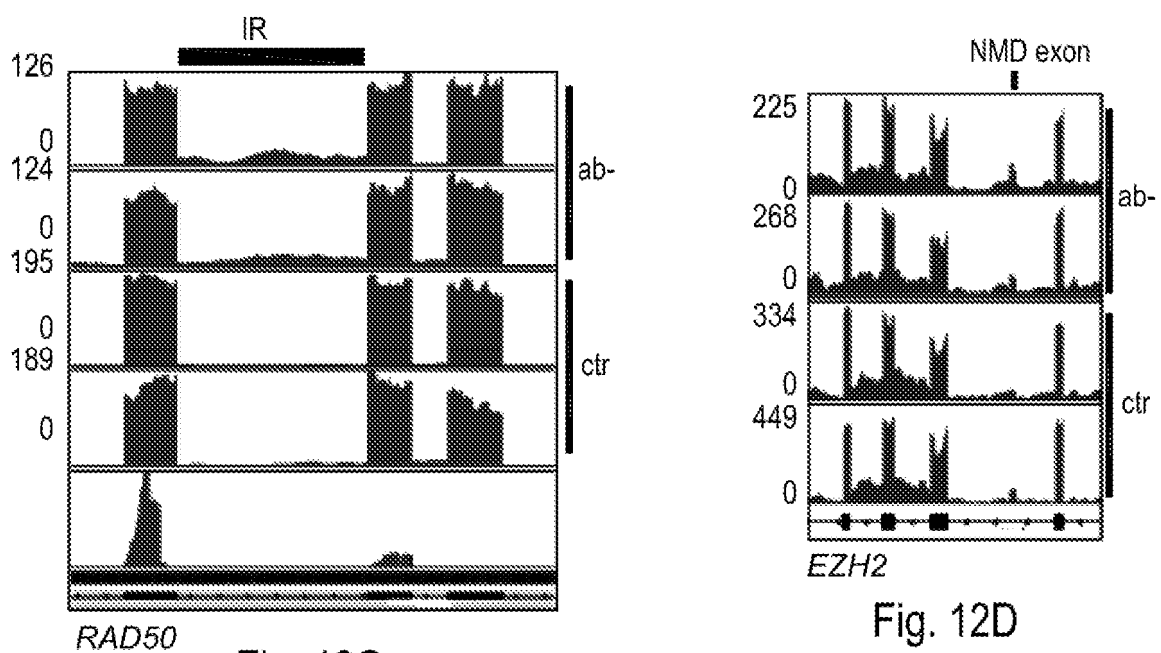


Fig. 12C

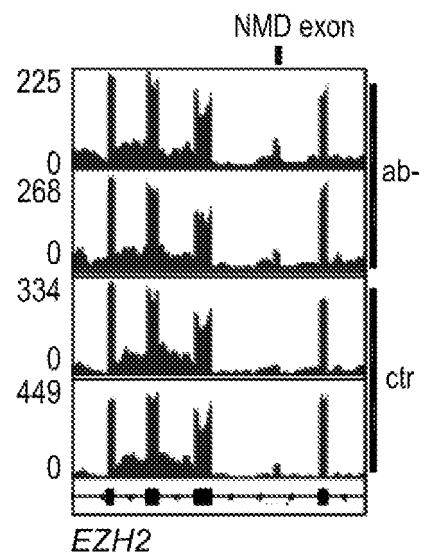


Fig. 12D

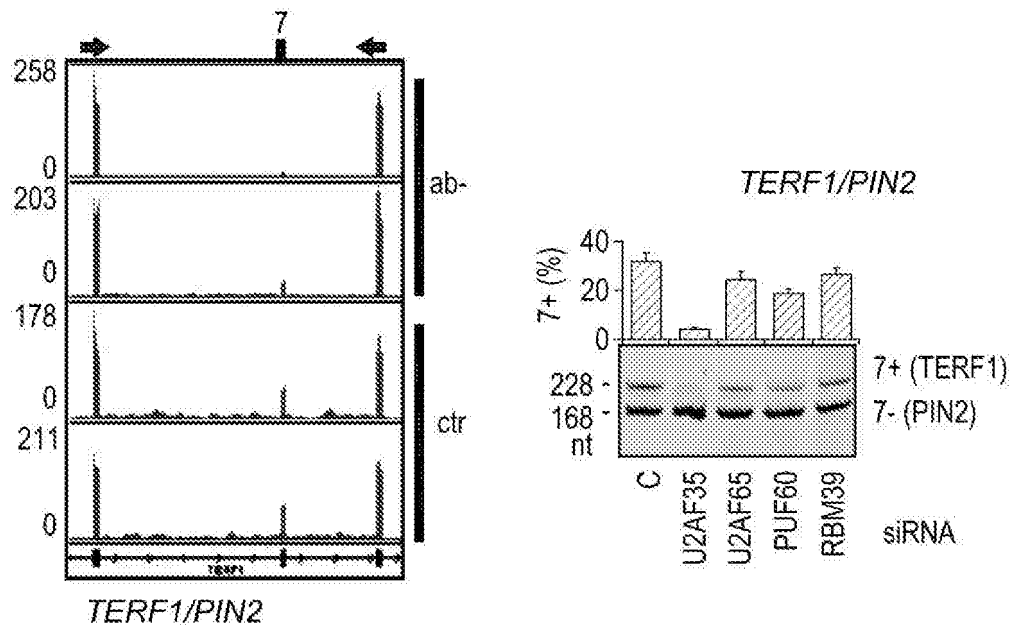


Fig. 13A

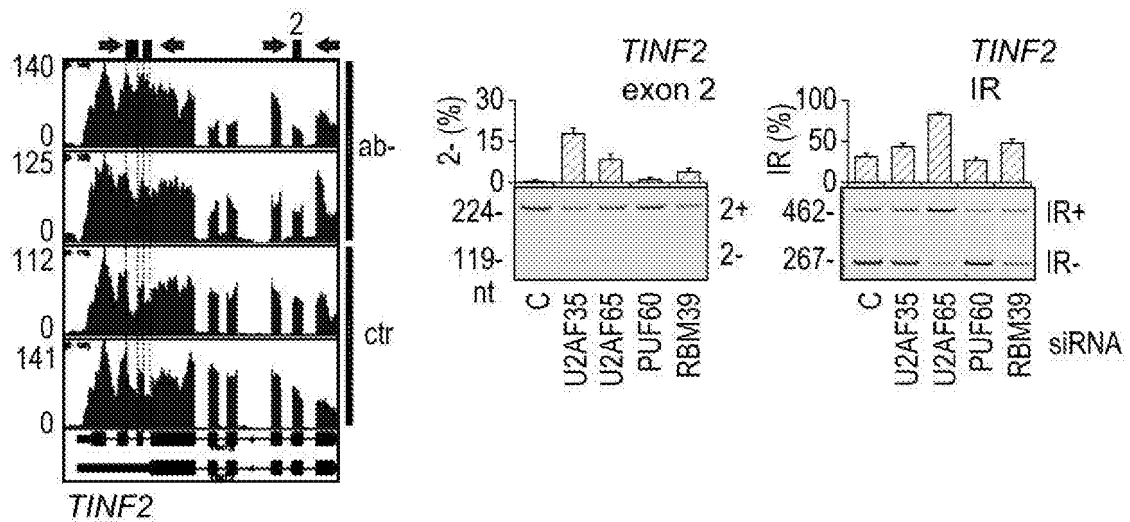


Fig. 13B

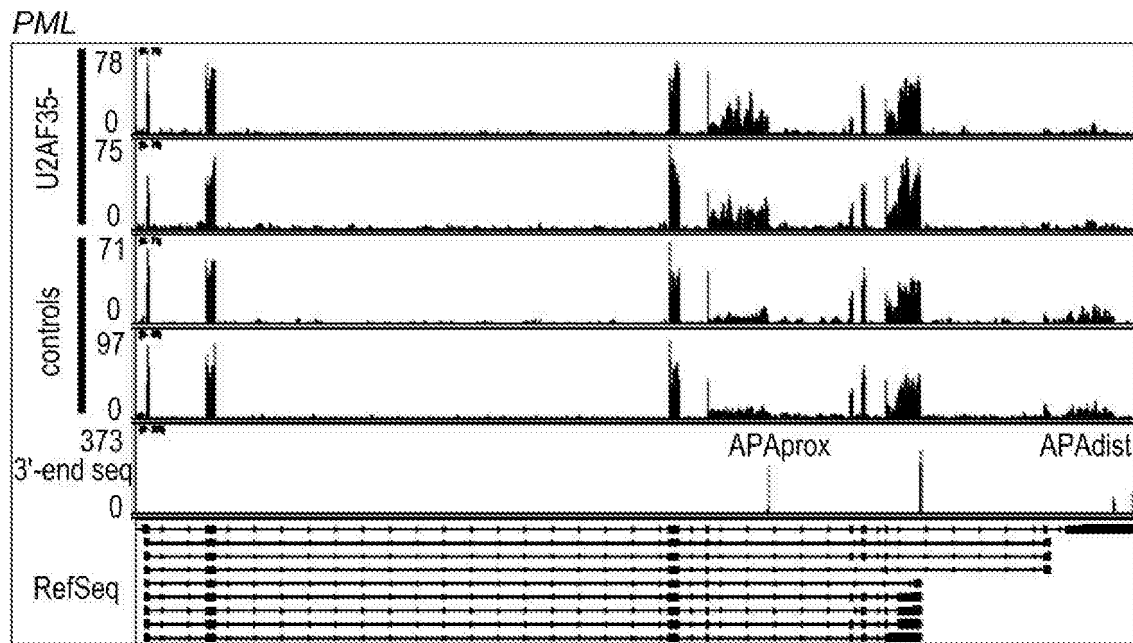


Fig. 14A

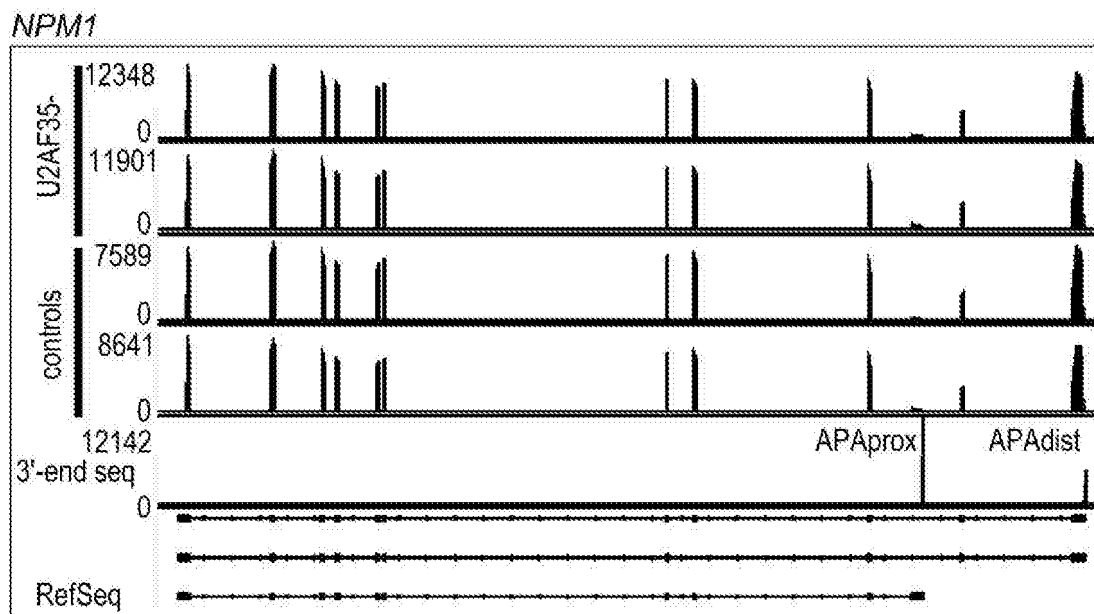


Fig. 14B

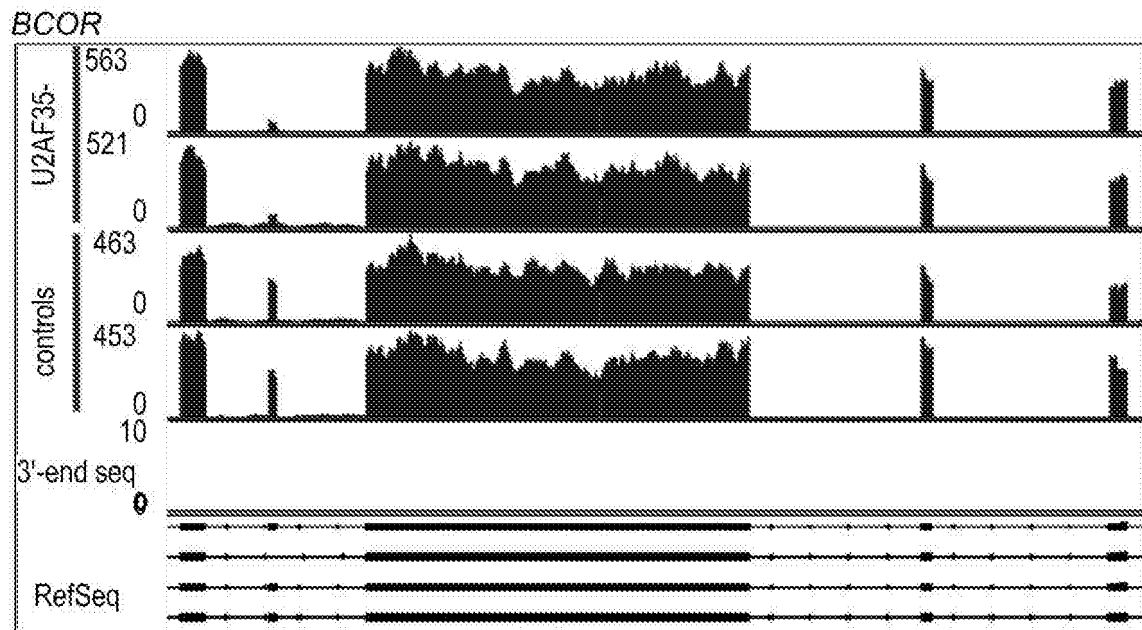


Fig. 14C

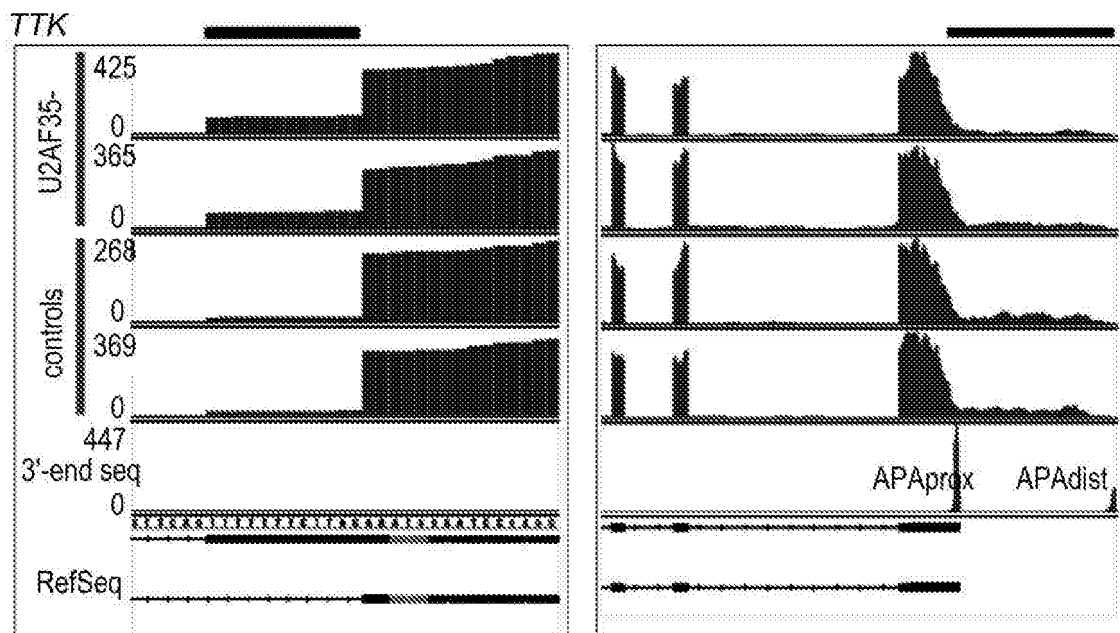


Fig. 14D

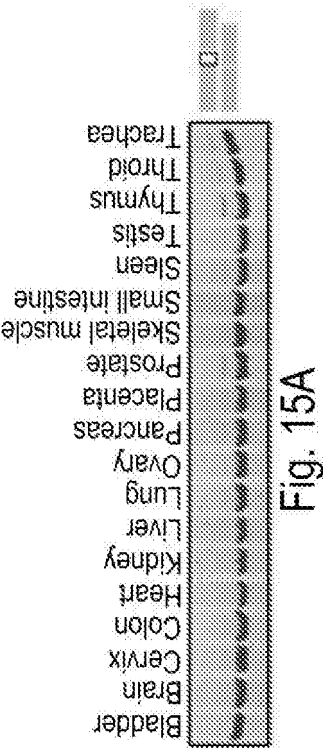
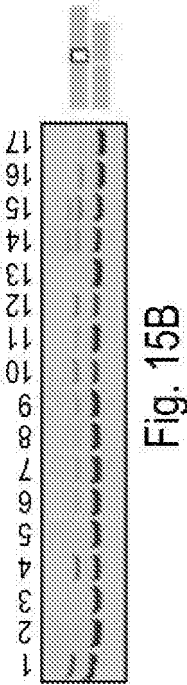
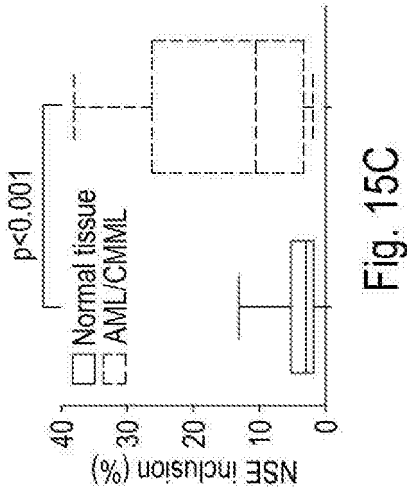
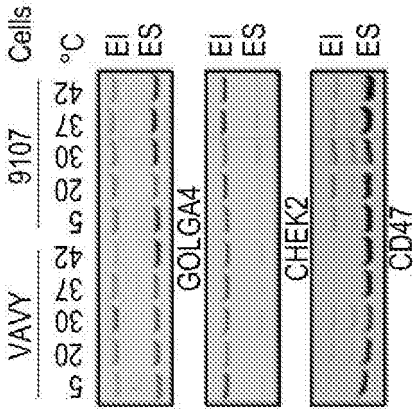


Fig. 15E

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

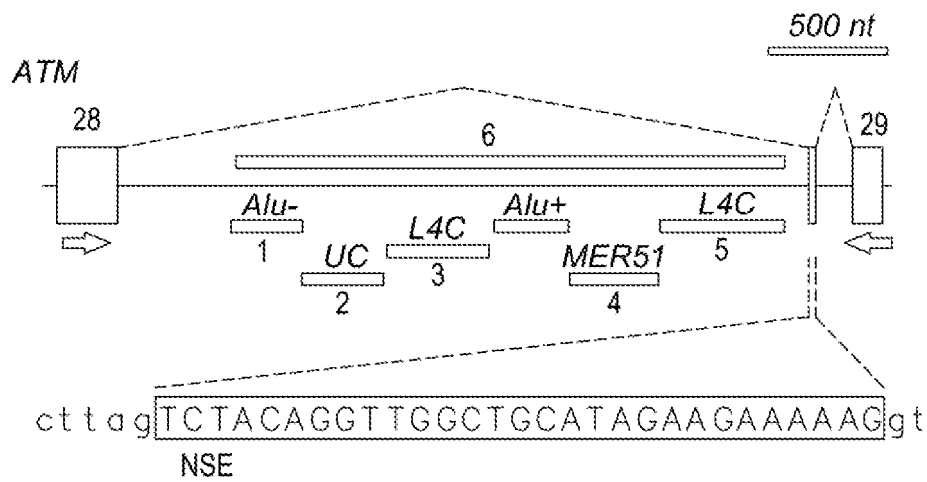


Fig. 16A

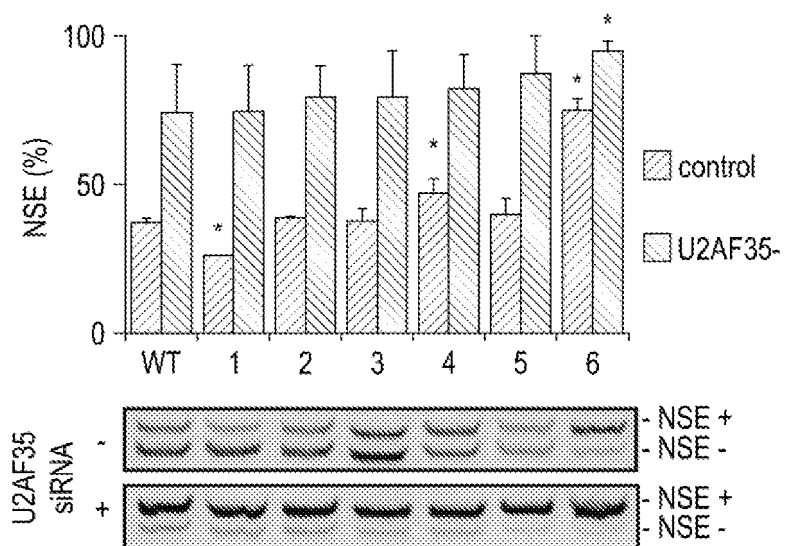


Fig. 16B

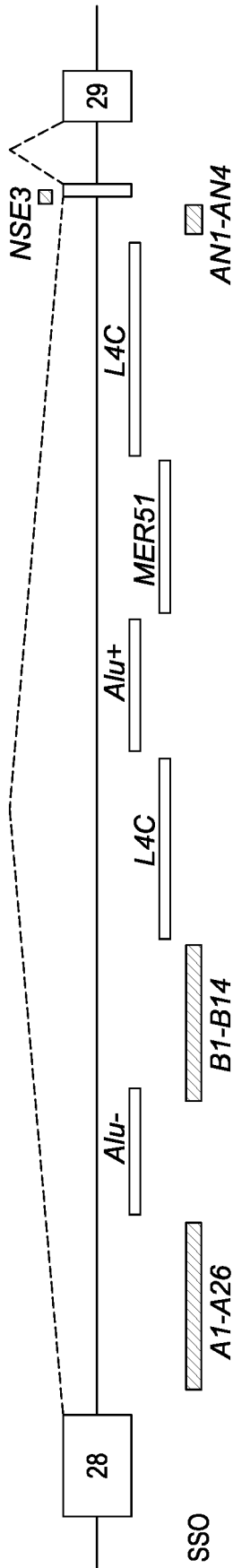


Fig. 17A

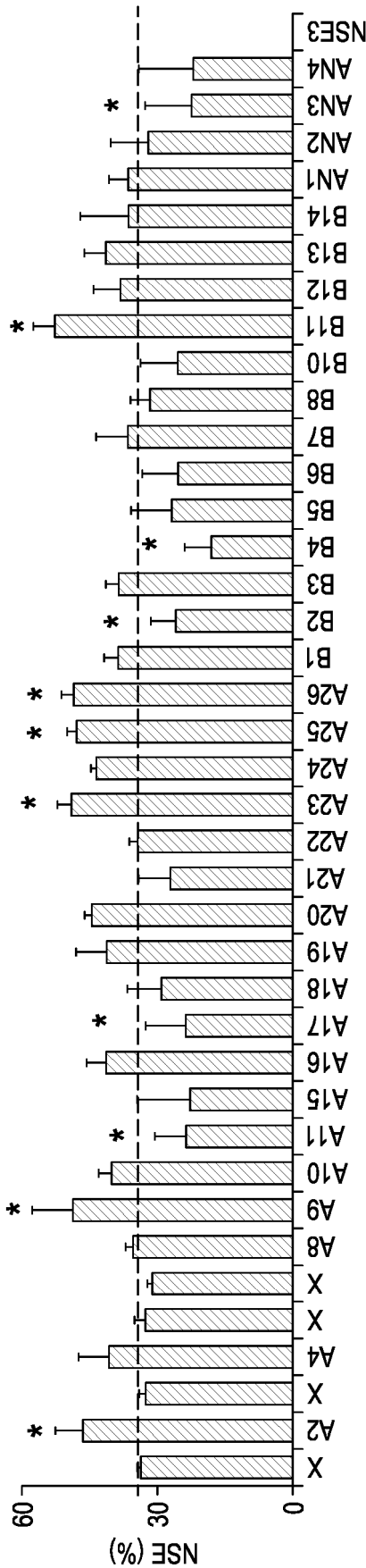


Fig. 17B

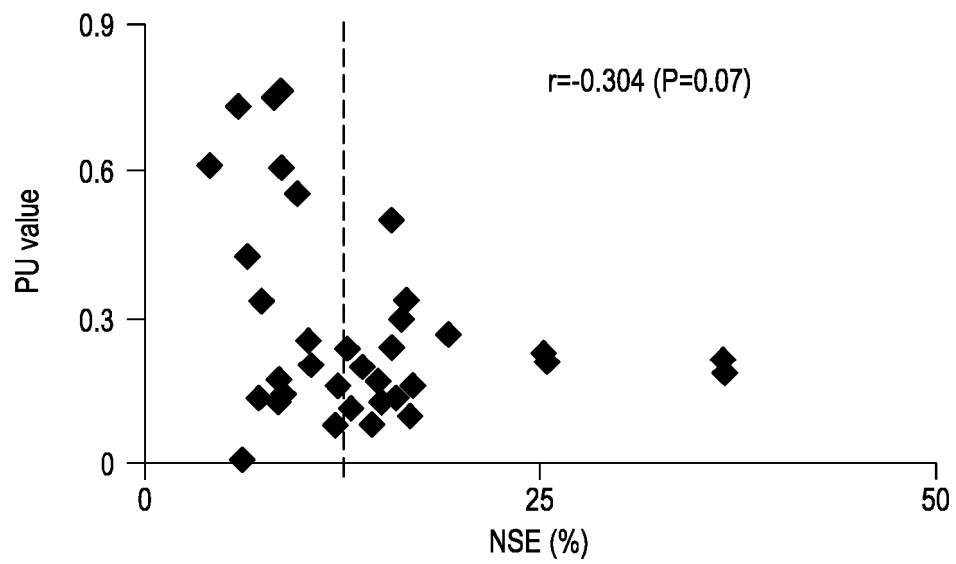


Fig. 17C

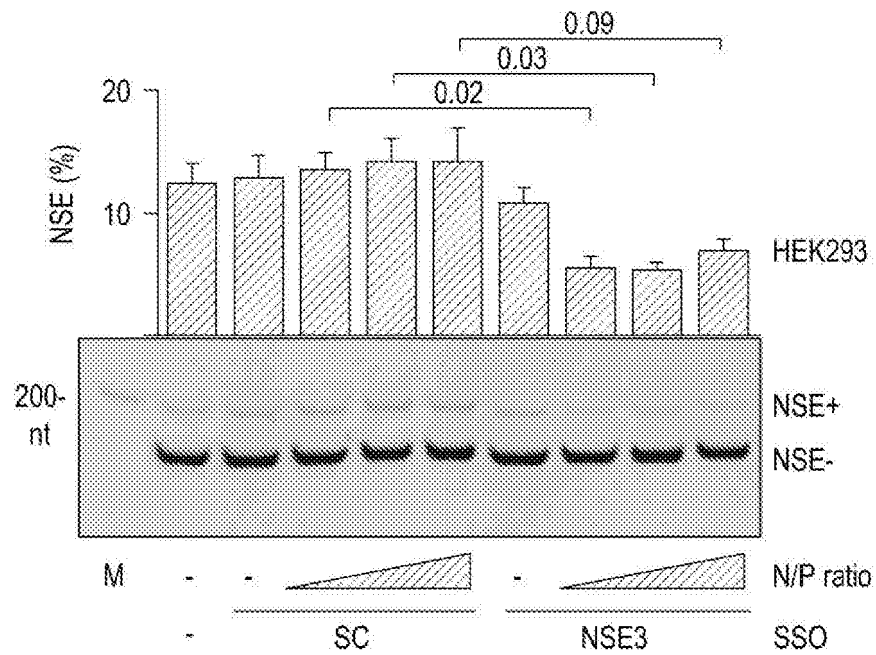


Fig. 18A

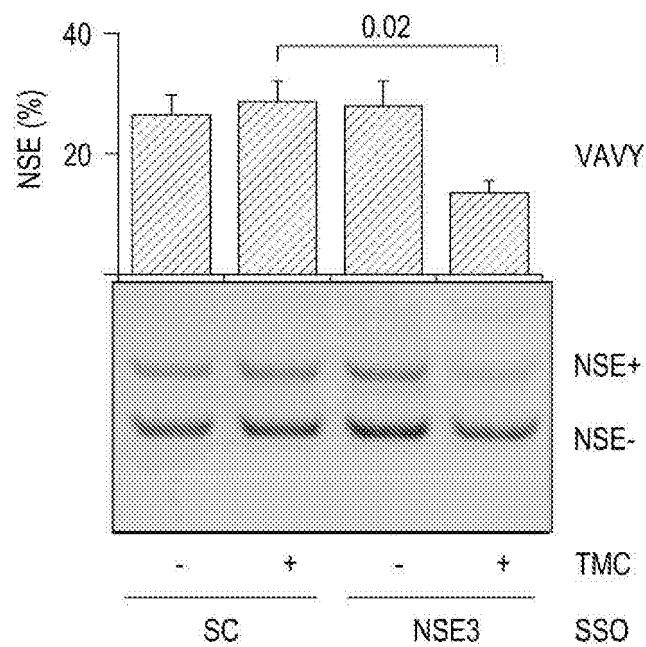


Fig. 18B

ATM intron 28	UUGUAUAAAACACACAAAACAAAGCAAGGAAAGAAUGAAGCAACAAAGCCA
MERS1A#LTR/ER	UUGGACAAAACGCACAAAACAAAGCAAGGAAAGAAUGAAGCAACAAAAGCA
ATM intron 28	GAGAUUUACUGAAAAUGAAAUUUAUACUCCACAGAGUGGGAGUG
MERS1A#LTR/ER	GAGAUUUUUUGAAAAACGAAAGUACACUCCACAGGGUGGGAGCGGGCCC-G
ATM intron 28	AGGAGUGG
MERS1A#LTR/ER	AGCAGCGGGCUCAAGGGGCCCGGUUACAGAAUUUCUGGGGUUAAAUACC
ATM intron 28	CUUCAGAGGUUUUCCAUGGUUACUUGGUUACACCCUAUGUAAAUGAAG
MERS1A#LTR/ER	CUCUAGAGGUUUUCCAUGGUUACUUGGUUACACCCUAUGUAAAUGAAG
ATM intron 28	UAGUGG
MERS1A#LTR/ER	UAGUGGCCCCGCAAUACAGUCUGAUUGGUUGCGGAAAGCGACCAUACAGAGG
ATM intron 28	UACAC-CCUAUGUAAAUGAAGUAGUGGUCUGUAAUACAGUCUGAUUGGUUA
MERS1A#LTR/ER	UACACUCCUAUGCAAAUGAAGACUUGGCCCGCGACCAGUCUGAUUGGUUG
ATM intron 28	UUCAAUUUCUUAUCUGCCA--CAGUAAAAGGG
MERS1A#LTR/ER	UUCAAUUUCCCAUUCUGCCACGCAG-AAAAGGUGGGGGGUUGCAAAGGGAG
ATM intron 28	GUCCUUUUUGUUAUUGAGCAUGGAAAGUUGGGGUUUUCCUU
MERS1A#LTR/ER	UAGCCUCUGGUCCUUUUUGUUAUUGGCCUGGAAAGUUGGGGUUUUCCUU
ATM intron 28	UUGAUUUUGGUUUAAGGAGGUCAGCAUGGAUUGACCUUAGGUUCCUGCCU
MERS1A#LTR/ER	UUGAUUUUAGUUCUAGGAAGUCAGCGUGAAUUGGCCUUAGGUUCCUGCCU
ATM intron 28	CCAGACCUUAUUGCCCUGCCUCA
MERS1A#LTR/ER	CCAGACCUUAUUCUCCUGCCUCA

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	TAGCTTCTTTCAGGCGTTTA	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	CCTGGCTTGTTGCTCTACC	This study
TIN2-R3	TGCTTCACTGCTGCTGTAATA	This study
TIN2-F6	GAAGAACATGCGATATACACA	This study
TIN2-R8	GTCTAAAACCAAGTCCCTAT	This study
PIN1-F	GAGGGAAGATGGCGGACGAG	This study
PIN1-R	TCCTCCTTGGTCCGGGTGAT	This study
TERF1-F	GCAGCGGCAAAAGTAGTAGA	This study
TERF1-R	GTCTTGTTGCTGGGTTCAC	This study
RAD50-cr5-F	AAAATCATCAAAACAGCGAG	This study
RAD50-cr5-R	TGGAGCAAGTCGAGTTTAG	This study
RAD50-E-F	GGCGACAGAAAGGTTATGAA	This study
RAD50-E-R	CGCCACAGGTCACGTATAAT	This study
Cloning primers		
ATM-XhoI	ATAGAATTCTCGAGGGGAGGGTTTTATTCTACTA	This study
ATM-XbaI	ATAGGGCCCTCTAGACTGTGGGGAGACTATGGTAA	This study
CHEK2-EcoRI	ATTAGAATTCTCTCGGGAGTCGGATGTTG	This study
CHEK2-NotI	ATTAGCGGCCGCGGTACATTCTTTCGTGTTCA	This study
Modified antisense oligonucleotides		
SSO-NSE3	CUUCUAUGCAGCCAACCUUGUAGACU	This study
SSO-NSE5	ACCUUUUUCUUCUAUGCAGCCAAC	This study
SSO-PE3	AUUUCCAAAAGUAUUUGAUGACUG	This study
SSO-PE5	UAUAUUACCUUAUUUCCAAAAGUA	This study
SSO-PEBP	CUGUAAAAGAAAAUAGAU GACUCAA	This study
SSO-PEdel	CUGUAAAAGAAAAUAGA	This study
SSO-CHEK2-ex9	ACUUACAAUCCAAAACAAUAUAAU	This study
SSO-C	AGGUGCUCGCGGGUGG	[3]
SSO-MIR loop	AGUUGCUUCAUCU	[4]
siRNA		
U2AF35ab	GGCUGUGAUUGACUUGAAU	[5]
U2AF65	GCAAGUACGGGCUUGUCA	[6]
RBM39	GGAUUACUGUCAUUUGUA	[7]
PUF60	GCAGAUGAACUCGGUGAUG	[6]
UPF1	AAGAUGCAGUCCGCUCCAUU	[8]

Fig. 20

[illegible]

Fig. 21

Pseudoboxon	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