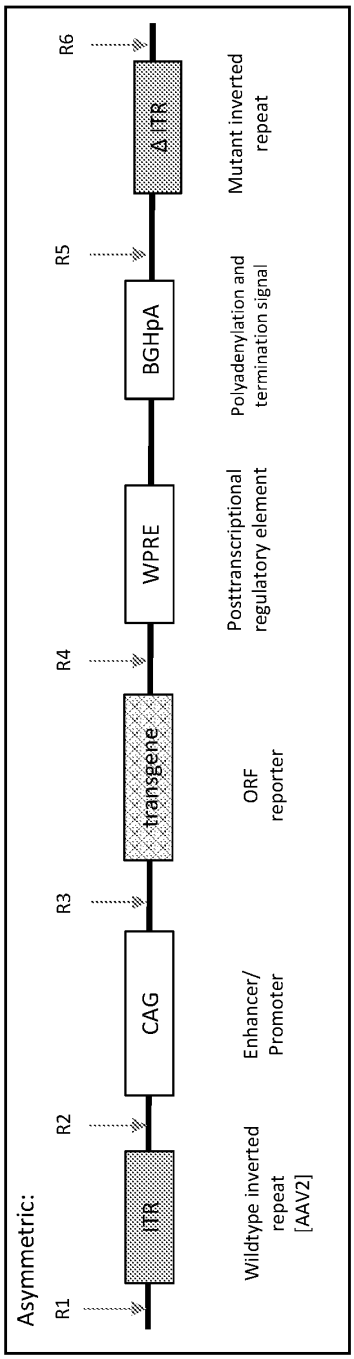


FIG. 1A

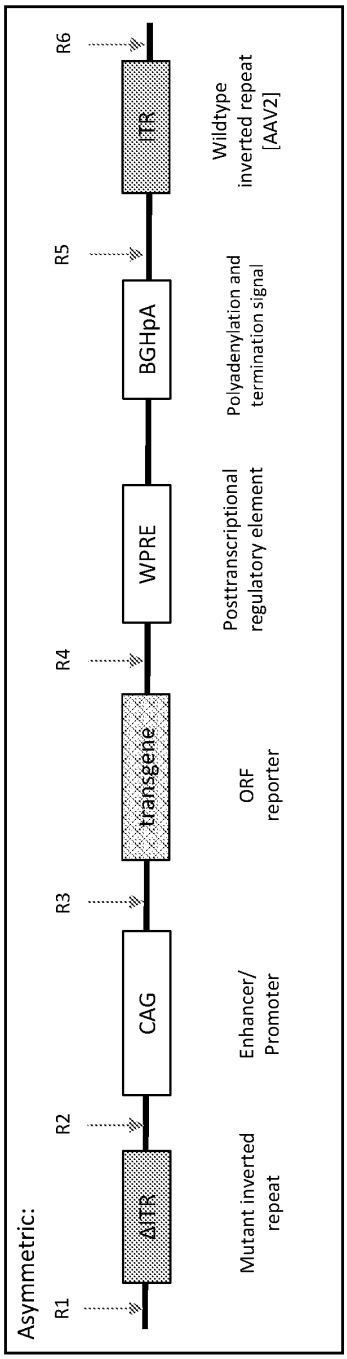


FIG. 1B

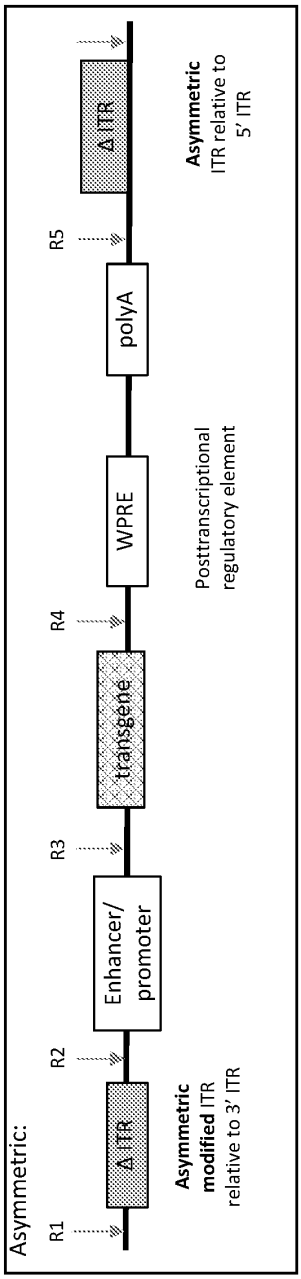


FIG. 1C

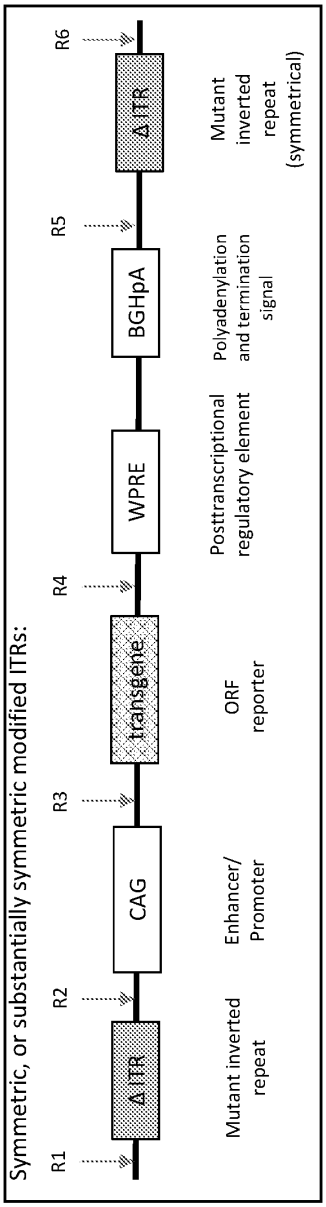

Symmetric, or substantially symmetric modified ITRs:
R1
R2
R3
R4
R5
R6
Δ ITR
CAG
transgene
WPRE
BGHpA
Δ ITR
Mutant inverted repeat
Enhancer/ Promoter
ORF reporter
Posttranscriptional regulatory element
Polyadenylation and termination signal
Mutant inverted repeat (symmetrical)

FIG. 1D

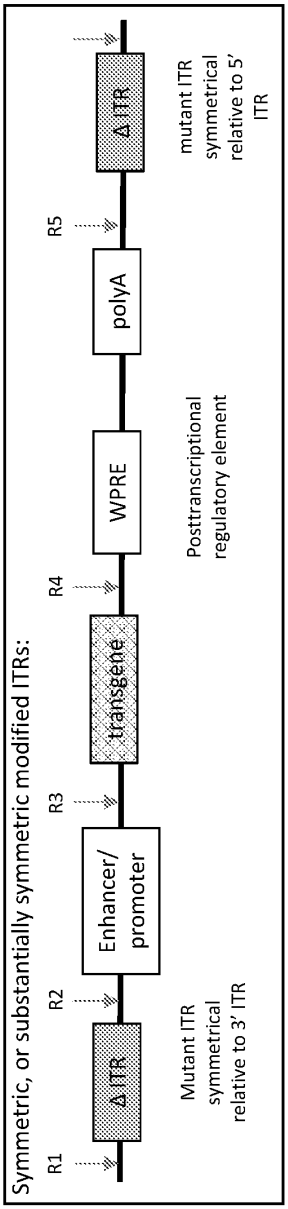

Symmetric, or substantially symmetric modified ITRs:
R1
R2
R3
R4
R5
Δ ITR
Enhancer/ promoter
transgene
WPRE
polyA
Δ ITR
Mutant ITR symmetrical relative to 3' ITR
Posttranscriptional regulatory element
mutant ITR symmetrical relative to 5' ITR

FIG. 1E

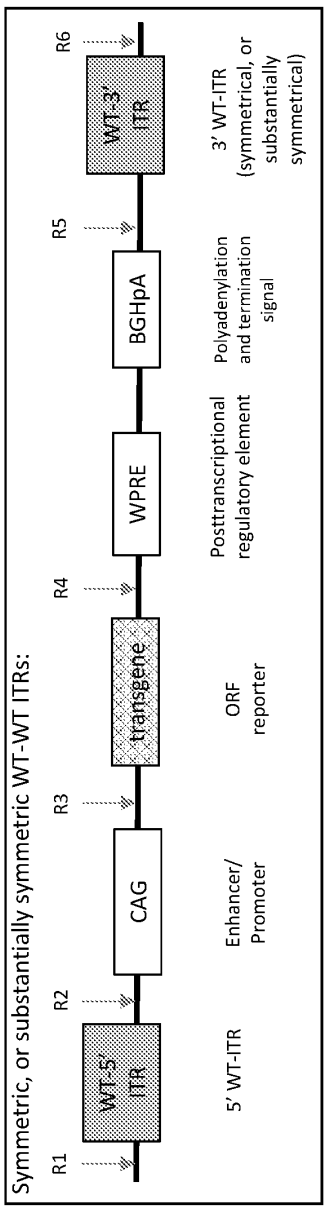

Symmetric, or substantially symmetric WT-WT ITRs:
R1
WT-5' ITR
5' WT-ITR
R2
CAG
Enhancer/ Promoter
R3
transgene
ORF reporter
R4
WPRE
Posttranscriptional regulatory element
R5
BGHpA
Polyadenylation and termination signal
R6
WT-3' ITR
3' WT-ITR (symmetrical, or substantially symmetrical)

FIG. 1F

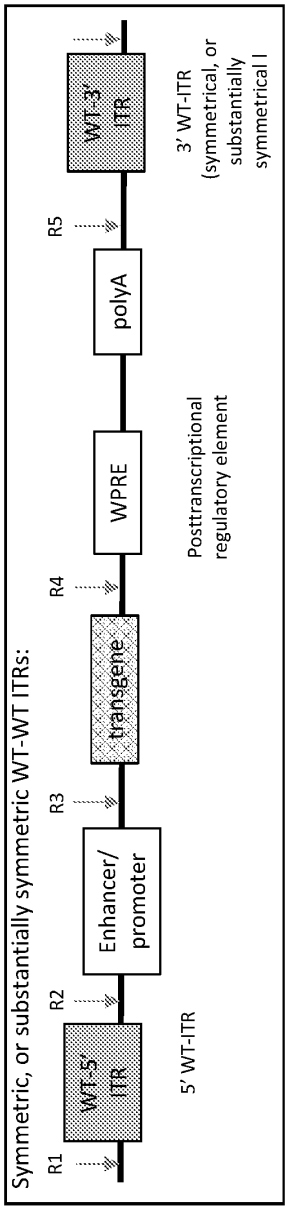

Symmetric, or substantially symmetric WT-WT ITRs:
R1
WT-5' ITR
5' WT-ITR
R2
Enhancer/ promoter
R3
transgene
R4
WPRE
Posttranscriptional regulatory element
R5
polyA
WT-3' ITR
3' WT-ITR (symmetrical, or substantially symmetrical I

FIG. 1G

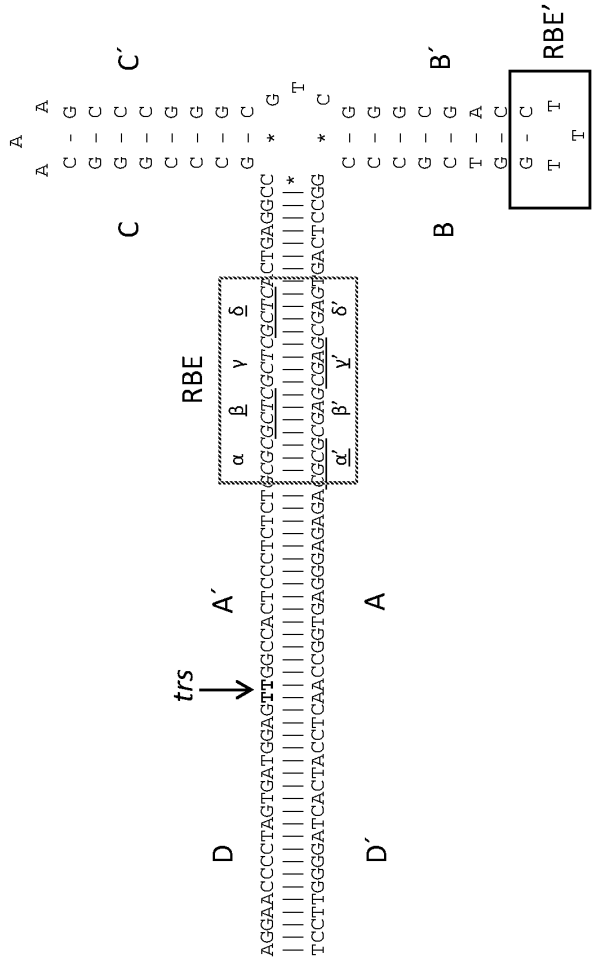


FIG. 2A

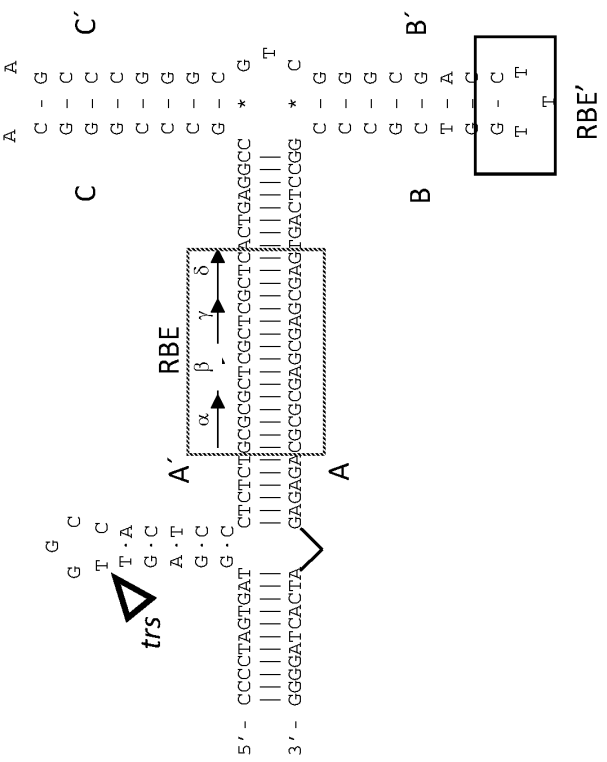

trs
RBE
A′
A
C
C′
B
B′
RBE′
α
β
γ
δ
5′ - CCCCTAGTGAT CTCTCTGCGCGCTCGCTCGCTCACTGAGGCC
3′ - GGGGATCACTA GAGAGACGCGCGAGCGAGCGAGTGACTCCGG

FIG. 2B

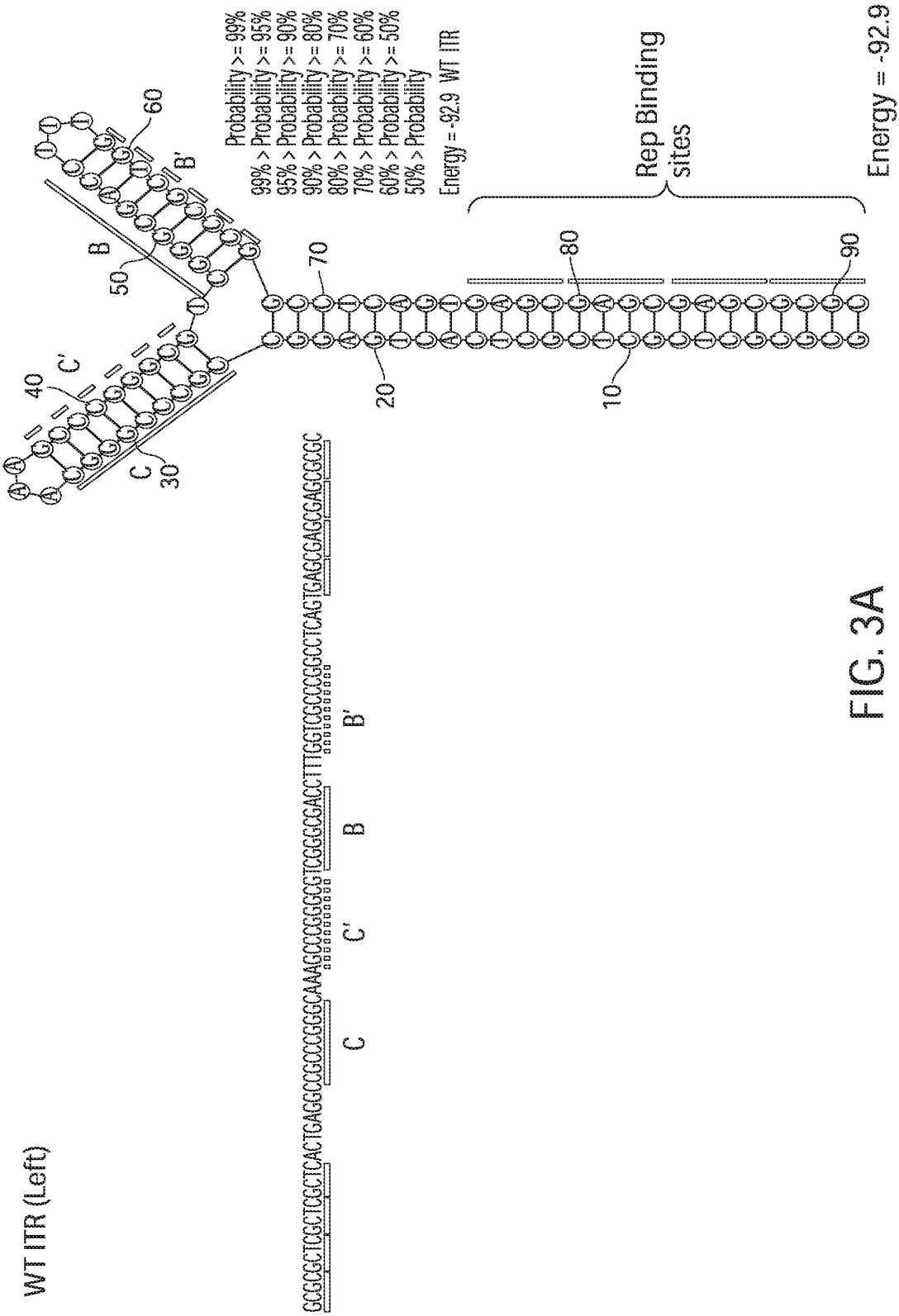

WT ITR (Left)
GCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGGCGTCGGGCGACCTTTGGTCGCCCGGCCTCAGTGAGCGAGCGAGCGCGC
C
C'
B
B'
Probability >= 99%
99% > Probability >= 95%
95% > Probability >= 90%
90% > Probability >= 80%
80% > Probability >= 70%
70% > Probability >= 60%
60% > Probability >= 50%
50% > Probability
Energy = -92.9 WT ITR
Rep Binding sites
Energy = -92.9
10
20
30
40
50
60
70
80
90

FIG. 3A

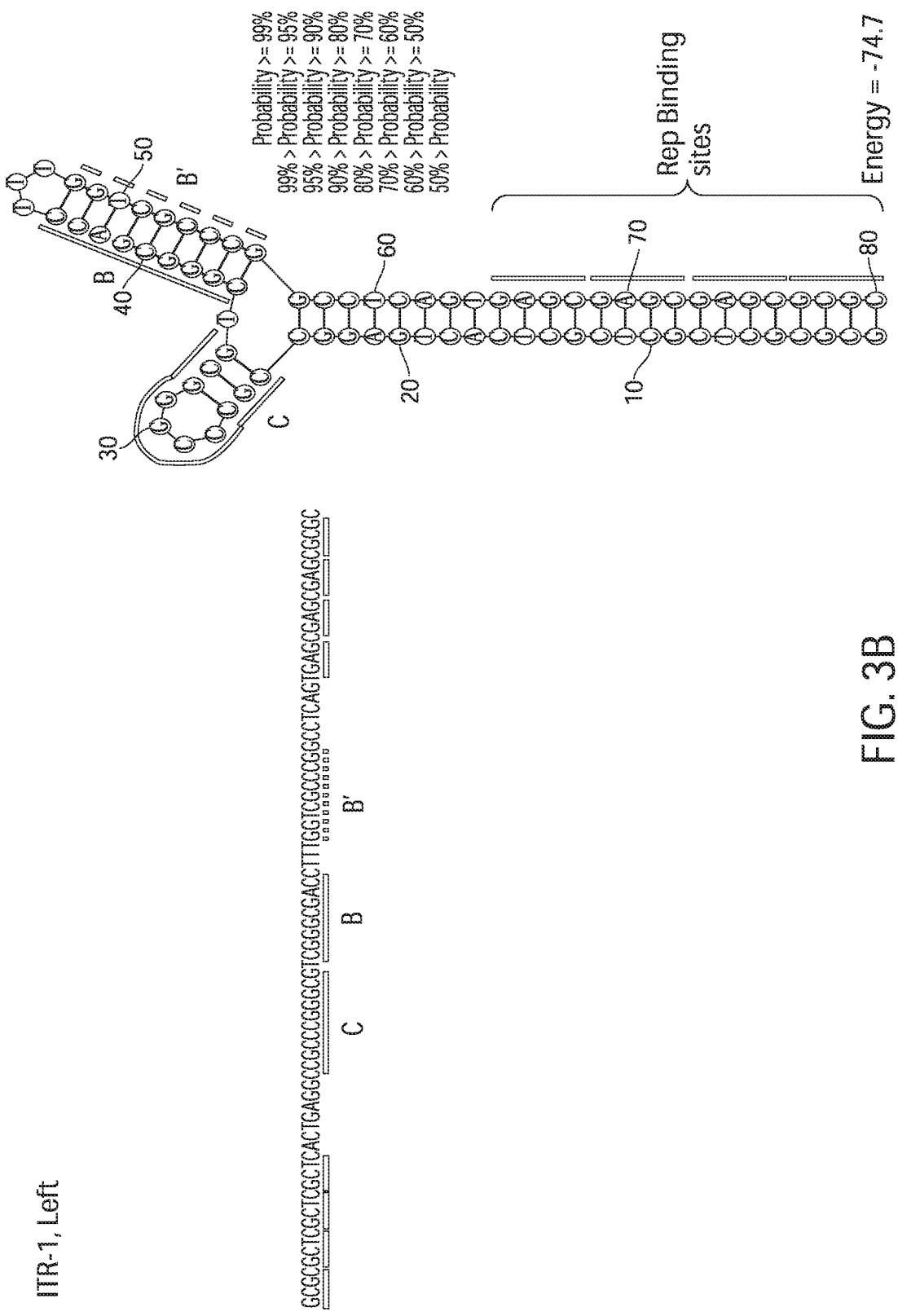

ITR-1, Left
GCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGGCGTCGGGCGACCTTTGGTCGCCCGGCCTCAGTGAGCGAGCGAGCGCGC
C
B
B'
Probability >= 99%
99% > Probability >= 95%
95% > Probability >= 90%
90% > Probability >= 80%
80% > Probability >= 70%
70% > Probability >= 60%
60% > Probability >= 50%
50% > Probability
Rep Binding sites
Energy = -74.7
10
20
30
40
50
60
70
80

FIG. 3B

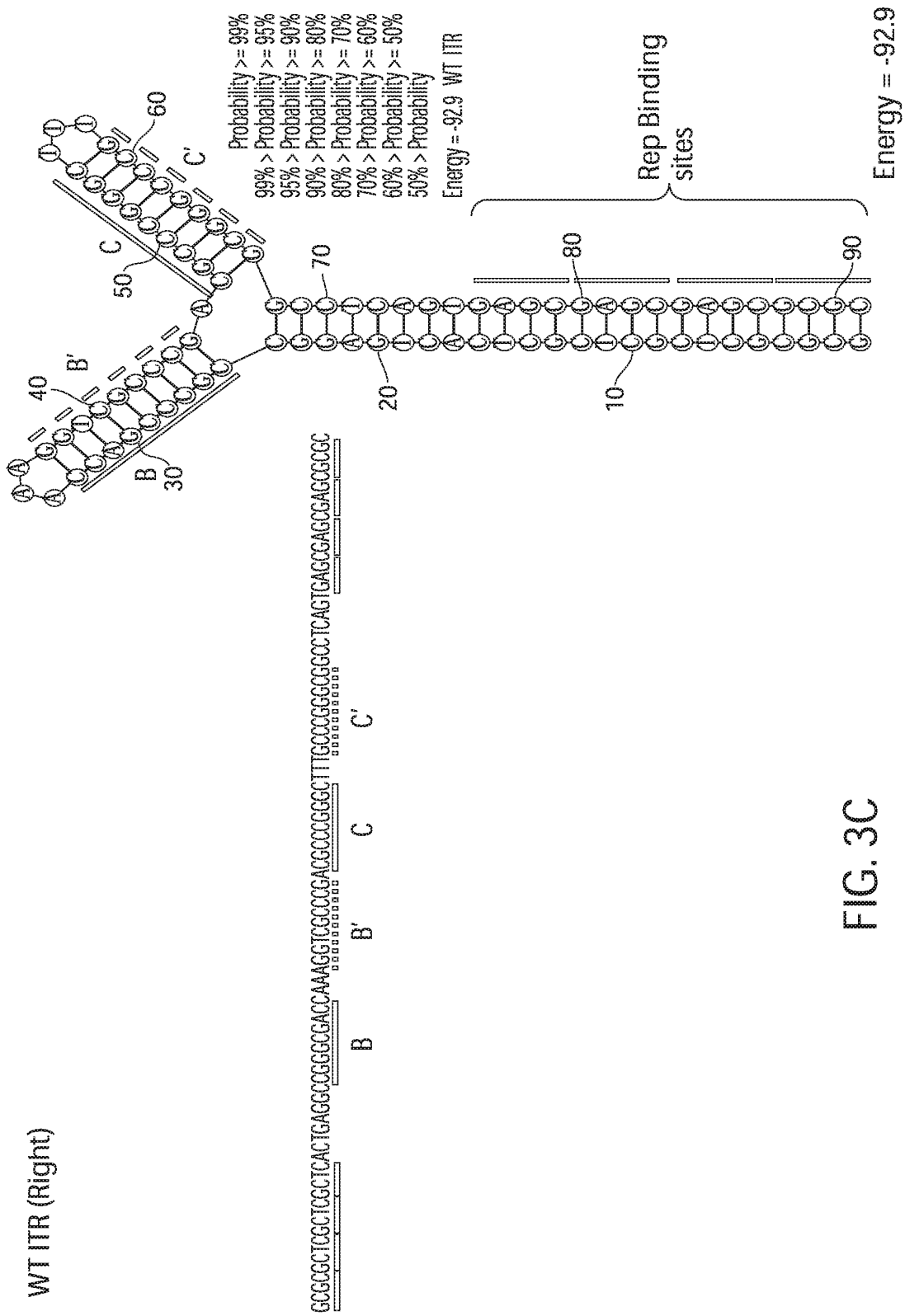

WT ITR (Right)
GCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGC
B
B'
C
C'
Probability >= 99%
99% > Probability >= 95%
95% > Probability >= 90%
90% > Probability >= 80%
80% > Probability >= 70%
70% > Probability >= 60%
60% > Probability >= 50%
50% > Probability
Energy = -92.9 WT ITR
Rep Binding sites
Energy = -92.9
10
20
30
40
50
60
70
80
90

FIG. 3C

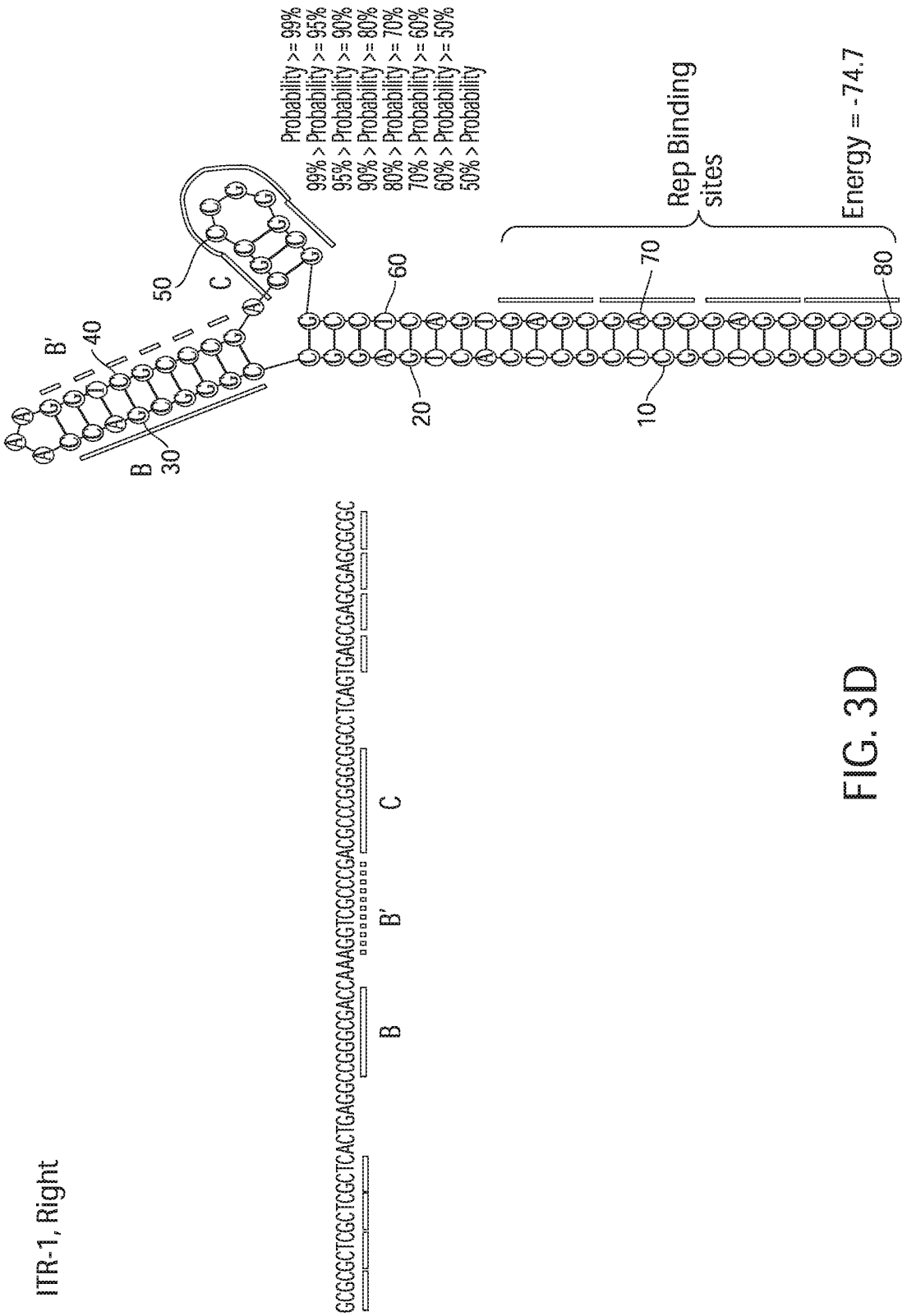

ITR-1, Right
GCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGC
B
B'
C
Probability >= 99%
99% > Probability >= 95%
95% > Probability >= 90%
90% > Probability >= 80%
80% > Probability >= 70%
70% > Probability >= 60%
60% > Probability >= 50%
50% > Probability
Rep Binding sites
Energy = -74.7
10
20
30
40
50
60
70
80
B
B'
C

FIG. 3D

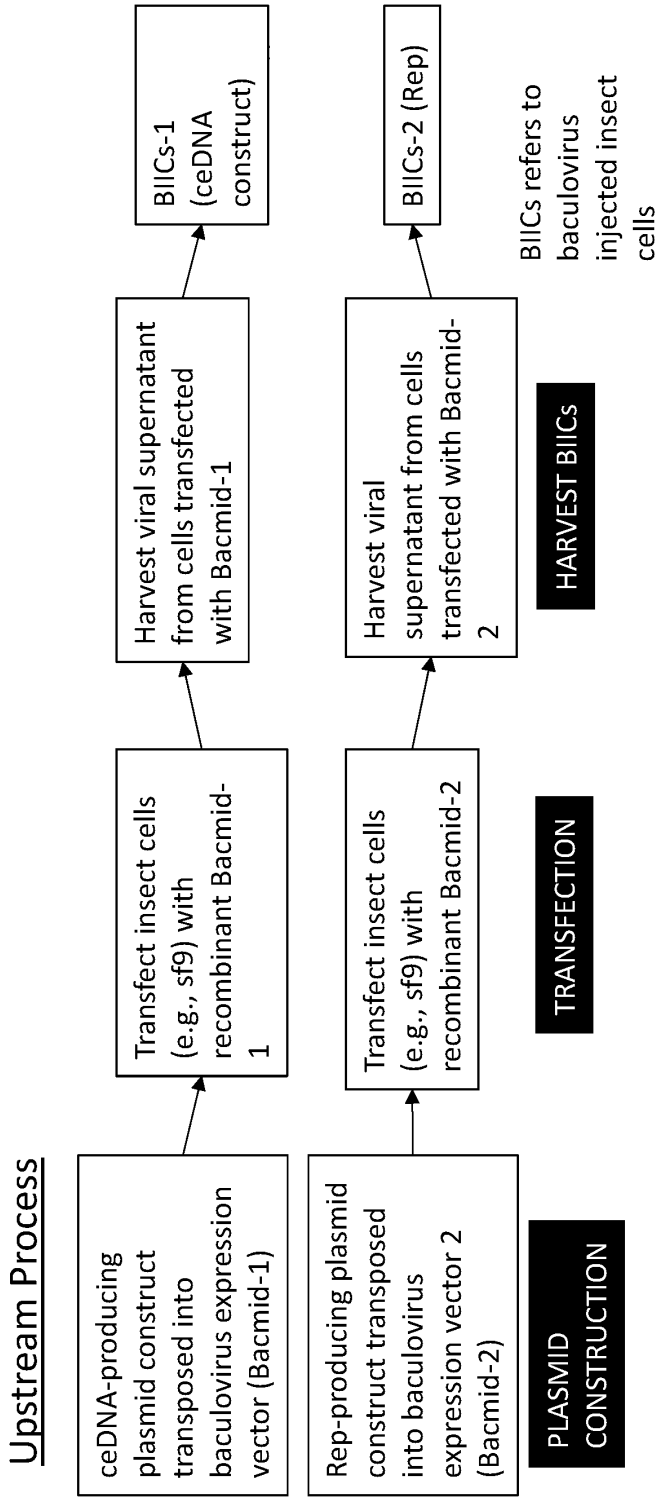

ceDNA Production
Upstream Process
ceDNA-producing plasmid construct transposed into baculovirus expression vector (Bacmid-1)
Rep-producing plasmid construct transposed into baculovirus expression vector 2 (Bacmid-2)
PLASMID CONSTRUCTION
Transfect insect cells (e.g., sf9) with recombinant Bacmid-1
Transfect insect cells (e.g., sf9) with recombinant Bacmid-2
TRANSFECTION
Harvest viral supernatant from cells transfected with Bacmid-1
Harvest viral supernatant from cells transfected with Bacmid-2
HARVEST BIICs
BIICs-1 (ceDNA construct)
BIICs-2 (Rep)
BIICs refers to baculovirus injected insect cells

FIG. 4A

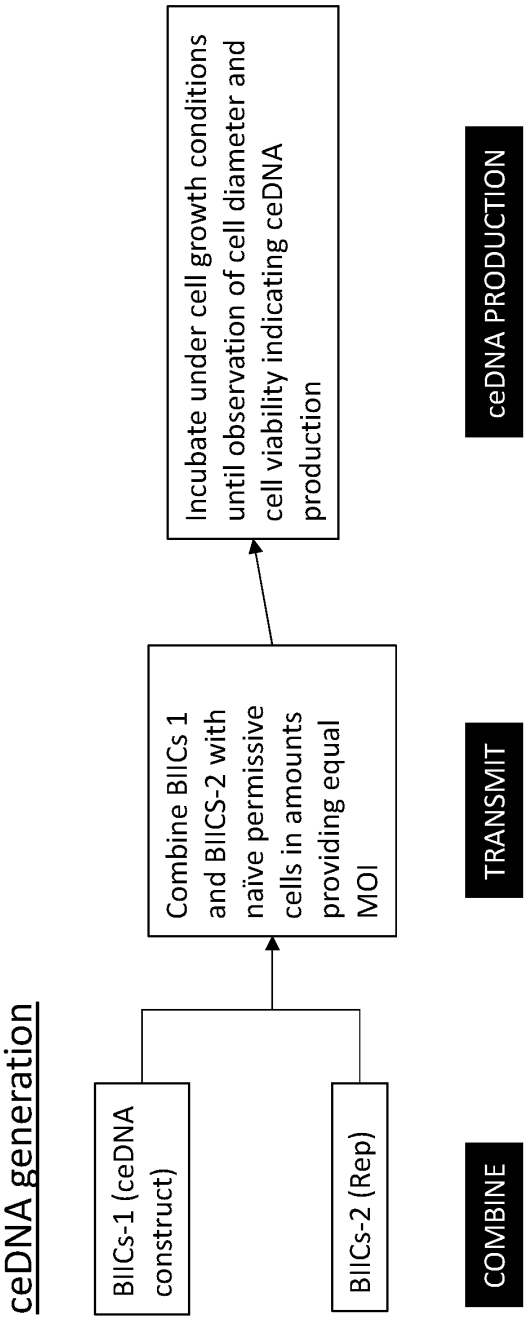

ceDNA Production
ceDNA generation
BIICs-1 (ceDNA construct)
BIICs-2 (Rep)
COMBINE
Combine BIICs 1 and BIICS-2 with naïve permissive cells in amounts providing equal MOI
TRANSMIT
Incubate under cell growth conditions until observation of cell diameter and cell viability indicating ceDNA production
ceDNA PRODUCTION

FIG. 4B

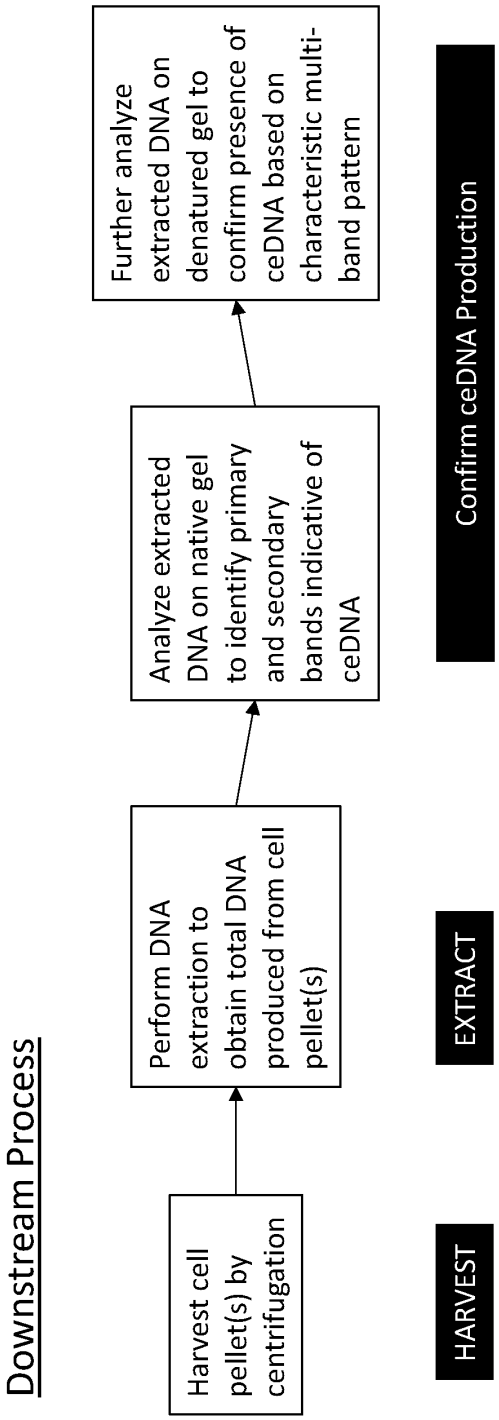

ceDNA Production
Downstream Process
Harvest cell pellet(s) by centrifugation
Perform DNA extraction to obtain total DNA produced from cell pellet(s)
Analyze extracted DNA on native gel to identify primary and secondary bands indicative of ceDNA
Further analyze extracted DNA on denatured gel to confirm presence of ceDNA based on characteristic multi-band pattern
HARVEST
EXTRACT
Confirm ceDNA Production

FIG. 4C

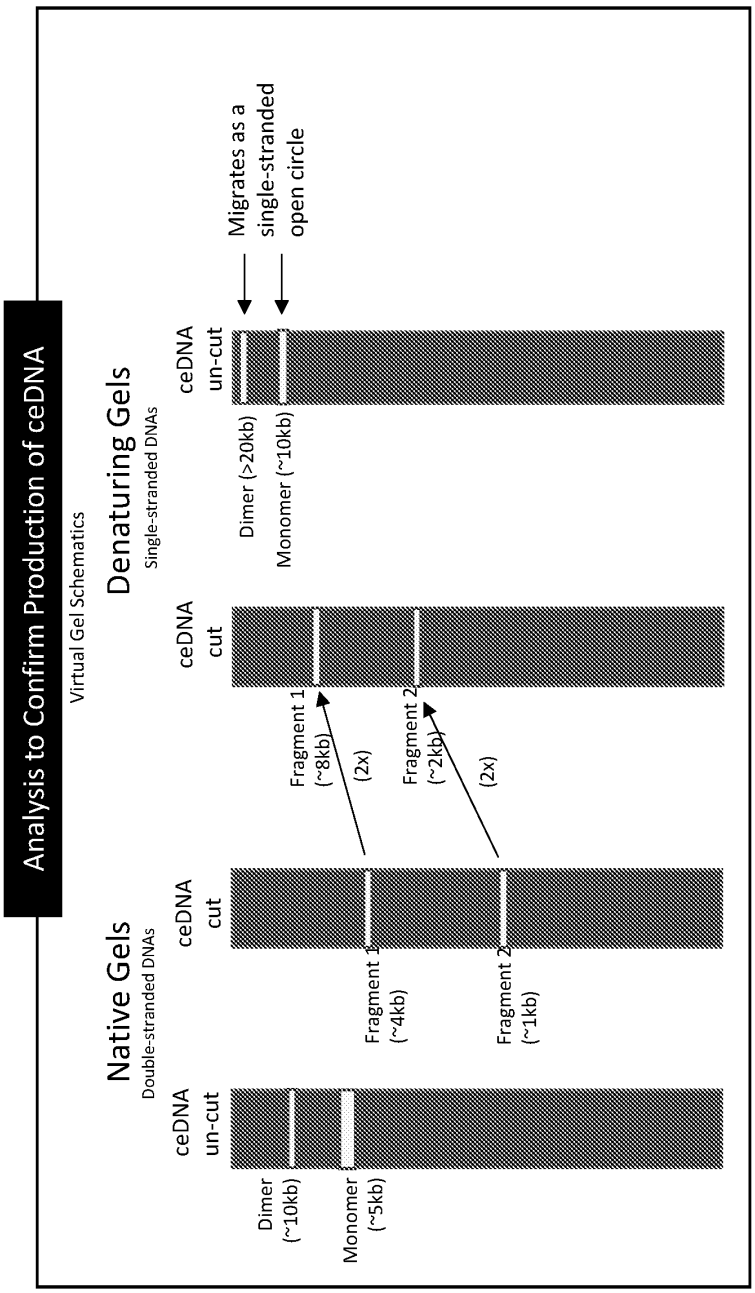
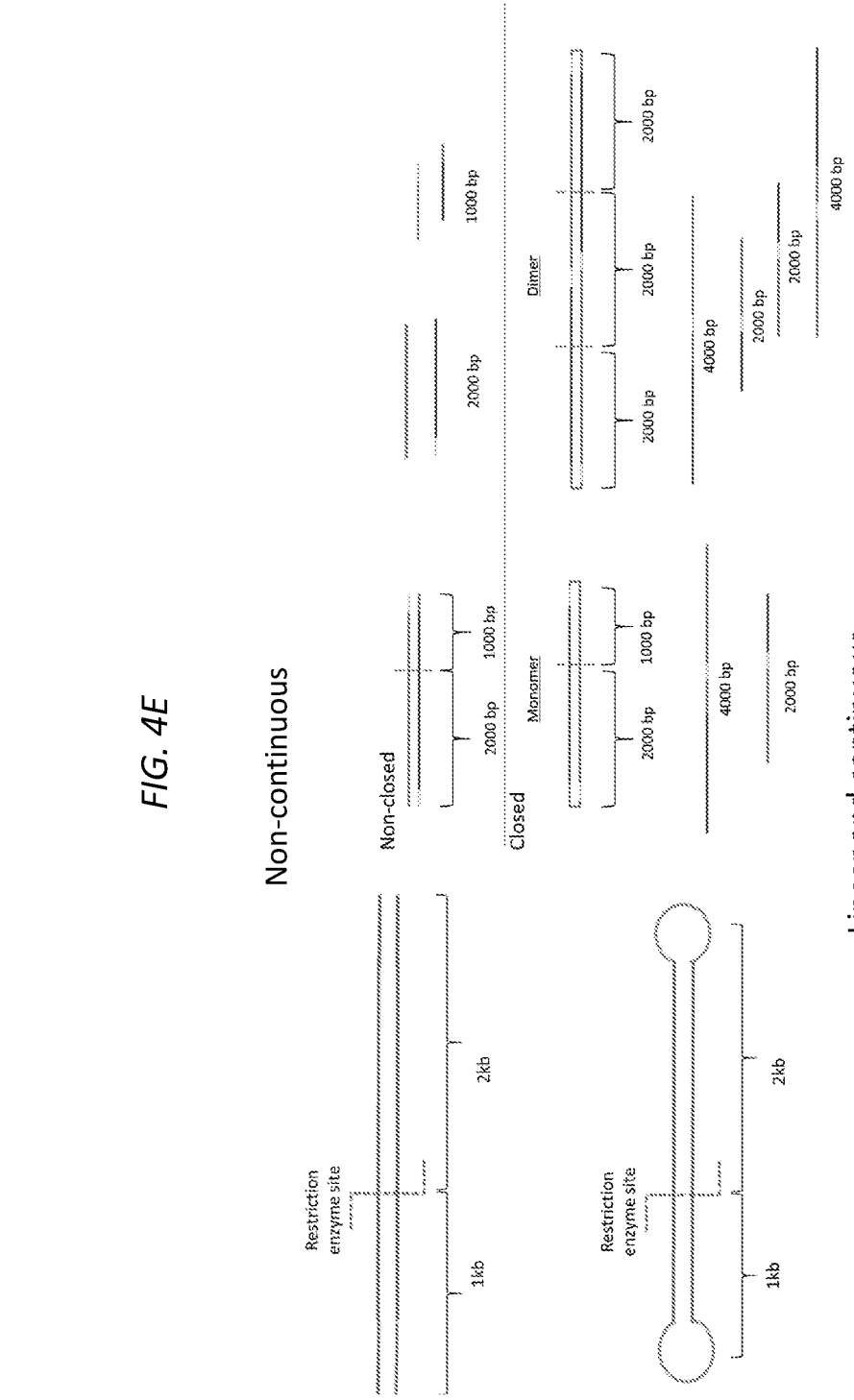

Analysis to Confirm Production of ceDNA
Virtual Gel Schematics
Native Gels
Double-stranded DNAs
ceDNA un-cut
Dimer (~10kb)
Monomer (~5kb)
ceDNA cut
Fragment 1 (~4kb)
Fragment 2 (~1kb)
Denaturing Gels
Single-stranded DNAs
ceDNA cut
Fragment 1 (~8kb)
(2x)
Fragment 2 (~2kb)
(2x)
ceDNA un-cut
Dimer (>20kb)
Monomer (~10kb)
Migrates as a single-stranded open circle

FIG. 4D

FIG. 4E


Non-continuous
Non-closed
Restriction enzyme site
1kb
2kb
2000 bp
1000 bp
Closed
Monomer
Dimer
2000 bp
1000 bp
2000 bp
2000 bp
2000 bp
4000 bp
Linear and continuous
Restriction enzyme site
1kb
2kb
4000 bp
2000 bp
2000 bp
2000 bp
4000 bp

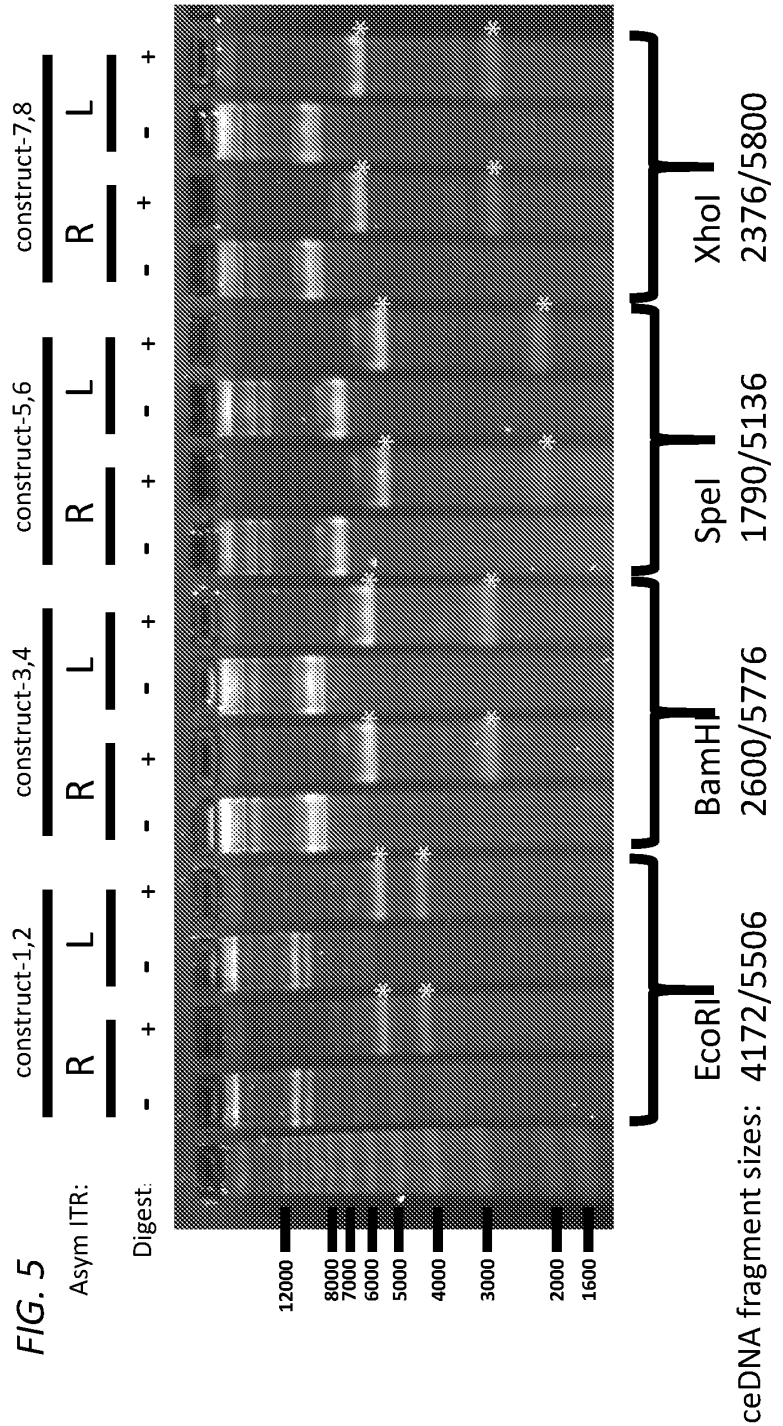

FIG. 5
Asym ITR:
Digest:
construct-1,2
construct-3,4
construct-5,6
construct-7,8
R
L
12000
8000
7000
6000
5000
4000
3000
2000
1600
EcoRI
BamHI
SpeI
XhoI
ceDNA fragment sizes: 4172/5506 2600/5776 1790/5136 2376/5800

FIG. 6

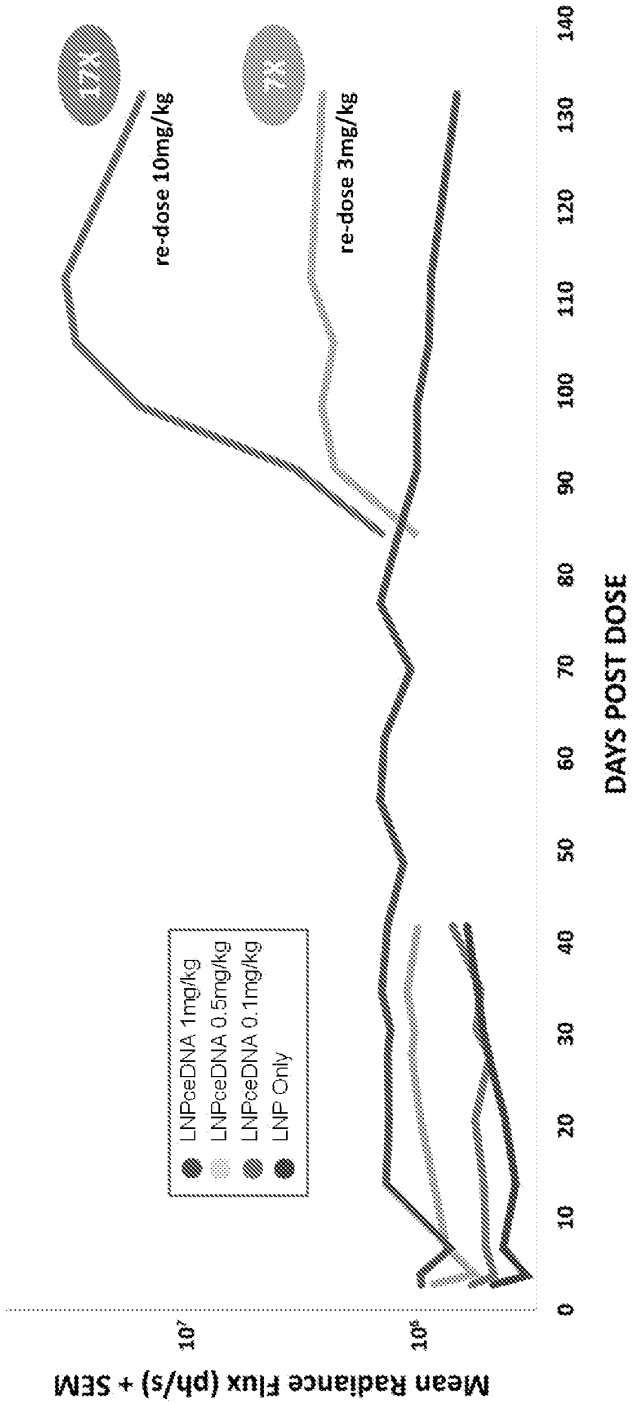

Repeat Dosing
re-dose 10mg/kg
re-dose 3mg/kg
LNPceDNA 1mg/kg
LNPceDNA 0.5mg/kg
LNPceDNA 0.1mg/kg
LNP Only
Mean Radiance Flux (ph/s) + SEM
10^7
10^6
0
10
20
30
40
50
60
70
80
90
100
110
120
130
140
DAYS POST DOSE

FIG. 7

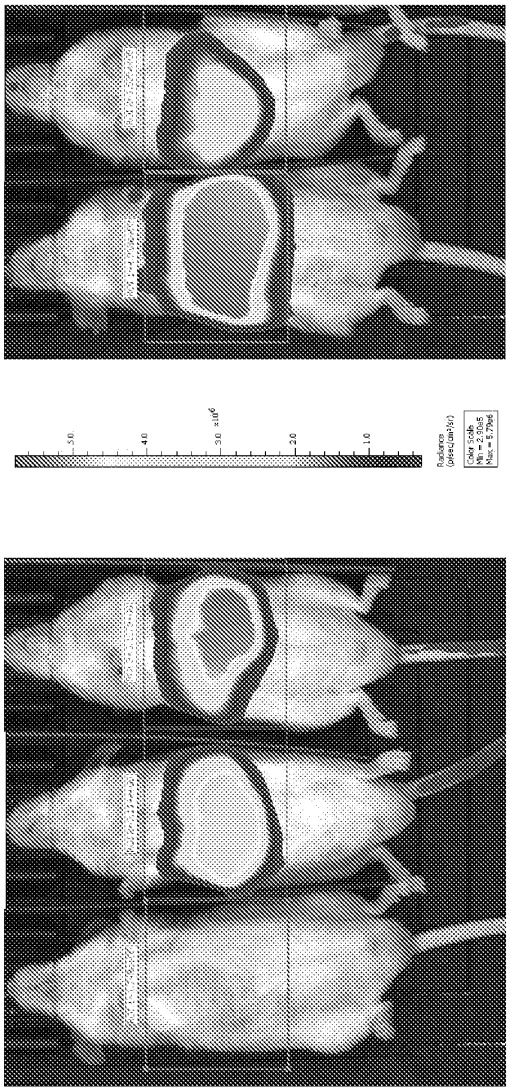
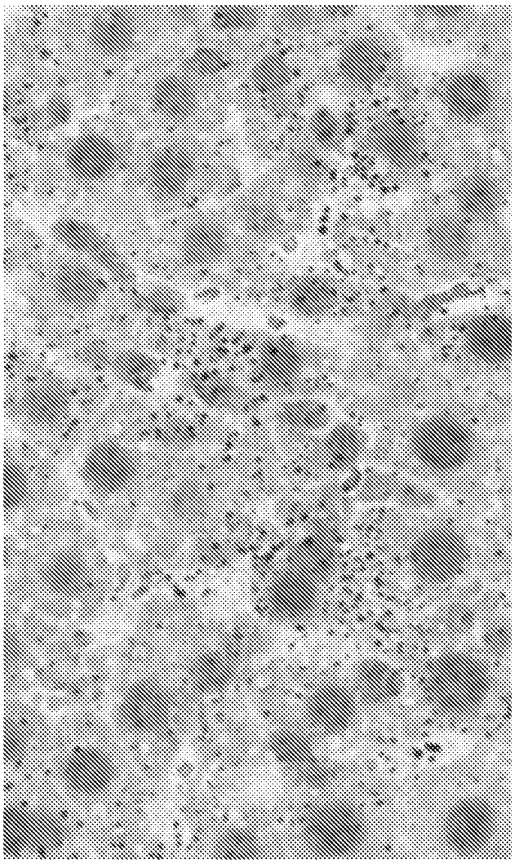


FIG. 8



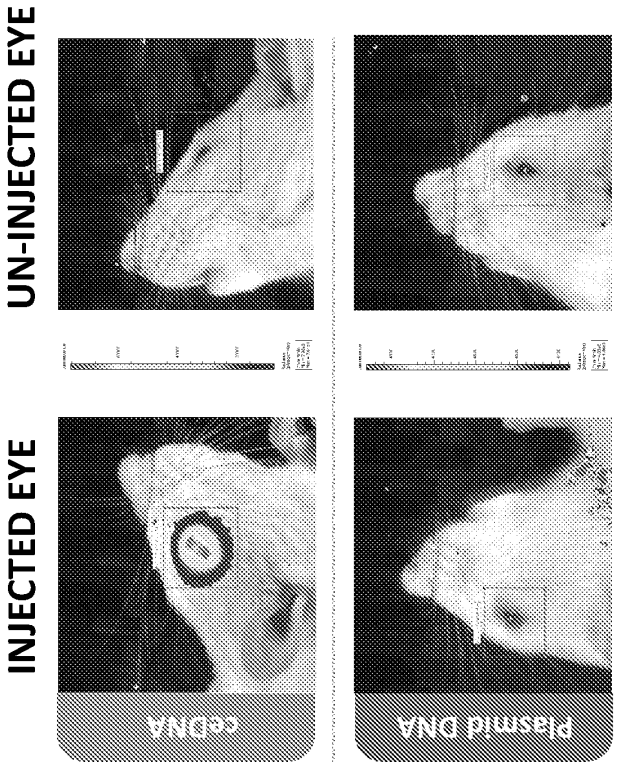


FIG. 9A

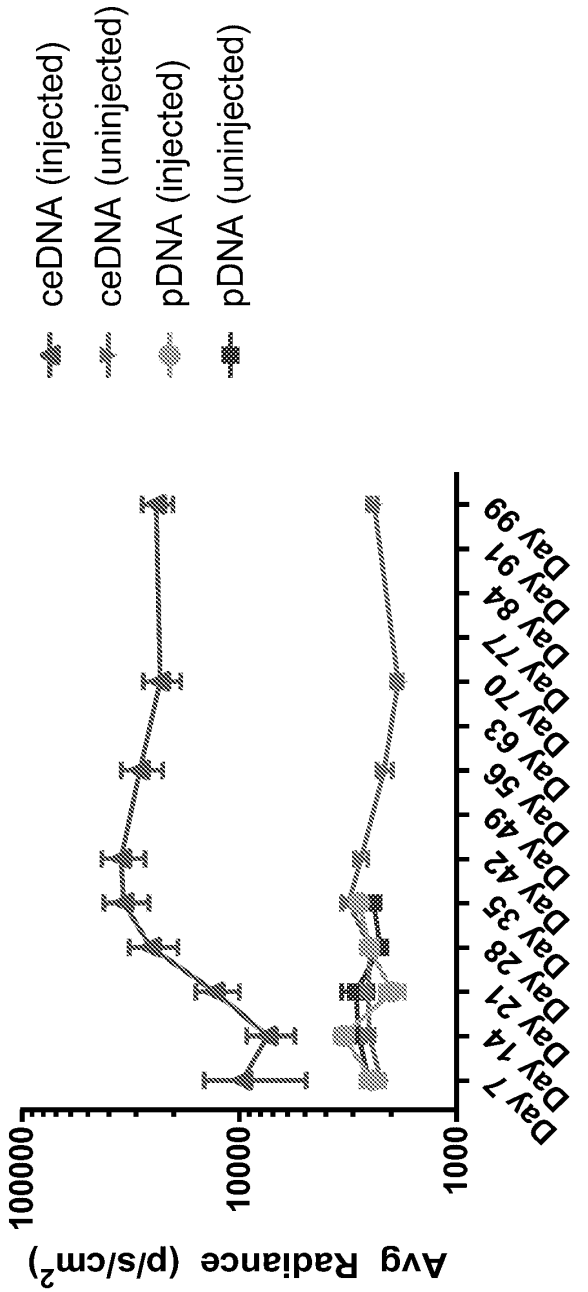

ceDNA (injected)
ceDNA (uninjected)
pDNA (injected)
pDNA (uninjected)
Avg Radiance (p/s/cm²)
100000
10000
1000
Day 7
Day 14
Day 21
Day 28
Day 35
Day 42
Day 49
Day 56
Day 63
Day 70
Day 77
Day 84
Day 91
Day 99
Days Post-Dose

FIG. 9B

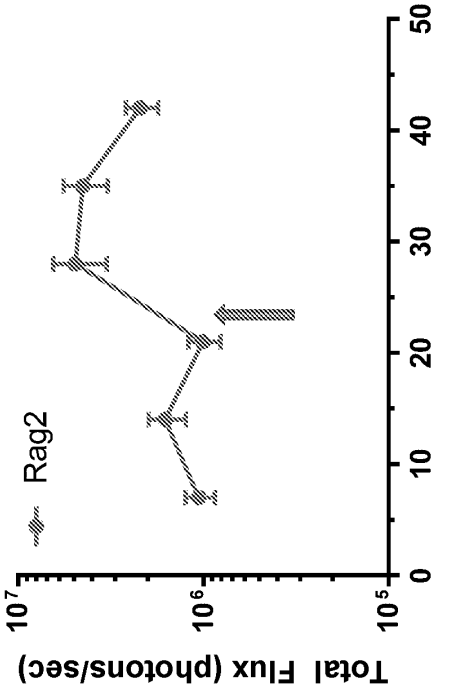


FIG. 10B

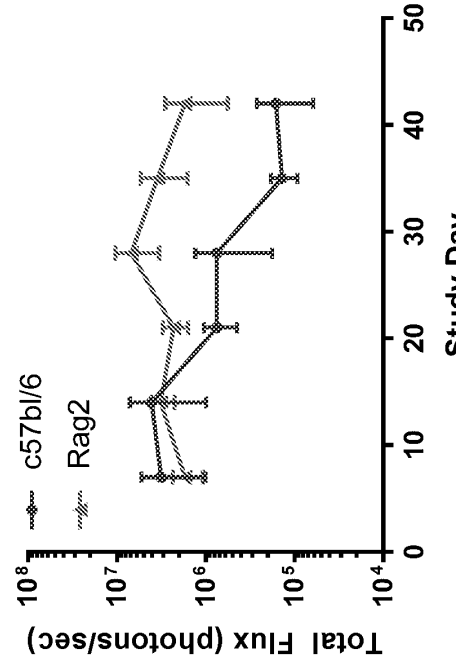


FIG. 10A

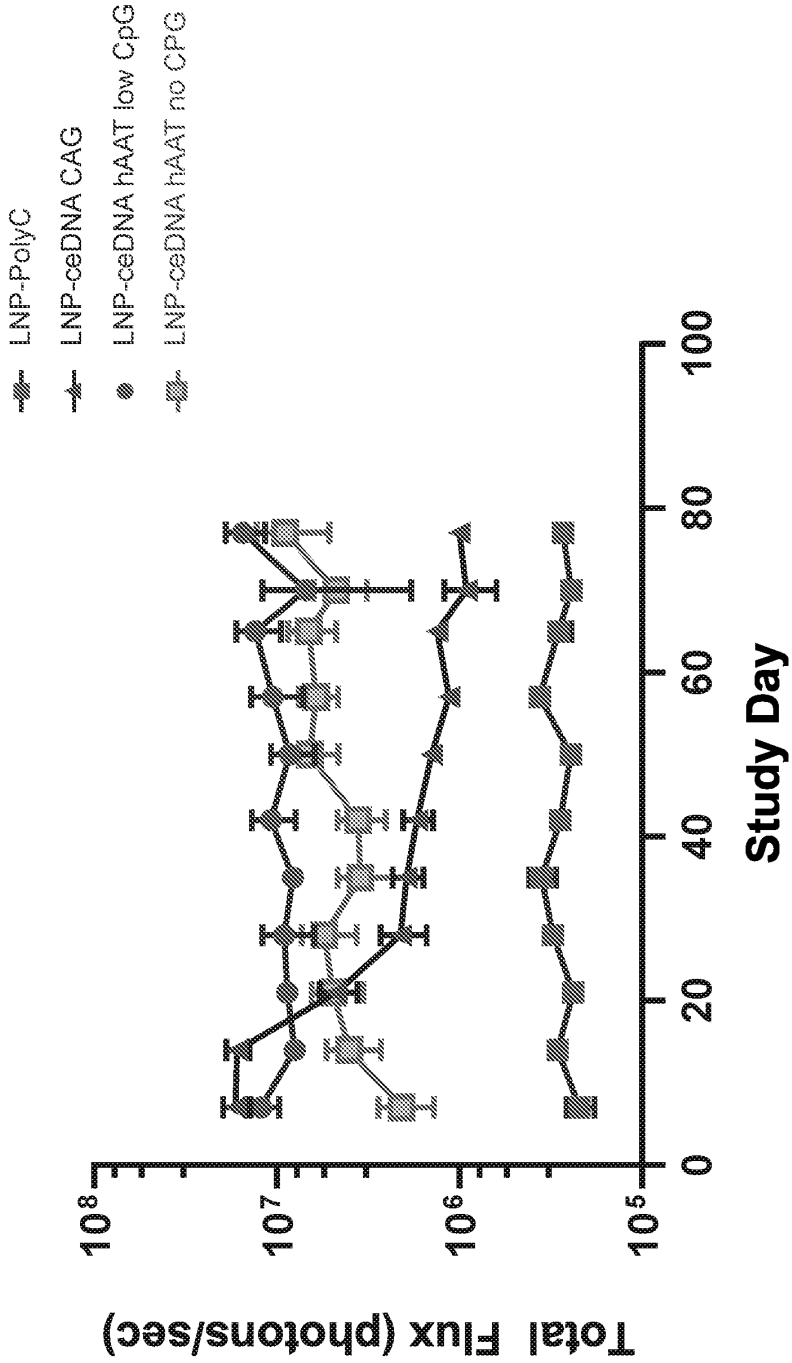

LNP-PolyC
LNP-ceDNA CAG
LNP-ceDNA hAAT low CpG
LNP-ceDNA hAAT no CPG
Total Flux (photons/sec)
10^8
10^7
10^6
10^5
0
20
40
60
80
100
Study Day

FIG. 11