

FIG. 1B

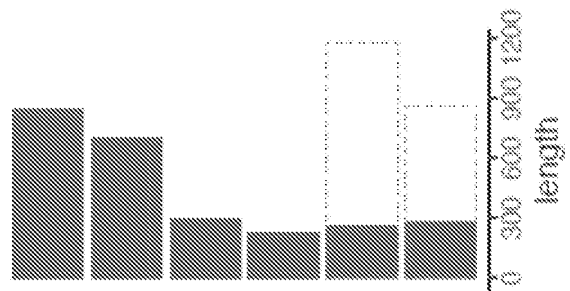


FIG. 1A

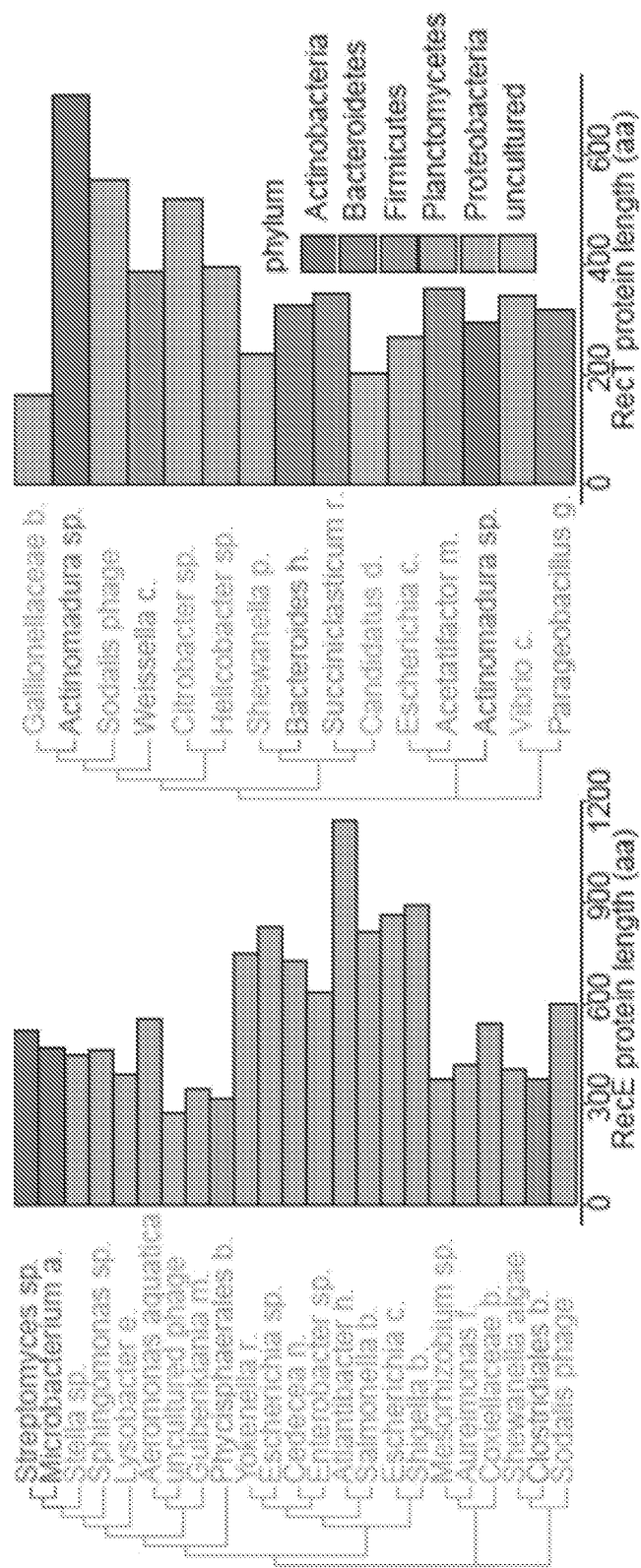


FIG. 2A

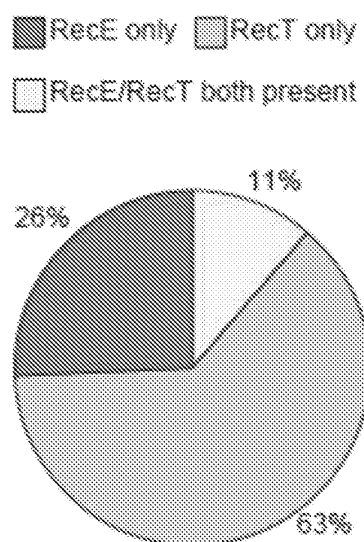


FIG. 2B

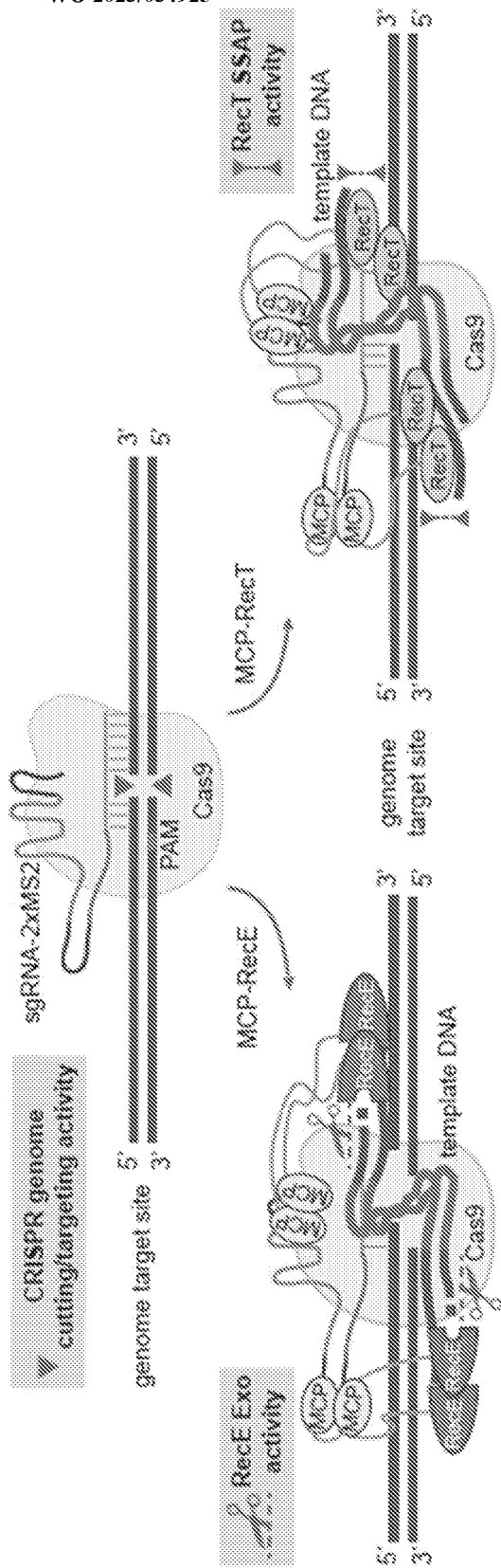


FIG. 2C

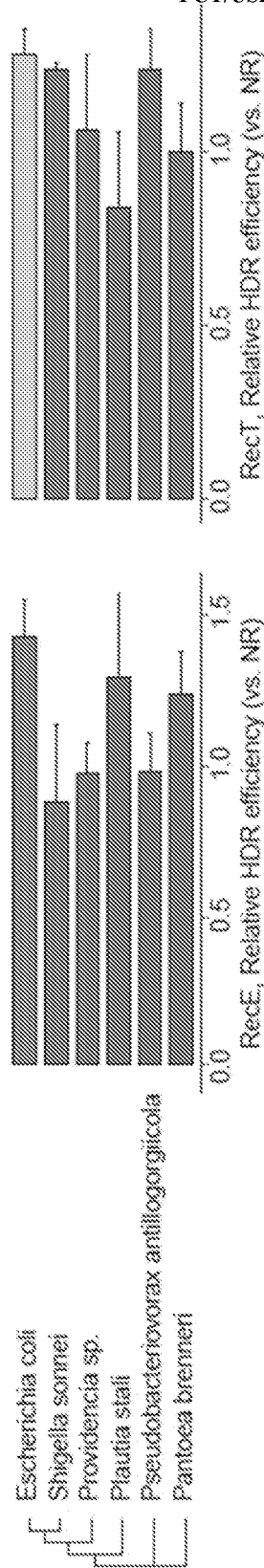


FIG. 2D

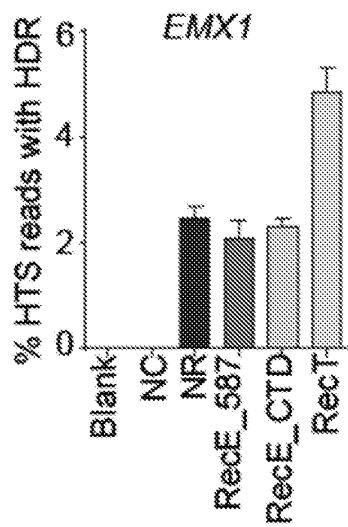


FIG. 3A

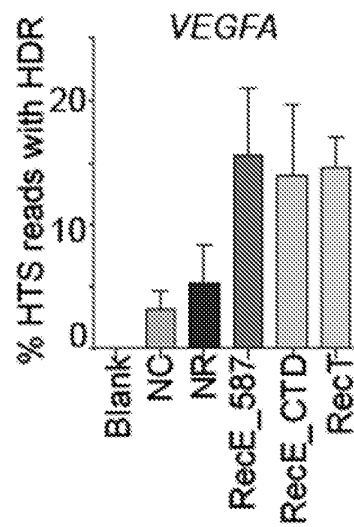


FIG. 3B

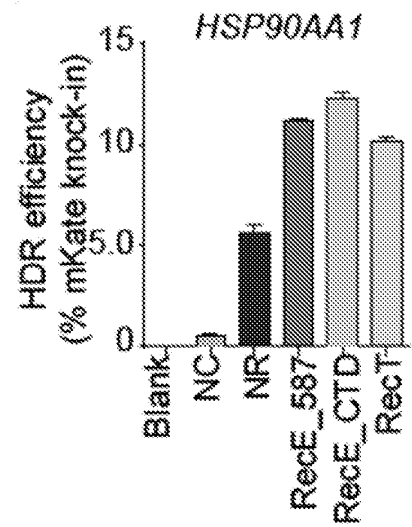


FIG. 3C

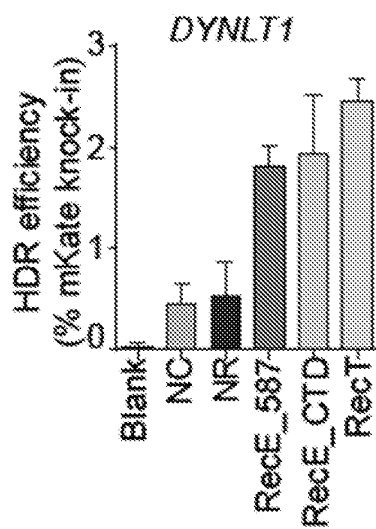


FIG. 3D

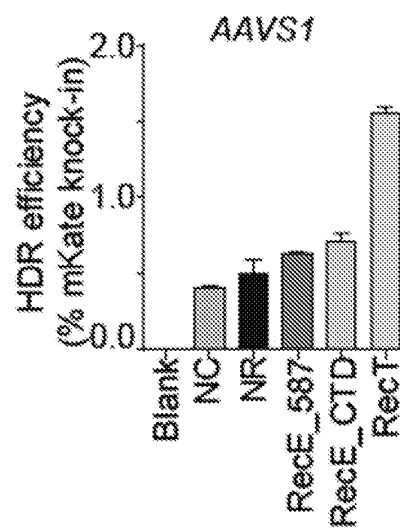


FIG. 3E

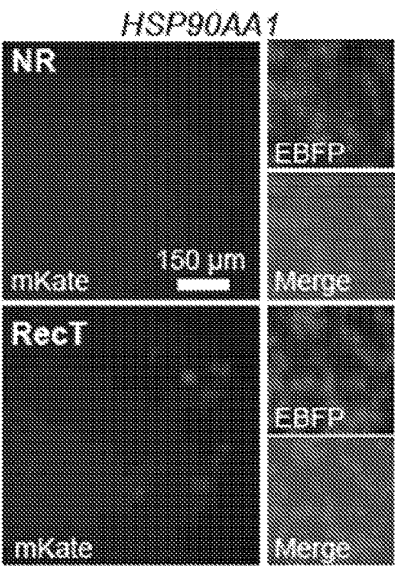


FIG. 3F

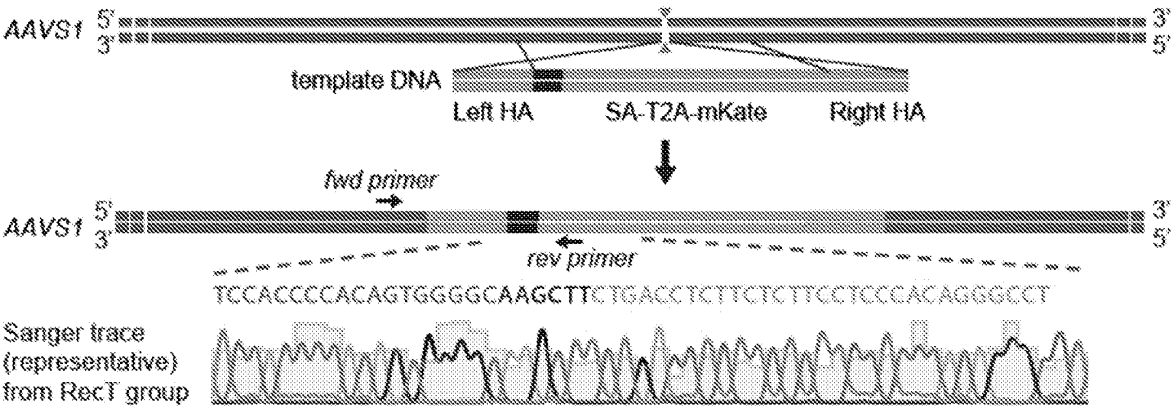


FIG. 3G

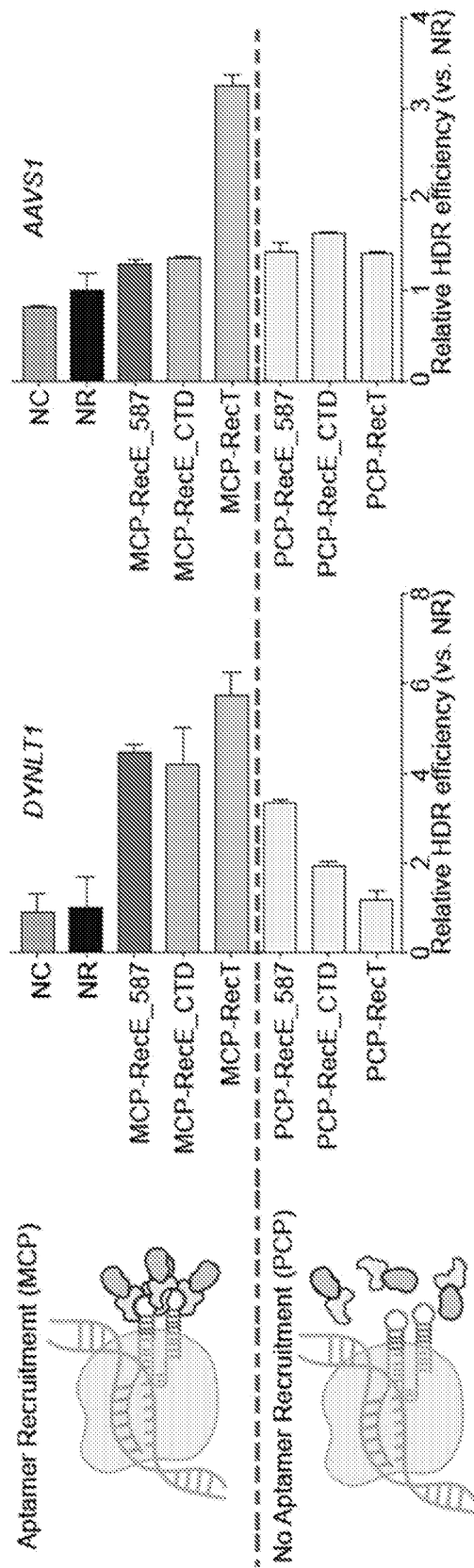


FIG. 3H

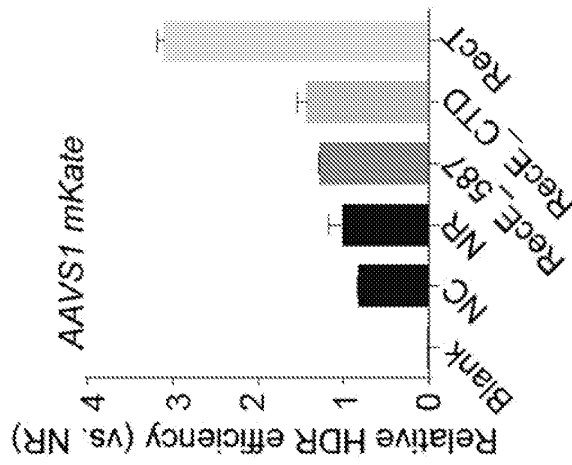


FIG. 4C

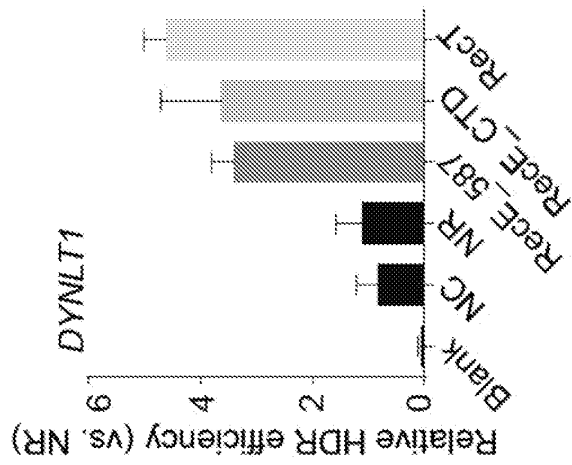


FIG. 4B

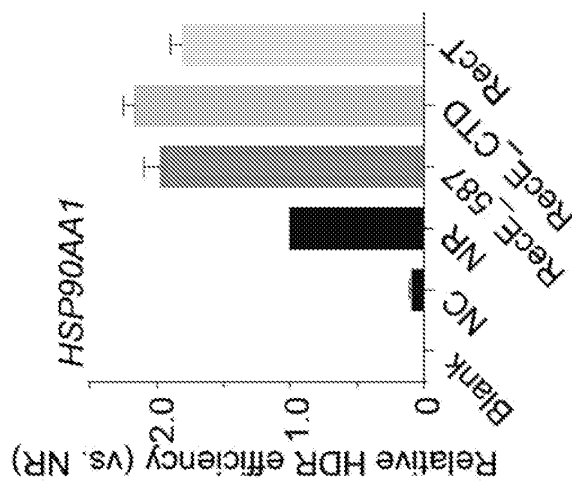


FIG. 4A

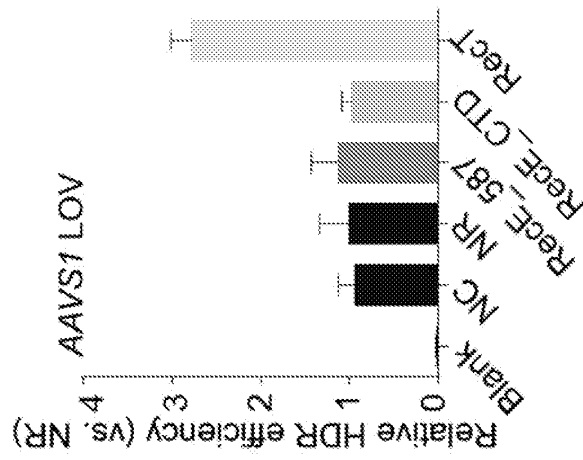


FIG. 4F

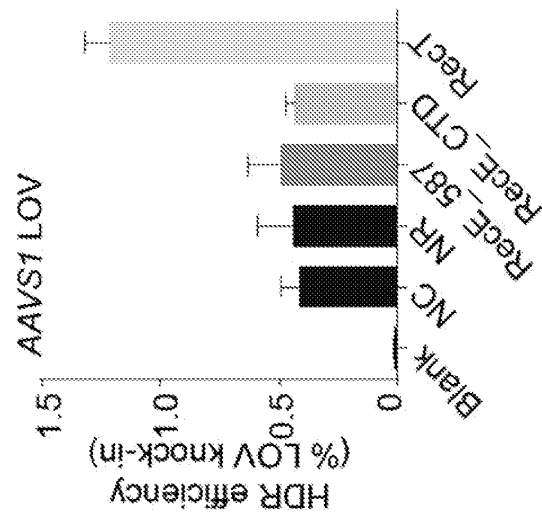


FIG. 4E

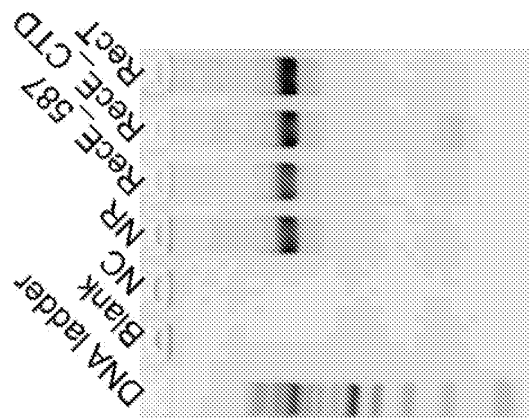


FIG. 4D

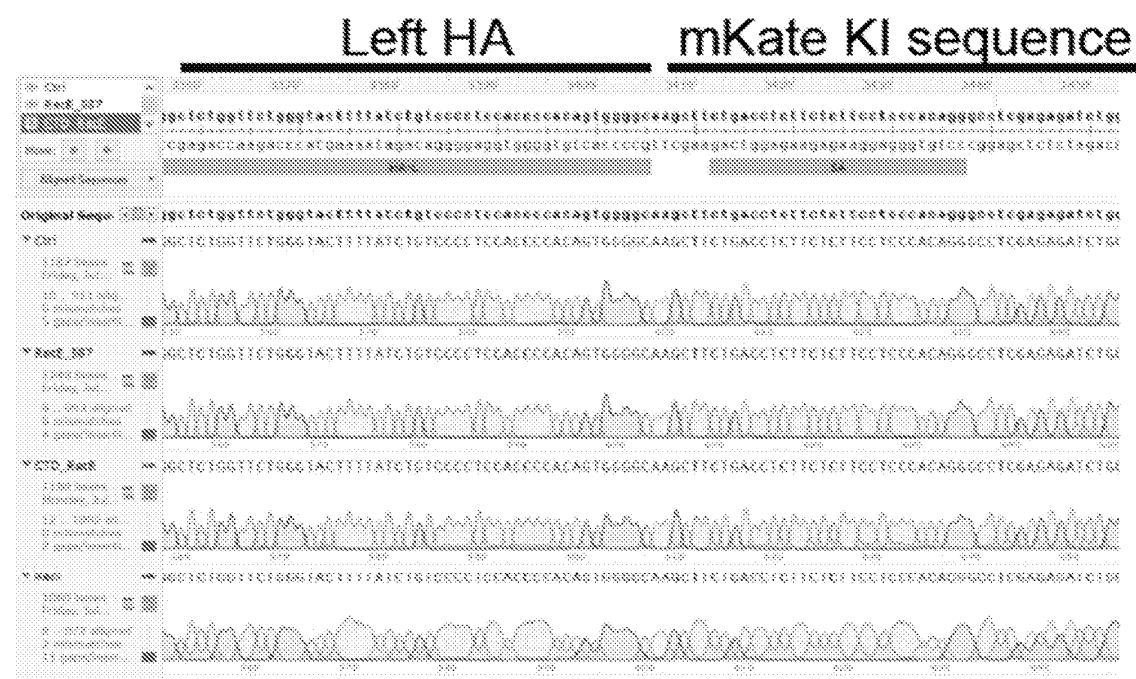
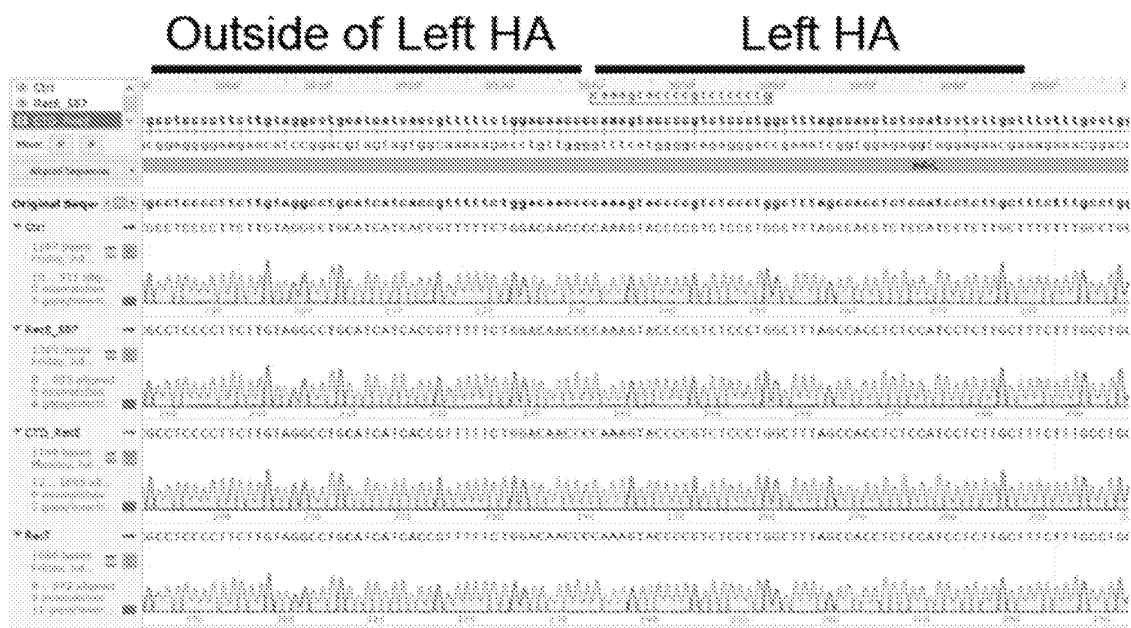


FIG. 4G

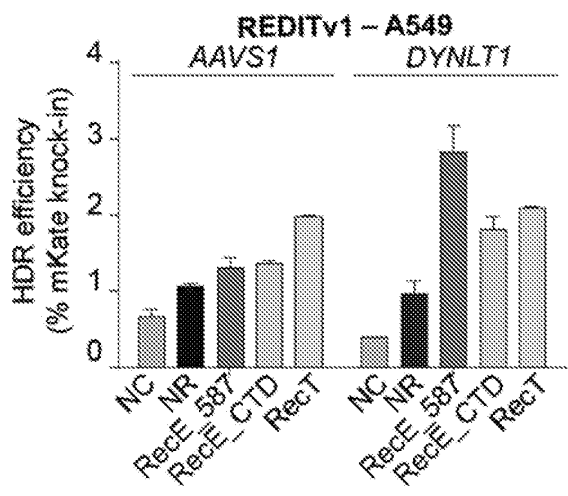


FIG. 5A

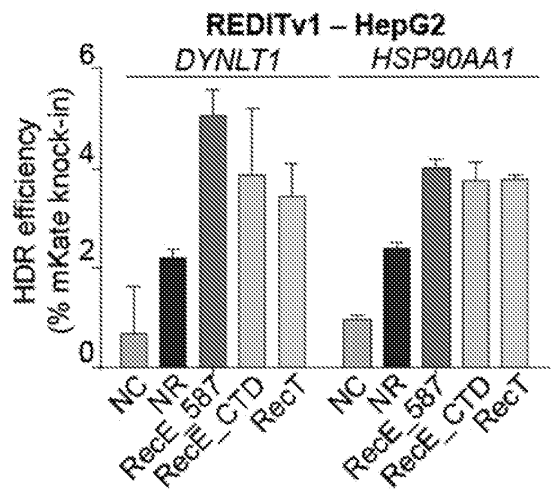


FIG. 5B

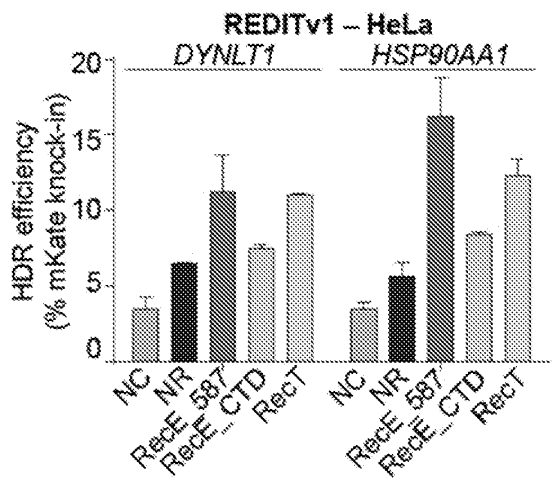


FIG. 5C

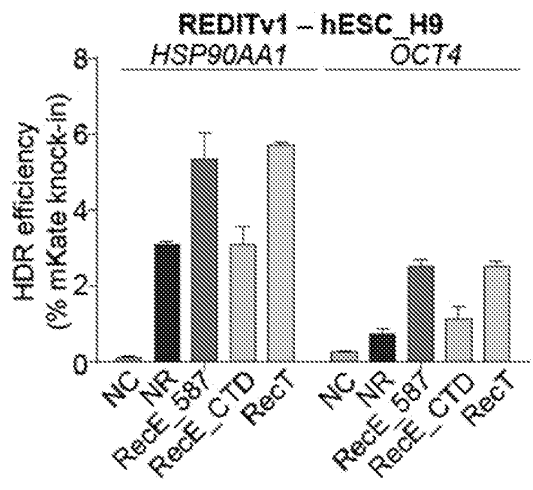


FIG. 5D

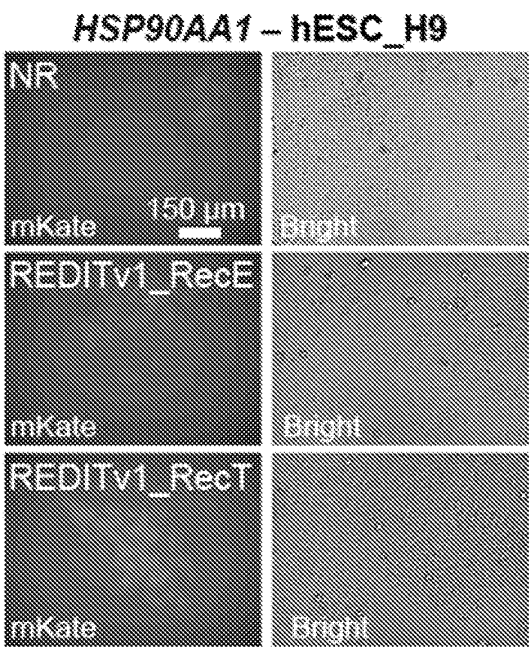


FIG. 5E

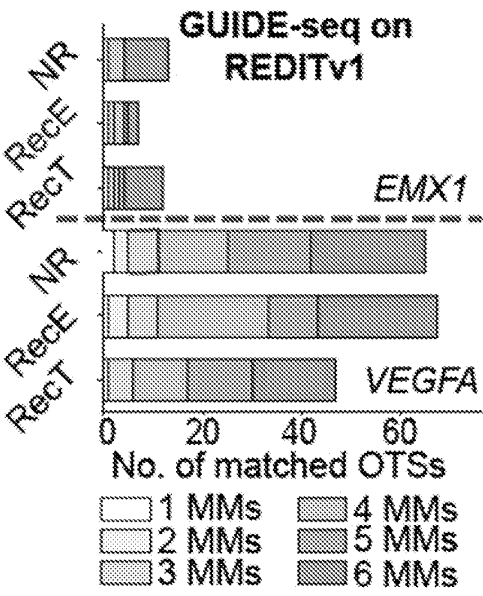
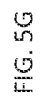


FIG. 5F



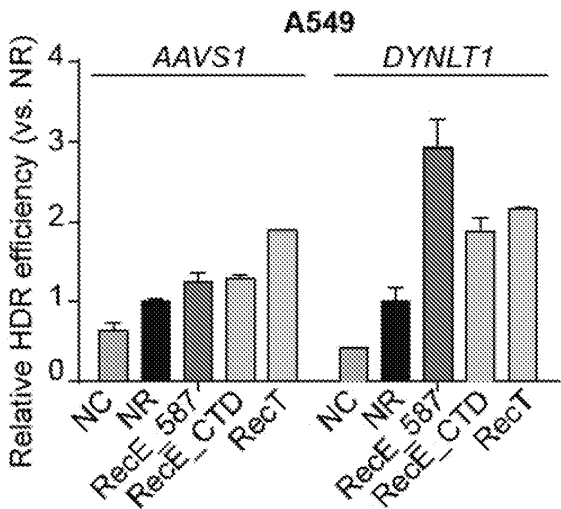


FIG. 6A

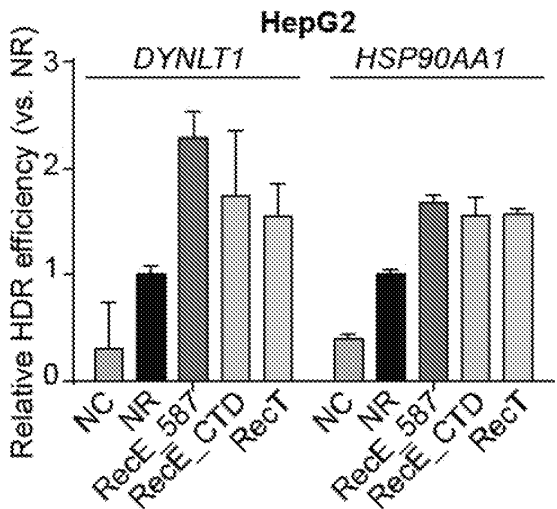


FIG. 6B

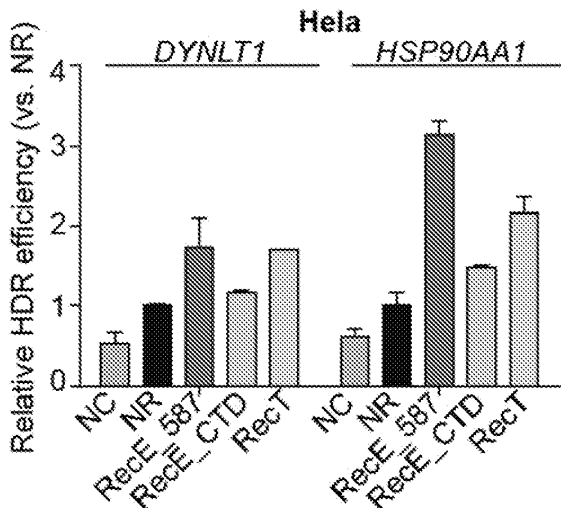


FIG. 6C

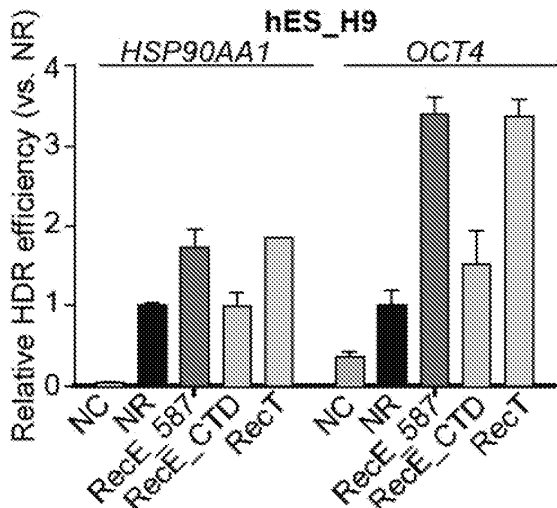


FIG. 6D

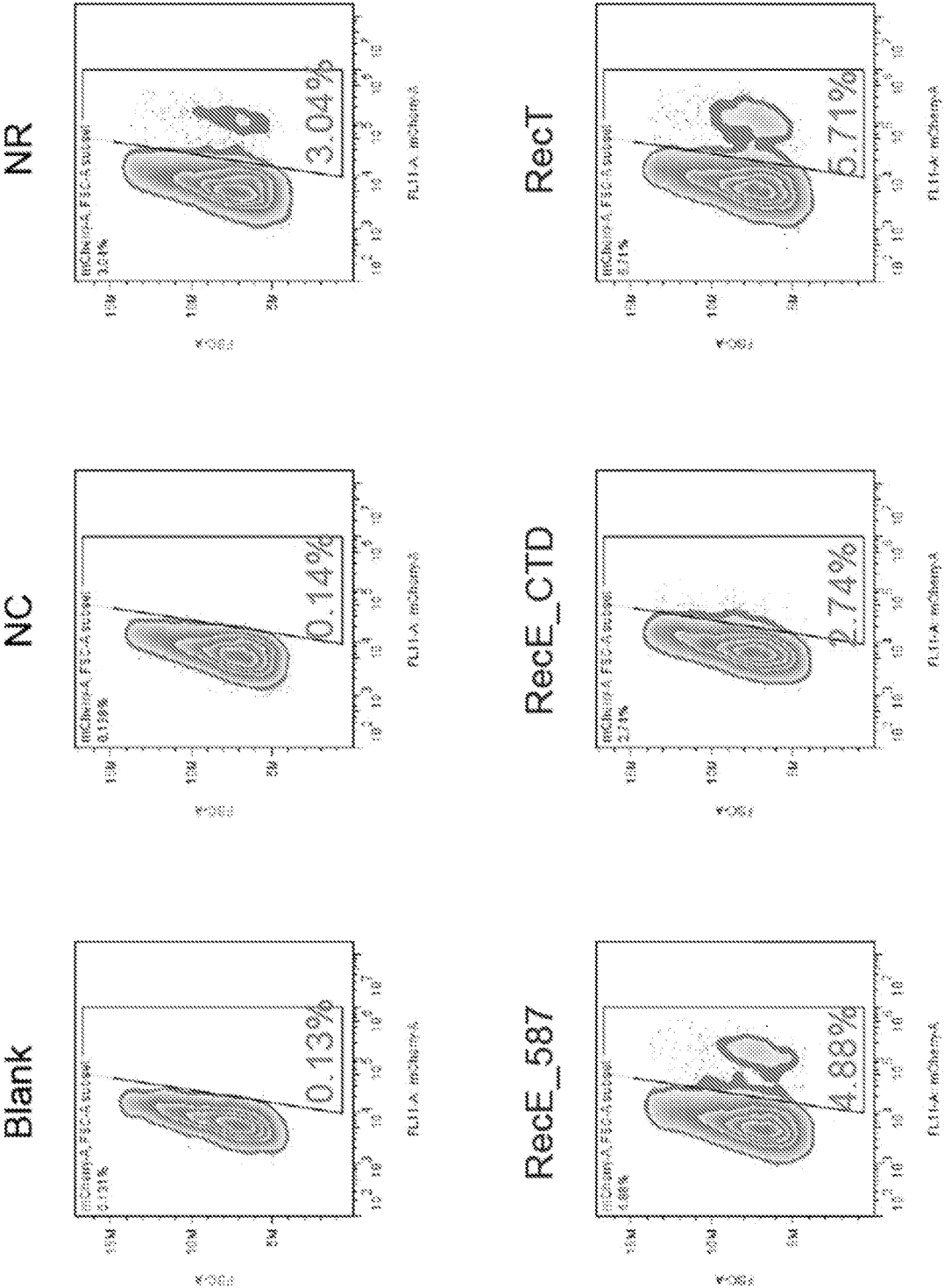


FIG. 6E

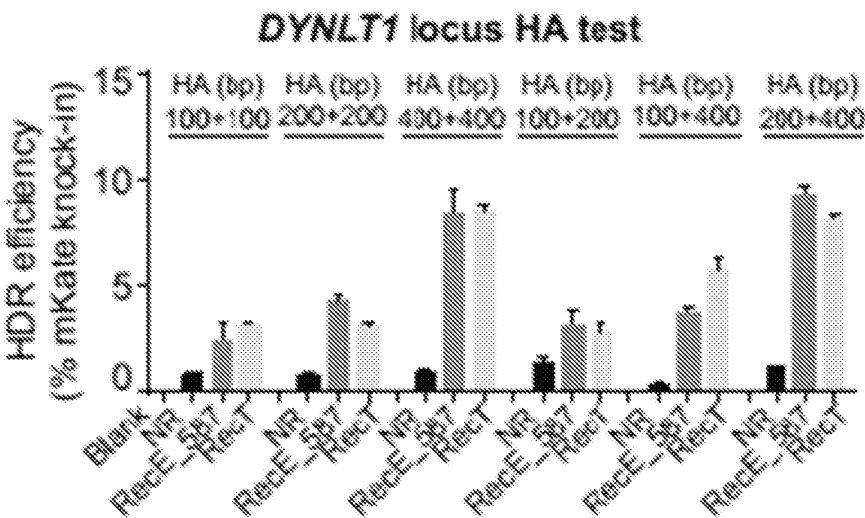


FIG. 7A

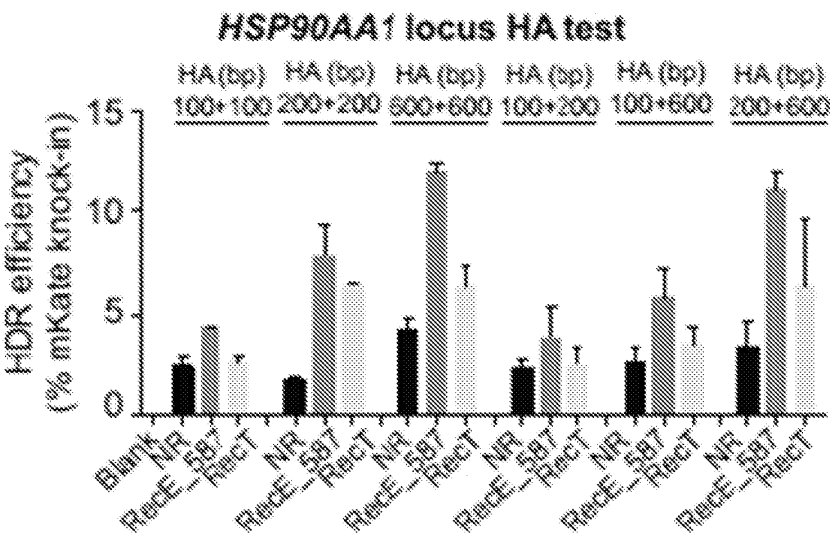


FIG. 7B

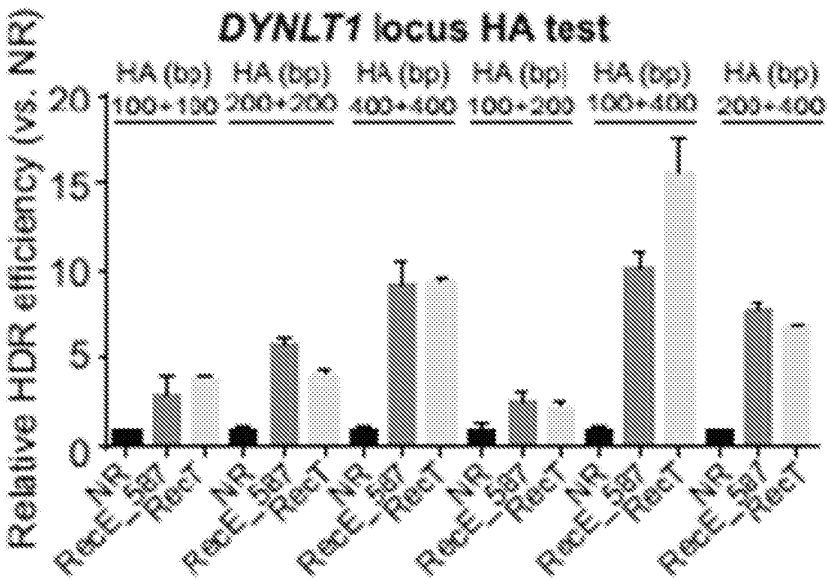


FIG. 7C

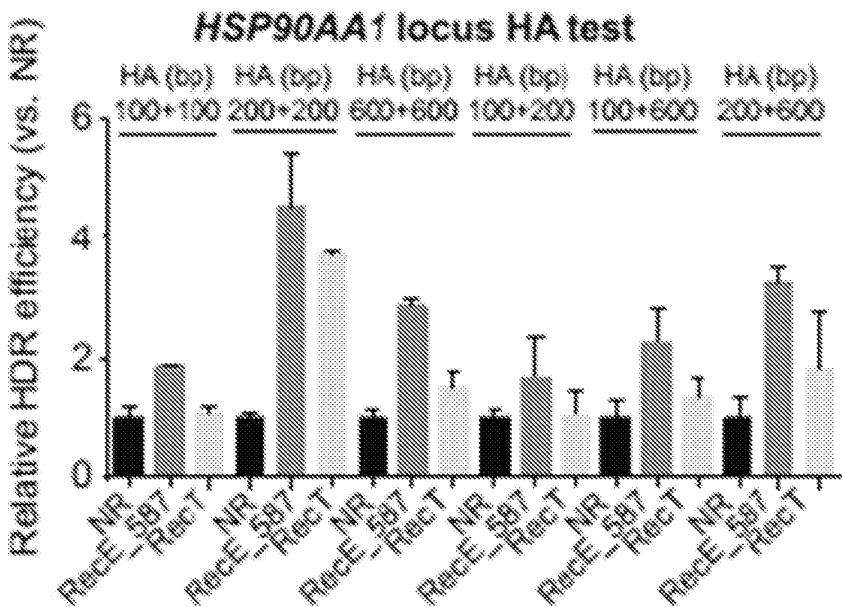


FIG. 7D

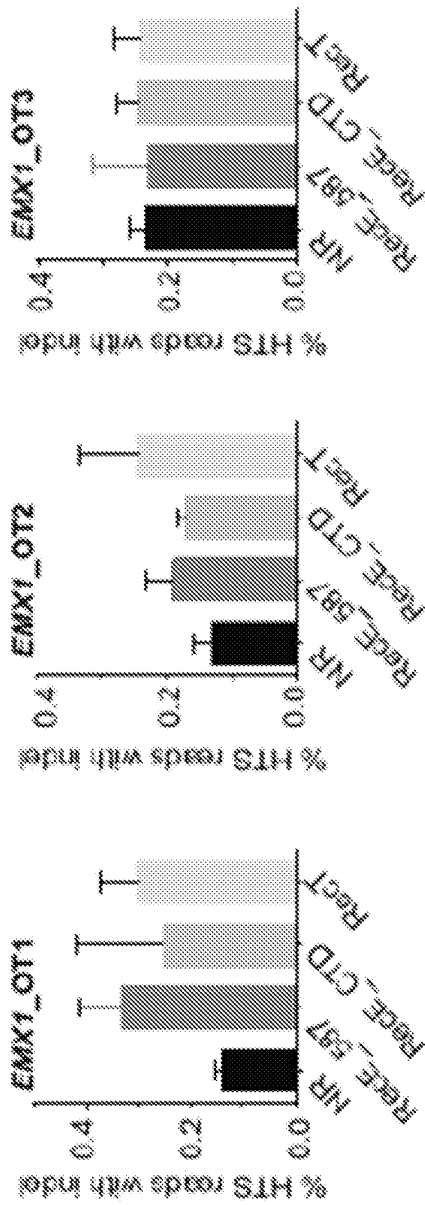


FIG. 8A

FIG. 8B

FIG. 8C

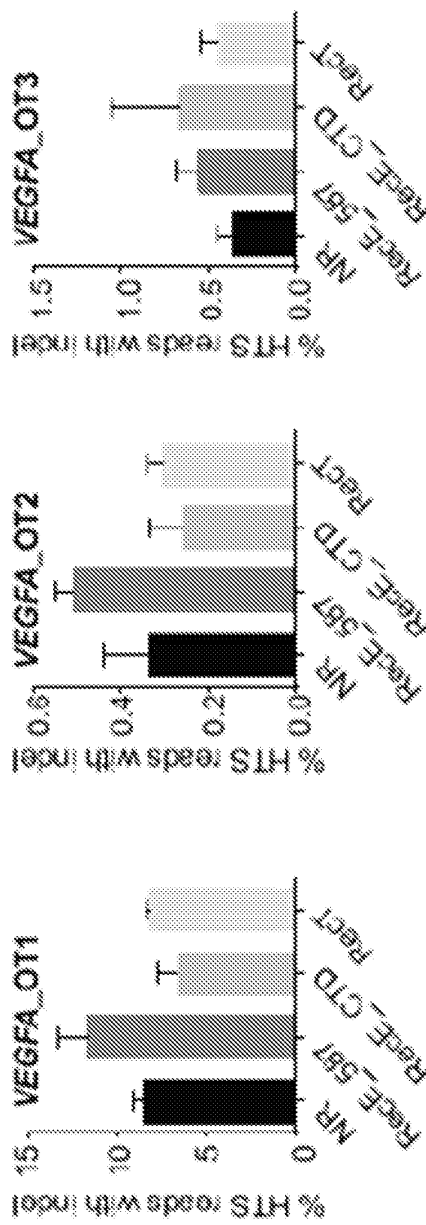


FIG. 8D

FIG. 8E

FIG. 8F

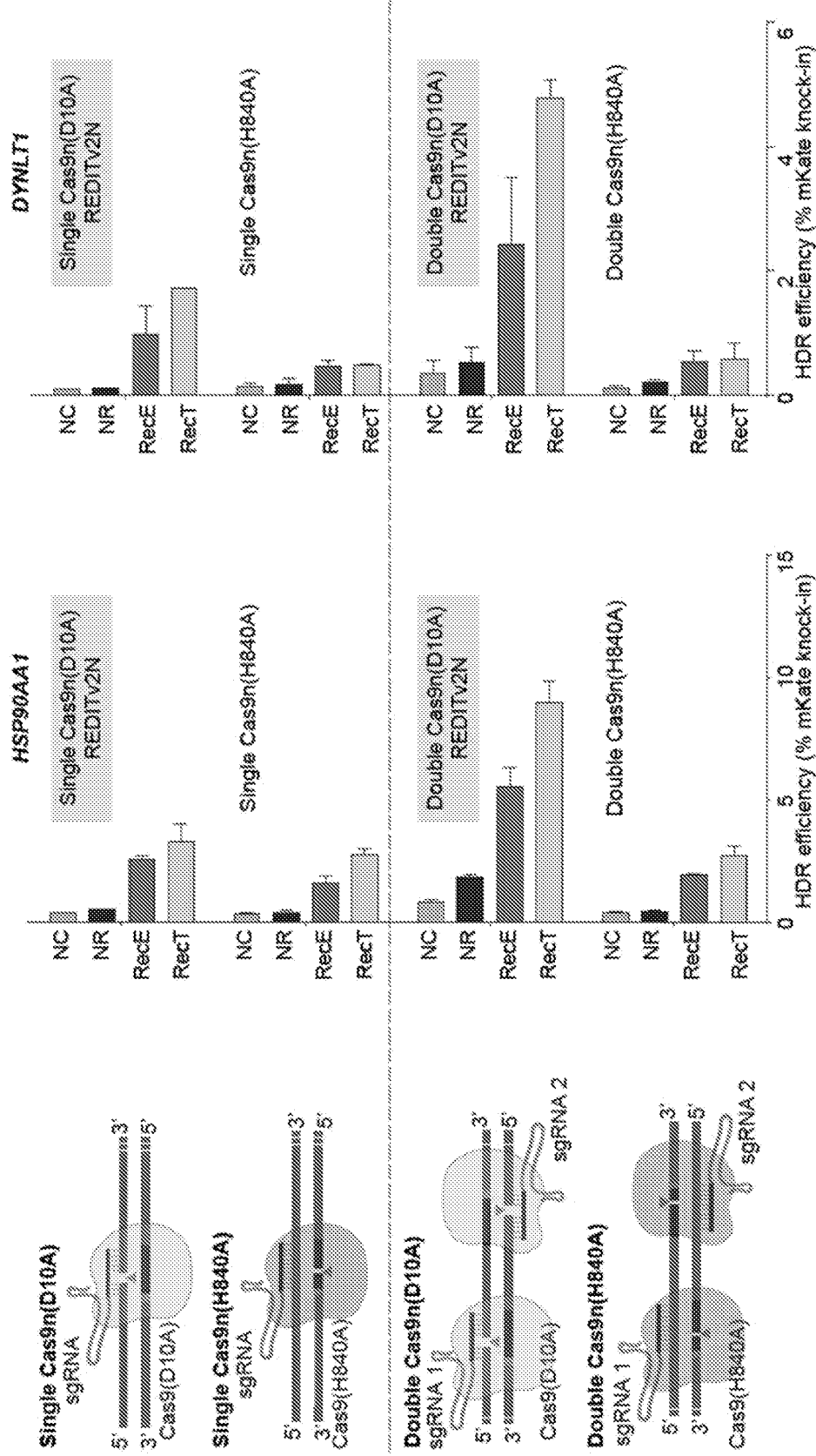


FIG. 9A

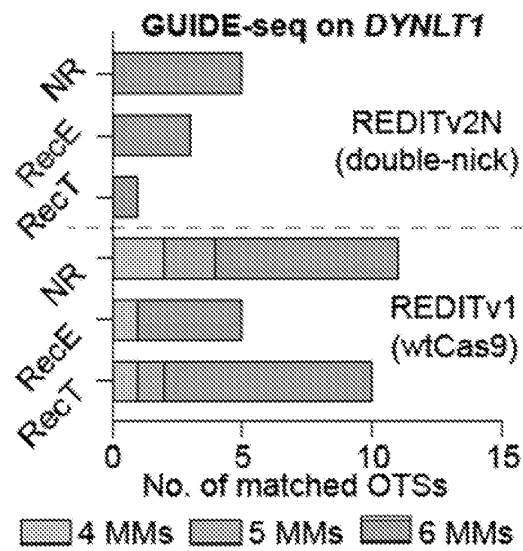


FIG. 9B

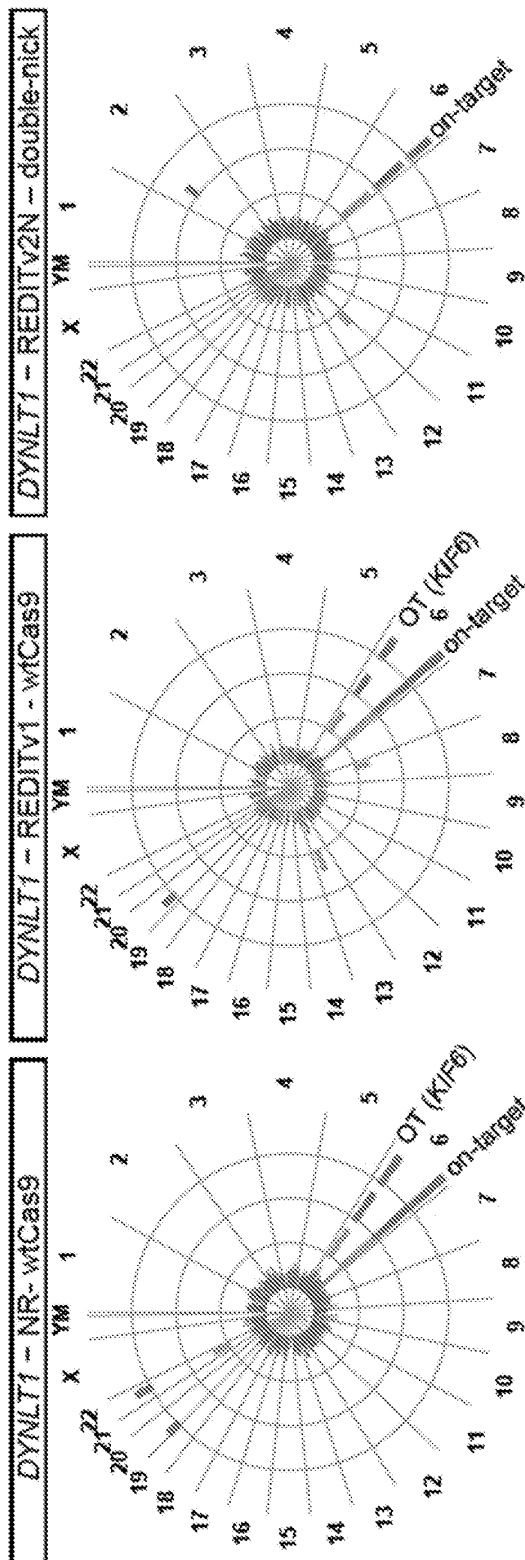


FIG. 9C

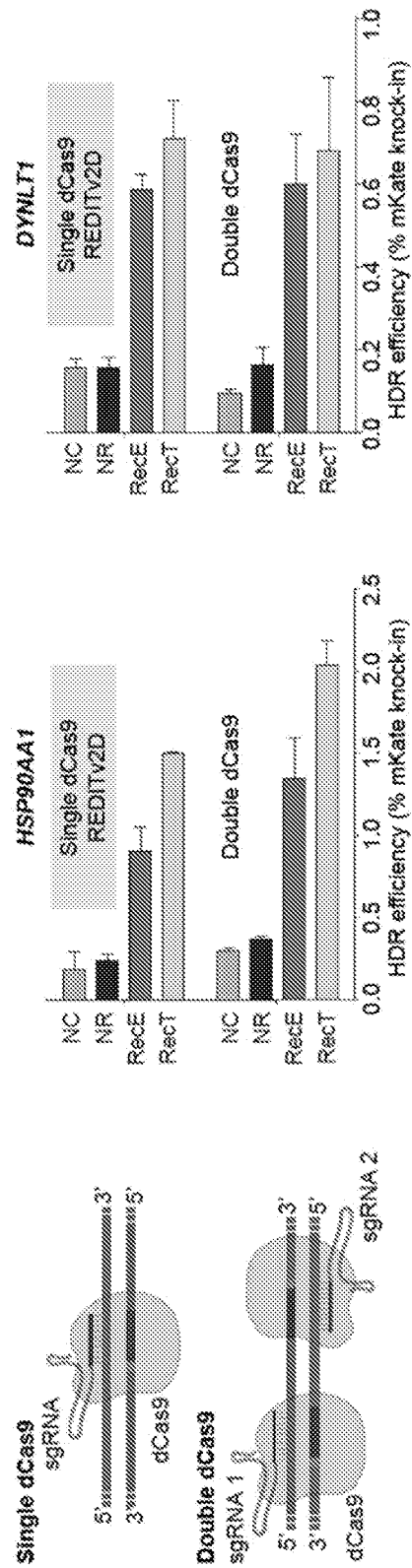


FIG. 9D

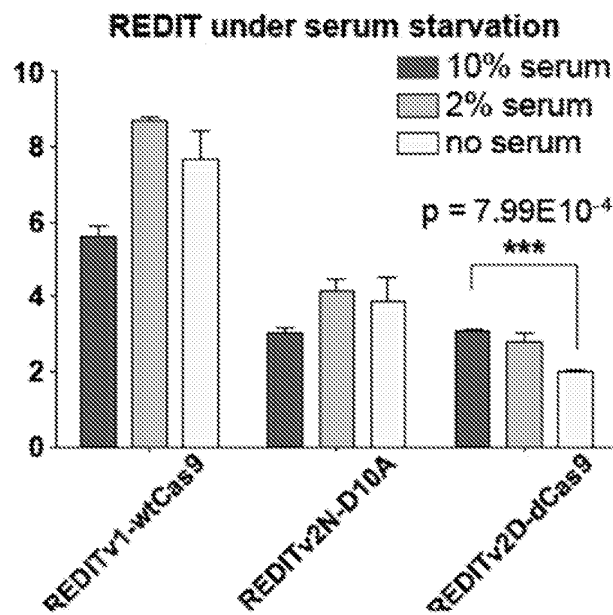


FIG. 9E

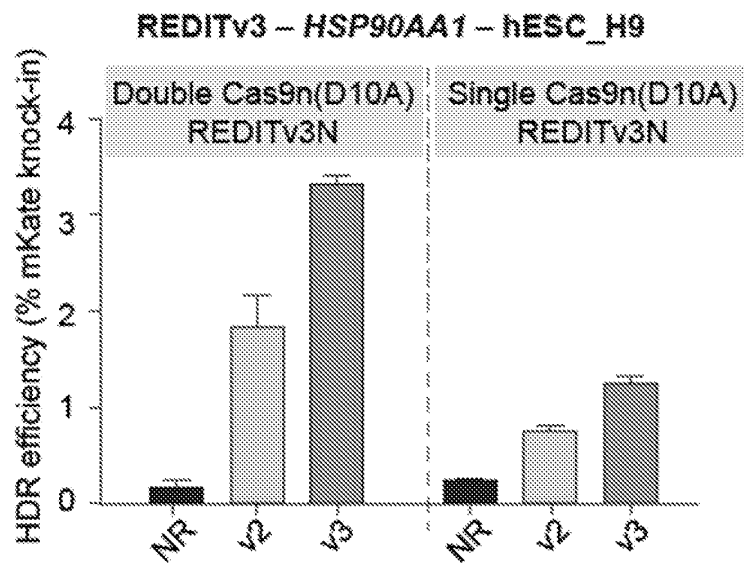
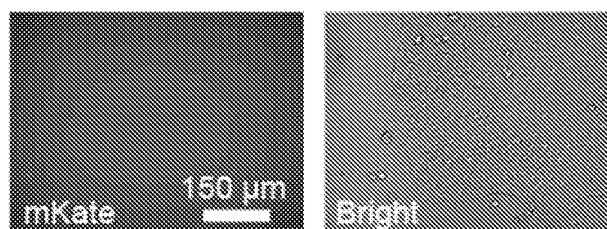


FIG. 9F

NR control – *HSP90AA1* – hESC_H9



REDITv3N – *HSP90AA1* – hESC_H9

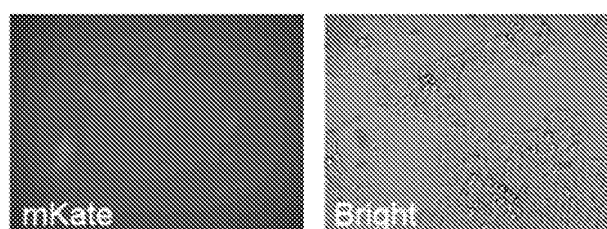


FIG. 9G

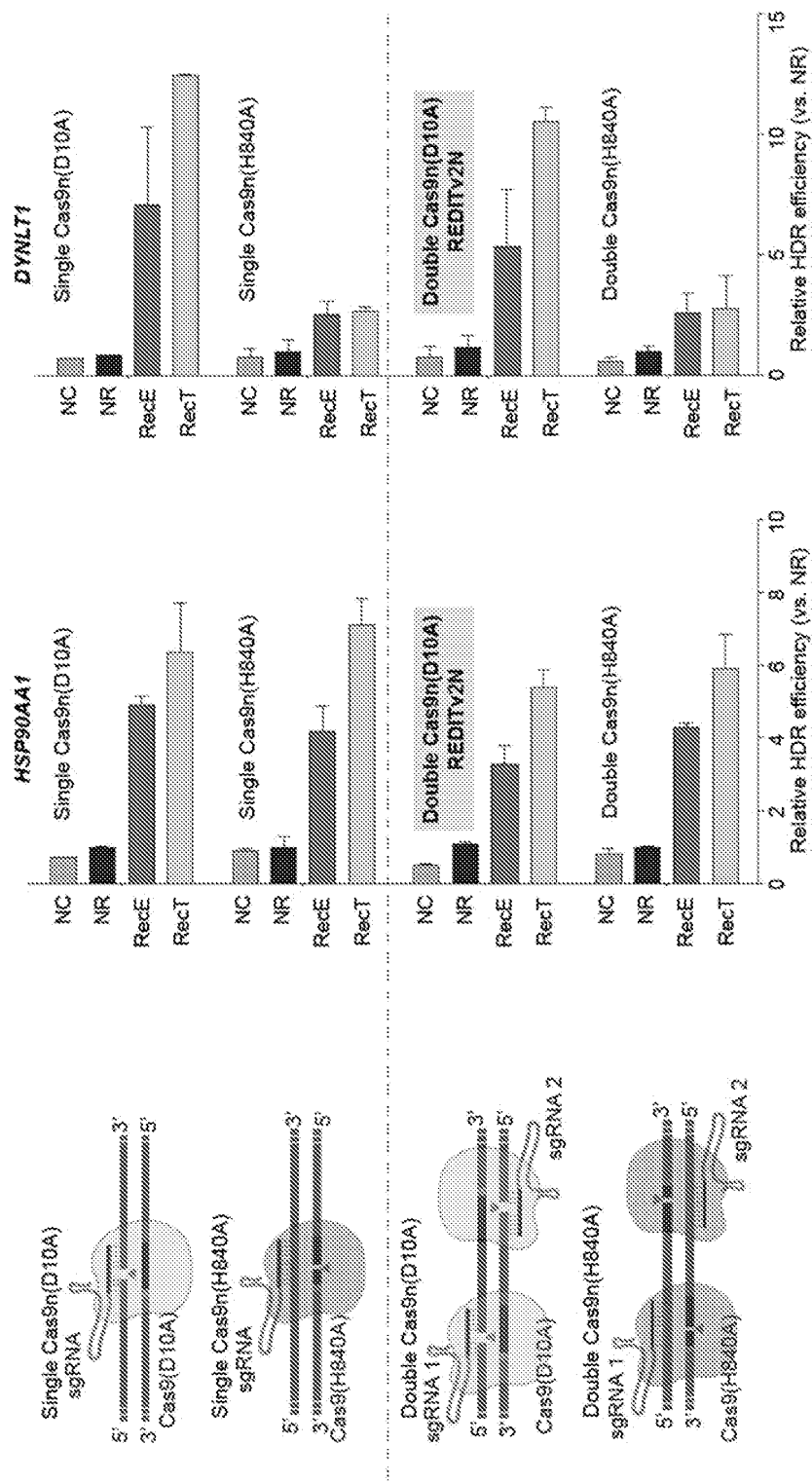


FIG. 10A

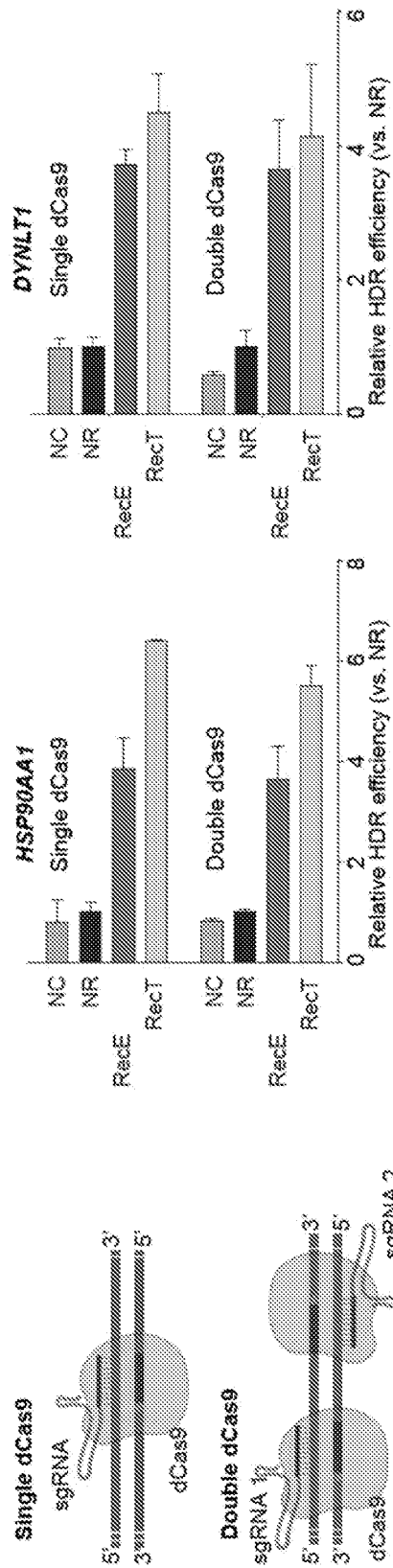


FIG. 10B

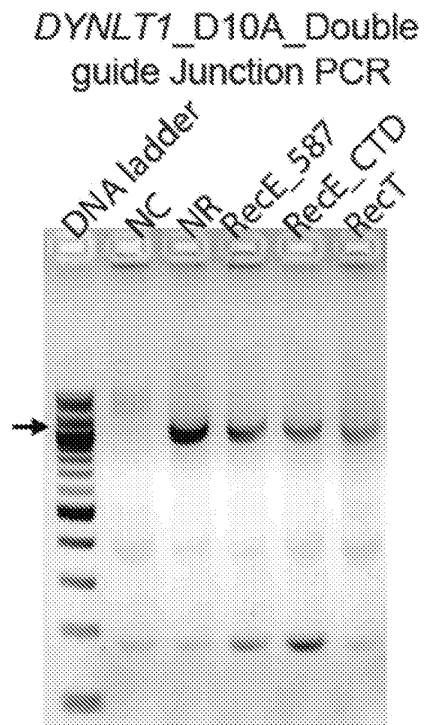


FIG. 11A

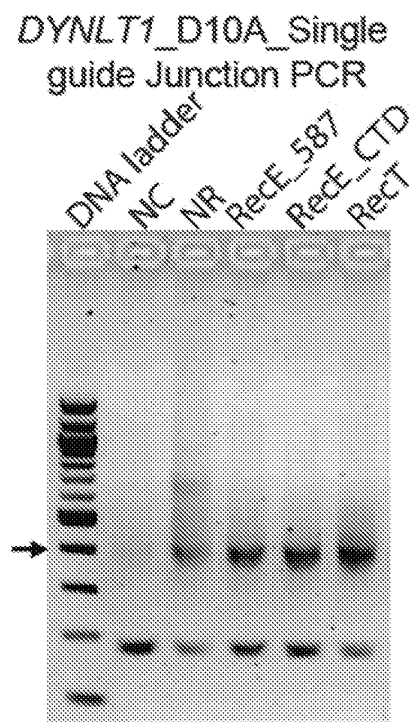


FIG. 11B

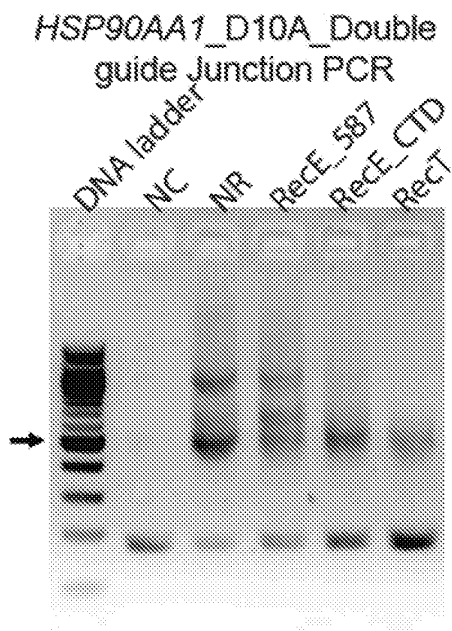


FIG. 11C

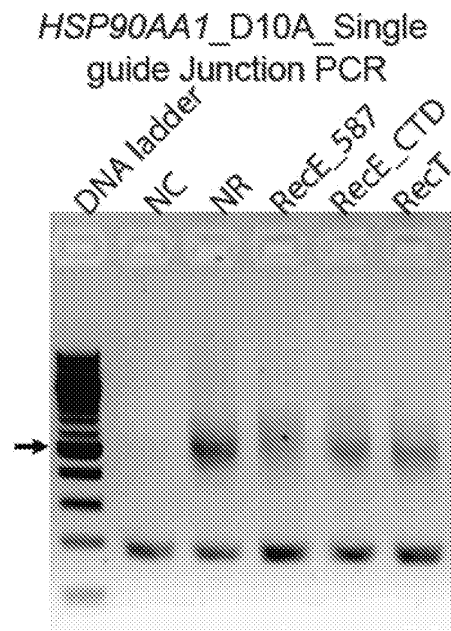
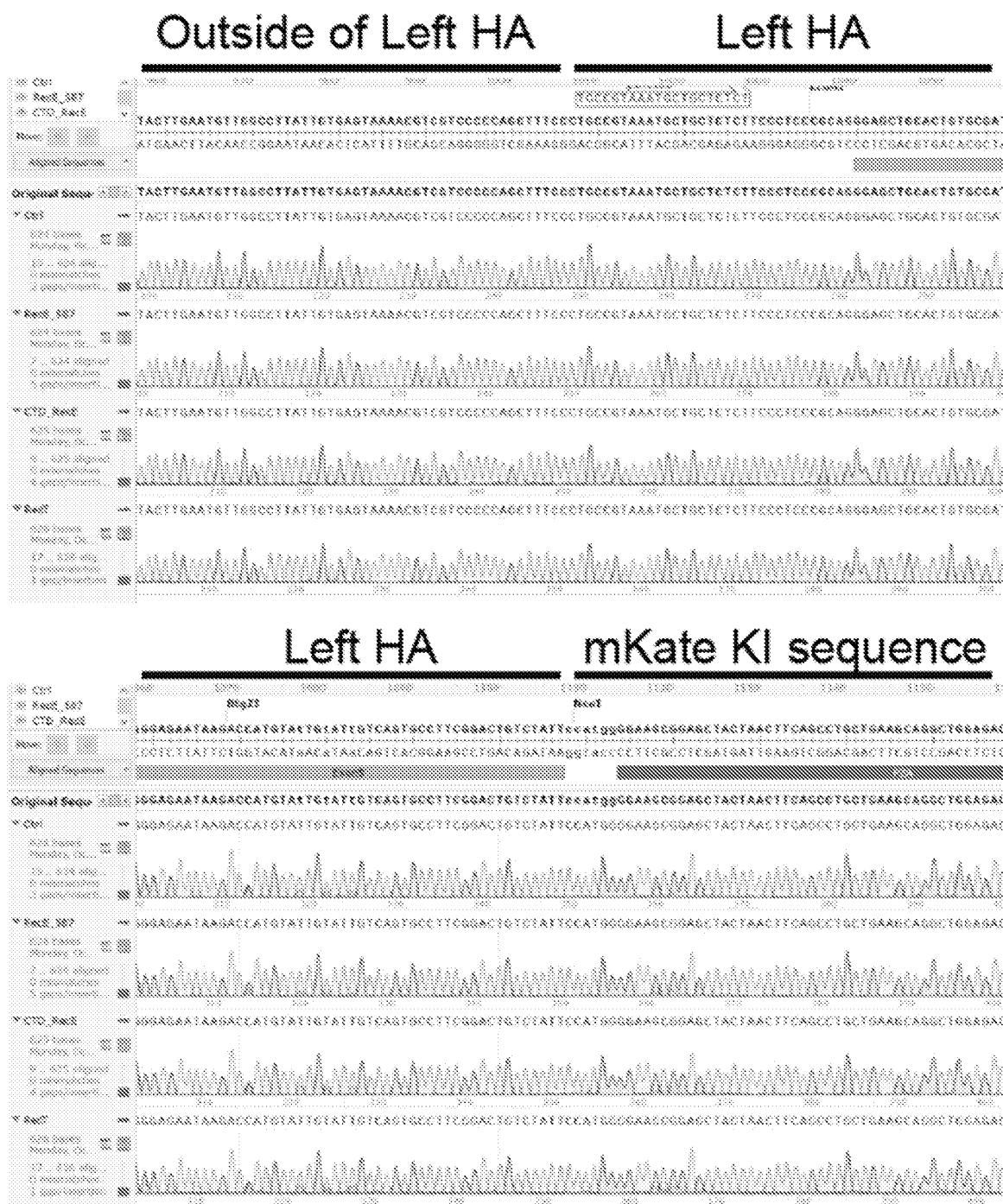
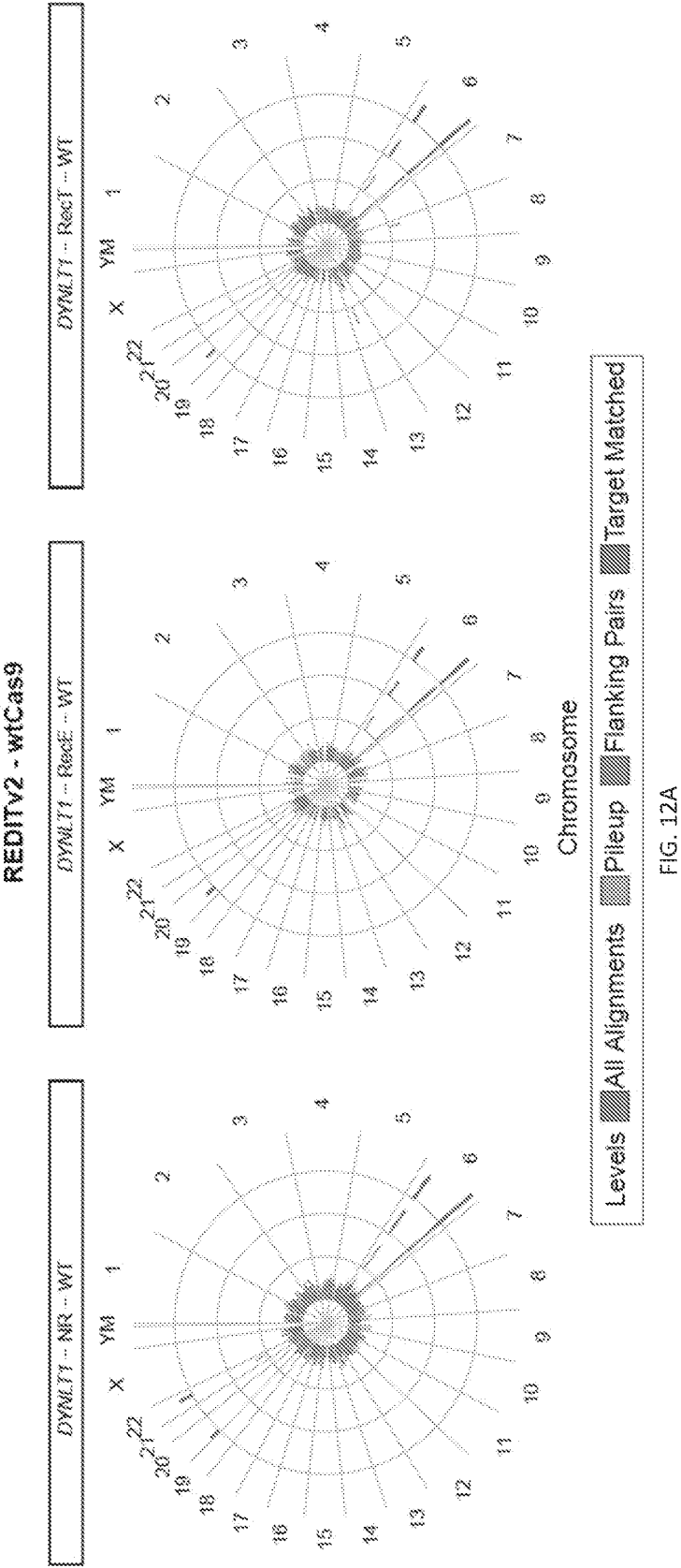


FIG. 11D





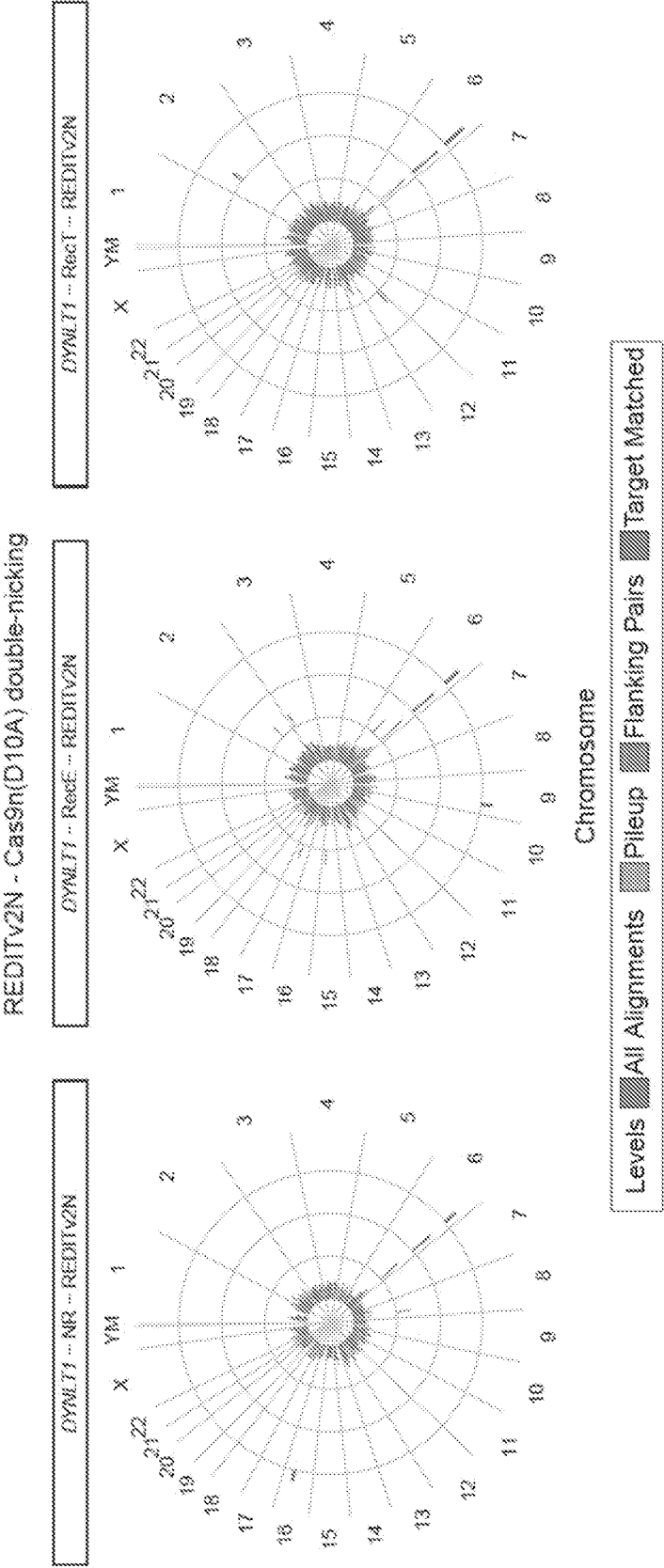


FIG. 12B

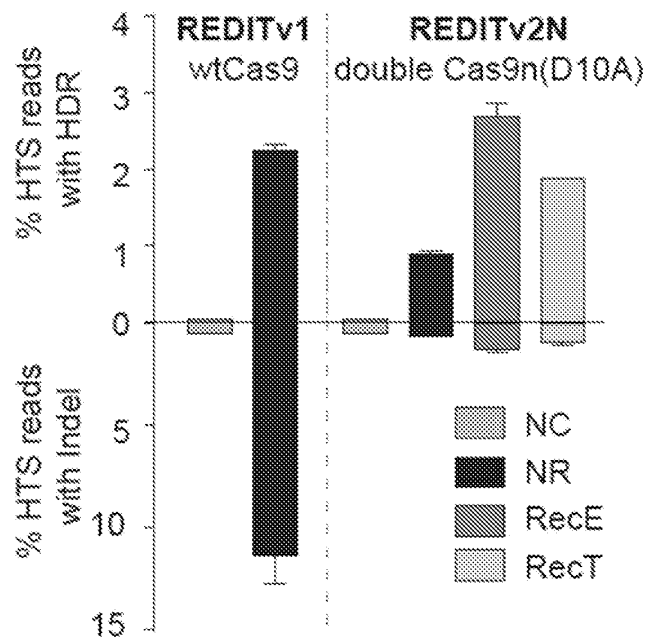


FIG. 12C

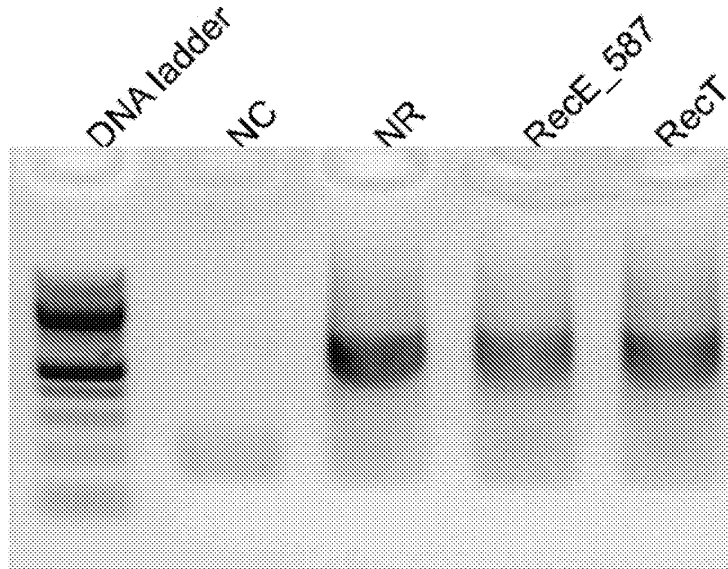


FIG. 13A

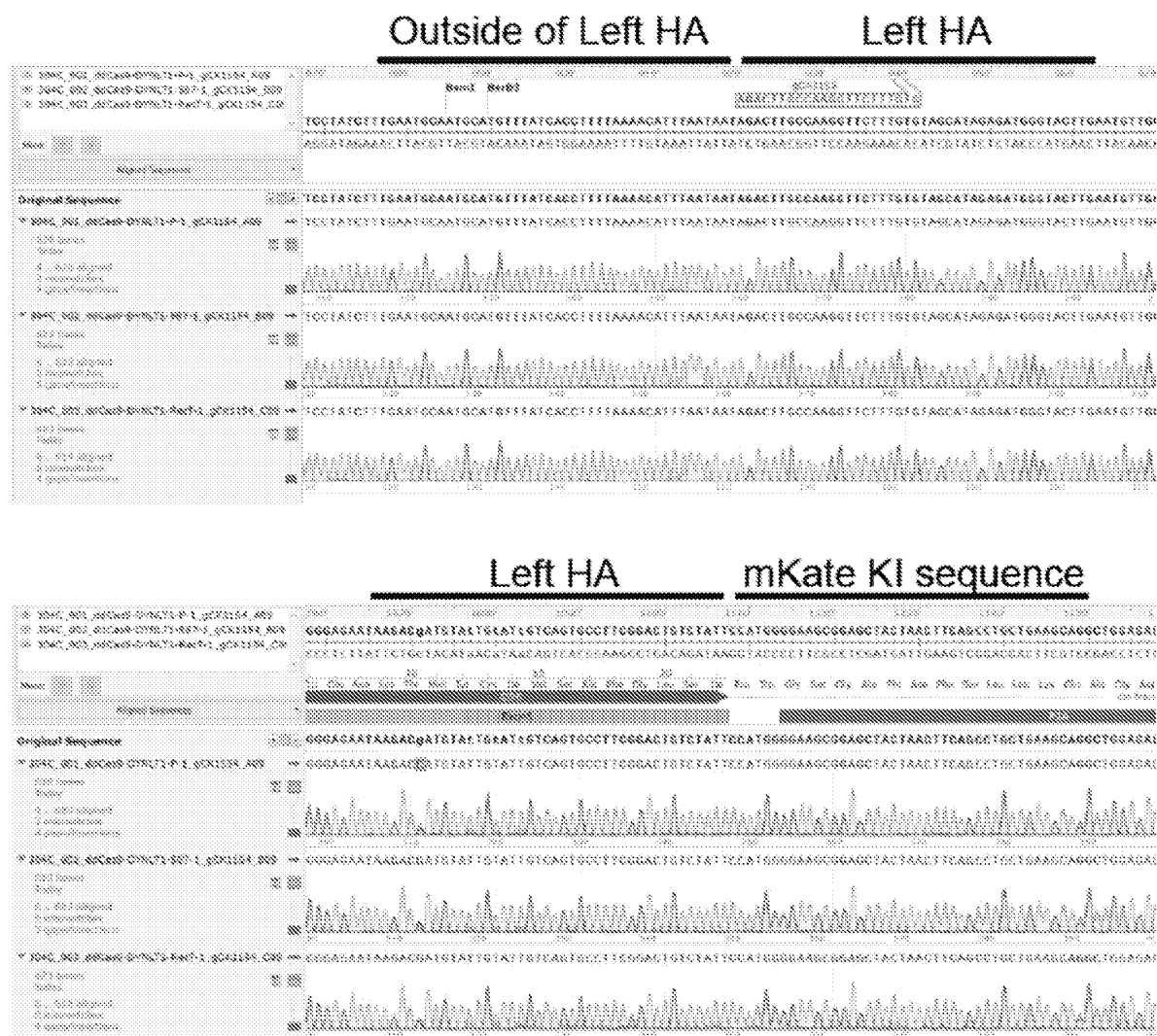


FIG. 13B

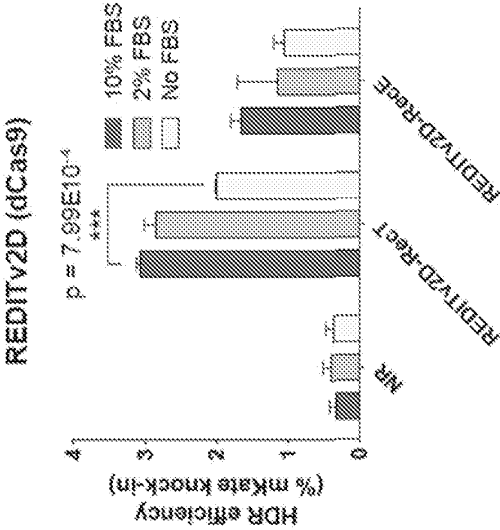


FIG. 14C

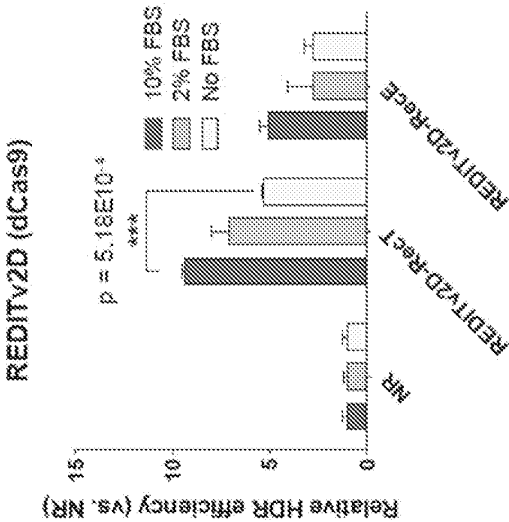


FIG. 14F

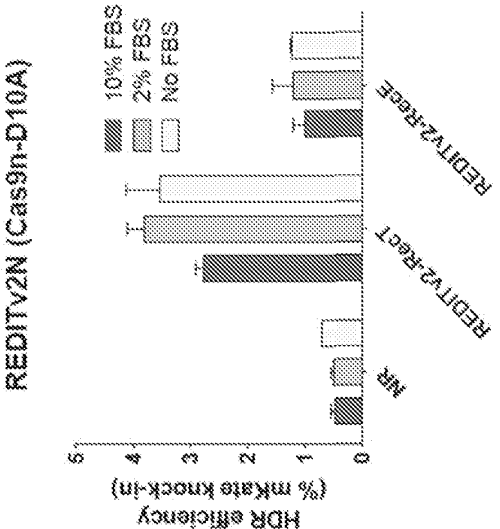


FIG. 14B

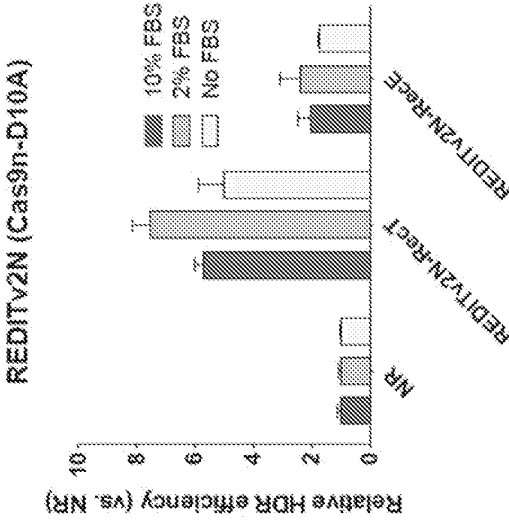


FIG. 14E

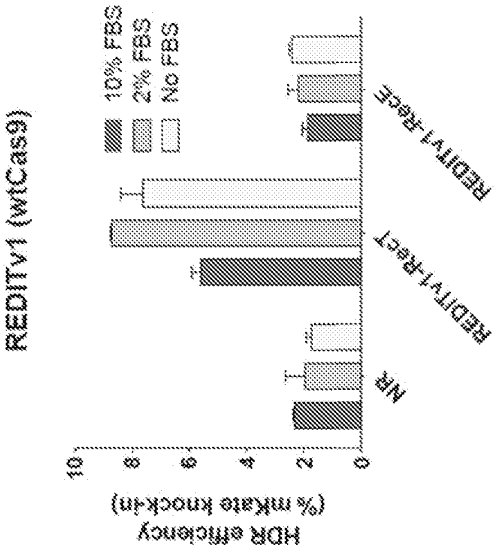


FIG. 14A

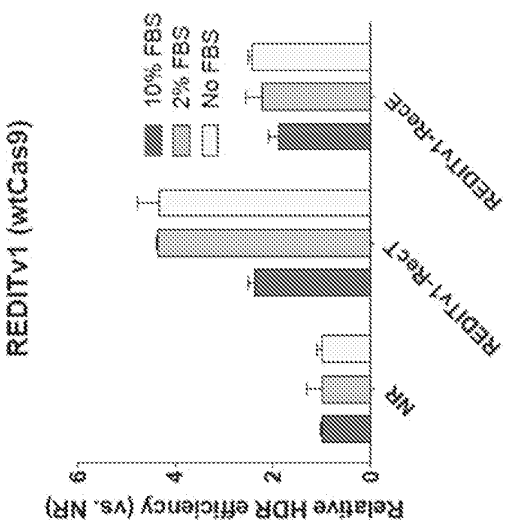


FIG. 14D

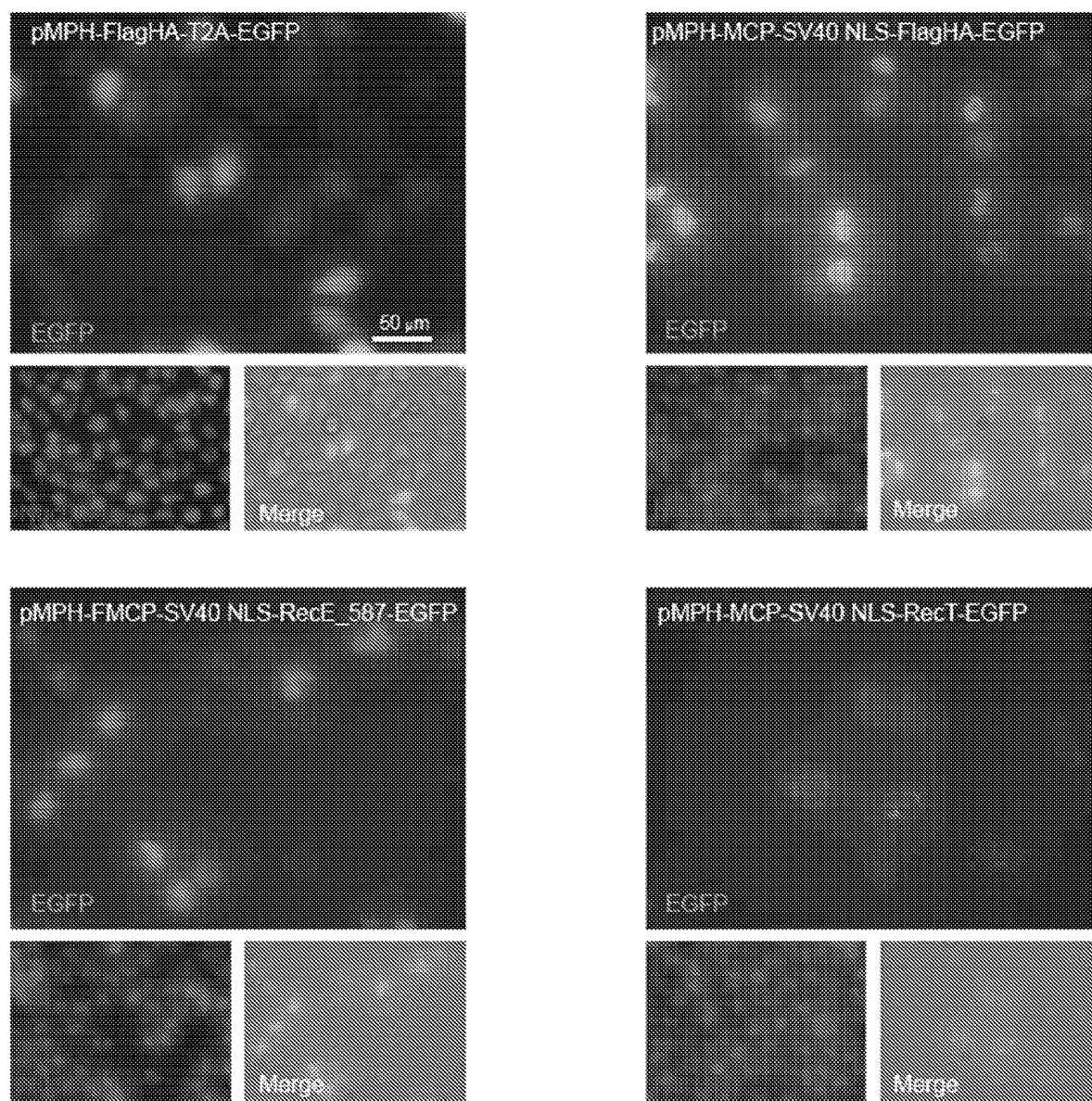


FIG. 15

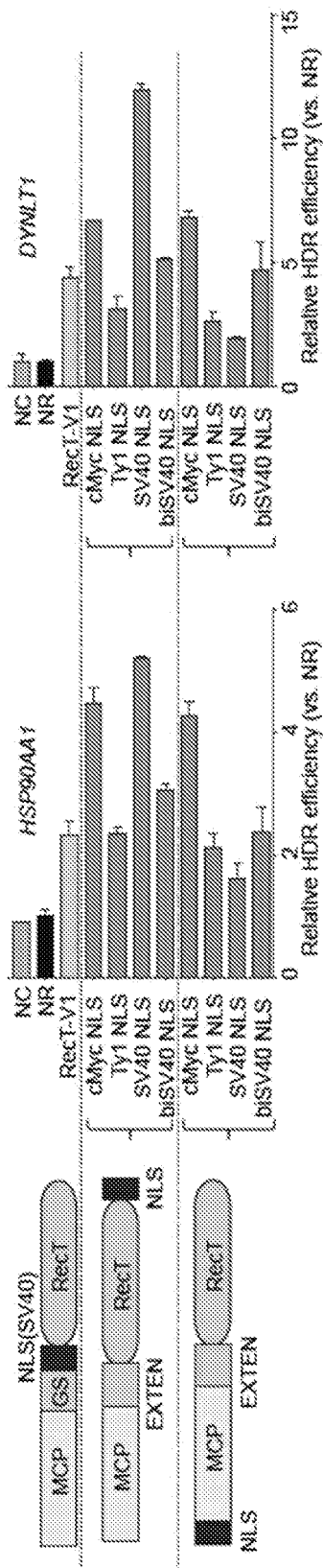


FIG. 16A

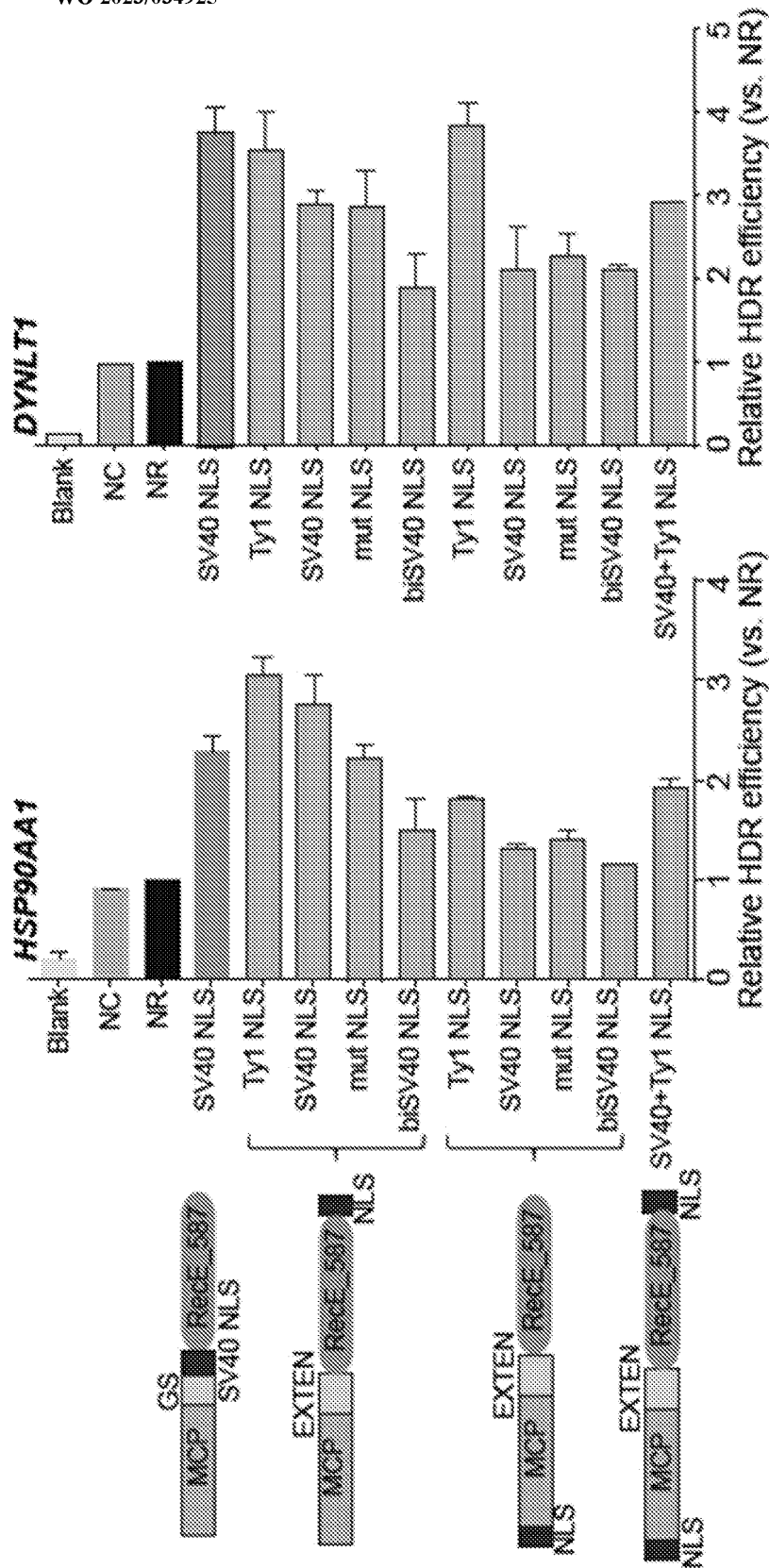
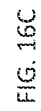
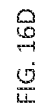


FIG. 16B





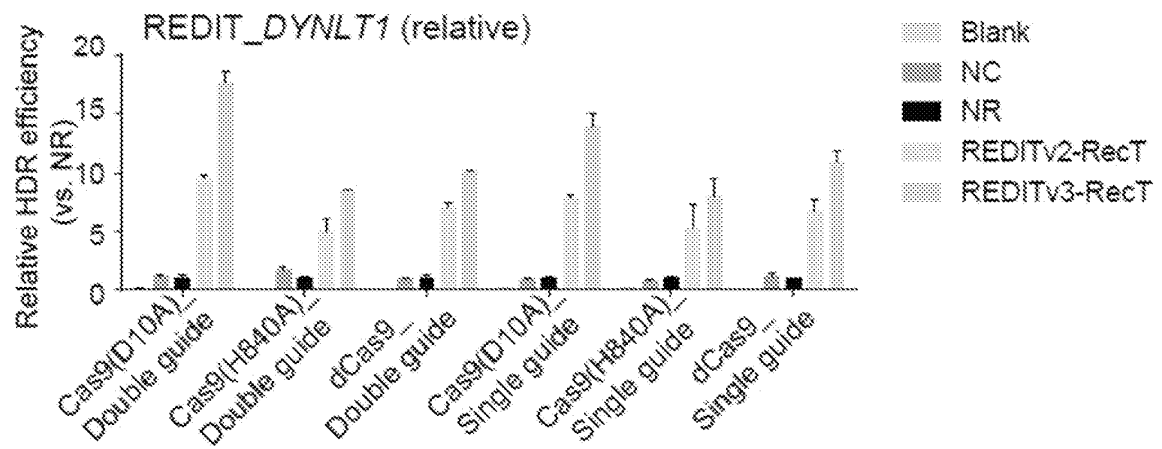


FIG. 17A

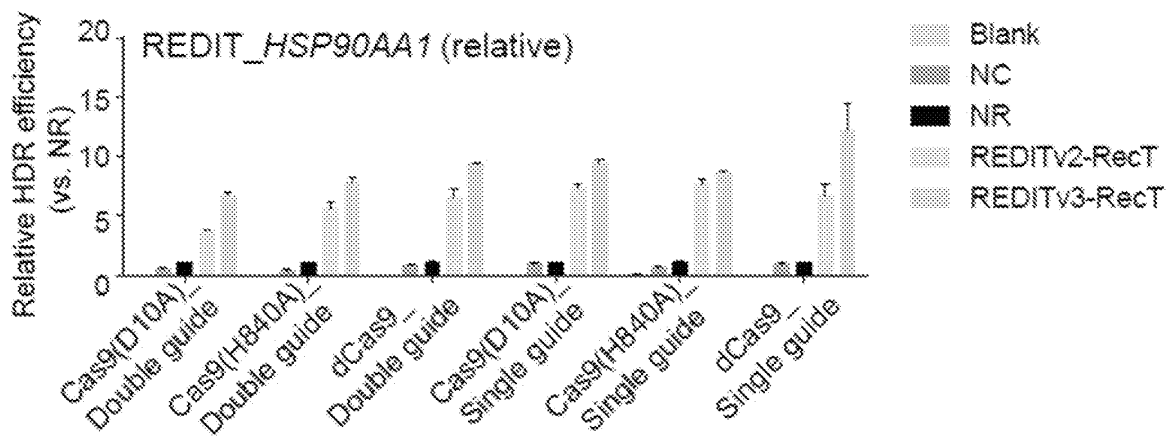


FIG. 17B

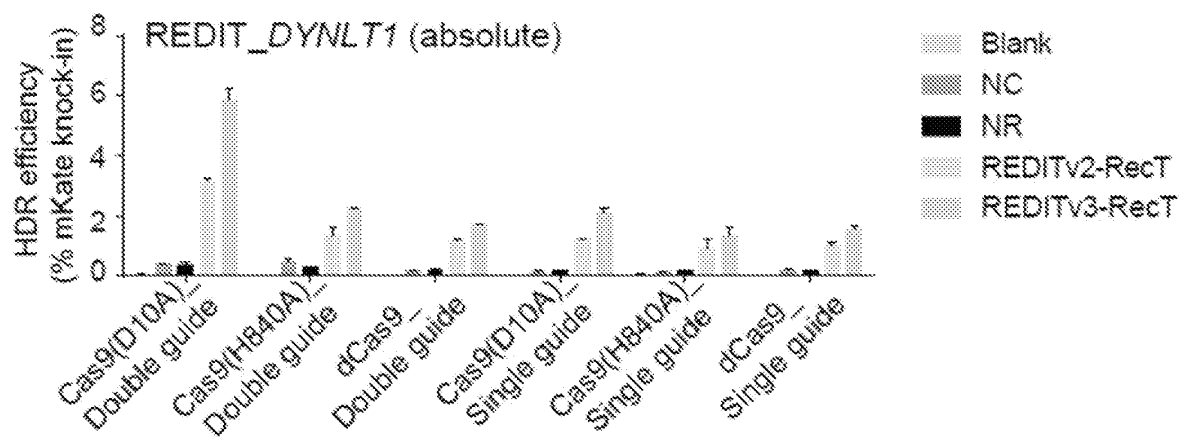


FIG. 17C

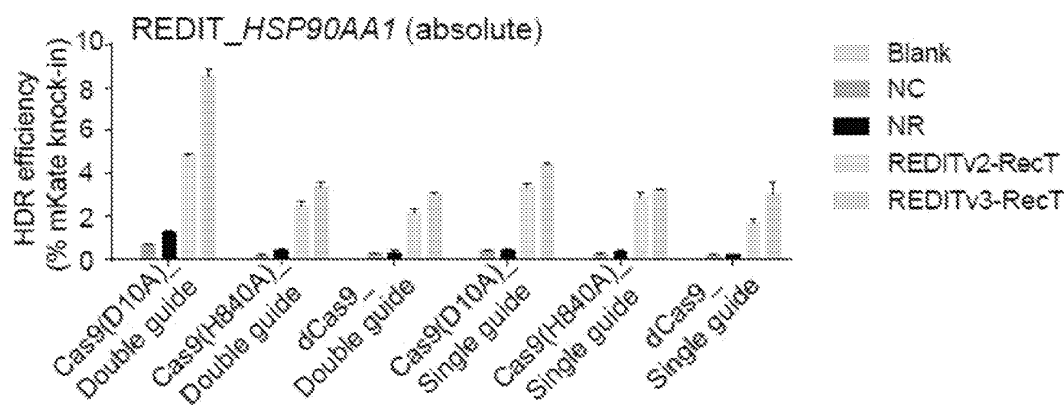


FIG. 17D

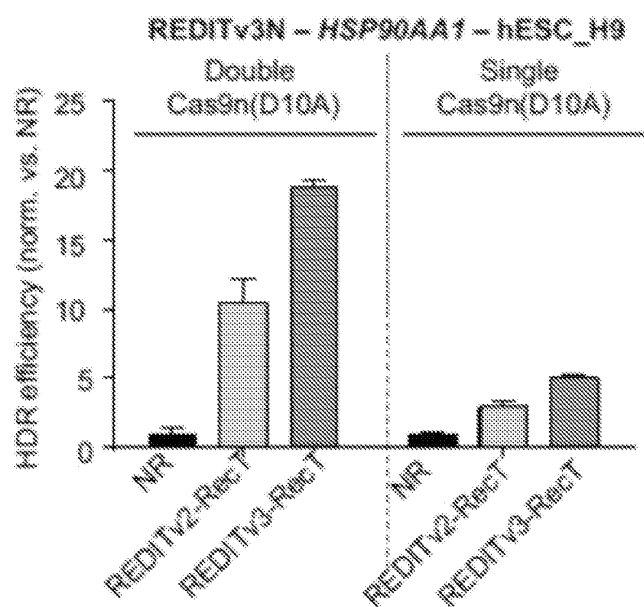


FIG. 18

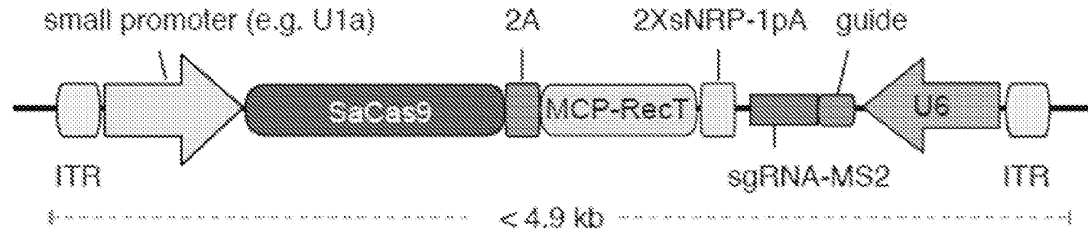


FIG. 19A

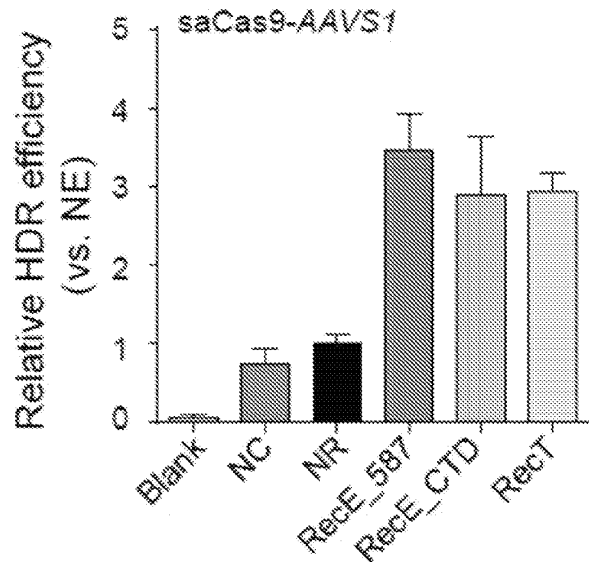


FIG. 19B

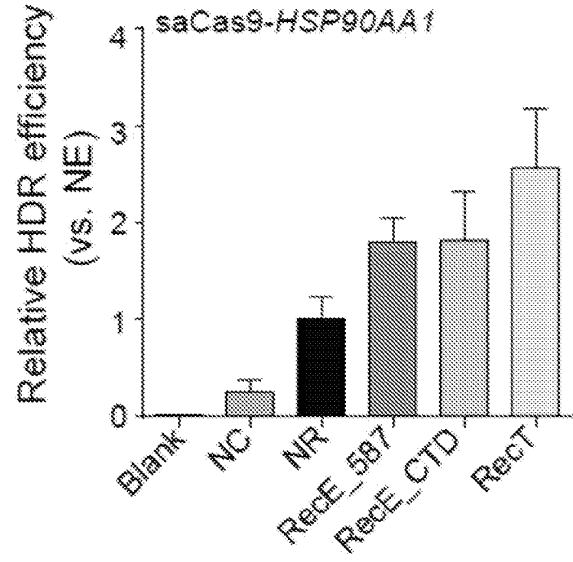


FIG. 19C

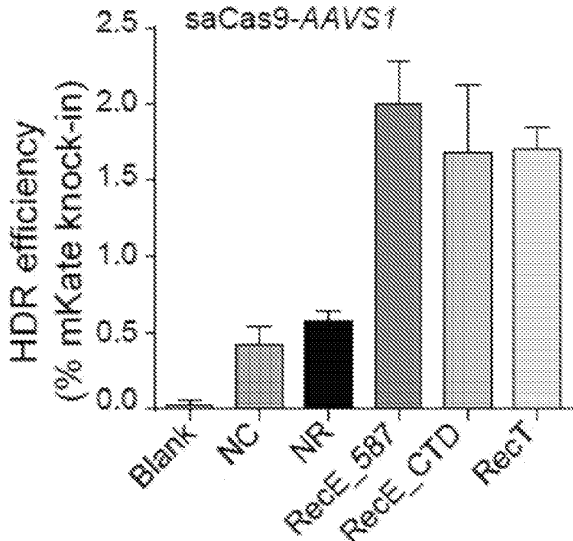


FIG. 19D

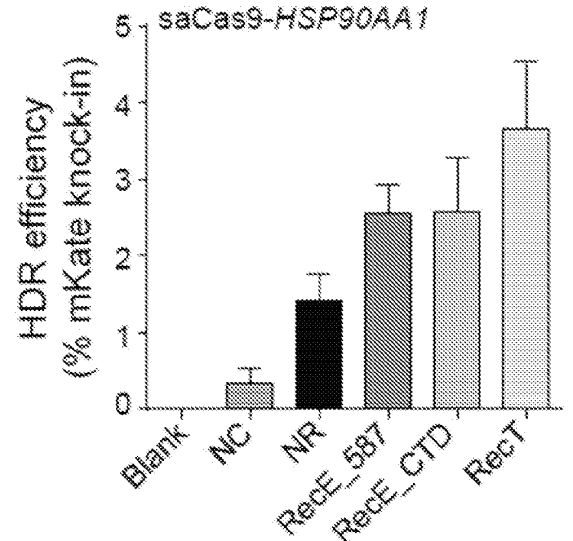


FIG. 19E

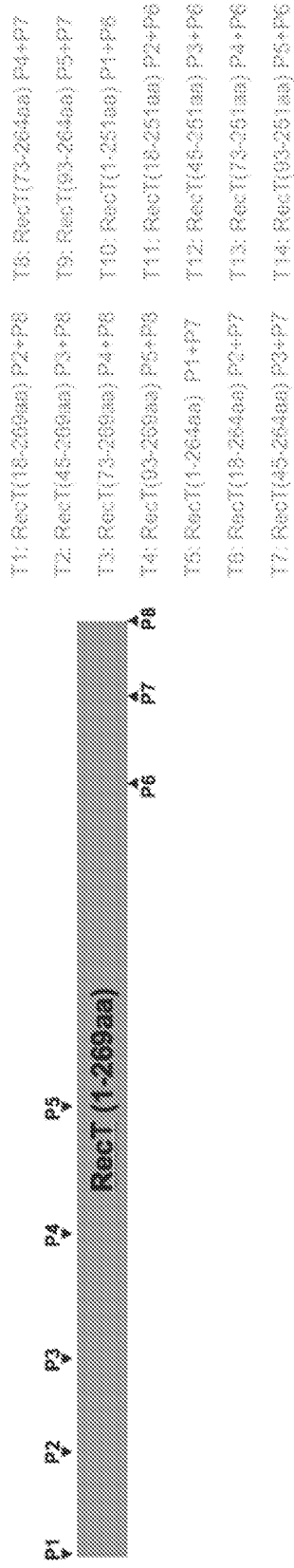


FIG. 20A

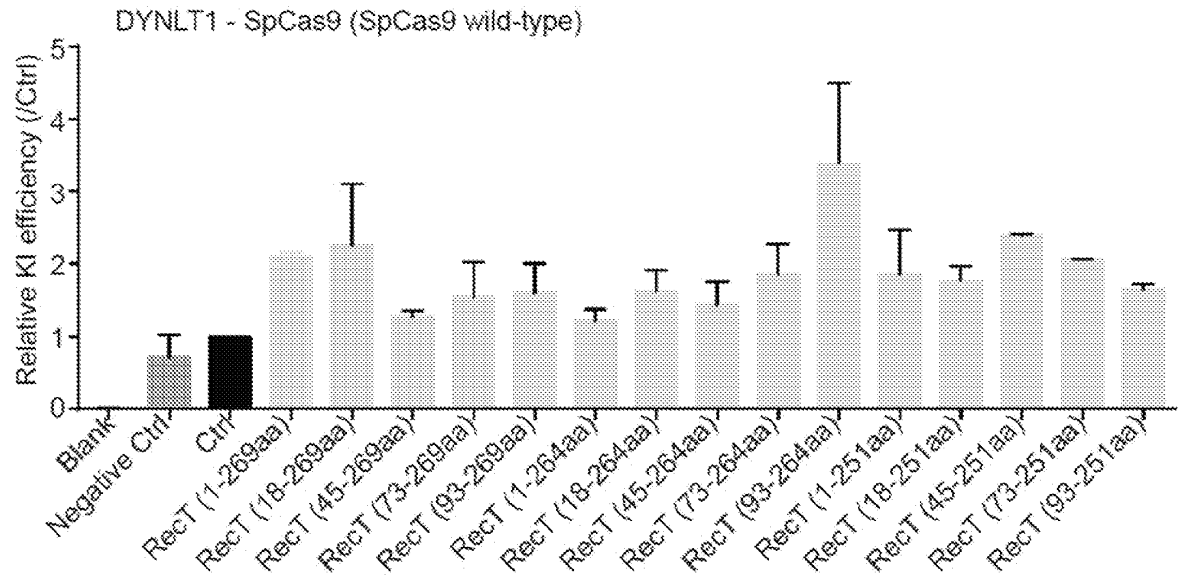


FIG. 20B

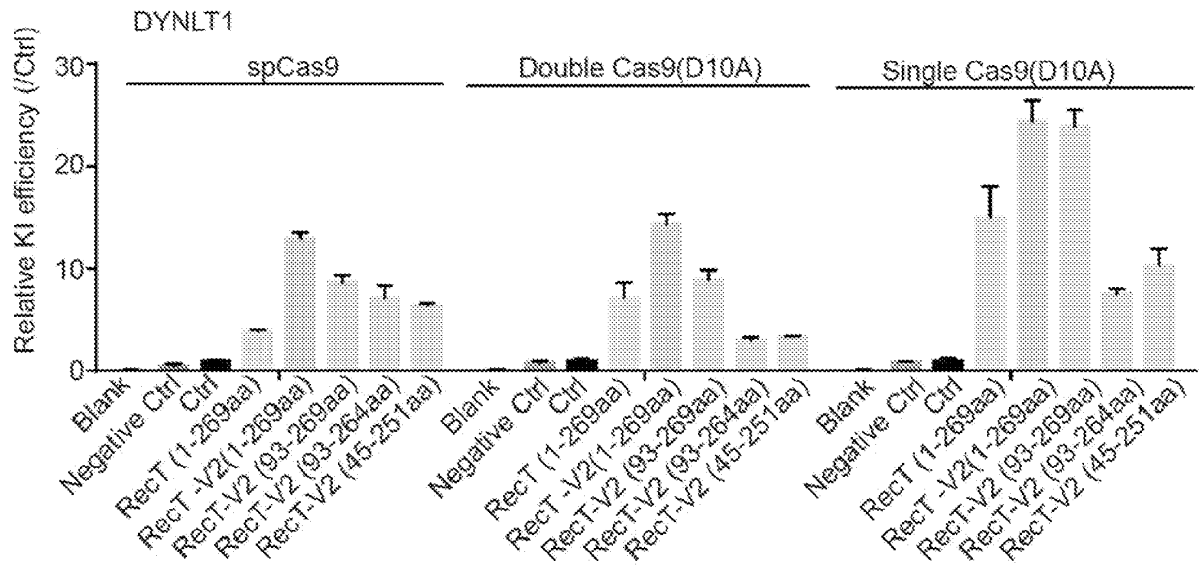


FIG. 20C

T15: RecE(61-260aa) P2+P8	T22: RecE(120-235aa) P3+P6
T16: RecE(120-280aa) P3+P9	T23: RecE(1-221aa) P1+P5
T17: RecE(1-280aa) P1+P7	T24: RecE(61-221aa) P2+P6
T18: RecE(61-260aa) P2+P7	T25: RecE(120-221aa) P3+P5
T19: RecE(120-260aa) P3+P7	T26: RecE(1-209aa) P1+P4
T20: RecE(1-235aa) P1+P6	T27: RecE(61-209aa) P2+P4
T21: RecE(61-235aa) P2+P6	T28: RecE(120-209aa) P3+P4



FIG. 21A

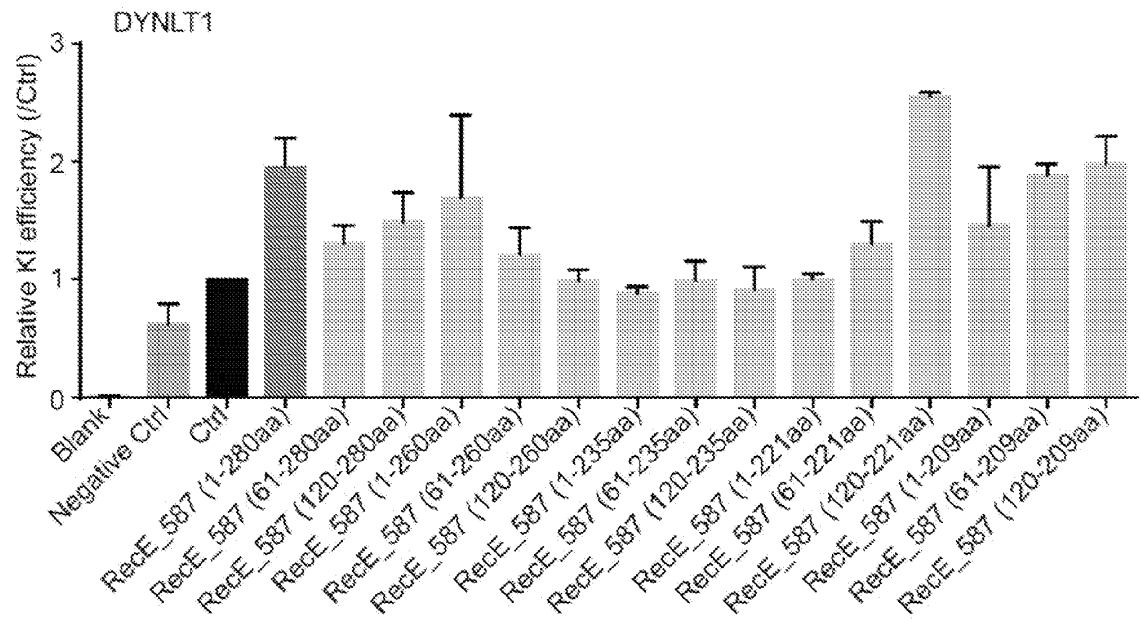


FIG. 21B

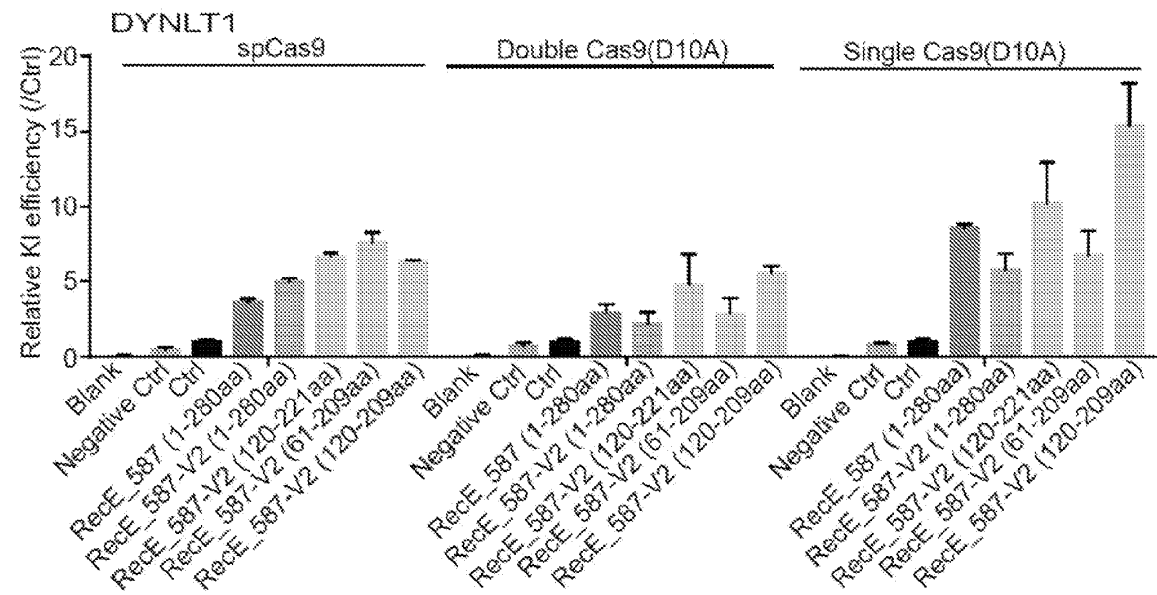


FIG. 21C

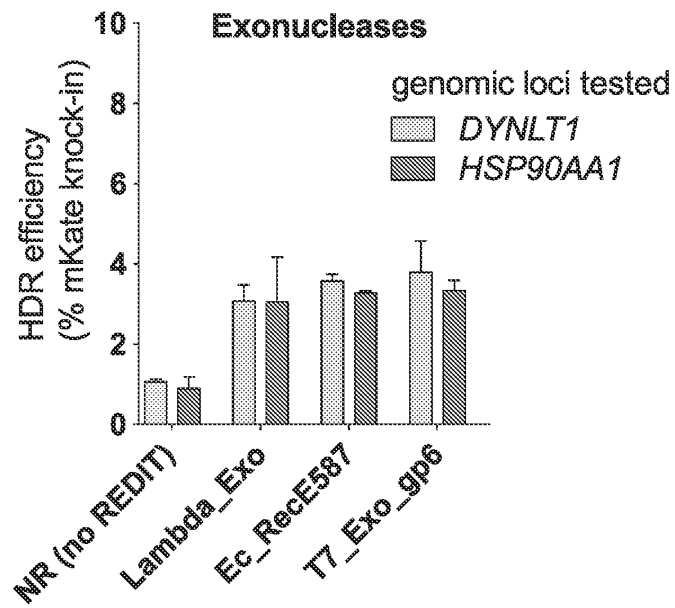


FIG. 22A

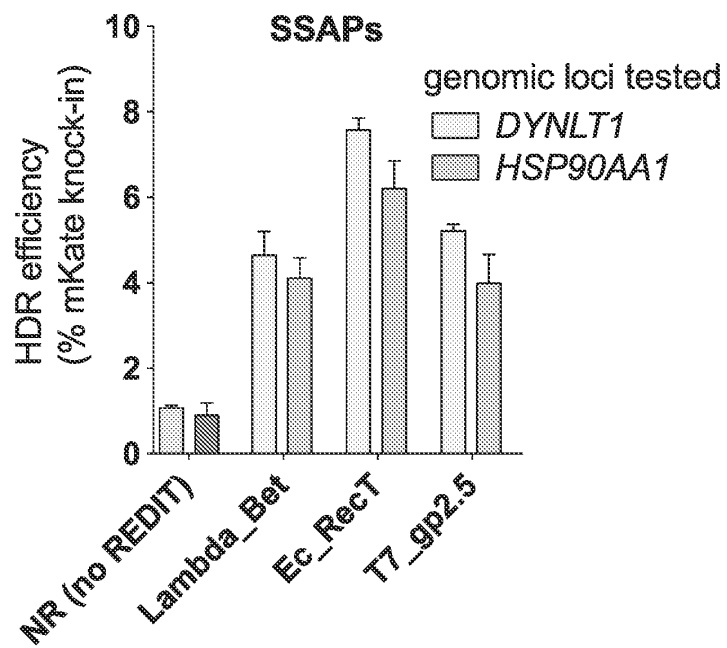


FIG. 22B

boxB-N22 recruitment system

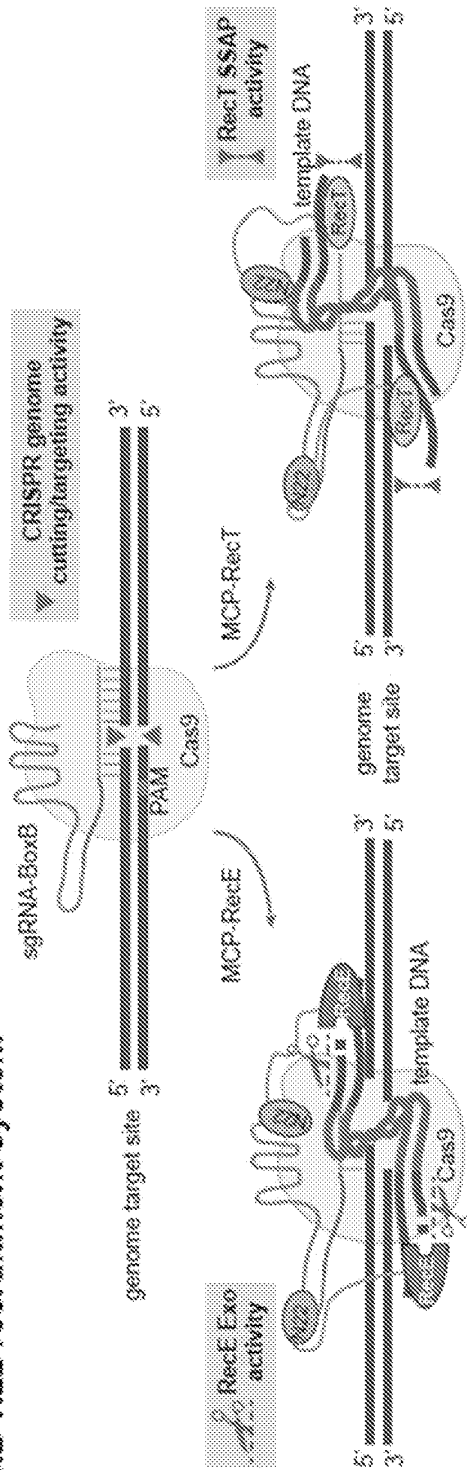


FIG. 23A

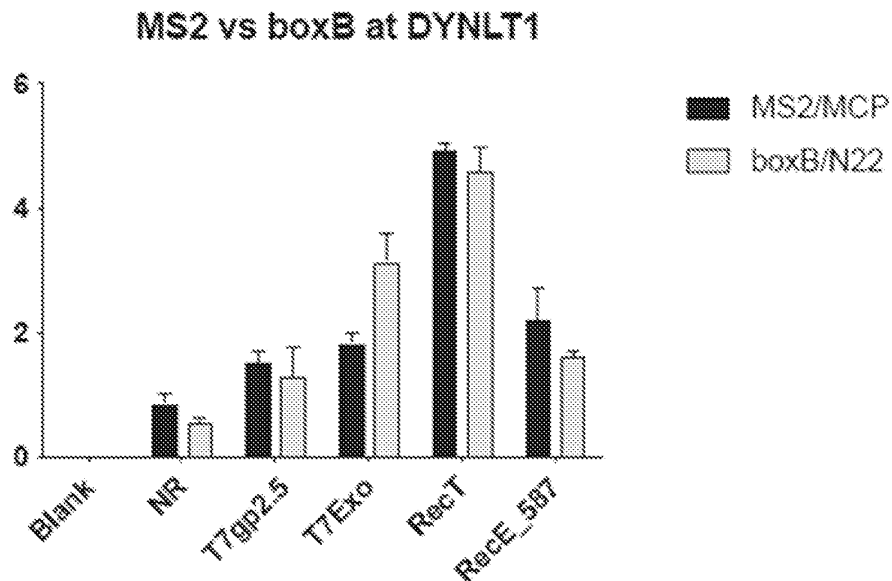


FIG. 23B

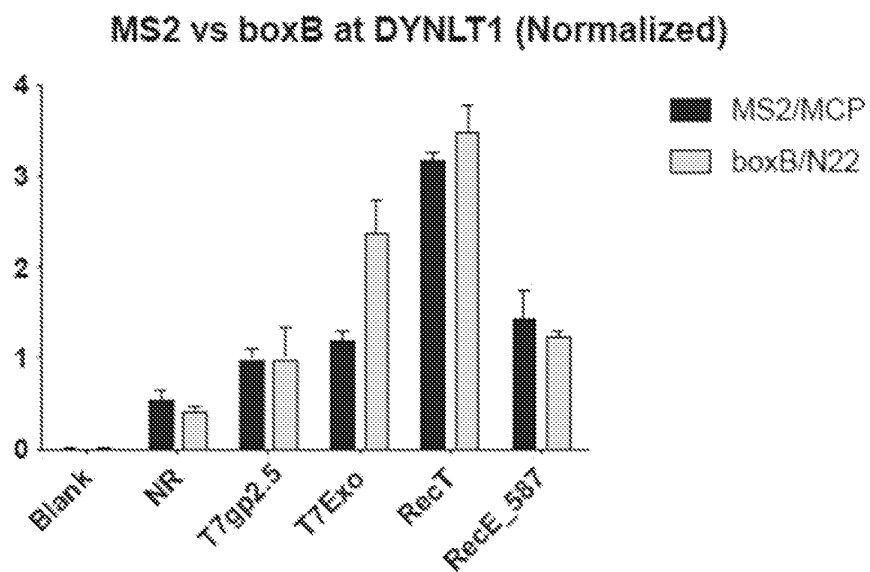


FIG. 23C

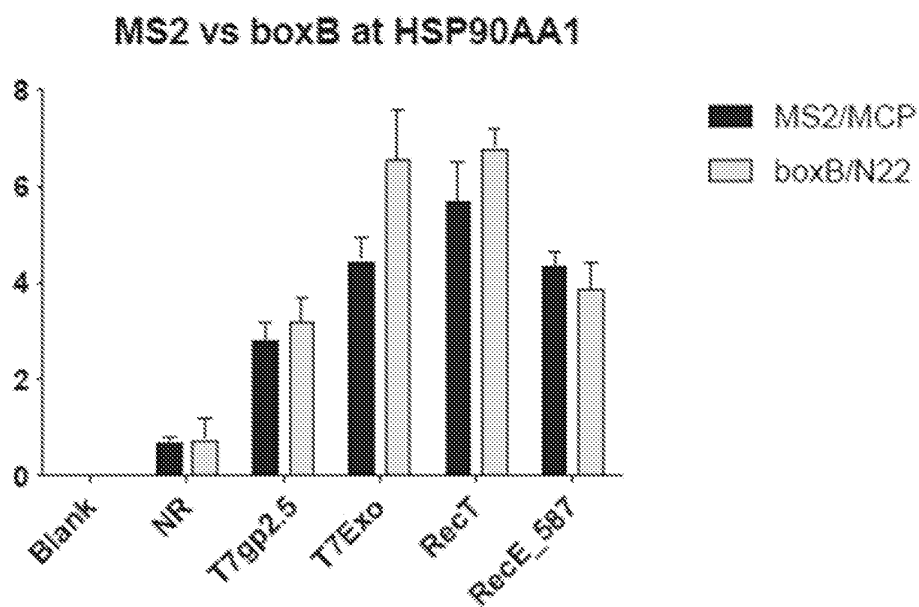


FIG. 23D

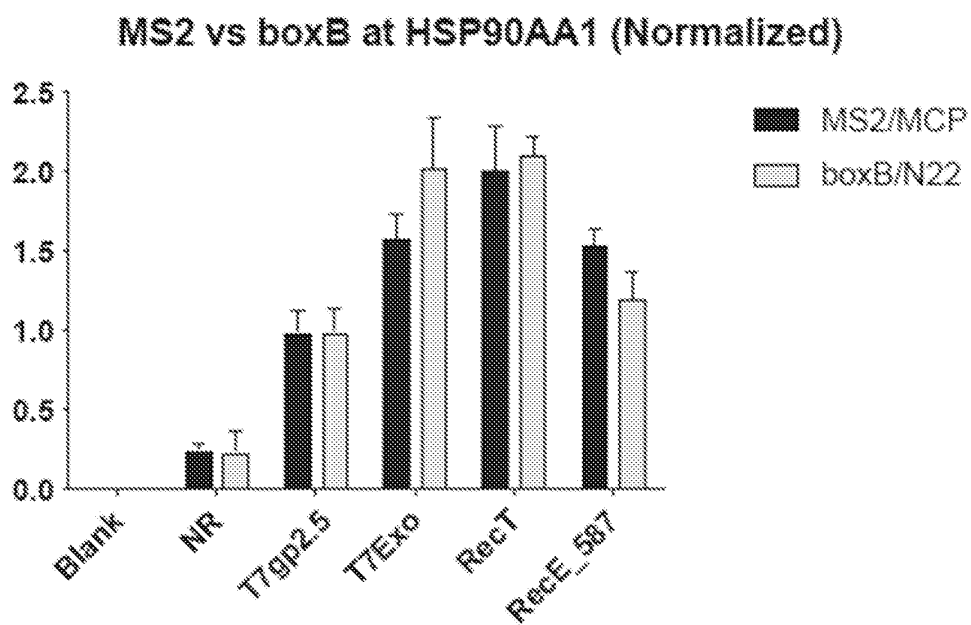


FIG. 23E

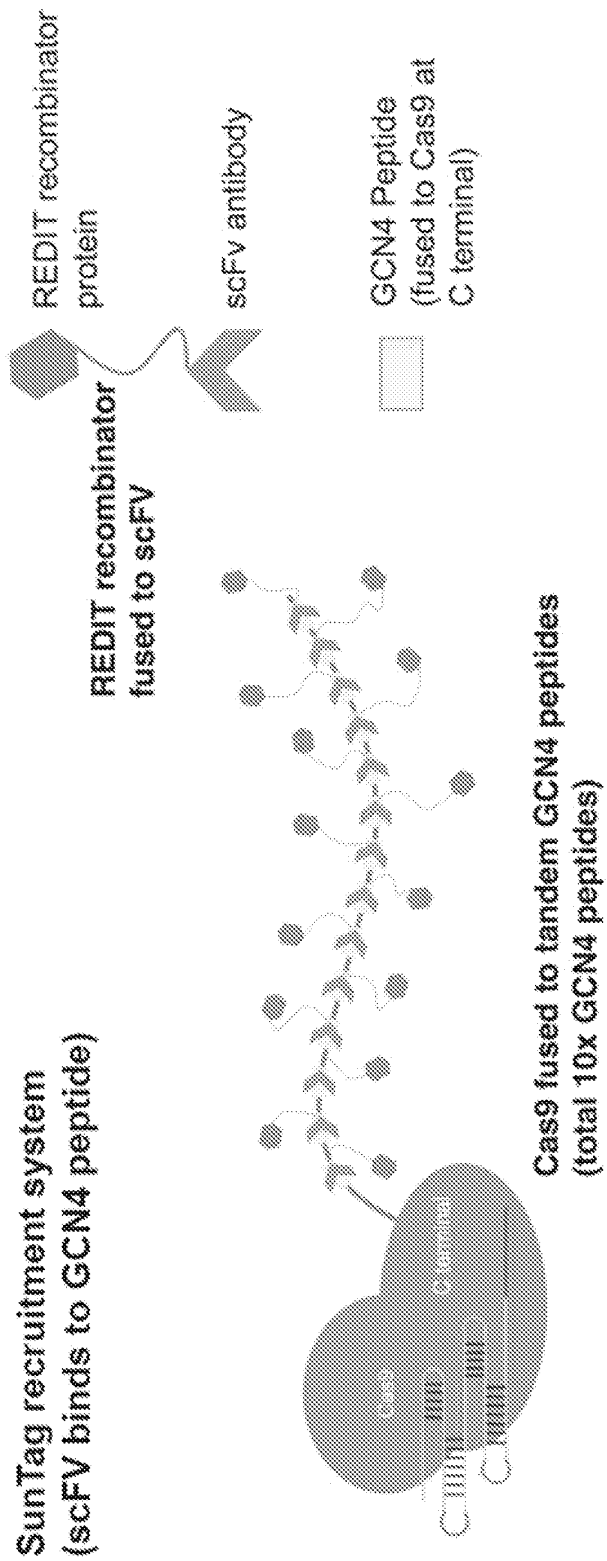
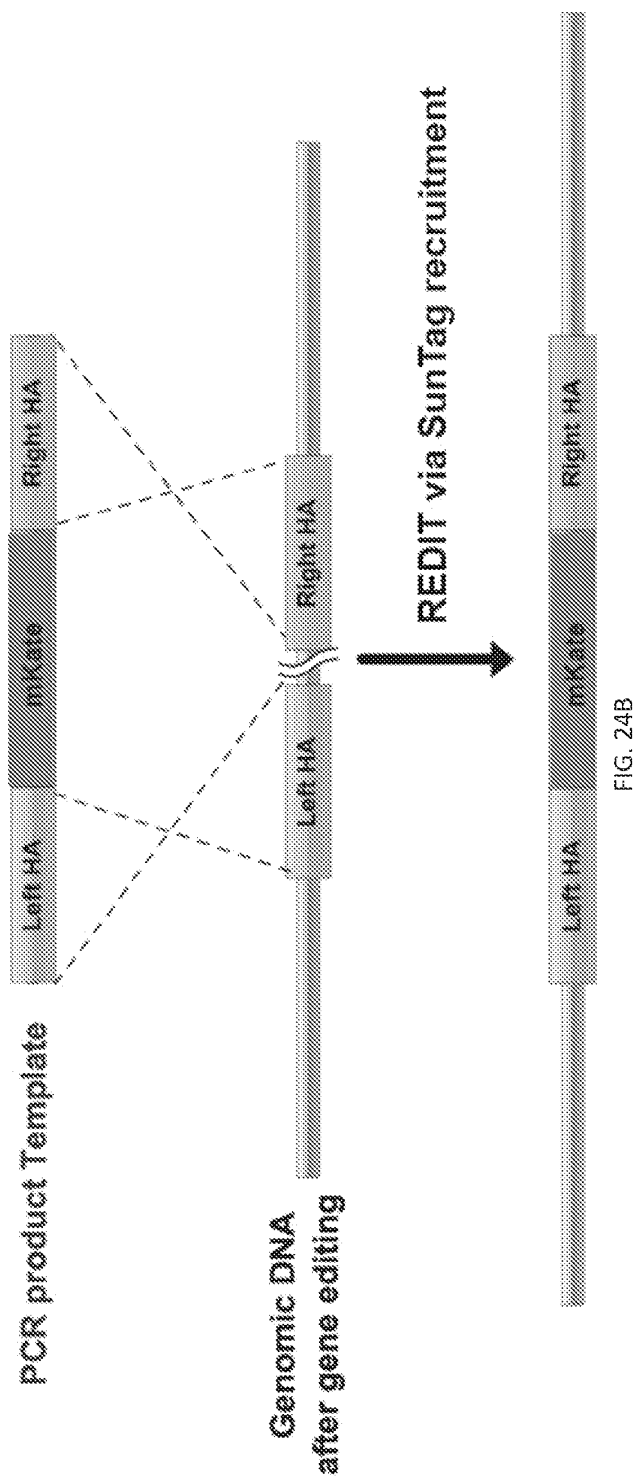


FIG. 24A



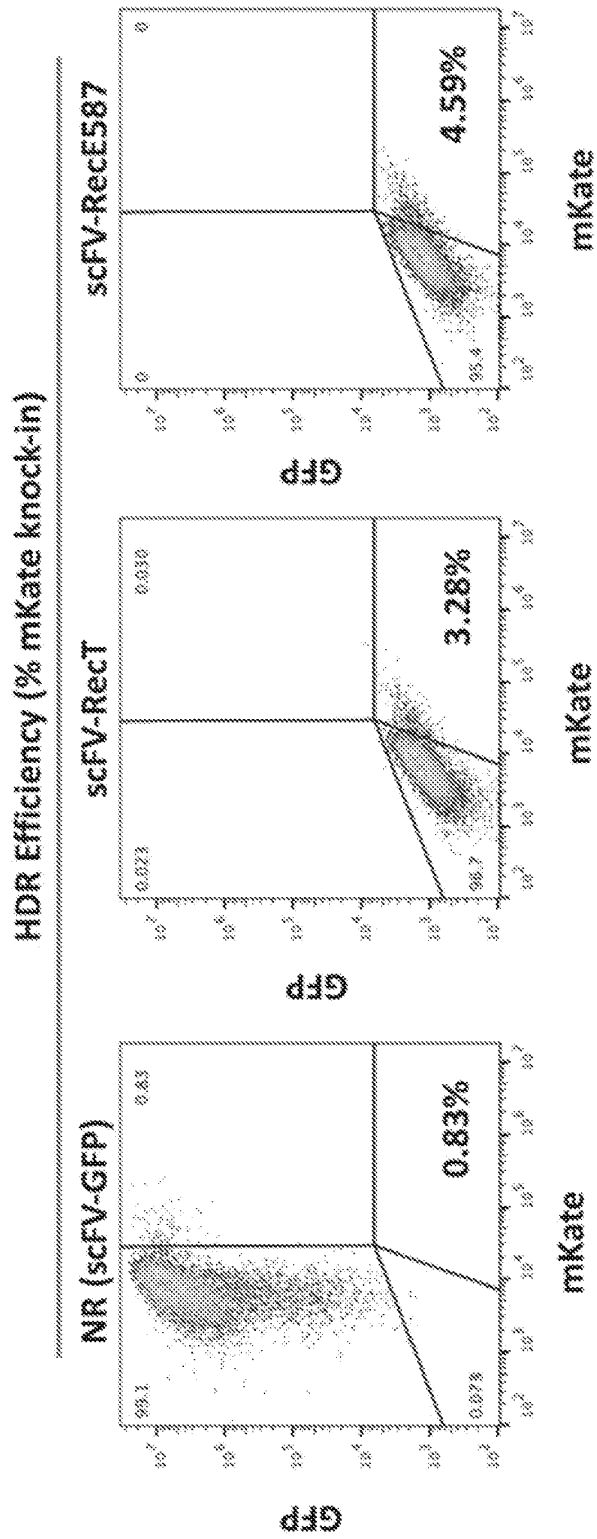


FIG. 24C

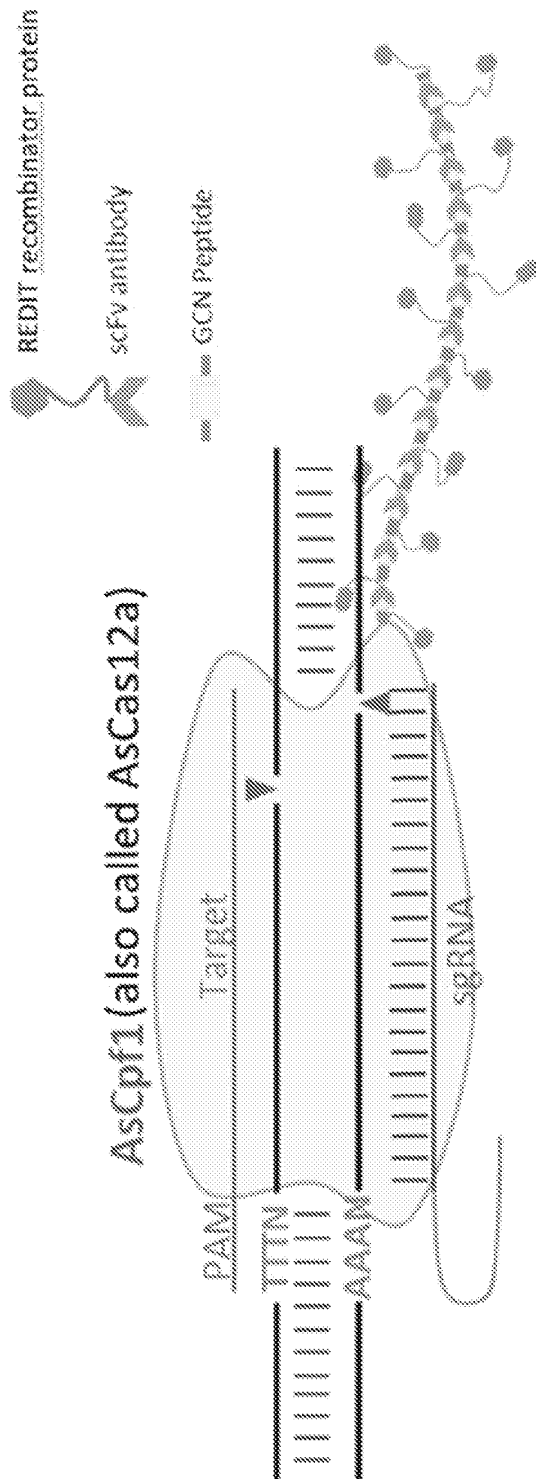


FIG. 25A

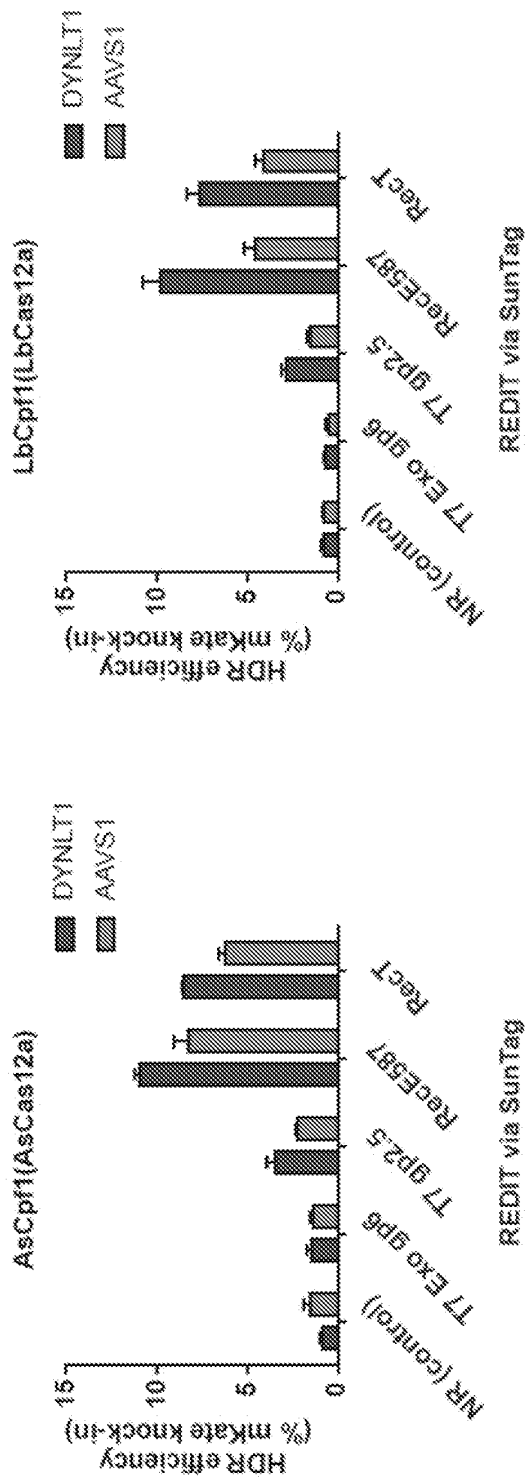


FIG. 25B

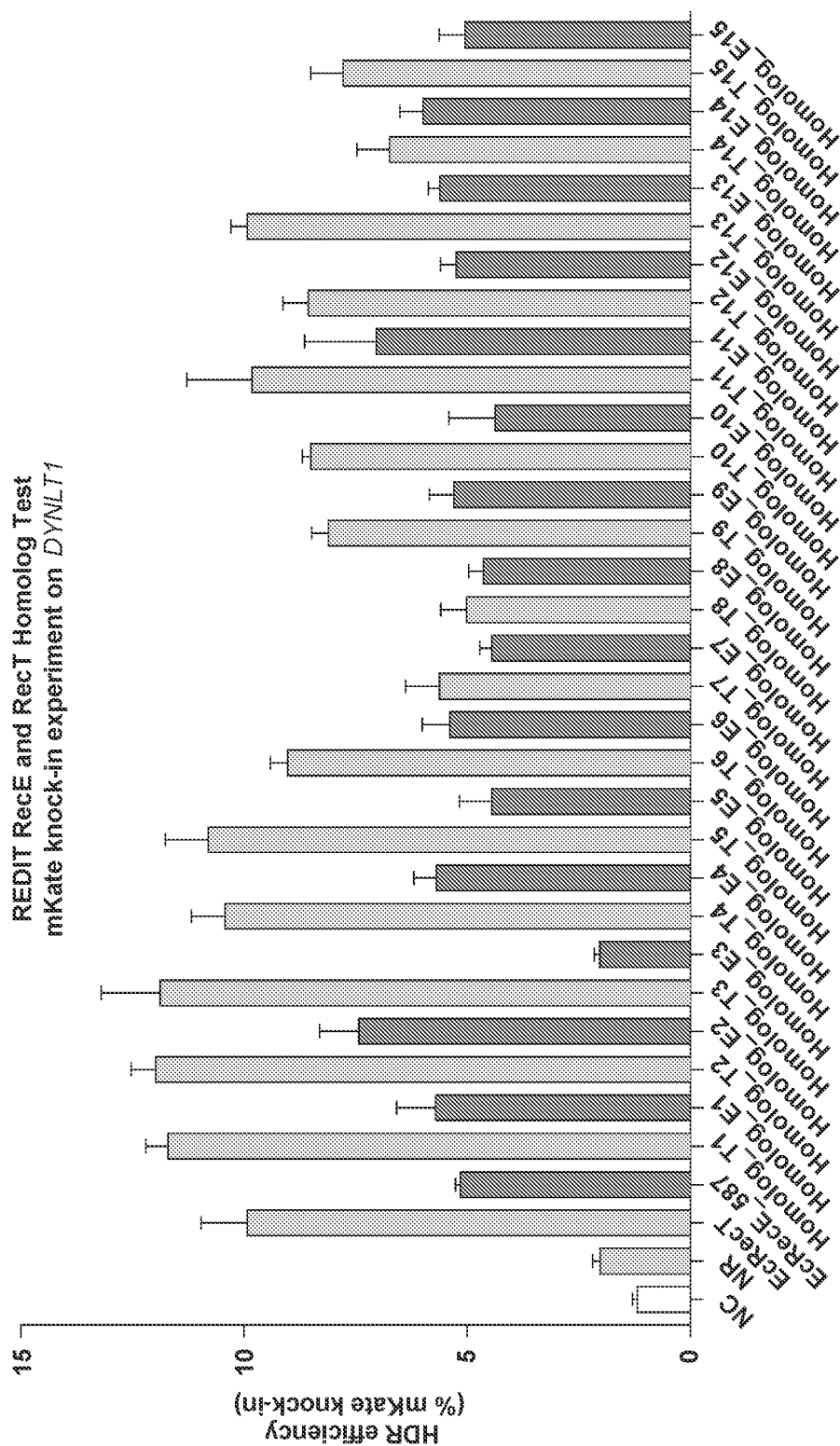


FIG. 26A

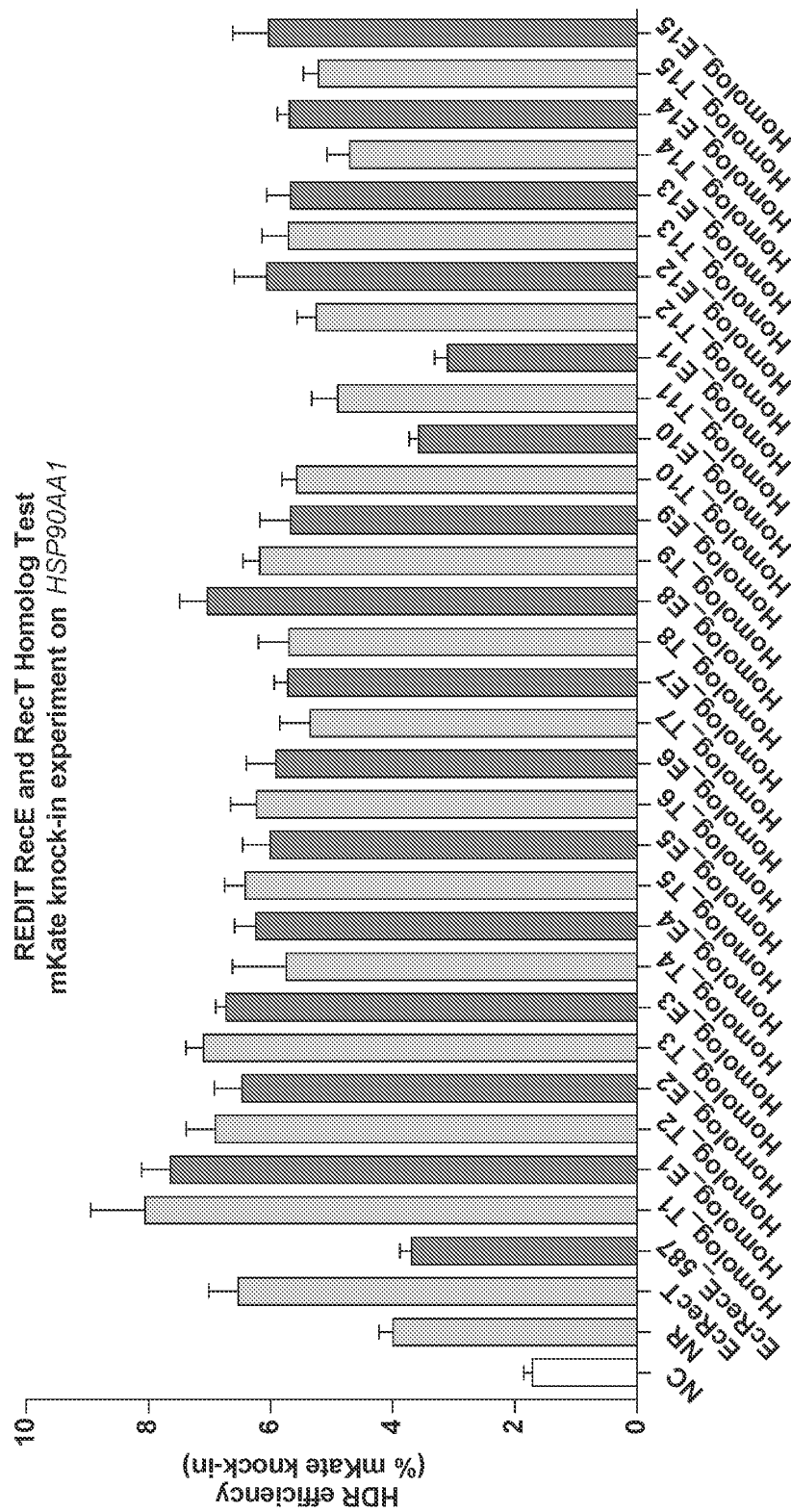


FIG. 26B

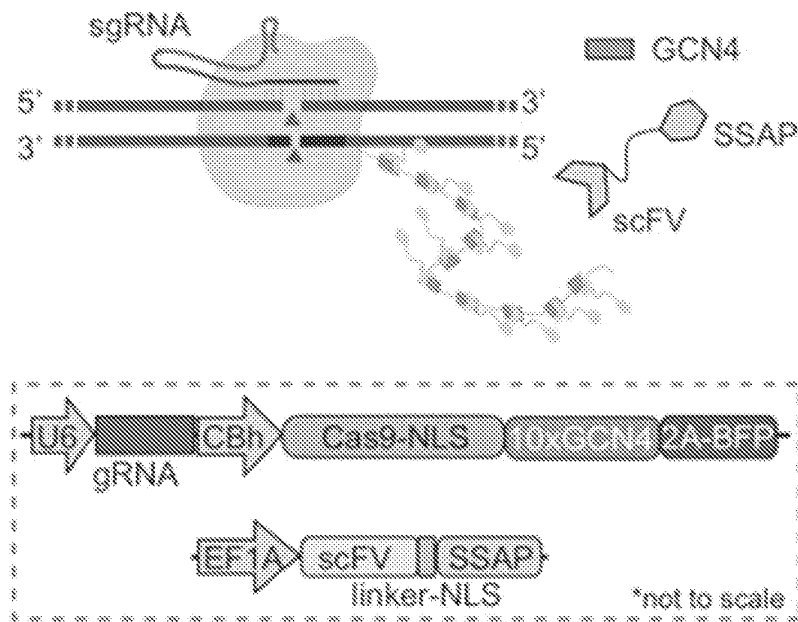


FIG. 27A

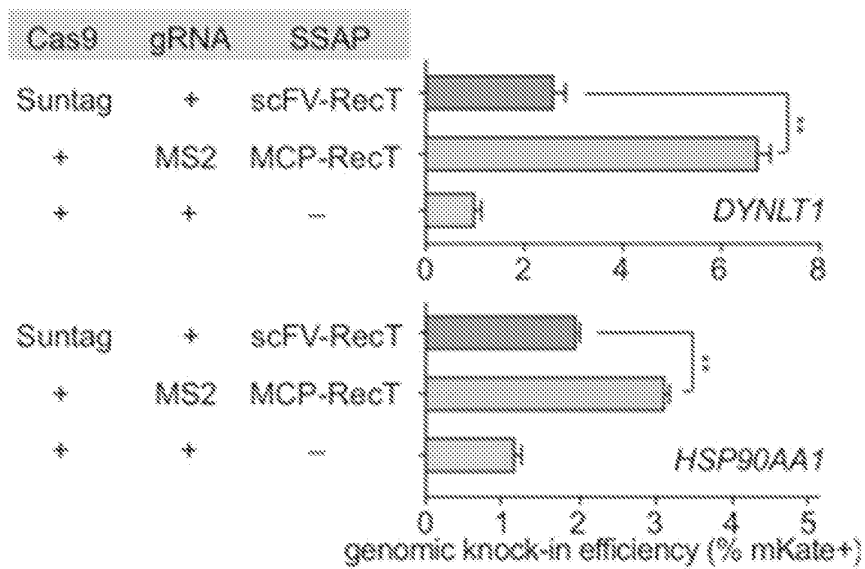


FIG. 27B

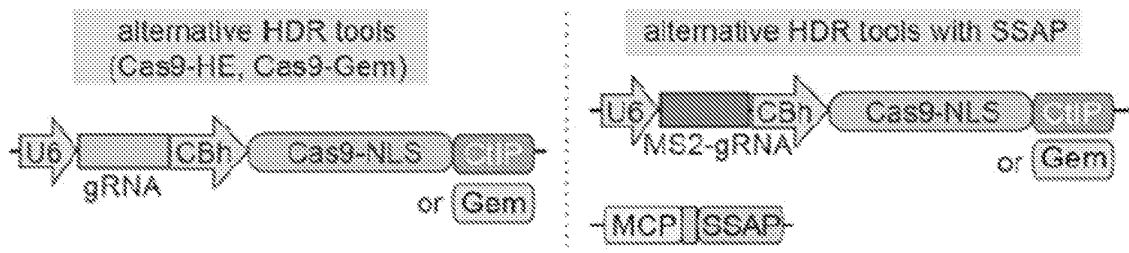


FIG. 28A

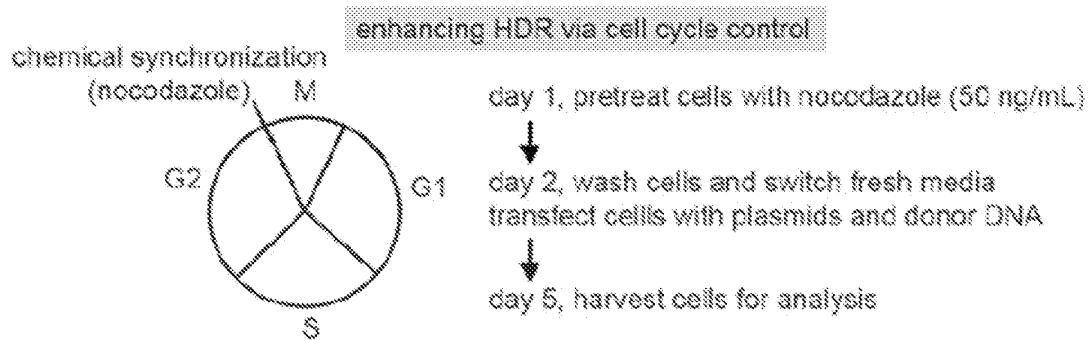


FIG. 28B

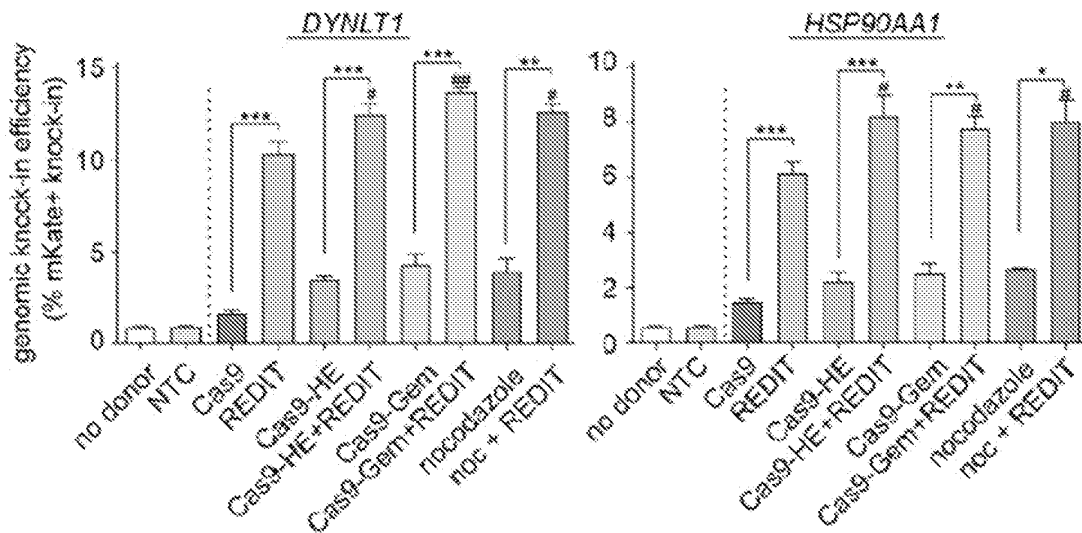


FIG. 28C

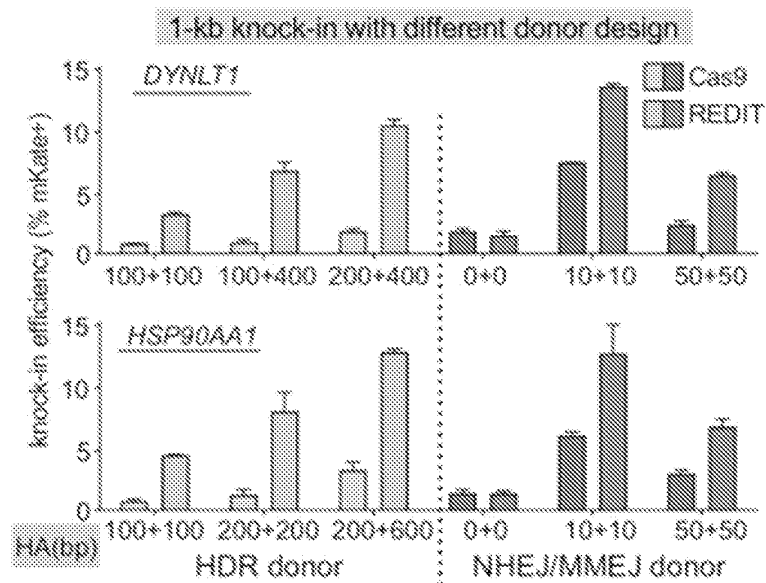


FIG. 29A

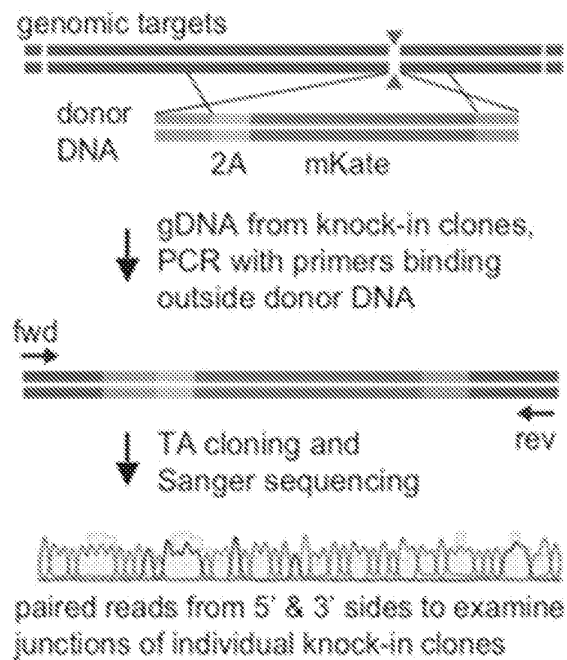


FIG. 29B

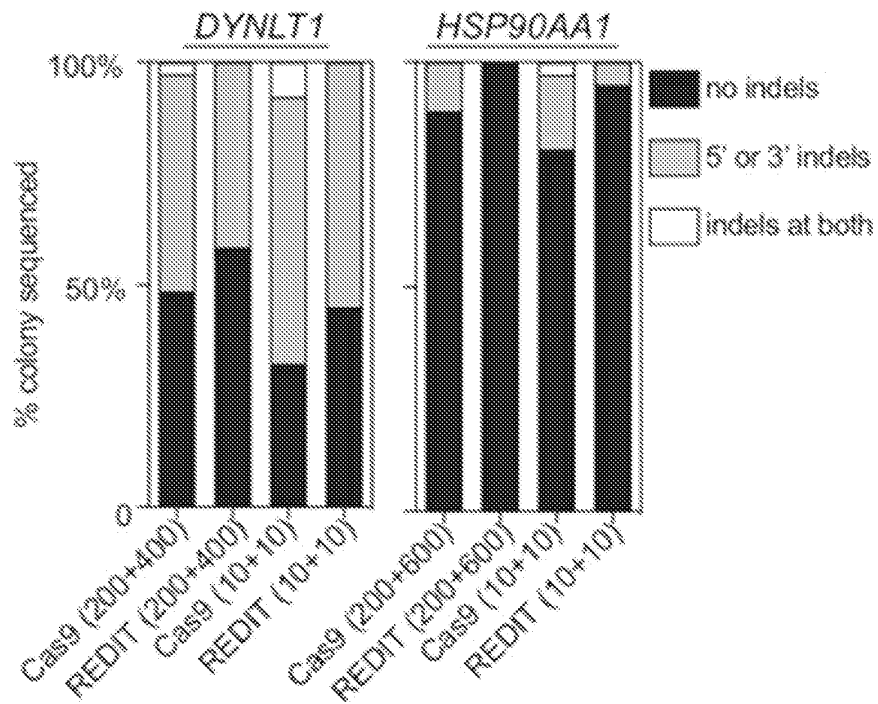


FIG. 29C

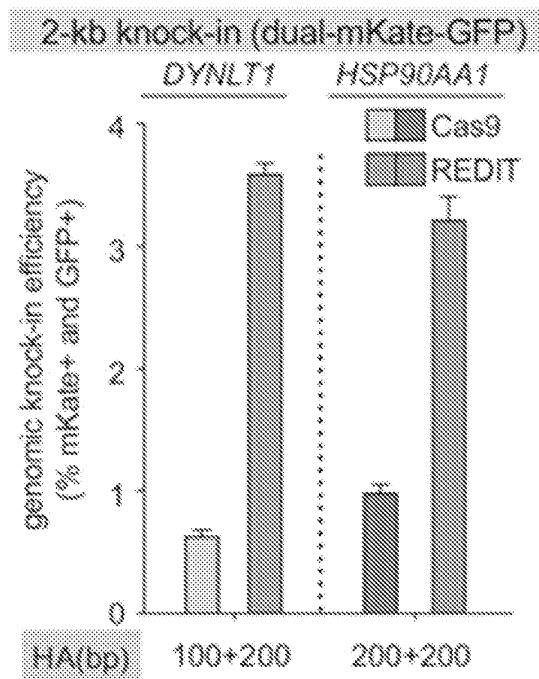


FIG. 29D

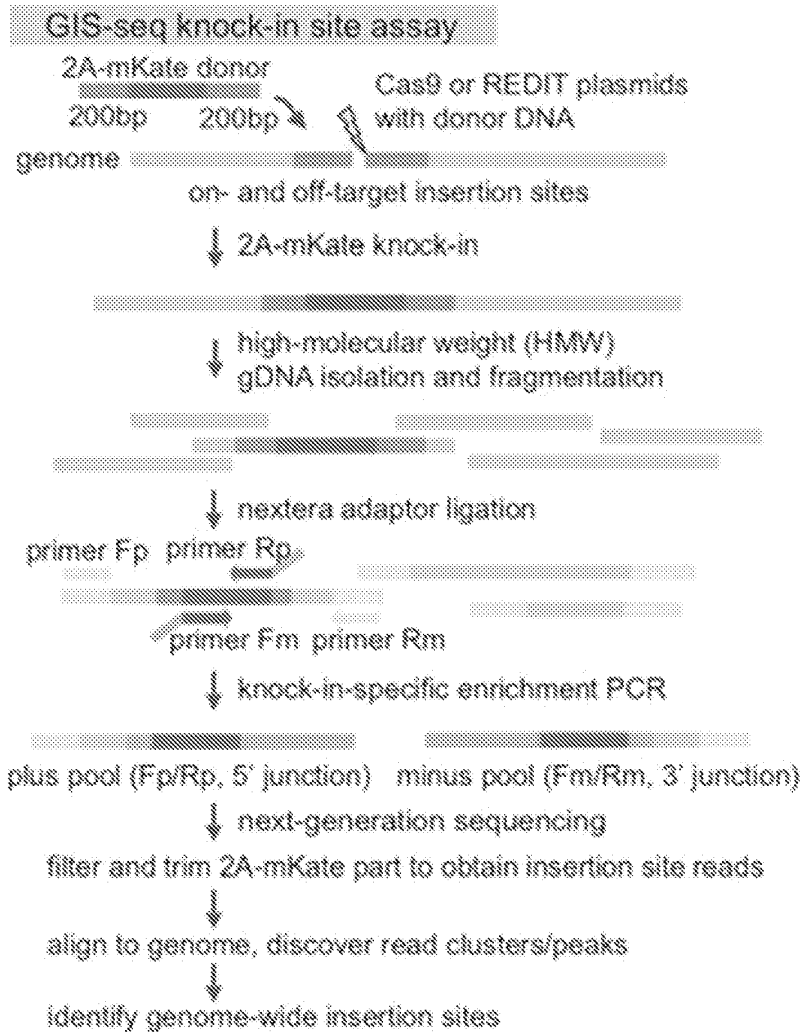


FIG. 30A

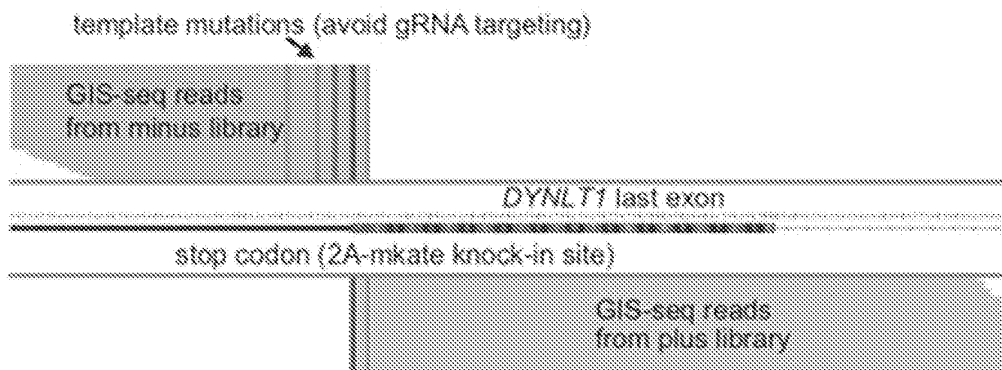


FIG. 30B

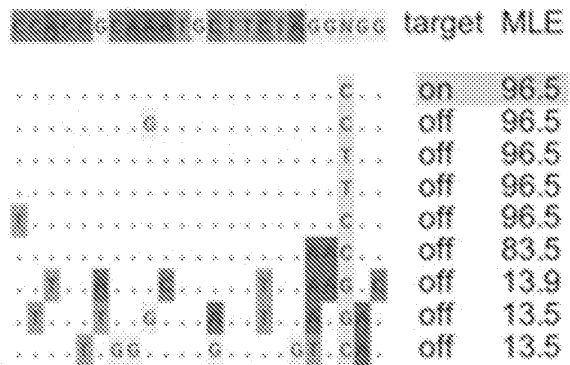
Cas9dn - GIS-seq insertion sites (*DYNLT1*)



REDITdn - GIS-seq insertion sites (*DYNLT1*)



Cas9dn - GIS-seq insertion sites (*ACTB*)



REDITdn - GIS-seq insertion sites (*ACTB*)



FIG. 30C

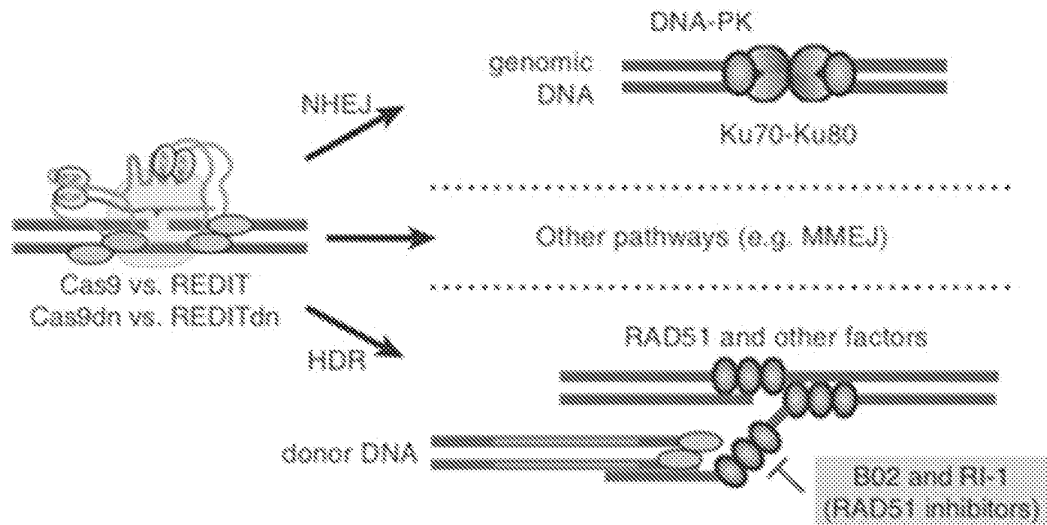


FIG. 31A

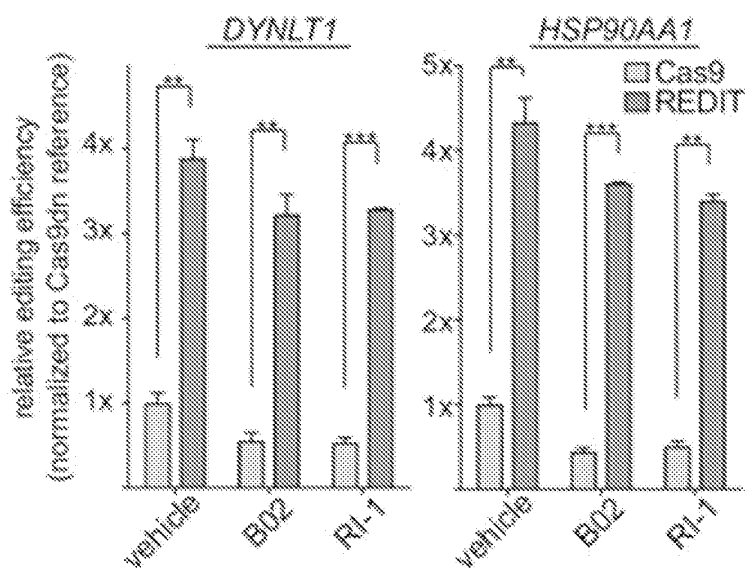


FIG. 31B

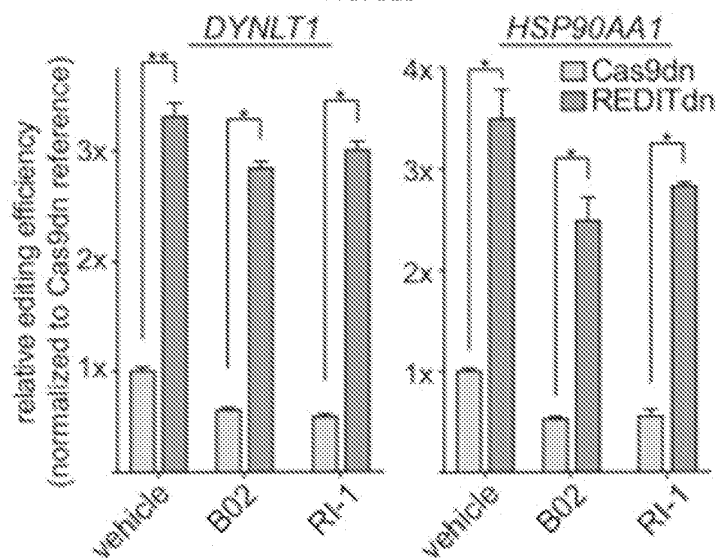


FIG. 31C

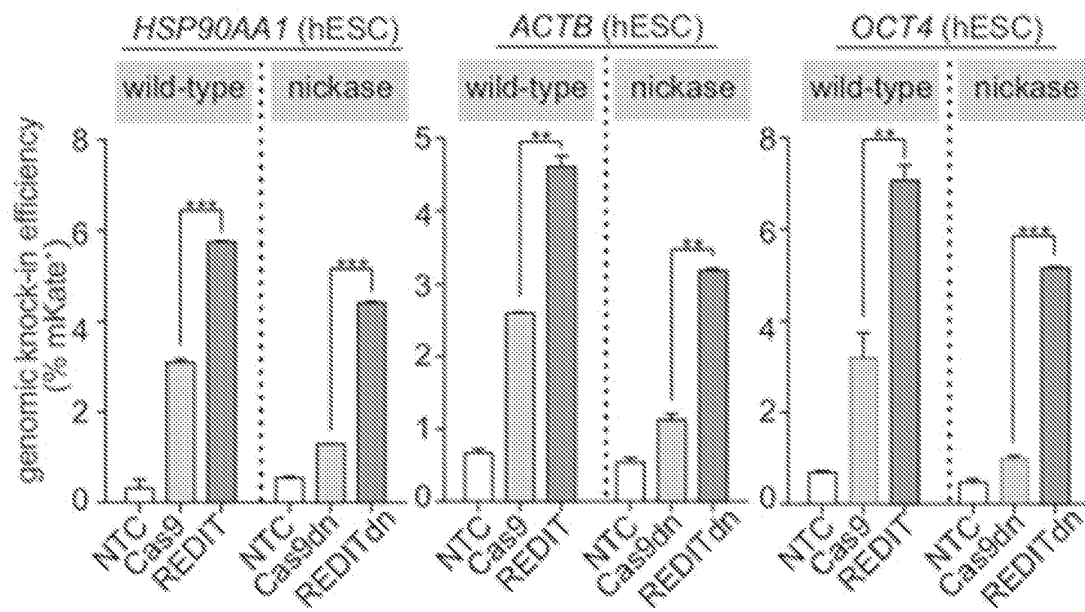


FIG. 31D

representative Cas9 results - OCT4 (hESC)

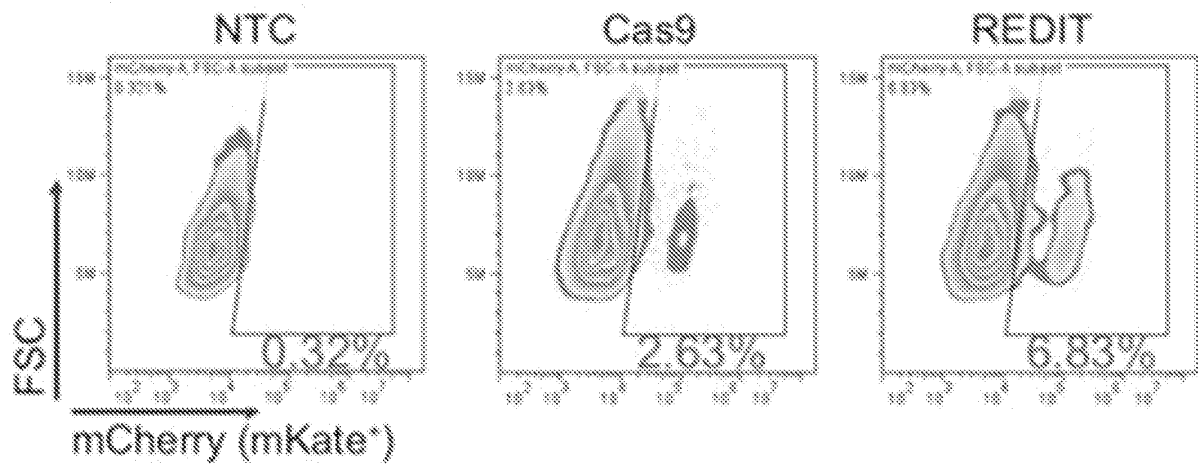


FIG. 31E

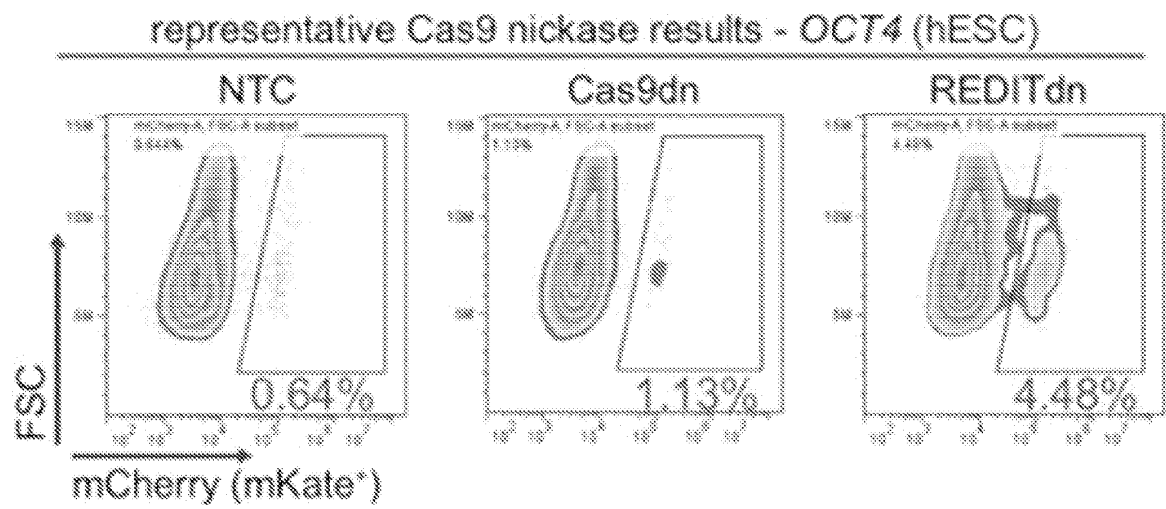


FIG. 31F

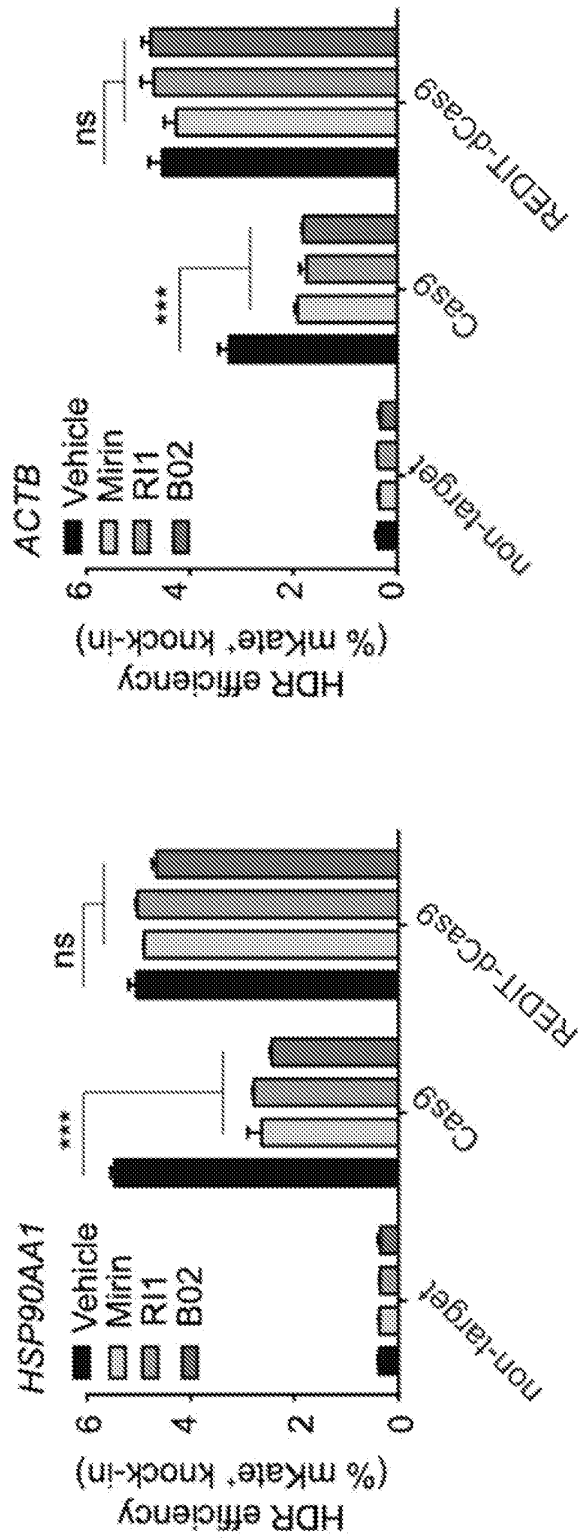


FIG. 32A

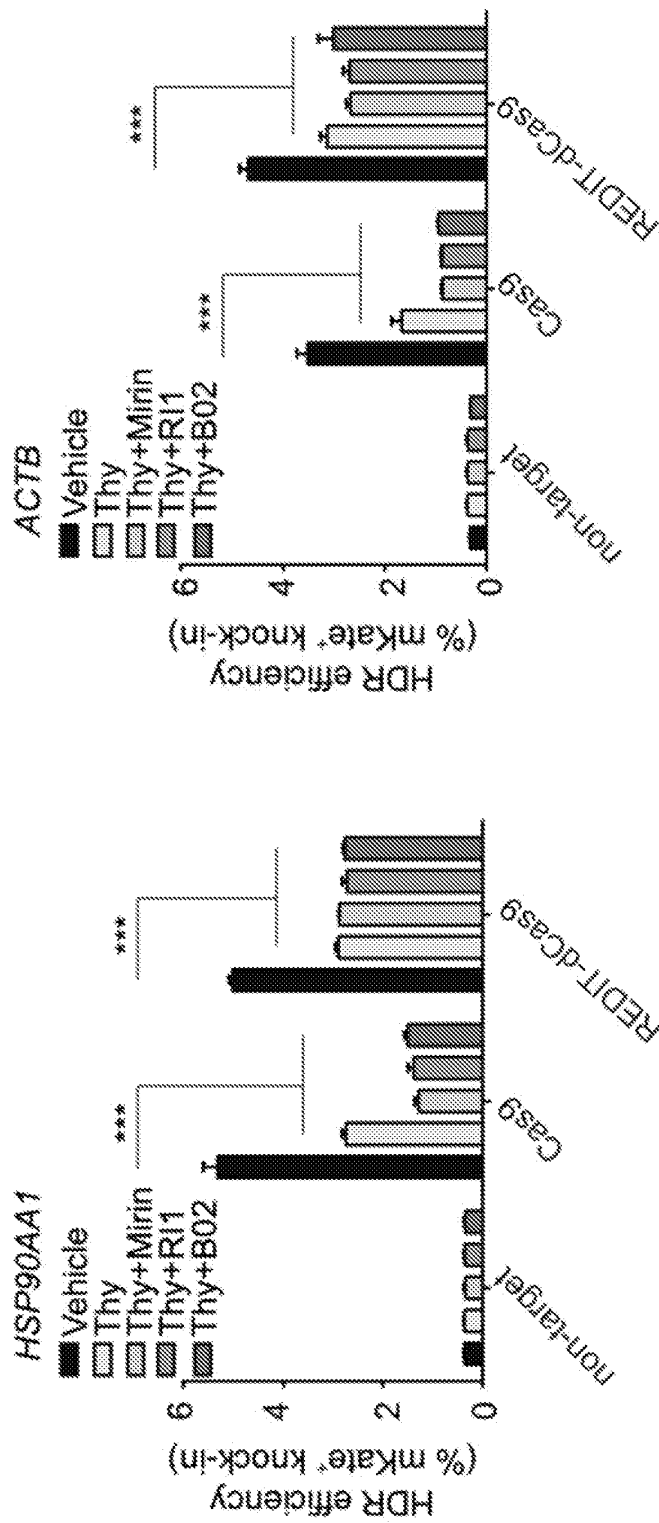
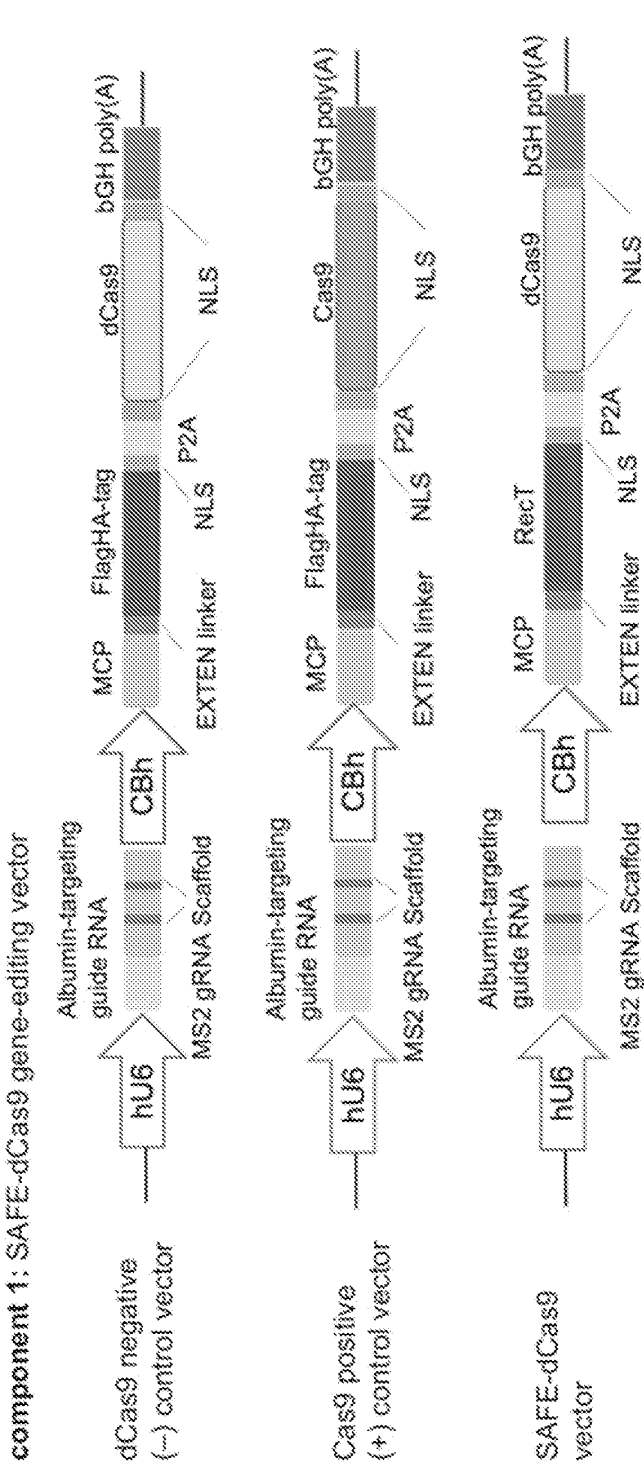


FIG. 32B



component 2: mouse Albumin knock-in template (for insertion of transgene into mouse Albumin genomic locus), shown below is a template used in this experiment where we inserted the purple-highlighted transgene, encoding SA-StrepIITag (SA = splice acceptor to express protein, StrepIITag is a polypeptide transgene) into mouse genome.

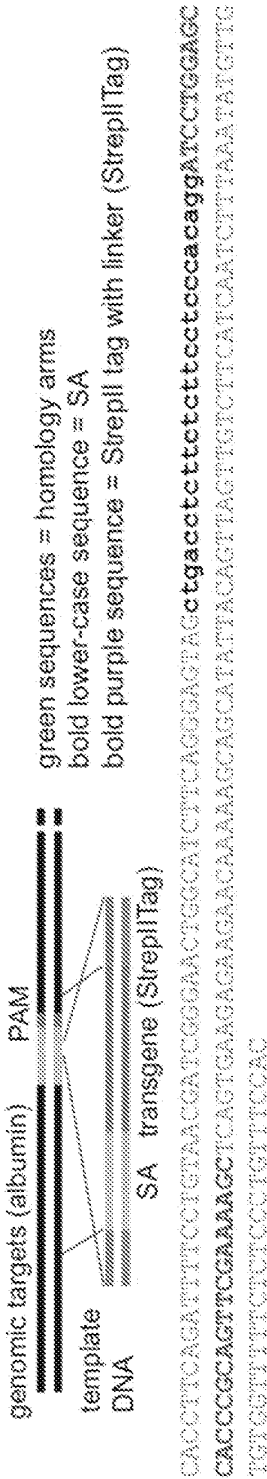


FIG. 33A

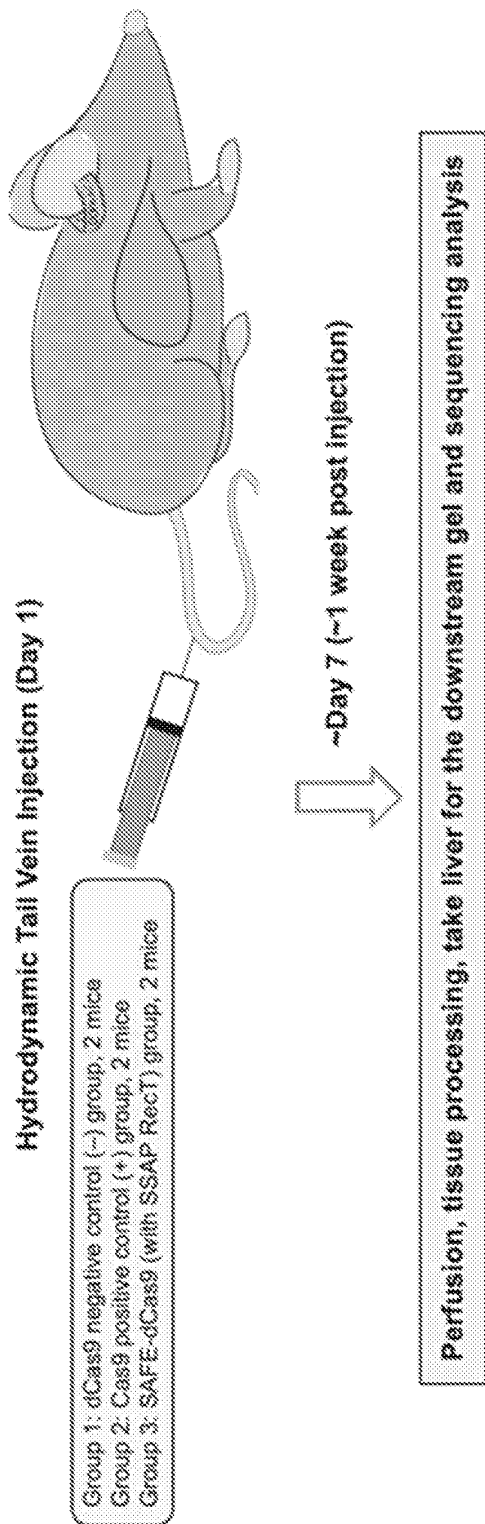


FIG. 33B

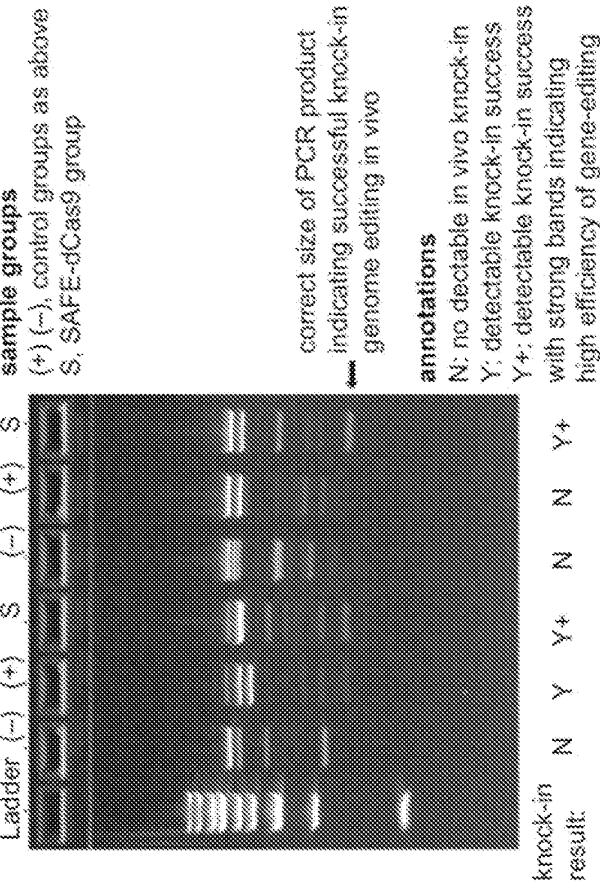


FIG. 34A

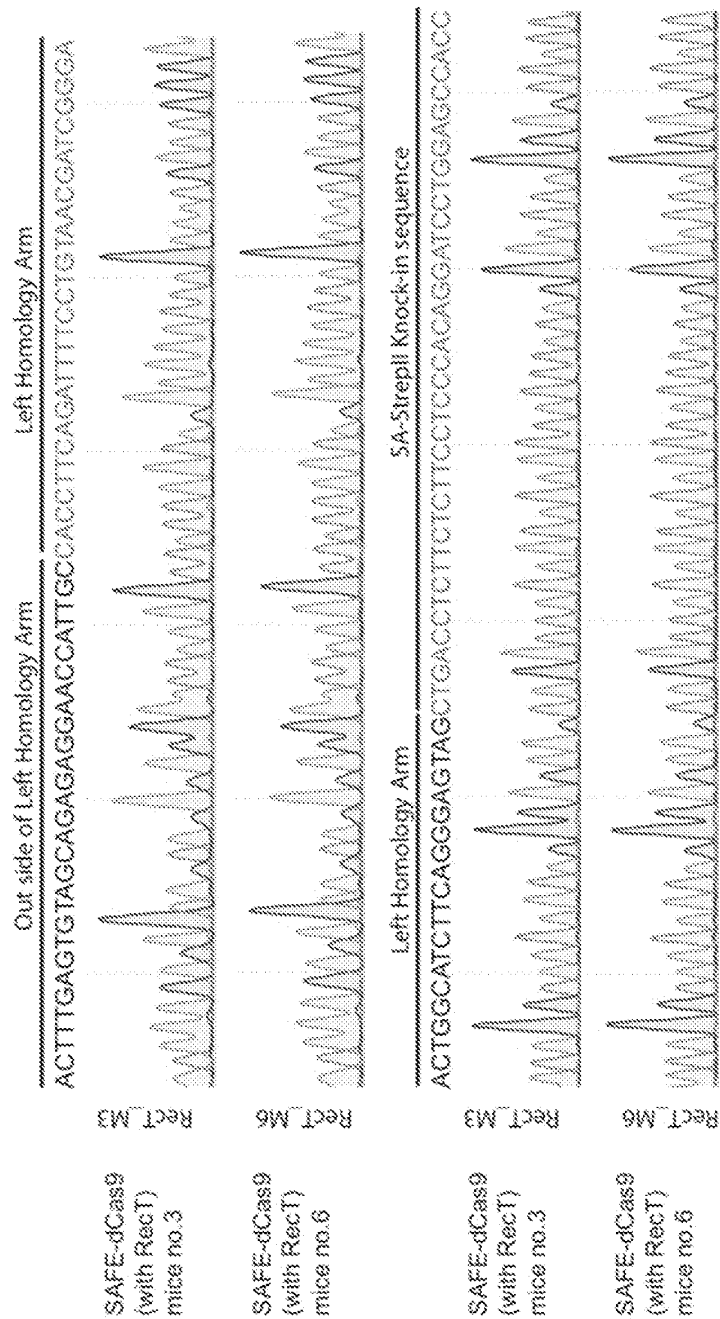


FIG. 34B

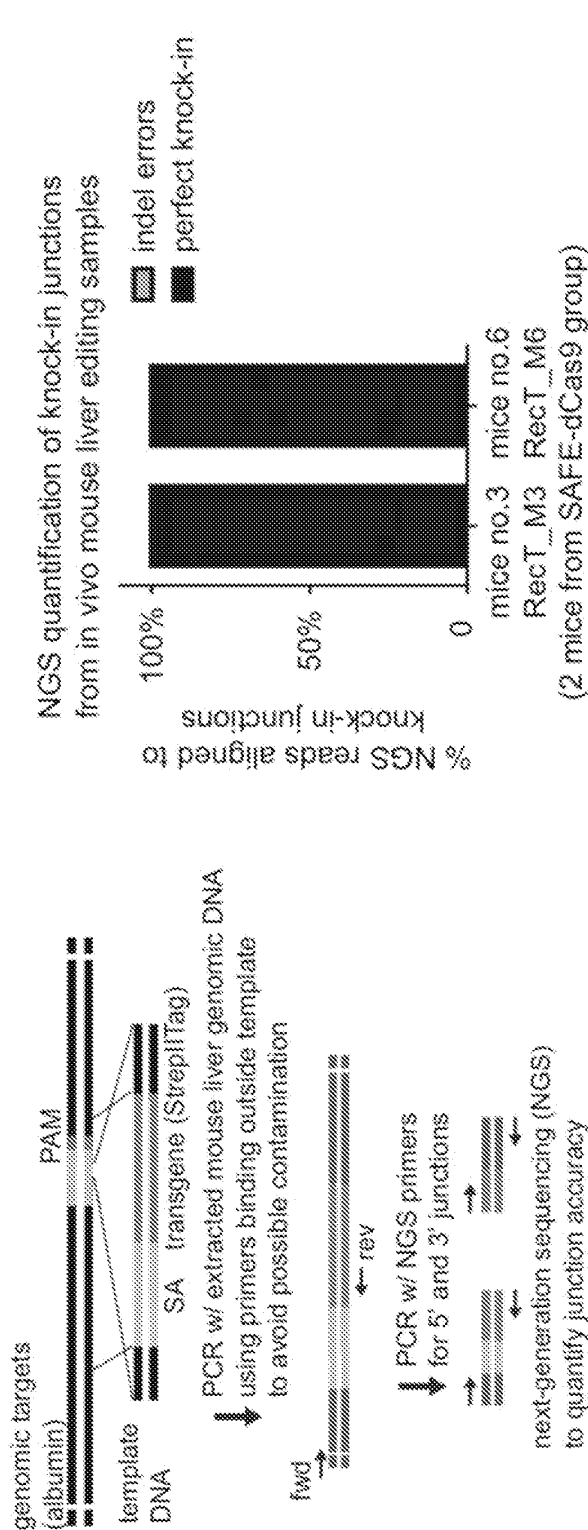


FIG. 34C

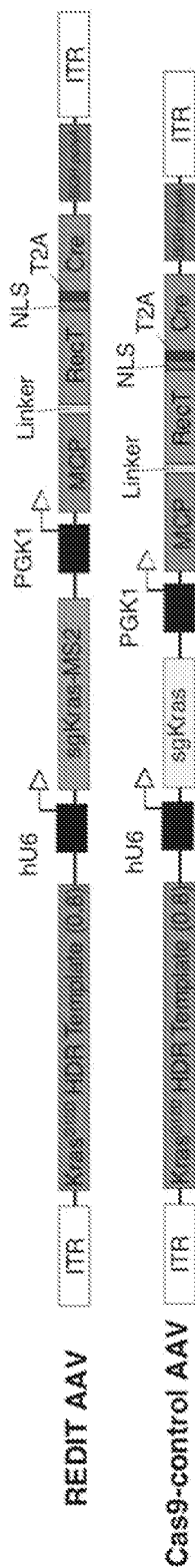


FIG. 35 A

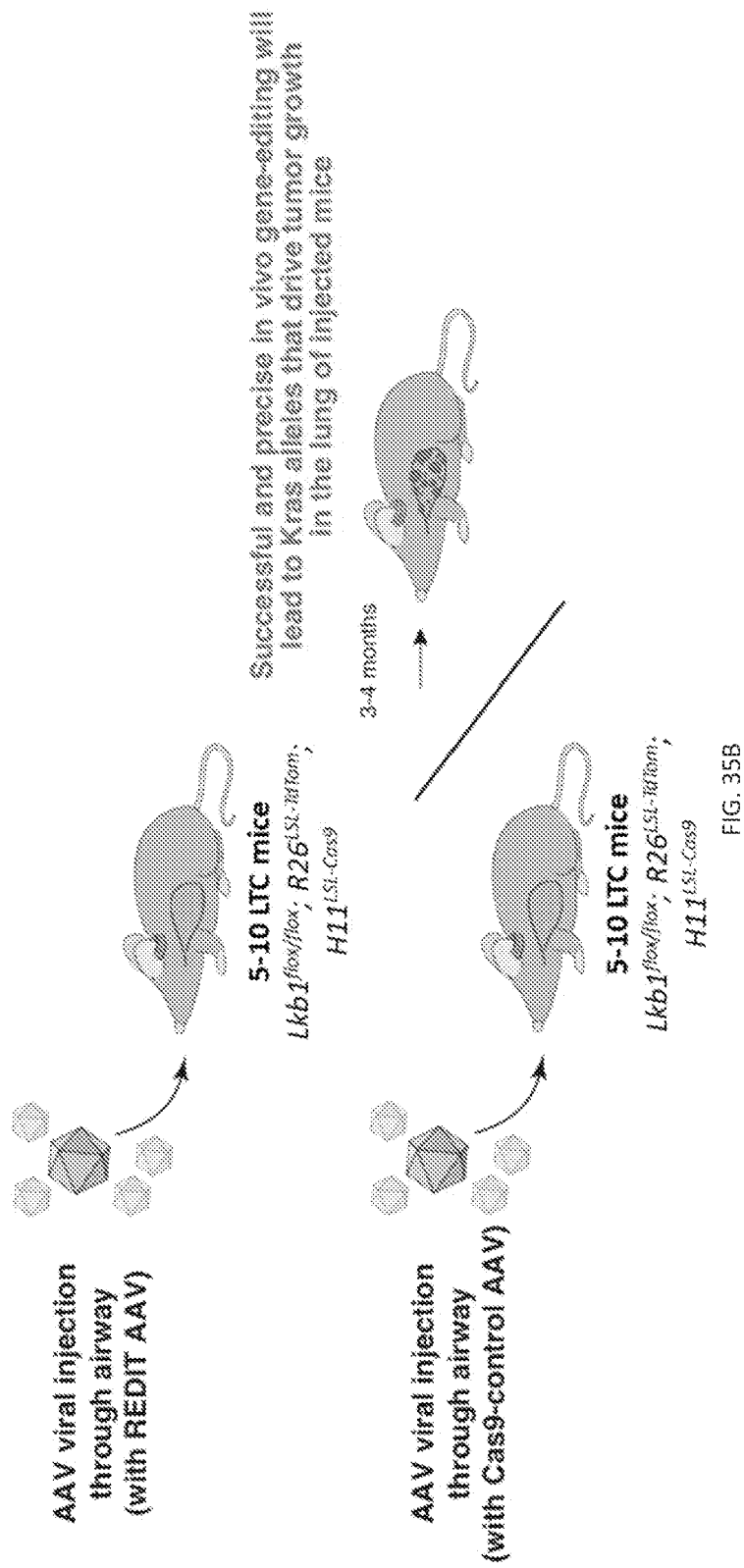


FIG. 35B

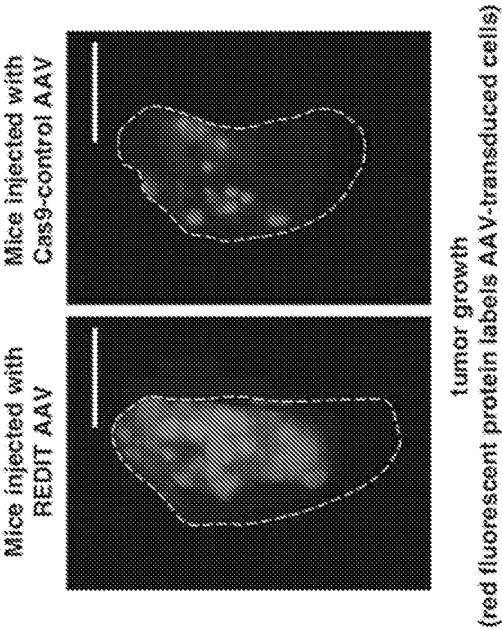
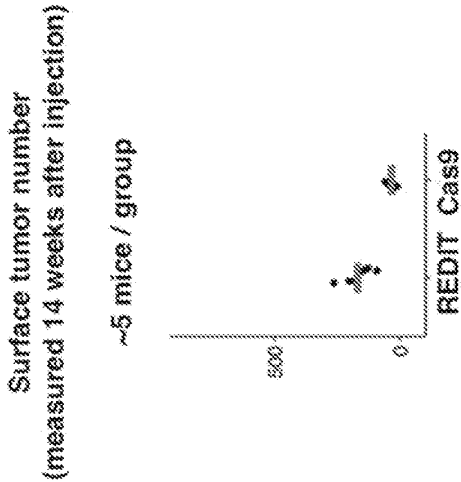


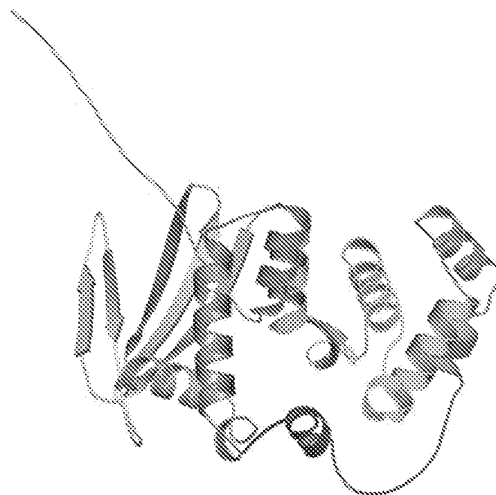
FIG. 35C

Before start:
AAV preparation

Week 1:
AAV viral injection
using ~4.00E+12 vg/mouse

Week 14:
sacrifice mice
perform lung tumor size analysis
perform lung imaging analysis

A.



B.



C.

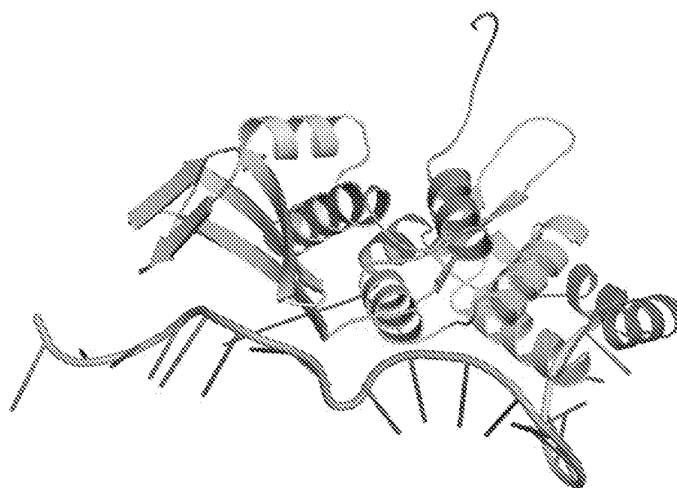


FIG. 36A-36C

# Receptor interface residue(s)			# Receptor-ligand interface residue pair(s)		
GLN	4A	4.107	4A	- 19D	4.107
VAL	24A	4.854	24A	- 30D	4.854
ASN	26A	2.727	26A	- 29D	3.837
SER	27A	3.416	26A	- 30D	2.727
ILE	30A	3.104	27A	- 30D	3.416
SER	31A	4.084	30A	- 29D	4.430
ASN	34A	3.111	30A	- 30D	3.104
LYS	39A	4.841	31A	- 30D	4.084
ARG	48A	3.943	34A	- 29D	3.111
HIS	49A	2.318	34A	- 30D	3.212
THR	51A	3.160	39A	- 29D	4.841
GLU	53A	2.512	39A	- 30D	4.925
ARG	54A	2.270	48A	- 24D	3.943
ILE	56A	3.968	49A	- 22D	4.536
ARG	57A	3.090	49A	- 23D	2.318
SER	85A	4.952	49A	- 24D	3.501
LEU	87A	4.951	49A	- 25D	4.897
GLY	88A	2.177	51A	- 25D	4.782
LEU	89A	3.838	51A	- 26D	3.160
LEU	95A	3.003	53A	- 26D	3.441
HIS	97A	3.069	53A	- 27D	2.512
ASP	126A	2.449	53A	- 28D	4.400
ARG	129A	3.757	54A	- 23D	3.414
ARG	130A	2.577	54A	- 24D	2.270
SER	136A	4.726	54A	- 25D	4.140
SER	138A	4.398	54A	- 26D	4.161
ARG	140A	2.675	56A	- 29D	3.968
PRO	162A	4.247	57A	- 24D	4.108
GLU	164A	2.527	57A	- 25D	3.581
GLU	166A	2.186	57A	- 26D	3.090
# Ligand interface residue(s):			57A	- 27D	4.720
DT	13D	2.527	85A	- 23D	4.952
DG	14D	3.334	87A	- 22D	4.951
DA	15D	2.186	88A	- 21D	4.303
DG	16D	4.247	88A	- 22D	2.177
DA	17D	2.675	88A	- 23D	4.533
DC	18D	2.871	89A	- 22D	3.838
DG	19D	3.757	95A	- 20D	3.793
DC	20D	3.793	95A	- 21D	3.003
DT	21D	3.003	97A	- 20D	4.980
DG	22D	2.177	97A	- 21D	3.069
DG	23D	2.318	97A	- 22D	3.237
DC	24D	2.270	126A	- 21D	3.330
DG	25D	3.581	126A	- 22D	2.449
DA	26D	3.090	129A	- 19D	3.757
DT	27D	2.512	130A	- 21D	4.980
DT	28D	4.400	130A	- 22D	2.577
DA	29D	3.111	136A	- 18D	4.726
DG	30D	2.727	138A	- 18D	4.398
			140A	- 16D	4.432
			140A	- 17D	2.675
			140A	- 18D	2.871
			162A	- 16D	4.247
			164A	- 13D	2.527
			164A	- 14D	3.334
			166A	- 14D	3.446
			166A	- 15D	2.186
			166A	- 16D	4.798

FIG. 37A

# Receptor interface residue(s):			# Receptor-ligand interface residue pair(s):		
ALA	45A	4.996	45A	- 24D	4.996
PRO	47A	2.815	47A	- 24D	3.973
ARG	48A	4.499	47A	- 25D	2.815
HIS	49A	2.553	47A	- 26D	3.660
ARG	54A	3.254	48A	- 26D	4.499
ARG	57A	3.694	49A	- 26D	2.553
GLN	83A	3.073	49A	- 27D	2.895
SER	85A	4.480	49A	- 28D	2.967
GLN	86A	2.789	54A	- 28D	3.254
LEU	87A	4.636	54A	- 29D	3.329
GLY	88A	4.263	57A	- 29D	3.694
GLU	90A	4.487	57A	- 30D	3.740
ASN	105A	3.540	83A	- 21D	3.073
ASN	107A	2.594	85A	- 25D	4.480
GLU	108A	4.448	86A	- 22D	2.903
ARG	130A	4.303	86A	- 23D	2.789
GLU	234A	2.961	86A	- 24D	3.058
ARG	237A	2.308	86A	- 25D	3.545
ALA	238A	4.651	87A	- 25D	4.636
MET	241A	3.086	88A	- 25D	4.263
LYS	244A	4.001	90A	- 28D	4.687
PRO	246A	3.605	90A	- 29D	4.487
THR	248A	4.878	105A	- 19D	3.540
ILE	249A	4.970	107A	- 18D	2.871
ASP	250A	3.074	107A	- 19D	2.594
PRO	251A	2.808	108A	- 19D	4.448
# Ligand interface residue(s):			130A	- 27D	4.303
DG	16D	4.833	234A	- 22D	4.302
DA	17D	2.808	234A	- 23D	2.961
DC	18D	2.871	237A	- 20D	2.308
DG	19D	2.594	237A	- 21D	4.221
DC	20D	2.308	237A	- 22D	4.990
DT	21D	3.073	238A	- 21D	4.651
DG	22D	2.903	241A	- 20D	3.133
DG	23D	2.789	241A	- 21D	3.086
DC	24D	3.058	244A	- 20D	4.001
DG	25D	2.815	246A	- 19D	3.605
DA	26D	2.553	248A	- 18D	4.878
DT	27D	2.895	249A	- 17D	4.970
DT	28D	2.967	250A	- 16D	4.833
DA	29D	3.329	250A	- 17D	3.074
DG	30D	3.740	251A	- 17D	2.808

FIG. 37B

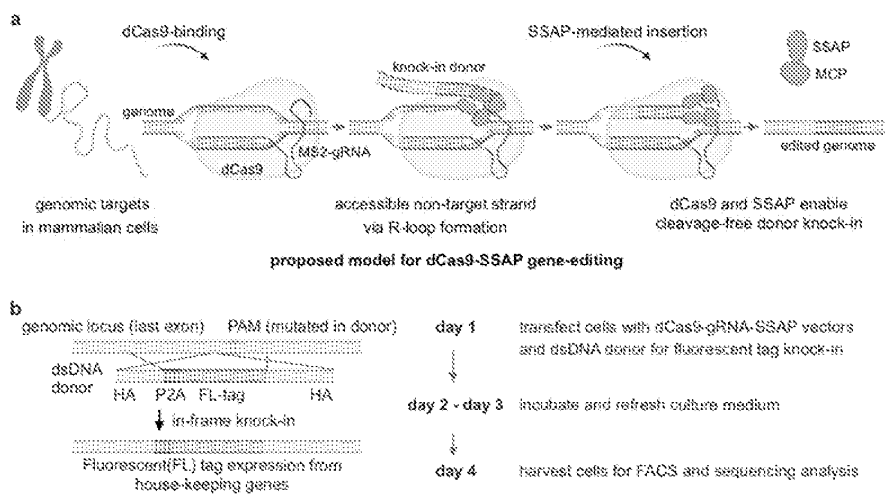


FIG. 38A-38B

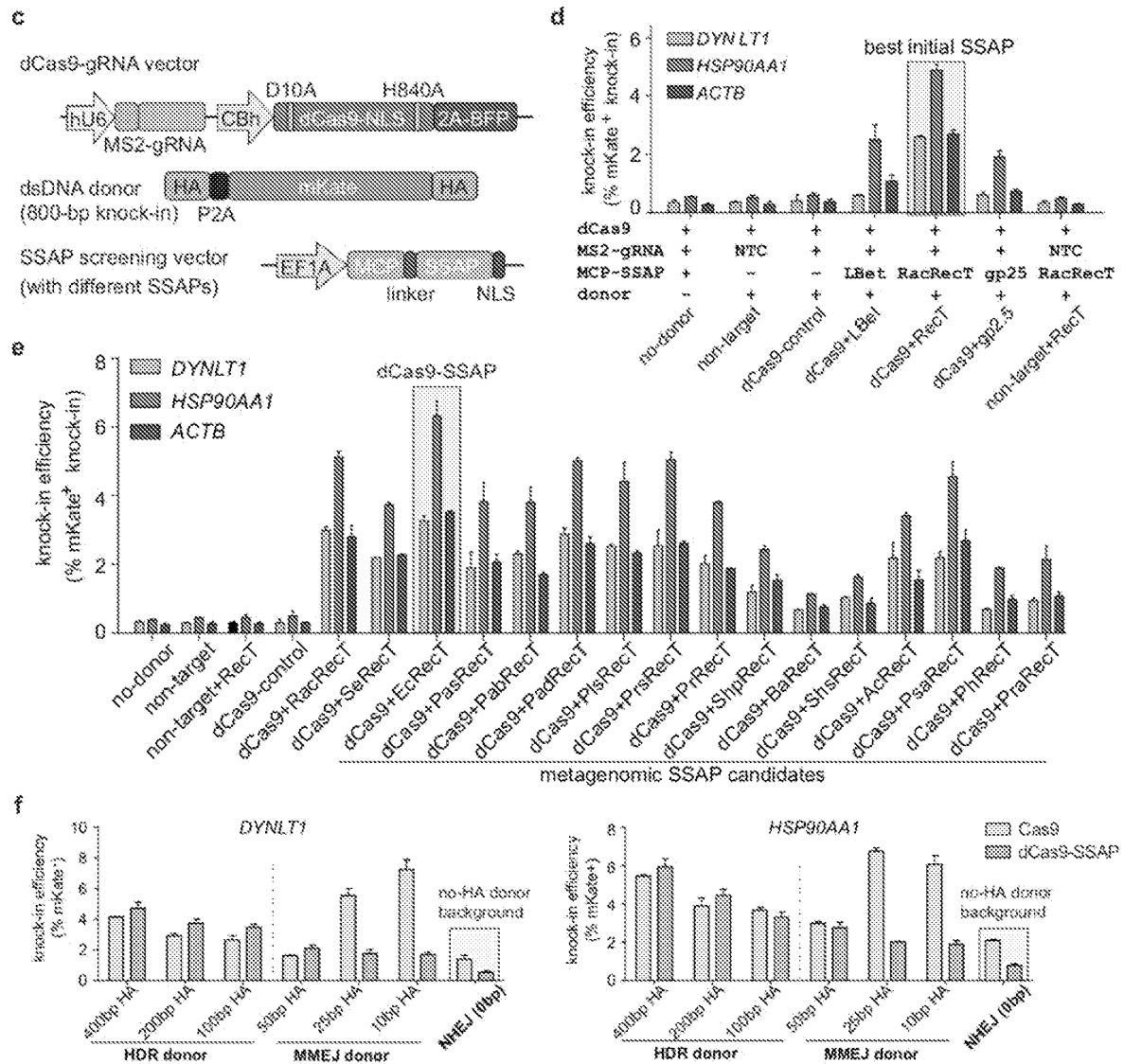


FIG. 38C-38F

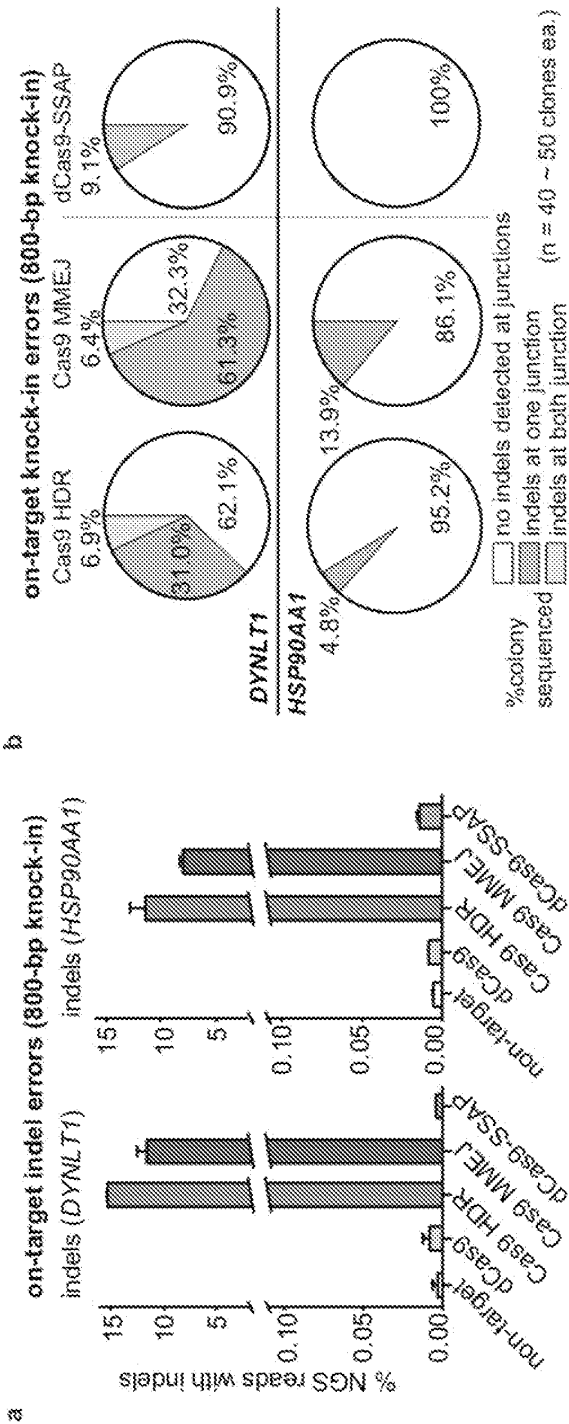


FIG. 39A-39B



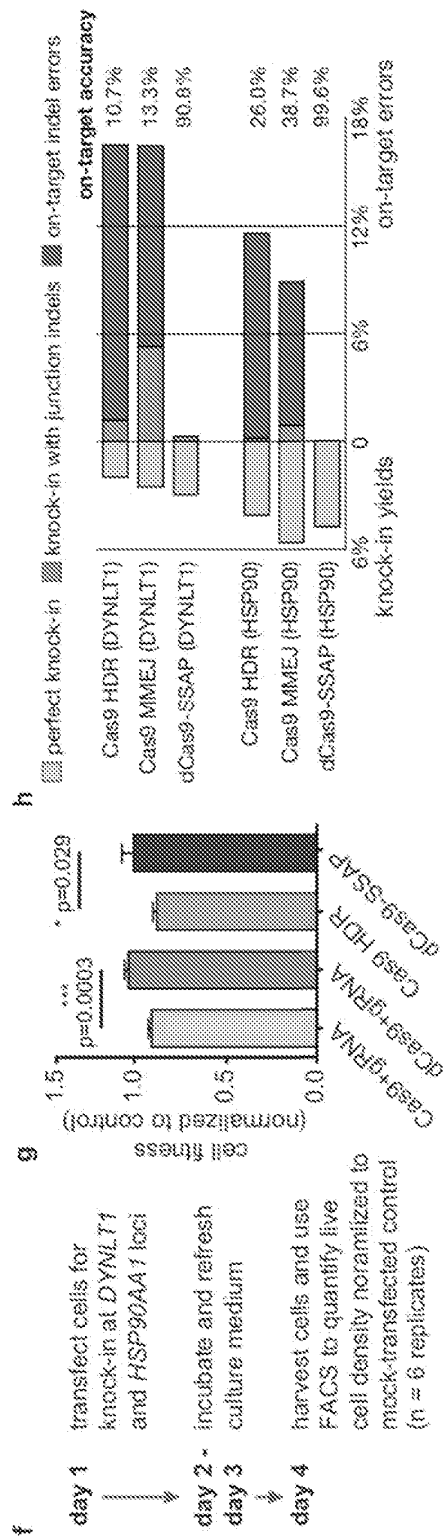
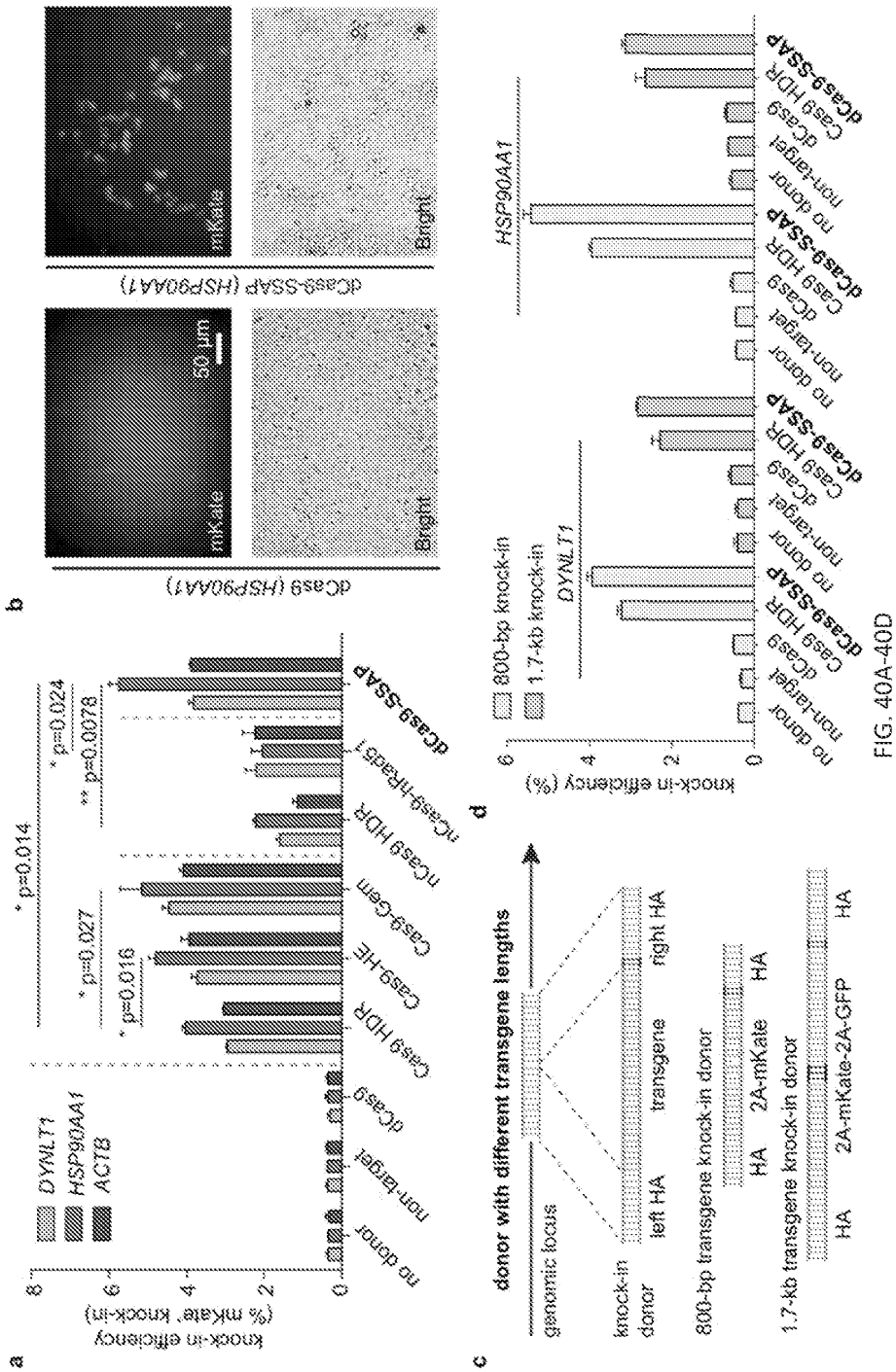


FIG. 39F-39H



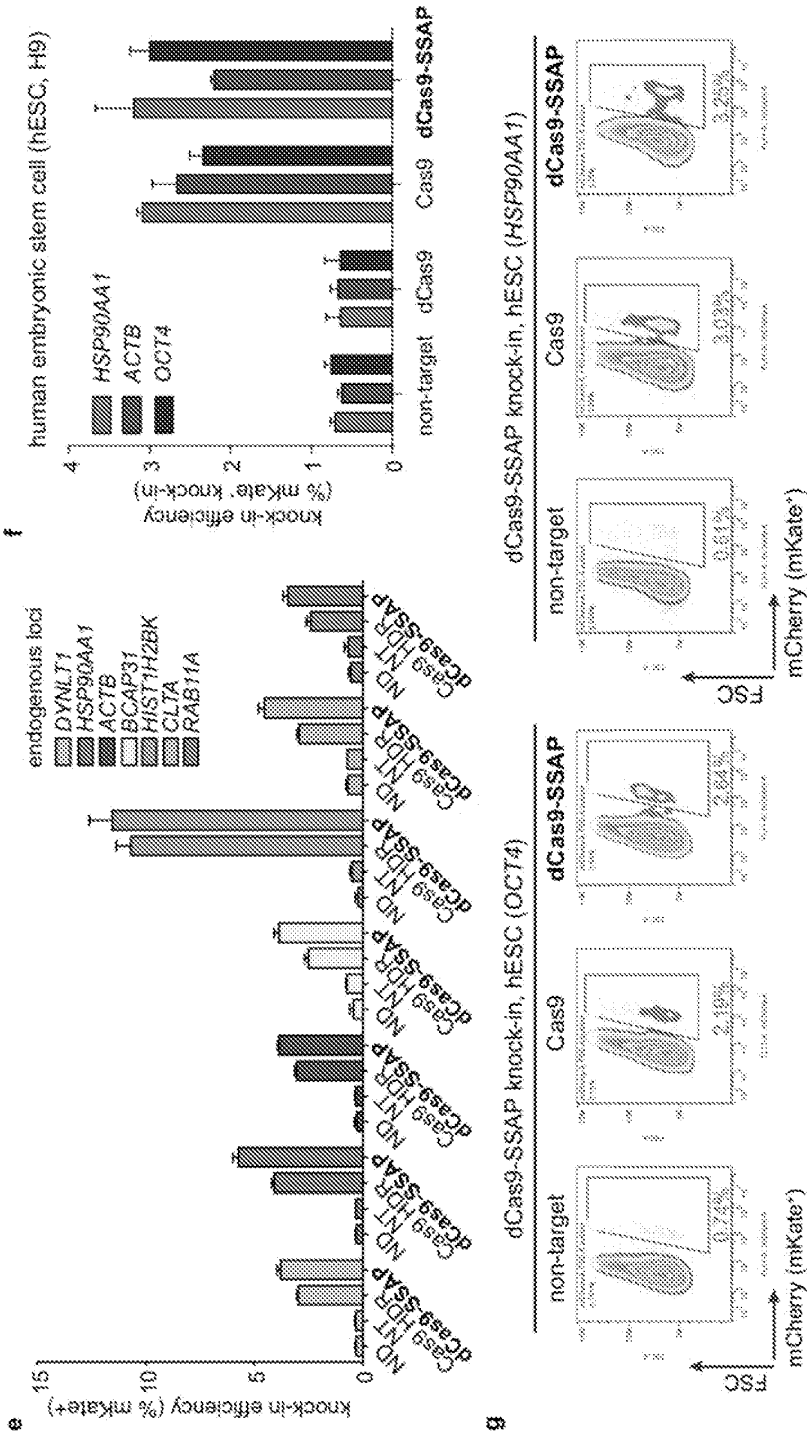
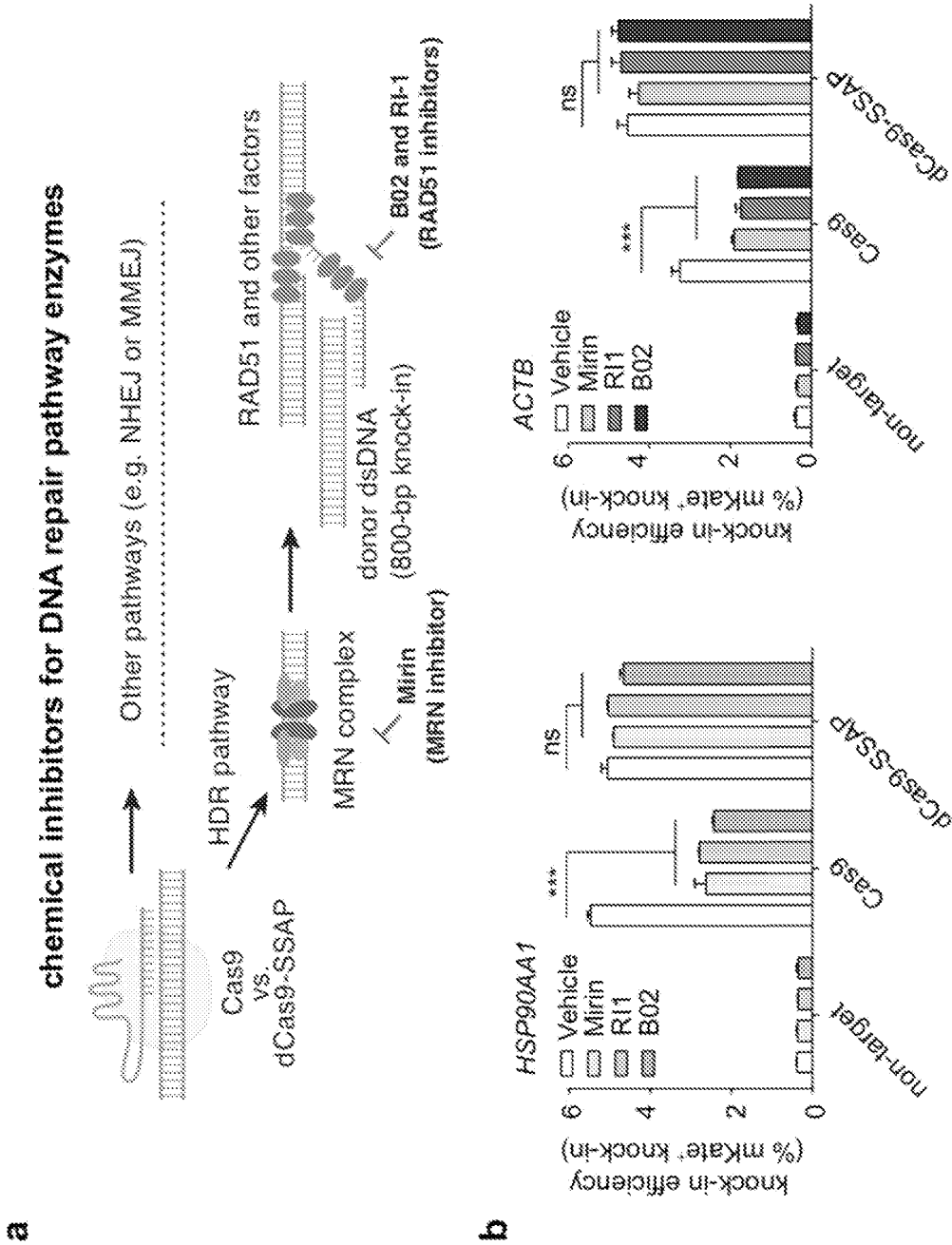


FIG. 40E-40G



c double Thymidine blocking (DTB) for cell cycle effects

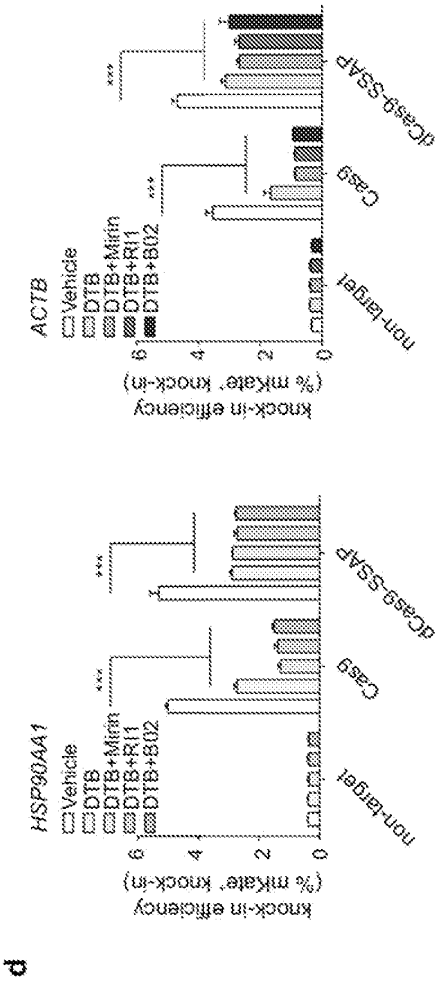
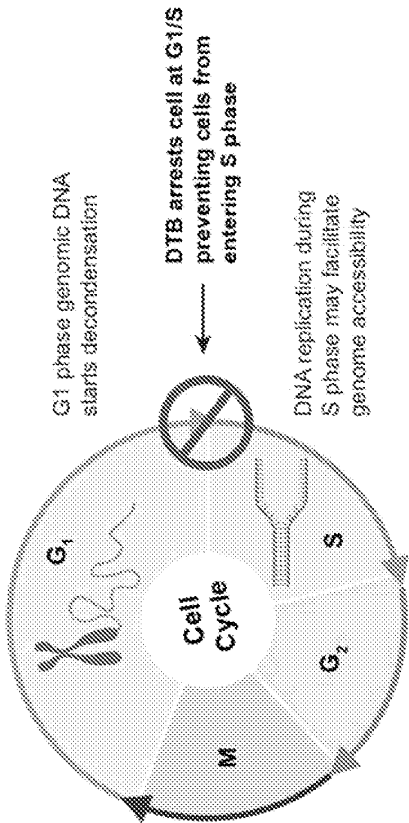


FIG. 41C-41D

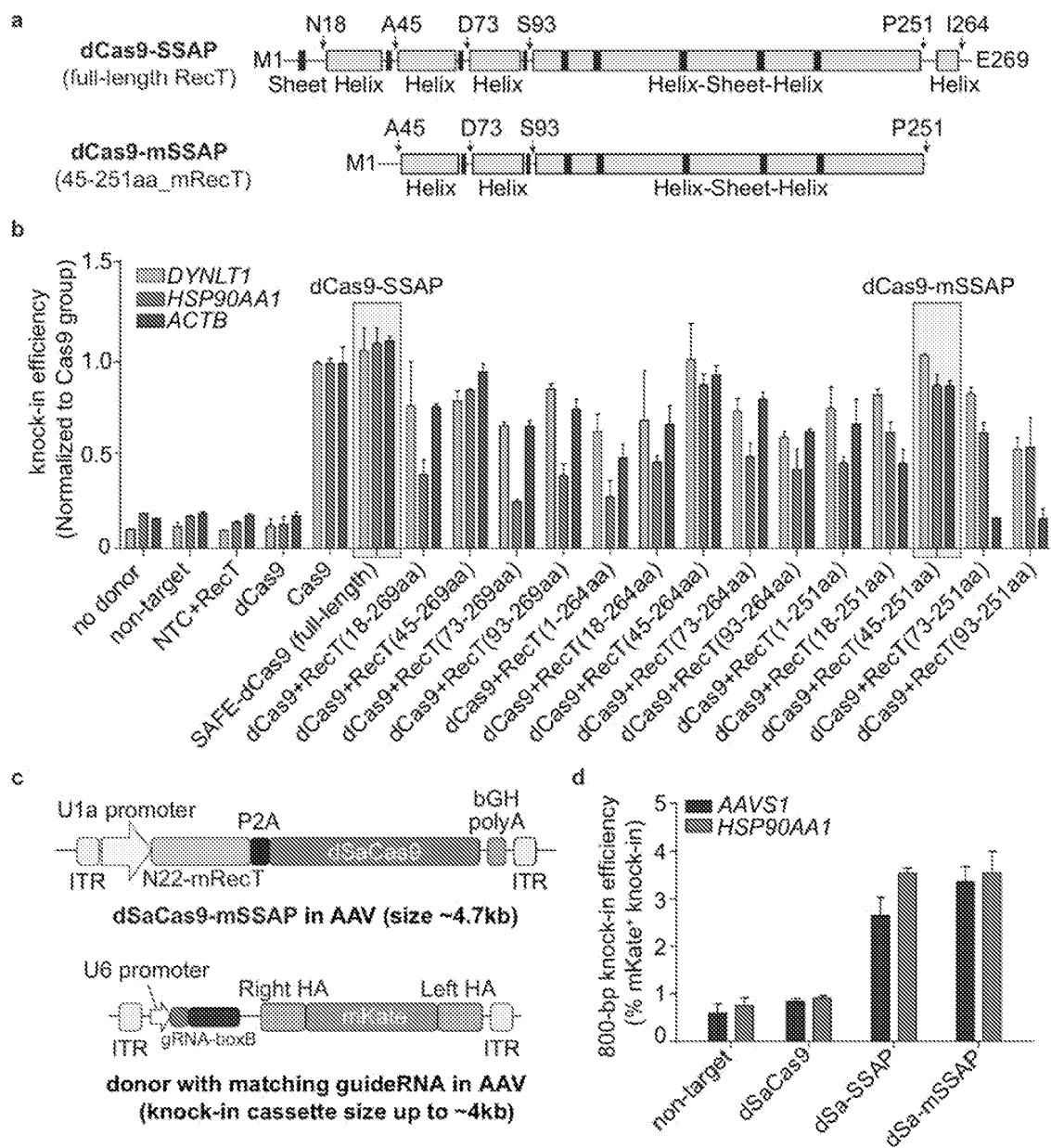


FIG. 42A-42D

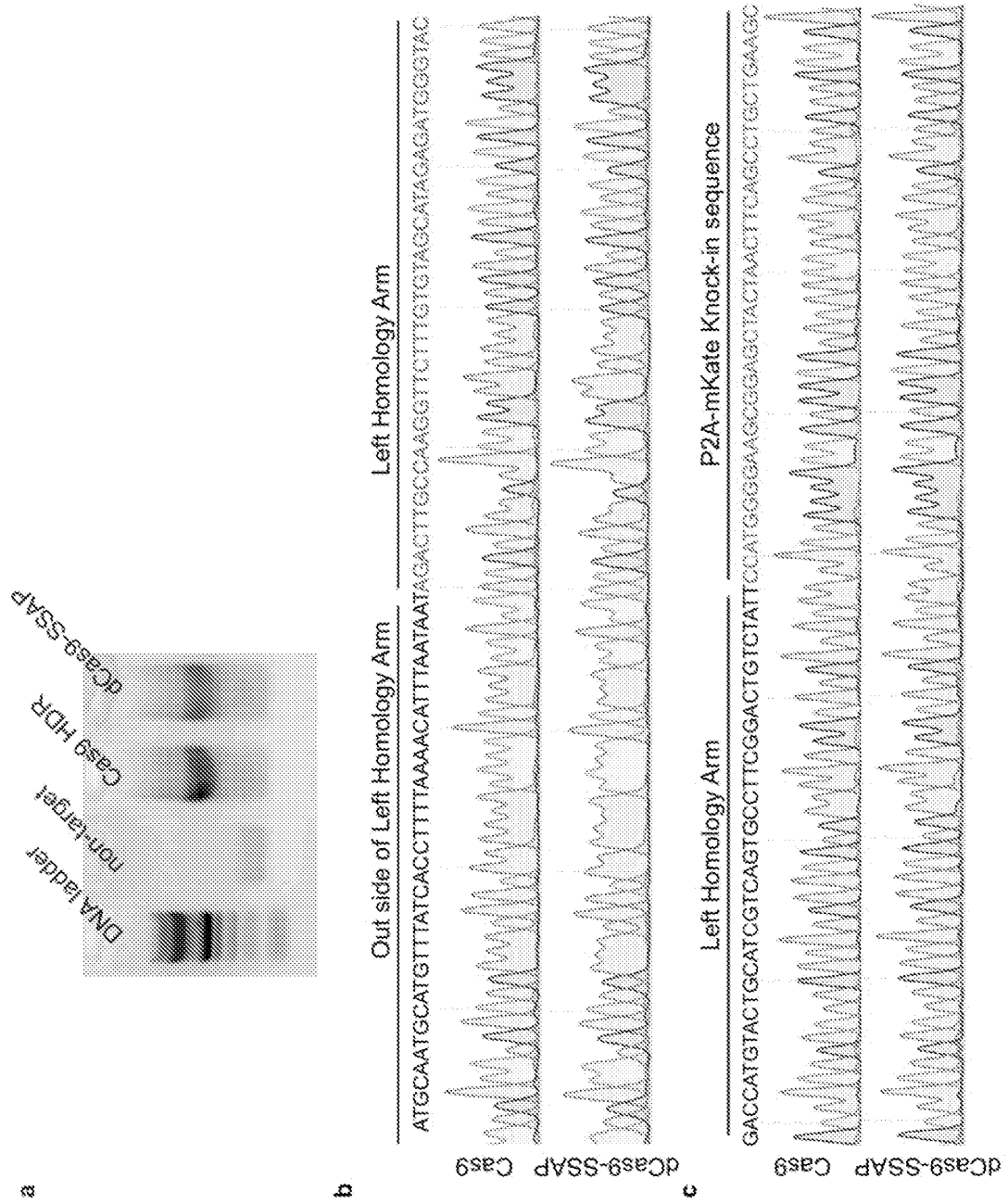


FIG. 43A-43C

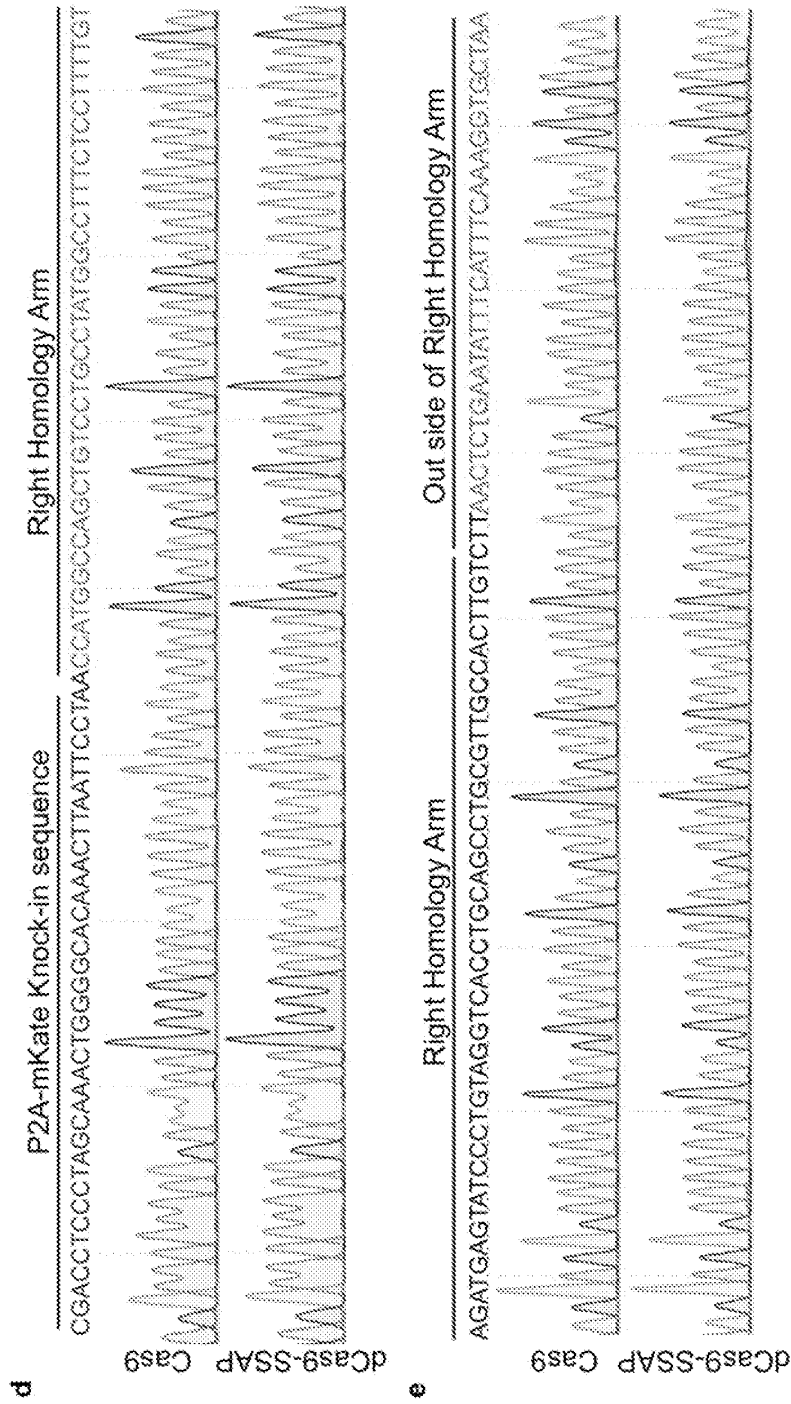


FIG. 43D-43E

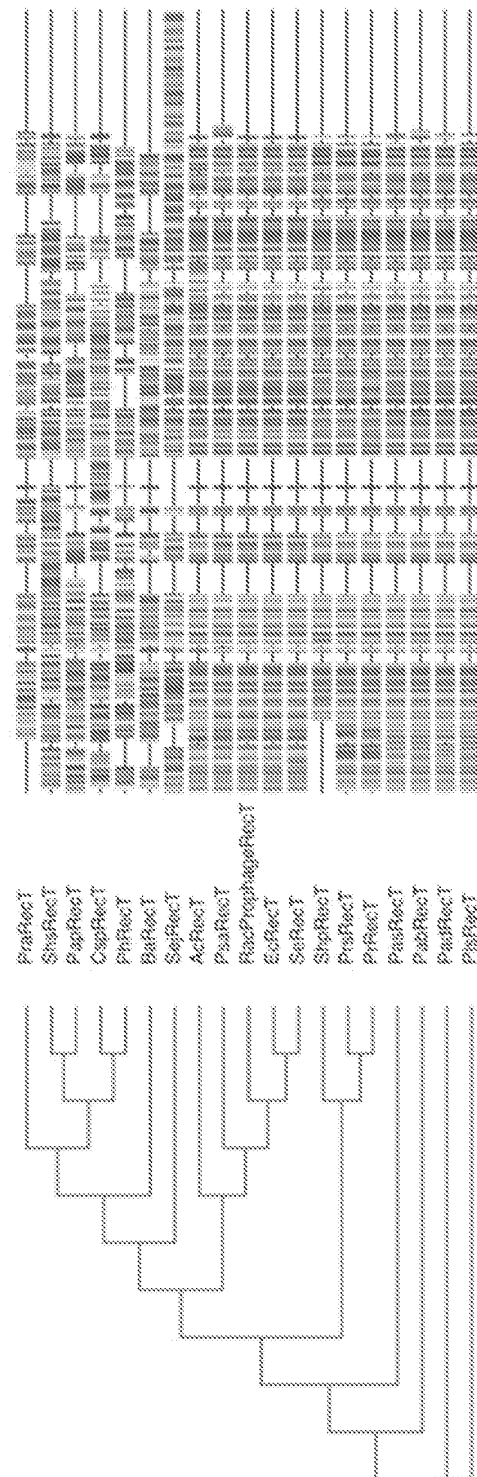


FIG. 44

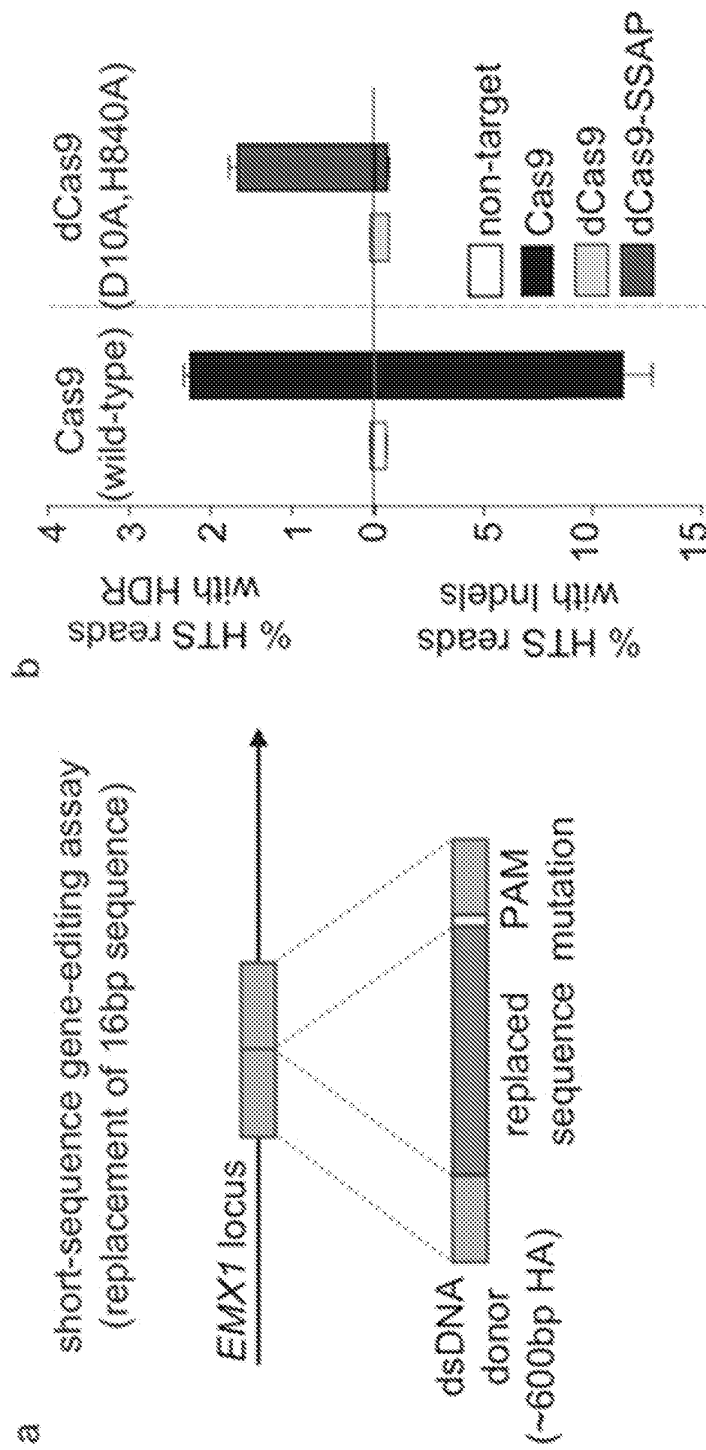


FIG. 45

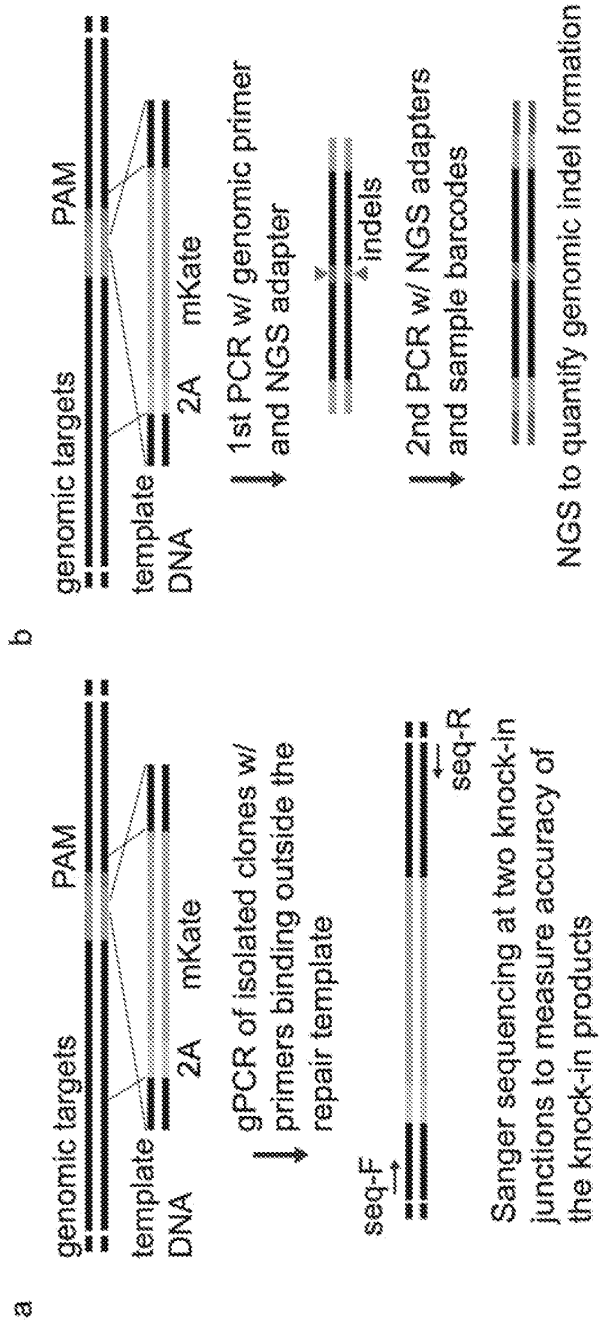
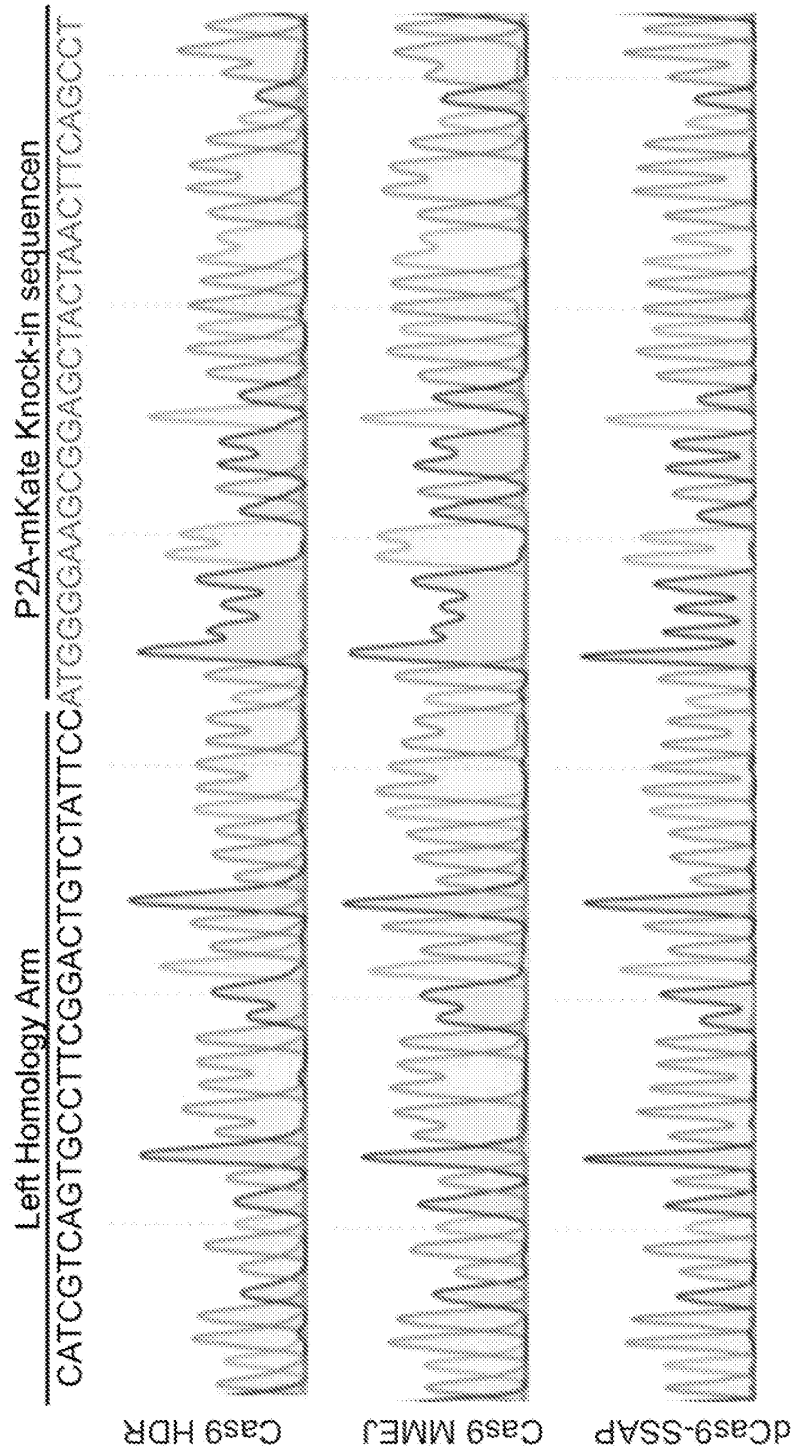


FIG. 46A-46B



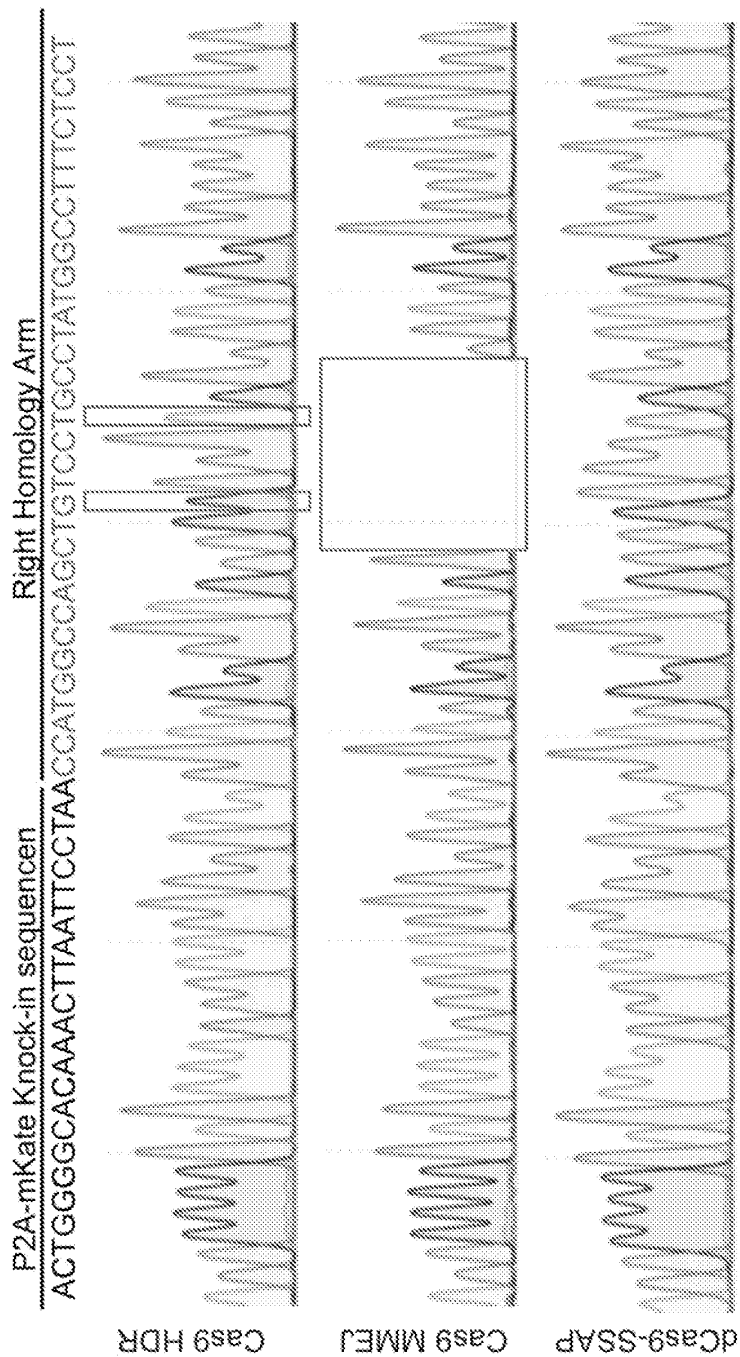
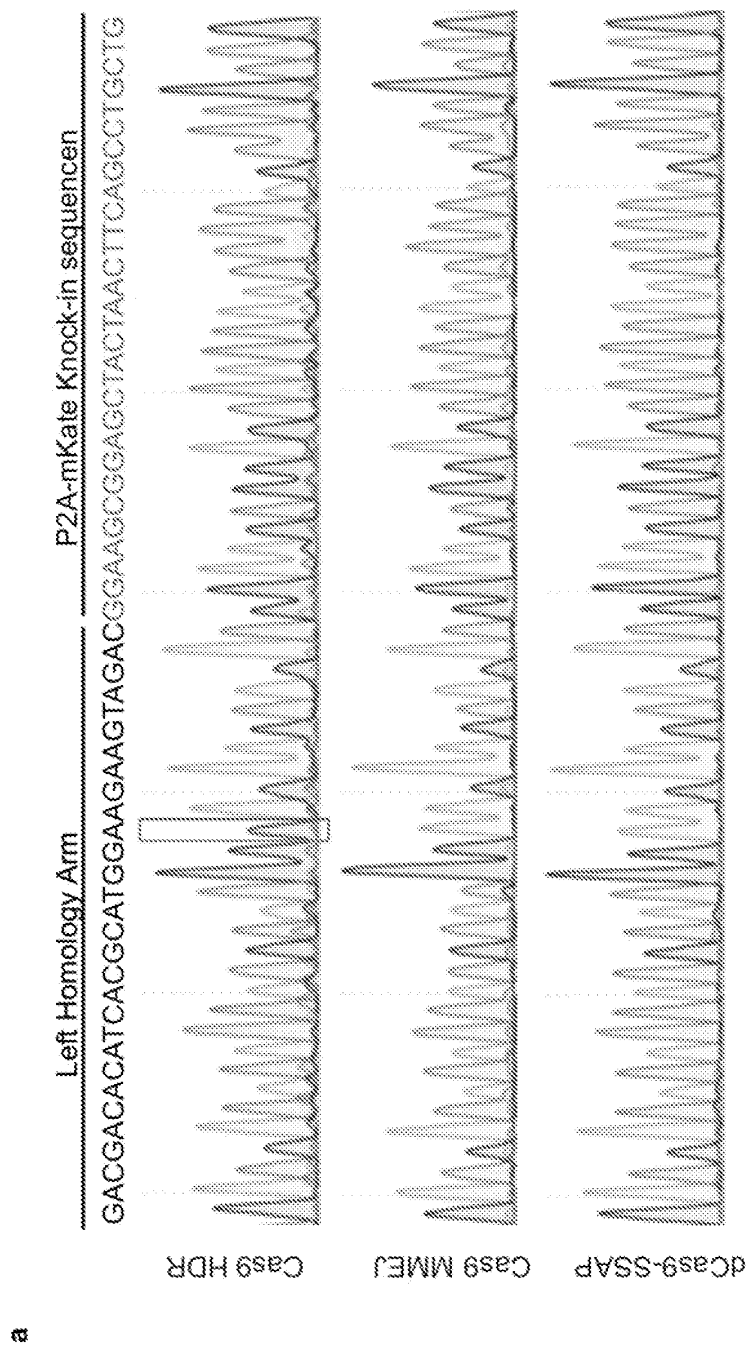


FIG 47B



b

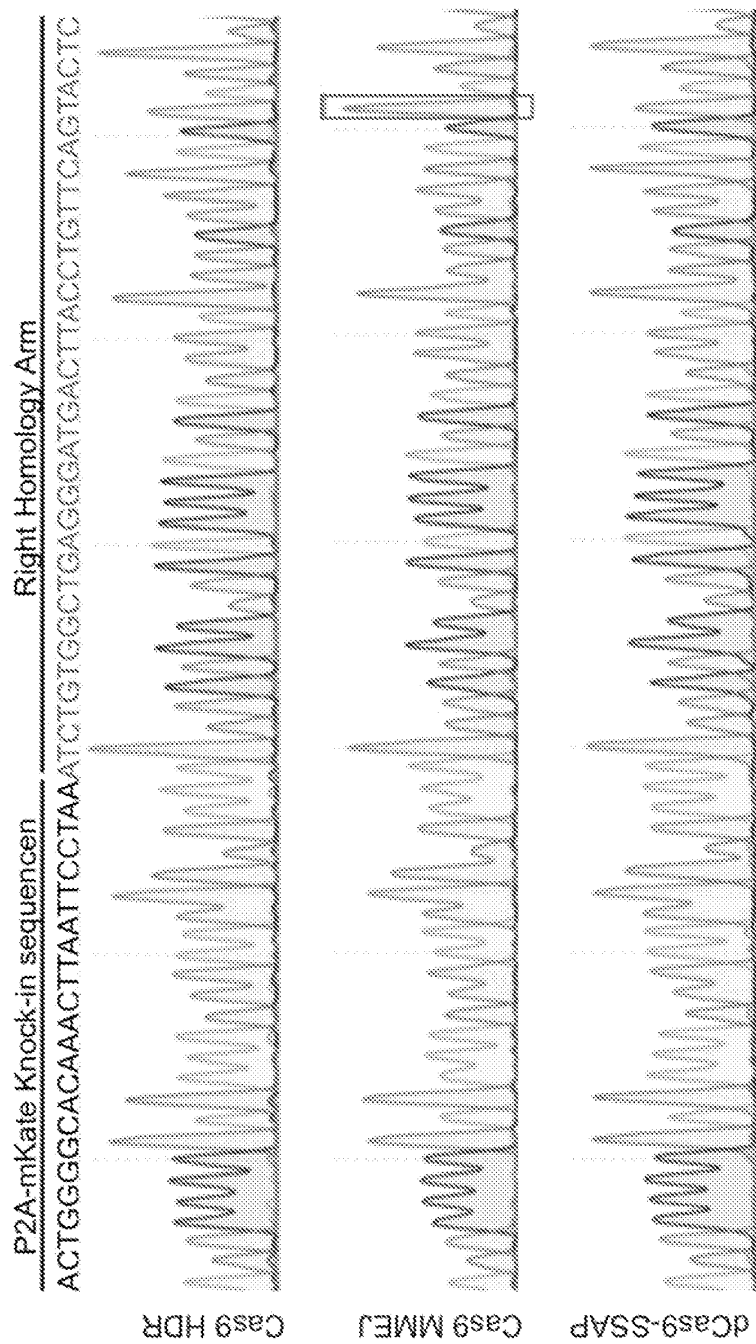


FIG. 48B

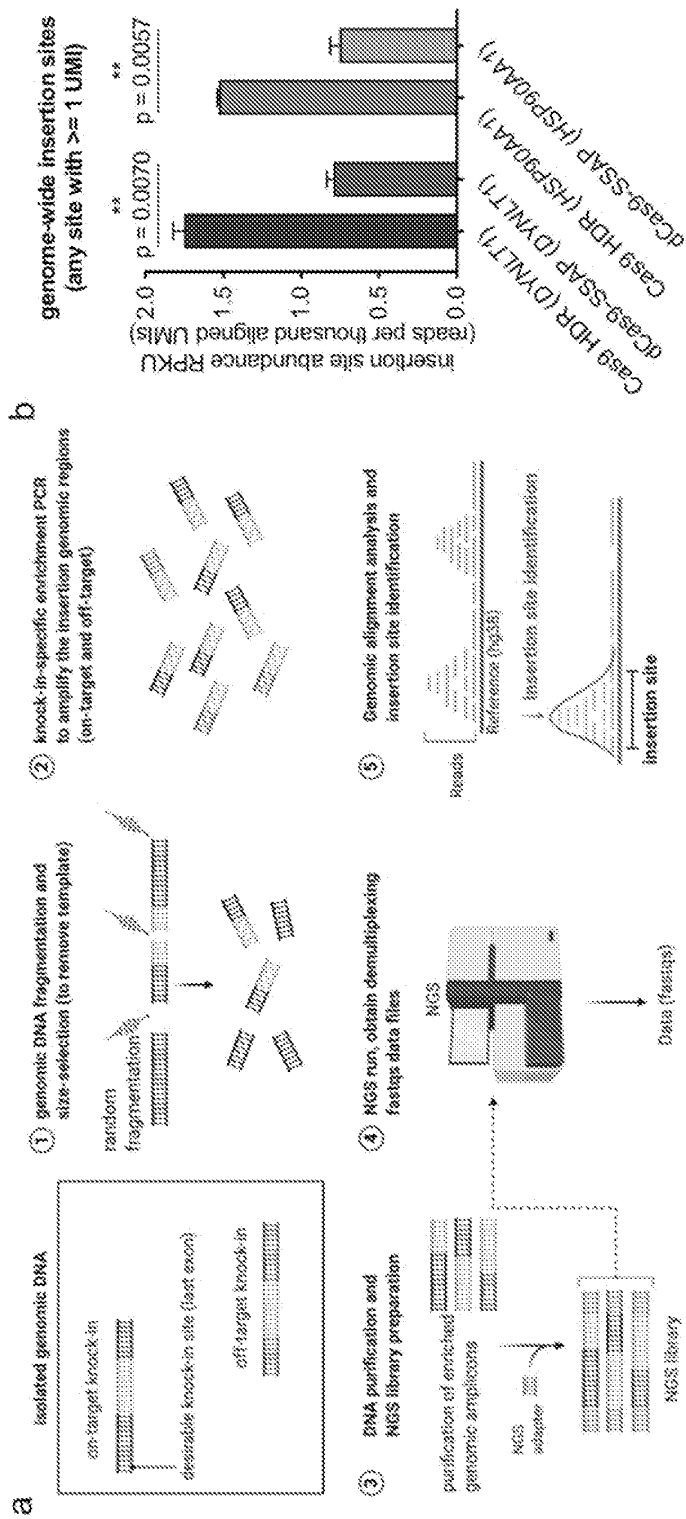


FIG. 49A-49B

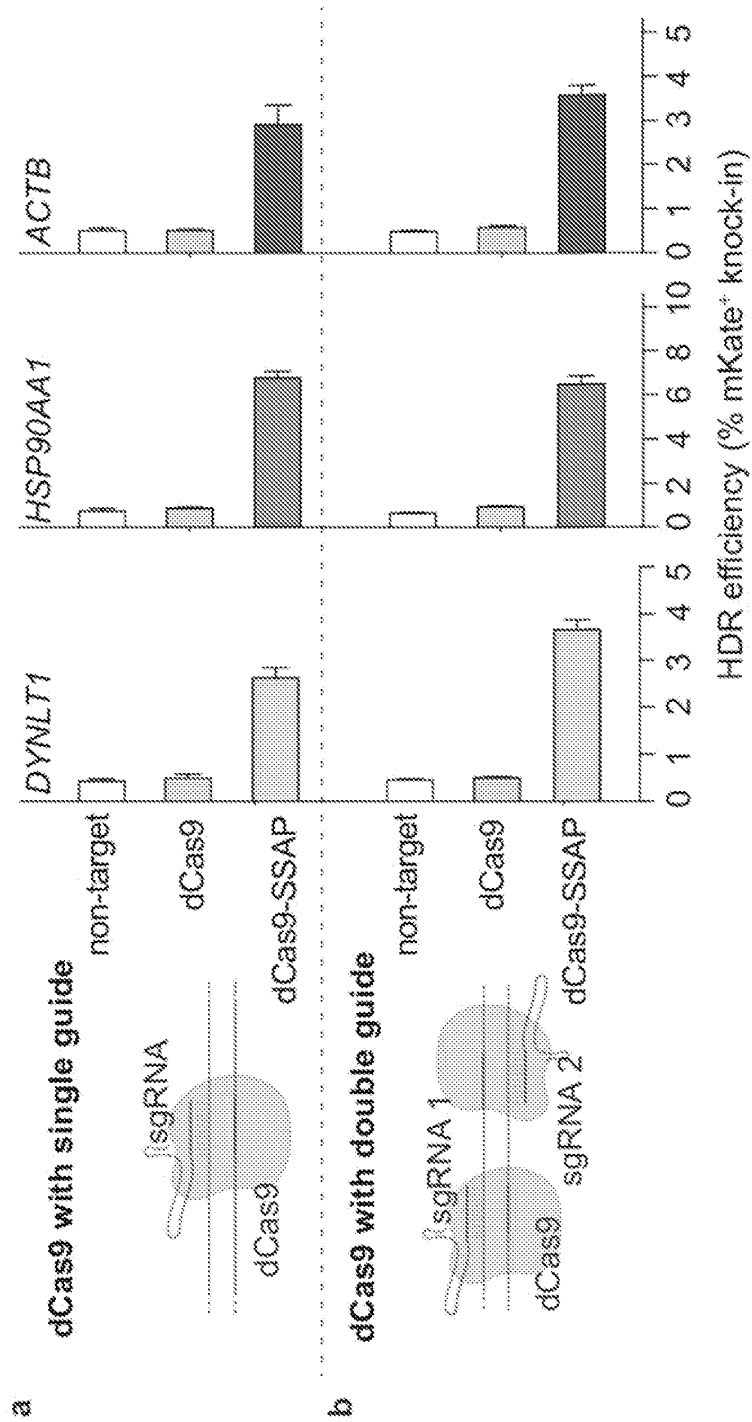


FIG. 50A-50B

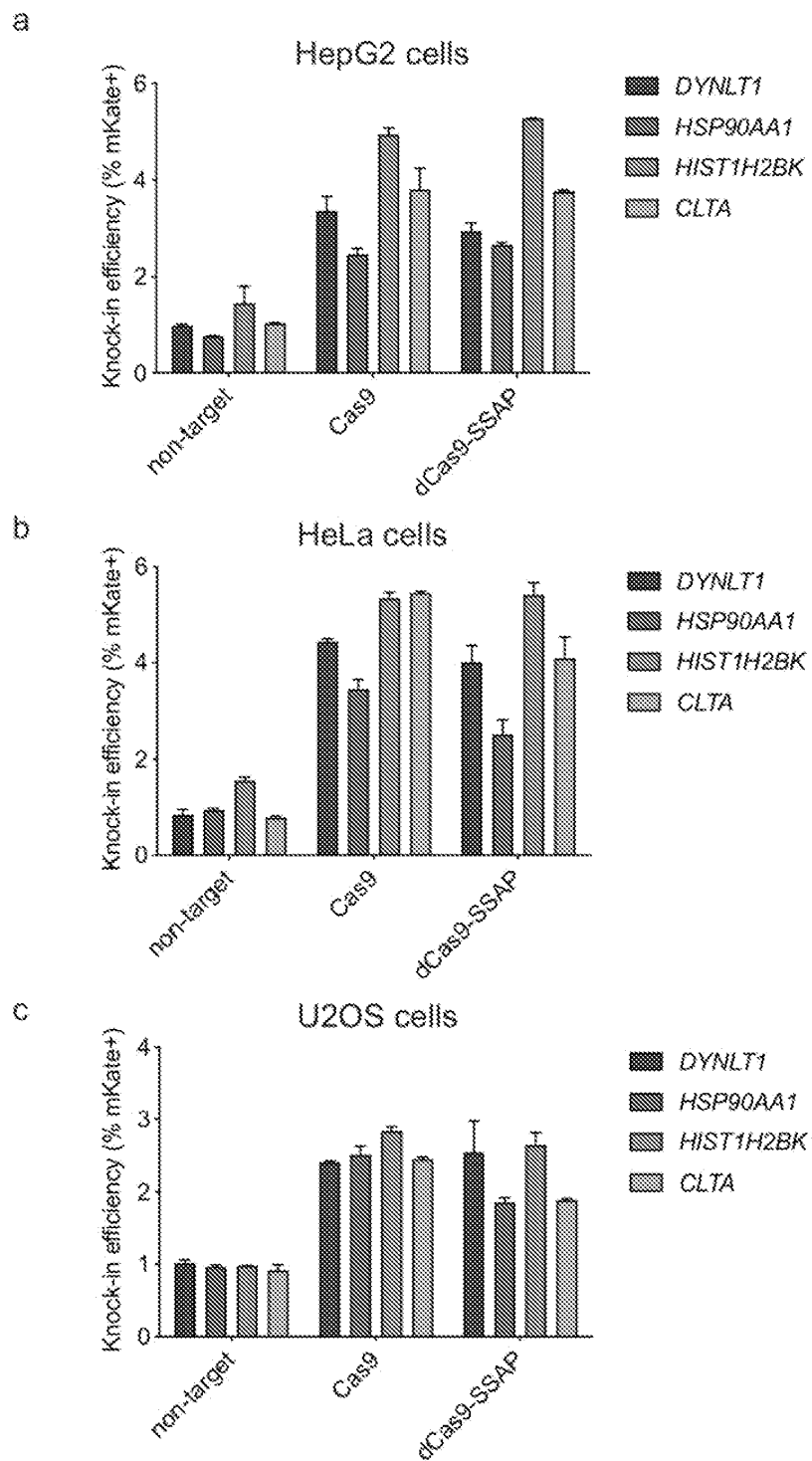


FIG. 51A-51C

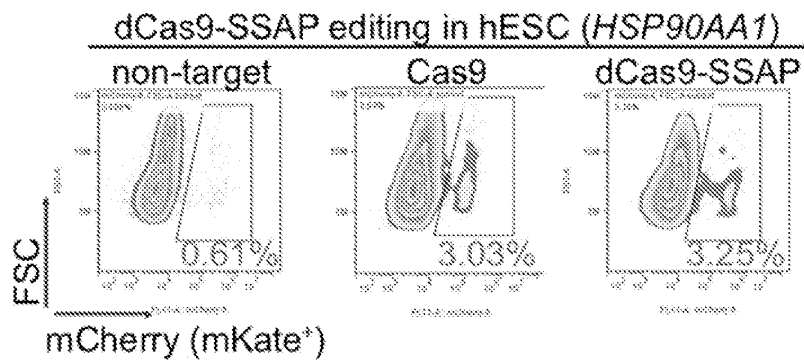
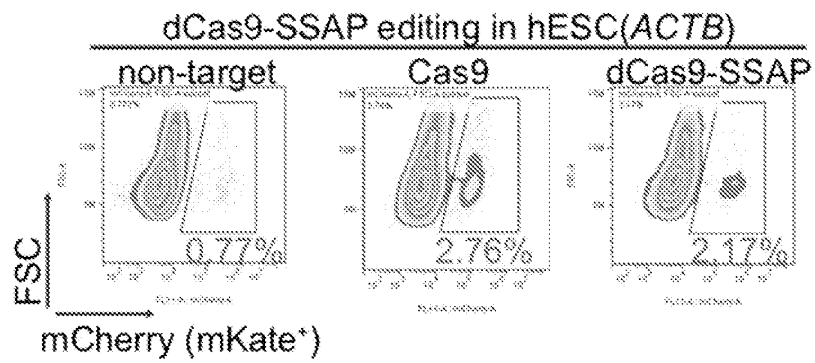
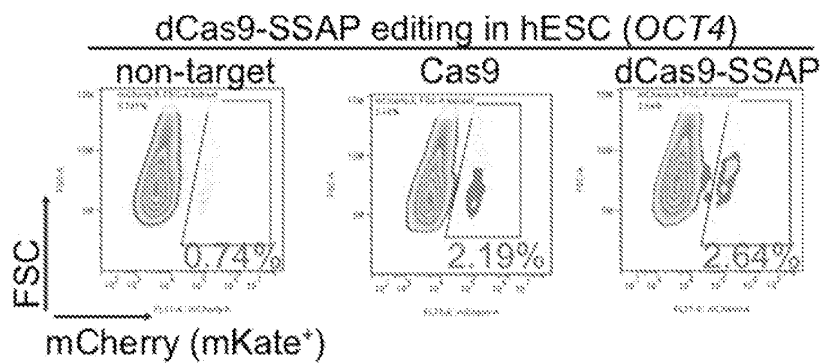
a**b****c**

FIG. 52A-52C

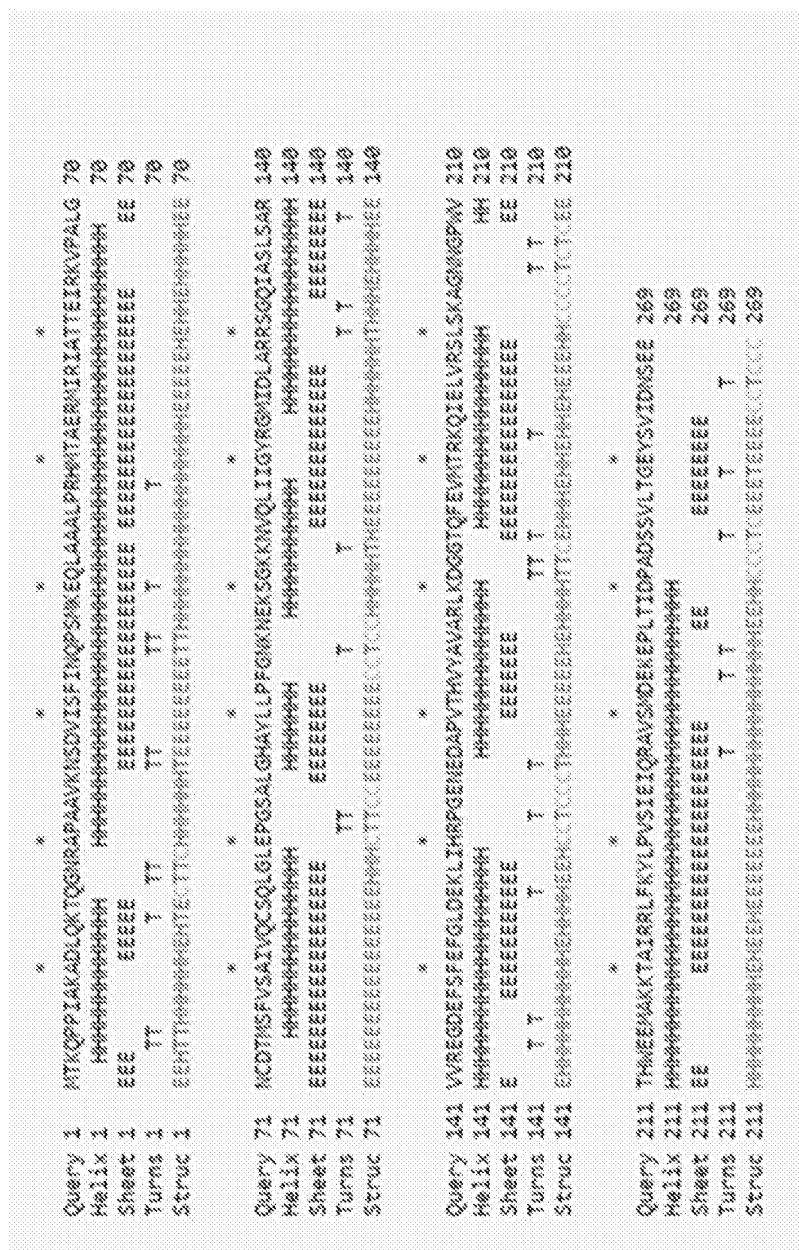


FIG. 53

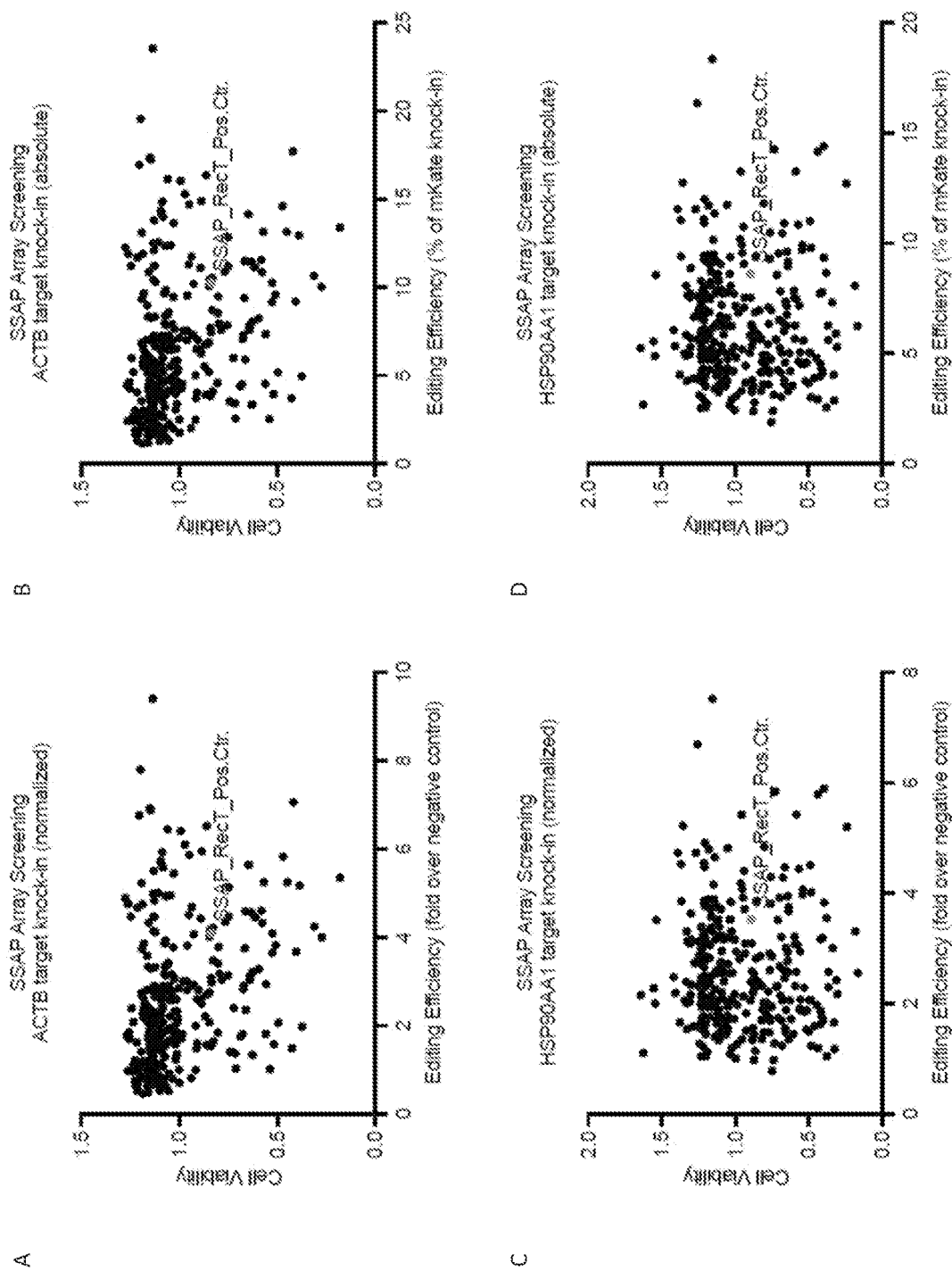


Fig. 54A-54D

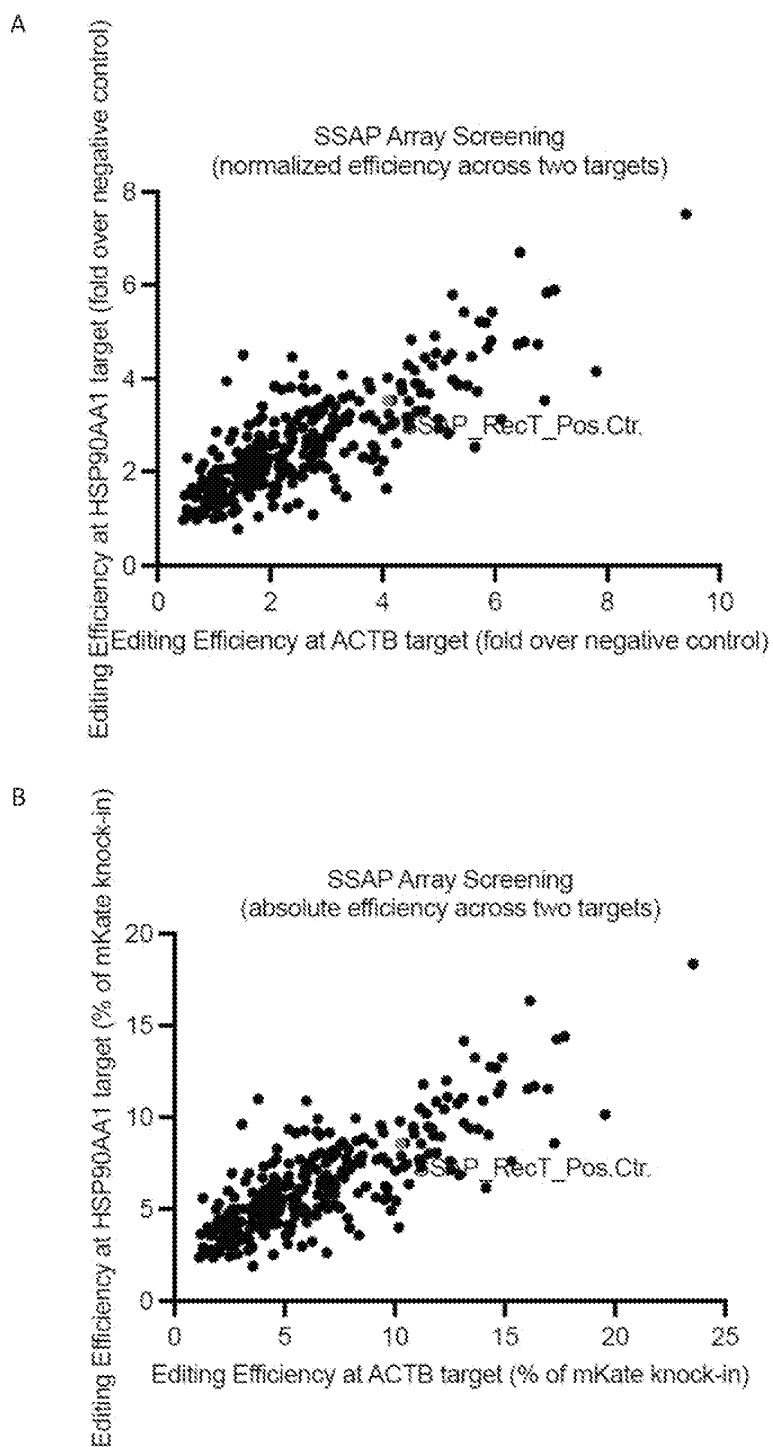


FIG. 55A-55B

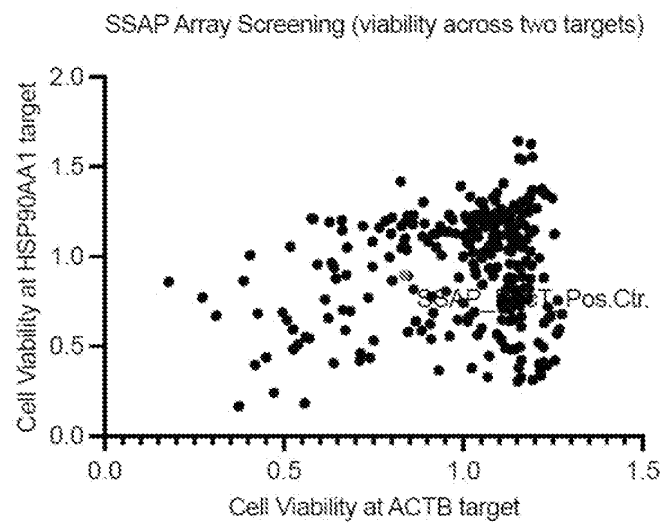


FIG. 55C

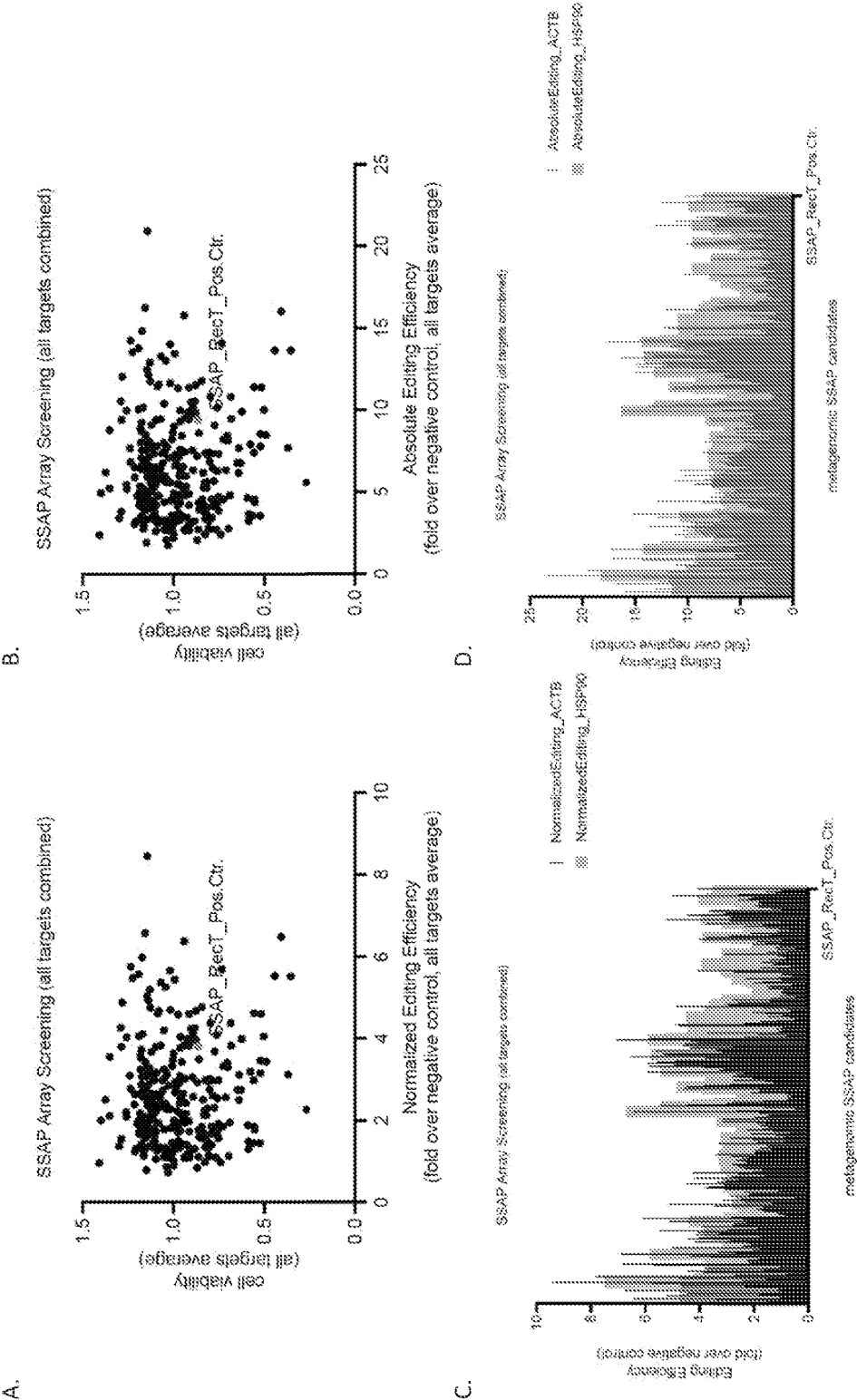


FIG. 56A-56D

					2 0.39884
					1 0.41069
					3 0.3789
					4 0.32729
					5 0.31762
					EcRecT 0.28714
2	-----	STALAHLAGELA-----	ERVGN	17	
1	-----	NAKENYSDPNKELLSSITTFEV	22		
3	-----	SSIAAAAEAEVTPAGIINKYRDDIATVLPFLERERIDRW----	49		
4	-----	SNLFALETNETKONSVTV--SNA-YAMXQLMIKMRGEITSALPTNL----SSERF----	49		
5	-----	-----	DADEM-----	5	
EcRecT	MYEQPPIAKA-DLQWFOGHRAPAAVKNSDVISTINQPMKEQLAAALPRHM--TAERM----			55	
2	DSVDVQBELITTLRQTAFKGD-----	ASDAQFIALLIVANQYGLNP--WTEEIYAPFPKGN--	70		
1	NGEEVVLGGNIIRDYLVSGN--AEVTDQELIMPLQLCKYQKL--	NPFLSEAFLVKKFKNTK	78		
3	-----	INLAIGAVNENPFLISRVRADQASMMQALMKCAALCHEPUGSLPH--LVPRGSR--	93		
4	-----	ENVALTAPNSNPKLQK-----	CDPFTPIAAMNQSAQLGLEPNTALGLAYLIPYEVK--	100	
5	-----	ARIALTLIRKNEPDLAT-----	CSGESFLGALMTCSQLGFEPGSPTEAFIVPYEGE--	56	
EcRecT	-----	IRIATTKIRKVPALGN-----	CDTNSFVSAIVQCSQLGLEPGSALGHAYLLFPCKKN	107	
	8	4 4 4	4 4 4 4	4	
2	-----	GIVPV-----	VCVDGWSKIINENQOFDGMDF-----	EQDN--ESCTCRIYKND	111
1	-----	GPDEPAQLIVSKEAFNKRATFHEQYDGFACVIVERGGETIELEGAVS-----		126	
3	-----	IEGWEDYKCILQRIDRSEVYARTVICVYVANDETSVDQNVDERPRHVR--ATGD		145	
4	-----	CINKVQFQIOYKCLLELANSKSNLSTLYAHEVRENDEPDIIDYGLEQKLINKPILLGN		157	
5	-----	ATFQLGYQGMVTLFTYQHPHASSVVKVEFVEENDYFEREERGLEEXLVHRPCETGP		169	
EcRecT	ERSCKKNVQLIIGYBGMIDLAKRSQIASLKAHVVEEGDEFPFEPGLDEKLIVPEGEED			167	
	1	1	1	1	
2	ENHPICVT-----	ENHDECE-----	REP-----	FFTEEGREITQFWQSHPRMLPHXAM	155
1	-----	LASDE--ELGGWAKVTHEDNRP--	VSVRISEKEFNKQSTWHTMPLTMKKTAV		177
3	RGEPISGYAYAVYPSGALTTVAAATPEQI--	ASKKKARGADNAASDWRAPGAPNKKVAV		204	
4	RCNVIGYYAVYHLEPSCVNFVFM--	TYDEVLEHCKKY--	SKSFEGGVNEKEFDMAKKTVI		214
5	RCKATAYYSVARLINGORTFKVM--	YPASI--	EEERKE--	LPSKNSPANESYDEMAKKTVL	165
EcRecT	--APVTHVYAVANLEDGGTQFEVM--	TRKQI--	ELVBSL--	SKAGNNGPWVTHWEEMAKKTAI	222
		1	1	1	
2	IQCARLAFQFA-----	GIYDEDEA-----	ERIVENTAYTAERQP--	ERDITPVNNETMQ	202
1	VNAMDEAFPDMLG-----	ANYTEEEQGSLOQTETETVQ--	QEIQNANAEVLDIPSQQNE--VP		231
3	KLEKN--VATSAEDRKEPISRS-----	AANDVVIDATADYYQEP--			242
4	KKLLKY--APLSIEMQRAIVFDESVMGSDSDMLLVDEKEDSIEGS--	ELN-----			261
5	KNSPKA--LPNSAELARANAHDCTVNTDWPDAIDVF--	PEYLSFPQSPFELGTGSTQ-----			218
EcRecT	RELPHY--LPVSTIEIQAVSMDEXEPLTIDPADSSVLTGEYSVIDNSEE-----				269
	1				
2	EINTLLIALDKTWUGDLLFLCSQIFRRDIRASSELTQAEAVKALGFLKQKATEQEVAA				250
1	DFKE-----	VREPERVEMPPFIYGE-----	QQST-----	PPAPY-----	250
3					242
4					261
5					218
EcRecT					269

FIG. 57



```

2      PICV-----TEWHDECKREFFKTRDGREIT-----GFWQSHPRKMLNHEAMIQCA
1      -----LASDKLLGCG-ANVFRKDRNEFPVSVRISEFEFNEKQSTWNTMFLTHMKKTAVVHAM
7      -----EIVLDLDNIXSOLRKINER-----YLIVMRMMLLALHL
3      FISSYAYAVYPCGAIITVAHATPDQIACGKSKARGADNAAGPWRAPGAPMHRKFAVELLE
6      IIAAYAIARLPNGE-VQFEIMNHEELEKVRKSGSEAAKNGGSPYDQWASEMMHRKAPIRRLF
6      IVKVIYAFKLNSGE-LVVEVMSRAGVEKIRDYVQSAKYDSSFWVKWFDHMLKTVIHRLA
9      MVGCVATARRHKQGG-TTWAYLTREQVEDERPSTWQE-----TPWGSHPDEMAKKTAVRALA
4      VIGIYAVYHLEPSC-YNFVFMTYDEVLENGKKYSKS-FEGGVNEKEFDSMAKKTVIKLL
5      AIAYYSVARLINGG-RTFFKVHYPAEIEERREKLPCK---NGPAWRNGYDEMAKKTVLRNHF
EcRecT VTHVYAVARLXDCG-TQFEVMTKQIQLVRSLSKAG---NNGPWWTHWEEMAKKTAIRRLF

```

1 2

```

2      RLAF---GFAGIYDEKDEAERIVENTAYTA-ERQPERDITPVNNETWQEINTILLIALDKTWD
1      REAFFDNLCAMYTEEEQGSGLQNTETSVQGEIFQMANAEVLDIPQQQN-----
7      R-----KISKG-----
3      R-----HVATSA-----EDEREPIGRSAANDVVID-----
8      K-----YLPKHNIPOQVINTLSLD-----EQNNGVDFFSAQEQEAFEG-----
6      R-----ELPCAS-----ELFSLFEVY-----EDANS-----TEKTLRM-----
9      K-----YLPKAT-----DLGRAIEADEQ-----KVQHVVEGLDEVTVTELDD-----
4
5
EcRecT

```

```

2      DULLPLCCQIFREDIRASCELTQAEAVKALGFLKQKATEQKVAA
1      -----EVPDFKEVNEPERVEMFFIYG-----EQQGTFFPARFY
7      -----
3      -----ATADYYQEP-----
8      -----KAADFFEDEPANTVDADYTDN-----SHEEADNELAA-----
6      -----APASFKRLSIN-----
9      -----EPETVVVQETTDANAATPVVAEVQP-----
4      -----LLVDKEDESIEGSELM-----
5      -----VPPEYLSEPORPELGTGSTQ-----
EcRecT -----LTGEYSVIDNSEE-----

```

FIG. 58 (cont)



FIG. 59