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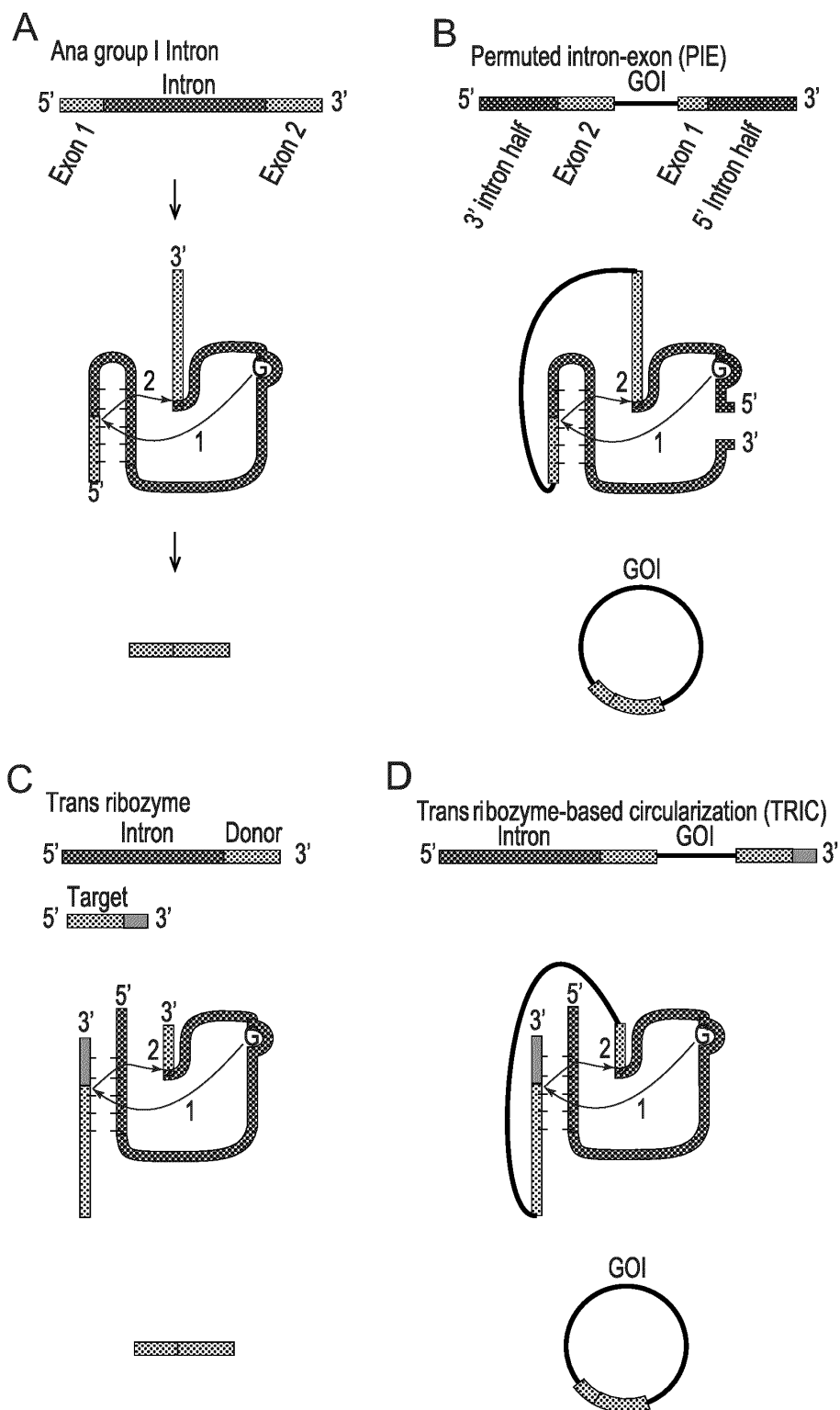


FIG. 1

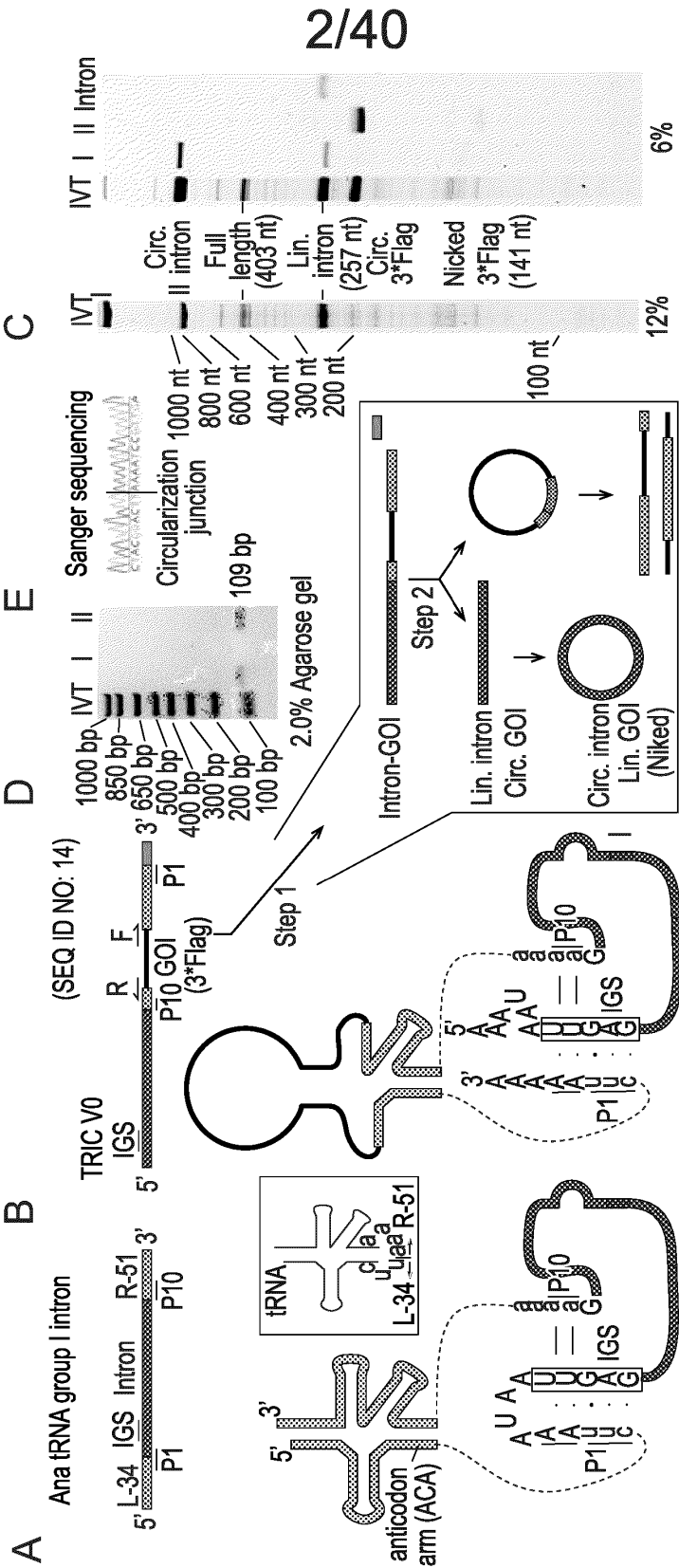


FIG. 2

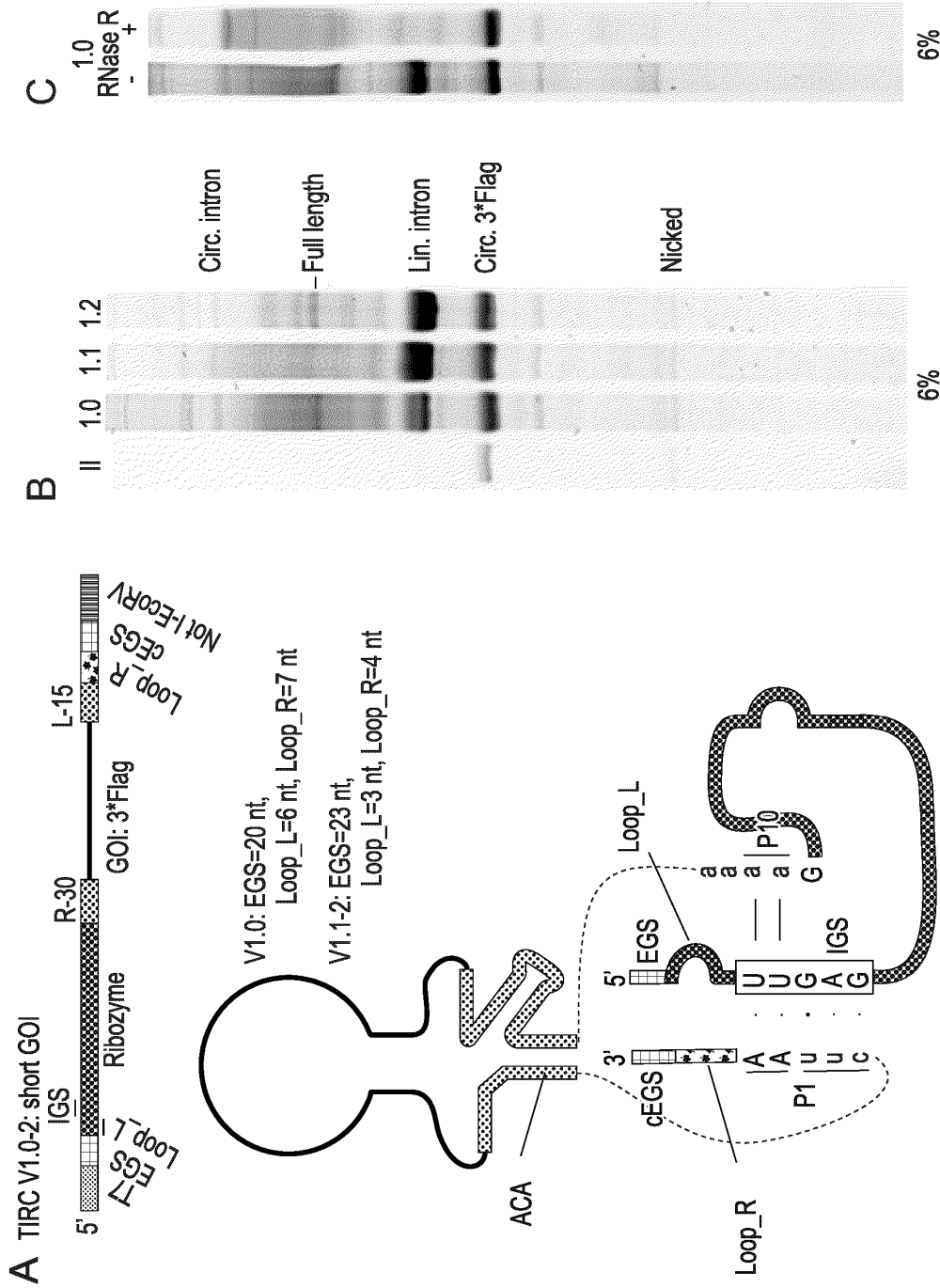


FIG. 3

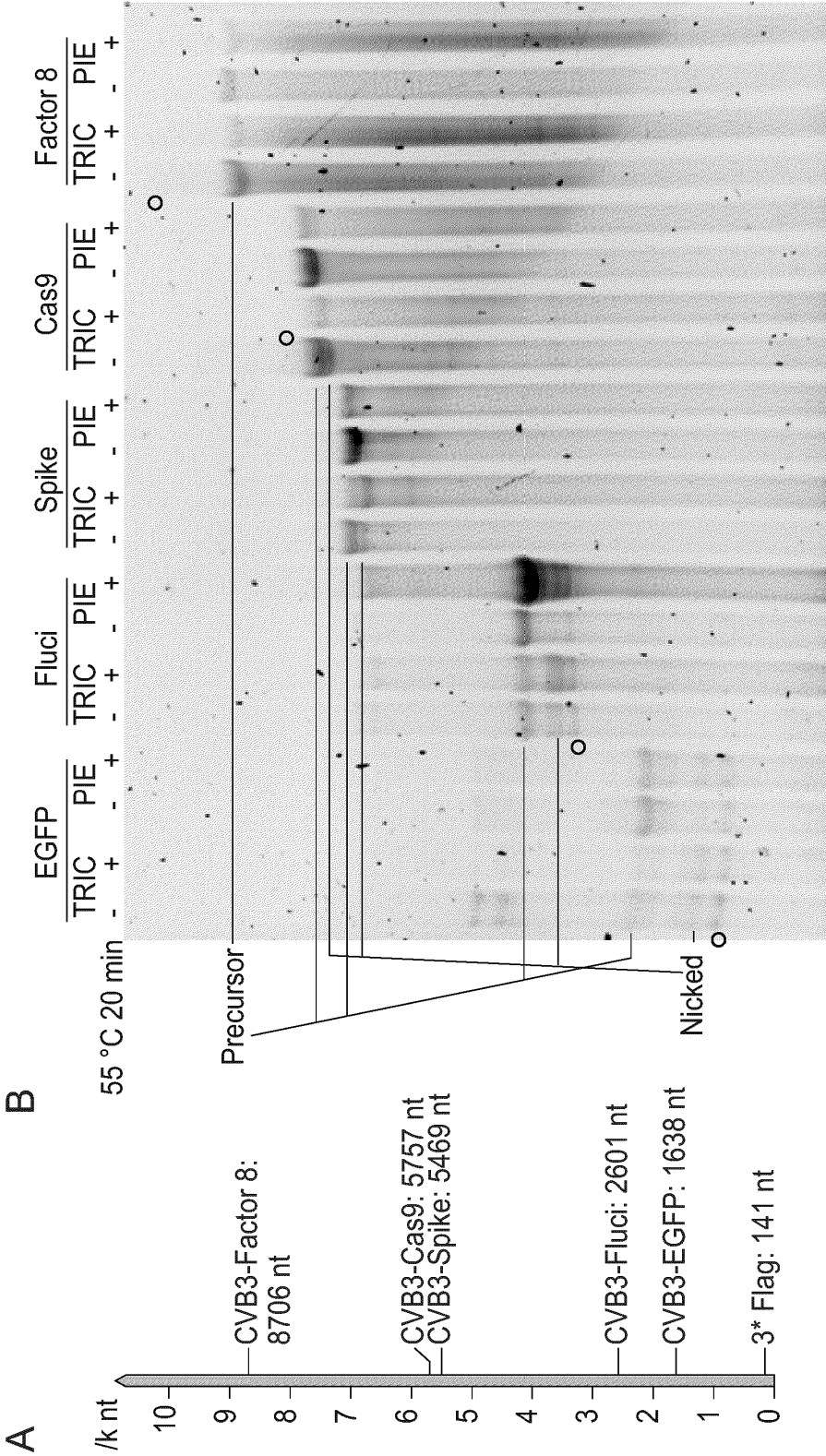


FIG. 4

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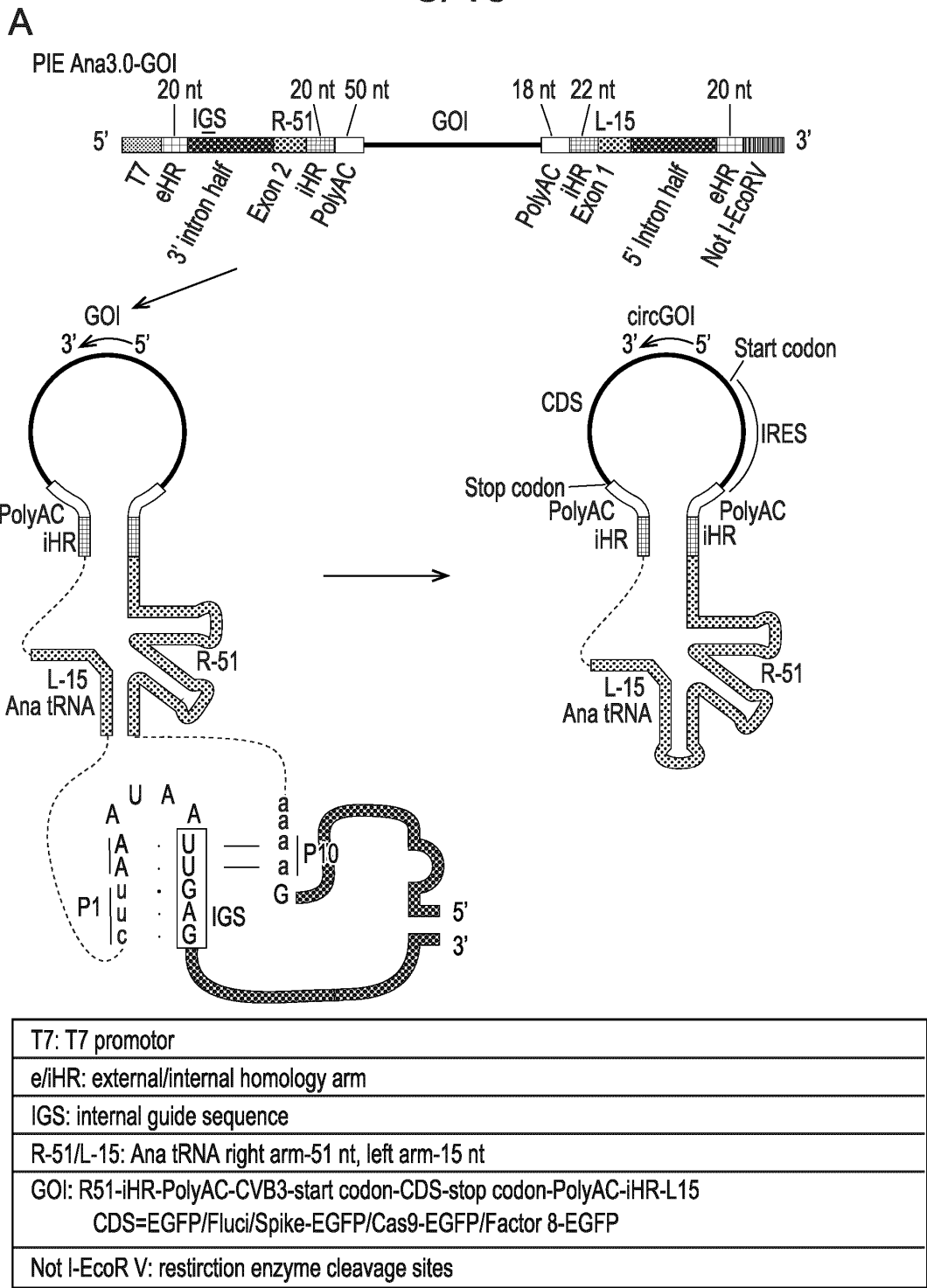


FIG. 5A

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A

PIE-Ana 3.0-GOI

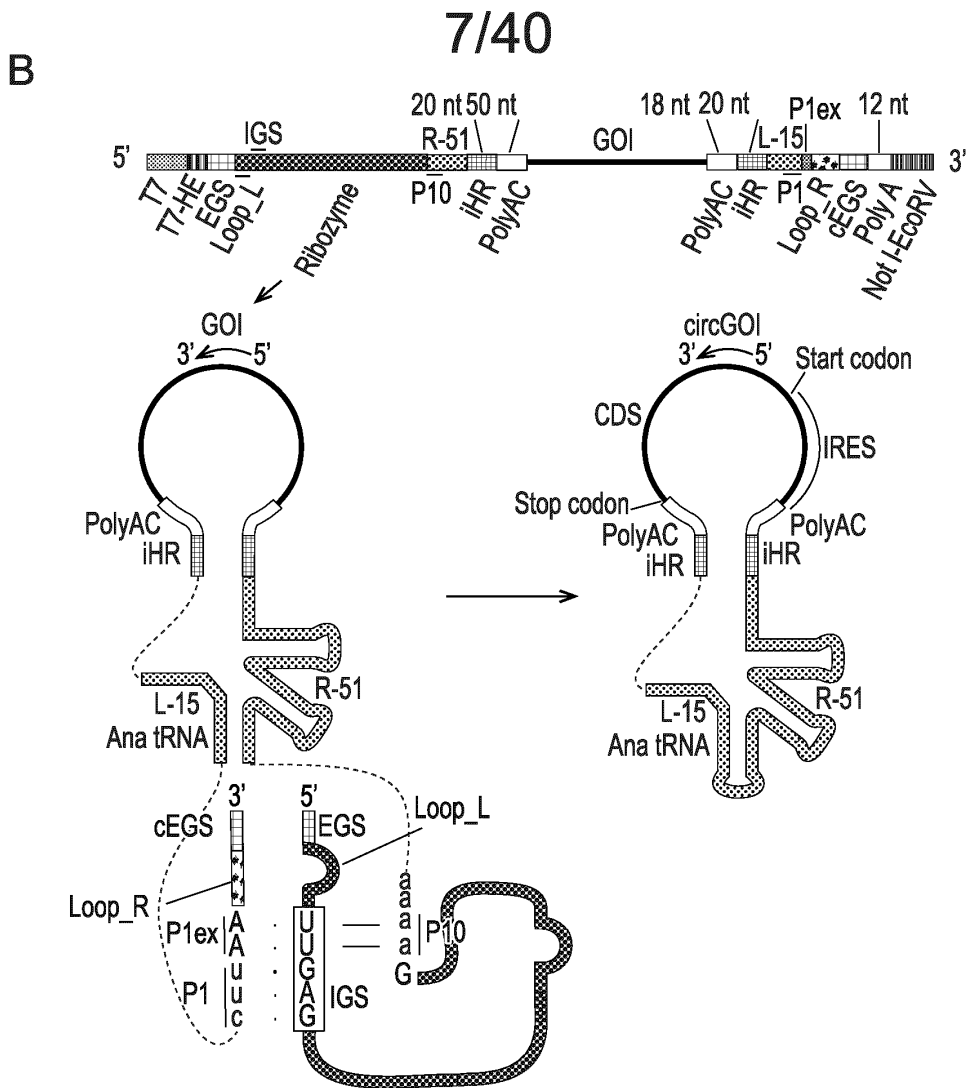
T7-HF [e_HR] [3' intron half] circGOI [Ana tRNA] [5' intron half] [IGS] Not I-EcoR V

GGGAGACCCUCGA CCGUCGAUUGUCCACUGGUC AACAAUAGAUGACUUACAACUAAU
 CGGAAGGUGCAGAGACUCGACGGGAGCUACCCUAACGUCAGACGAGGGUAAAGAGAG
 AGUCCAAUUCUCAAGCCAAUAGGCAGUAGCGAAAGCUGCAAGAGAAUG AAAAUCCGU
 UGACCUUAAACGGUCGUGUGGGUUCAAGUCCUCCACCCCCA CGCCGGAACGCAUA
 GCCGAAAAACAAAAACAAAAAAACAAAAAAACAAAAAAACAAAAACACAUUAAAAC
 AGCCUGUGGGUUGAUCCACCCACAGGCCCAUUGGGCGCUAGCACUCUGGUUACACGG
 UACCUUUGUGCGCCUGUUUUAUACCCCCUCCCCAACUGUAACUUAGAAGUAACACACA
 CCGAUCAACAGUCAGCGUGGCACACCAGCCACGUUUUGAUCAAGCACUUCUGUUACCCC
 GGACUGAGUAUCAAUAGACUGCUCACGCGGUUGAAGGAGAAAGCGUUCGUUAUCCGGC
 CAACUACUUCGAAAAACCUAGUAACACCGUGGAAGUUGCAGAGUGUUUCGCUCAGCACU
 ACCCCAGUGUAGAUCAAGGUCGAUGAGUACCCGAUUCCCCACGGGCGACCGUGGCGGU
 GGCUGCGUUGGCGGCCUGCCCAUGGGGAAACCAUGGGACGCUCUAAUACAGACAUGG
 UGCGAAGAGUCUAUUGAGCUAGUUGGUAGUCCUCCGGCCCCUGAAUGCGGCUAAUCCU
 AACUGCGGAGCACACACCCUCAAGCCAGAGGGCAGUGUGUCGUAACGGGCAACUCUGC
 AGCGGAACCGACUACUUUGGGUGUCCGUGUUUCAUUUUAUCCUUAUACUGGCUGCUUA
 UGGUGACAAUUGAGAGAUCCGUUACCAUAUAGCUAUUGGAUUGGCCAUCCGGUGACUAA
 UAGAGCUAUUAUAUAUCCCUUUGUUGGGUUUAUACCACUUAAGCUUGAAAGAGGUUAAAA
 CAUUACAUAUUAUUGUUAAGUUGAAUACAGCAAAAUUGGUGAGCAAGGGCGAGGAGCUGU
 UCACCGGGGUGGUGGCCAUCCUGGUCGAGCUGGACGGCGACGUAACGGCCACAAGUU
 CAGCGUGUCCGGCGAGGGCGAGGGCGAUGCCACCUACGGCAAGCUGACCCUGAAGUUC
 AUCUGCACCCACCGGCAAGCUGCCCGUGCCUUGGCCACCCUCGUGACCCACCCUGACCU
 ACGGCGUGCAGUGCUUCAGCCGUACCCCGACCAUGAAGCAGCAGACUUCUUCAA
 GUCCGCCAUGCCCGAAGGCUACGUCCAGGAGCGCACCAUCUUCUUAAGGACGACGGC
 AACUACAAGACCCGCGCCGAGGUGAAGUUCGAGGGCGACACCCUGGUGAACCGCAUCG
 AGCUGAAGGGCAUCGACUUAAGGAGGACGGCAACAUCUUGGGGCAAGCUGGAGUA
 CAACUACAACAGCCACAACGUCUUAUUAUGGCCGACAAGCAGAAGAACGGCAUCAAGG
 UGAACUUAAGAUAUCCGCCACAACUUGAGGACGGCAGCGUGCAGCUCGCCGACCACUAC
 CAGCAGAACACCCCCAUCGGCGACGGCCCCGUGCUGCUGCCCGACAACCACUACCUGA
 GCACCCAGUCCGCCUGAGCAAAGACCCCAACGAGAAGCGCGAUCACAUGGUCCUGCU
 GGAGUUCGUGACCGCCGCCGGGAUCACUCUCGGCAUGGACGAGCUGUACAAGUAAAA
 AAACAAAAACAAACGGCUAUUAUGCGUUAACGGCGAGACGCUACGGACUU AAAUAA
 UUGAGCCUUAAGAAGAAAUUCUUUAAGUGGAUGCUCUCAAACUCAGGGAAACCUAAAU
 UAGUUUAUAGACAAGGCAAUCCUGAGCCAAGCCGAAGUAGUAAUUAAGUAA GACCAGUGG
 ACAAUUCGACGG AUAACAGCAUAUCUAGCGGCCGCGAU (SEQ ID NO: 52)

circGOI: R51-iHR-PolyAC-CVB3-start codon-CDS-stop codon-PolyAC-iHR-L15

CDS=EGFP/Fluci/Spike-EGFP/Cas9-EGFP/Factor 8-EGFP

FIG. 5A (continued)



T7: T7 promotor
T7-HE: T7 high efficiency sequence
EGS: external guide sequence (20 nt random sequence)
Loop_L/R: loop_left (6 nt)/loop_right (5nt)
IGS: internal guide sequence
R-51/L-15: Ana tRNA right arm-51 nt, left arm-15 nt
iHR: internal homology arm
GOI: R51-iHR-PolyAC-CVB3-start codon-CDS-stop codon-PolyAC-iHR-L15 CDS=EGFP/Fluci/Spike-EGFP/Cas9-EGFP/Factor 8-EGFP
P1/P10: paired structure 1/10
P1ex: P1 extension
cEGS: complementary sequence of EGS
Not I-EcoR V: restirction enzyme cleavage sites

FIG. 5B

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TRIC-V1: long GOIs

T7-HE EGS Ribozyme Loop_L IGS circGOI Ana tRNA P1ex Loop_R cEGS PolyA Not I-EcoR V

GGGAUAAUAC GGUCAAUCAGUUGGCUUCCG AAAUAAUUGAGCCUAGAGAAGAAUU
CUUUAAGUGGAUGCUCUCAAACUCAGGGAAACCUAAAUCUAGCUAUAGACAAGGCAAUC
CUGAGCCAAGCCGAAGUAGUAAUUAAGUUAACAACAGAUAAACUACAGCUAAUCCGG
AAGGUGCAGAGACUCGACGGGAGCUACCCUAAACGUAAGACGAGGGUAAAGAGAGAGU
CCAAUUCUCAAAGCCAAUAGGCAGUAGCGAAAGCUGCGGGAGAAUG AAAAUCCGUUGA
CCUUAACGGUCGUGUGGGUUAAGUCCCUCCACCCCCACGCCGGAACGCAAUAGCC
GAAAAACAAAAACAAAAAAACAAAAAAACAAAAAAACAAAAACAAUUAACAGCC
UGUGGGUUGAUCCCAACCCACAGGCCCAUUGGGCGUAGCACUCUGGUUACACGGUACC
UUUGUGCGCCUGUUUUAUACCCCUCCCAACUGUAACUUAAGAAGUAAACACACACCGA
UCAACAGUCAGCGUGGCACACCAGCCACGUUUUGAUCAAGCACUUCUGUUAACCCCGGA
CUGAGUAUCAAUAGACUGCACGCGGUUGAAGGAGAAAGCGUUCGUUAUCCGGCCAA
CUACUUCGAAAAACCUAGUAAACACCGUGGAAGUUGCAGAGUGUUUCGCUCAGCACUACC
CCAGUGUAGAUACAGGUCGAUGAGUCACCGCAUUCACCGGGCGACCGUGGCGGUGGC
UGCGUUGGCGGCCUGCCCAUGGGGAAACCAUGGGACGCUCUAAUACAGACAUGGUGC
GAAGAGUCUAAUUGAGCUAGUUGGUAGUCCUCCGGCCCCUGAAUGCGGCUAAUCCUAAAC
UGCGGAGCACACACCCUCAAGCCAGAGGGCAGUGUGUCGUAACGGGCAACUCUGCAGC
GGAACCGACUACUUUGGGUGUCCGUGUUUUAUUAUCCUUAUACUGGCGUCUUAUGG
UGACAAUUGAGAGAUCCGUUACCAUUAUAGCUAUUGGAUUGGCCAUCCGGUGACUAAUAGA
GCUAAUUAUUAUCCCUUUGUUGGGUUUAUACCACUUAAGCUUGAAAGAGGUUAAACAUU
ACAAUUAUUGUUAAGUUGAAUACAGCAAAUUGGUGAGCAAGGGCGAGGAGCUGUUCAC
CGGGGUGGUGCCCAUCCUGGUCGAGCUGGACGGCGACGUAACGGCCACAAGUUCAGC
GUGUCCGGCGAGGGCGAGGGCGAUGCCACCUACGGCAAGCUGACCCUGAAGUUAUC
UGCACCACCGGCAAGCUGCCCGUGCCCGUGGCCACCCUCGUGACCACCCUGACCUACG
GCGUGCAGUGCUUACAGCCGCUACCCCGACCACAUGAAGCAGCACGACUUCUUAAGUC
CGCCAUGCCCGAAGGCUACGUCCAGGAGCGCACCAUCUUCUUAAGGACGACGGCAAC
UACAAGACCCGCGCCGAGGUGAAGUUCGAGGGCGACACCCUGGUGAACCGCAUCGAGC
UGAAGGGCAUCGACUUAAGGAGGACGGCAACAUCUGGGGCACAAGCUGGAGUACAA
CUACAACAGCCACAACGUCUUAUUAUGGCCGACAAGCAGAAGAACGGCAUCAAGGUGA
ACUUAAGAUCGCCACAACAUCGAGGACGGCAGCGUGCAGCUCGCCGACCACUACCA
GCAGAACACCCCAUCGGCGACGGCCCCGUGCUGCUGCCCGACAACCACUACCUGAGC
ACCCAGUCCGCCUGAGCAAAGACCCCAACGAGAAGCGCGAUCACAUGGUCCUGCUGG
AGUUCGUGACCGCCGCCGGGAUCACUCUGGCAUGGACGAGCUGUACAAGUAAAAAA
ACAAAAACAAACCGGCUAUUAUGCGUUAACGGCGAGACGCUACGGACUU AA ACACC
GGUCAAUCAGUUGGCUUCCG AAAAAAAAAA GCGGCCGCGAU (SEQ ID NO: 53)

circGOI: R51-iHR-PolyAC-CVB3-start codon-CDS-stop codon-PolyAC-iHR-L15
CDS=EGFP/Fluci/Spike-EGFP/Cas9-EGFP/Factor 8-EGFP

FIG. 5B (continued)

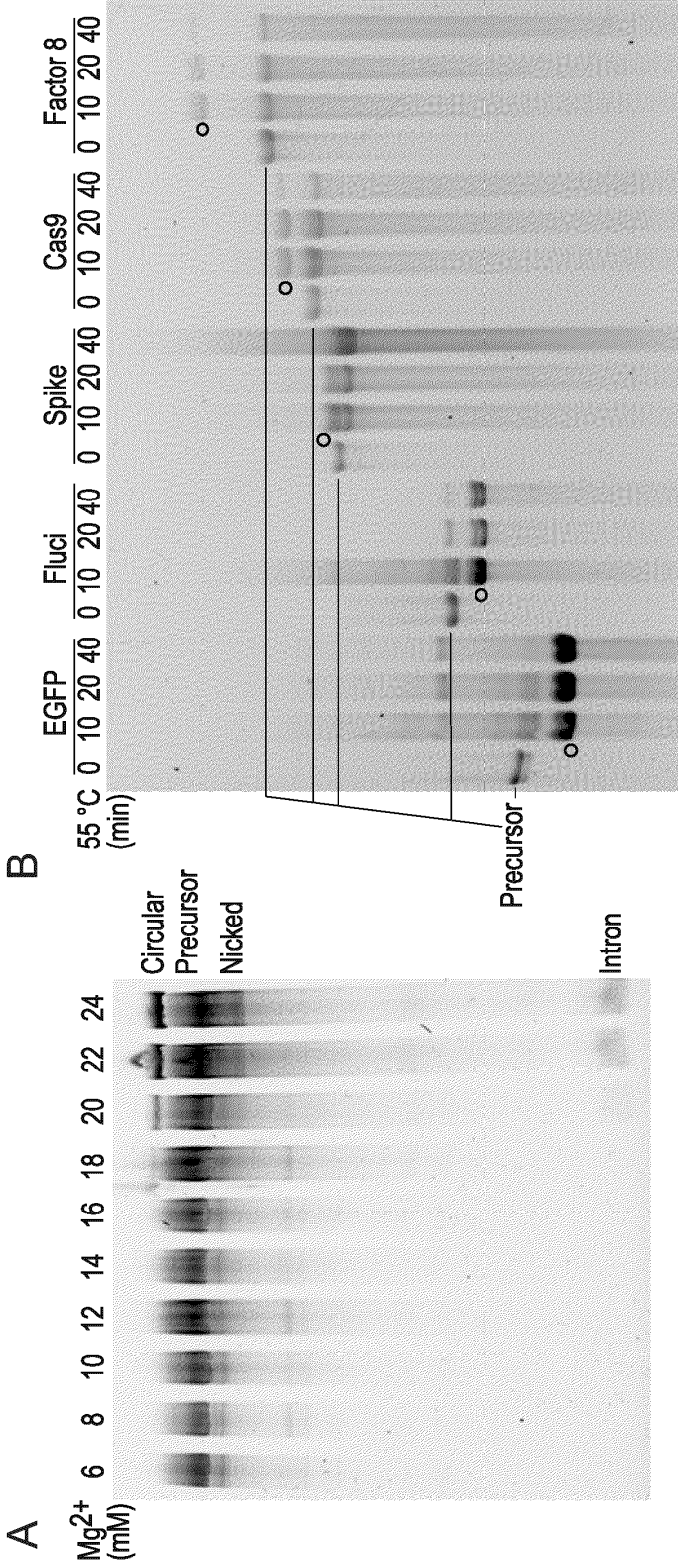


FIG. 6

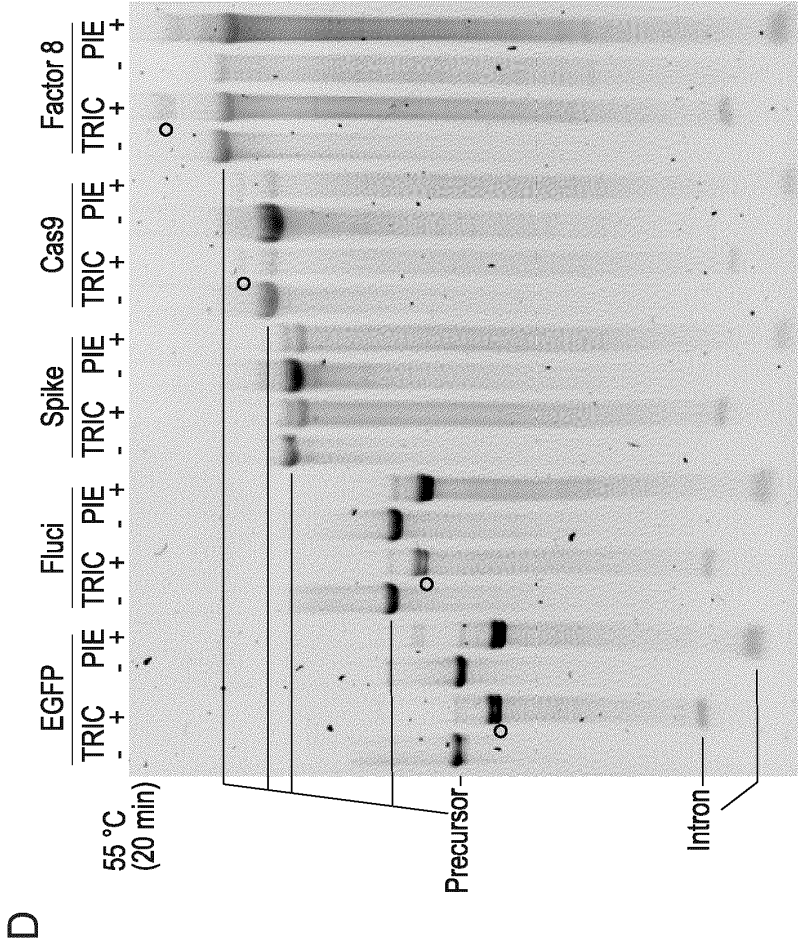
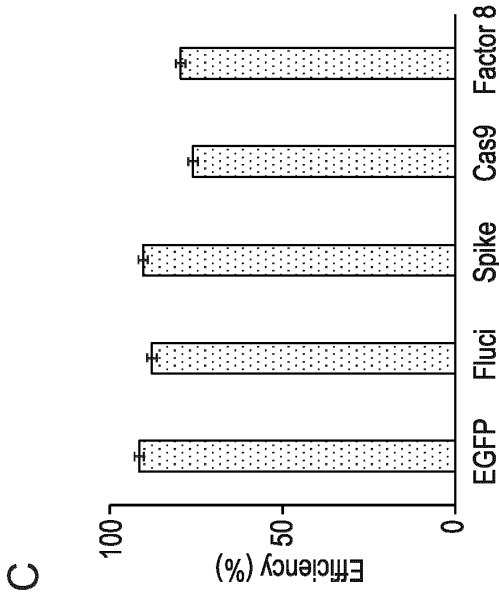


FIG. 6B (continued)



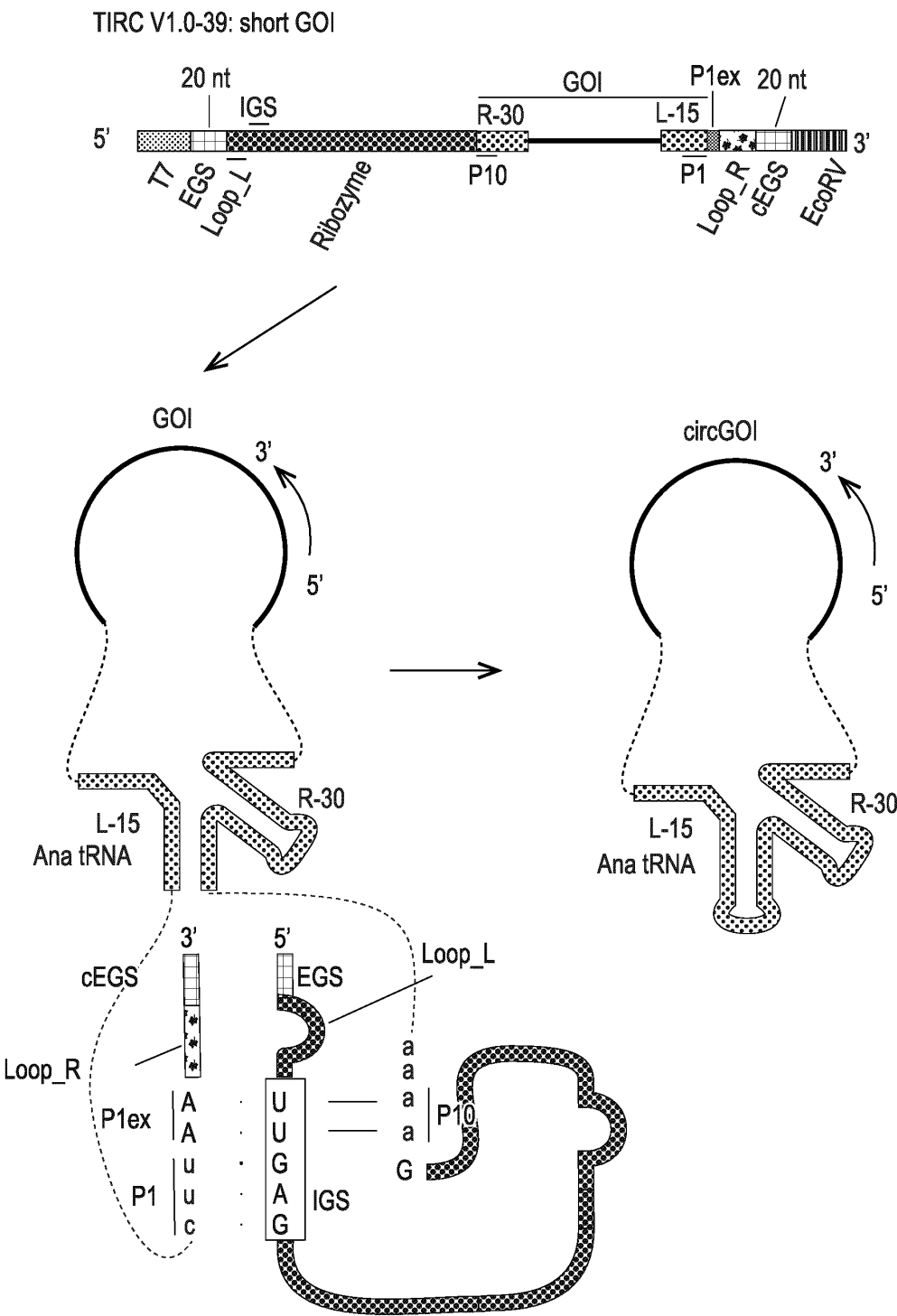


FIG. 7A

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TRIC-V1: 1.0-2, short GOI

EGS

Ribozyme

Loop_L

IGS

circGOI

Ana tRNA

P1ex

Loop_R

cEGS

EcoR V

G

GGUCAAUCGGUUGGCUUCCG

AAAUAAUUGAGCCUAGAGAAG

AAAUUCUUUAAGUGGAUGCUCUCAAACUCAGGGAAACCUAAAUCU

AGCUAUAGACAAGGCAAUCCUGAGCCAAGCCGAAGUAGUAAUUAG

UAAGUUAACAACAGAUAAACUACAGCUAAUCGGAAGGUGCAGAGA

CUCGACGGGAGCUACCCUAACGUCAAGACGAGGGUAAAGAGAGA

GUCCAAUUCUCAAAGCCAAUAGGCAGUAGCGAAAGCUGCGGGAG

AAUG

AAAAUCCGUUGACCUUAAACGGUCGUGUGG

UACACUCGA

UCUGGACUAAAGCUGCUCAUGGAUUACAAAGAUACACGAUGGUGA

UUAUAAAGAUACGACAUCGAUUACAAGGAUGAUGAUGAUAAAG

AGACGCUACGGACUU

AA

ACACC

GGUCAAUCGGUUGGCUUCCG

GAU

(SEQ ID N0: 63)

circGOI: R30-3*Flag-L15

T7: T7 promotor
EGS: external guide sequence (20 nt random sequence)
Loop_L/R: loop_left (6 nt)/loop_right (5nt)
IGS: internal guide sequence
R-51/L-15: Ana tRNA right arm-30 nt, left arm-15 nt (1.0-2)
circGOI: R30-3*Flag-L15
P1/P10: paired structure 1/10
P1ex: P1 extension
cEGS: complementary sequence of EGS
EcoR V: restriction enzyme cleavage sites

V1.3	0	1	2	3	4	5	6	7	8	9
R	2	2	2	30	25	16	9	16	9	9
L	3	3	15	3	3	3	3	15	15	8

FIG. 7B

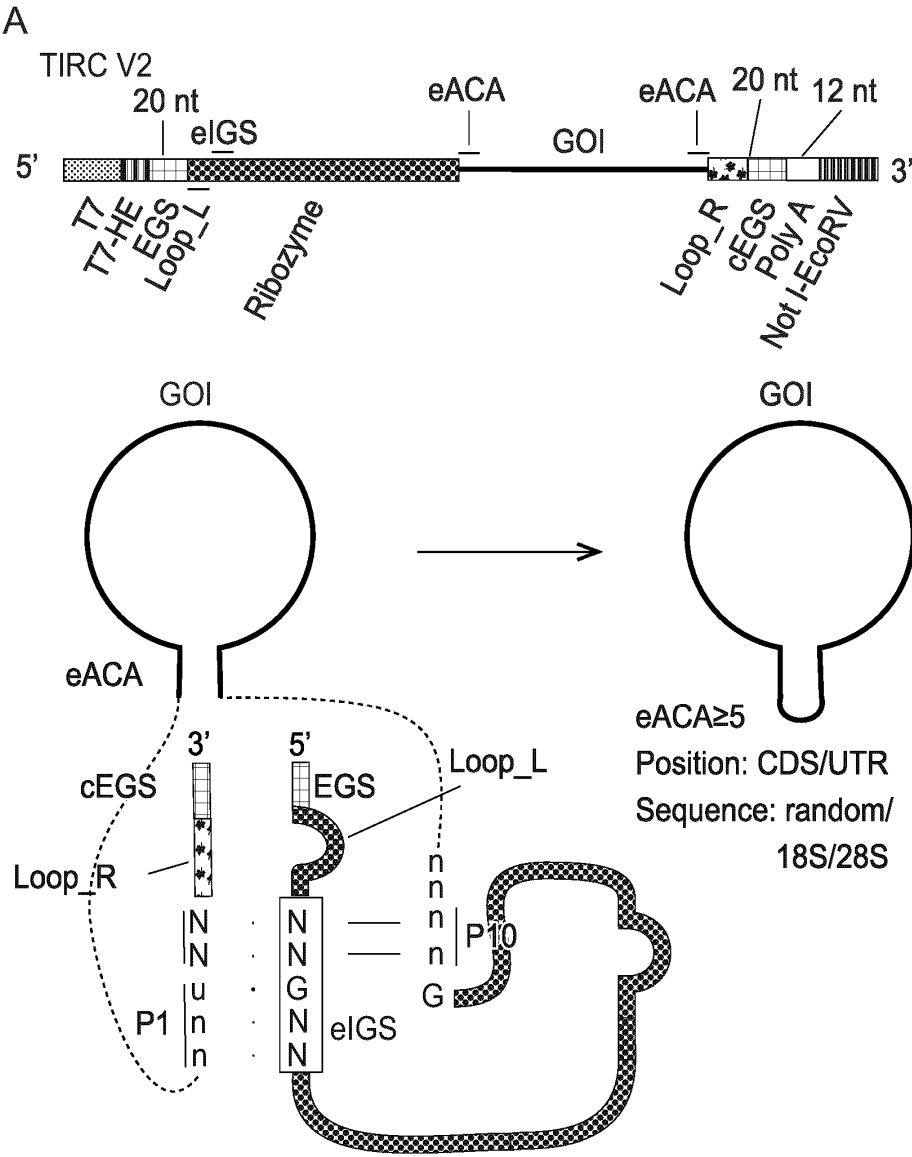


FIG. 8

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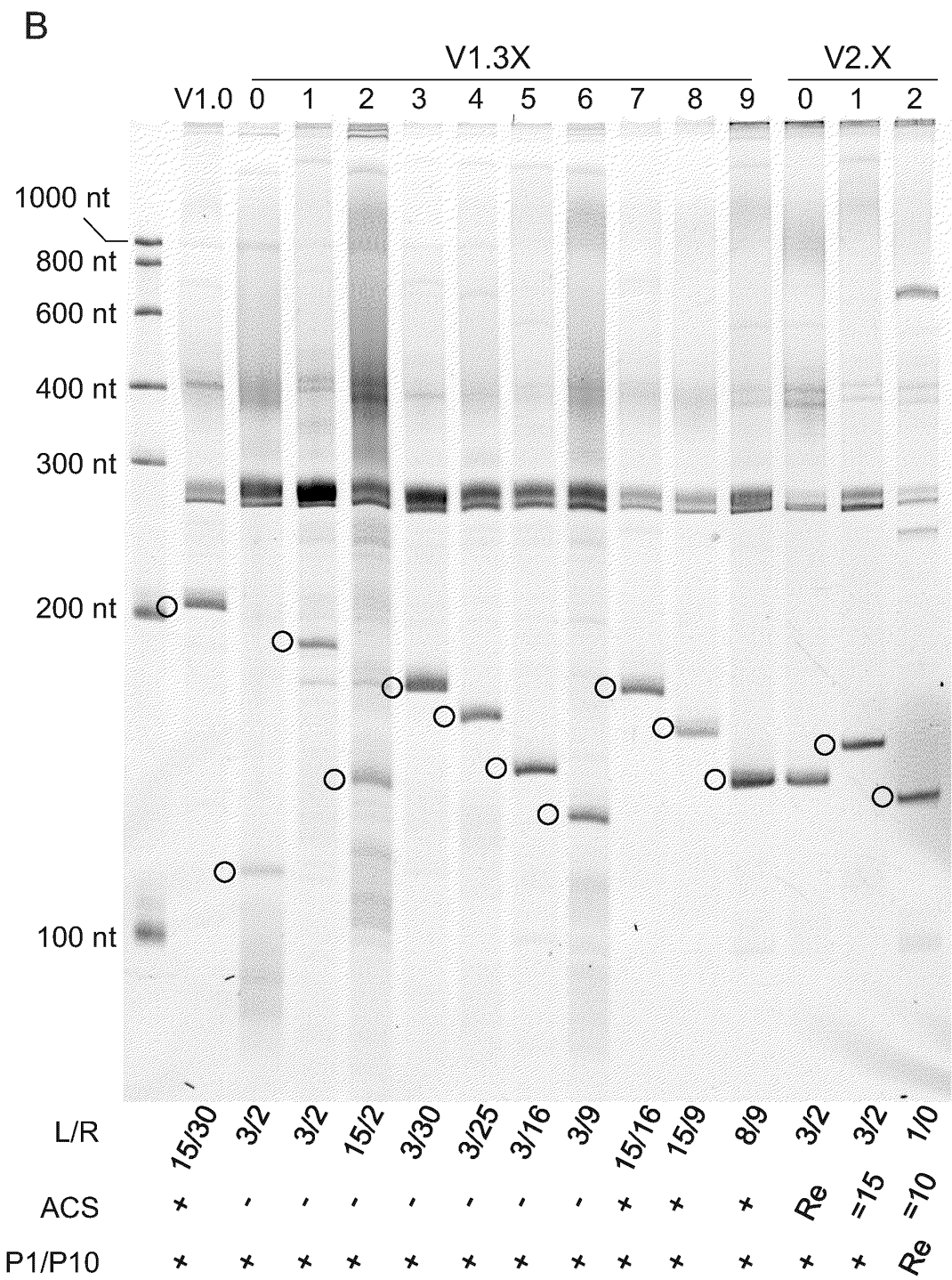


FIG. 8 (continued)

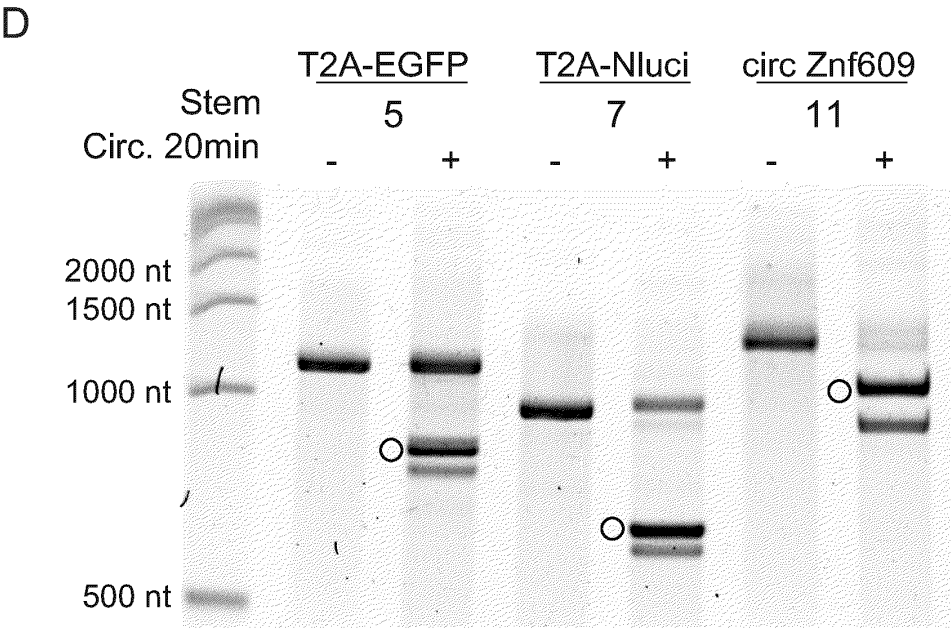
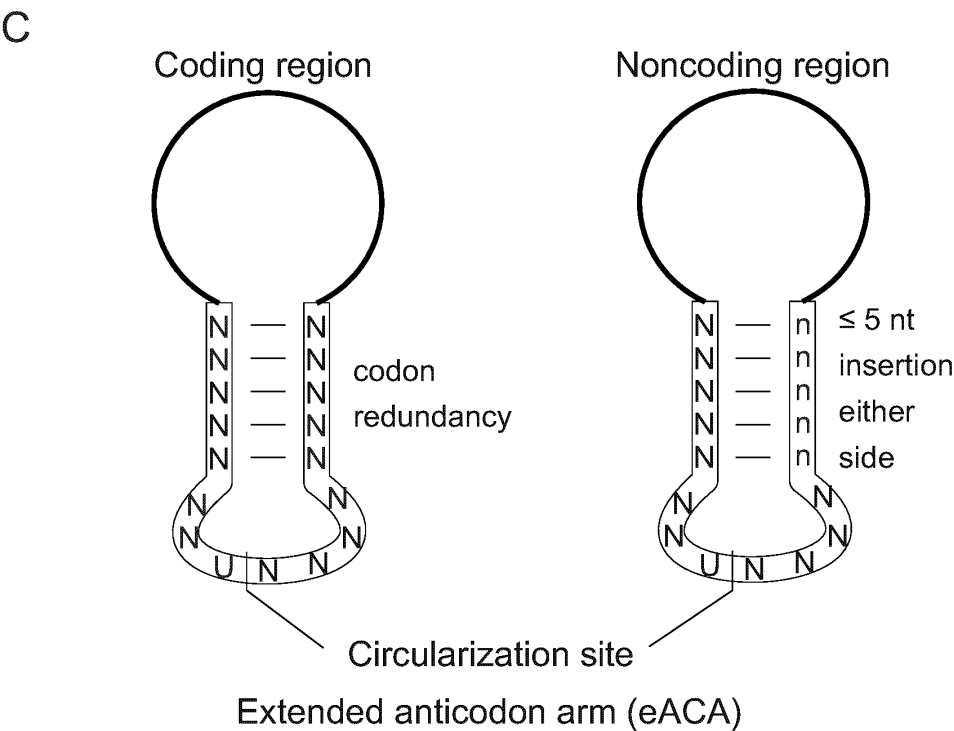


FIG. 8 (continued)

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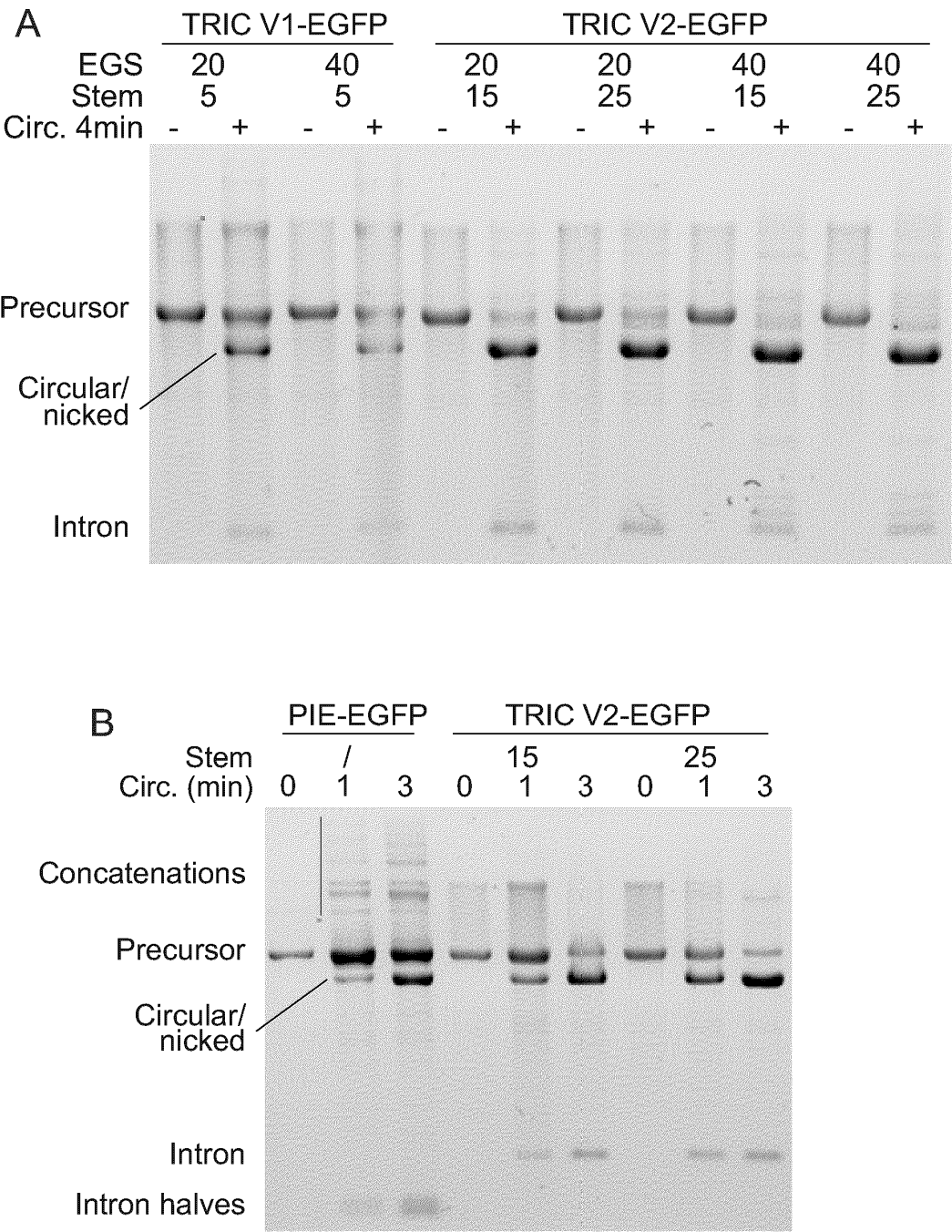


FIG. 9

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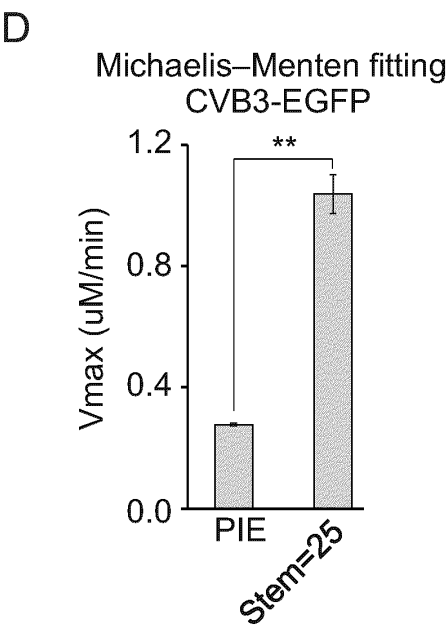
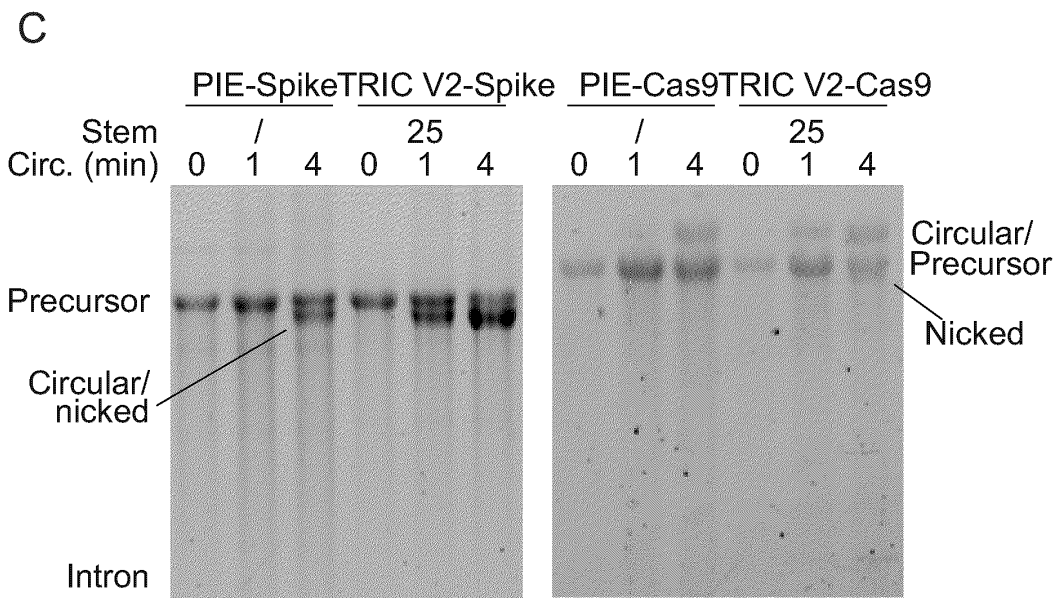


FIG. 9 (continued)

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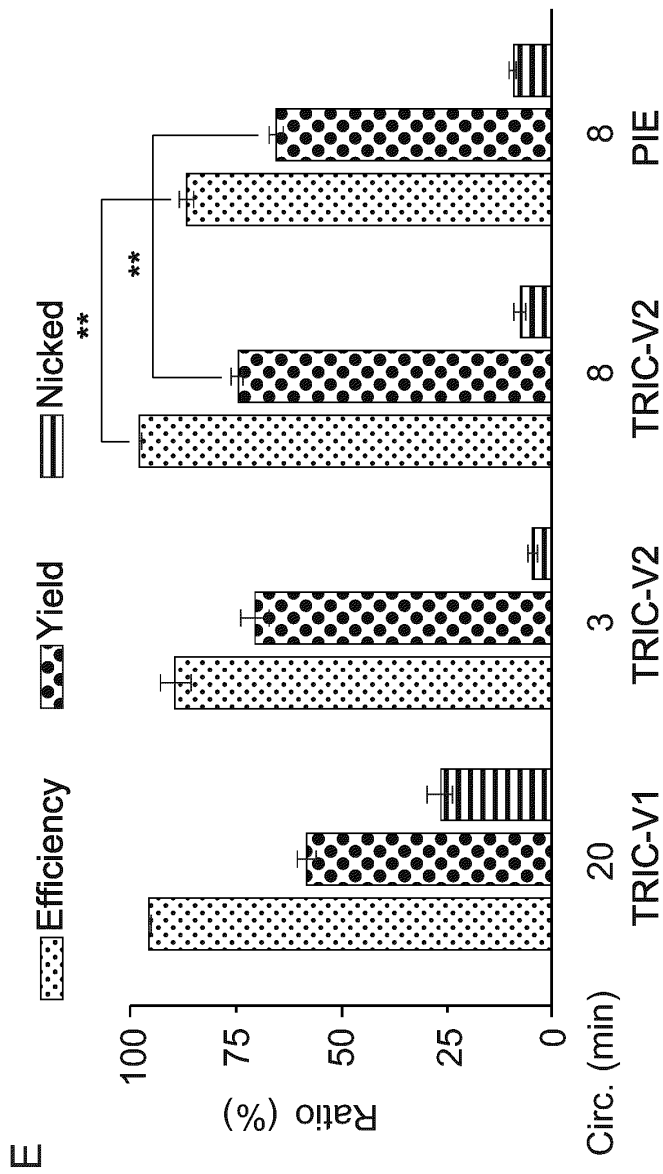


FIG. 9 (continued)

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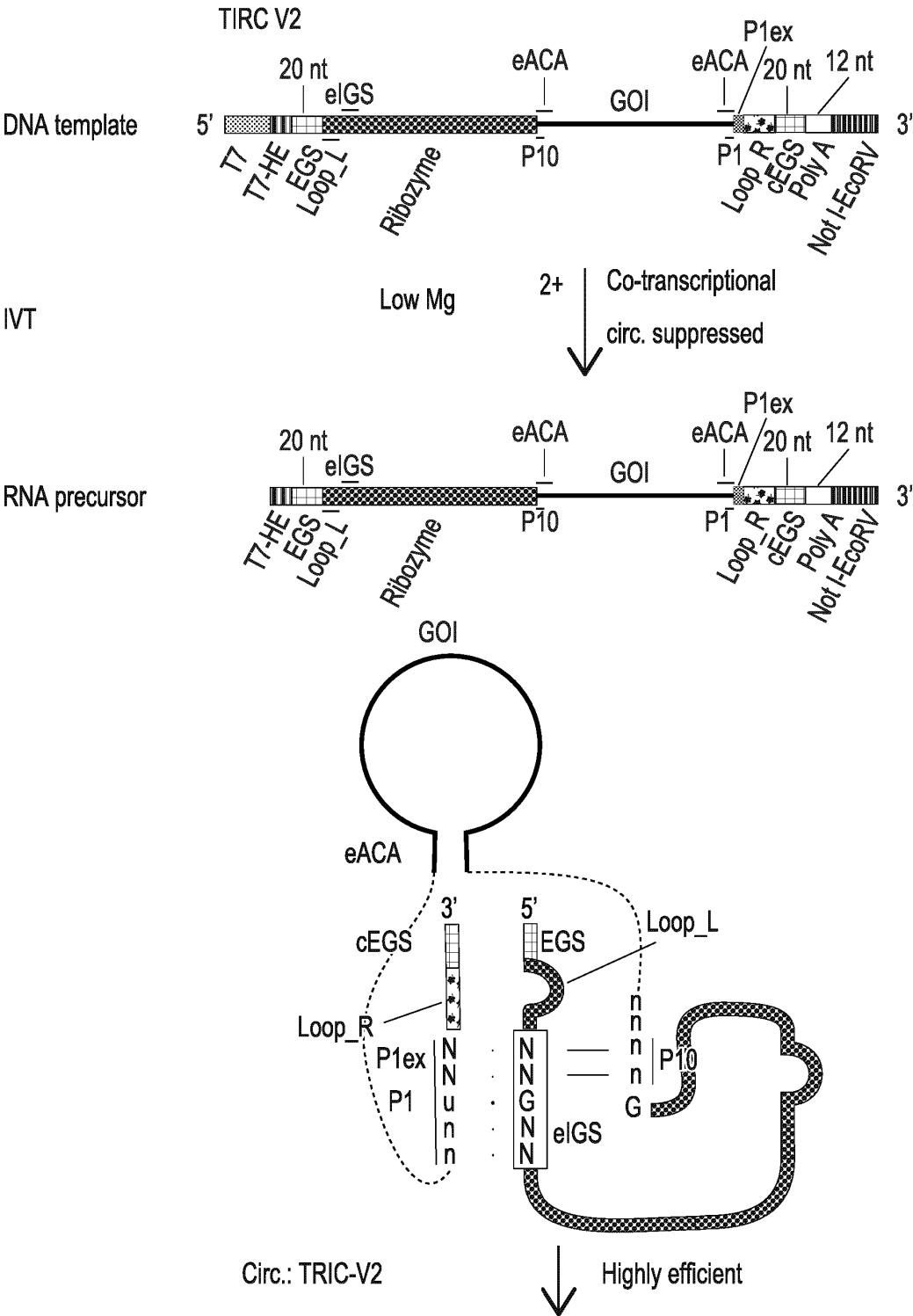


FIG. 10A

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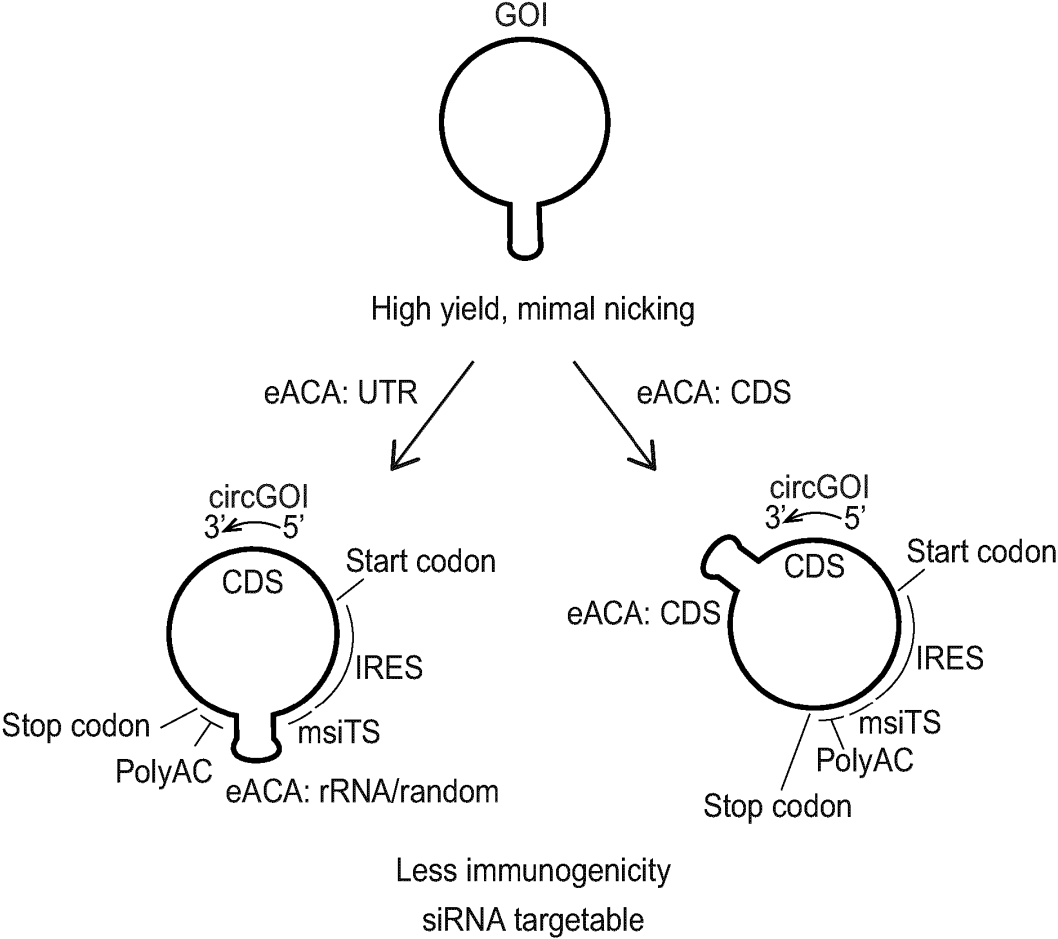


FIG. 10A (continued)

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T7: T7 promotor
T7-HE: T7 high efficiency sequence
EGS: external guide sequence (20/40 nt random sequence)
Loop_L/R: loop_left (6 nt)/loop_right (5nt)
eIGS: extended internal guide sequence (random with G 3 rd)
eACA: extended anticodon arm sequence: random with an U-3 rd 7 nt loop/18S/28S; position; UTR/CDS stem length: 5-25 nt (tested: 5, 7, 10, 11, 15, 17, 24, 25)
circ.GOI-short: 3*Flag circ.GOI-long: 1: eACA (UTR)-msiTS-IRES-start codon-CDS-stop codon-PolyAC-eACA (UTR) 2: eACA (CDS)-stop codon-PolyAC-msiTS-IRES-start codon-eACA (CDS) IRES= CVB3, CSFV, CroV, CDS= EGFP, Spike-EGFP, Cas9-EGFP, Nluc, circZNF609, T2A-EGFP
P1/P10: paired structure 1/10
P1ex: P1 extension
msiTS: multiple siRNA target sequence
cEGS: complementary sequence of EGS
Not I-EcoR V: restriction enzyme cleavage sites

FIG. 10B

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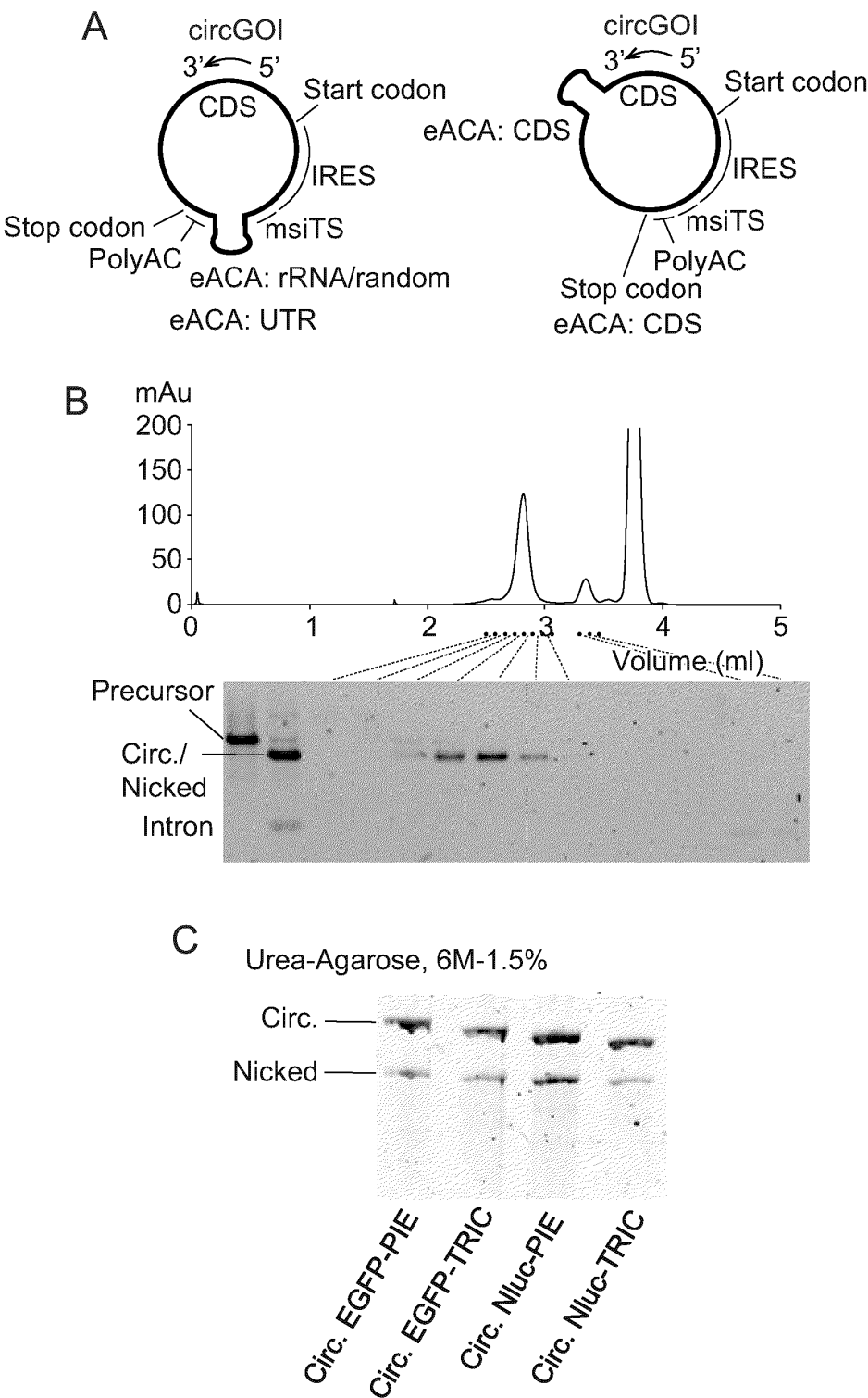


FIG. 11

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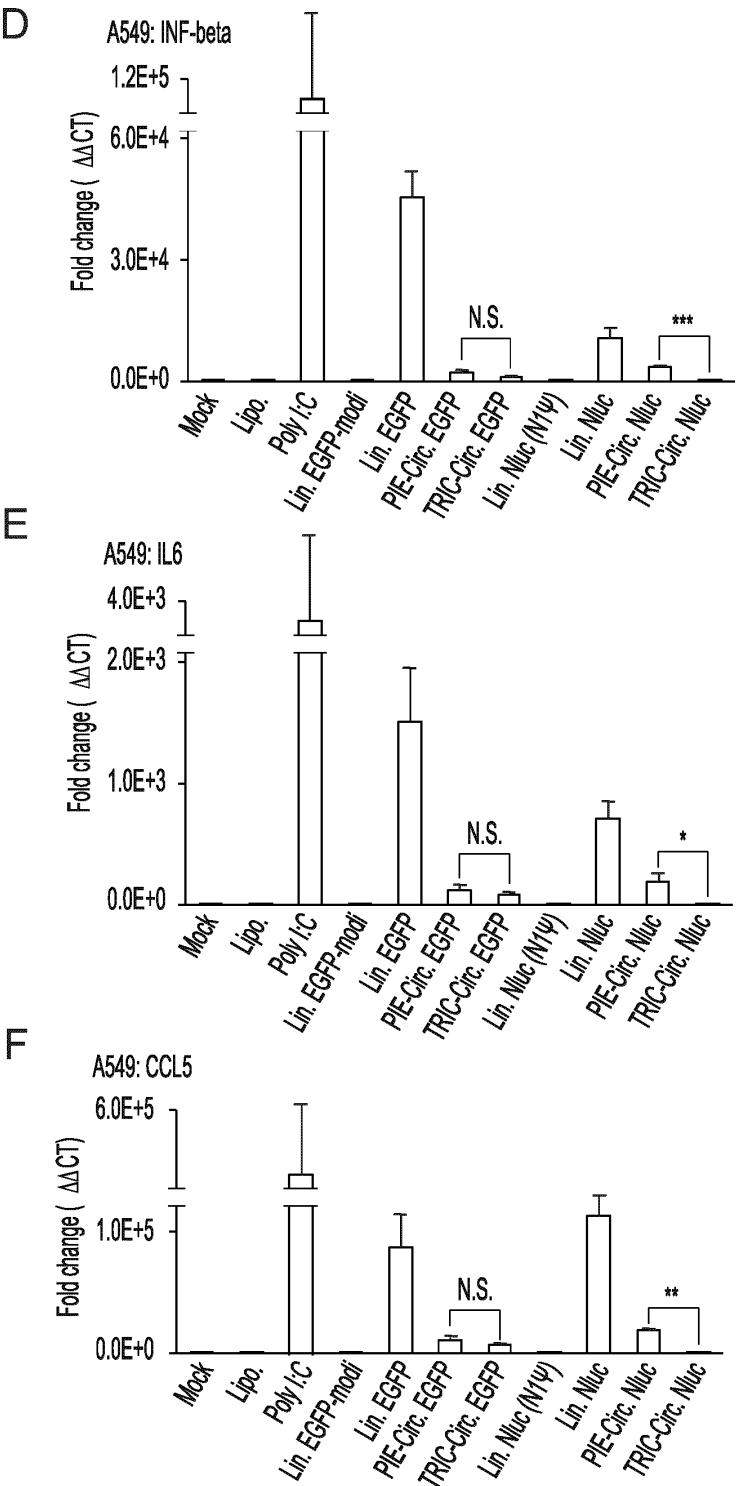


FIG. 11 (continued)

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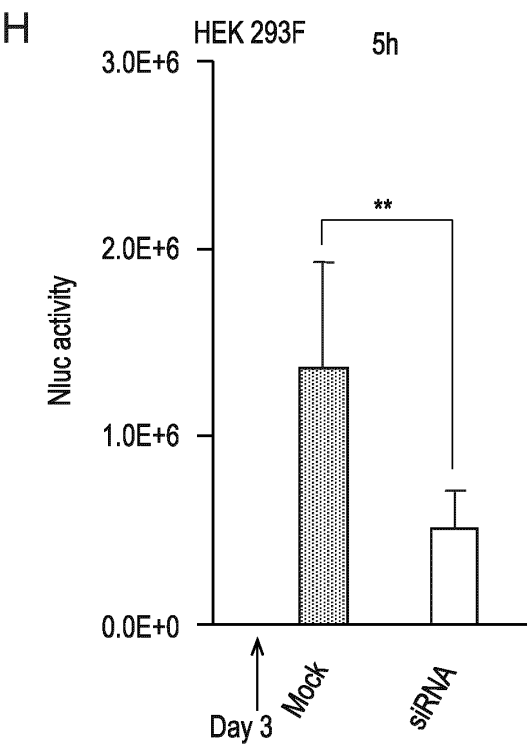
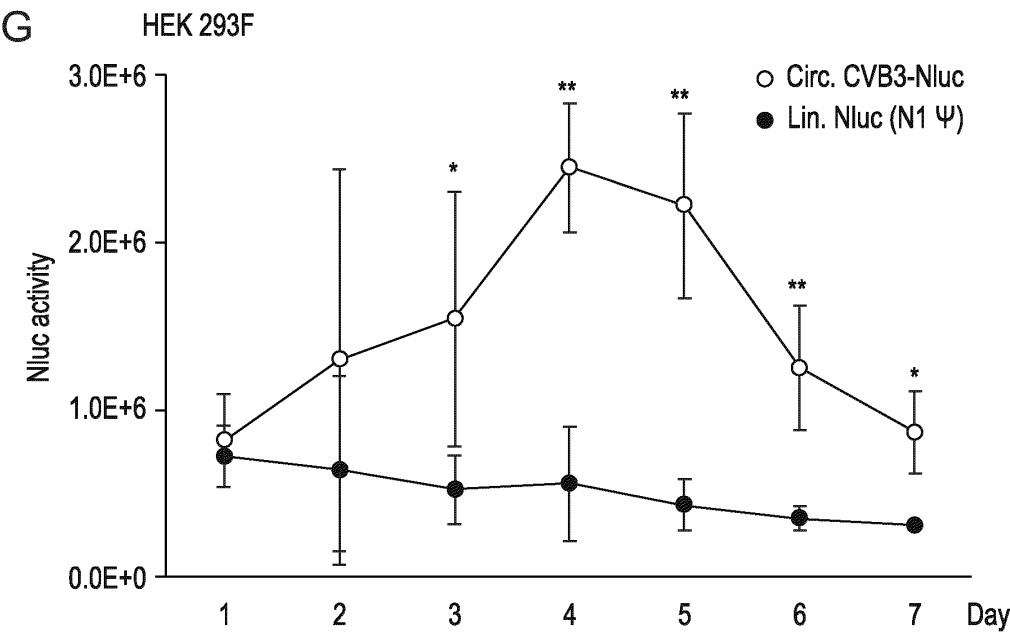


FIG. 11 (continued)

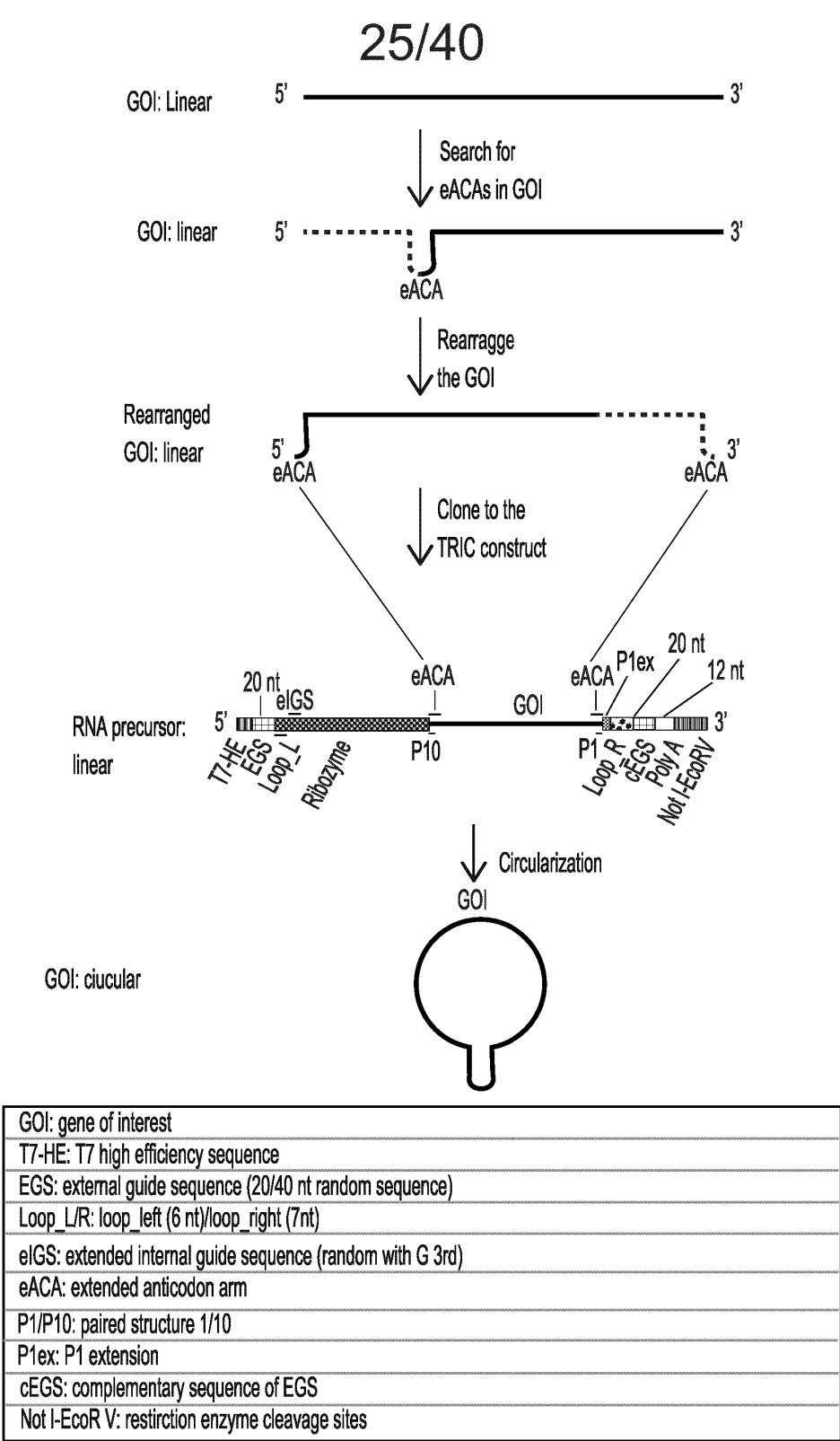
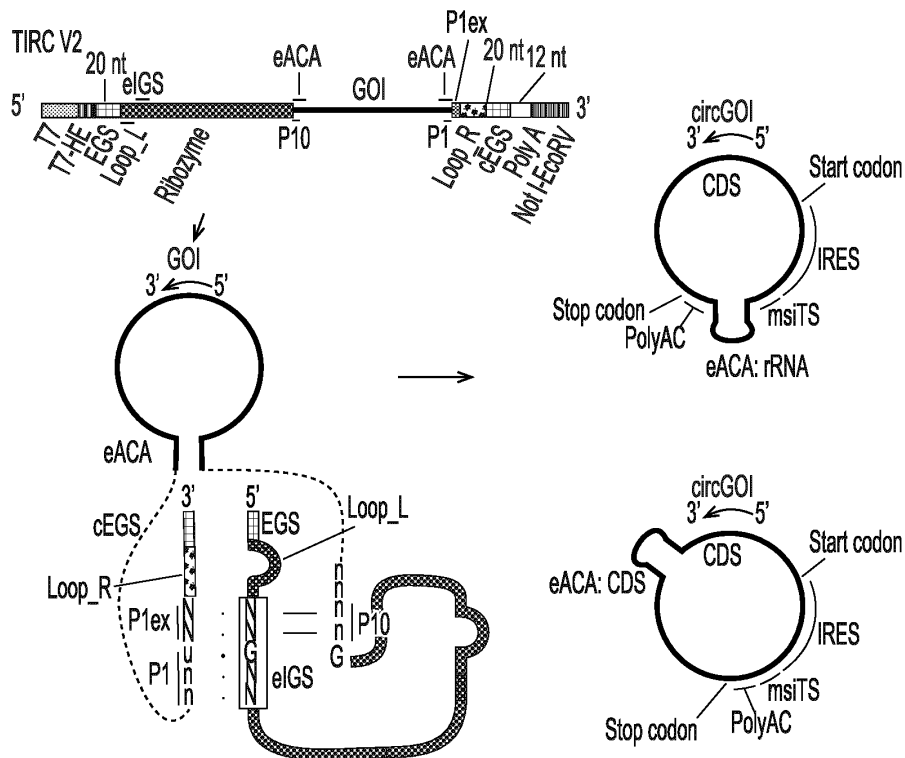


FIG. 12

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T7: T7 promotor
T7-HE: T7 high efficiency sequence
EGS: external guide sequence (20/40 nt random sequence)
Loop_L/R: loop_left (6 nt)/loop_right (5nt)
eIGS: extended internal guide sequence (random with G 3 rd)
eACA: extended anticodon arm sequence: random with an U-3 rd 7 nt loop/18S/28S; position: UTR/CDS stem length: 5-25 nt (tested: 5, 7, 10, 11, 15, 17, 24, 25)
circ.GOI-short: 3*Flag circ.GOI-long: 1: eACA (UTR)-msiTS-IRES-start codon-CDS-stop codon-PolyAC-eACA (UTR) 2: eACA (CDS)-stop codon-PolyAC-msiTS-IRES-start codon-eACA (CDS) IRES= CVB3, CSFV, CroV, CDS= EGFP, Spike-EGFP, Cas9-EGFP, Nluc, circZNF609, T2A-EGFP
msiTS: multiple siRNA target sequence
P1/P10: paired structure 1/10
P1ex: P1 extension
cEGS: complementary sequence of EGS
Not I-EcoR V: restriction enzyme cleavage sites

FIG. 13A

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TIRC V2-Nluc: eACA placed in UTR

T7-HE|EGS|Ribozyme|Loop_L|IGS|circGOI|eACA|P1ex|Loop_R|cEGS|PolyA|Not I-EcoR V

GGGAAUAAUAC GGUCAAUCAGUUGGCUUCCG|AAUAAUUGAGCCUUAGAGAAGAAAUU|
 CUUUAAAGUGGAUGCUCUCAAACUCAGGGAACCUAAAUCUAGCUAUAGACAAGGCCAAUC|
 CUGAGCCAAGCCGAAGUAGUAAUAGUAAGUUAACAACAGAUAAUACAGCUAAUCCG|
 AAGGUGCAGAGACUCGACGGGAGCUACCCUAACGUCAGAGAGGGUAAAGAGAGAGU|
 CCAAUUCUCAAAGCCAAUAGGCAGUAGCGAAAGCUGCGGGAGAAUG|AAAAGGAGGGCG|
 CGCGGGUUCGGGGCGGGG|AAAACAAUUGGGCCAGAUCGAAAAAACGAACAUGAUCGA
 CUUUUACACACAUUAAAACAGCCUGUGGGUUGAUCCACCCACAGGCCCAUUGGGCGC
 UAGCACUCUGGUUACAGGUACCUUUUGUGCGCCUGUUUUUUAACCCCUCCCCCAACUG
 UAACUUAGAAGUAACACACACCGAUCAACAGUCAGCGUGGCACACCAGCCACGUUUUGA
 UCAAGCACUUCUGUUACCCCGGACUGAGUAUCAAUAGACUGCUCACGCGGUUGAAGGA
 GAAAGCGUUCGUUAUCCGGCCAACUACUUCGAAAAACCUAGUAACACCGUGGAAGUUG
 CAGAGUGUUUCGCUCAGCACUACCCAGUGUAGAUACAGGUCGAUGAGUACCGCAUUC
 CCCACGGGCGACCGUGGGCGGUGGCUGCGUUGGCGGCCUGCCCAUGGGGAAACCCAUG
 GGACGCUCUAAUACAGACAUGGUGCGAAGAGUCUAAUUGAGCUAGUUGGUAGUCCUCCG
 GCCCCUGAAUGCGGCUAAUCCUAAUCUGCGGAGCACACCCUCAAGCCAGAGGGCAGU
 GUGUCGUAAACGGGCAACUCUGCAGCGGAACCGACUACUUUGGGUGUCCGUGUUUCAU
 UUAUCCUUAUACUGGCUGCUUAUGGUGACAAUUGAGAGAUCGUUACCAUUAAGCUAUU
 GGAUUGGCCAUCCGGUGACUAAUAGAGCUAAUUAUUAUCCCUUUGUUGGGUUUAUACC
 ACUUAAGCUUGAAAGAGGUUAAAACAUUACAUAUUAUUGUUAAGUUGAAUACAGCAAAU
 GGUCUUCACACUCGAAGAUUUCGUUGGGGACUGGCGACAGACAGCCGGCUACAACCUG
 GACCAAGUCCUUGAACAGGGAGGUGUGUCCAGUUUGUUUCAGAAUCUCGGGGUGUCC
 GUAACUCCGAUCCAAAGGAUUGUCCUGAGCGGUGAAAAUGGGCUGAAGAUCGACAUC
 AUGUCAUCAUCCCGUAUGAAGGUCUGAGCGGCGACCAAUUGGGCCAGAUCGAAAAAU
 UUUUAAGGUGGUGUACCCUGUGGAUGAUCAUCACUUUAAGGUGAUCCUGCACUAUGGC
 ACACUGGUAAUCGACGGGGUACGCCGAACAUAGUACGACUAAUUCGGACGGCCGUAUG
 AAGGCAUCGCCGUGUUCGACGGCAAAAAGAUACUGUAACAGGGACCCUGUGGAACGG
 CAACAAAAUUAUCGACGAGCGCCUGAUCAACCCCGACGGCUCUCCUGCUGUCCGAGUA
 ACCAUCAACGGAGUGACCGGCUGGCGGCUGUGCGAACGCAUUCUGGCGUGAAAAAAC
 AAAAAACAAAACCGCCCCCGGCCCGCGUCCUCCU|AA|ACACC CGGAAGCCAACU
 GAUUGACC AAAAAAAAAA GCGGCCGCGAU (SEQ ID NO: 61)

circ.GOI-long:

eACA (UTR)-msiTS-IRES-start codon-CDS-stop codon-PolyAC-eACA (UTR)

IRES= CVB3, CDS= EGFP, Spike-EGFP, Cas9-EGFP, Nluc

FIG. 13B

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TIRC V2-EGFP: eACA placed in CDS

T7-HE[EGS] [Ribozyme] [Loop_L] [IGS] circGOI [eACA] [P1ex] [Loop_R] cEGS PolyA Not I-EcoR V

GGGAUAAUAC [GGUCAUACAGUUGGCUUCCG] [AAUAAUUGAGCCUAGAGAAGAAAUU]
CUUUAAGUGGAUGCUCUCAACUCAGGGAAACCJAAAUCUAGCUAUAGACAAGGCAAUC
CUGAGCCAAGCCGAAGUAGUAAUAGUAAGUUAACAACAGUAACUACAGCUAAUCGG
AAGGUGCAGAGACUCGACGGGAGCUACCCUAACGUAAGACGAGGGUAAAGAGAGAGU
CCA AUUCUCAAAGCCAAUAGGCAGUAGCGAAAGCUGCGGGAGAAUG [AACGGUCACAAG
UUCAGCGUGUCCGGCGAGGGCGAGGGCGAUGCCACCUACGGCAAGCUGACCCUGAAGU
UCAUCUGCACCACCGGCAAGCUGCCGUGCCUGGCCACCCUCGUGACCAACCCUGAC
CUACGGCGUGCAGUGCUUCAGCCGCUACCCGACCAUGAAGCAGCAGCAGCUUCUUC
AAGUCCGCCAUGCCCGAAGGCUACGUCCAGGAGCGCACCAUCUUCUUAAGGACGACG
GCAACUACAAGACCCGCGCCGAGGUGAAGUUCGAGGGCGACACCCUGGUGAACCGCAU
CGAGCUGAAGGGCAUCGACUUAAGGAGGACGGCAACAUCUGGGGCACAAGCUGGAG
UACAACUACAACAGCCACAACGUCUAUAUCAUGGCCGACAAGCAGAAGAACGGCAUCAA
GGUGAACUUAAGAUCGCCACAACUUCGAGGACGGCAGCGUGCAGCUCGCCGACCAC
UACCAGCAGAACACCCCAUCGGCGACGGCCCCGUGCUGCUGCCCGACAACCACUACC
UGAGCACCCAGUCCGCCUGAGCAAAGACCCCAACGAGAAGCGCGAUCACAUGGUCCU
GCUGGAGUUCGUGACCGCCGCCGGGAUCACUCUCGGCAUGGACGAGCUGUACAAGUG
AAAAAACAAAAACAAAAAAACAAACAAUUGGGCCAGAU CGAAAAAACGAACAUGAUCG
ACUAAUUCACACAUUAAAACAGCCUGUGGGUUGAUCCACCCACAGGCCCAUUGGGCG
CUAGCACUCUGGUUAUCACGGUACCUUUGUGCGCCUGUUUUAUACCCCUCCCCAACU
GUAACUUAAGAAGUAACACACACCGAUCAACAGUCAGCGUGGCACACCAGCCACGUUUUG
AUCAAGCACUUCUGUUAACCCGGACUGAGUAUCAUAGACUGCUCACGCGGUUGAAGG
AGAAAGCGUUCGUUAUCCGGCCAACUACUUCGAAAAACCUAGUAACACCGUGGAAGUUG
CAGAGUGUUUCGCUAGCACUACCCAGUGUAGAUACAGGUCGAUGAGUCACCGCAUUC
CCCACGGGCGACCGUGGCGGUGGCUUGCGUUGGCGGCCUGCCCAUGGGGAAACCCAUG
GGACGCUCUAAUACAGACAUGGUGCGAAGAGUCUAUUGAGCUAGUUGGUAGUCCUCCG
GCCCCUGAAUGCGGCUAUCCUAACUGCGGAGCACACCCUCAAGCCAGAGGGCAGU
GUGUCGUAACGGGCAACUCUGCAGCGGAACCGACUACUUUGGGUGUCCGUGUUUCAU
UUAUCCUAUACUGGCUUUAUGGUGACAAUUGAGAGAU CGUUAACUAUAGCUAUUG
GAUUGGCCAUCCGGUGACUAAUAGAGCUAAUUAUUAUCCCUUUGUUGGGUUUAUACCA
CUUAGCUUGAAAGAGGUUAAAACAUUACA AUUUAUAGUUAAGUUGAAUACAGCAAAUUG
GUGAGCAAGGGCGAGGAGCUGUUCACCGGGUGGUGCCCAUCCUGGUCGAGCUGGAC
[GGUGACGUU] [AA] ACACC CGGAAGCCAACUGAUUGACC AAAAAAAAAA GCGGCCG
GAU

(SEQ ID NO: 62)

circ.GOI-long:

eACA (CDS)-stop codon-PolyAC-msiTS-IRES-start codon-eACA (CDS)

IRES= CVB3, CSFV, CroV, CDS= EGFP, Nluc, circZNF609, T2A-EGFP

FIG. 13B (continued)

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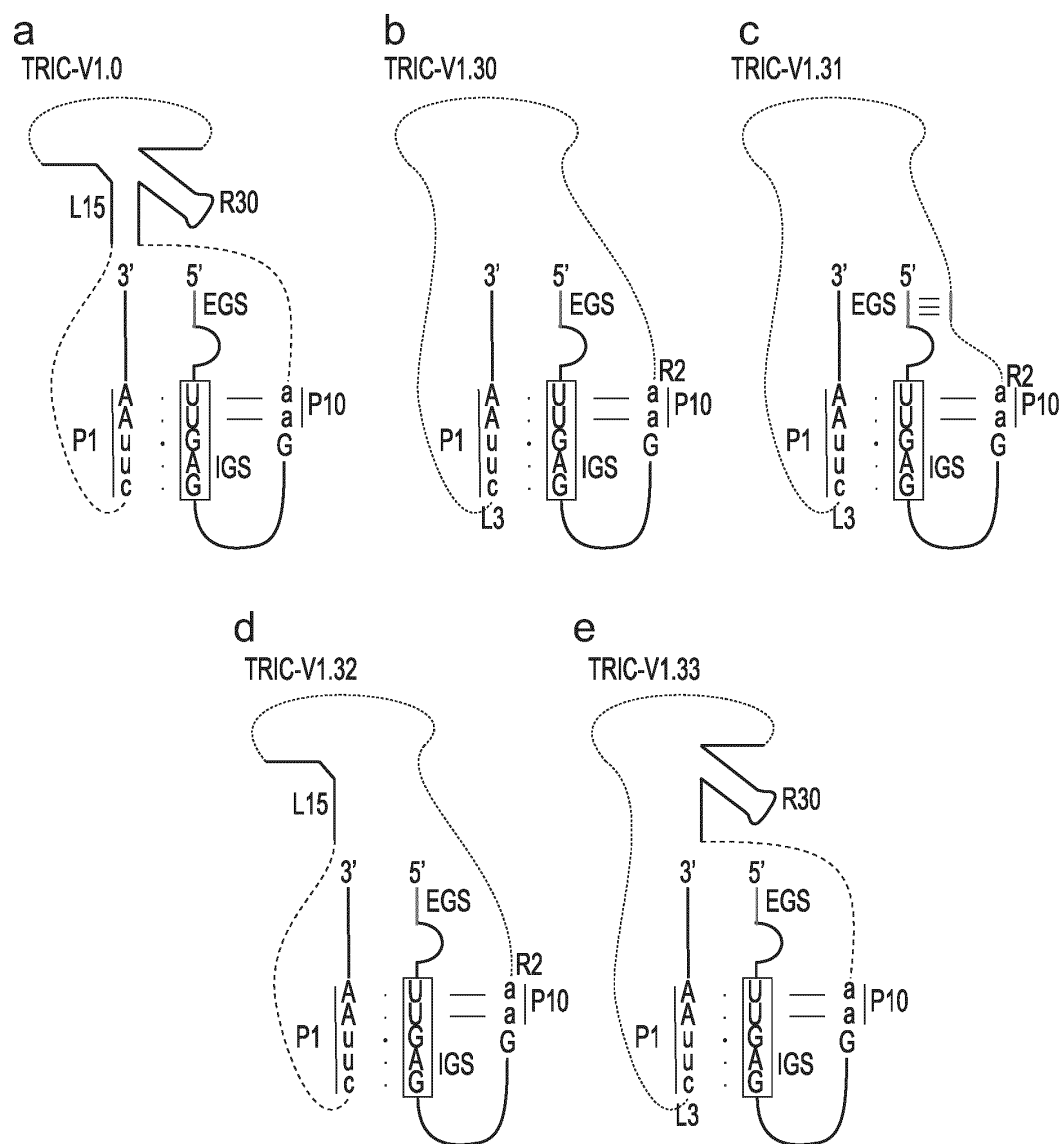


FIG. 14

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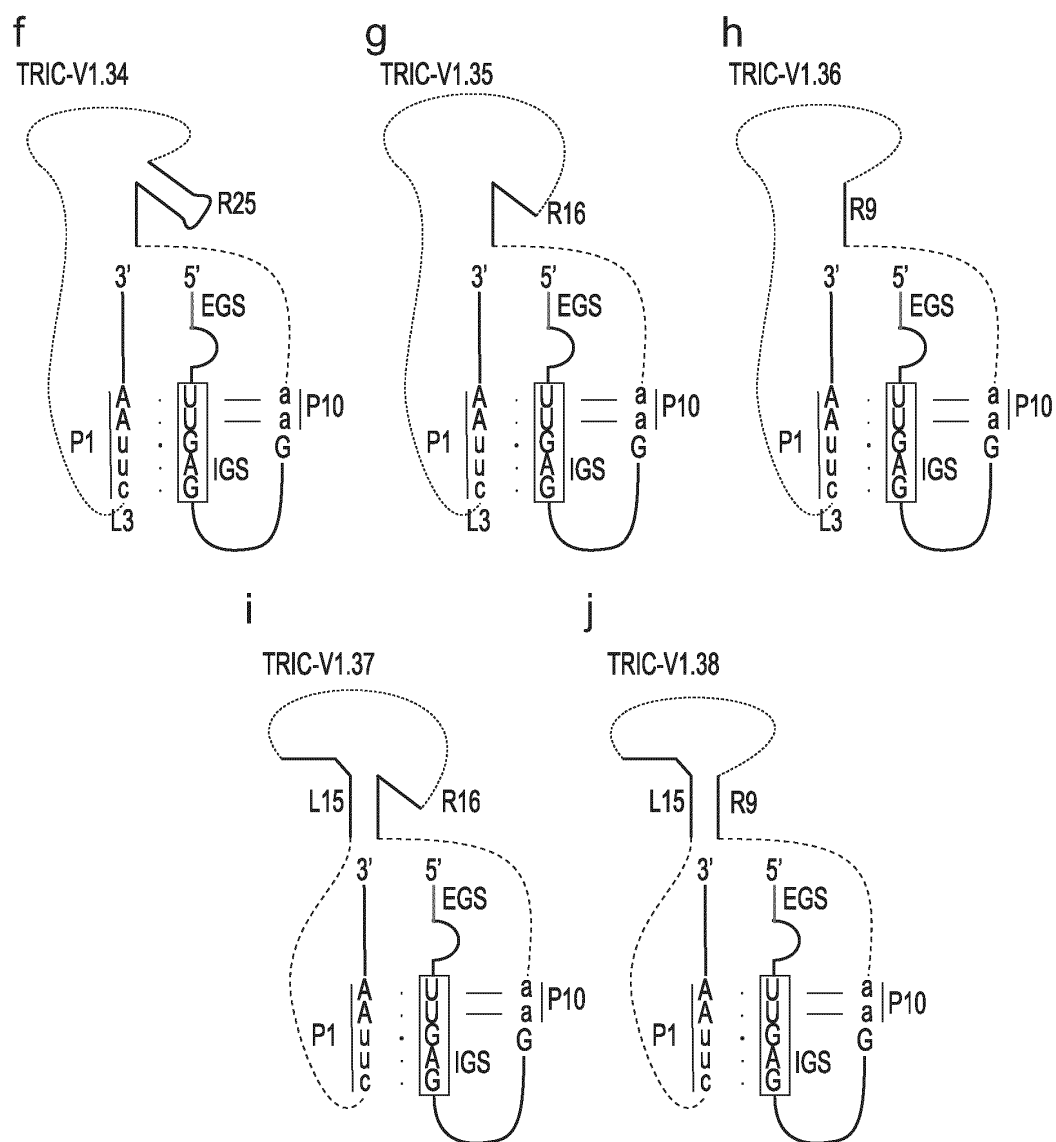


FIG. 14B (continued)

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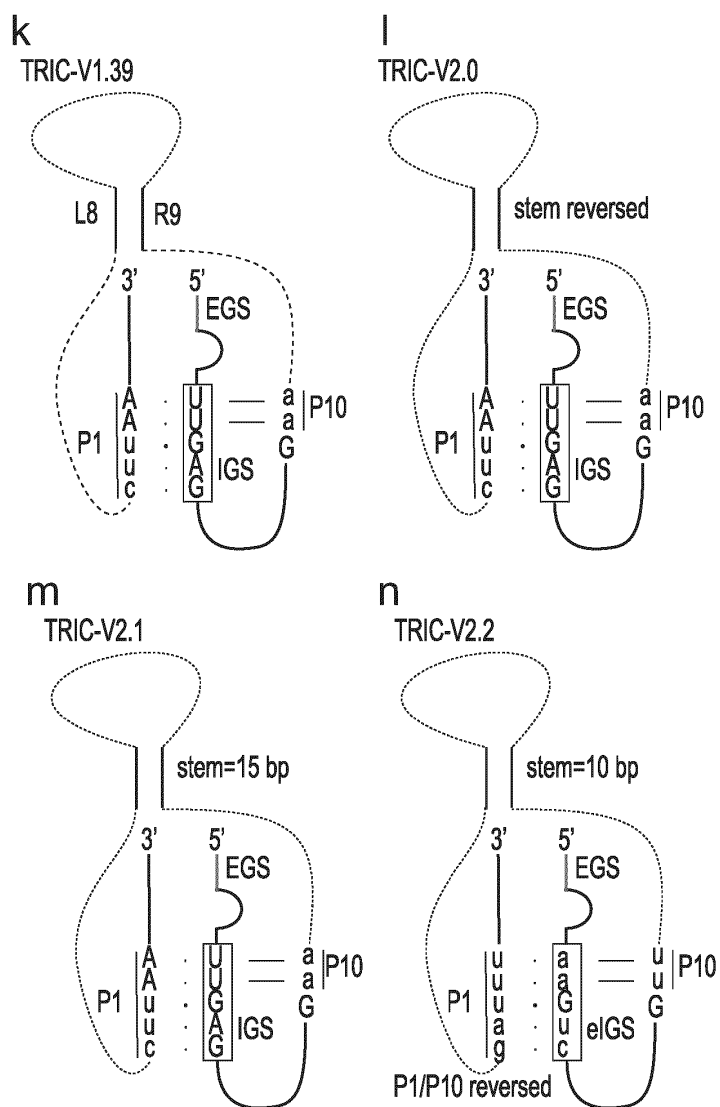


FIG. 14B (continued)

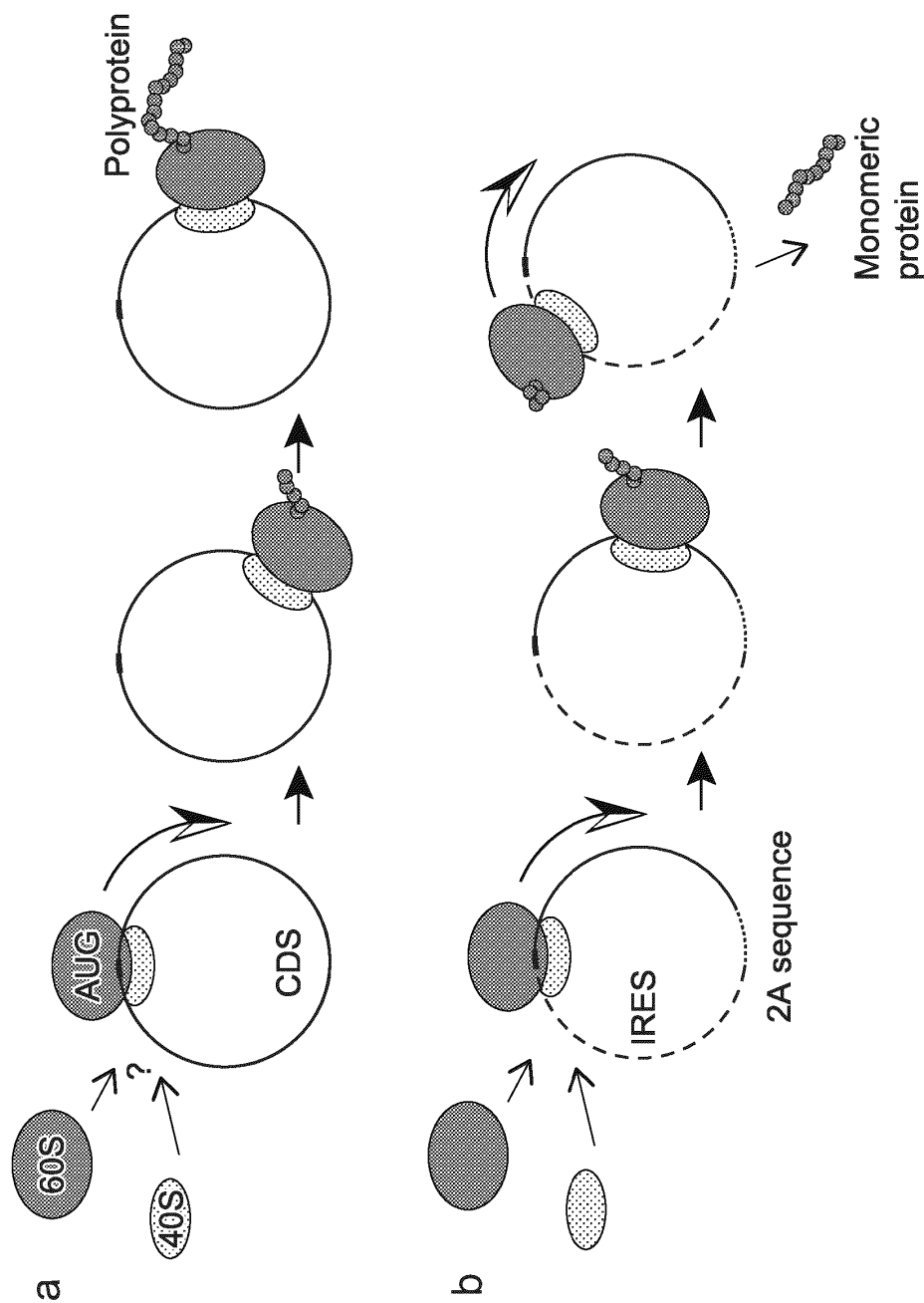
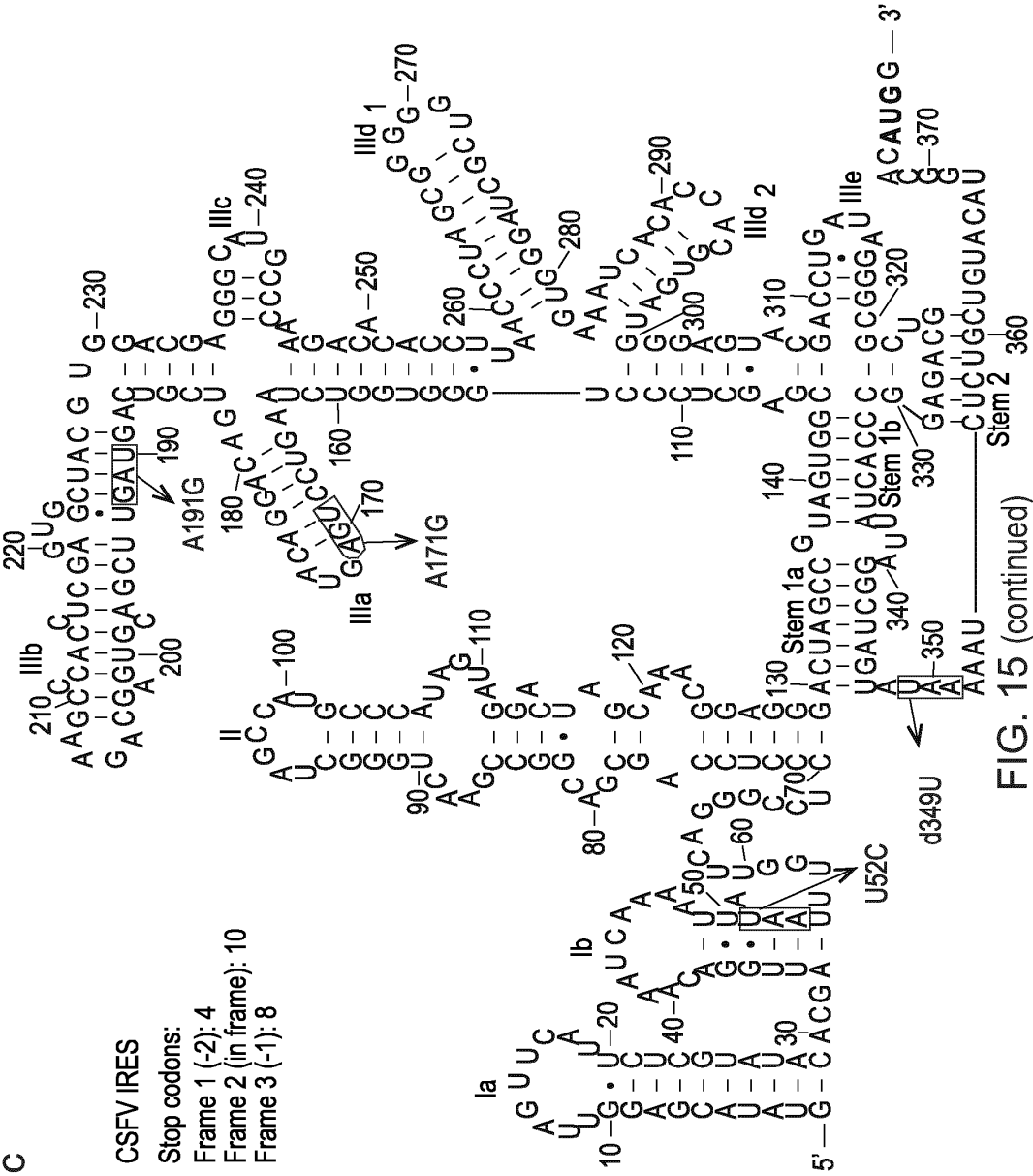


FIG. 15



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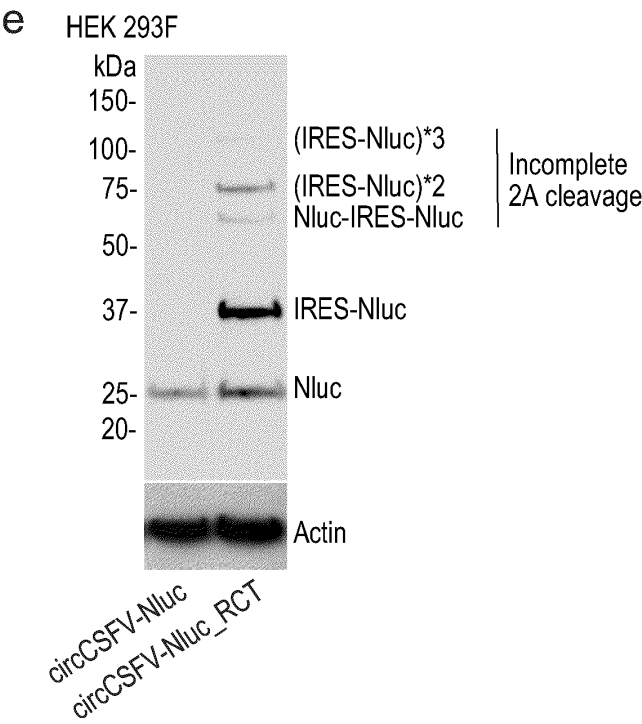
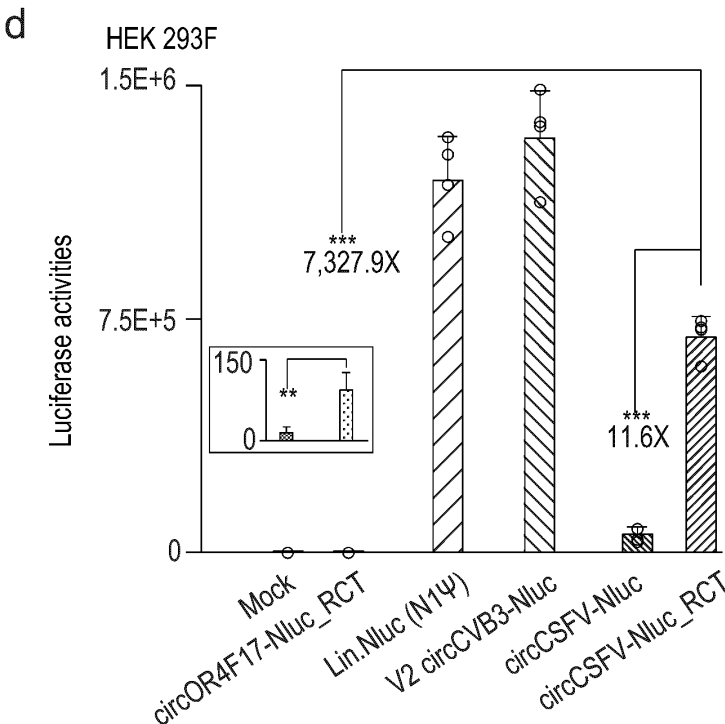


FIG. 15 (continued)

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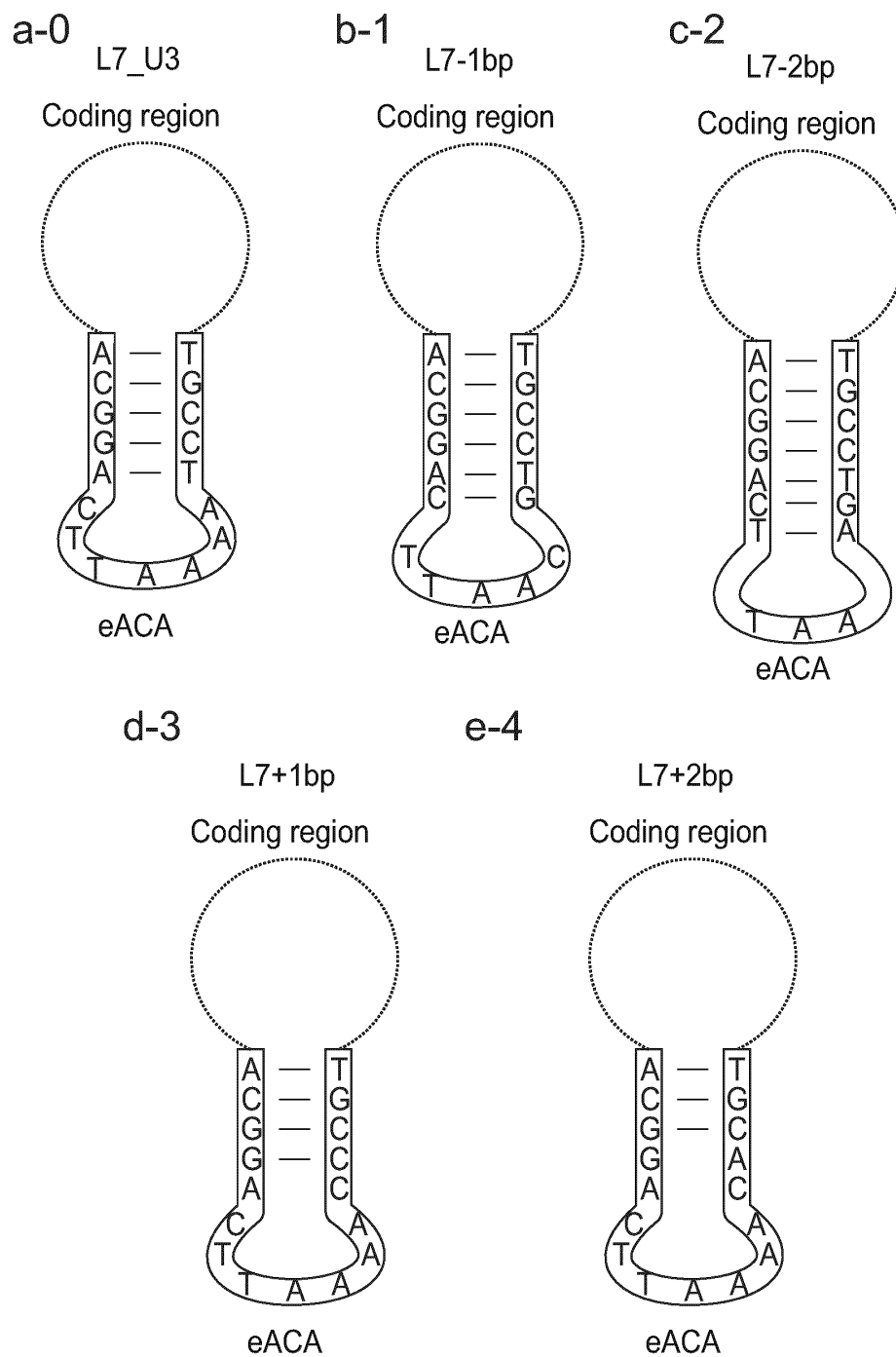
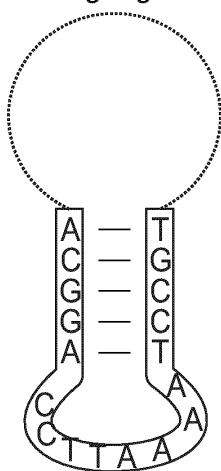


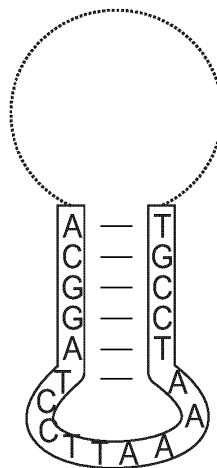
FIG. 16A

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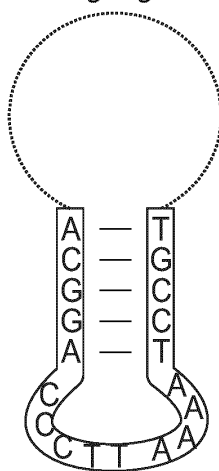
f-5

L7_p1+1nt
Coding region

g-6

L7_p1+1nt_p1ex-1nt
Coding region

h-7

L7_p1+2nt
Coding region

i-8

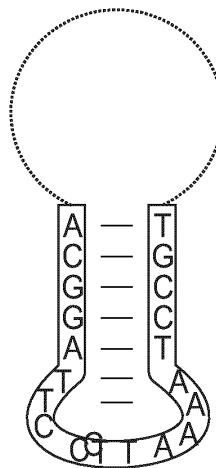
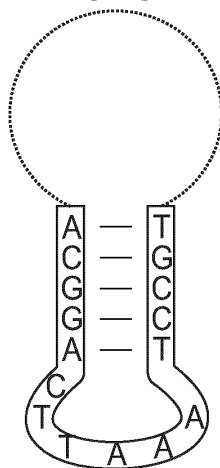
L7_p1+2nt_p1ex-2nt
Coding region

FIG. 16A (continued)

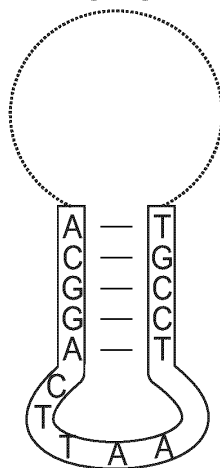
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j-9

L7_p1ex-1nt
Coding region

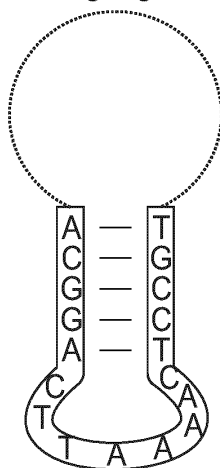
eACA

k-10

L7_p1ex-2nt
Coding region

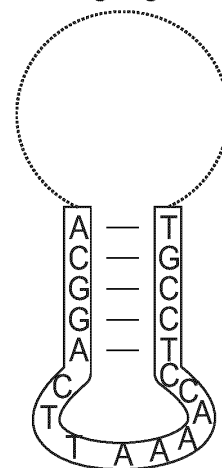
eACA

l-11

L7_p1ex+1nt
Coding region

eACA

m-12

L7_p1ex+2nt
Coding region

eACA

FIG. 16A (continued)

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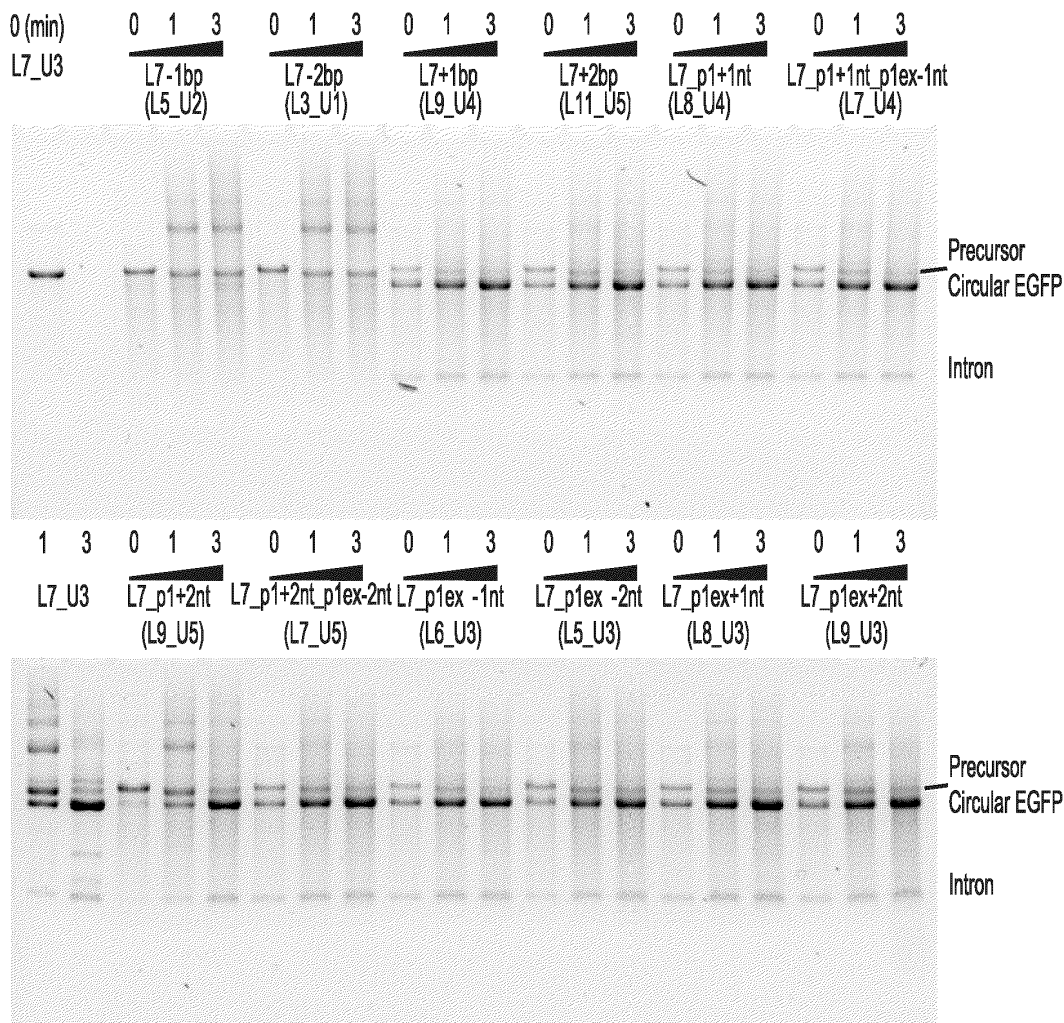


FIG. 16B

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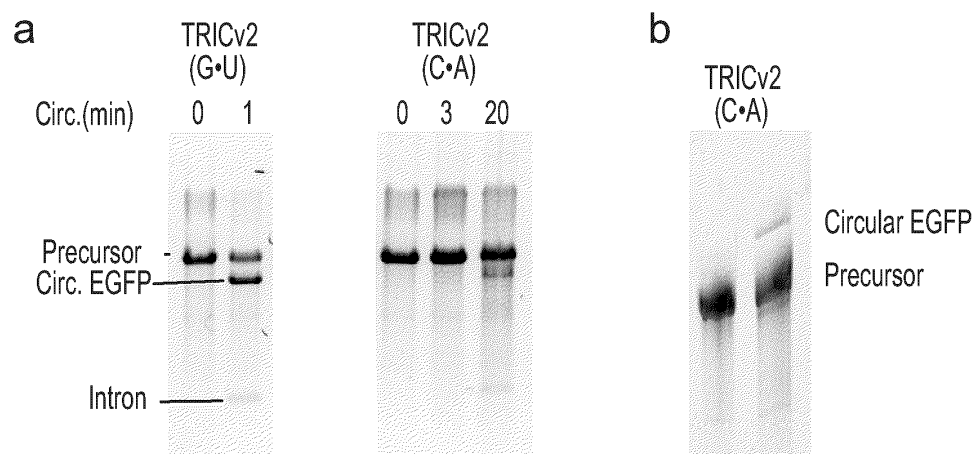
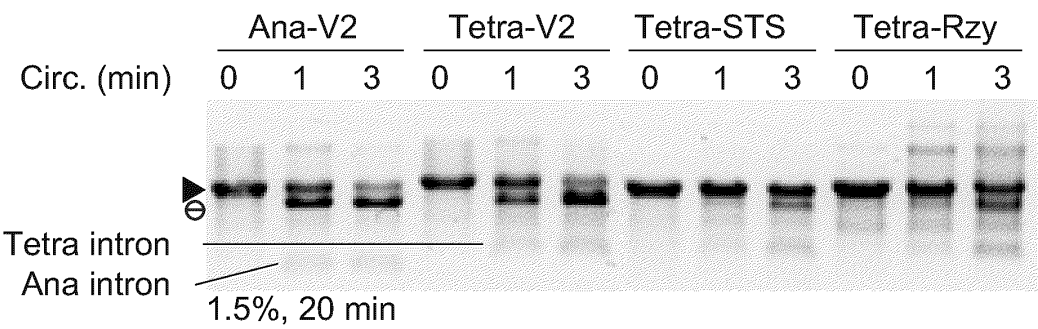


FIG. 17

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a



b

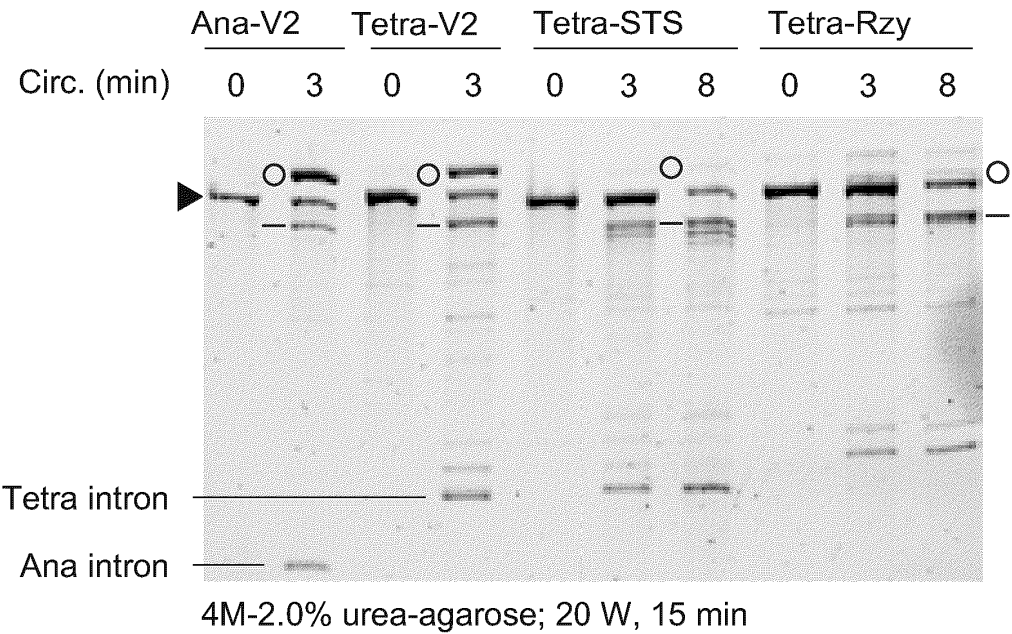


FIG. 18