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FIG. 1A

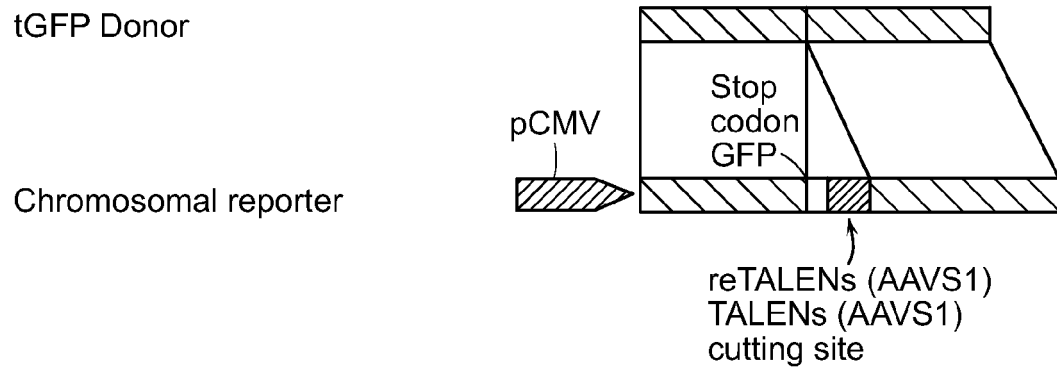
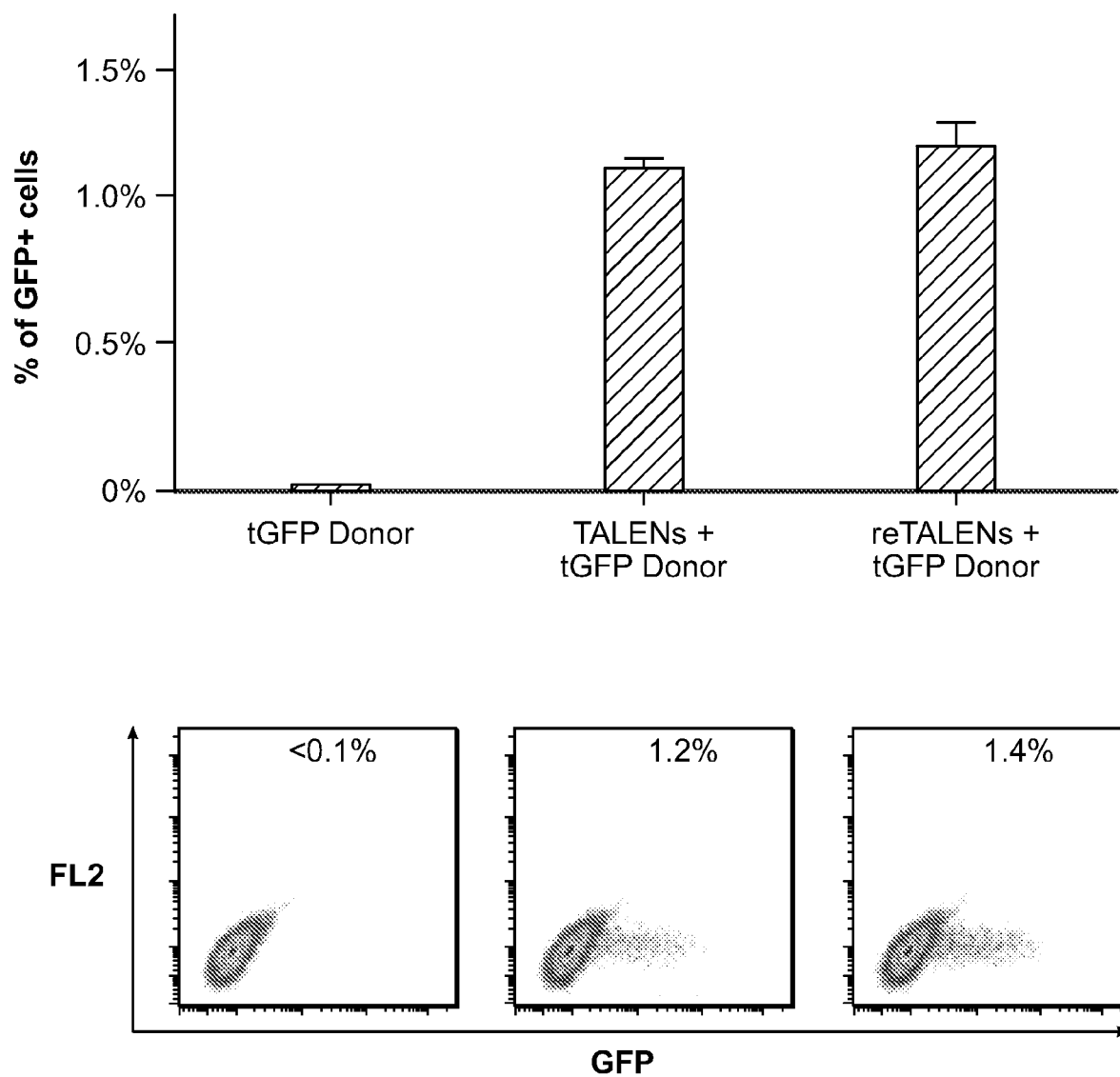
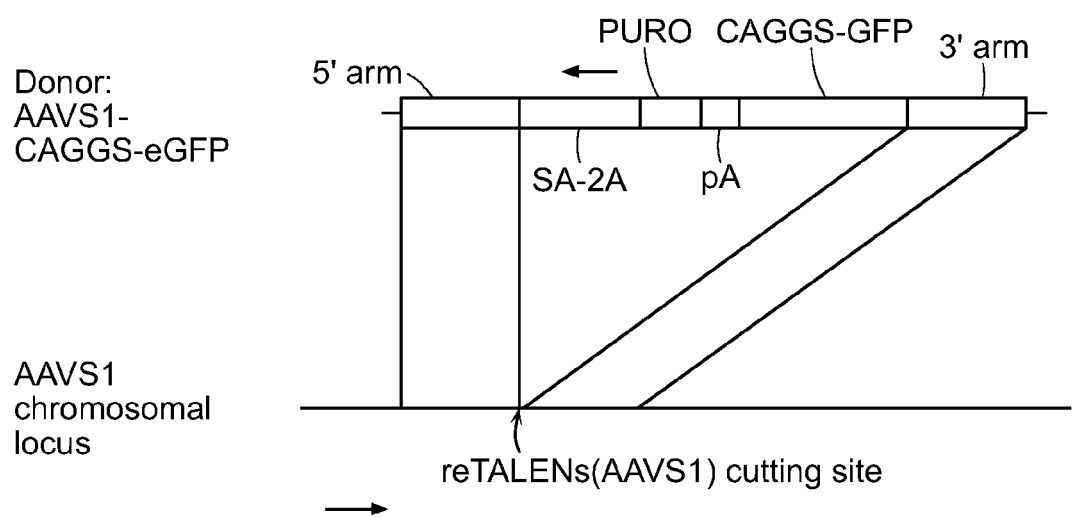


FIG. 1B



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FIG. 1C



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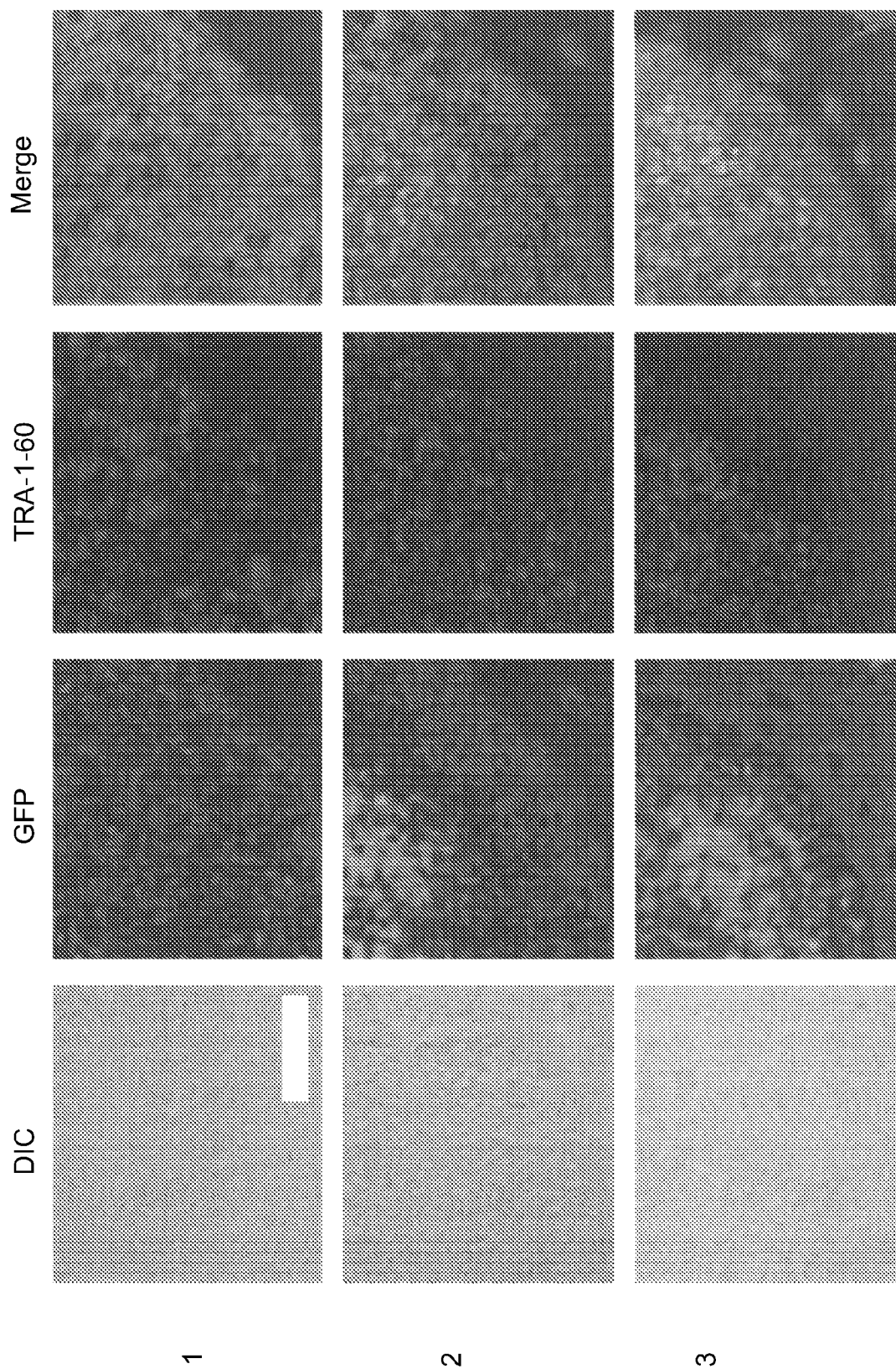


FIG. 1D

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FIG. 1E

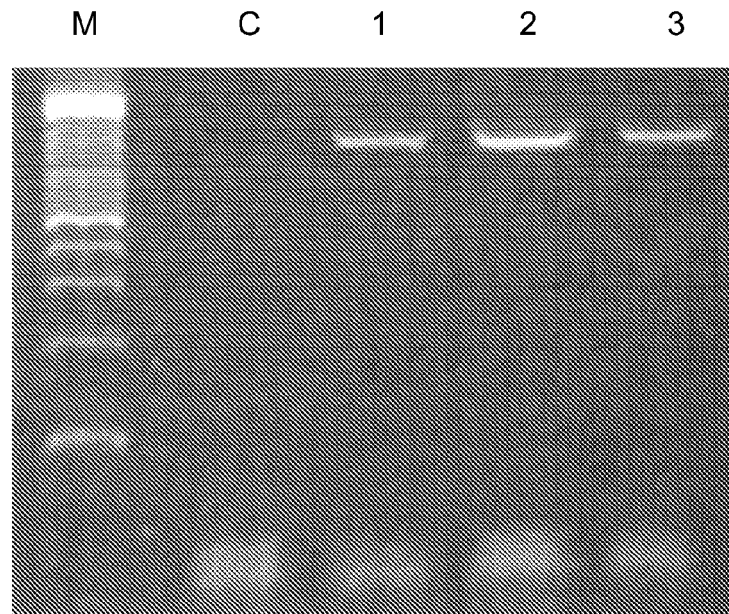


FIG. 1F

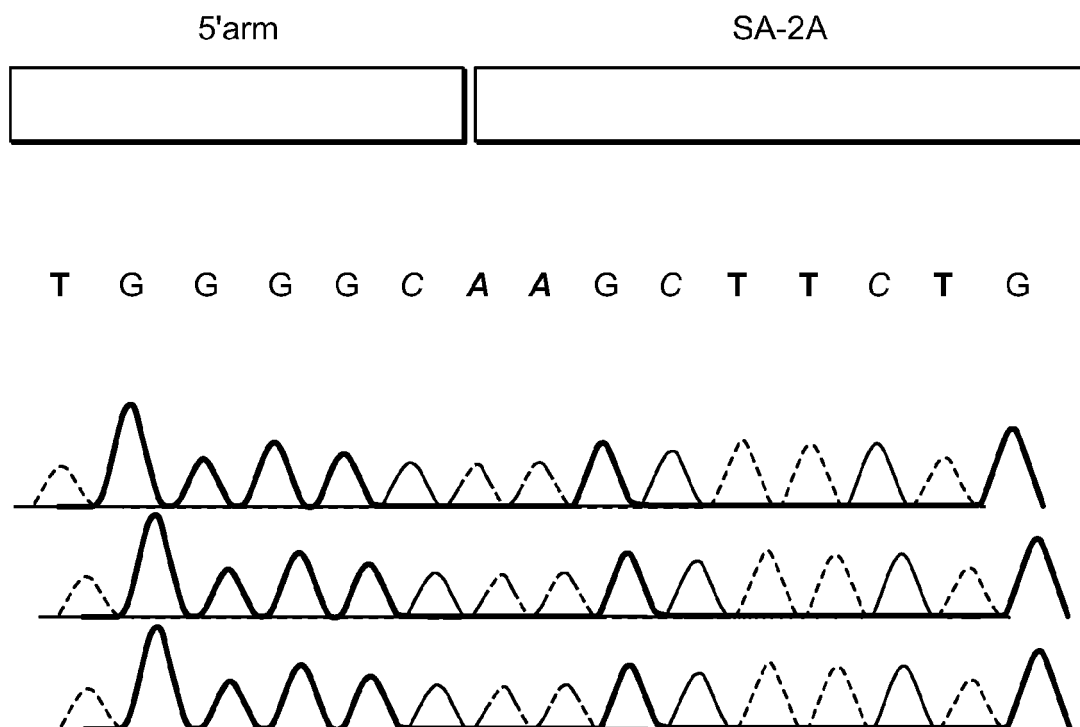


FIG. 2A

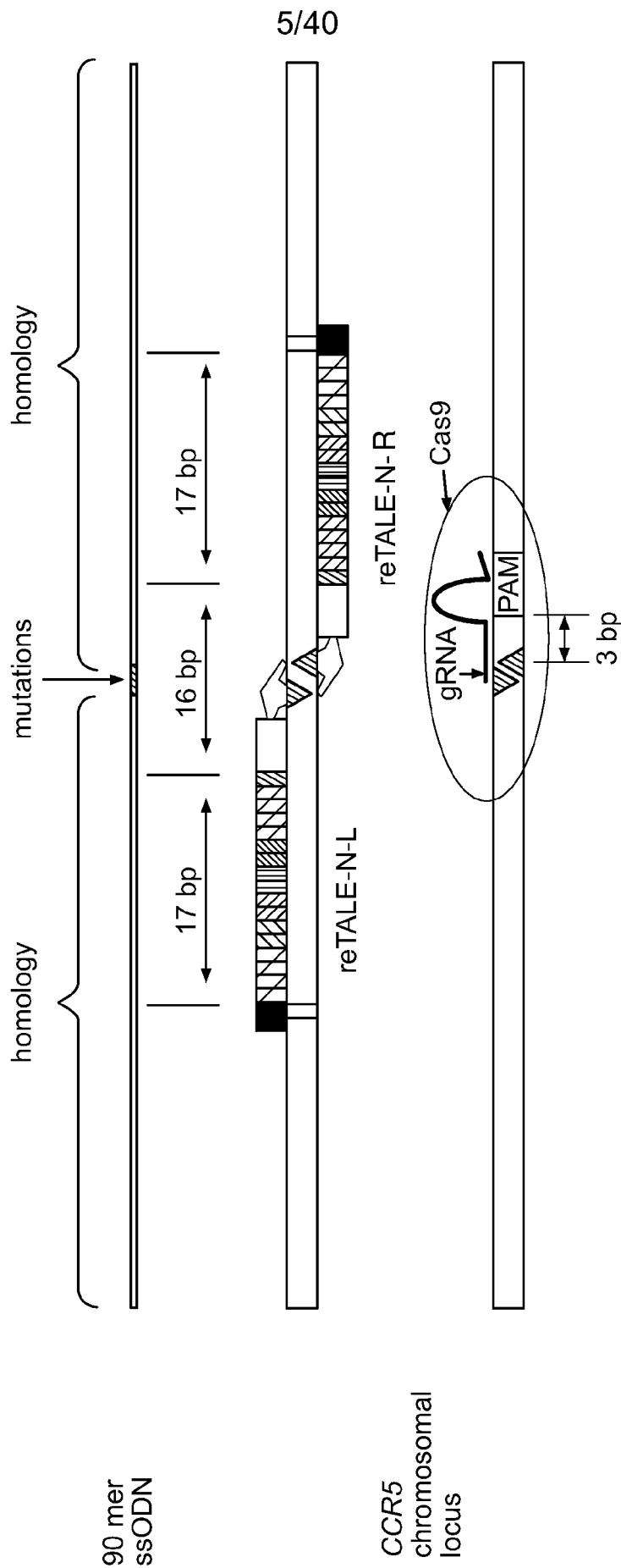
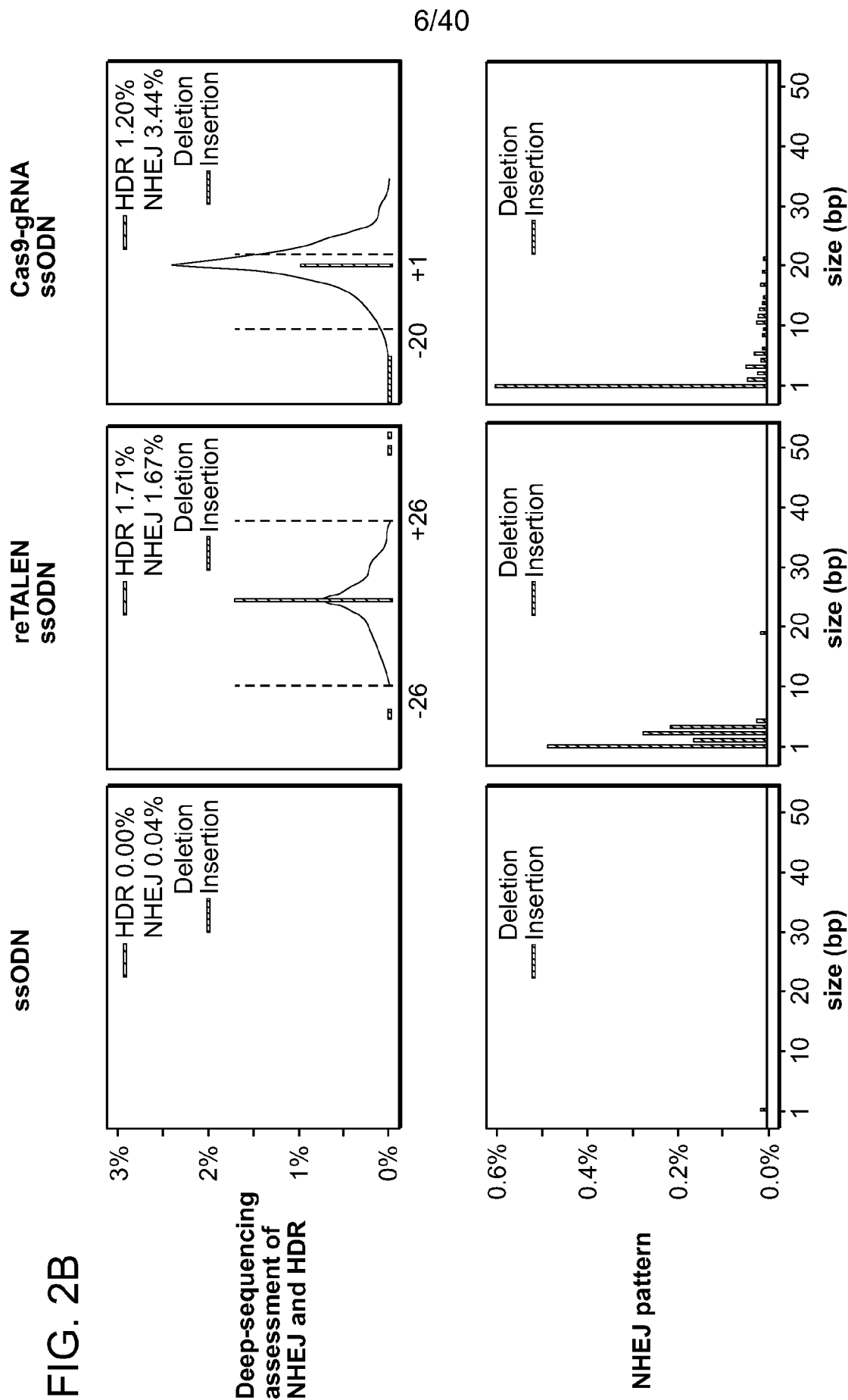
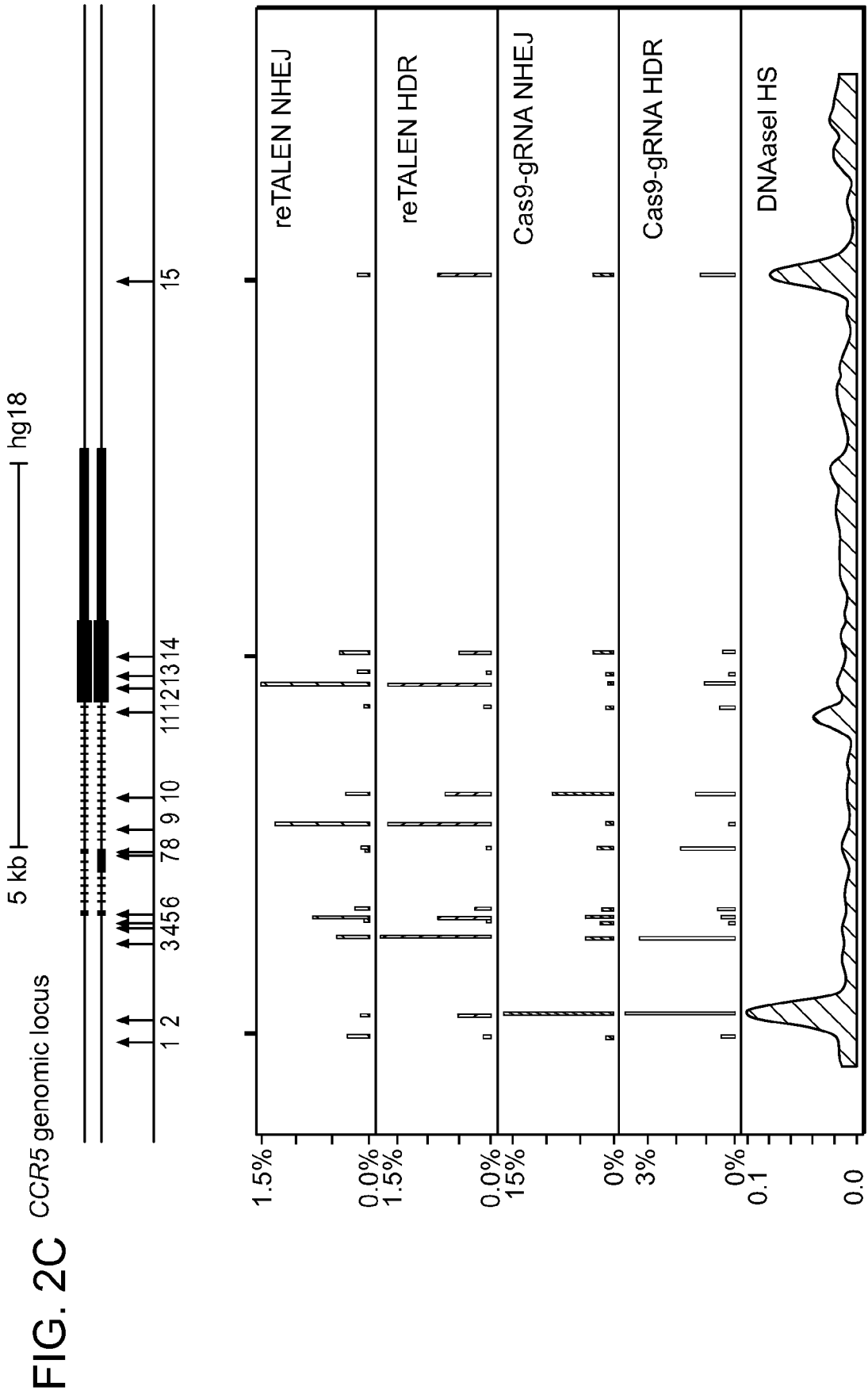


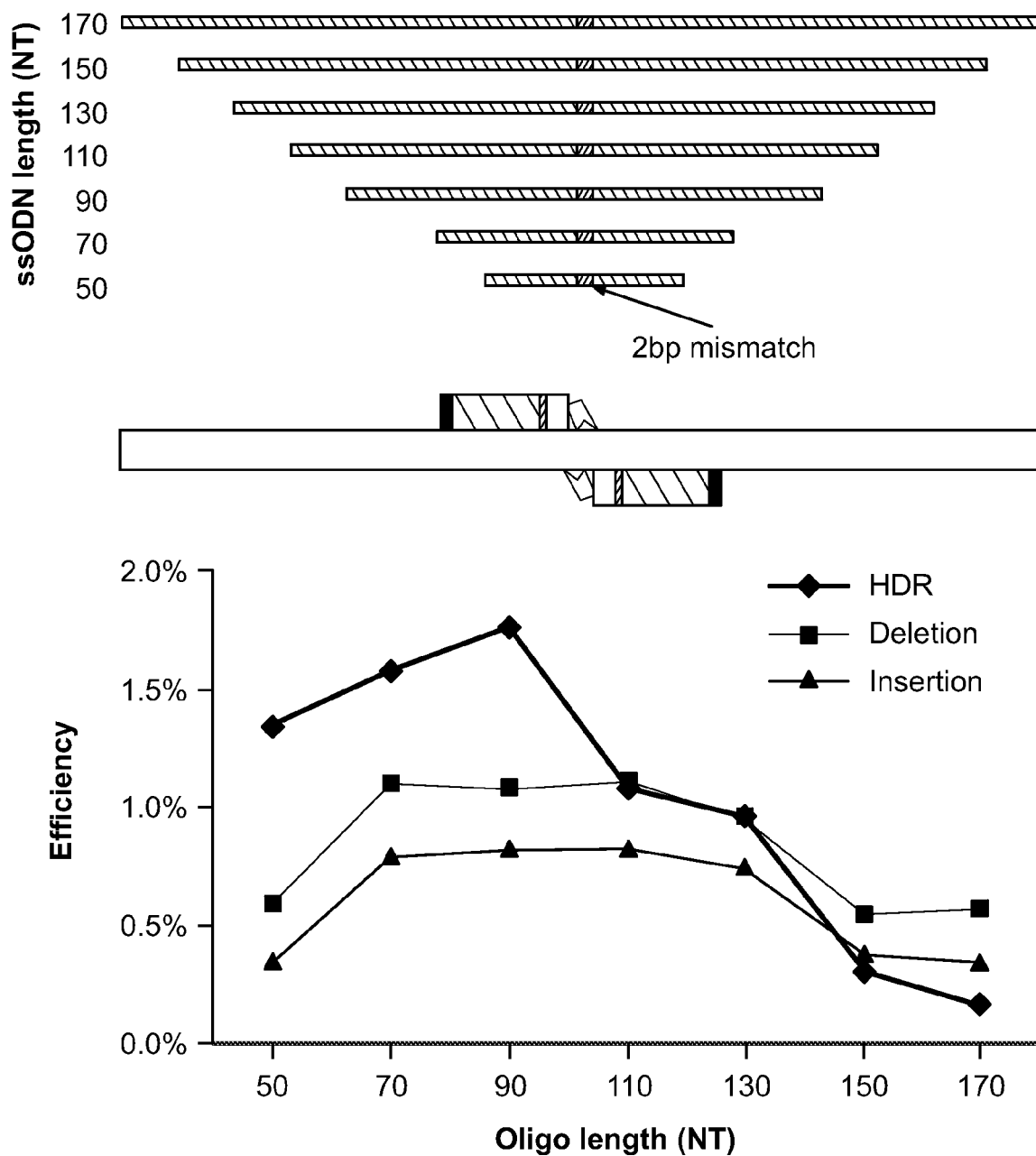
FIG. 2B





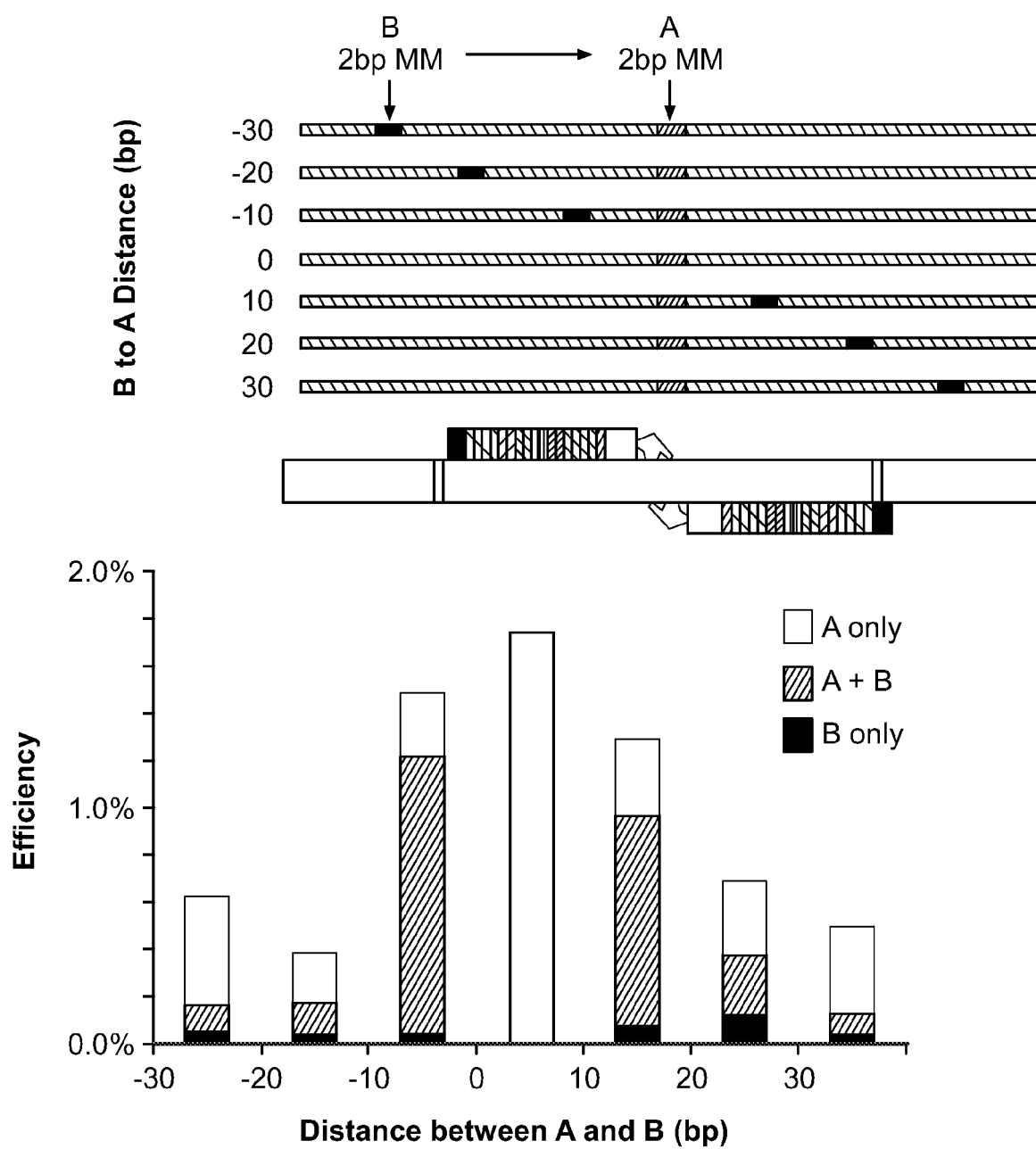
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FIG. 3A



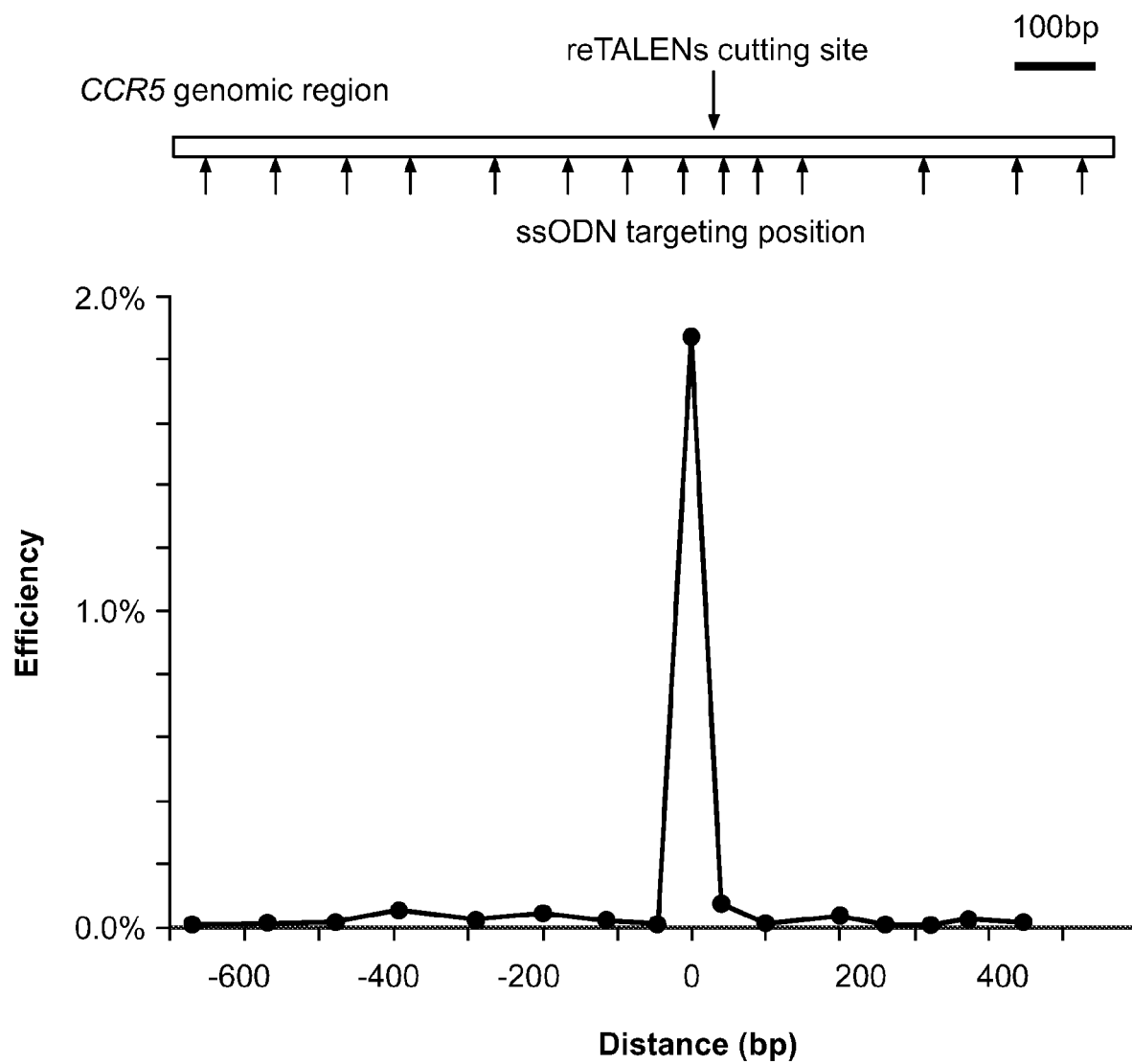
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FIG. 3B



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FIG. 3C



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FIG. 3D

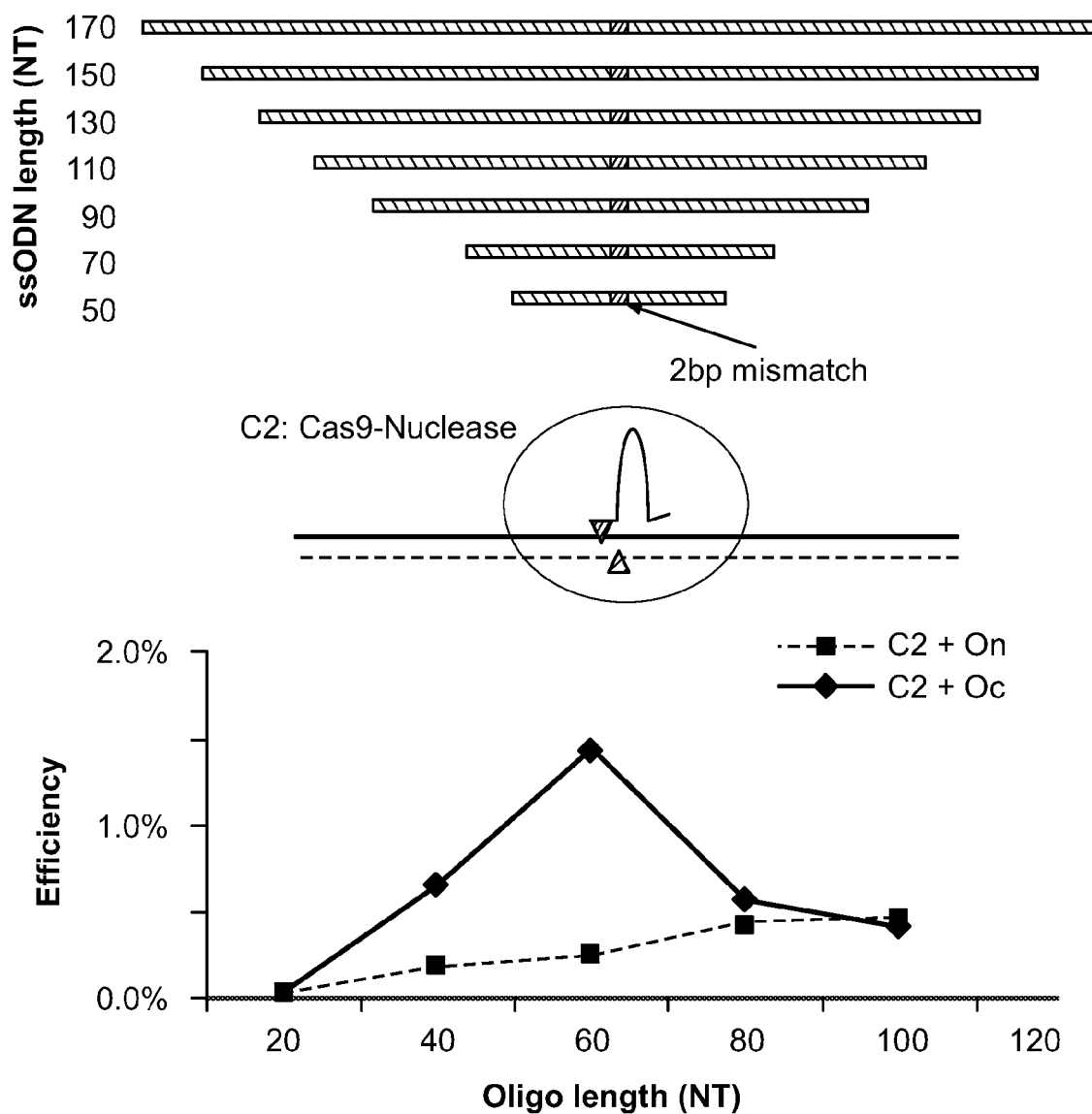


FIG. 4A

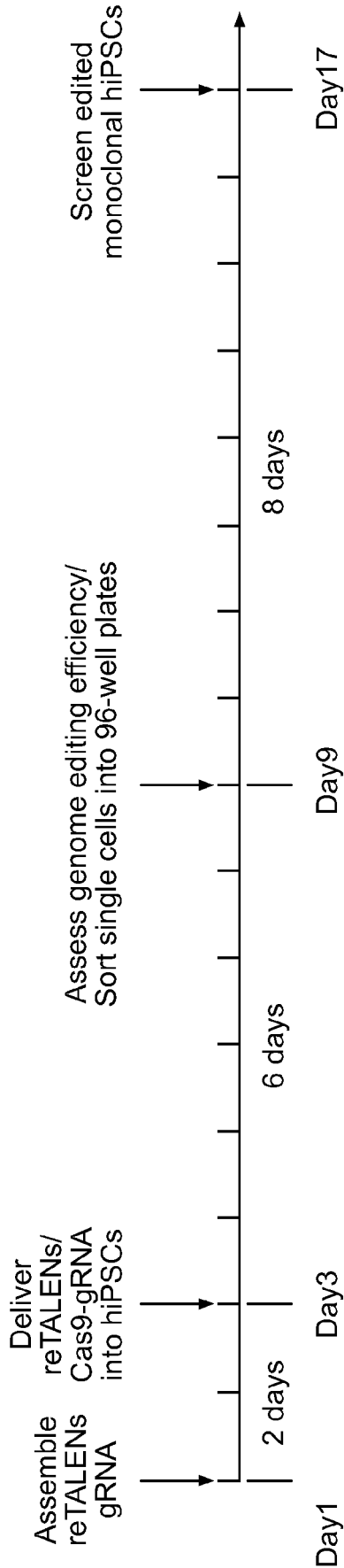


FIG. 4B

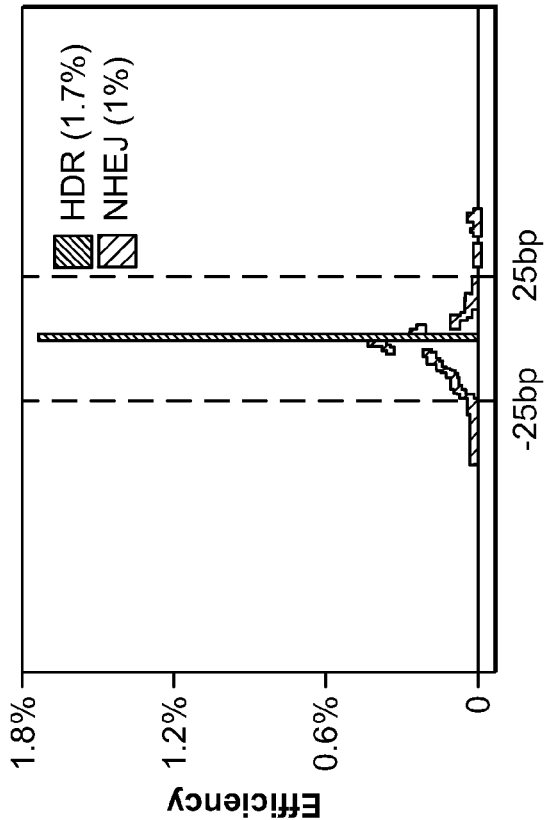
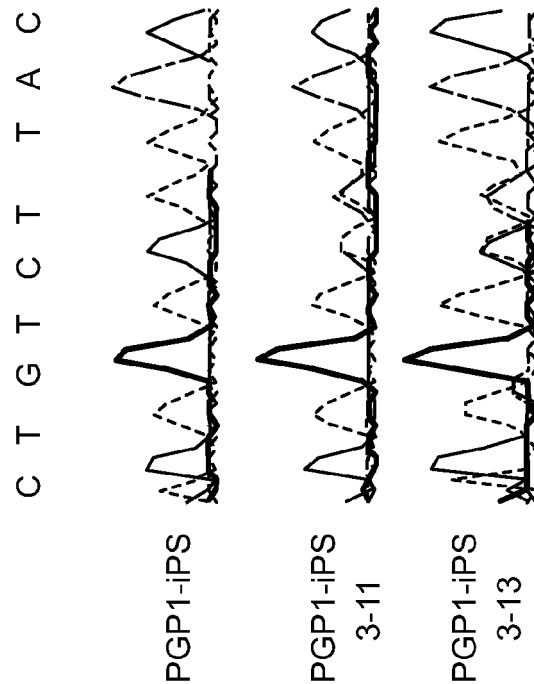
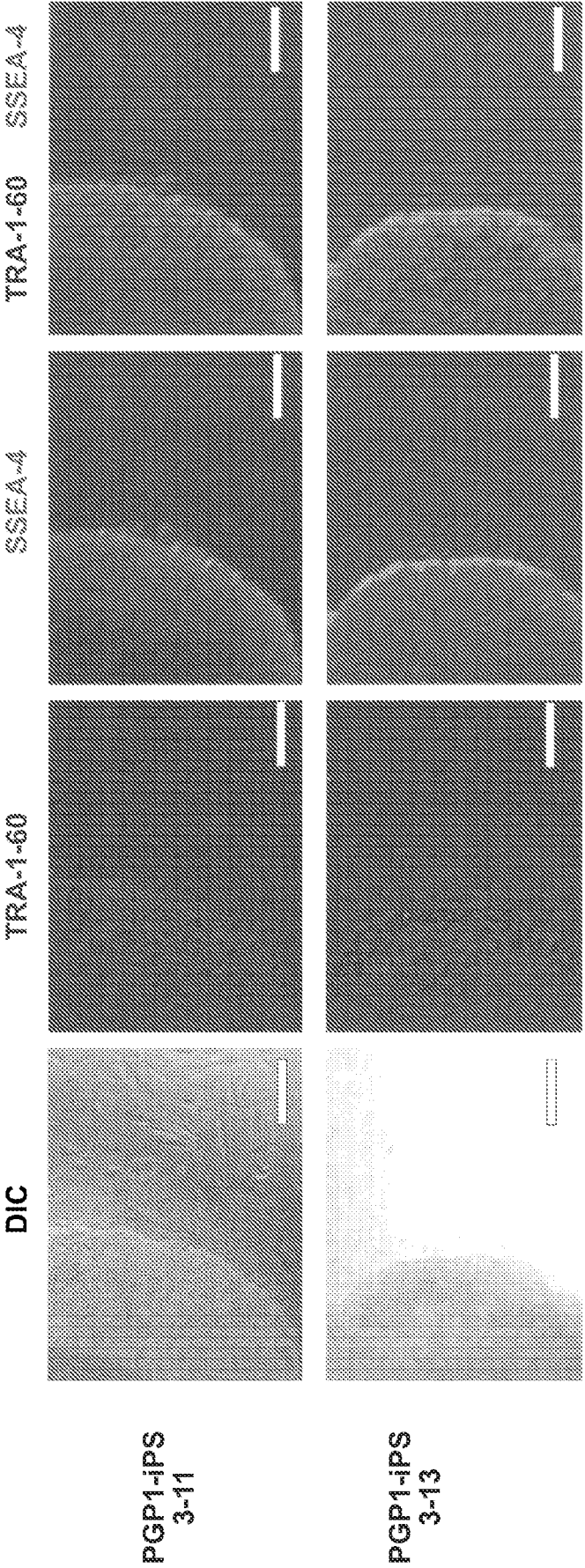


FIG. 4C



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FIG. 4D



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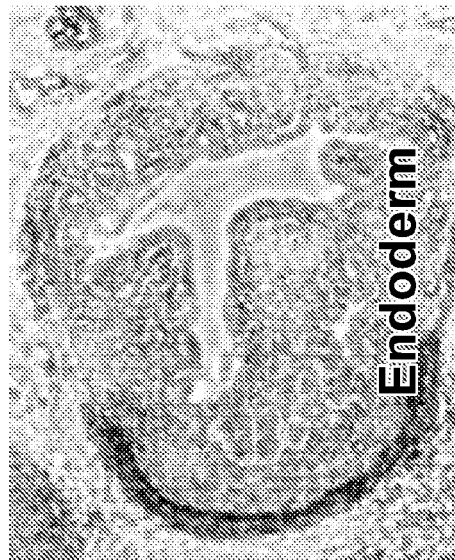
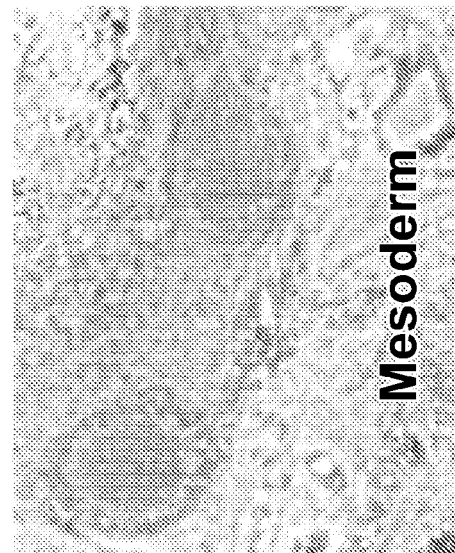
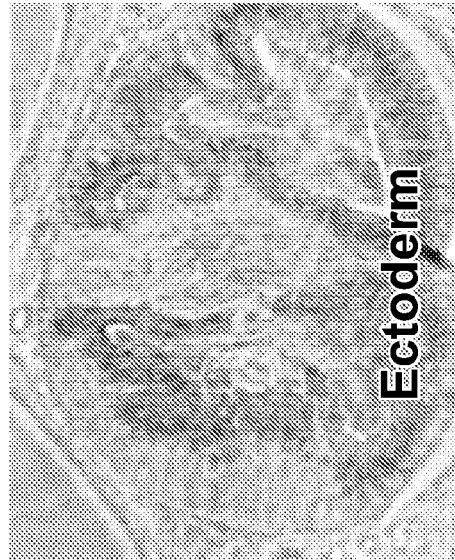
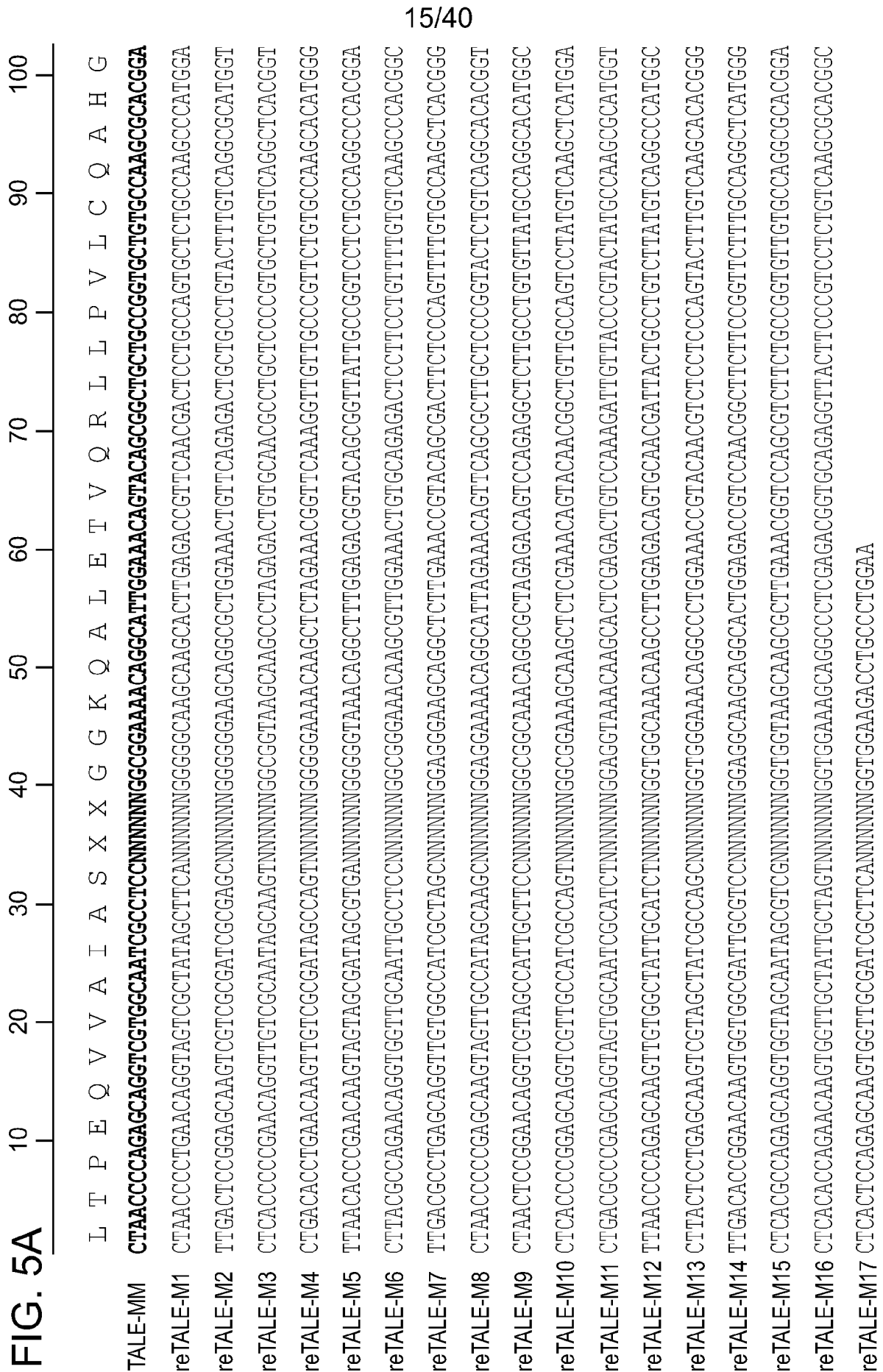
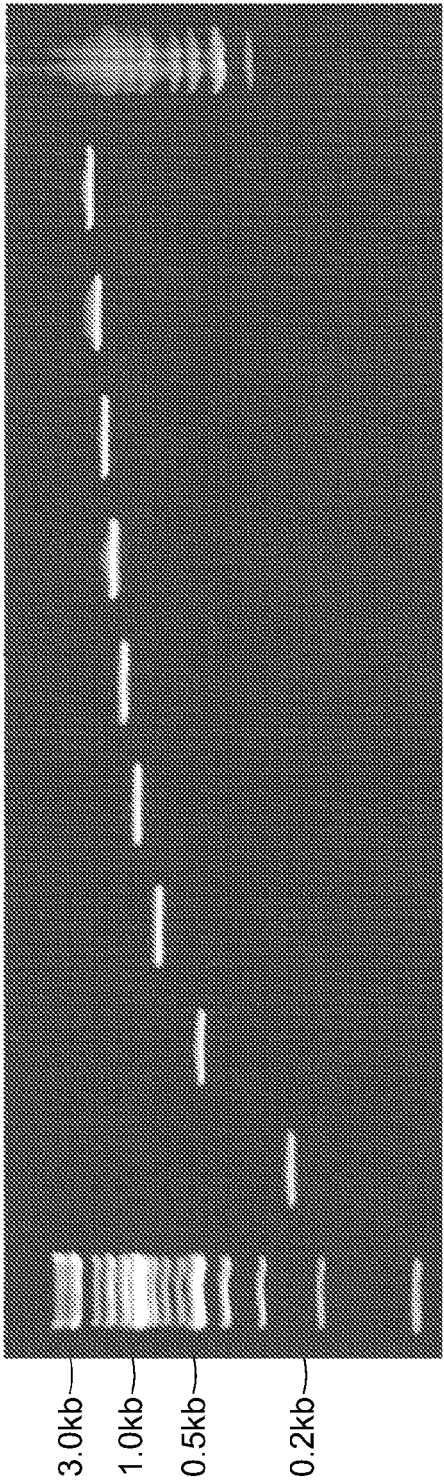
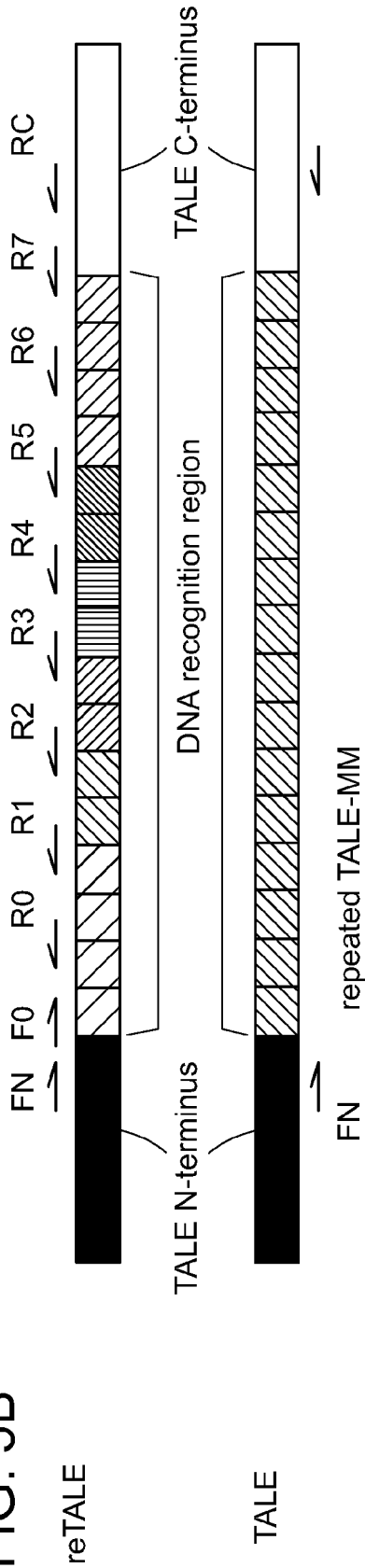


FIG. 4E



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FIG. 5B



Template	reTALE	reTALE	reTALE	reTALE	reTALE	reTALE	reTALE	reTALE	TALE
Primer1	F0	F0	F0	F0	F0	F0	F0	F0	FN
Primer2	R0	R1	R2	R3	R4	R5	R6	R7	RC

FIG. 6A

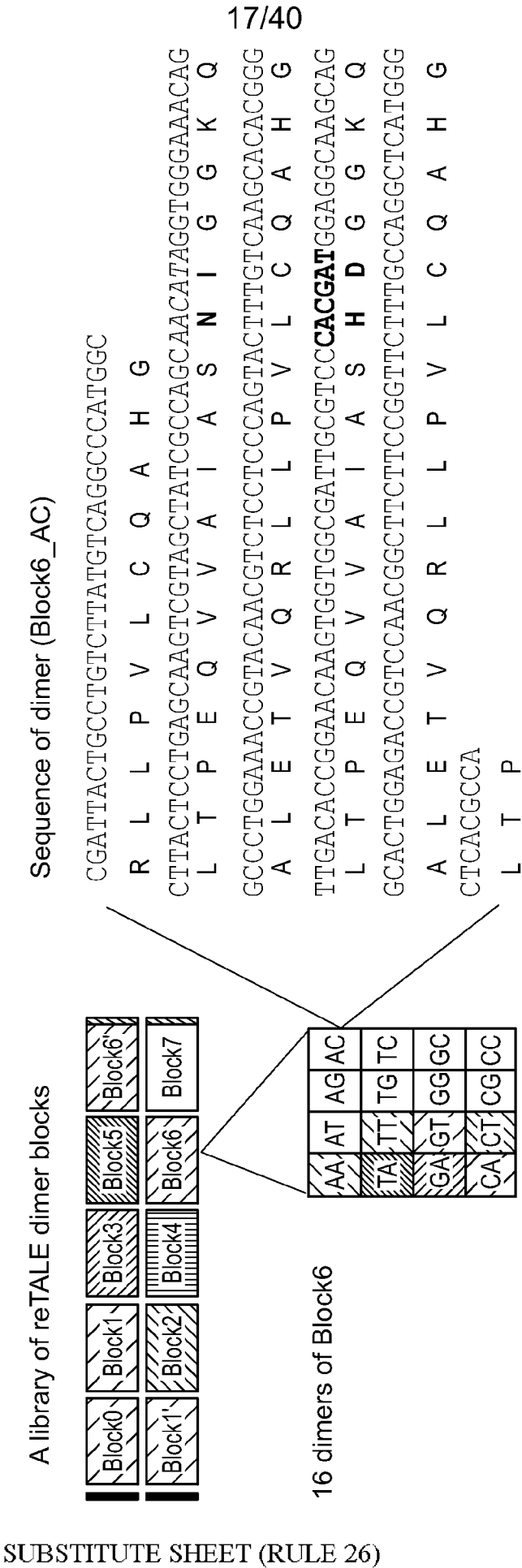


FIG. 6B

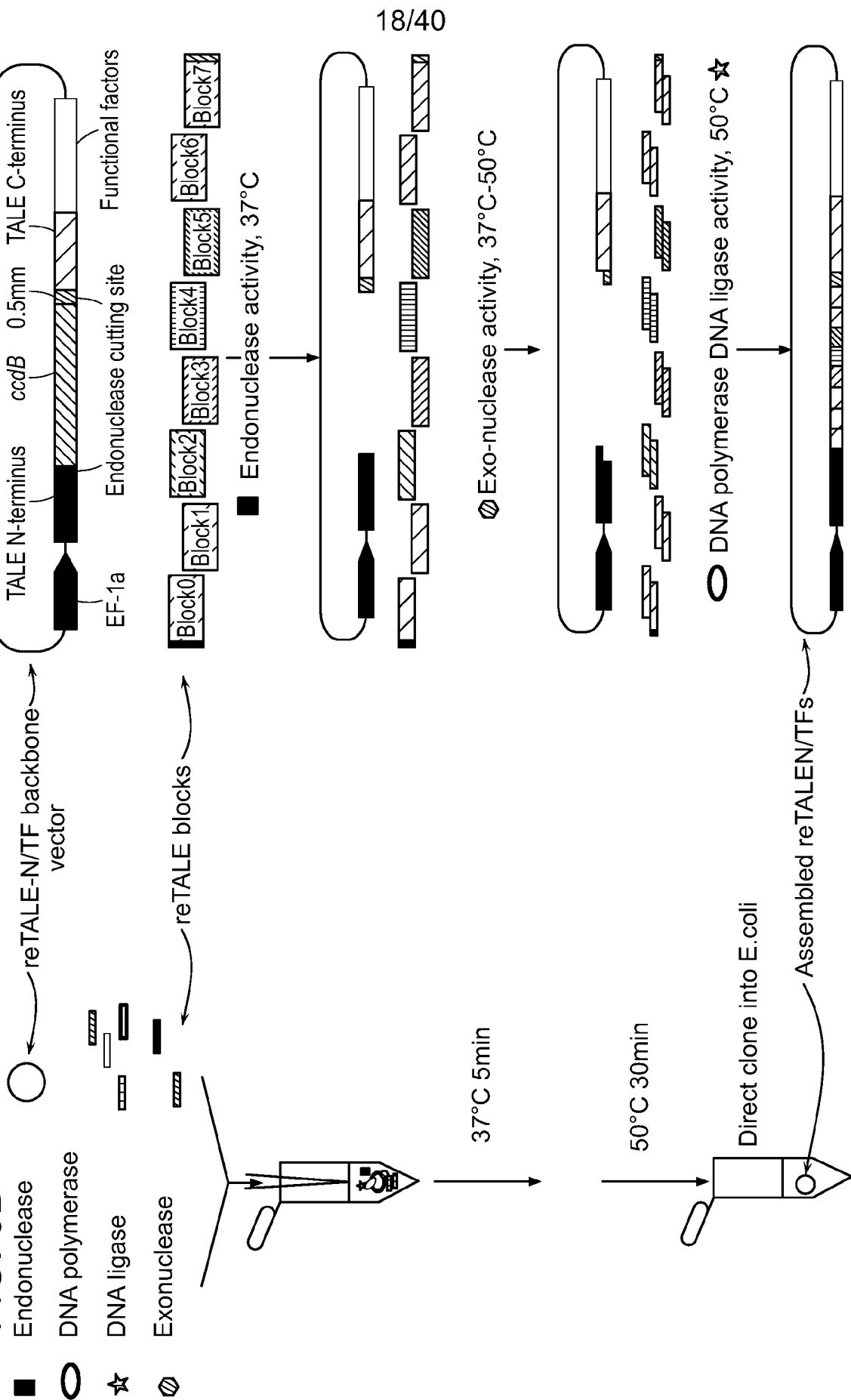
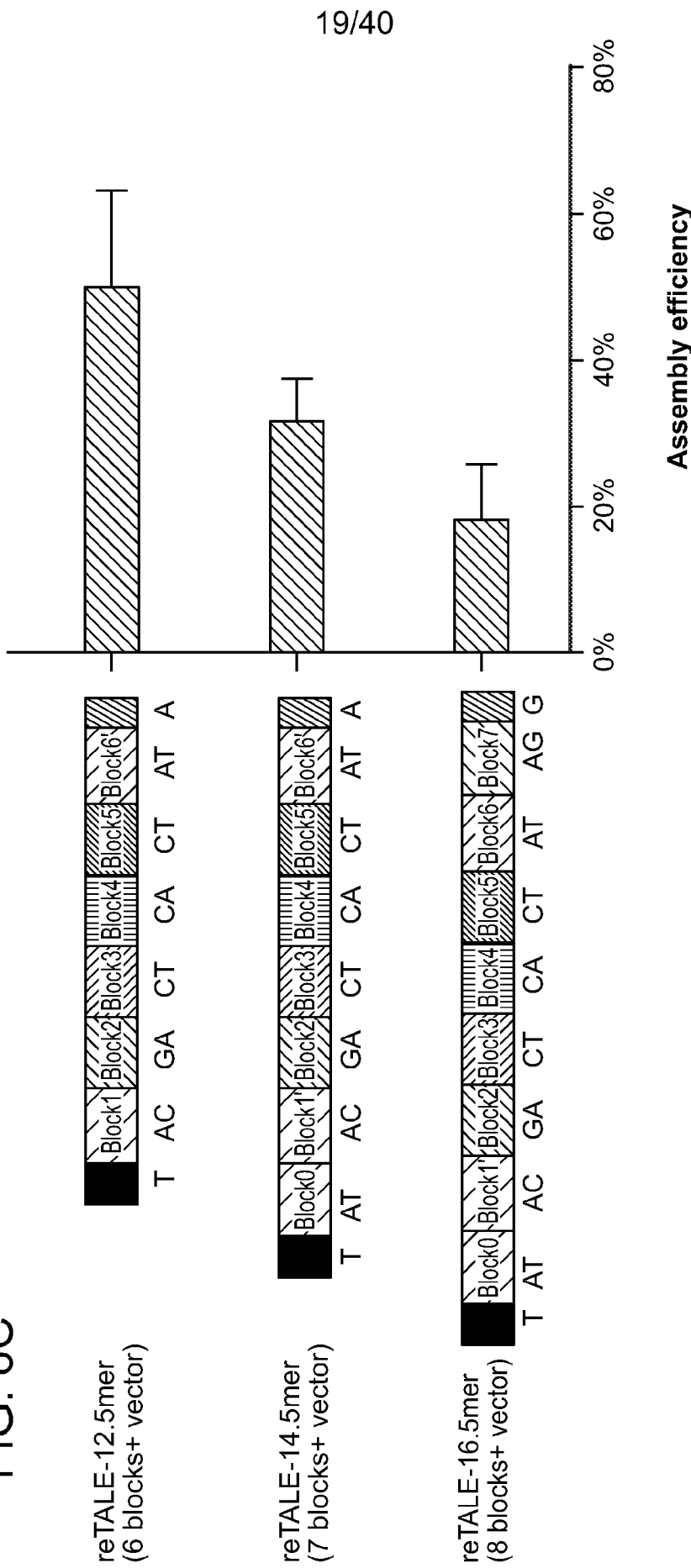


FIG. 6C



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FIG. 7A

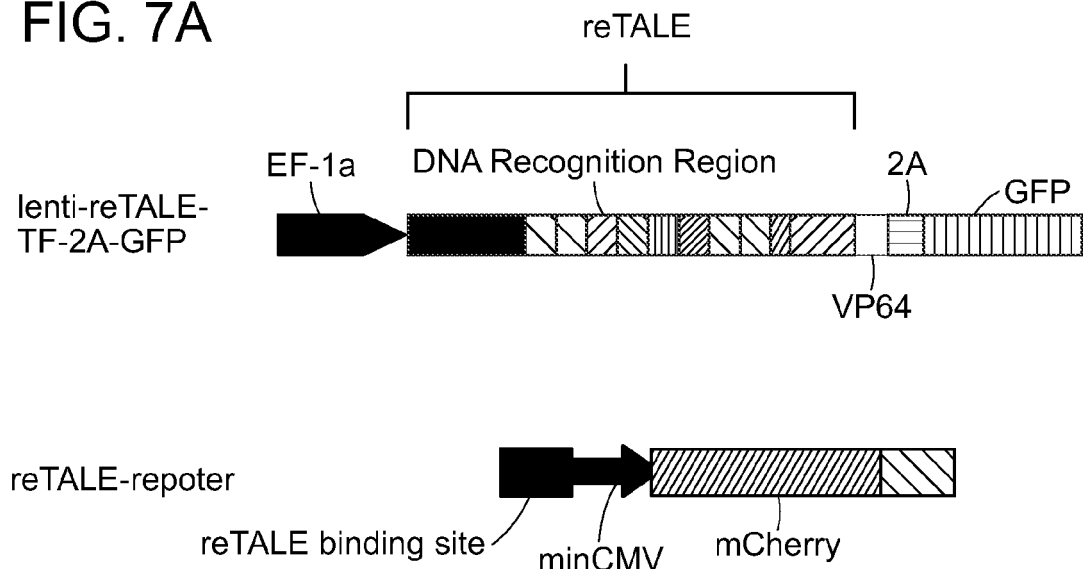
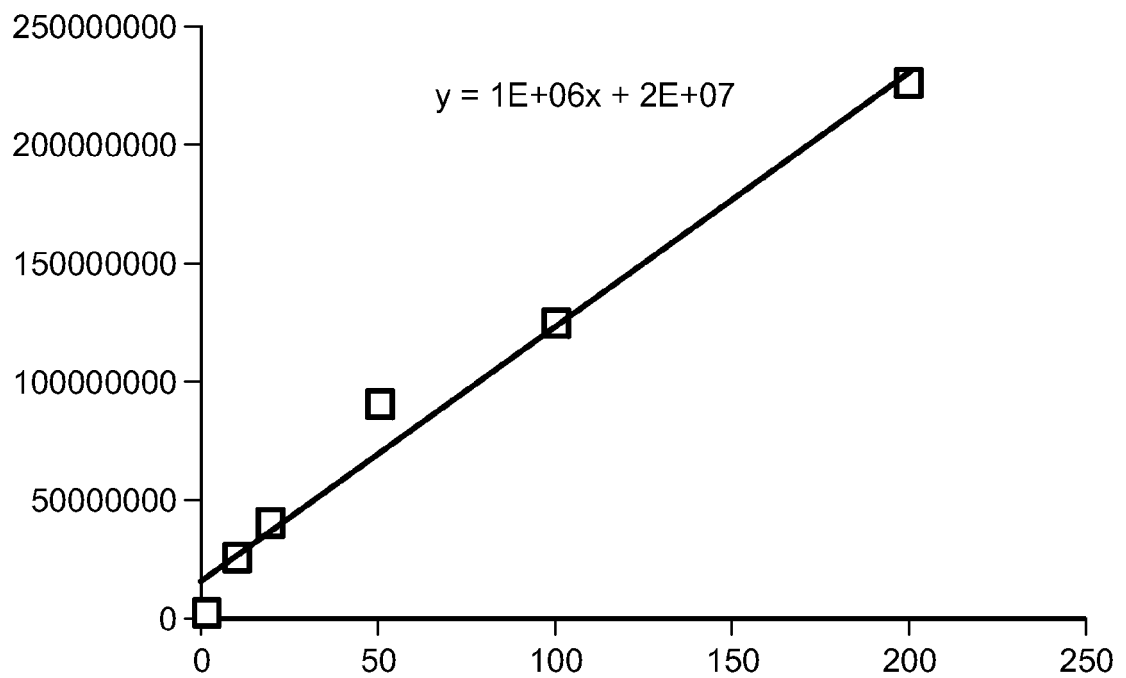
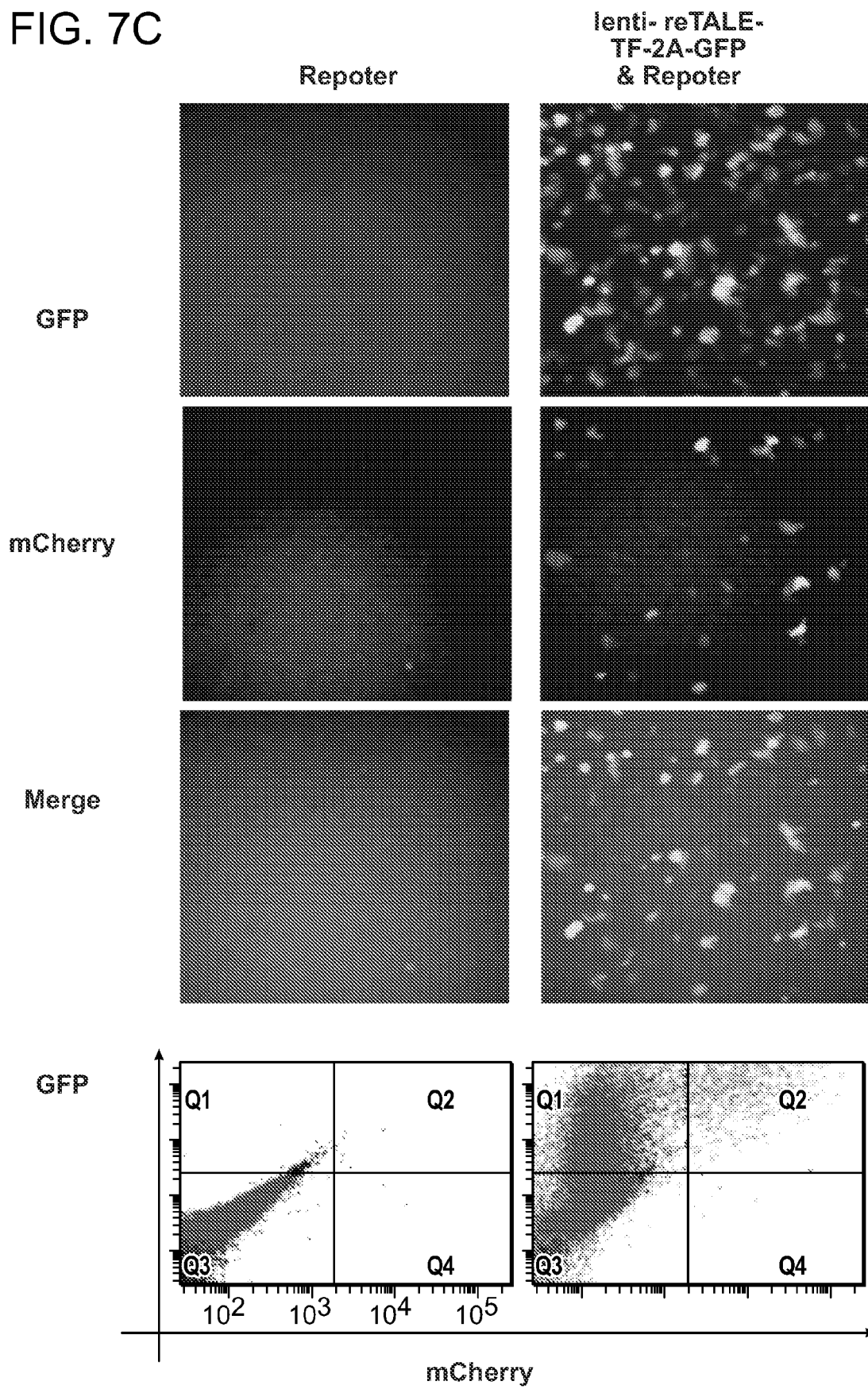


FIG. 7B



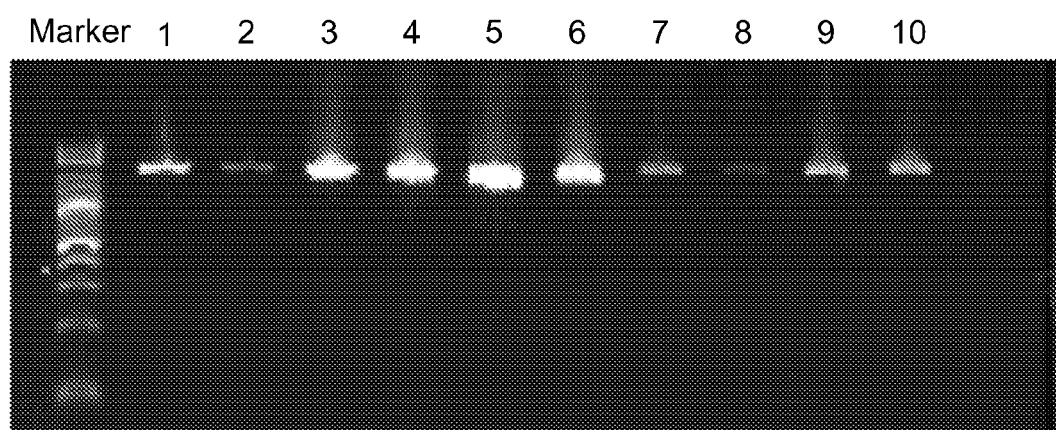
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FIG. 7C



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FIG. 7D



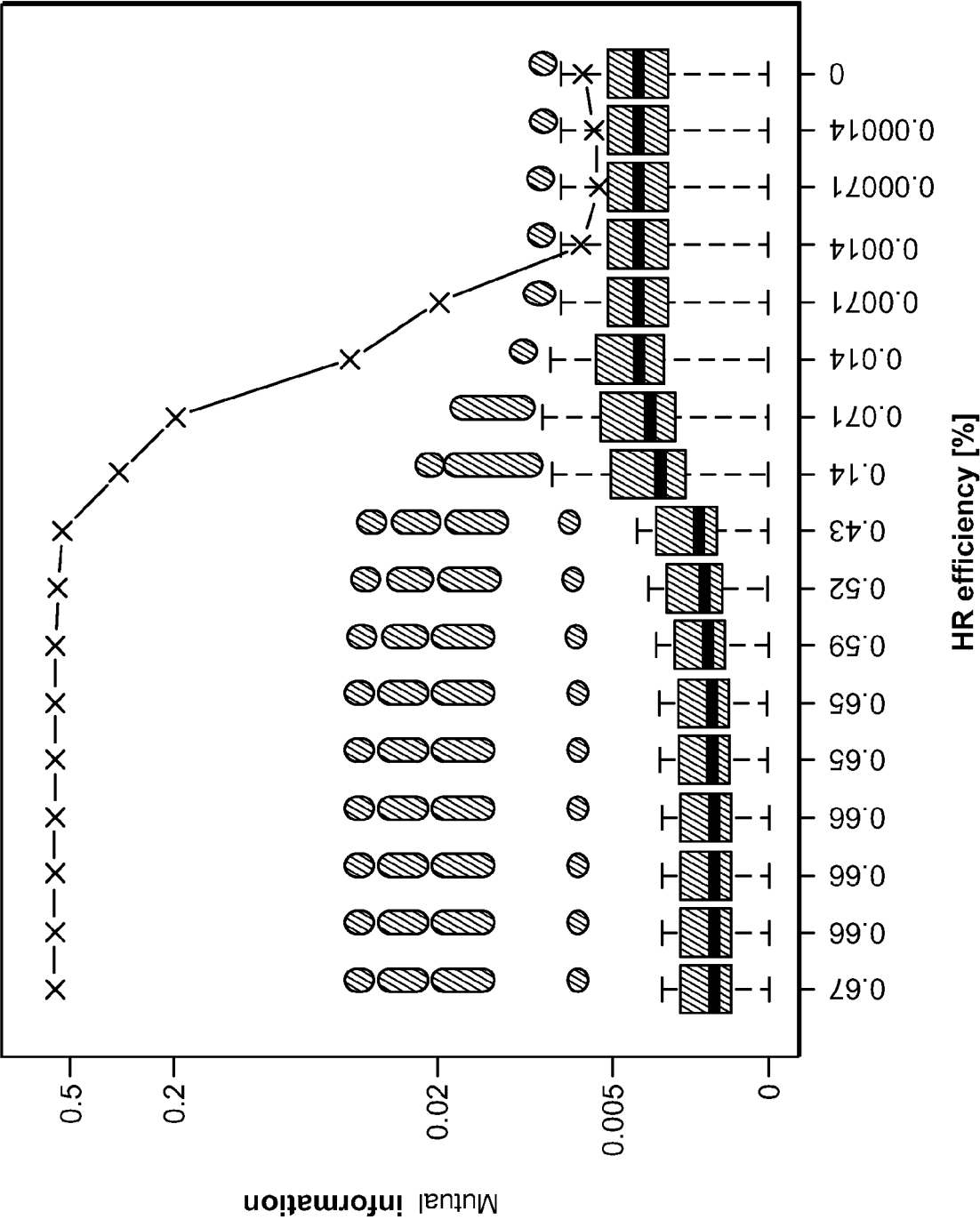
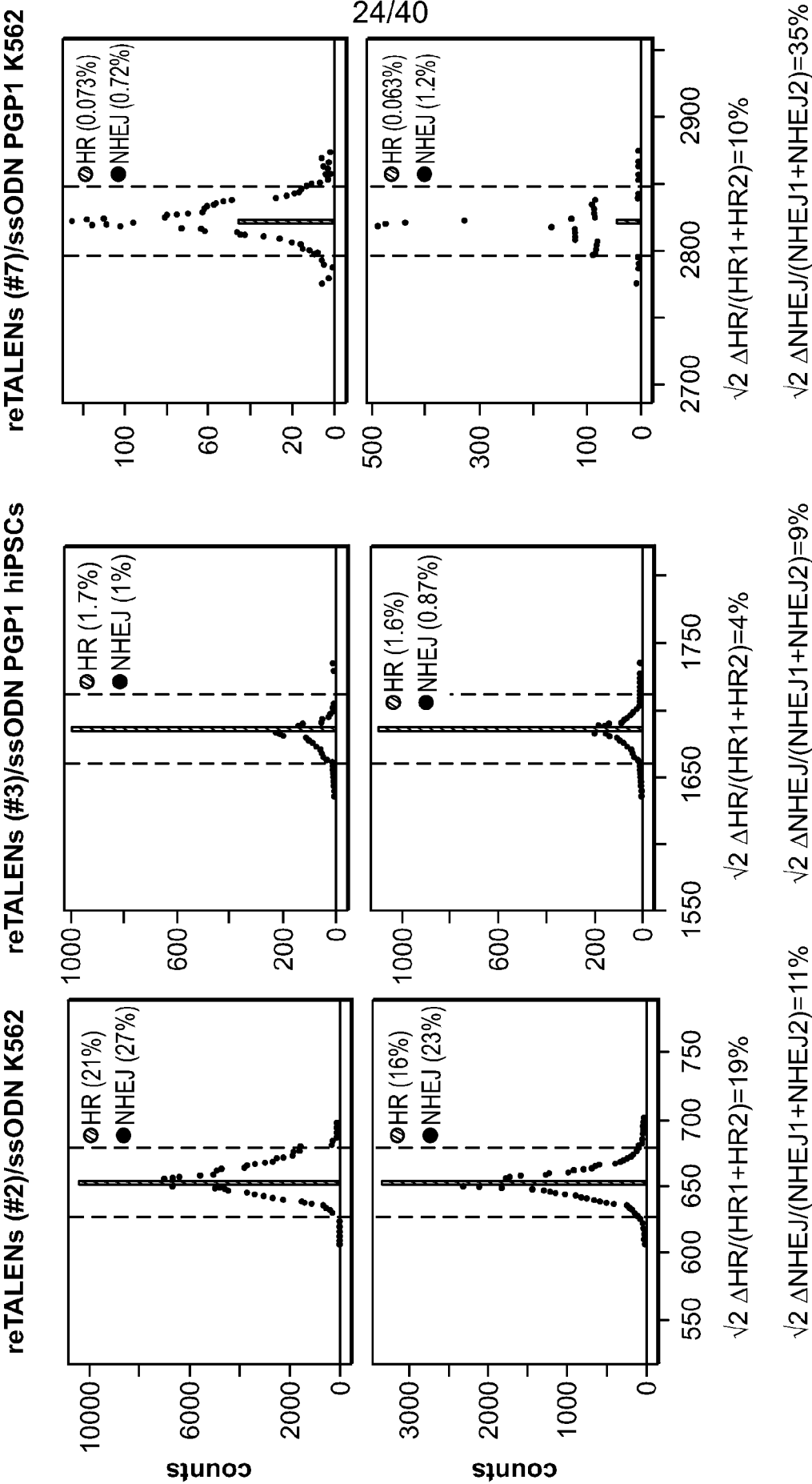


FIG. 8A

FIG. 8B



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FIG. 9A

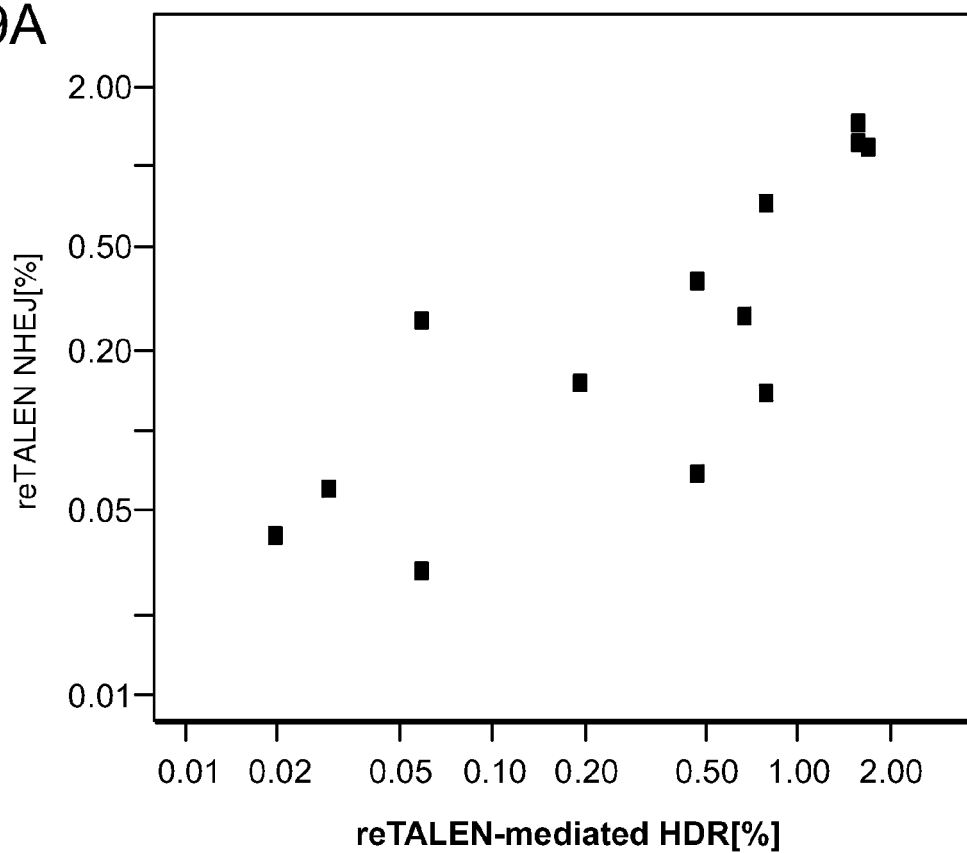
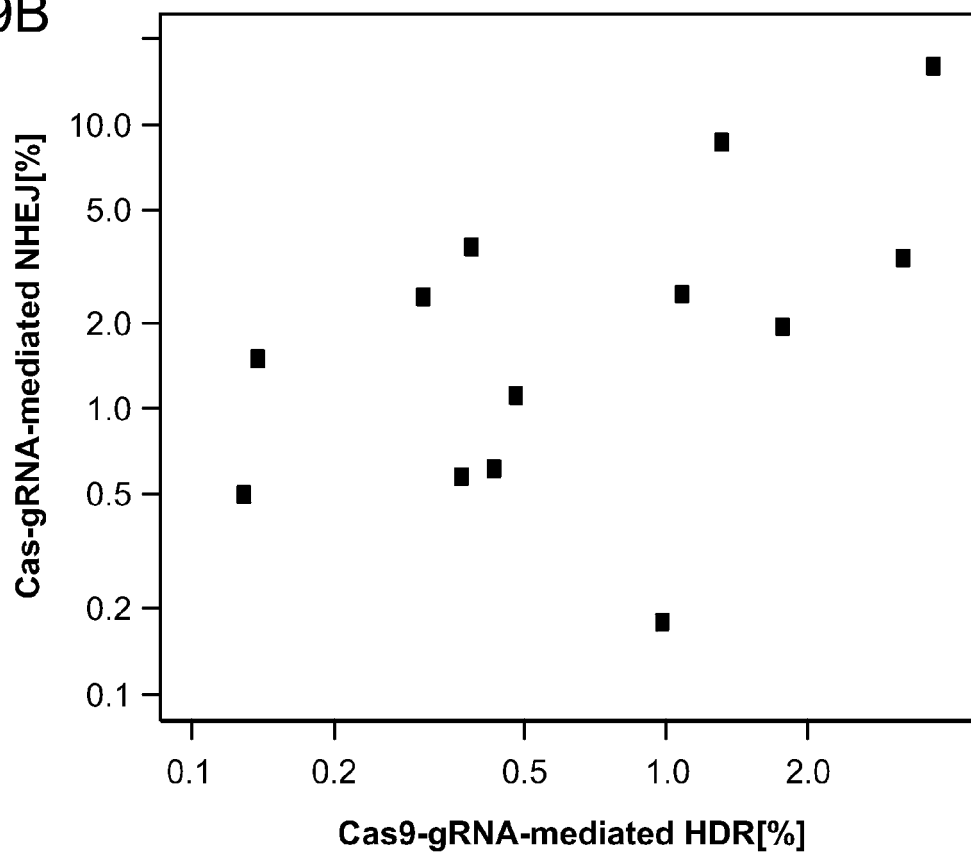


FIG. 9B



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FIG. 9C

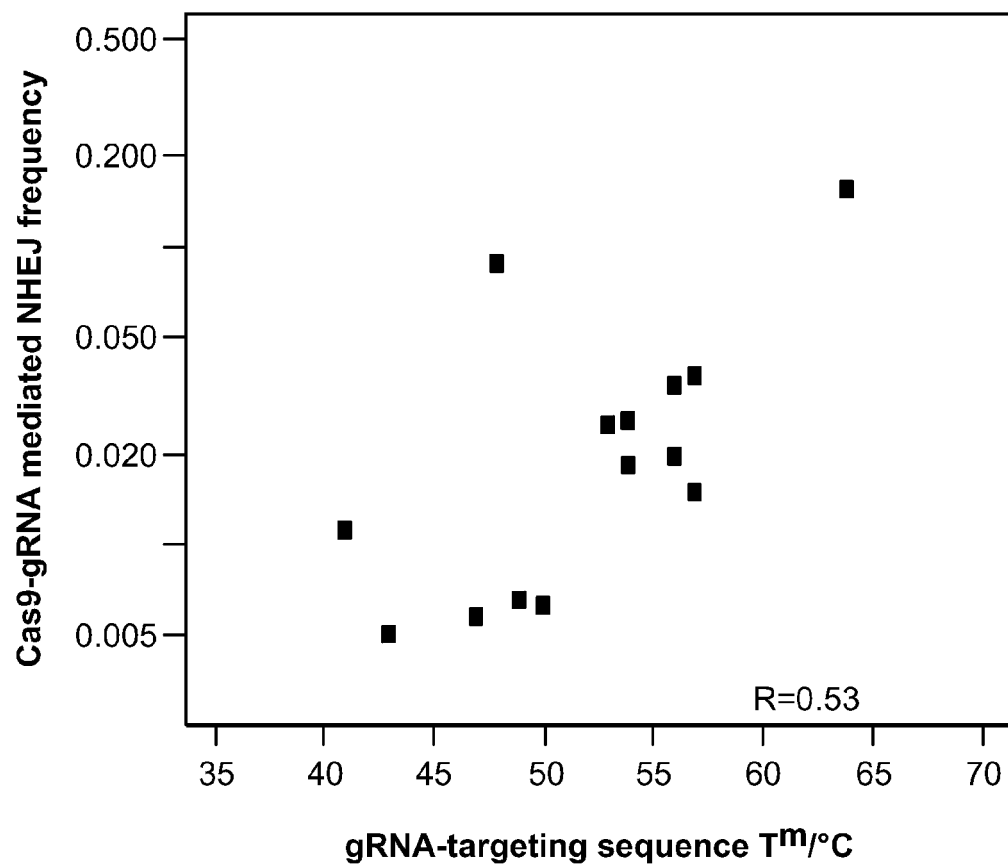
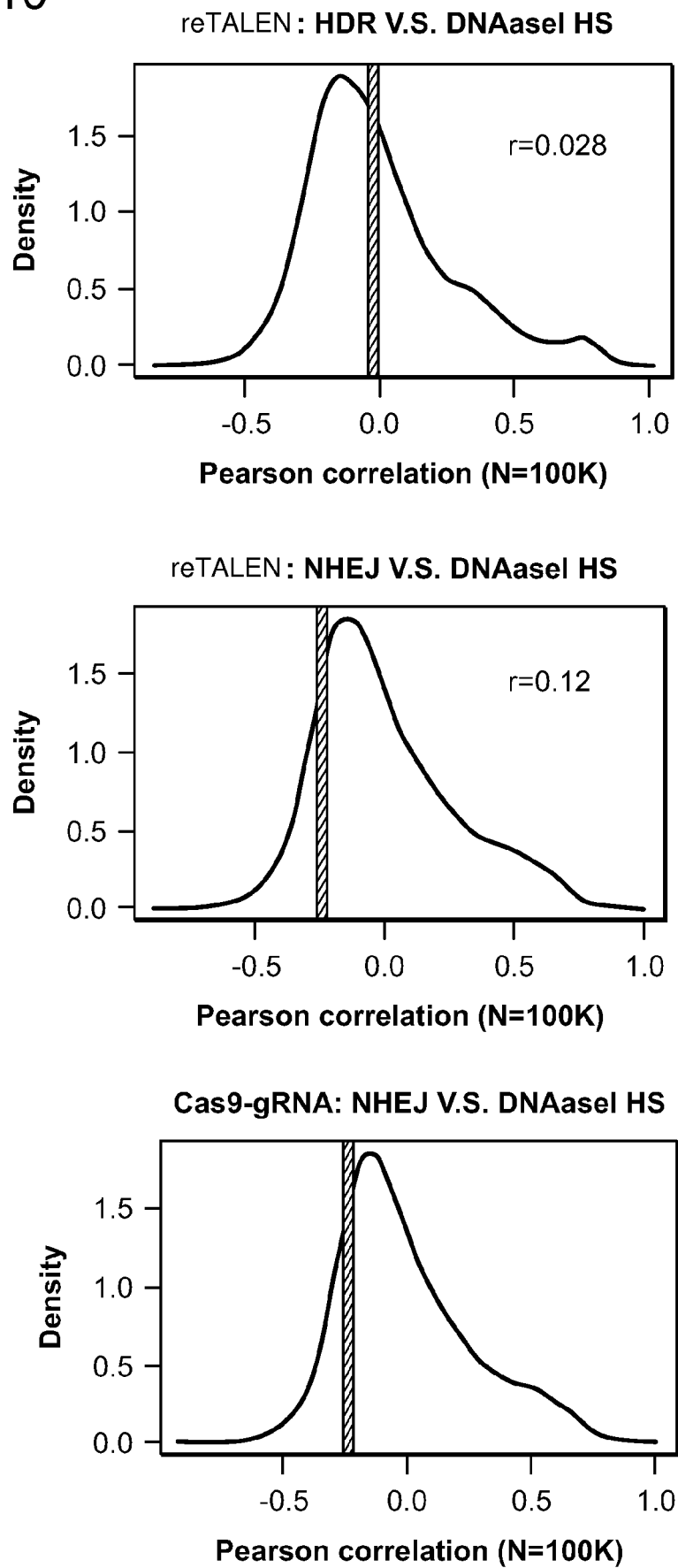


FIG. 10

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FIG. 11A

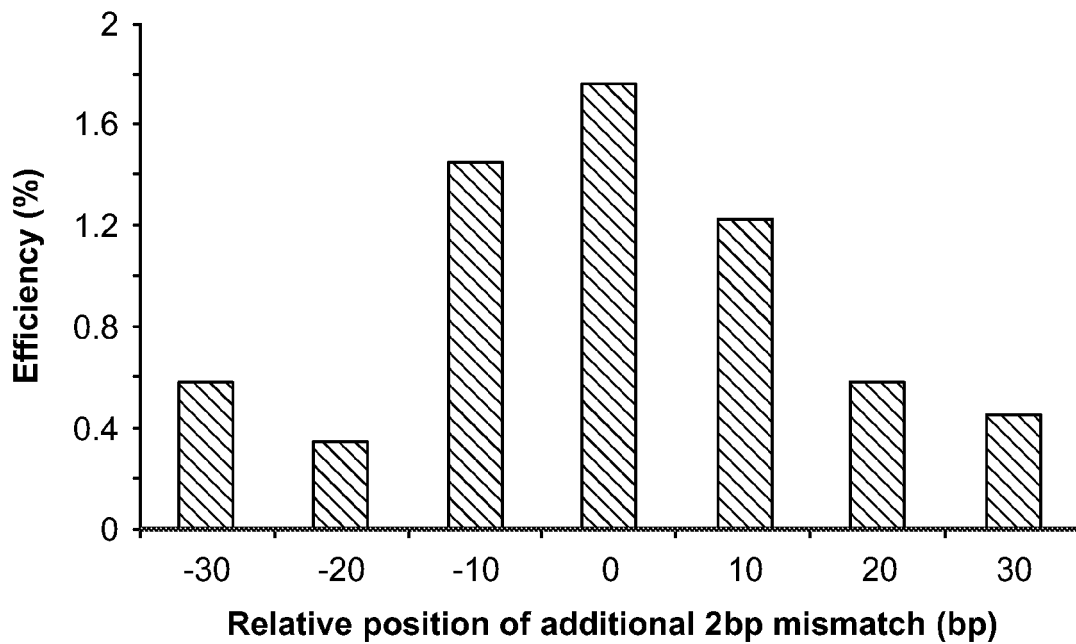


FIG. 11B

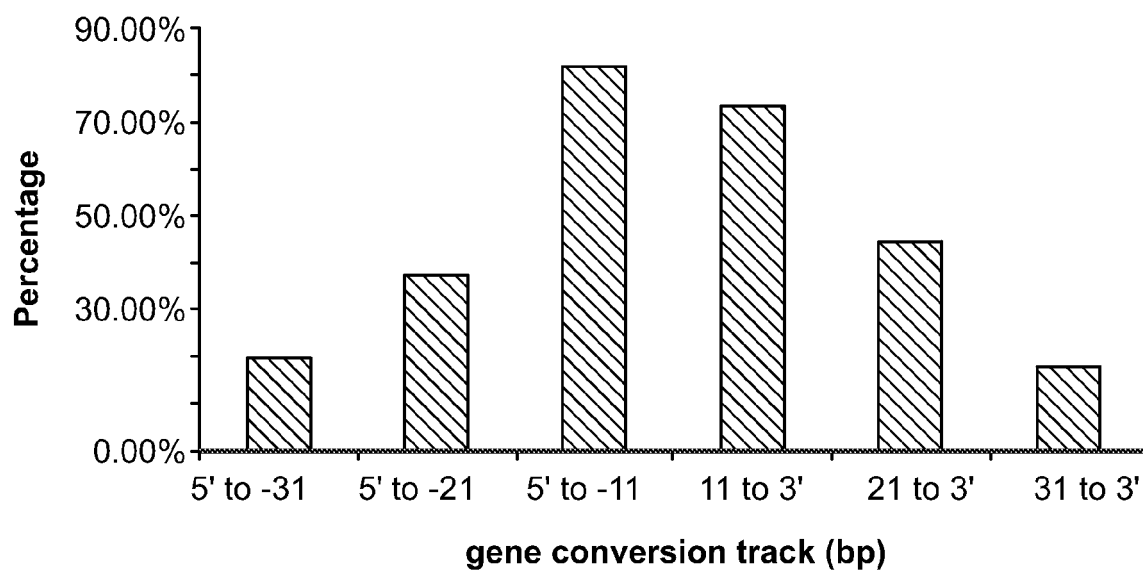
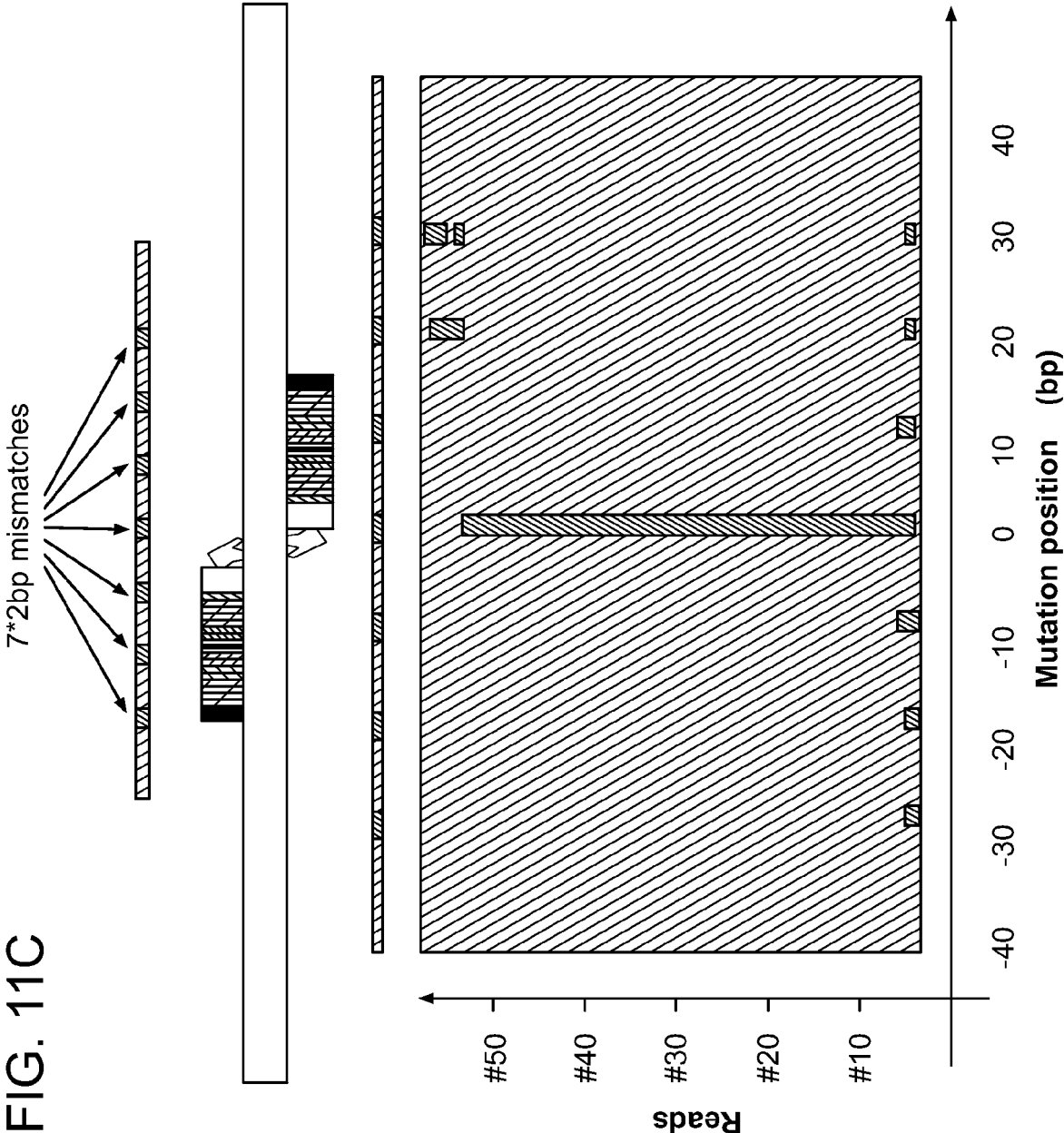
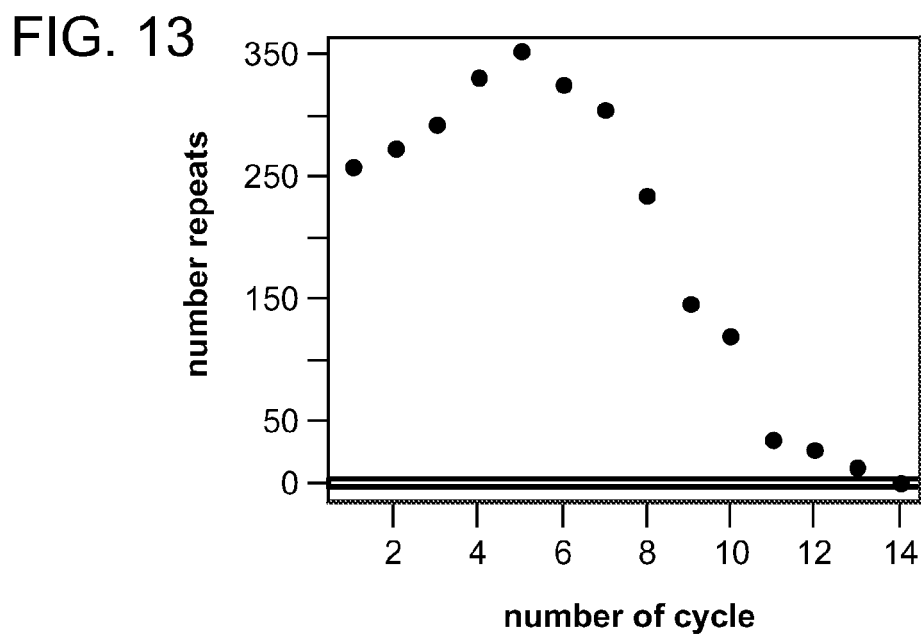
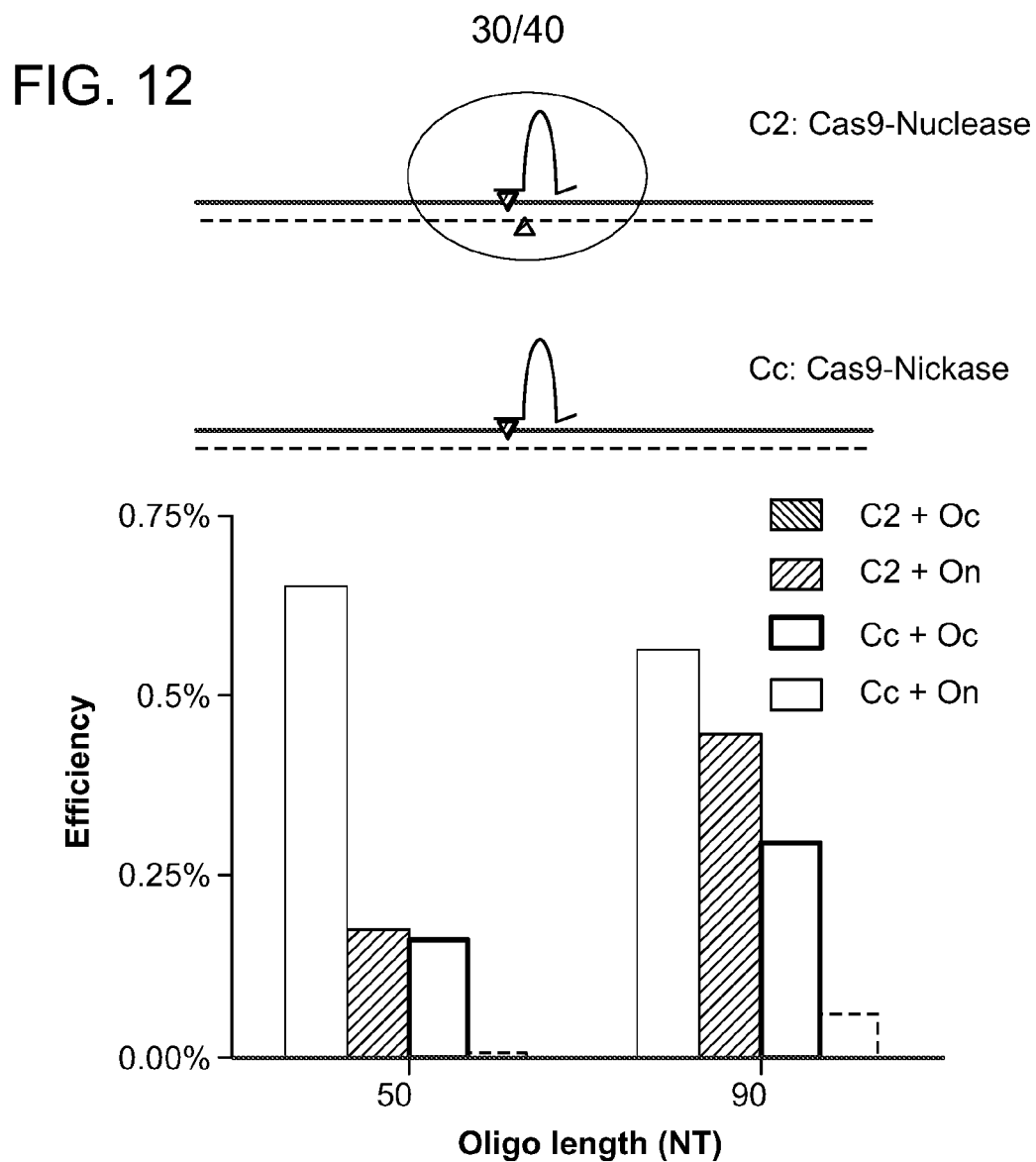


FIG. 11C





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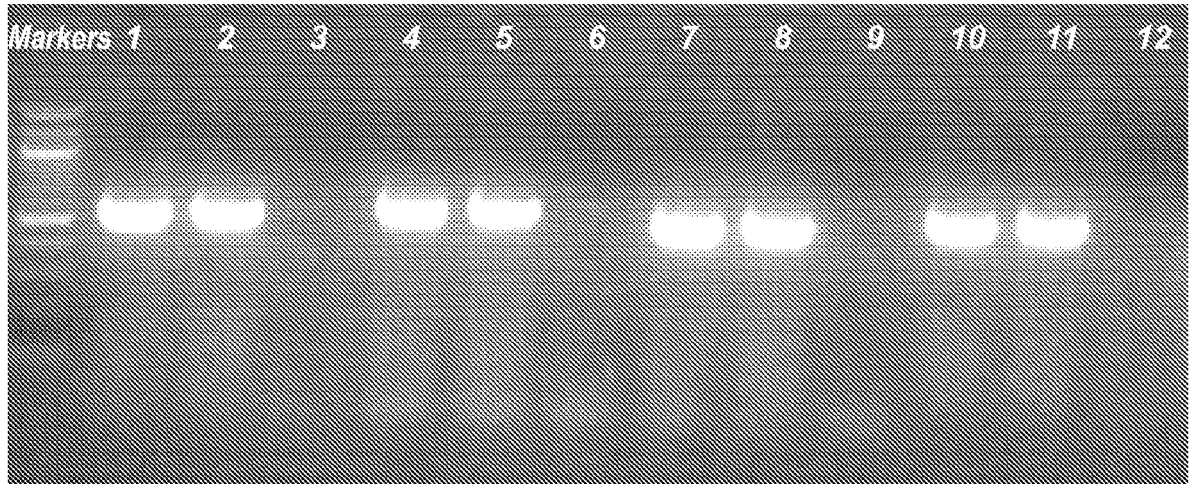


FIG. 14

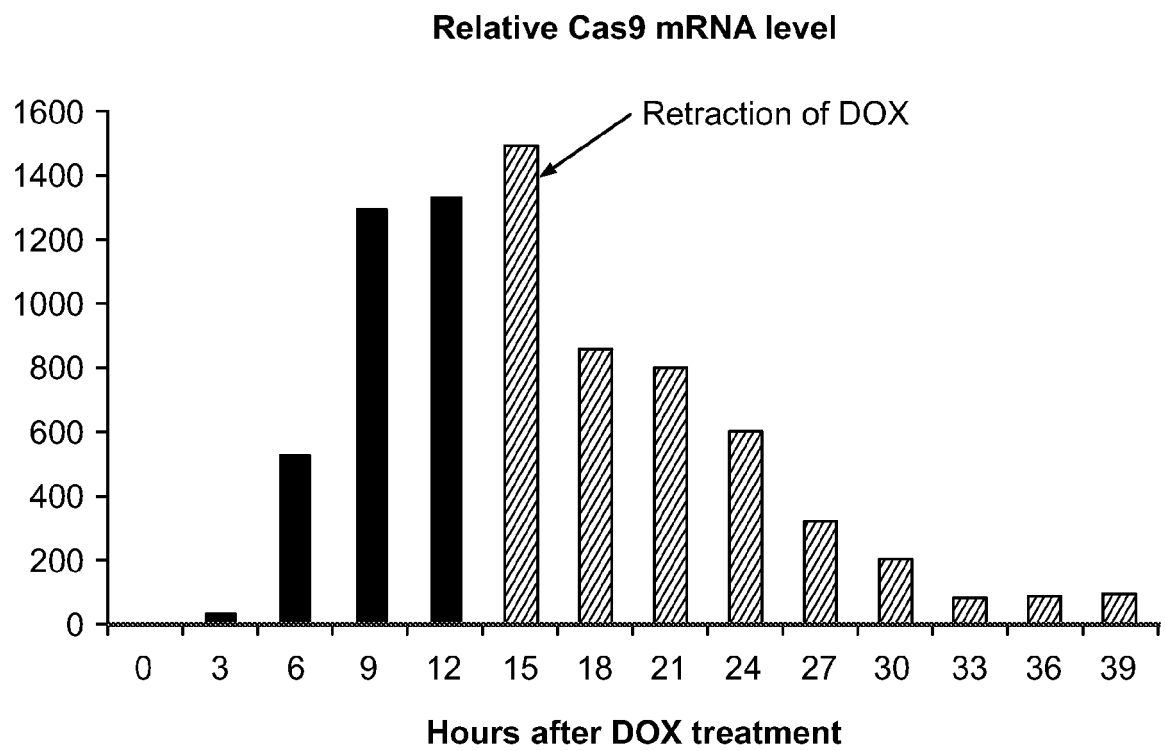


FIG. 15

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FIG. 16

Genome editing efficiency in hiPSCs

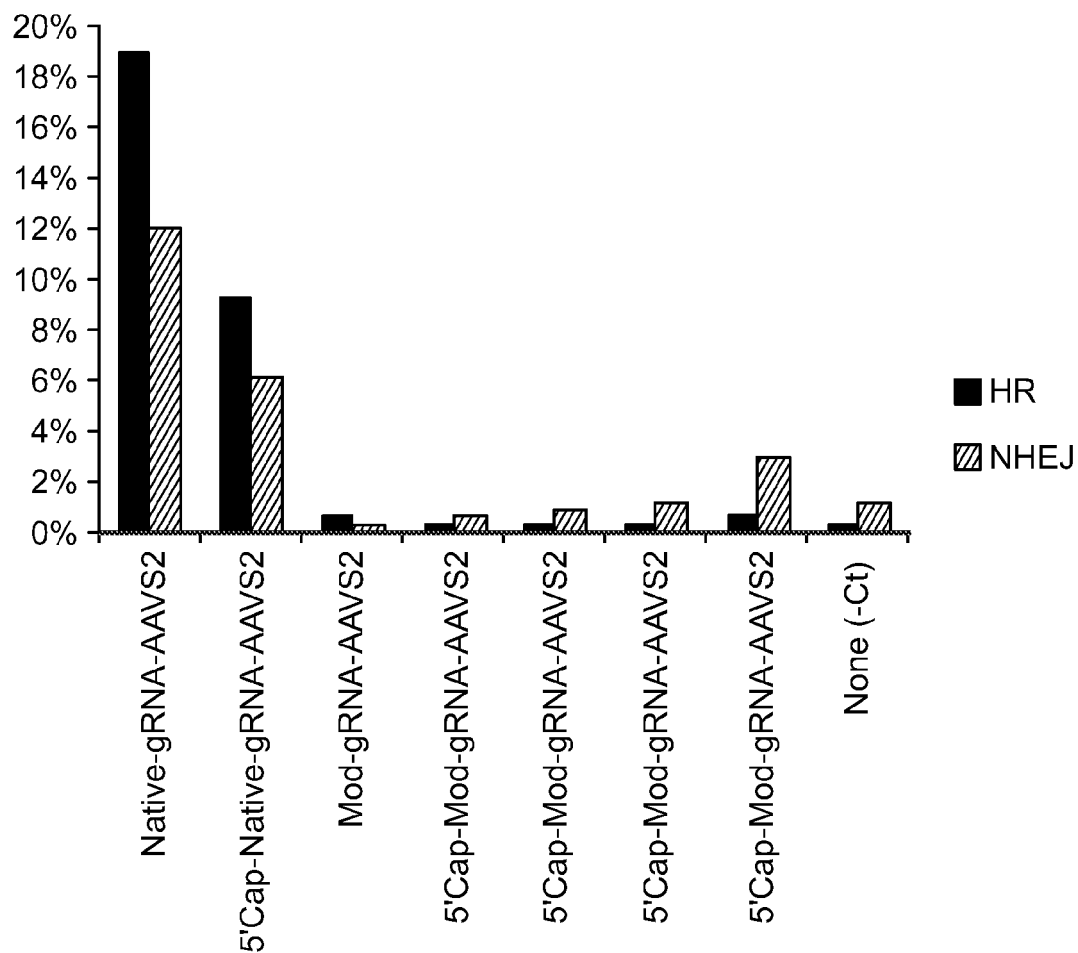


FIG. 17

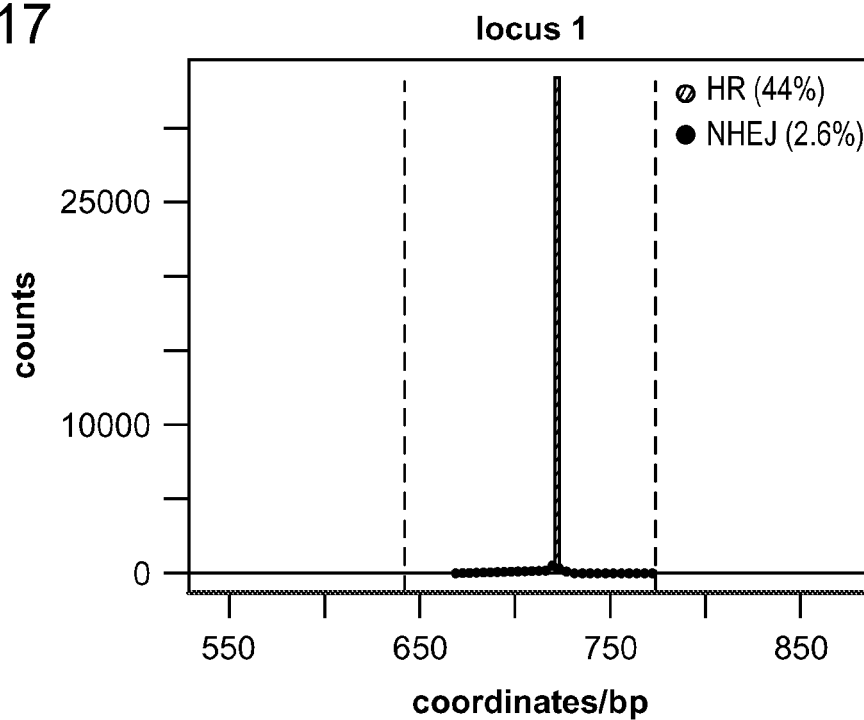
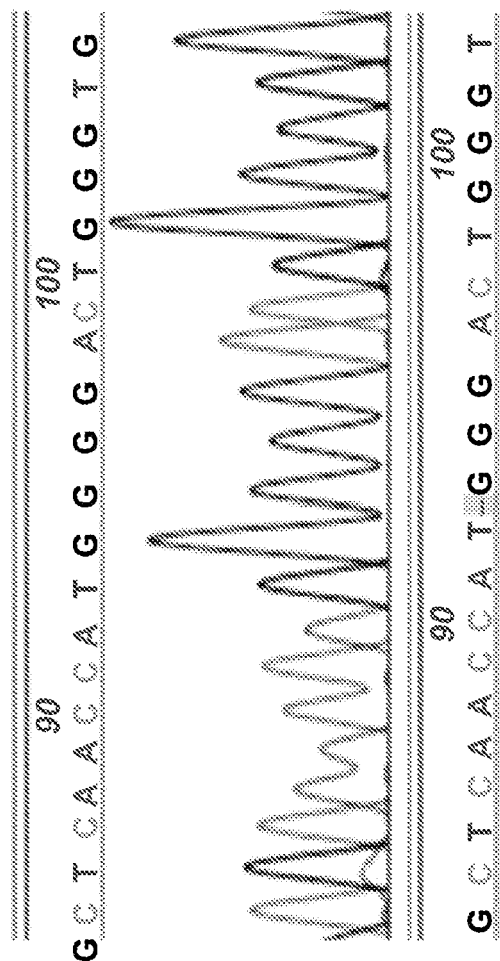
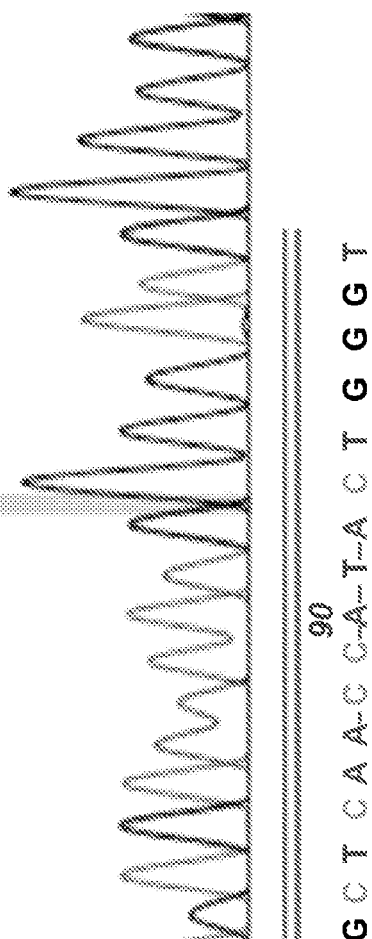


FIG. 18

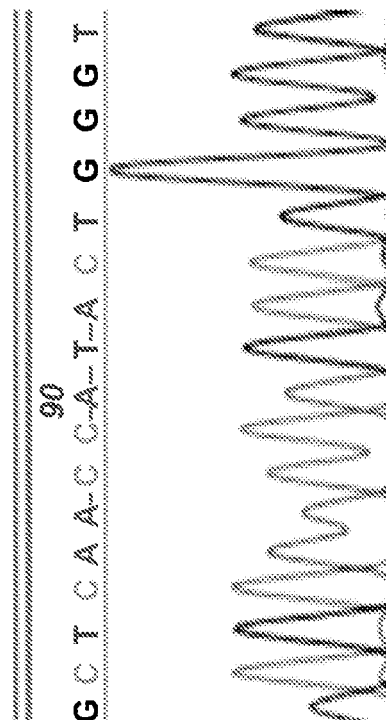
PGP1-iPS-NT



PGP1-iPS-BTHH

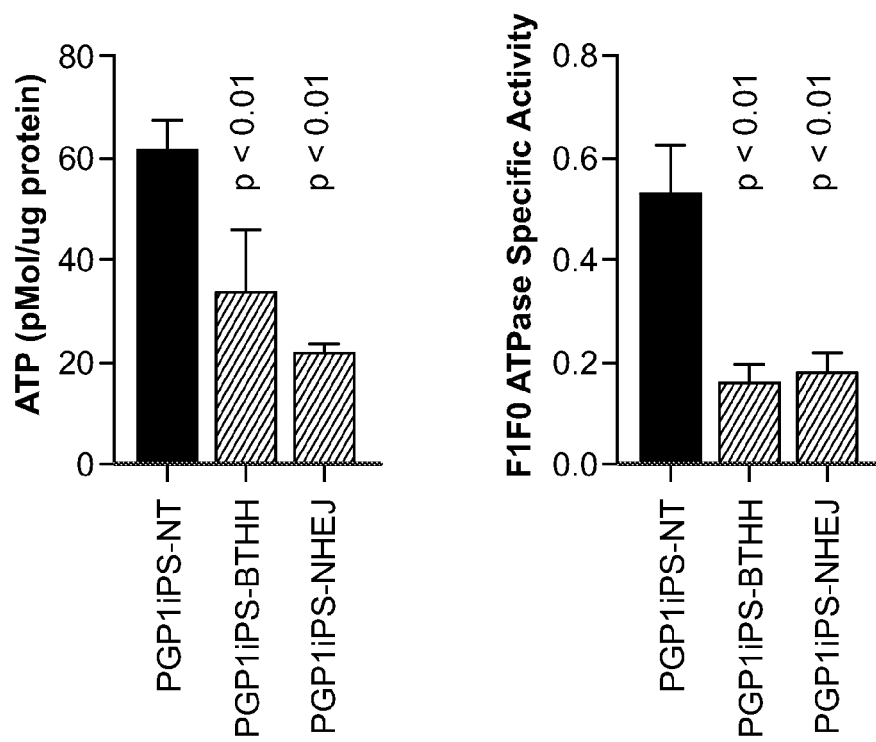


PGP1-iPS-NHEJ



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FIG. 19



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FIG. 20A

re-TALEN-backbone sequence

(purple: re-TALE-N; red: SapI site; green: 0.5 monomer; blue: re-TALEN-C; orange: FokI)

ATGTCGGACCCGGCTCCCTCCCAACCCGACCCAGCCAGCGTTTTCGGCCGAC
 TCGTTCTCAGACCTGCTTAGGCAGTTCGACCCCTCACTGTTTAACACATCGTTGTTG
 ACTCCCTTCCCTCCGTTTGGGCGCACCATACGGAGCGGCCACCGGGAGTGGGAT
 GAGGTGAGTCGGGATTGAGAGCTGCGGATGCACCAACCCCAACCATGCGGGTGGC
 CGTCACCGCTGCCCGACCGCCGAGGCGAAGCCCGCACCAAGCGGAGGCGAGCGC
 AACCGTCCGACGCAAGCCCCGAGCGCAAGTAGATTGAGAACTTTGGGATATTCA
 CAGCAGCAGCAGGAAAAGATCAAGCCCAAGTGAGGTCGACAGTCGCGCAGCATC
 ACGAAGCGCTGTTGGTCAATGGGTTTACACATGCCCACTCGTAGCCTTGTGCGCAGC
 ACCCTGCAGCCCTTGGCACGGTCGCCGTCAAGTACCAGGACATGATTGCGGCGTTGC
 CGGAAGCCACACATGAGCGGATCGTCGGTGTGGGAAACAGTGGAGCGGAGCCCCG
 AGCGCTTGAGGCCCTGTTGACGGTCGCGGGAGAGCTGAGAGGGCCTCCCCCTTCAGC
 TGGACACGGGCCAGTTGCTGAAGATCGCGAAGCGGGGAGGAGTCACGGCGGTGAG
 GCGGTGCACGCGTGGCGCAATGCGCTCACGGGAGCACCCCTCAACAGTTCACGTG
 ACAGAGACCGGGCCGCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCG
 TATAATGTGTGGATTTTGAGTTAGGATCCGTCGAGATTTTCAGGAGCTAAGGAAGCT
 AAAATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCG
 TAAAGAACATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTATAACCGACCCGT
 TCAGCTGGATATTACGGCCTTTTTAAGACCGTAAGAAAAATAAGCACAAAGTTTAA
 TCCGGCCCTTTATTACACATTCCTTGCCCGCCTGATGAATGCTCATCCGGAATCCGTATG
 GCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTACCCCTTGTACACCCGTT

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FIG. 20B

TTCCATGAGCAAACTGAAACGTTTTTCATCGCTCTGGAGTGAATACCACGACGATTTC
CGGCAGTTTCTACACATATATTGCAAGATGTGGCGTTTACGGTGAAACCTGGCC
TATTTCCCTAAAGGTTTATTGAGAAATATGTTTTTTCGCTCAGCCAAATCCCTGGGTGA
GTTTCACCAGTTTGTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTT
CACCATGGGCAAAATATTATACGCAAGCGACAAAGTGCTGATGCCGCTGGCGATTTC
AGGTTTCATCATGCCGTTTGTGATGGCTTCCATGTCTGGCAGAAATGCTTAAATGAATTAC
AACAGTACTGCCGATGAGTGGCAGGGCGGGCGTAAAGATCTGGATCCGGCTTACTA
AAAGCCAGATAACAGTATGCCGTAATTTCGCCGCTGATTTTTTGGGGTATAAGAAATATAT
ACTGATATGTATACCCGAAGTATGTCAAAAAGAGGTATGCTATGAAGCAGCGTATT
ACAGTGACAGTTGACAGCGACAGCTATCAGTTGCTCAAGGCATATATGATGTCAATA
TCTCCGGTCTGGTAAGCACAAACCATGCAGAAATGAAGCCCGTCTGCTGCGTGCCGAAC
GCTGGAAAGCGGAAAATCAGGAAGGGATGGCTGAGGTGCGCCCGTTTTATTGAAATG
AACGGCTCTTTTGCTGACGAGAACACAGGGCTGGTGAAATGCAGTTTAAAGTTTACAC
CTATAAAGAGAGAGCCGTTATCGTCTGTTTGTGGATGTACAGAGTGATATTATTGA
CACGCCGGCGACGGATGGTGATCCCCCTGGCCAGTGACGCTCTGCTGTACAGATA
AAGTCTCCCGTGAACTTTACCCGGTGGTGCAATATCGGGGATGAAAGCTGGCGCATGA
TGACCAACCGATATGGCCAGTGTGCCGCTCTCCGTTATCGGGGAAGAGTGGCTGATC
TCAGCCACCGCGAAAATGACATCAAAAACGCCATTAAACCTGATGTTCTGGGGAATA
TAAATGTCAGGCTCCCTTATACACAGCCAGTCTGCAGGTCGACGGTCTC**GCTCTTCG**
AAGGTTACTTCCCGTCTCTGTCAAGCGCACGGCCCTCACTCCAGAGCAAGTGGTTGC
GATCGCTTCAAACAACGGTGGAGACCTGCCCTGGGAATCAATCGTGGCCACGCTTTC

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FIG. 20C

GAGCCGGACCCGCGCTGGCCGCACTACTAATGATCATCTTGTAGCGCTGGCCTG
CCTCGCGGACGACCCGCTTGGATGCGGTGAAGAAGGGCTCCCGCACGGCCTG
CATTGATTAAAGCGGACCAACAGAAAGGATTCCCCGAGAGGACATCACATCGAGTGGCA
GTTCCCAACTCGTGAAGAGTGAACTTGAGGAGAAAAAGTCGGAGCTCGGCACAA
ATTGAAATACGTACCGCATGAATACATCGAACTTATCGAAATTGCTAGGAACTCGAC
TCAAGACAGAAATCCTTGAGATGAAGGTAATGGAGTTCTTTATGAAGTTTATGGATA
CCGAGGGAAGCATCTCGGTGATCACGAAAACCCGACGGAGCAATCTATACGGTGG
GGAGCCCGATTGATTACGGAGTGATCGTCGACACGAAAGCCTACAGCGGTGGTAC
AATCTTCCCATCGGCGAGCAGATGAGATGCAACGTTATGTCGAAGAAAATCAGAC
CAGGAACAAACACATCAATCCAAATGAGTGGTGGAAAGTGATCCTTCATCAGTGA
CCGAGTTTAAAGTTTGTGTTGTTCTCTGCGCATTTCAAAGGCAACTATAAGGCCAGCT
CACACGGTTGAATCACATTACGAACTGCAATGGTGCGGTTTTGTCCGTAGAGGAACT
GCTCATTTGGTGAGAAAATGATCAAAAGCGGGAACCTGTGACACTGGAAGAAAGTCAGAC
GCAAGTTTAAACAAATGGCGAGATCAATTTCCGC

re-TALE-TF backbone sequence

(purple: re-TALE-N; red: SapI site; green: 0.5 monomer; blue: re-TALEN-C; orange: NLS-VP64;
 2A-GFP)

ATGTCGGGACCCGGCTCCCTTCCCCACCCGACCCAGCCAGCGTTTTCGGCCGAC
 TCGTTCTCAGACCTGCTTAGGCAGTTCGACCCCTCACTGTTTAAACACATCGTTGTTCG

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FIG. 20D

ACTCCCTTCCTCCGTTTGGGGCGCACCATACGGAGCGGCCACCGGGAGTGGGAT
GAGGTGAGTCGGGATTGAGAGCTGCGGATGCACCAACCCCAACCATGCGGGTGGC
CGTCACCGCTGCCGACCGCCGAGGCGAAGCCCGCACCAAGCGGAGGCGACGCGC
AACCGTCCGACGCAAGCCCCGACGCGCAAGTAGATTGAGAACTTTGGGATATTCA
CAGCAGCAGCAGGAAAAGATCAAGCCCCAAAGTGAGGTCGACAGTCGCGCAGCATC
ACGAAGCGCTGGTGGGTCA TGGGTTTACACATGCCCCACATCGTAGCCTTGTGCGCAGC
ACCCTGCAGCCCTTGGCACGGTCGCCGTCAAGTACCAGGACATGATTGCGGCGTTGC
CGGAAGCCACACATGAGGCGATCGTCGGTGTGGGAAACAGTGGAGCGGAGCCCCG
AGCGCTTGAGGCCCTGTTGACGGTCGCGGGAGAGCTGAGAGGGCCTCCCCCTTCAGC
TGGACACGGGCCAGTTGCTGAAGATCGCGAAGCGGGGAGGAGTCACGGCGGTGAG
GCGGTGCACGCGTGGCGCAATGCGCTCACGGGAGCACCCCTCAACAGTTCACGCTG
ACAGAGACCGGGCCGCATTAGGCACCCCGAGGCTTTACACTTTATGCTTCCGGCTCG
TATAATGTGTGGA TTTTGAGTTAGGATCCGTCGAGATTTTCAGGAGCTAAGGAAAGCT
AAAAATGGAGAAAAAATCACTGGATATACCAACCGTTGATATATCCCAAATGGCATCG
TAAAGAACATTTTGAGGCA TTTTCAGTCAGTTGCTCAATGTACCTATAACCCAGACCGT
TCAGCTGGATATTACGGCC TTTTAAAGACCGTAAAGAAAAATAAGCACAAAGTTTAA
TCCGGCC TTTATTCACATTTCTTGCCCGCCTGATGAATGCTCATCCGGAATTCGGTATG
GCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCC TTTGTACACCGTT
TTCCATGAGCAAACTGAACG TTTTCATCGCTCTGGAGTGAAATACCACGACGATTTC
CGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTACGGTGAAAAACCTGGCC
TATTTCCCTAAAGGG TTTATTGAGAAATATGTTTTCGTCTCAGCCAATCCCTGGGTGA
GTTTCACCAGTTTGTATTTAAACGTGGCCAAATATGGACAACTTCTTCGCCCCCGTTT

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FIG. 20E

CACCATGGGCAAAATATTATACGCAAGCGACAAAGTGCTGATGCCGCTGGCGATTCC
AGGTTTCATCATGCCGTTTGTGATGGCTTCCATGTCCGAGAAATGCTTAATGAATTAC
AACAGTACTGCGATGAGTGGCAGGGCGGCGTAAAGATCTGGATCCGGCTTACTA
AAAGCCAGATAACAGTATGCCGTATTTGCCGCGCTGATTTTTCGGGTATAAGAATATAT
ACTGATATGTATACCCGAAGTATGTCAAAAAGAGGTATGCTATGAAGCAGCGTATT
ACAGTGACAGTTGACAGCGACAGCTATCAGTTGCTCAAGGCATATATGATGTCAATA
TCTCCGGTCTGGTAAGCACAAACCATGCAGAAATGAAGCCCGTCTGCTGCCGCGAAC
GCTGGAAAGCGGAAAATCAGGAAGGGATGGCTGAGGTCGCCCGGTTTATTGAAAATG
AACGGCTCTTTTGCTGACGAGAACACAGGGCTGGTGAAATGCAGTTTAAAGTTTACAC
CTATAAAGAGAGAGCCGTTATCGTCTGTTTGTGGATGTACAGAGTGATATTATTGA
CAGCCCCGGCGACGGATGGTGATCCCCCTGGCCAGTGACAGTCTGCTGTCAGATA
AAGTCTCCCGTGAACTTTACCCGGTGGTGCAATATCGGGGATGAAAGCTGGCGCATGA
TGACCAACCGATATGGCCAGTGTGCCGCTCTCCGTTATCGGGGAAGAGTGGCTGATC
TCAGCCACCGCGAAAATGACATCAAAAACGCCATTAACTGATGTTCTGGGAATA
TAAATGTCAGGCTCCCTTATACACAGCCAGTCTGCAGGTCGACGGTCTC**GCTCTTCG**
AAGGTTACTTCCCGTCTCTGTCAAGCGCACGGCCCTCACTCCAGAGCAAGTGGTTGC
GATCGCTTCAACAACGGTGAAGACCTGCCCTGGAAATCAATCGTGGCCAGCTTTC
GAGCCGGACCCCGCTGGCCGCACCTACTAATGATCATCTTGTAGCGCTGGCCCTG
CCTCGGGGACGACCCGCCCTTGATGCGGTGAAGAAGGGCTCCCGCACGGCCCTG
CATTGATTAAGCGGACCAACAGAAGGATTCCCGAGAGGACATAGCCCCAAGAAGAA
GAGAAAGTGGAGGCCAGCGGTTCCGGACGGGCTGACGCATTGGACGATTTTGATC

TGGATATGCTGGGAAGTGACGCCCTCGATGATTTTGACCTTGACATGCTTGGTTCCG
ATGCCCTTGATGACTTTGACCTCGACATGCTCGCAGTGACGCCCTTGATGATTTCC
ACCTGGACATGCTGATTAAGTCTAGAGGCAGTGGAGAGGGCAGAGGAAGTCTGCTA
ACATGCCGCTGACGTCGAGGAGAAATCTGCGCCAGTGAGCAAGGGCGAGGAGCTGT
CACCGGGGTGGTGCCCATCTGTCGAGCTGGACGGCGAGCTAAACGCCCAAGT
TCAGCGTGTCCGGCGAGGGCGAGGCGGATGSCACCTACGGCAAGCTGACCTGAAG
TTTANCTGCAACCGGCAAGCTGCGCGTGGCTGGCCACCTCGTGACCACTCGTG
ACCTACGGCGTGCAAGTGTCTTCAGCGCTACCGCGACCACTGAAGCAGCAGACTTC
TTSAAGTCCGCCATGCTCCGAAGGCTATGTTCSAGAGCGCACATCTTTCTCAAGGAC
GAGGGCACTACAAGACTCCGCGCGAGGTGAAGTTGAGGGCCACACCTGGTGA
CCGCTTCGAGGCTGAAGGCACTCGACTTCAGAGGAGGACGGCAACTCTCGGGCA
AGGTGGAGTACAACTACAAGCAACAAGCTCTATACTATGGCGGACCAAGCAAG
AAGGGCACTCAAGGTGAACCTTCAGATCCGCGCAACAATCGAGGACGGGAGCGTGA
GCTCCCGAGCACTACAGCAGAACAACCTCTGGCGAGCGCGCTGCTGCTGCTG
CCGACAACCACTAGGCACTGAGGCACTCGCGCTGAGCAAAAGACCTCAAGCAAG
CGCGATCAATGCTGCTGAGGTTCGTCAGCGCGCGGATCACTCTCGGCACTG
GAGGAGCTGTACAG