

FIG. 1A-C

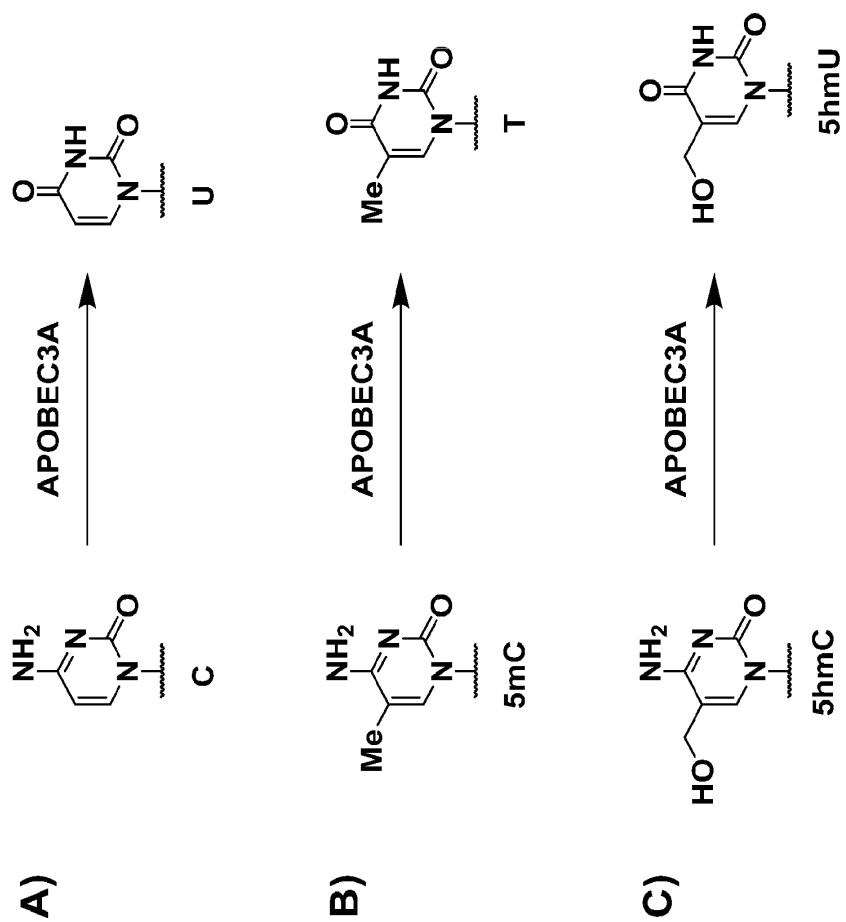


FIG. 1D

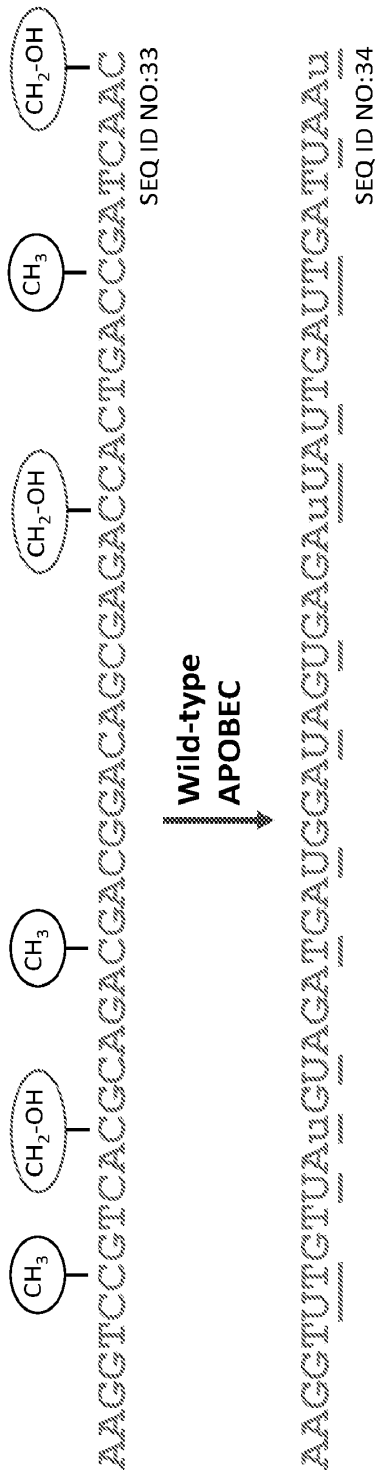


FIG. 1E

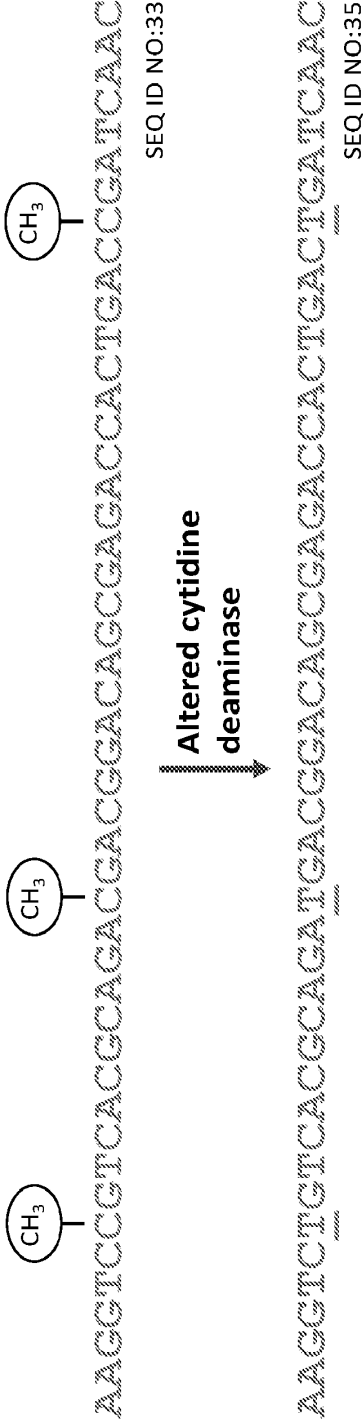


FIG. 1F

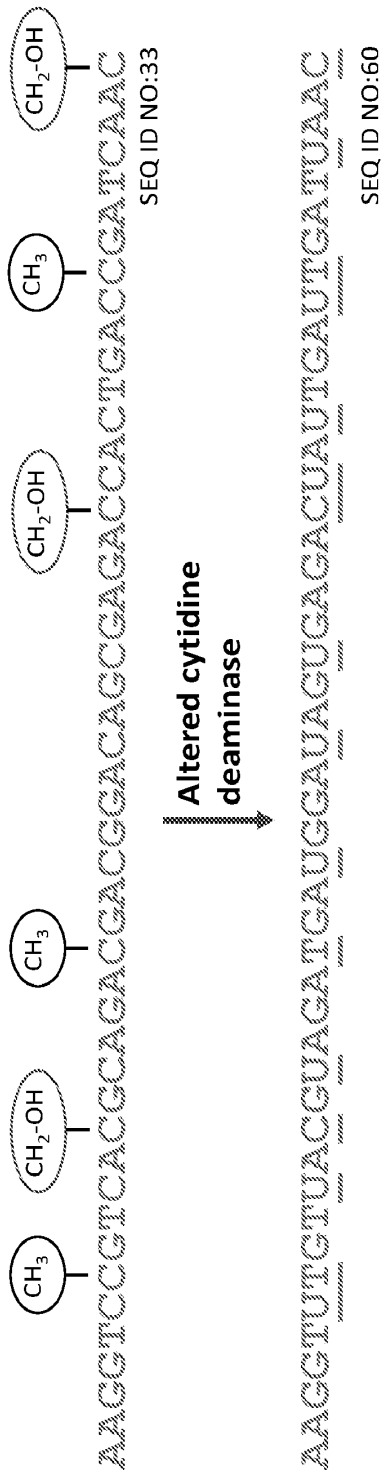
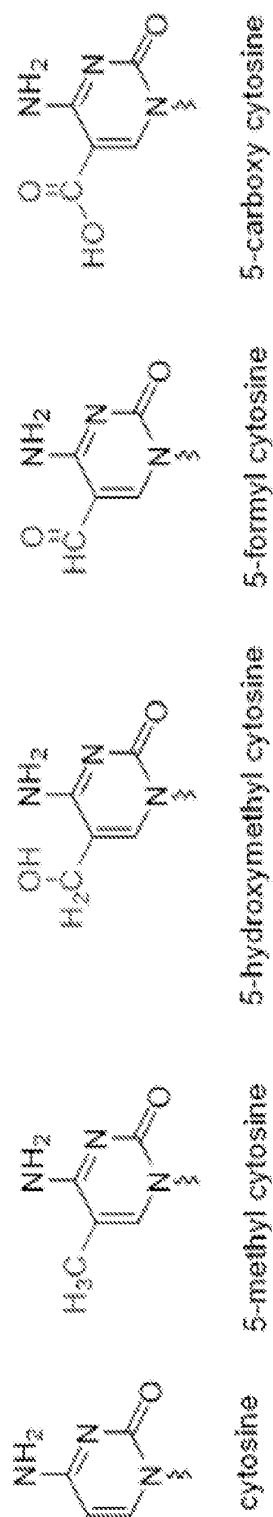


FIG. 2



[illegible]

FIG. 4

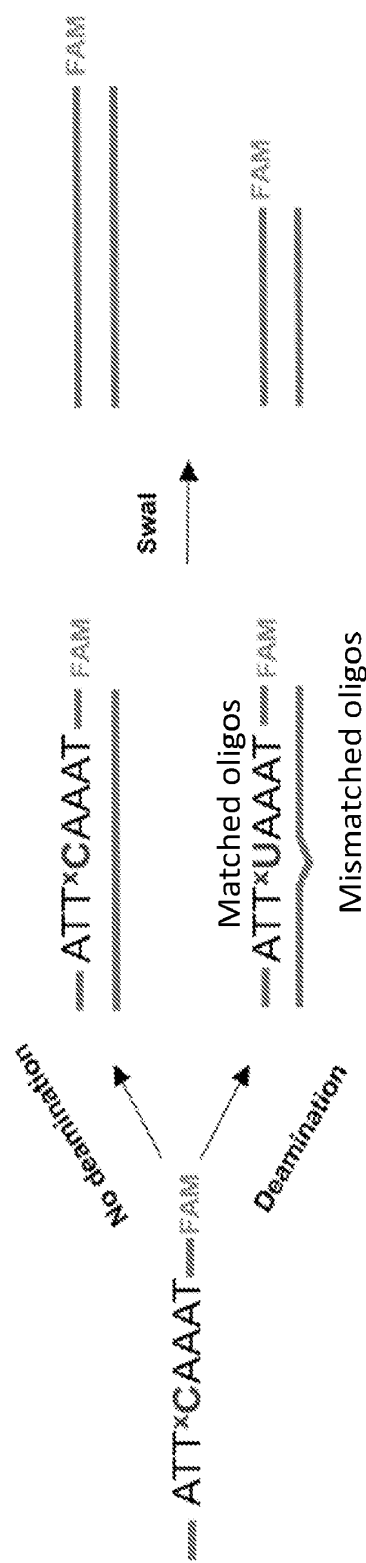
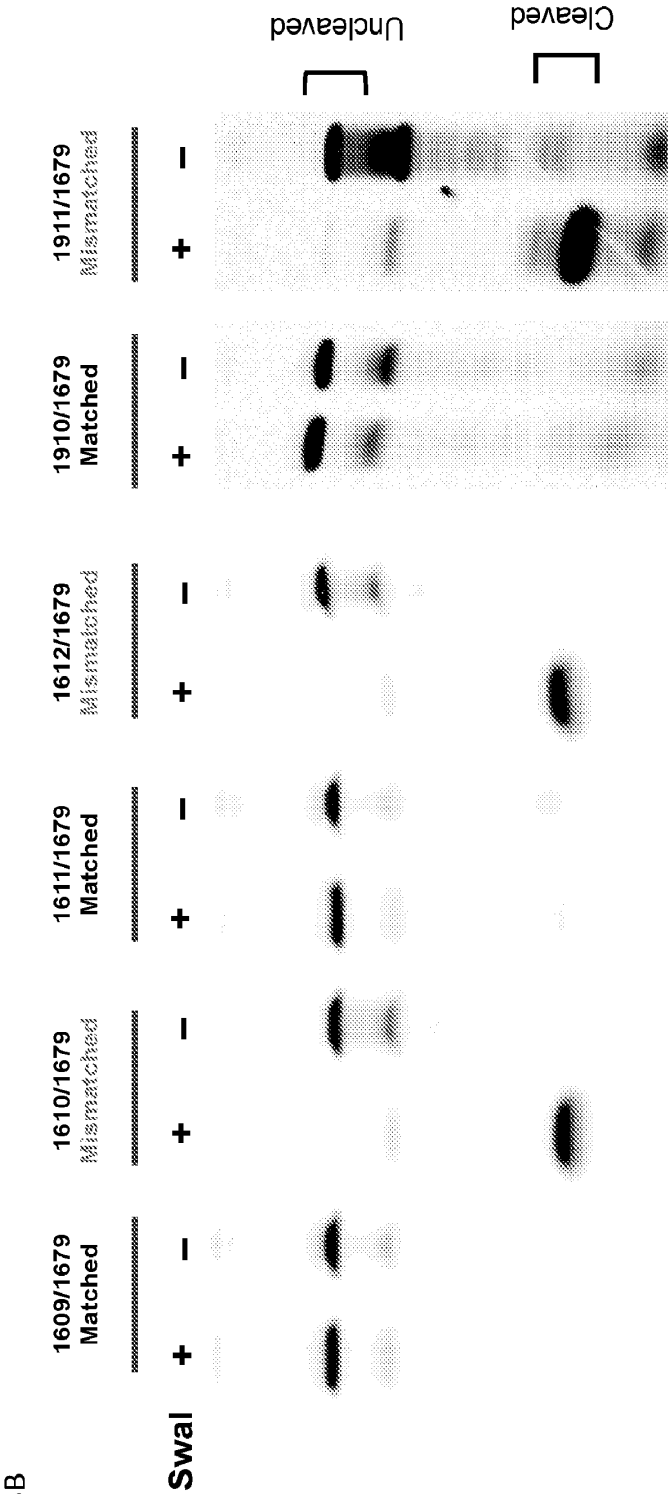


FIG. 5A

Oligo ID	Sequence
oLB1609	TGAGGAATGAAAGTTGATTCAAATGTGATGAGGTGA/36-FAM/
oLB1610	TGAGGAATGAAAGTTGATT/deoxyU/AAATGTGATGAGGTGA/36-FAM/
oLB1611	TGAGGAATGAAAGTTGATT/Me-dC/AAATGTGATGAGGTGA/36-FAM/
oLB1612	TGAGGAATGAAAGTTGATTIAAATGTGATGAGGTGA/36-FAM/
oJT 1910	TGAGGAATGAAAGTTGATT/5hm-dC/AAATGTGATGAGGTGA/36-FAM/
oJT1911	TGAGGAATGAAAGTTGATT/5hm-dU/AAATGTGATGAGGTGA/36-FAM/
oLB1679	TCACCTCATCACATTGAATCAACTTCATTCTCA



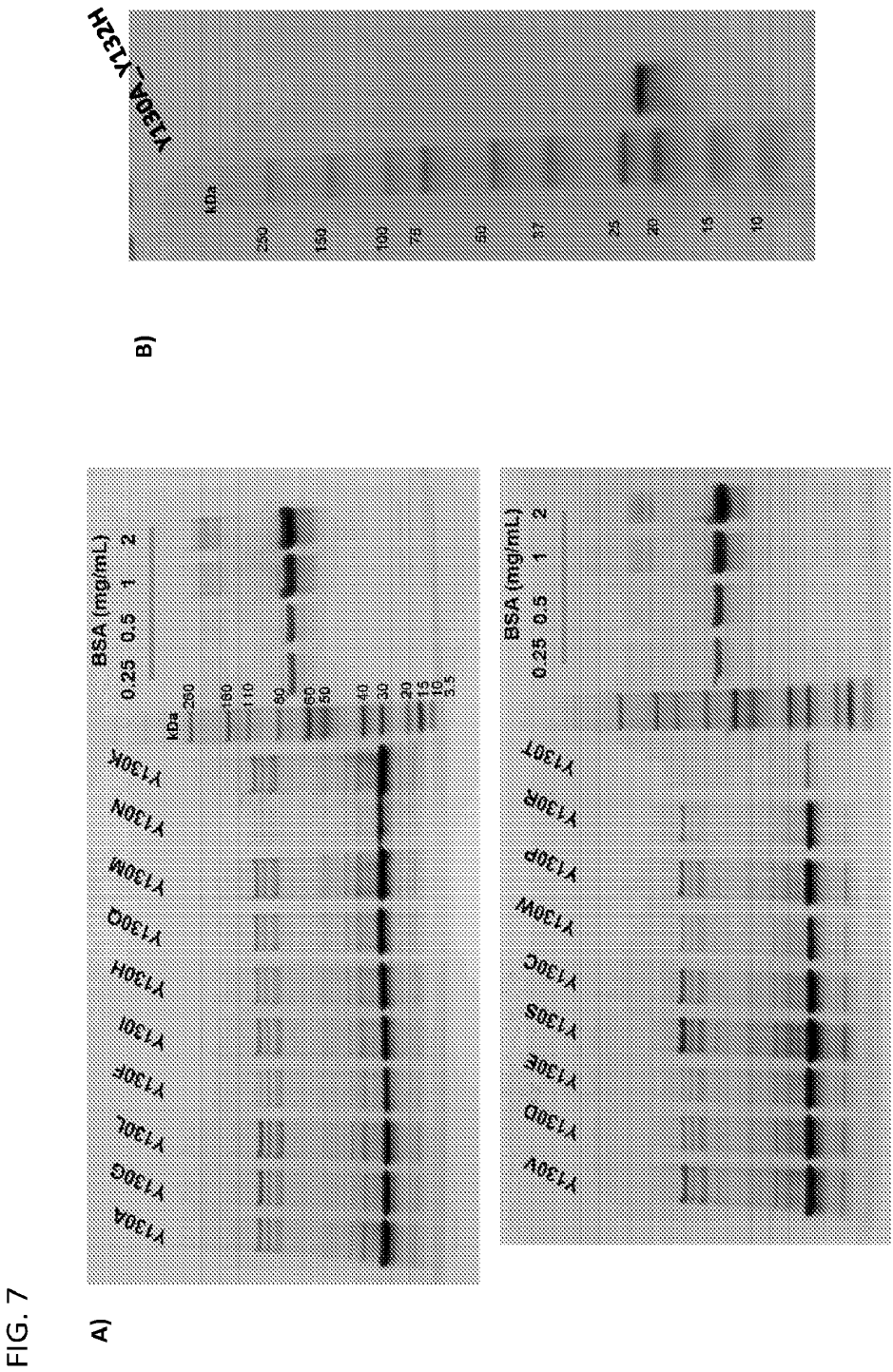


FIG. 8

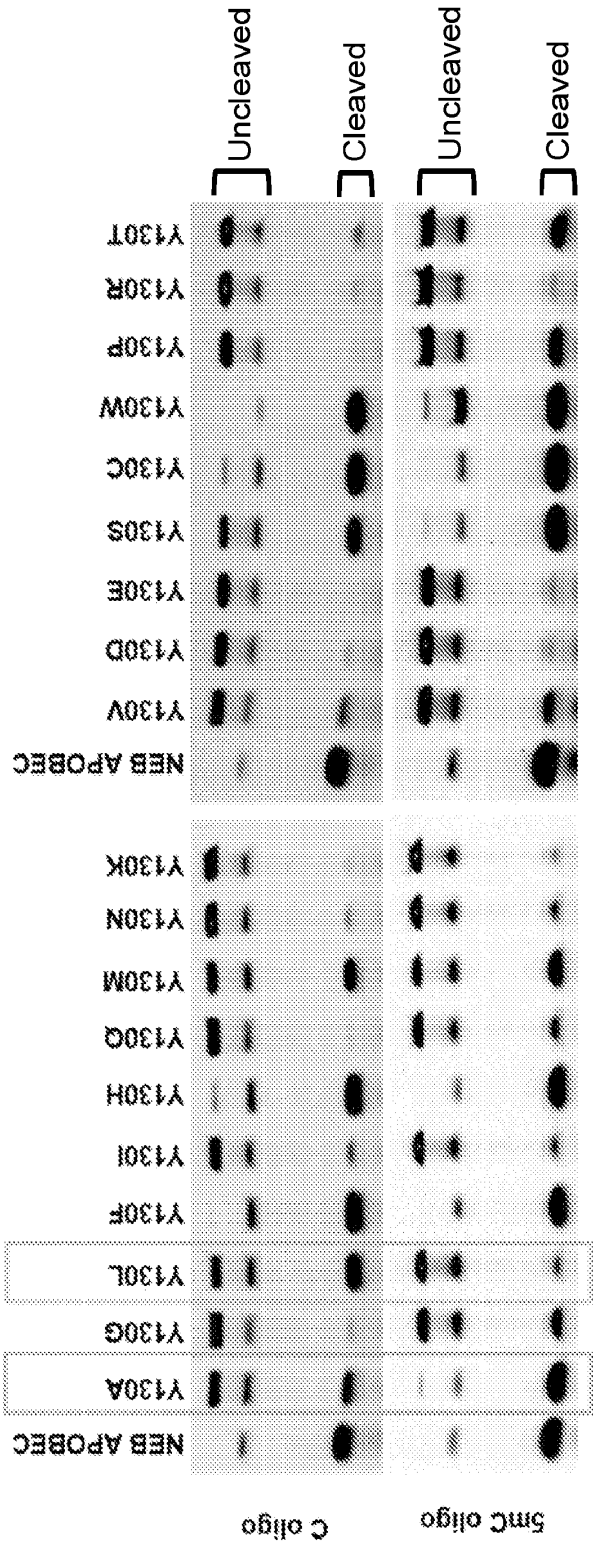


FIG. 9

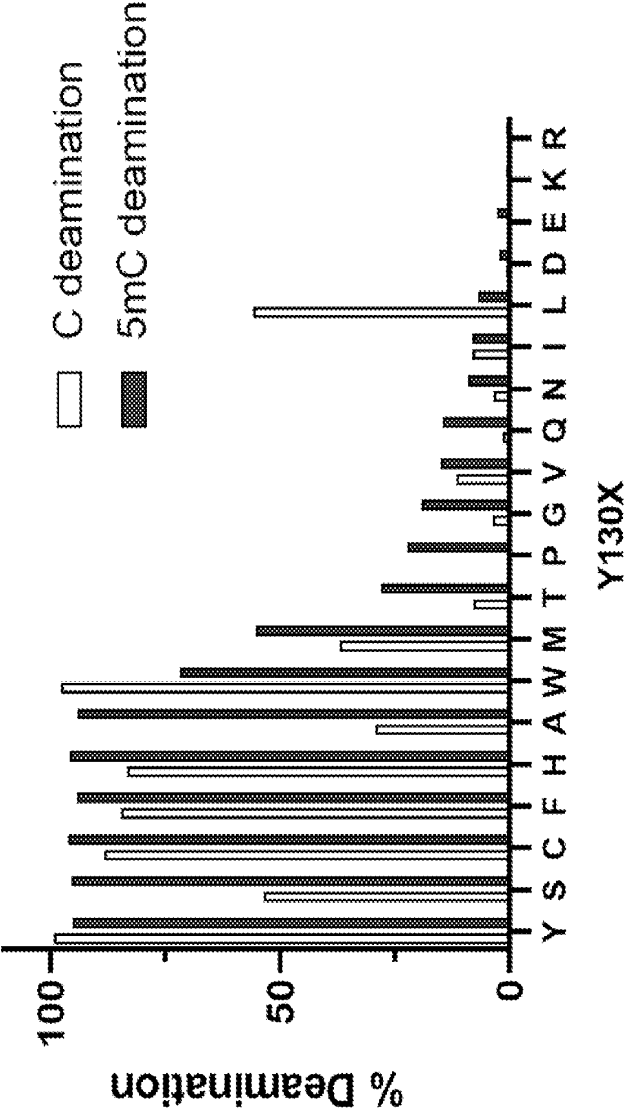


FIG. 10

Protein	% C deamination	% 5mC deamination
NEB APOBEC	99.3	47
(Y130 to A)	29.4	39
(Y130 to G)	3.7	21.7
(Y130 to L)	56	0
(Y130 to F)	84.6	92.7
(Y130 to I)	8.1	0
(Y130 to H)	83.4	55.4
(Y130 to Q)	1.6	29.8
(Y130 to M)	37	0
(Y130 to N)	3.6	27.8
(Y130 to K)	0.3	0
(Y130 to V)	11.6	0
(Y130 to D)	0.8	0
(Y130 to E)	0	0
(Y130 to S)	53.5	42.2
(Y130 to C)	88.2	92.7
(Y130 to W)	97.6	0
(Y130 to P)	0.2	0
(Y130 to R)	0.6	0
(Y130 to T)	8	13.9

Protein	% C deamination	% 5mC deamination
NEB APOBEC	92	94.9
(Y130 to A)	29.4	94.2
(Y130 to G)	3.7	19.1
(Y130 to L)	56	6.8
(Y130 to F)	84.6	94.3
(Y130 to I)	8.1	8.1
(Y130 to H)	83.4	95.8
(Y130 to Q)	1.6	14.6
(Y130 to M)	37	55.4
(Y130 to N)	3.6	9.1
(Y130 to K)	0.3	0.9
(Y130 to V)	11.6	15
(Y130 to D)	0.8	2.3
(Y130 to E)	0	2.9
(Y130 to S)	53.5	95.4
(Y130 to C)	88.2	96.2
(Y130 to W)	97.6	71.6
(Y130 to P)	0.2	22.3
(Y130 to R)	0.6	0.8
(Y130 to T)	8	28.1

FIG. 11A-C

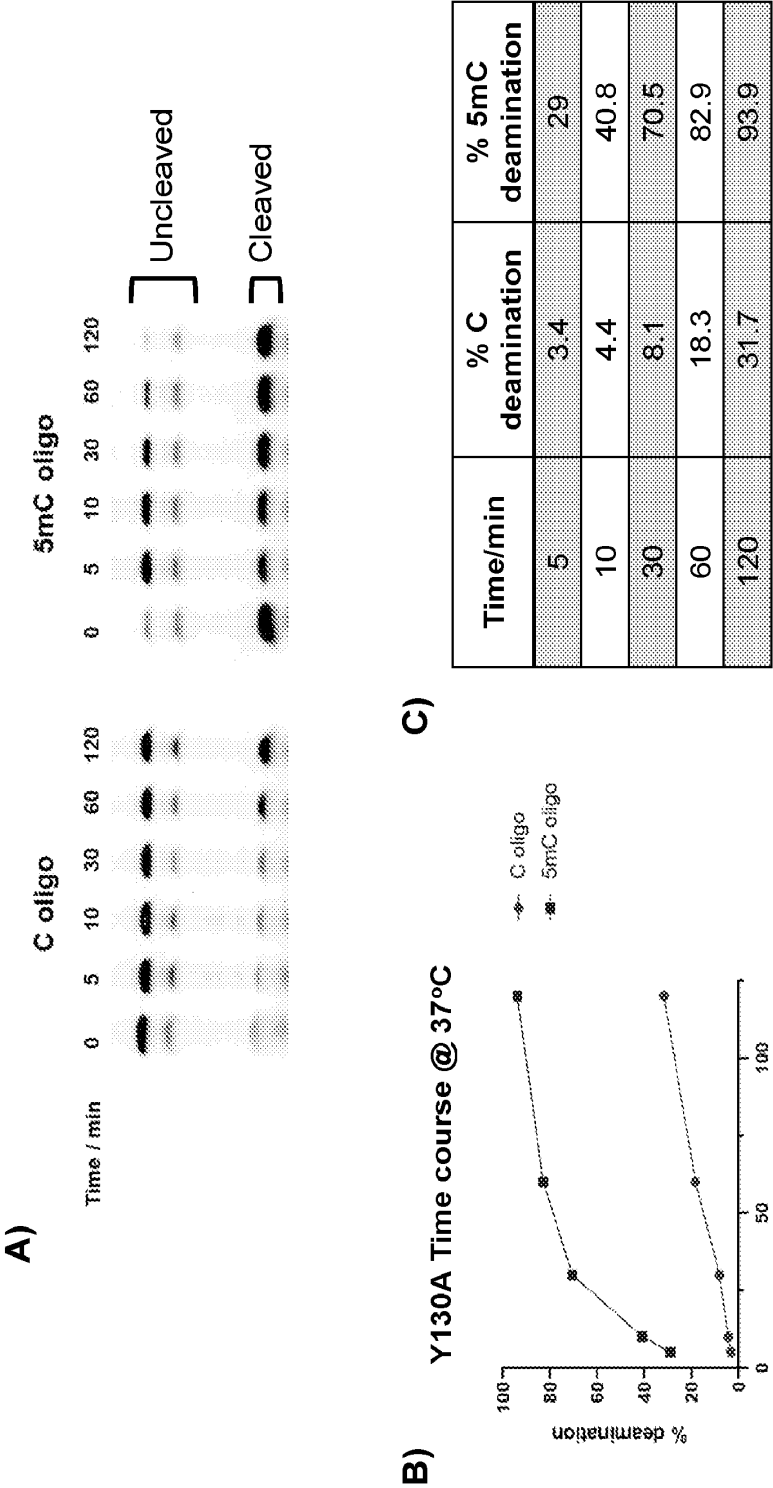
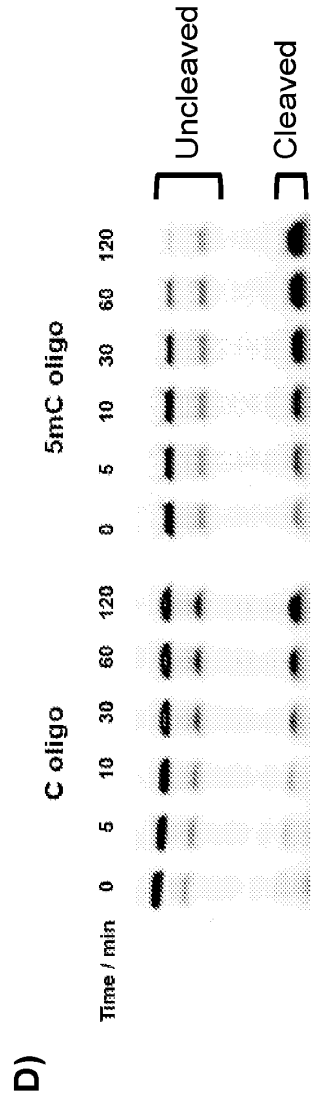
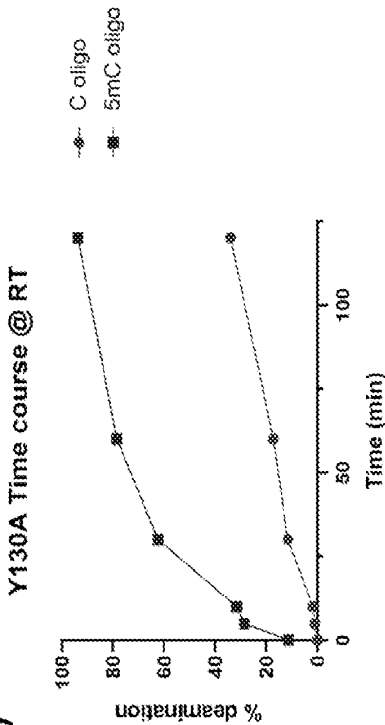


FIG. 11D-F



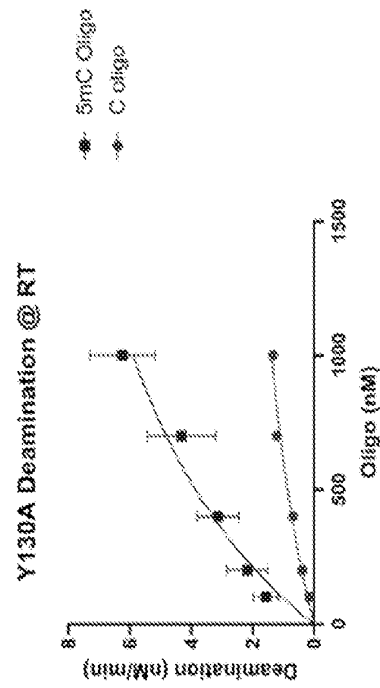
E)



F)

Time/min	% C deamination	% 5mC deamination
0	0	11.4
5	1	28.6
10	1.7	31.7
30	11.6	62.4
60	17.2	78.5
120	34	93.8

FIG. 12



Parameter	C oligo	5mC oligo
K _{cat} (min ⁻¹)	3.1X10 ⁻⁴	2.5X10 ⁻²
K _m (nM)	1659	1110
V _{max} (nM/min)	3.7	12.43
K _{cat} /K _m (nM ⁻¹ min ⁻¹)	1.85X10 ⁻⁷	2.25X10 ⁻⁵

FIG. 13

Set (A)

5' GAGGTGTATGGTTGTAATAA/5mC/ACT/5mC/CTGGA/5mC/GAATCTTAA/5mC/ACAA/5mC/GTGCAG/5mC/CAAA/5mC/GCTT/5mC/GC/5mC/ACGG/5mC/AACGGT/5mC/GGACT/5mC/GTCG/5mC/CTTA/5mC/AATCG/5mC/GCAGGT/5mC/ACGTTGAAGATGAGGATG-3'

Set (B)

GAGGTGTATGGTTGTAG/5mC/GCAAATCGTAAAA/5mC/GCAAAGCGAAAAA/5mC/GCAAACCGTAAAC/5mC/GAAAAACCGTTGAAGATGAGGATG
GAGGTGTATGGTTGTAG/5mC/GGAAAAACGGAAAT/5mC/GGAAAAACGTAAAG/5mC/GTAAATCGGAAAC/5mC/GAAAAACCGGTTGAAGATGAGGATG
GAGGTGTATGGTTGTAA/5mC/GTAAACCGCAAAAC/5mC/GGAAAAACGAAAAAT/5mC/GCAAACCGAAAAAC/5mC/GTAAACCGCTTGAAGATGAGGATG
GAGGTGTATGGTTGTAA/5mC/GAAAAACGGGAAAT/5mC/GAAAAACGTAAAT/5mC/GTAAATCGCAAAA/5mC/GGAAATCGATTGAAGATGAGGATG

C = unmethylated
/5mC/ = methylated

FIG. 14

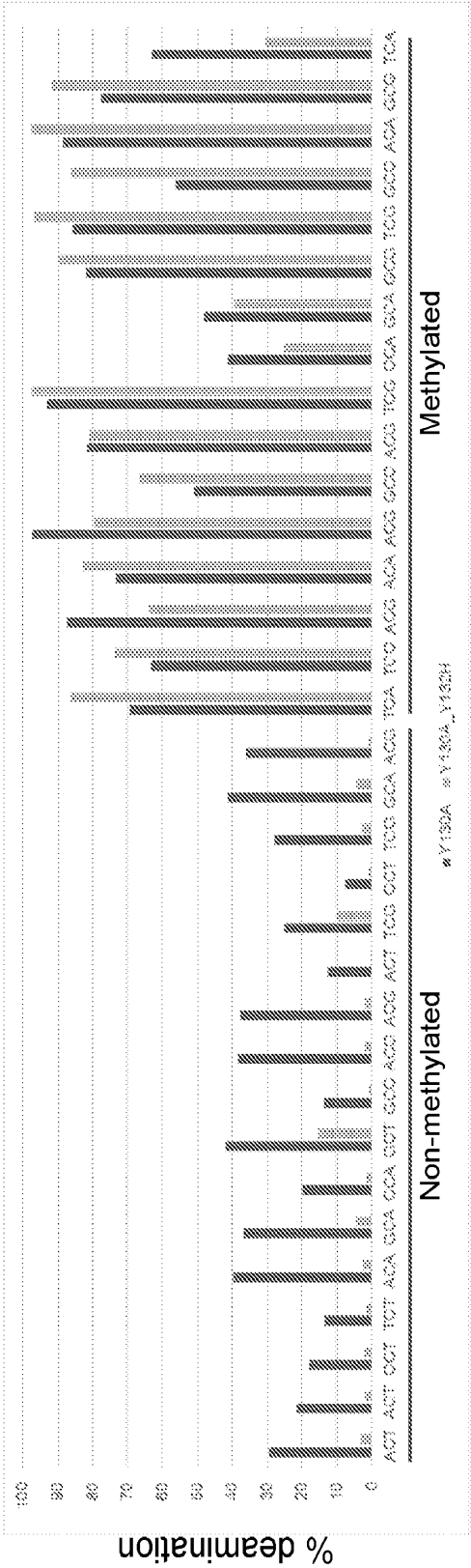
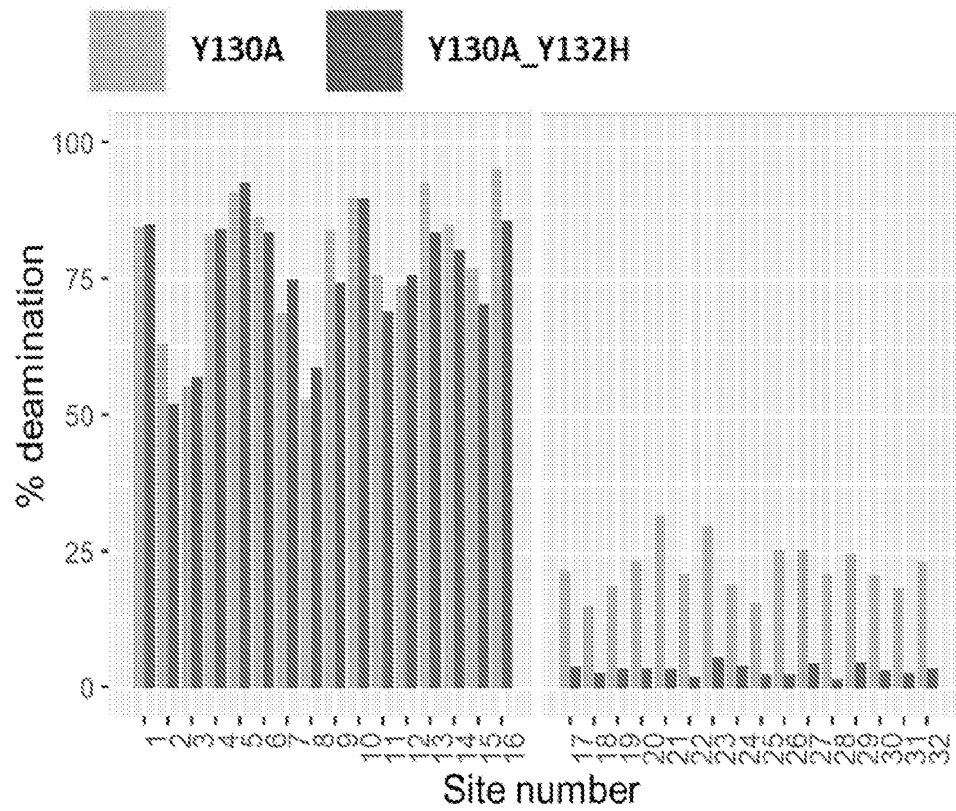


FIG. 16



Site number

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
CGCG	ACGC	CCGC	CCGA	CGCG	TCGG	GCCT	GCGA	ACGT	CCGG	TCGC	CCGT	ACGA	TCGA	TCGT	ACCG

Methylated CpG

17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
TCGT	GCGA	CCGT	CGCG	ACCG	ACGT	TCGG	GCGG	CCGC	ACGA	CCGA	ACGC	CCGG	GCCT	TCGC	TCGA

Non-methylated CpG

FIG. 17

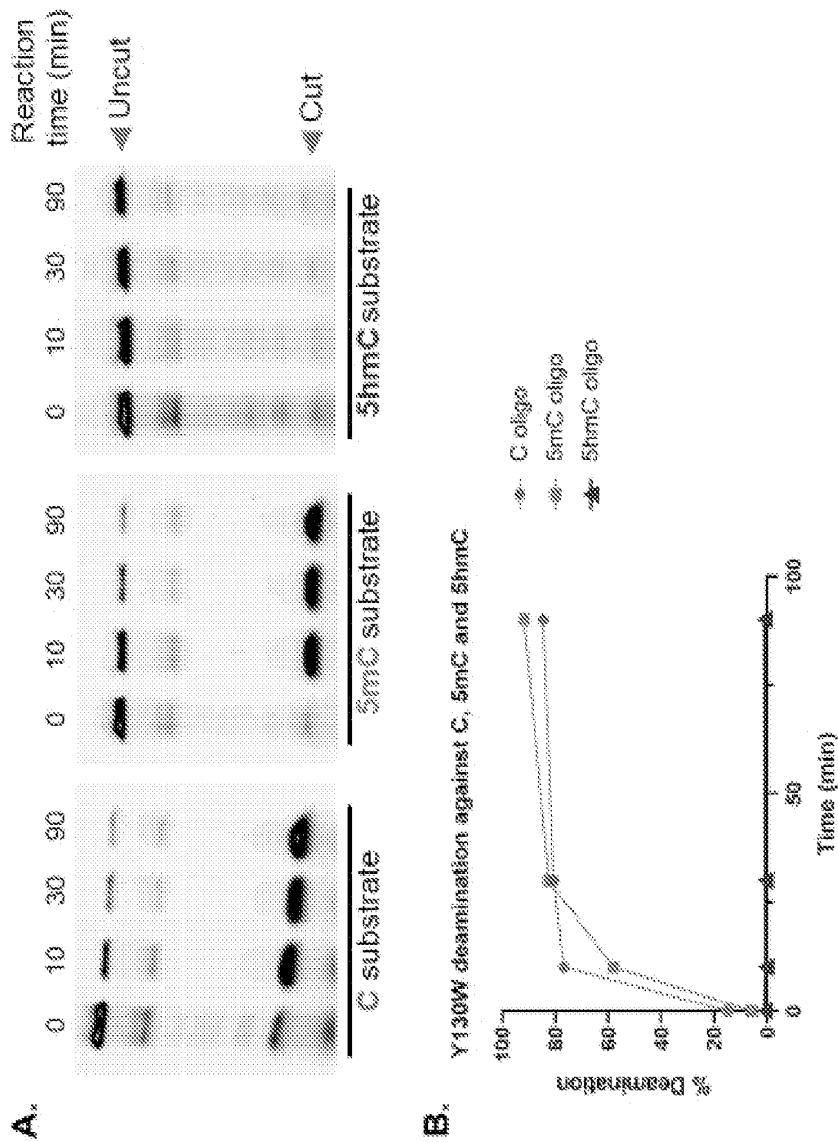
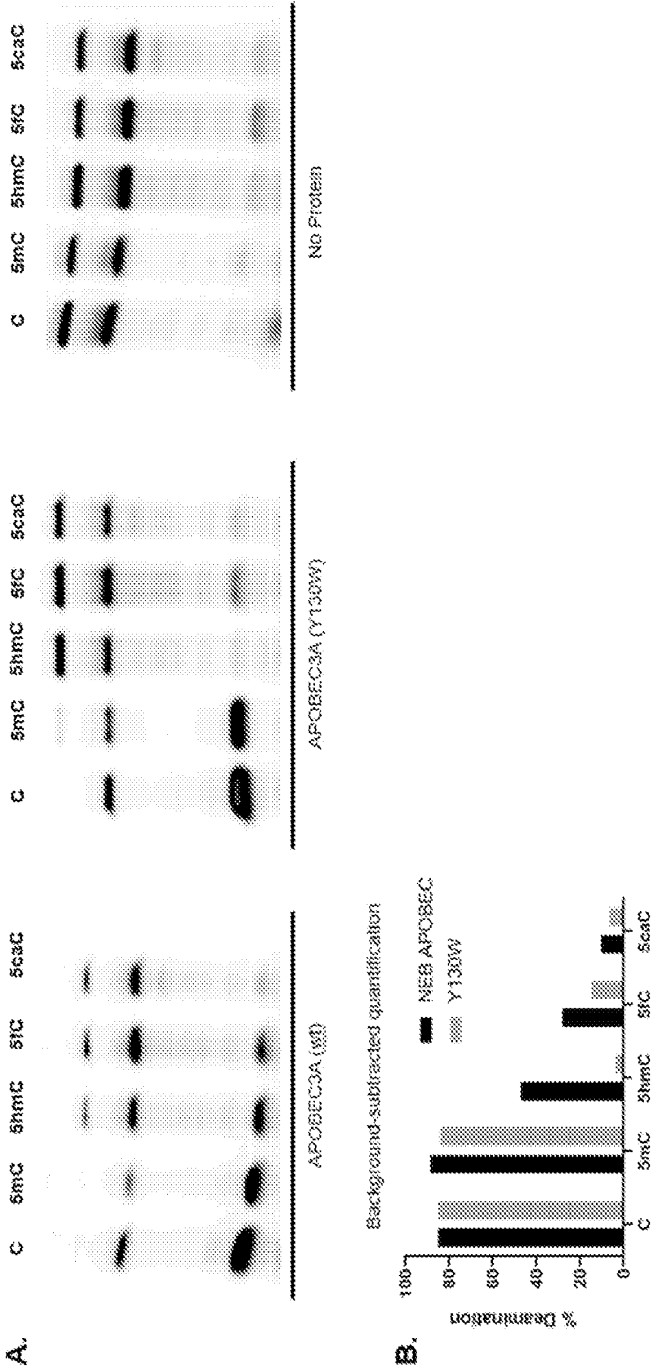


FIG. 18



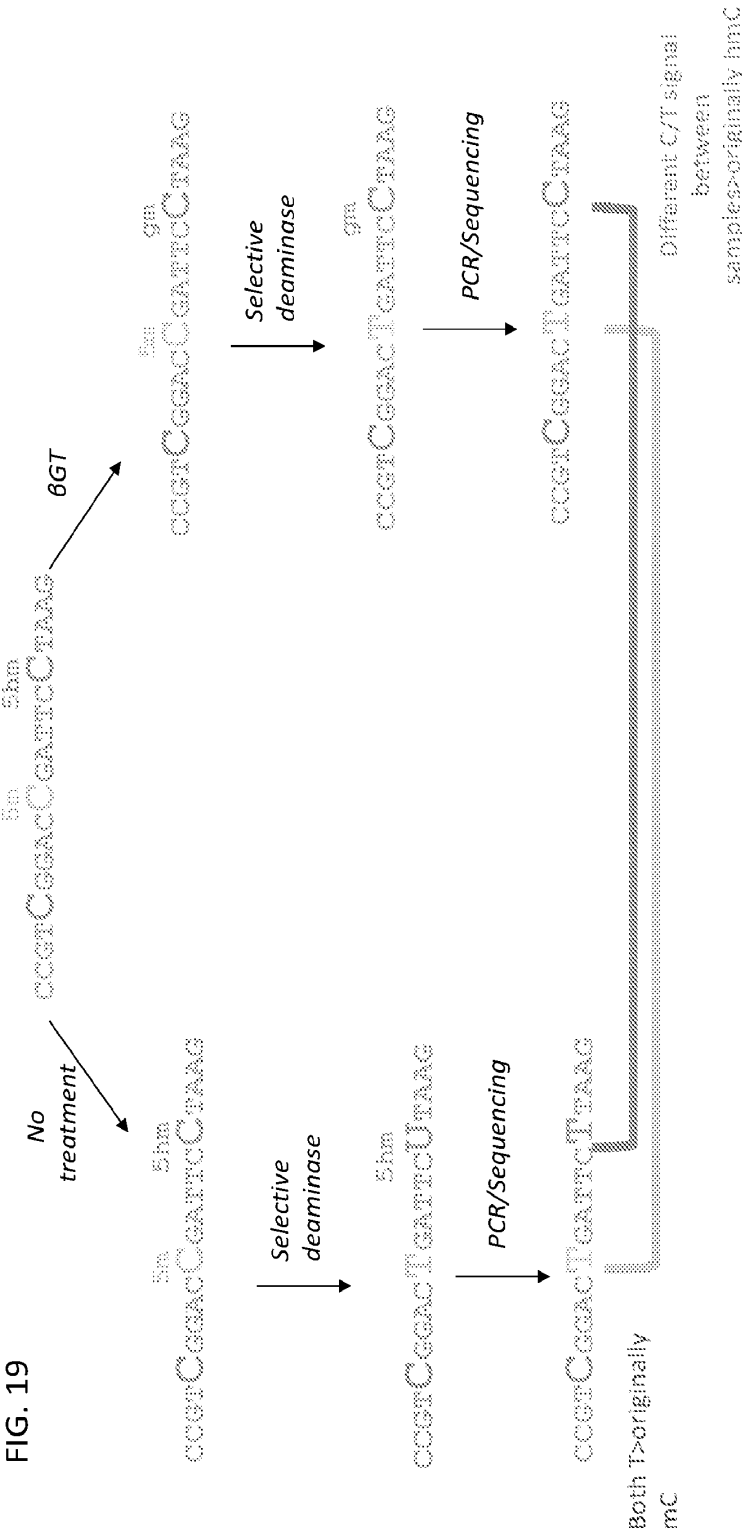


FIG. 20

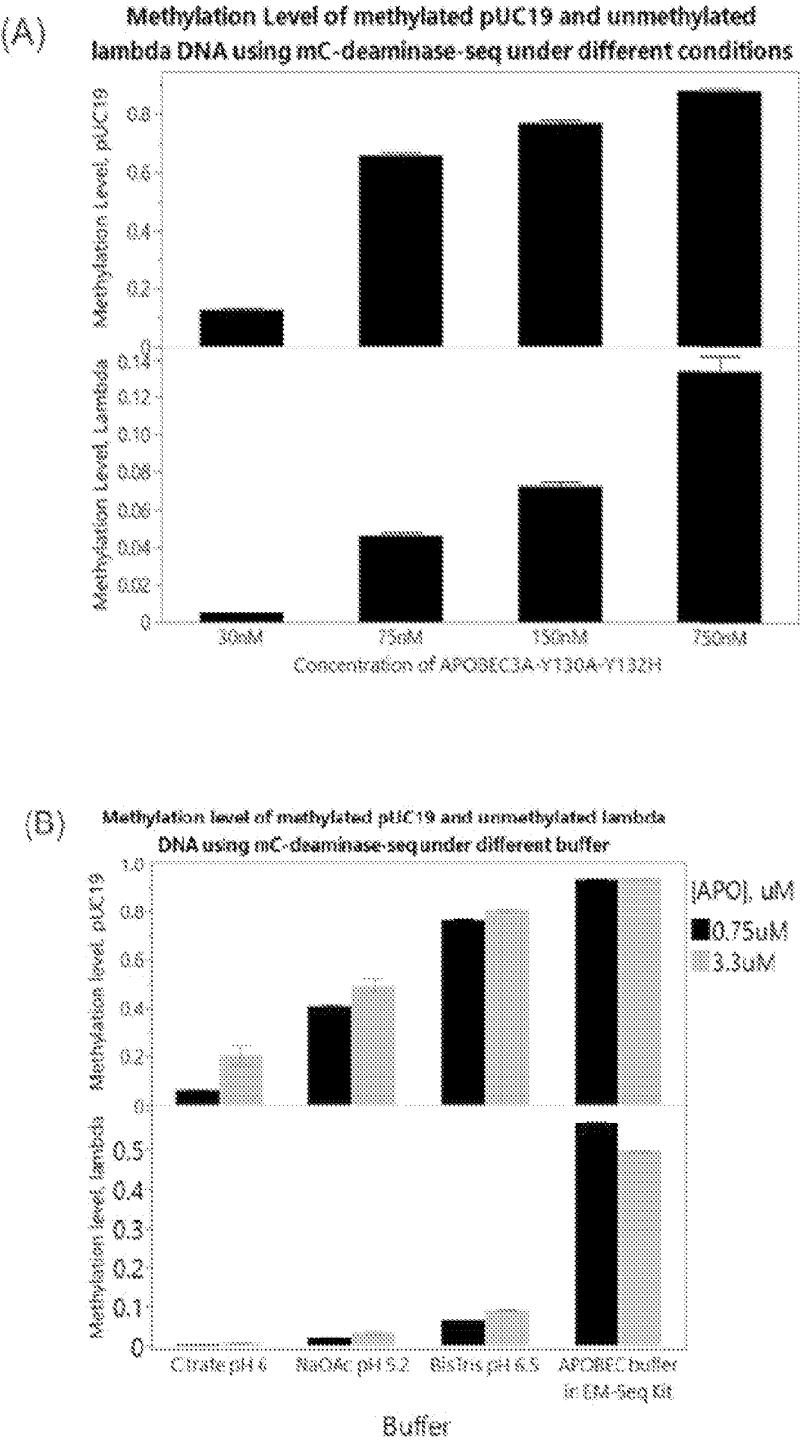


FIG. 21

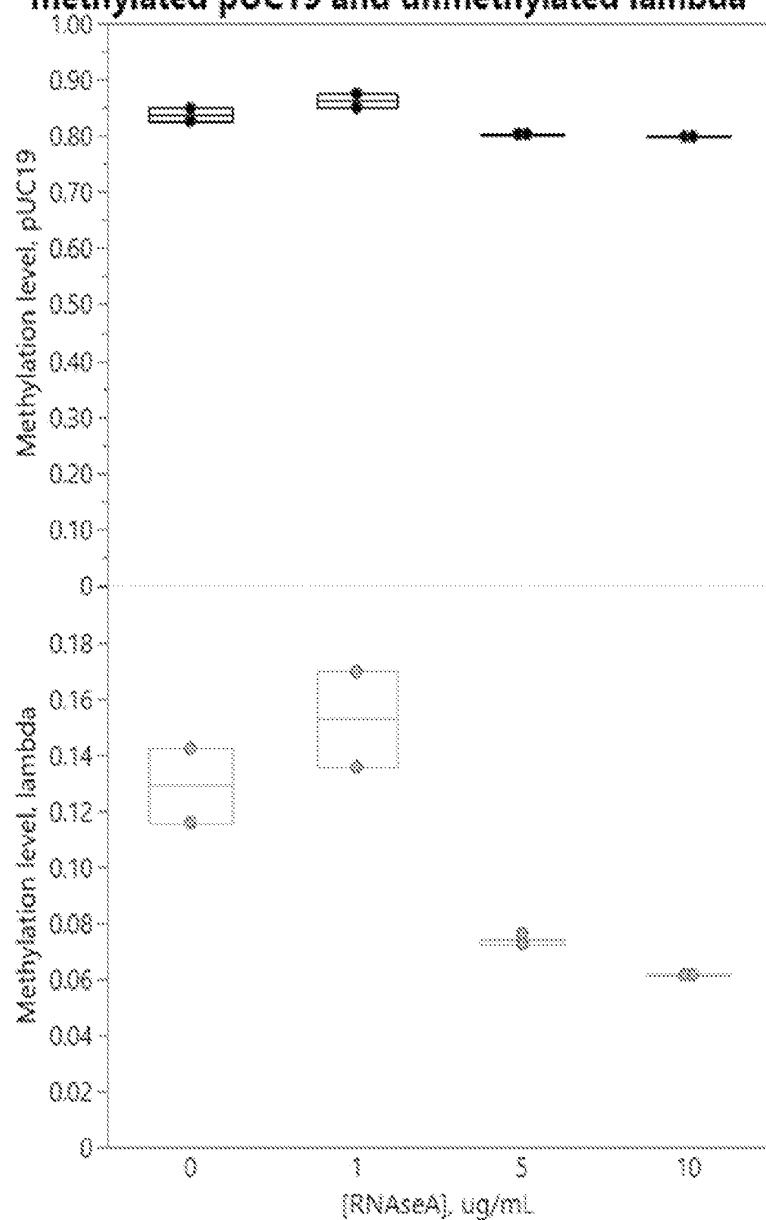
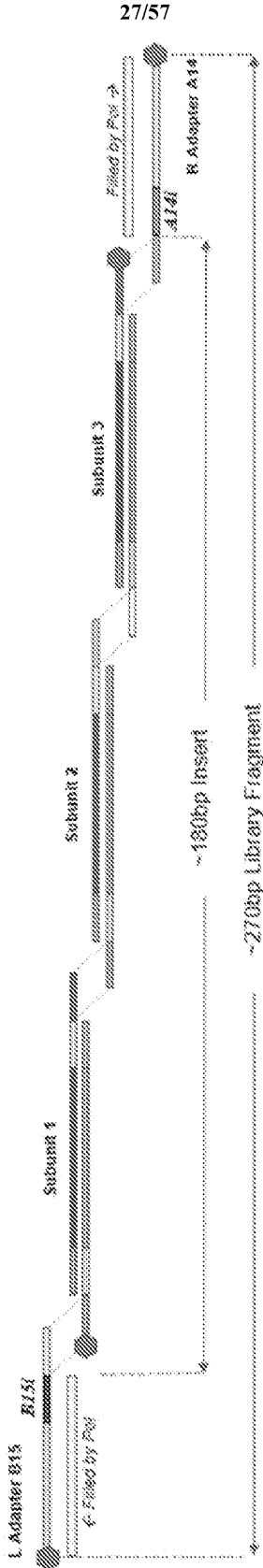
Impact of RNase A on the methylation level of methylated pUC19 and unmethylated lambda

FIG. 22A



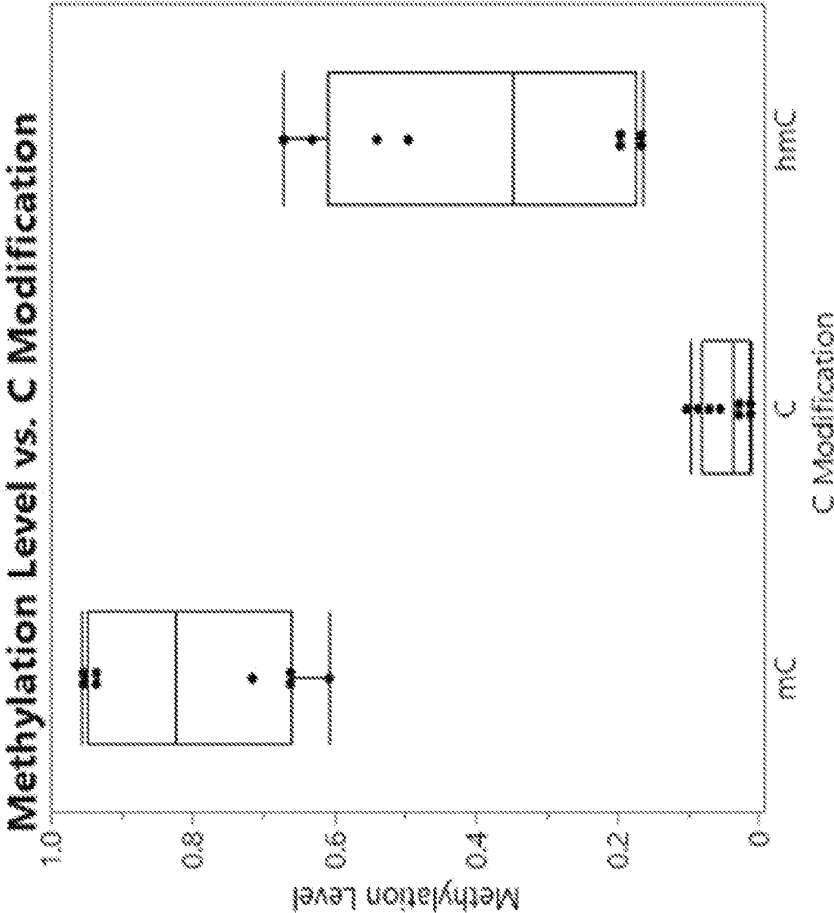


FIG. 22B

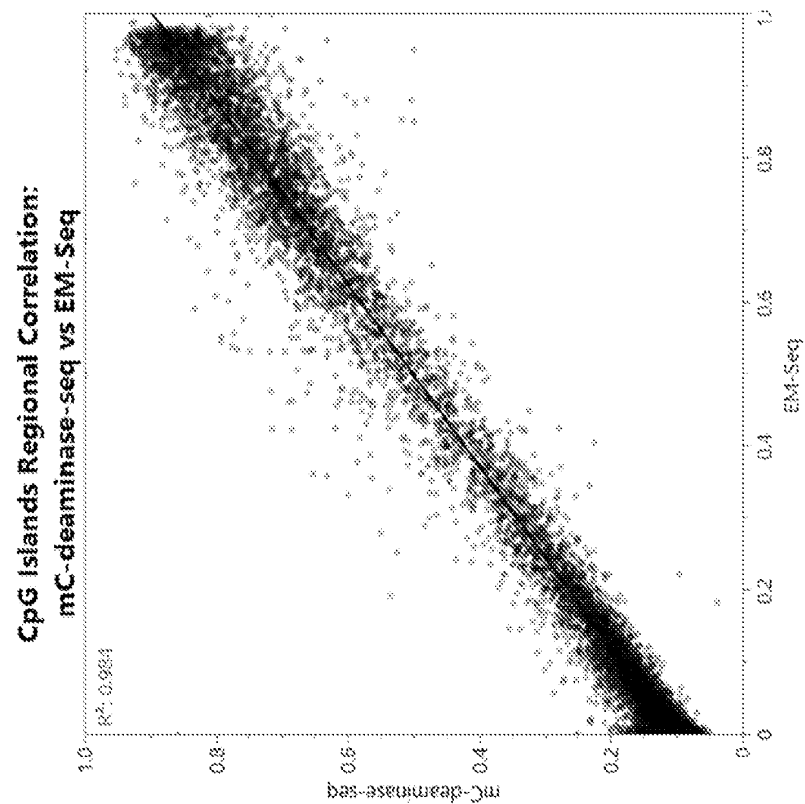


FIG. 23

FIG. 24

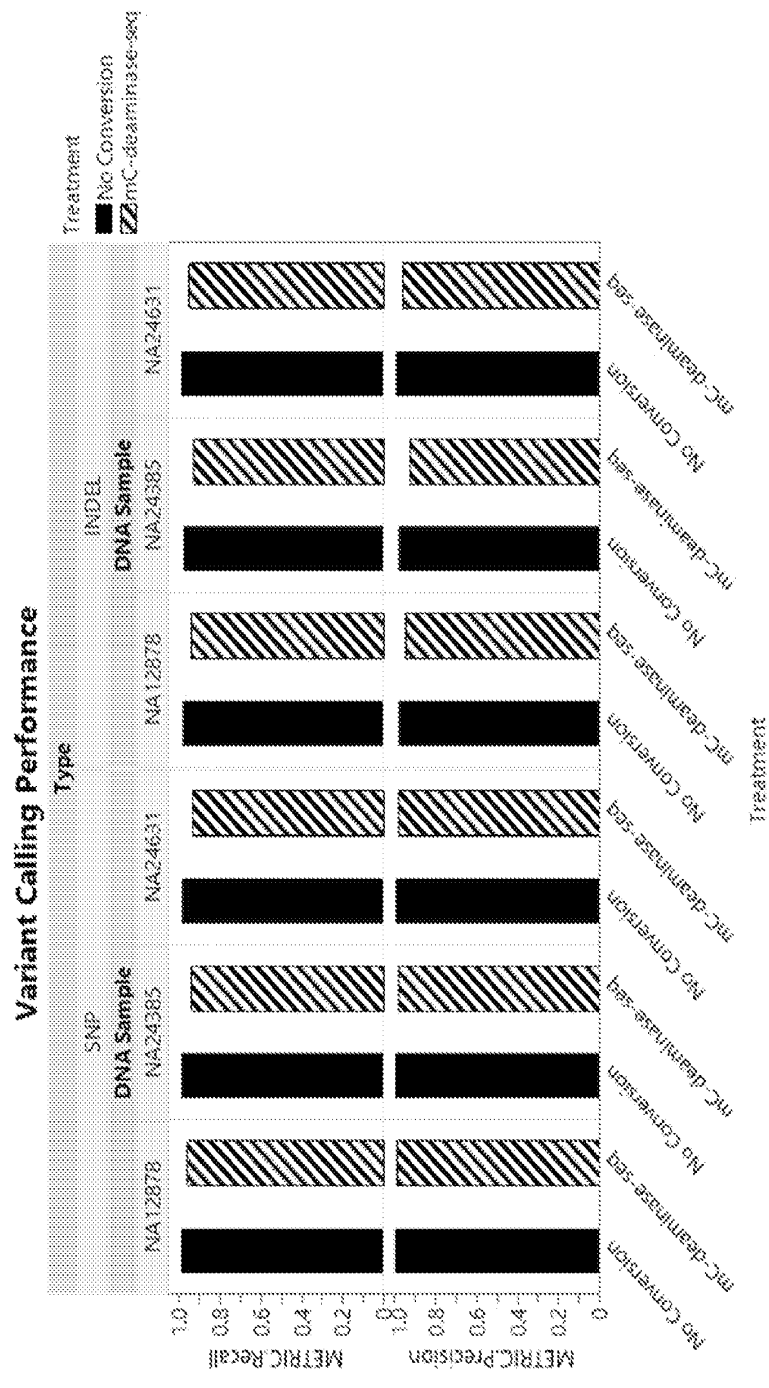


FIG. 25

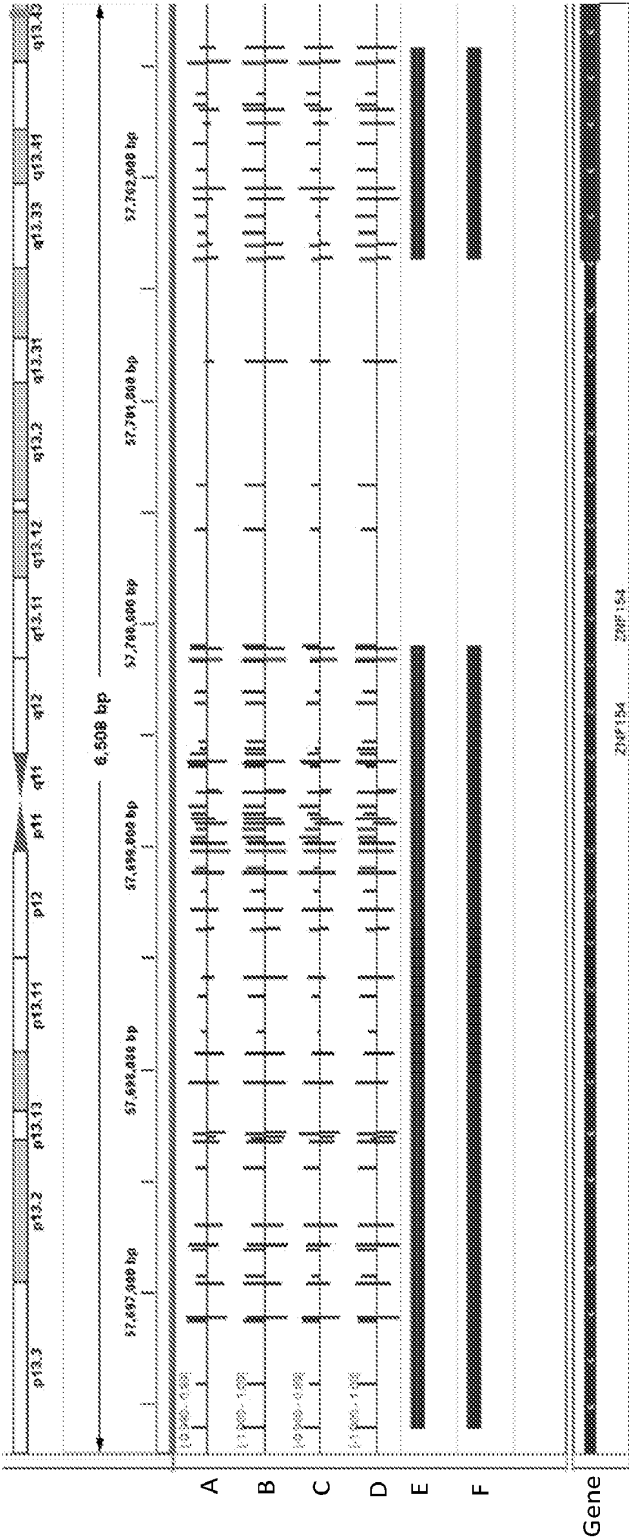


FIG. 26

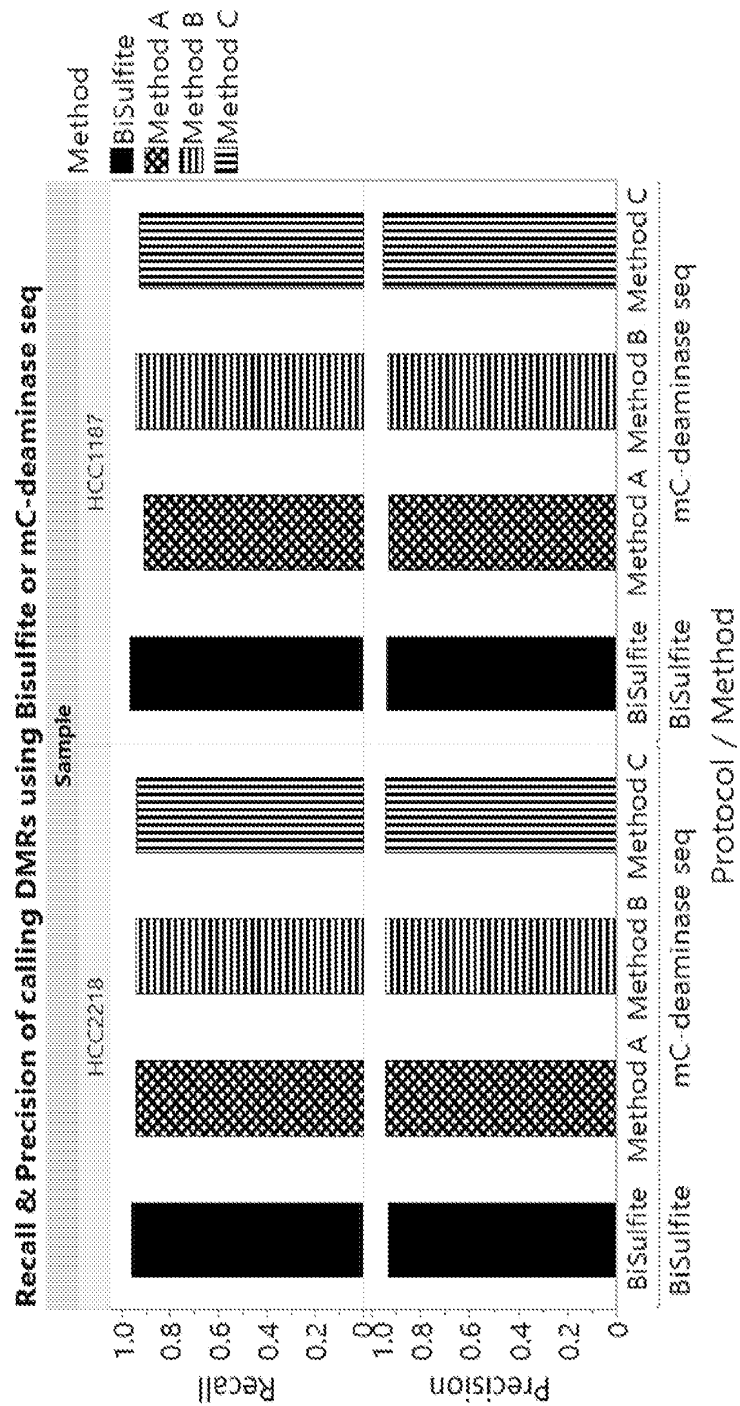
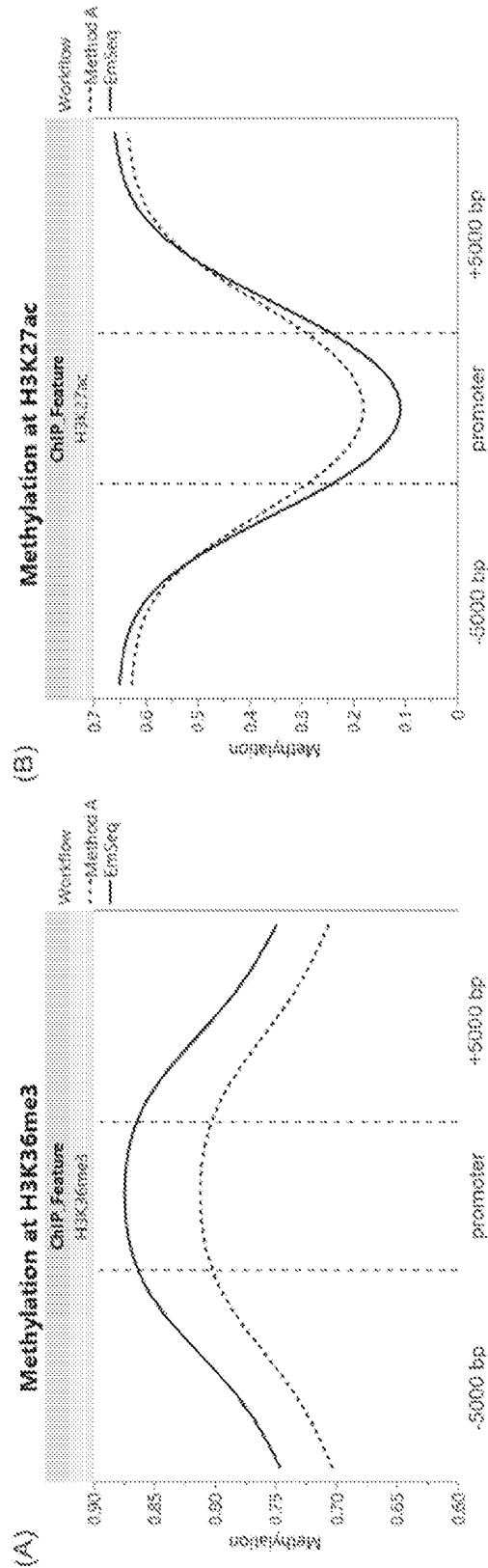


FIG. 27



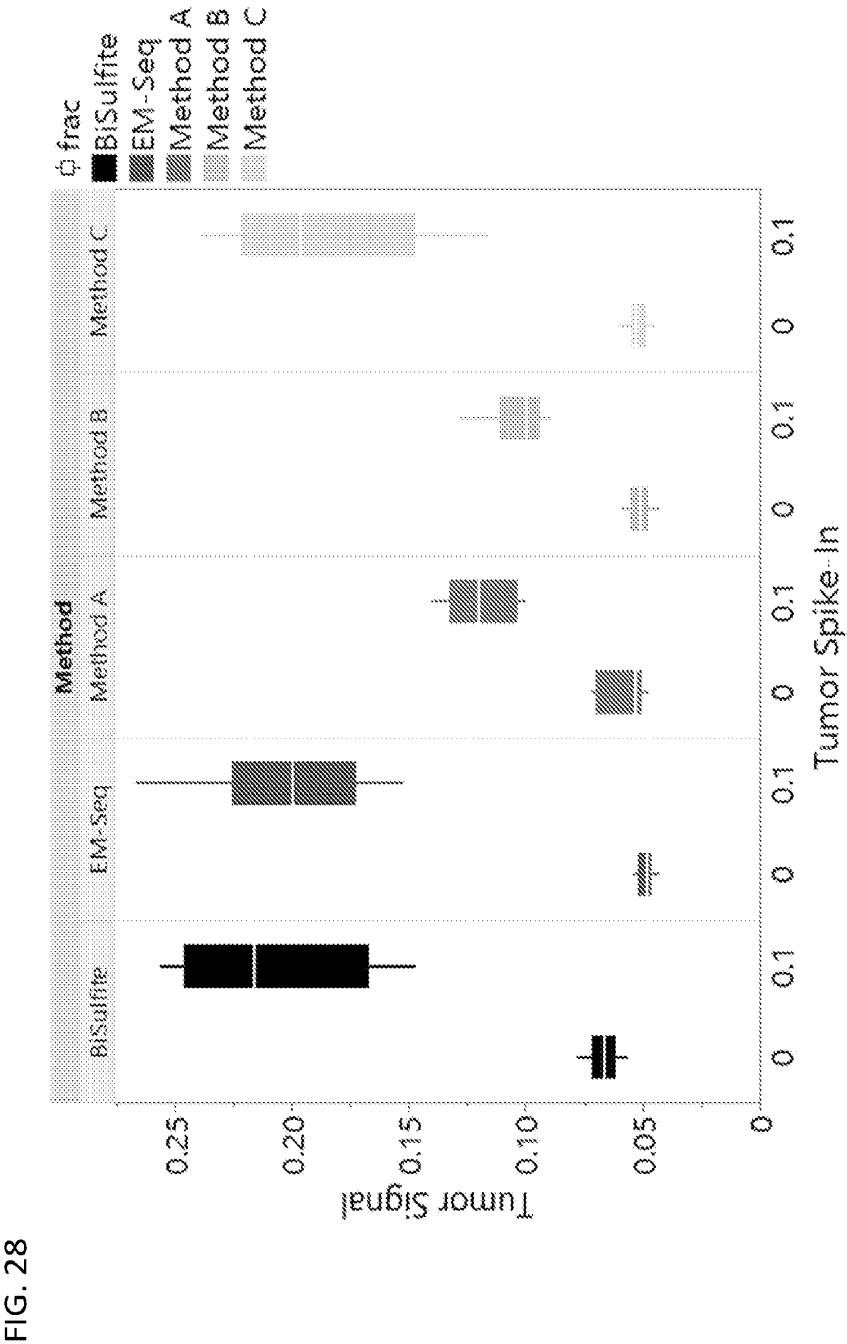
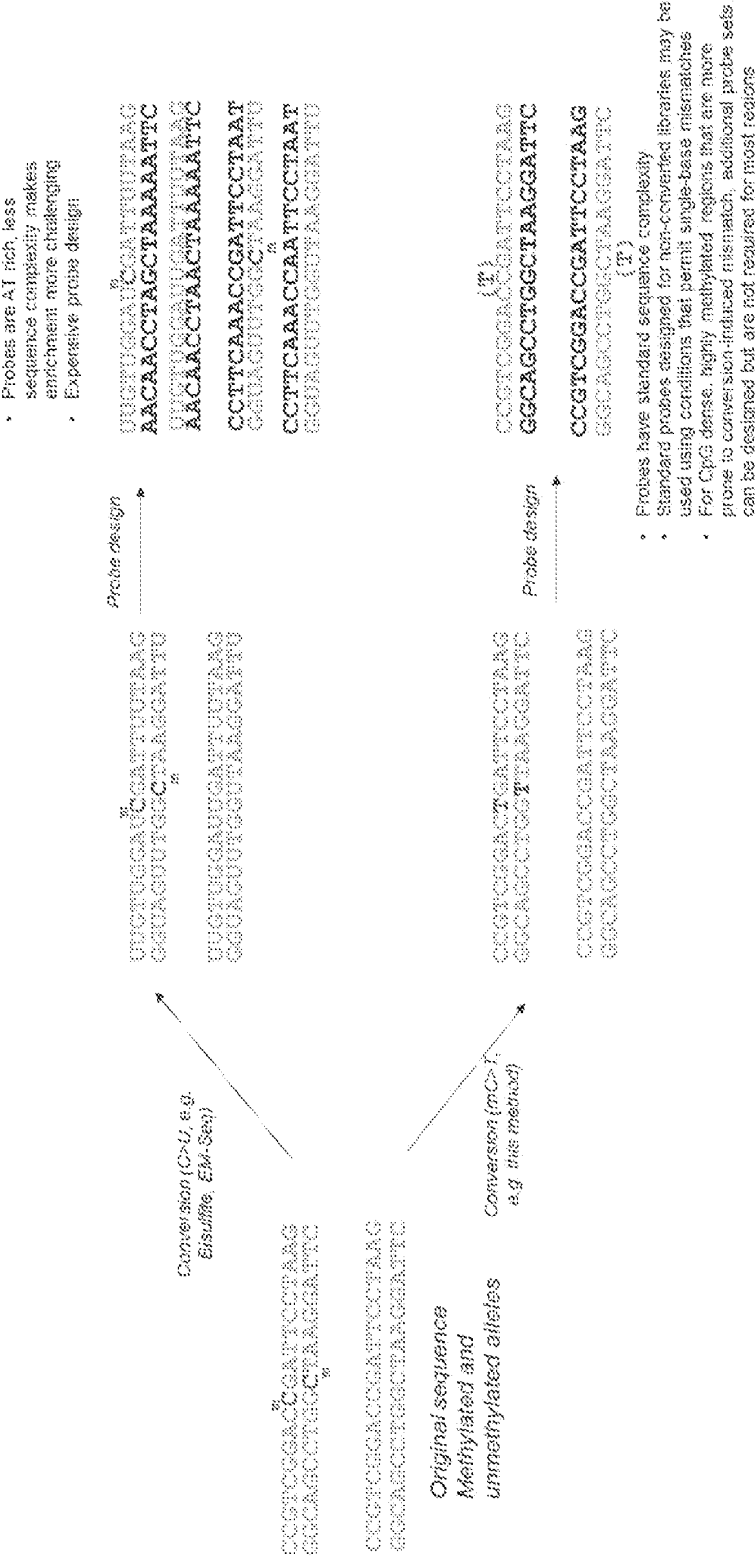


FIG. 29



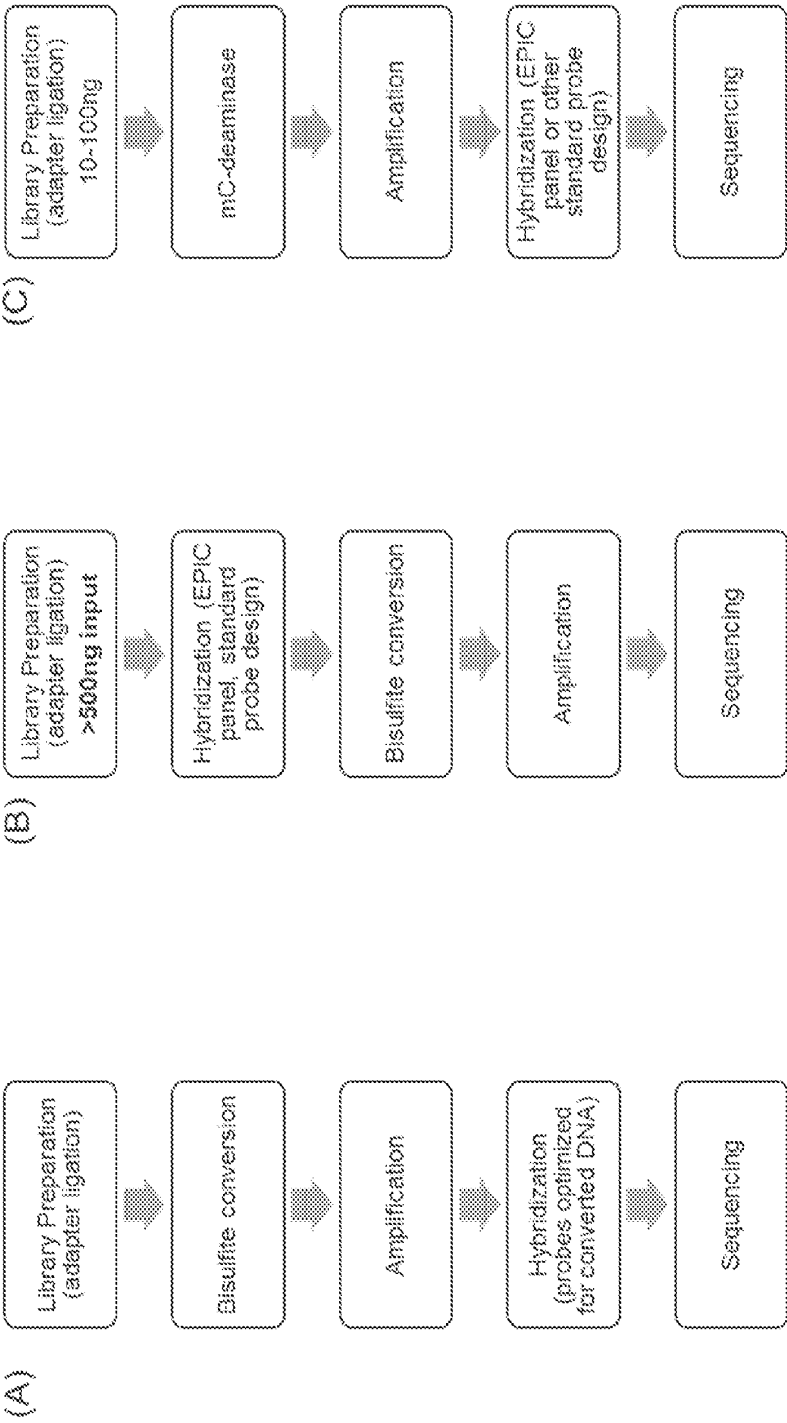


FIG. 30

FIG. 31

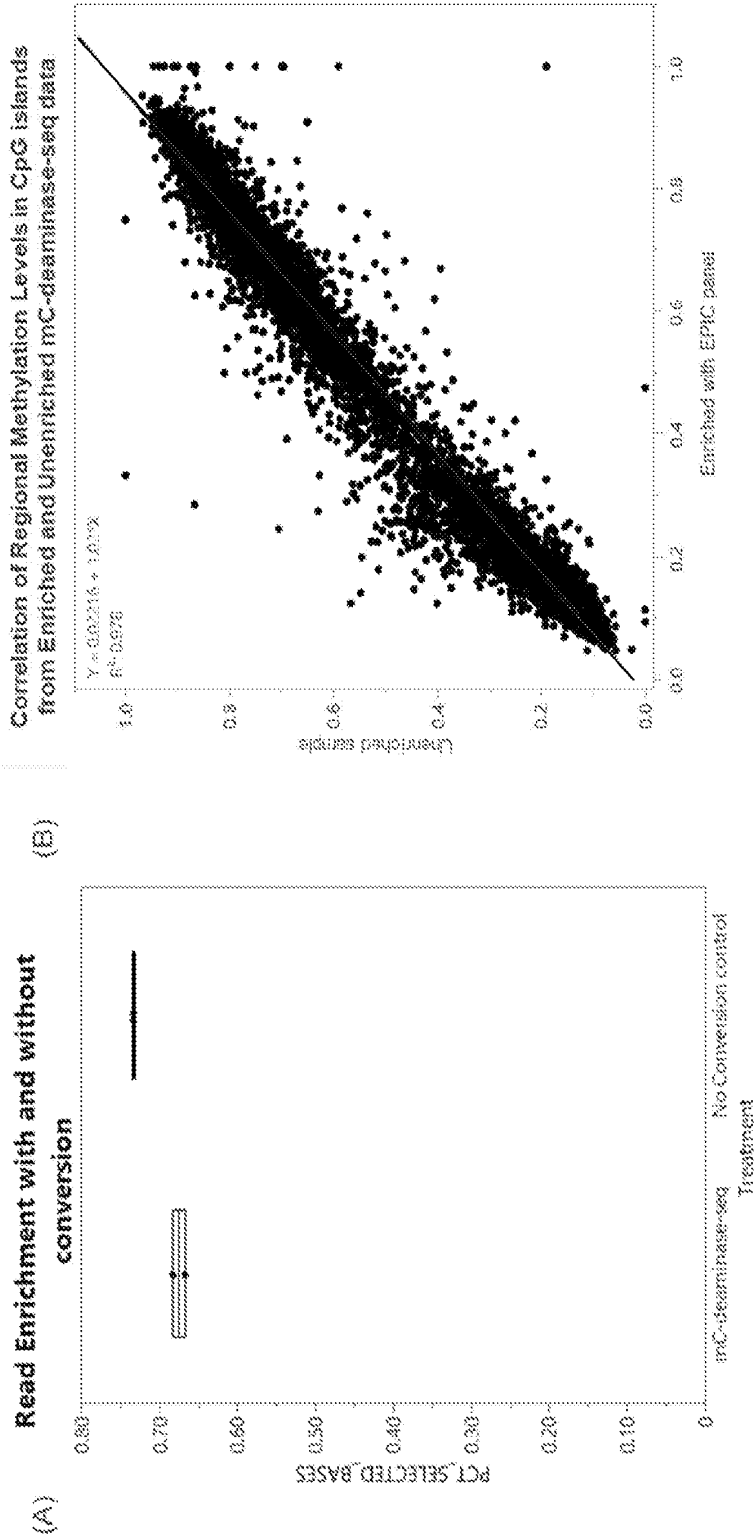
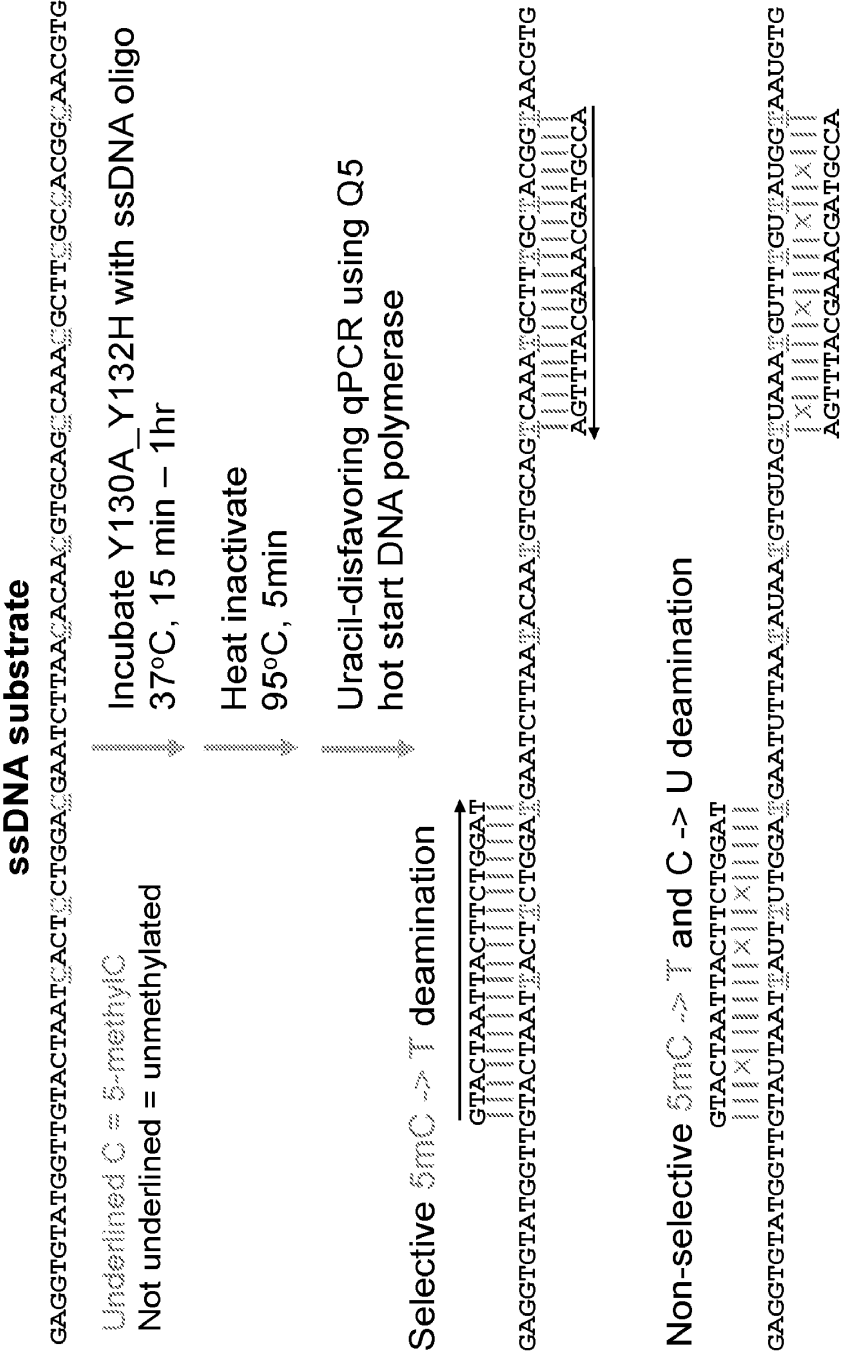


FIG. 32



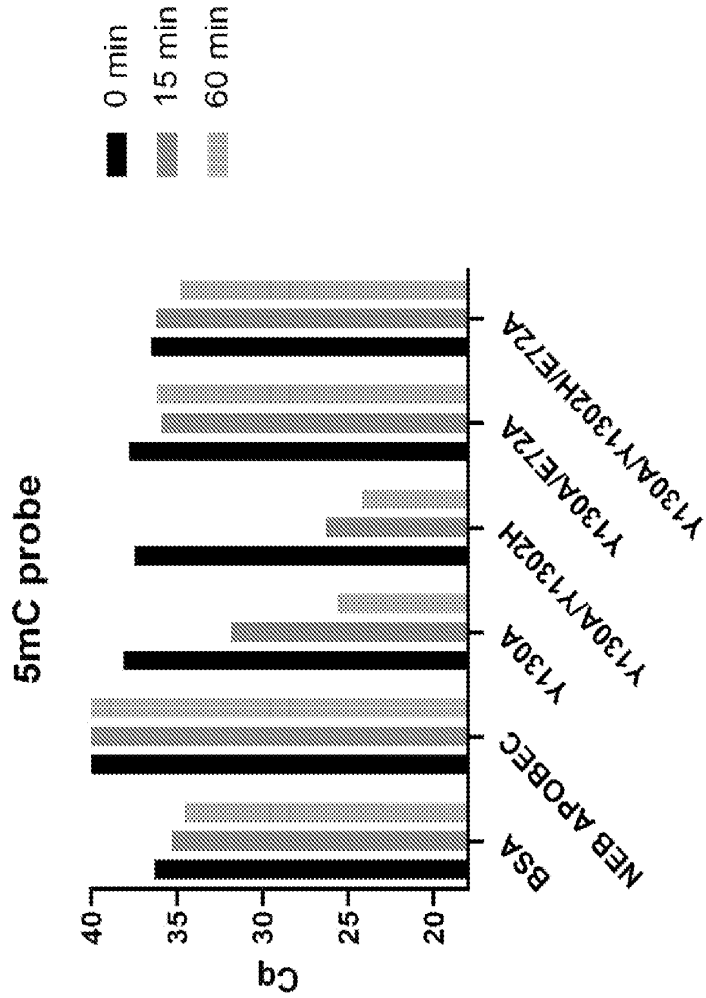
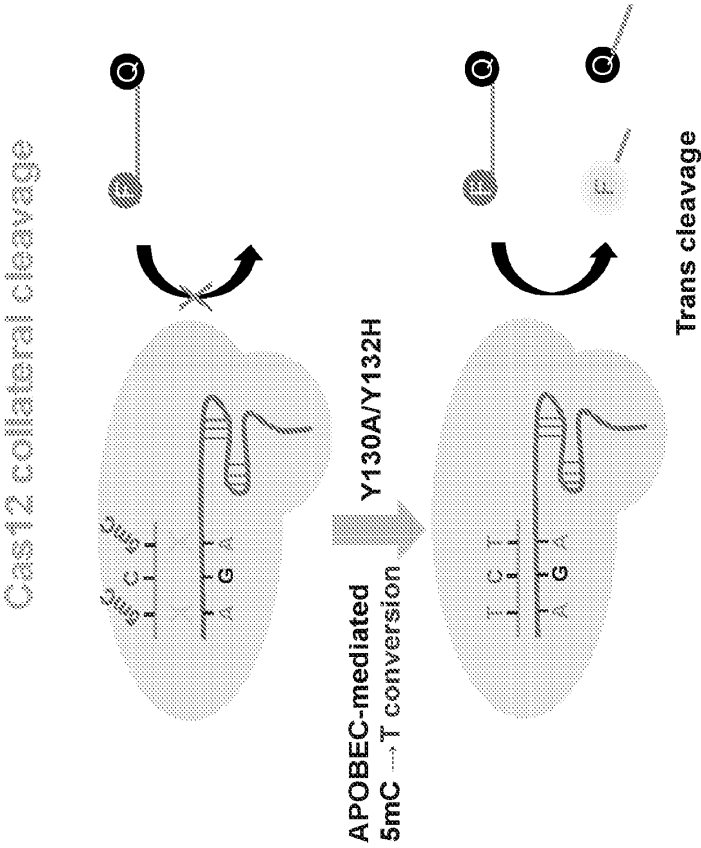


FIG. 33

FIG. 34



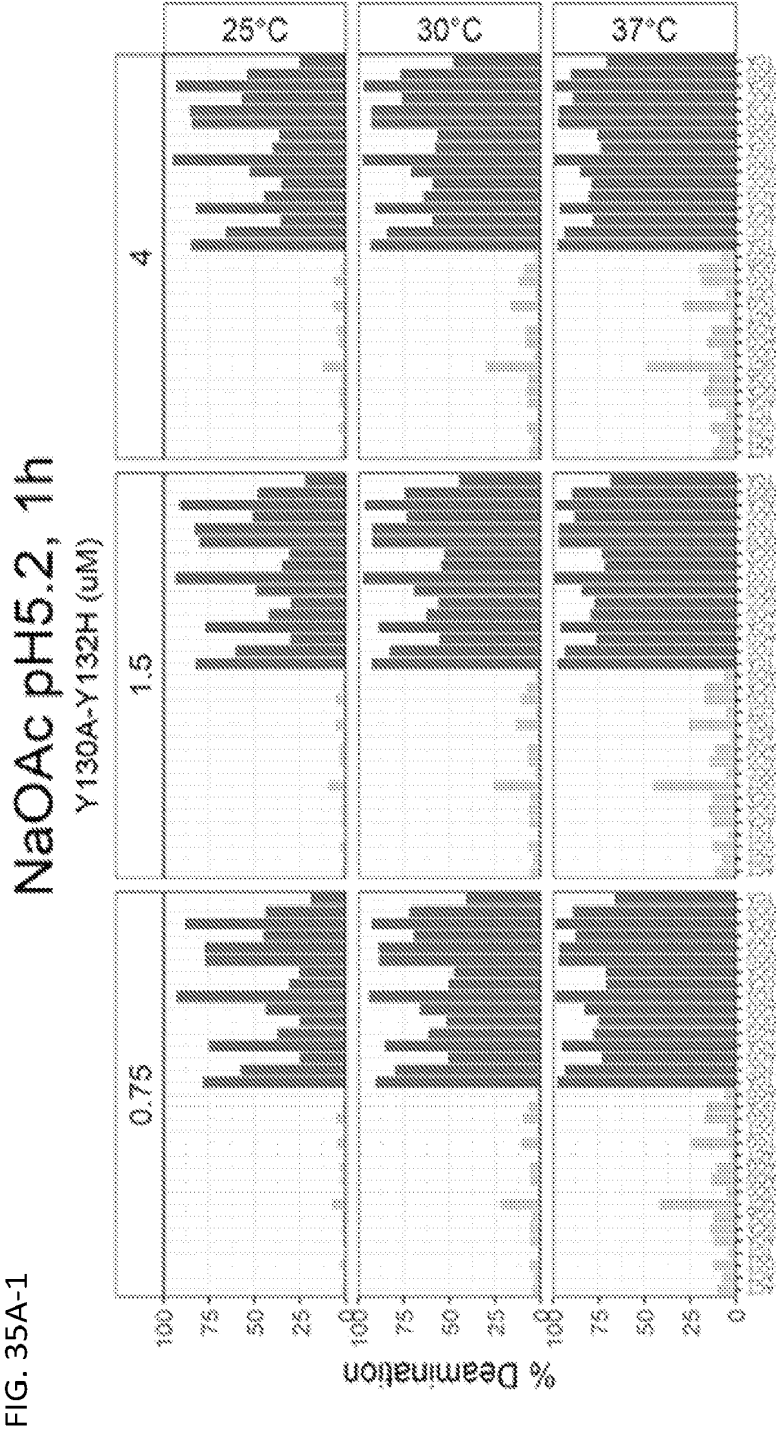
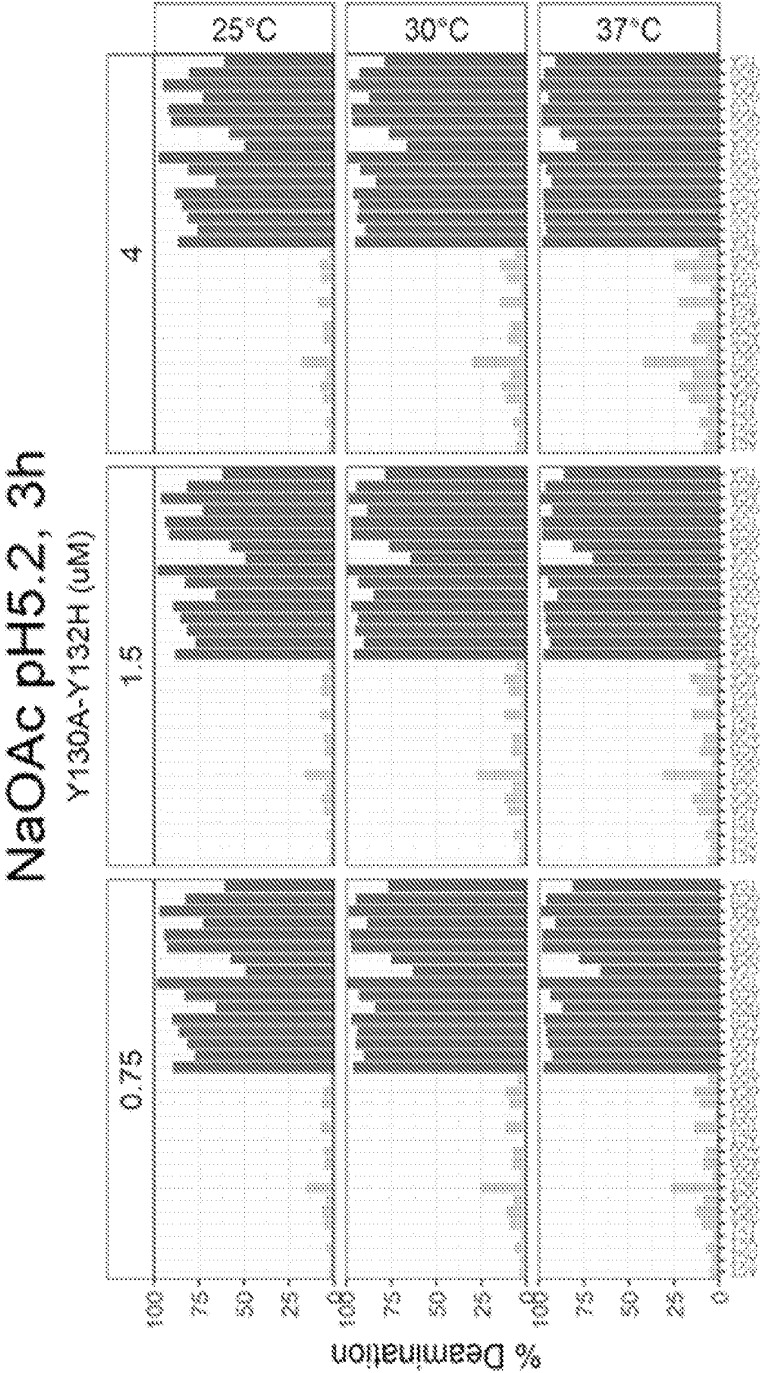


FIG. 35A-2



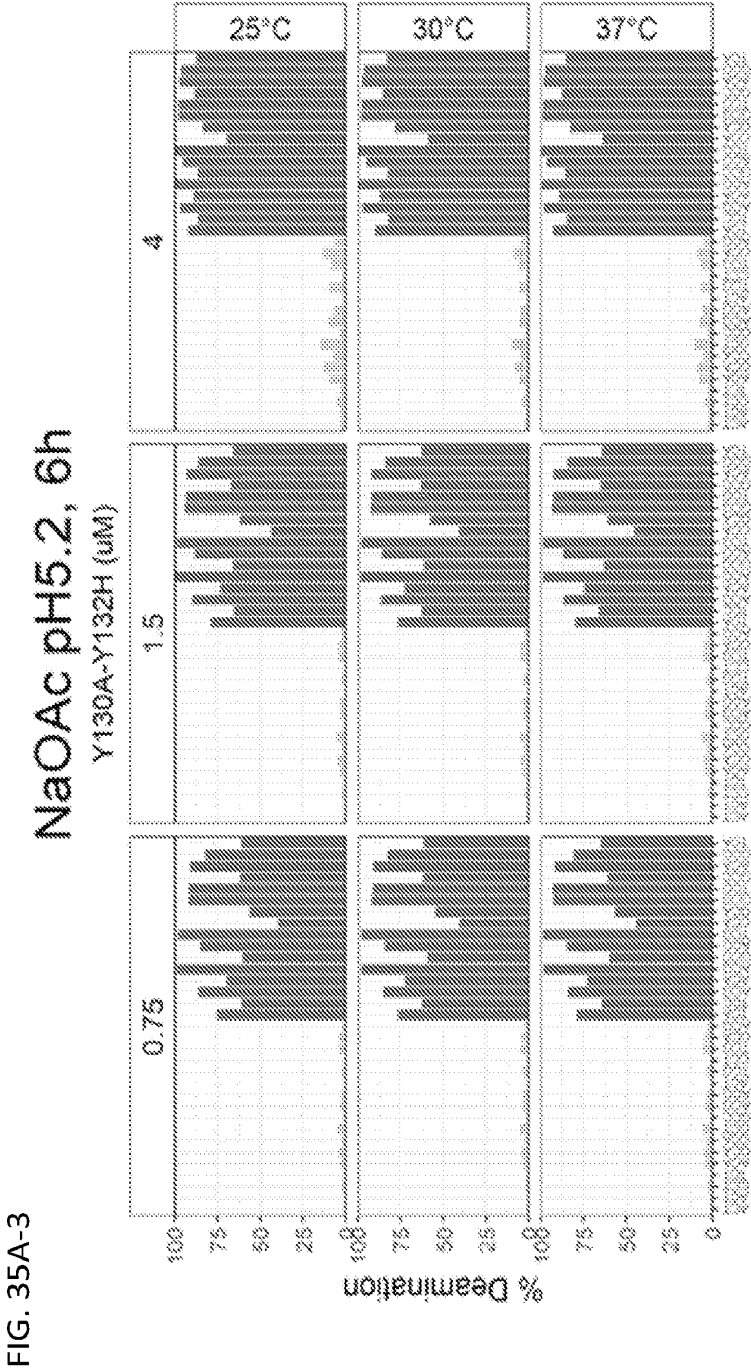


FIG. 35B-1

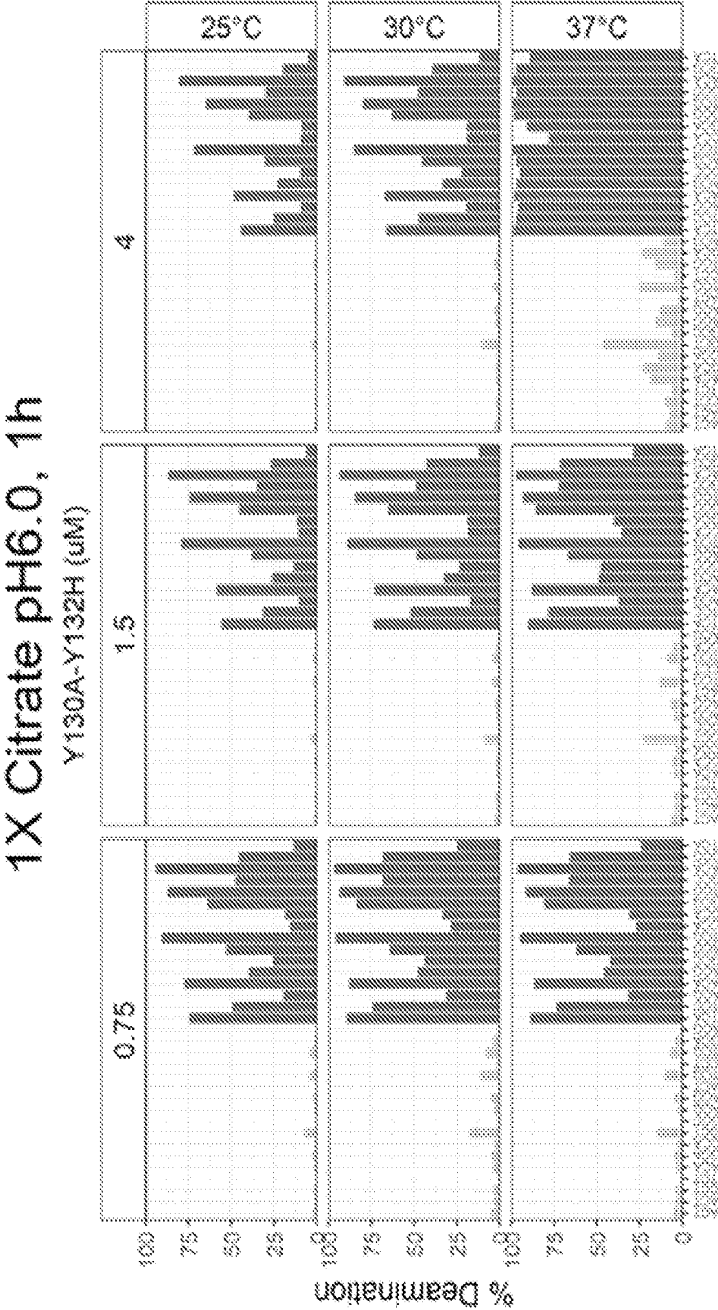


FIG. 35B-2

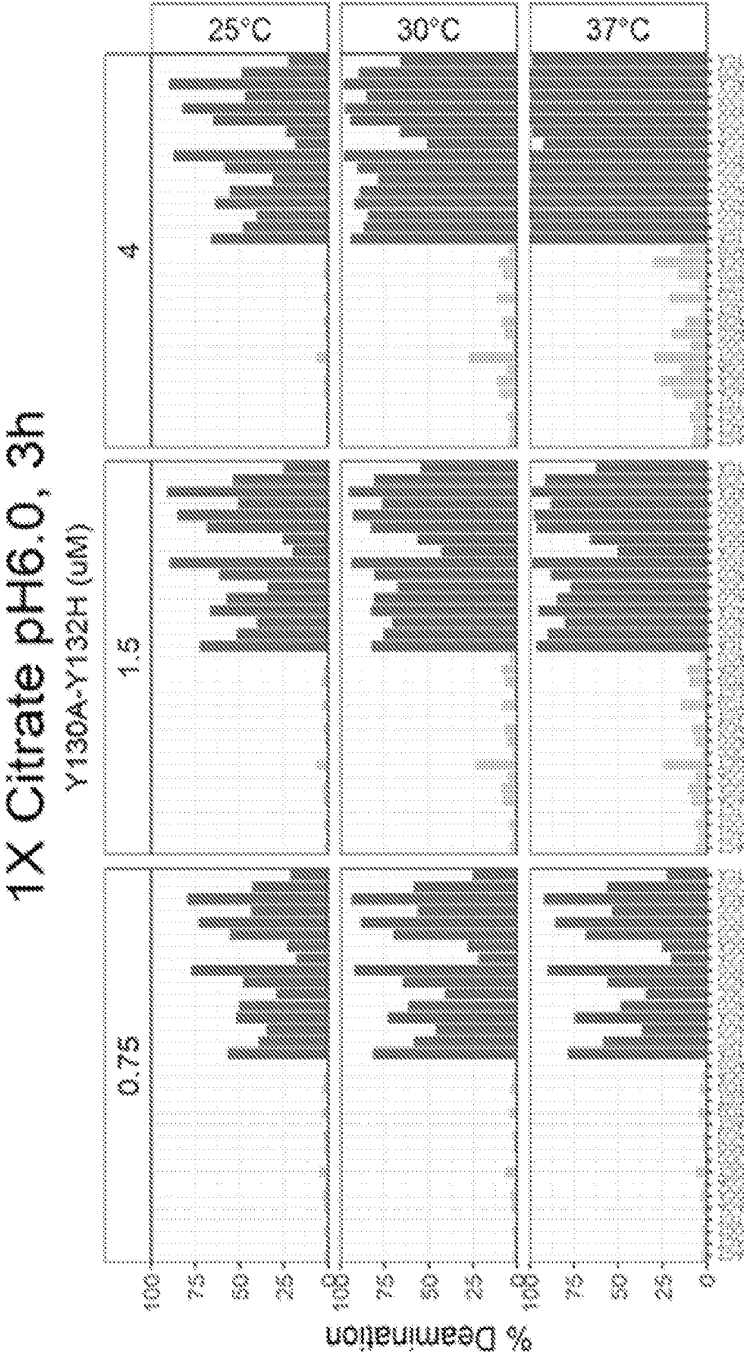


FIG. 35B-3

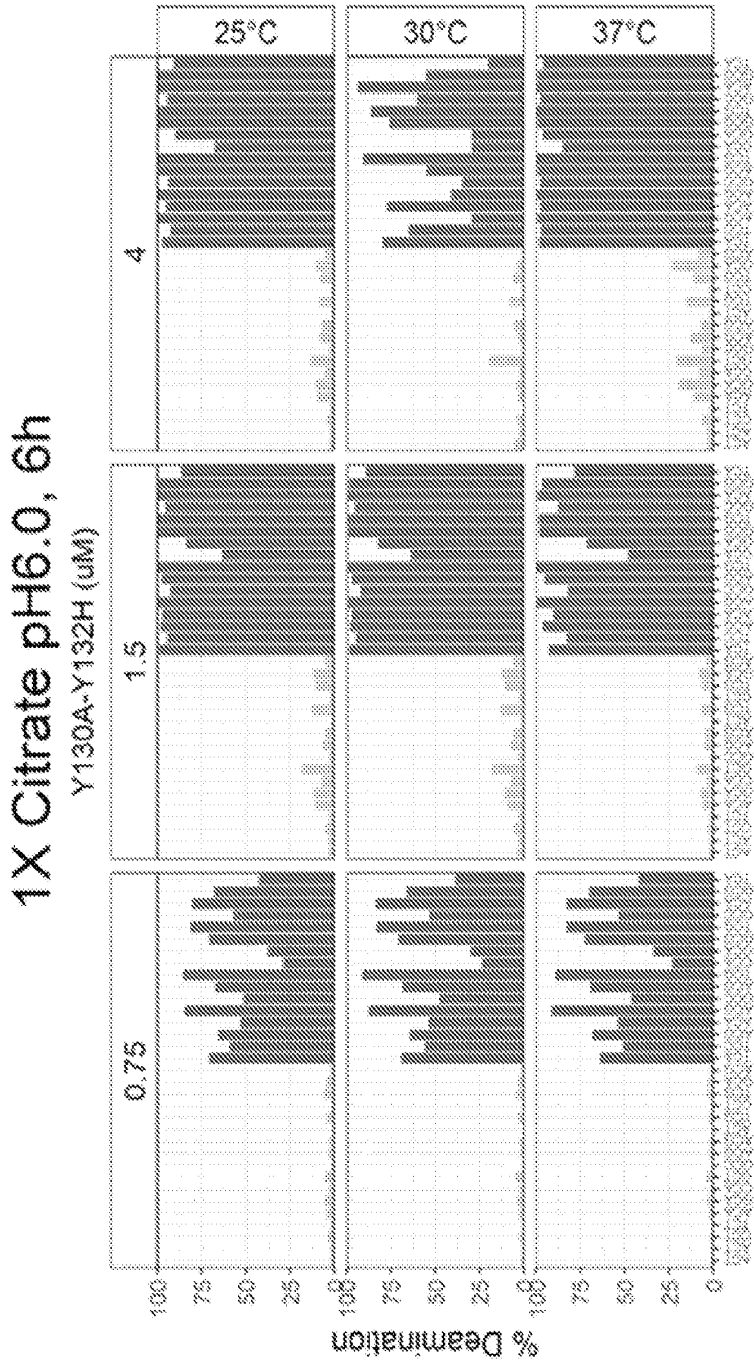


FIG. 35C-1

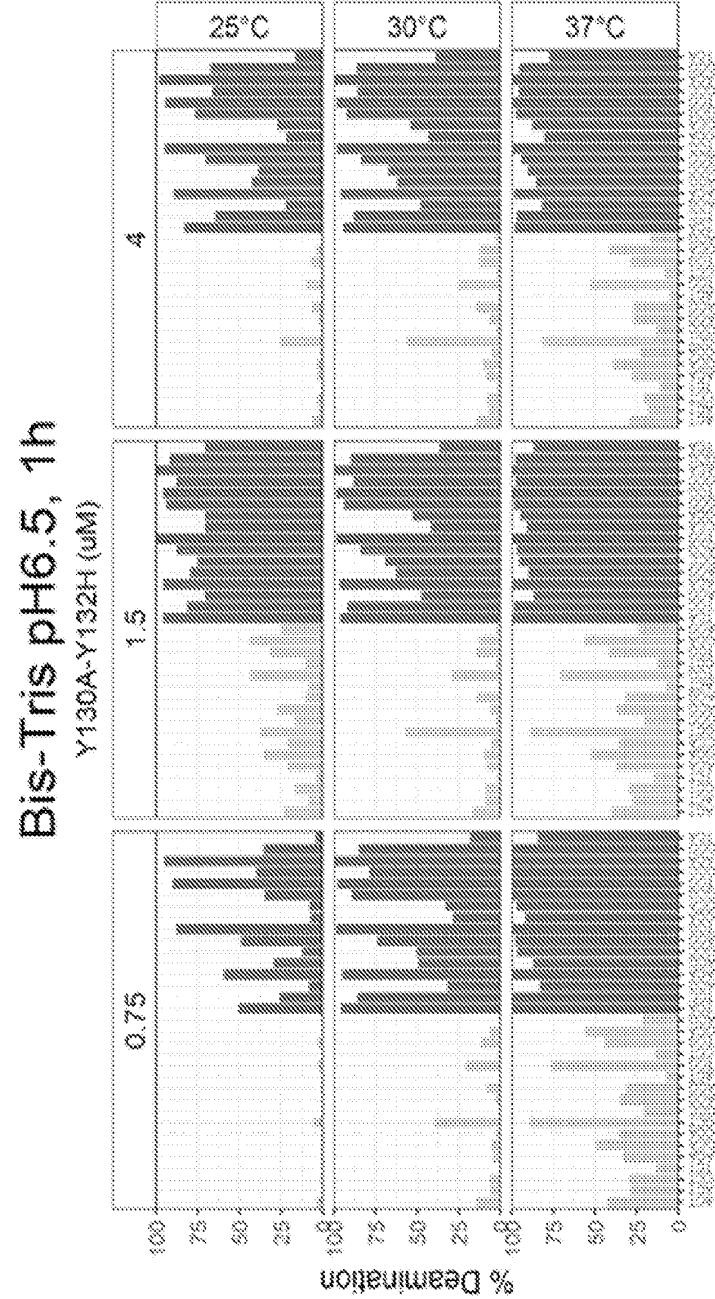
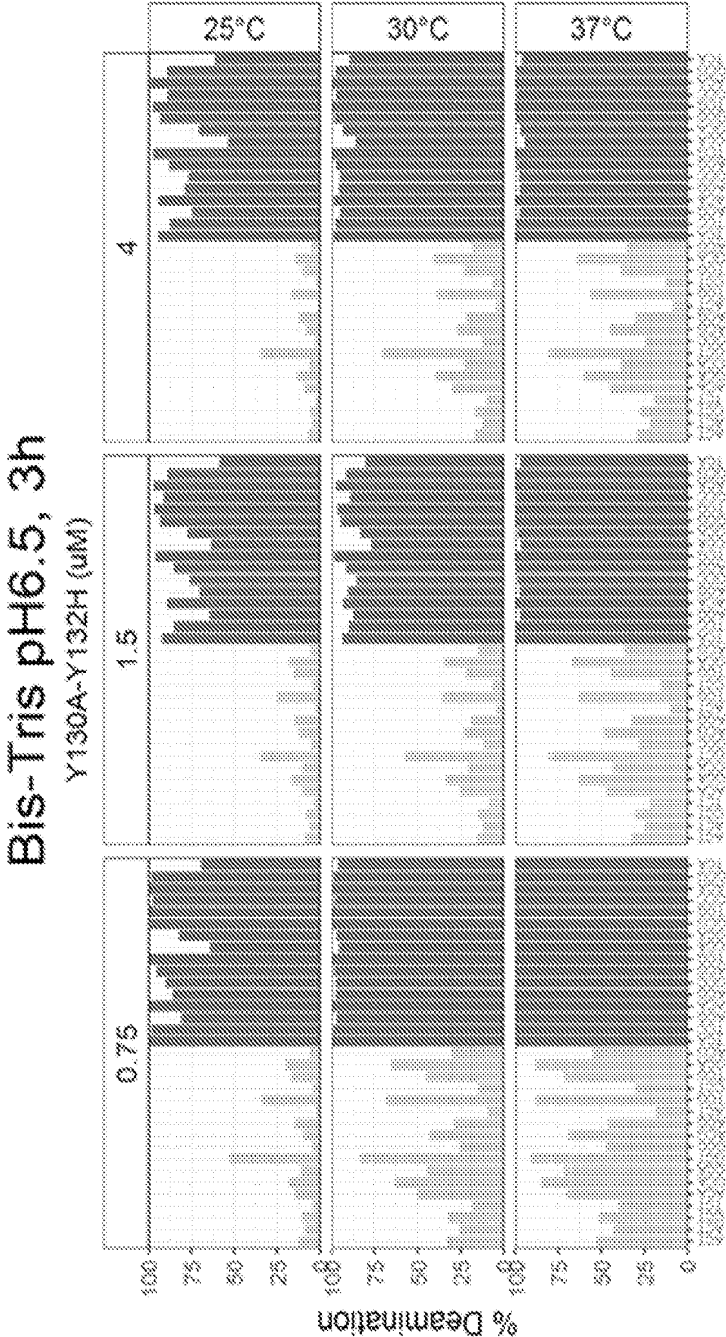


FIG. 35C-2



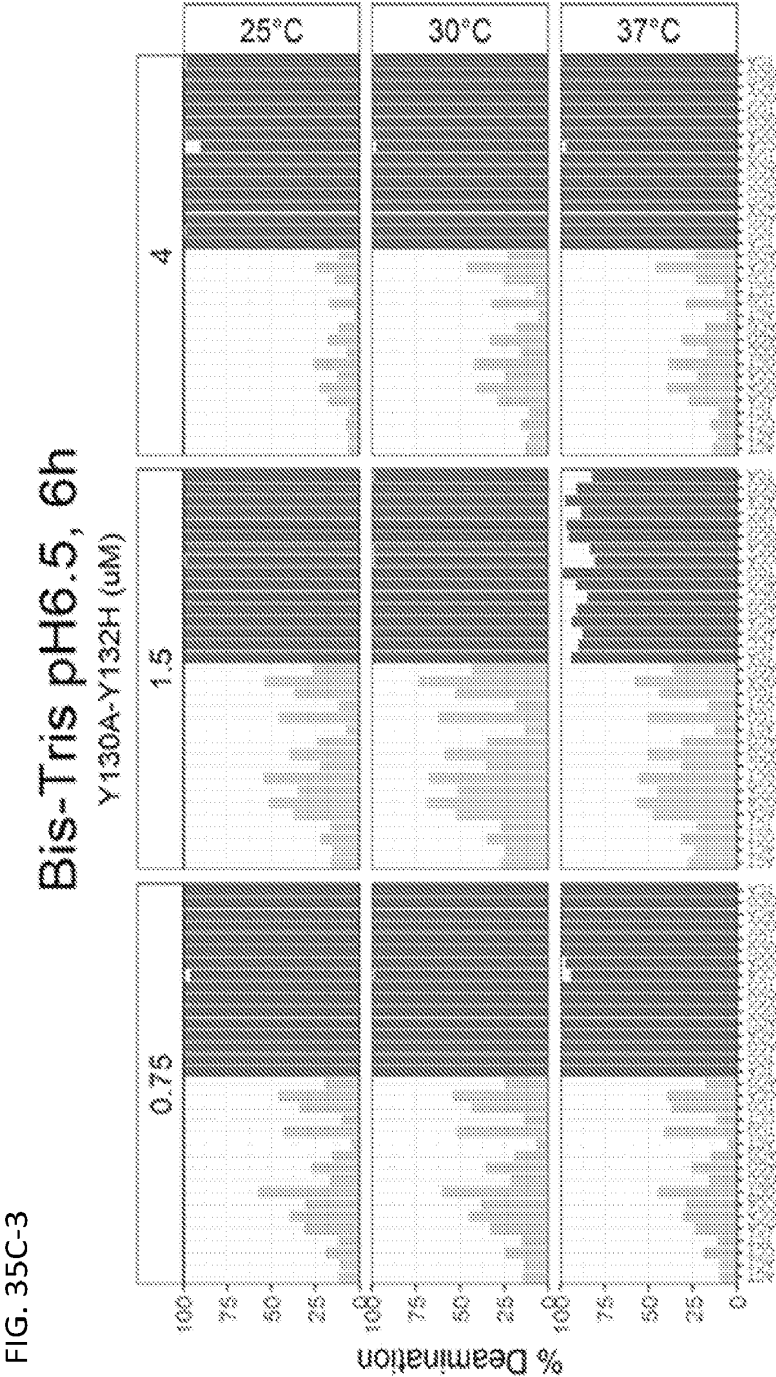


FIG. 36

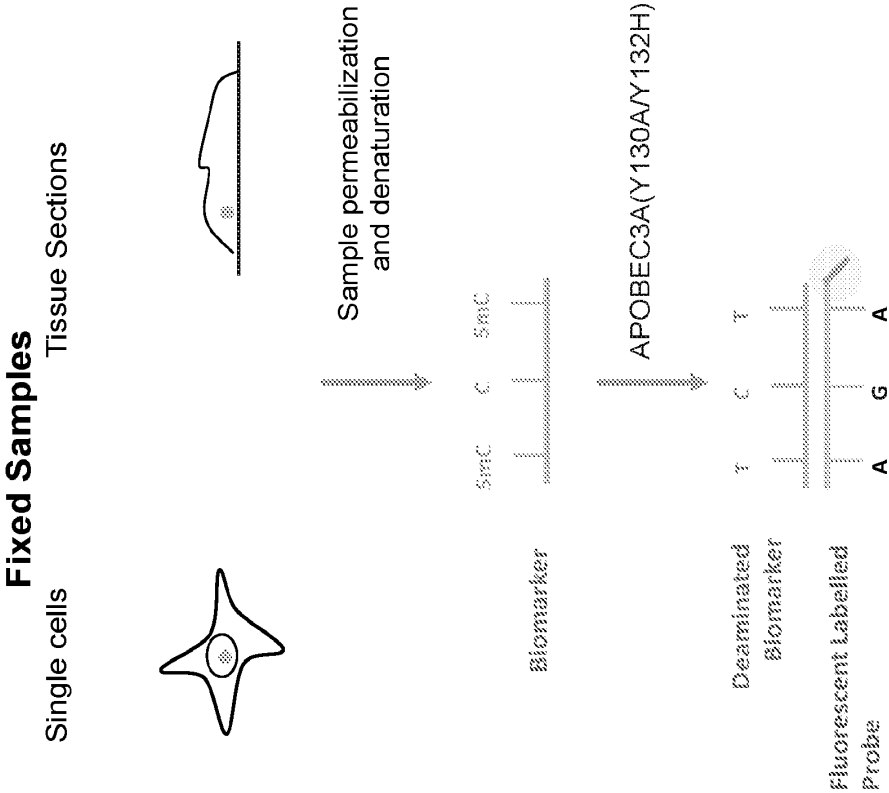


FIG. 37A

SEQ ID NO: 16

MEASPASGERHLMDFHIFTSNFNNGIGRHKTYLCYEVEERLDNGTSVKMDQHRGFLHNQAK
NLLCGFYGRHAELEFLDLVPSQLDPAQIYRVTWFI SWSPCF SWGCAGEVRAFLQENTHV
RLRIFAARIADYDEPLYKEALQMLRDAGAQSIMTYDEFKHCWDTFVDHQGCCPFQPWDGLD
EHSQALSGRLRAILQNQGN

SEQ ID NO: 17

MEASPASGERHLMDFHIFTSNFNNGIGRHKTYLCYEVEERLDNGTSVKMDQHRGFLHNQAK
NLLCGFYGRHAELEFLDLVPSQLDPAQIYRVTWFI SWSPCF SWGCAGEVRAFLQENTHV
RLRIFAARIADHDEPLYKEALQMLRDAGAQSIMTYDEFKHCWDTFVDHQGCCPFQPWDGLD
EHSQALSGRLRAILQNQGN

FIG. 37B

SEQ ID NO:37
MDSLIMNRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKGCHVELLFLRYISDWDL
DPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMT
FKENHRTFKAWEGLENHNSVRLSRQLRRIILPLYEVDLIRDAFRTLGL

SEQ ID NO:38
MDSLIMKQKKFLYHFKNVRWAKGRHETLYCYVVKRRDSATSCSLDFGHLRNKSGCHVELLFLRYISDWDL
DPGRCYRVTWFTSWSPCYDCARHVAEFLRWPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIGIMT
FKDYFCWNTFVENRERTFKAWEGLENHNSVRLTRQLRRIILPLYEVDLIRDAFRMLGF

SEQ ID NO:39
MSRKIWRSSGKNTTNHVEVNFIIKKFTSERHEHPSISCSITWFLSWSPCECSQAIREELSQHFGVTIYI
VARLEWHMDQNRQGLRDLVNSGVTIQIMRASEYYHCWRNFVNYPGDEAHWPQYPLMMMLYALELHCI
ILSLFPCLKTSRRWQNHLLTFERLHQNCHYQTIPPHILLATGLIHPSVAWR

SEQ ID NO:40
MSSETGPVAVDPFLRRRIEPHEFEVFFDPRRLRKETCLLYEINWGRHSHVRHTSQNTSNHVEVNFLEKF
TTERYFRPNTRCSITWFLSWSPCECSRAITEFLSRHPYVTLFIYIARLYHHTDQRNQGLRDLISGVT
IQIMTEQEYCWCWRNFVNYPSPNEAYWPRYFHLWVLYVLELYCIILGLPCLKILRKQPLTFFTTITL
QTCHYQRIPPHLLWATGLK

SEQ ID NO:41
MAQKEEAAAAATEAAAAEAAASQNGEDLENLDDPEKLELIELPFEIVTGERLPANFFKFQFRNVEYSSG
RNKTFLCYVVEAQGGQVQASRGYLEDEHAAHAEEAFFNTIILPAFDPALRYNVTWYVSSSPCAACADR
IIKTLKTKNLRLIILVGRLFMWEEPEIQAAALKKEAGCKLRIMKPDPEYVWQNFVEQEEGESKAFQP
WEDIQENFLYYEEKLADILK

FIG. 37C

SEQ ID NO: 42
MAQKEEAAEAAAPASONGDDLENLEDPEKIKELIDLPPFEIYTGVRLPVNFYKQFRNVEYSSGRNKTFL
CYVVEVQSGGQAQATQGYLEDEHAGAHAEAFNTILPAFDPAKYNVTWYVSSPAAACADRILKTL
KTKNLRLLILVSRLFMWEEPEVQAALKKLEAGCKLRIMKPDFFEYIWQNFVEQEEGESKAFEPWEDIQE
NFLYYEKLADIILK

SEQ ID NO: 43
MNPQIRNPMERMRYGTFFYNNFENEPILYGRSYNWLCYEVKIKRGRSNLLWNTGVFRGQMSQPEHHAEMC
FLSWFCGNQLPAYKCFQITWFSWTPCPDCVAKLAELAEYPNVTLTISTARLYYWERYRRAICRLSQ
AGARMKIMDYEECAYCWENFVYKEGQQFMPWYKFDENYAFLLHHTLKEILRHLMDDPTFTFNNDPLVLR
RHQTYLCYEVERLDNGTWVMDRHMGLCNEAKNLLCGFYGRHAELRFLDLPVSLQDPAQIYRVTWFTS
WSPCFSWGACQVCEFLQENTHMLRIFAARIYDYDPLYKKALQMLRDAGAQVSIMTYDEFKHCWDTFVY
RQCGFFQPWDGLEEHSQALSGRLLQAILQNGN

SEQ ID NO: 44
MNPQIRNPMERMRYRTFNYNFENEPILYGRSYTWLCYEVKIRKDPKLPWDTGVFRGQMSKPEHHAEMC
FLSWFCGNQLPAHKRFQITWFSWTPCPDCVAKVAEEFLAEYPNVTLTISAARLYYWETDYRRAICRLRQ
AGARVKIMDYEEFAFCWENFVYNEDQSFMPWYKFDNNAFLHHKLKEILRHLMDDPTFTSNFNNDLSVLG
RHQTYLCYEVERLDNGTWVMDQHWGFLCNQAKNVPBGDYGCHAECLFDDQVSWQLDPAQTYRVTWFTS
WSPCFSWGACADQVYAFLOENTHVLRLIFAARIYDYNPLYQALRTLRDAGAQVSIMTYDEFECWDTFVD
RQGRPFQPWDGLDEHSQALSGRLLRAILQNGN

SEQ ID NO: 45
MNPQIRNPMKAMYPGTFYFQFKNLWEANDRNETWLCFTVEGIKRRSVSWKTGVFRNQVDSETHCHAE
FLSWFCDDILSPNTNYQVWTWYTSWSPCECAGEVAEFLARHSNVNLTIFTARLYYFQDQDYQEGRLSLQ
EGVAVKIMDYKFCWENFVYNDDEPFPEWKGLKYNFRFLKRLQEIIE

FIG. 37D

SEQ ID NO: 46
MNPQIRNPMKAMDEGTFYFQFKNLWEANNRNETWLCFTTVEVIKQHSTVSWETGVFRNQVDLETHCHAERC
FLSWFCEDILSPNTDYQVTWYTSWSPCLDCAGEVAKFLARHNNVMLTIYTARLYYSQYPNYQQGLRSLSE
KGVSVKIMDYEDFKYCWKEKVVYDDGEPFKPWKGLKTSFRFLKRRRLREILQ

SEQ ID NO: 47
MNPQIRNPMERMYPRTFYNHFENEPILYGRSYTWLCYEVKIKRGCSNLIWDTGVFRGPVLPKLQSNHRQE
VYFQFENHAEMCFFSWFCGNRLPANRRFQITWFVSWNPCLPVVKVTKFLAEHENVTLTI SAARLYYYQD
REWRRVLRRLHKAGARVKIMDYKDFAHCWENFVYNEGQQFMPWYKFDDNYASLHRTLKEILRNPMEMAMP
HVYFHFKNLLKACGRNESWLCFTVDTEHHPVYSWKRGVFRNPVDETHCHAERCFLSWFCDDILSPNT
NYQVTWYTSWSPCECAREVAEFLARHSNVKLTIFTARLYHFWNTDYQEGLCSLSQEGASVKIMSYKDFV
SCWKNEVYSDDEPFKPKWKGKLTNFRLLKTMLEILQ

SEQ ID NO: 48
MNPQIRNPMERMYPRTFNYPFENEPILYGRSYTWLCYEVKIRKDP SKLPWDTGVFRGQVFPQYHAEMC
FLSWFCGNQLPAYKRFQITWFVSWNPCDCVAKVTEFLAEHPNVTLTISVARLYYYRGKDWRRALCRLHQ
AGARVKIMDYEEFAYCWENFVYNEGQSFMPWDKDDNYAFLHKLKEILRNPMKAMPHTFYFHFENLQK
AYGRNETWLCFAVEIIKQHSTVPWKTGVFRNQVDPETHCHAERCFLSWFCDDNTLSPKKNYQVTWYISWSP
CPECAGEVAEFLATHSNVKLTITYTARLYYFWDTDYQEGRLSLSEEGASMEIMGYEDFKYCWENFVYNDGE
PFKPKWGINTNFRFLERLWKILQ

SEQ ID NO: 49
MKPQFRNTVERMYRGTFSYNFNNRPILSRNTVWLCYEVKTKGSPRPPLDAKIFRGQVYFQYHAEMCF
LSWFCGNQLPAYKCFQITCFVSWTPCPCDCVAKLAEF LAEHPNVTLTISAAARLYYYWERDYRRALRRLPQA
GARVKIMDDEEFAYCWENFVYSEGQPEMPWHKDDNYAFLHRTLKEILRNPMEMAMPPIFYFHFKNLLKA
YGRNESWLCFTMEVIKHSFVSWKRGVFRNQVDSETHCHAERCFLSWFCDDILSPNTNYQVTWYTSWSPC
PECAGEVAEFLARHSNVNLTIFTARLYYFWDTDYQEGRLSLNQEGASVKIMGYKDFKYCWENFVYNDDEP
FKPWKGLKYNFLFLDSKLQEILE

FIG. 37E

SEQ ID NO: 50
MQPQYRNTVERMYRGTFYFNFNRPILSRNTVWLCYEVKTRGFSMPWTDTKIFRGQVYSKEPHEHMCFLSRFCGNQLPAYKRFOITWFSWTPCPDCVAKVAEFLAEHNVTLTI SAARLYYWETDYRRALCRLROA GARVKIMDYEEFAFCWENFVYNEGQSEMPWDKFDNNYAFLLHKLKEILRNPMETYPHIFYFHEKNLRKAYGRNETWLCFTMEILIKQHSVSWETGVFRNQVDPSRCHAEKCFLSWFCEDILSPNTDYQVTWYTSWSPCLDCAGEVAEFLARHNSVKLAI FAARLYYFWDTHYQOGLRSLSEKGA SVEIMGYKDFKYCWENFVYNGDEP EKPWKGLKYNFLFLDSKLQEIIE

SEQ ID NO: 51
MTPQFRNTVERMYRDTFSYNFNRPILSRNTVWLCYEVKTKDPSRPPLDAKIFRGQVYSELKYHPEMRF FHWFSKWRKLHRDQYEVWTYISWSPCTKCTRNATFLAEDPKVTLTIFVARLYYFWDQDYQEALRSLCQ KRDGPRATMKIMNYDEFQHCWSKFVYSQRELFEFNNLPKYTMLLHIMLGEILRHSMDPPTT SNFNNEH WVRGRHETYL CYEVERLHNDTWLLNQRRGFLCNQAPHKHGFLEGRHAELCFLDVIPFWKLDLHQDYRVTCFTSWSPCFSCAQEMAKFISNKKHVS LCIFAARIYDDQGRQCEGLRTLAEAGAKISIMTYSEFKHCWDTF VYHQGCPFQPWDGGLDEHSQALSGRLOAILQNQGN

SEQ ID NO: 52
MNPQIRNMVEPMDPRTFVSNFNRPILSGLNTVWLCCEVTKDPSGPPLDAKIFQKVLRSKAKYHPEMR FLQWFREWFQLHHDQYKVTWYVSWSPCTRCANSVATFLAKDPKVTLTIFVARLYYEWKPNYQQAALRILC OKRDGPHATMKIMNYNEFQDCWNKFVDGRGKPFKPWNNLPKHYTL LQATLGELLRHLMDPGTFTSNFNNK PWSGQHETYL CYKVERLHNDTWVPLNQHRGFLRNQAPNIHGFPKGRHAELCFLDLIPFWKLDGQQYRVTCFTSWSPCFSCAQEMAKFISNNEHVS LCIFAARIYDDQGRYQEGGLRTLHRDGAKIAMMNYSEFEYCWDTF VDCQGCPFQPWDGGLDEHSQALSERLRAILQNQGN

SEQ ID NO: 53
MALLTAETFRLQFNKKLRLRRPYRRKTL CYQLTPQNGSMPTRGYFKNKKKCHAEICFINEIKSMGLDE TQCYQVTCYLTWSPCS CAWKLVDFIKAHDLNLRIFASRLYHWCKRQOEGRLLCGSQVPEVMGFPE FADCWENFVDHEKPLSFDPSKMLEELDKN SQAIKRRLERIKRSRVDVLENGLRSLQLGPVTPSSRSNSR

FIG. 37F

SEQ ID NO: 54

SMALLTAKTSLQFNKRVRKPYPRKALLCYQLTPQNGSTPTRGHLNKKKKDHAEIRFINIKIKSMGLUDE
TQCYQVTCYLTWSPCSCAGELVDFIKAHRLNLRIFASRLYHWRPNVQEGLLLCGSGQVPEVVMGLPE
FTPDQWENFVDHKPEPSPNPSSEKUEELDKNQSOKRRLERIKSPSDVJLENGRLSLQGLGVTPSSSIRNRS

SEQ ID NO: 55

MEPI YEEYLANHGTVKPYWJUSFSLDCSNCPYHJTGEEARVSLTEFCQIFGFPYGTTFPOTKHLTFYE
LKTSSGSLVQKGHASSCTGNYIHPESMLEWNGYLDSAIYNND SIRHILYSNNSPCNEANHCCISKMYN
FLFTYPGITLSIYFSQLYHTEMDFPASAWNREALRSLASLPFRVLSPTSGGIMFSLHSFTSGVSGSHV
FQPI LTGRALADRHNAYEINATGVKPYTVDVLQTKRNPNTKAQEALESYPLNNAFPQSQTQMPSPGOLQ
PDVRAEYFVLVRLDLPMMHGQNPKNPRNIVRHLNMPQMSFQETEDLGRLTGTRSVVEIVEITER
FASCKEADKKKKKKKK

SEQ ID NO: 56

MEELYEEILTOGGTIVKPYWLSLSLGCNCPYHUTGTEEARVPYTEFHQTGFFWSTYPQTKHLTTFVEL
RSSS KNLIQKGLASNCTGSHNPEAMLFEKNGYLDVIFHNSNI RHII LYSNNSPCEAKHCCI SKMYNF
LMMNYPEVTLISVFFSOLYHTEKQFTSAMNRKALQSLASLPQVLTSPICGGLWHAILKEKFSVNI SGSTVP
QPTIAGRIILADRYNTVEINSITAAKPYTFDGLLSROKENQNRAAWAFETKHP LGSAA PAQOFTRGQDPR
TTPAVMLVSNRDLPIIHVGSTPQKPTVTVYHLMNLQLSSEKYDKVKKPSGRPVEEVEVMKESARSQKAN
KNRNSQWKKOTLVIKPIRCLLER

FIG. 37G

SEQ ID NO:61
MEASPASGERHLMDEPHIFTSNFNNGIGRHKTYLCYEVEVERLDNGTSVRMDQHRGFLHNQAKNLLCGFYGRH
AELRFLDLVPSLQLDPAQIYRVTWFI SWSPCF SWGCAGEVRAFLQENTHVRRLRIFAARI~~X~~DYDPLYKEAL
QMLRDAGA~~Q~~VSIMTYDEFKHCWDTFVDH~~Q~~GCPFPQPDGLDEHS~~Q~~ALSGRLRAILQ~~N~~QGN
(where X is A, G, F, H, Q, M, N, K, V, D, E, S, C, P, or T)

SEQ ID NO:62
X26-GRXXTXLCYXV-X15-G-X16-HAEXXF-X14-YYXTWXXSWSPC-X4-CA-X5-FL-X7-LXIFXXR
(L/I) ~~Z~~-X8-GLXXLXXG-X5-M-X4-FXXCWXXFV-X6-FXPW-X13-LXXI-X6
(where Z is A, G, F, H, Q, M, N, K, V, D, E, S, C, P, or T, and
the number after an X refers to the number of amino acids present)

SEQ ID NO:63
MEASPASGERHLMDEPHIFTSNFNNGIGRHKTYLCYEVEVERLDNGTSVRMDQHRGFLHNQAKNLLCGFYGRH
AELRFLDLVPSLQLDPAQIYRVTWFI SWSPCF SWGCAGEVRAFLQENTHVRRLRIFAARI~~X~~DYDPLYKEAL
QMLRDAGA~~Q~~VSIMTYDEFKHCWDTFVDH~~Q~~GCPFPQPDGLDEHS~~Q~~ALSGRLRAILQ~~N~~QGN
(where X is A, L, or W, and Z is R, H, L, or Q)