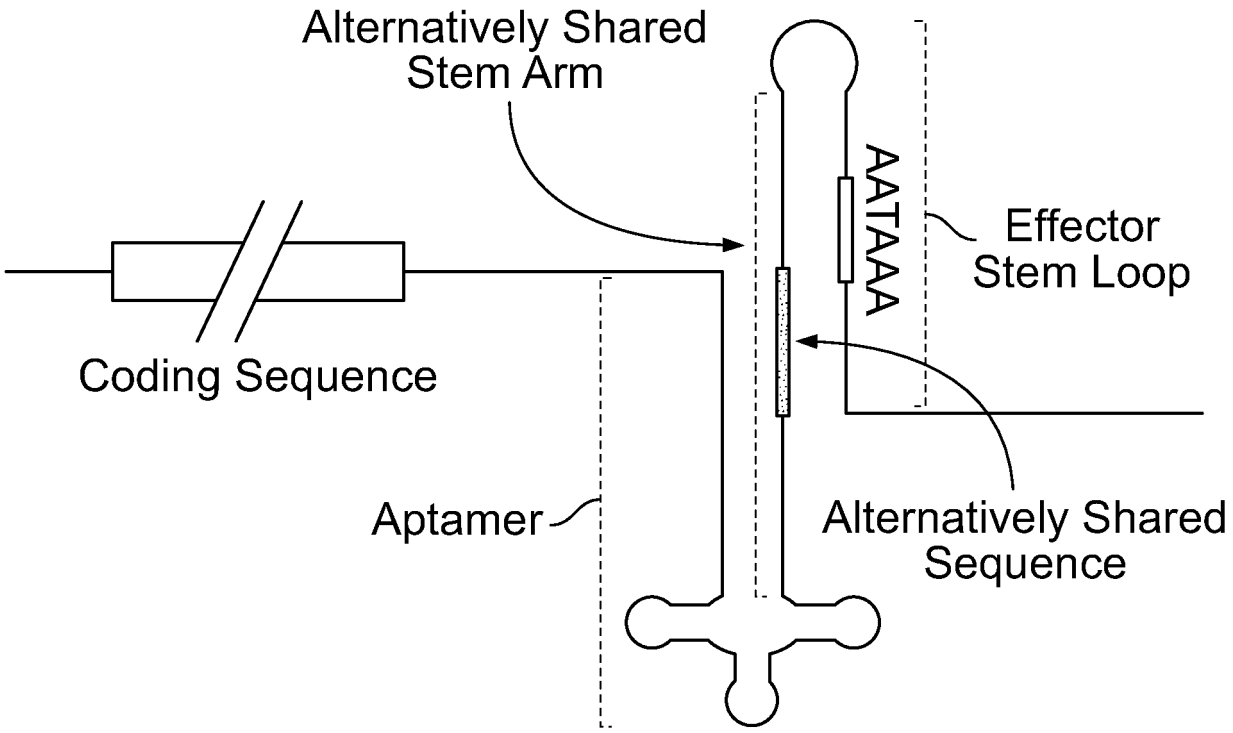

Alternatively Shared
Stem Arm
AATAAA
Effector
Stem Loop
Coding Sequence
Aptamer
Alternatively Shared
Sequence

FIG. 1a

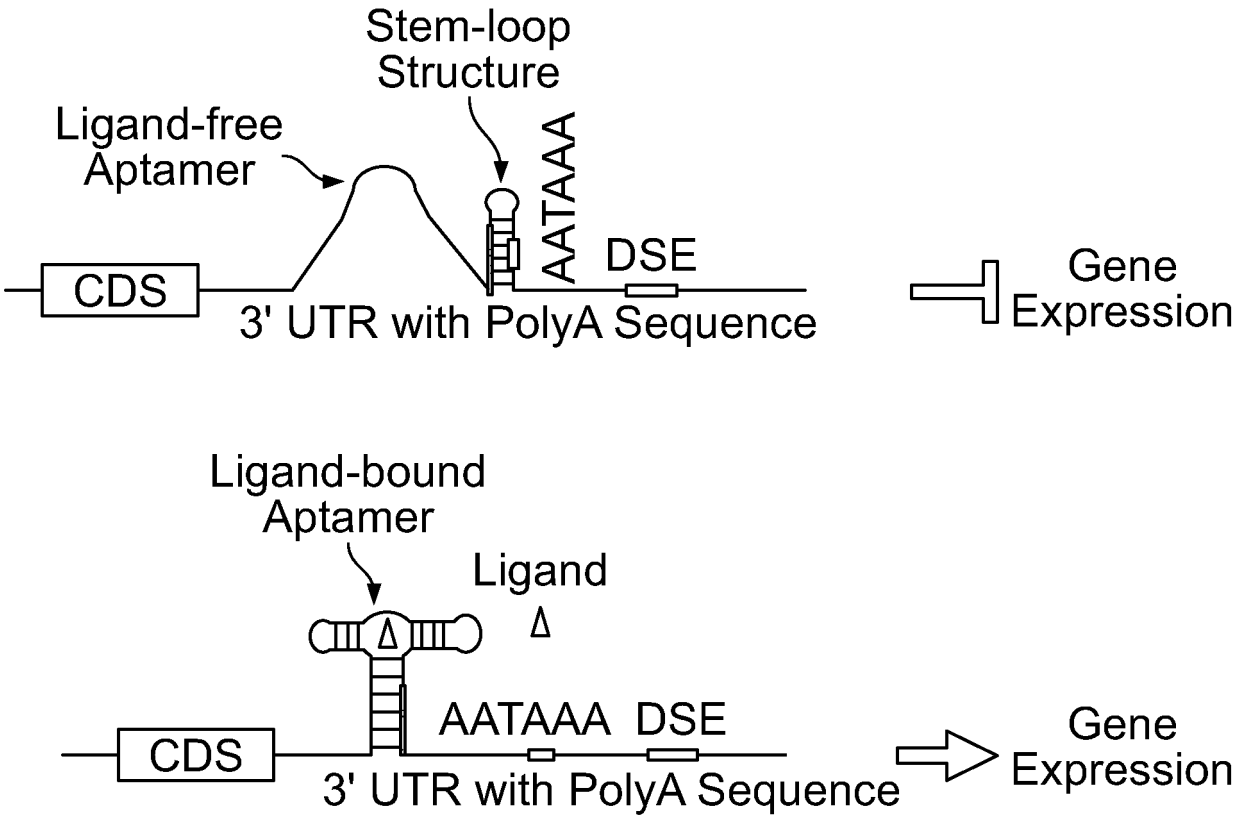

Stem-loop
Structure
Ligand-free
Aptamer
AATAAA
DSE
CDS
3' UTR with PolyA Sequence
Gene
Expression
Ligand-bound
Aptamer
Ligand
AATAAA DSE
CDS
3' UTR with PolyA Sequence
Gene
Expression

FIG. 1b

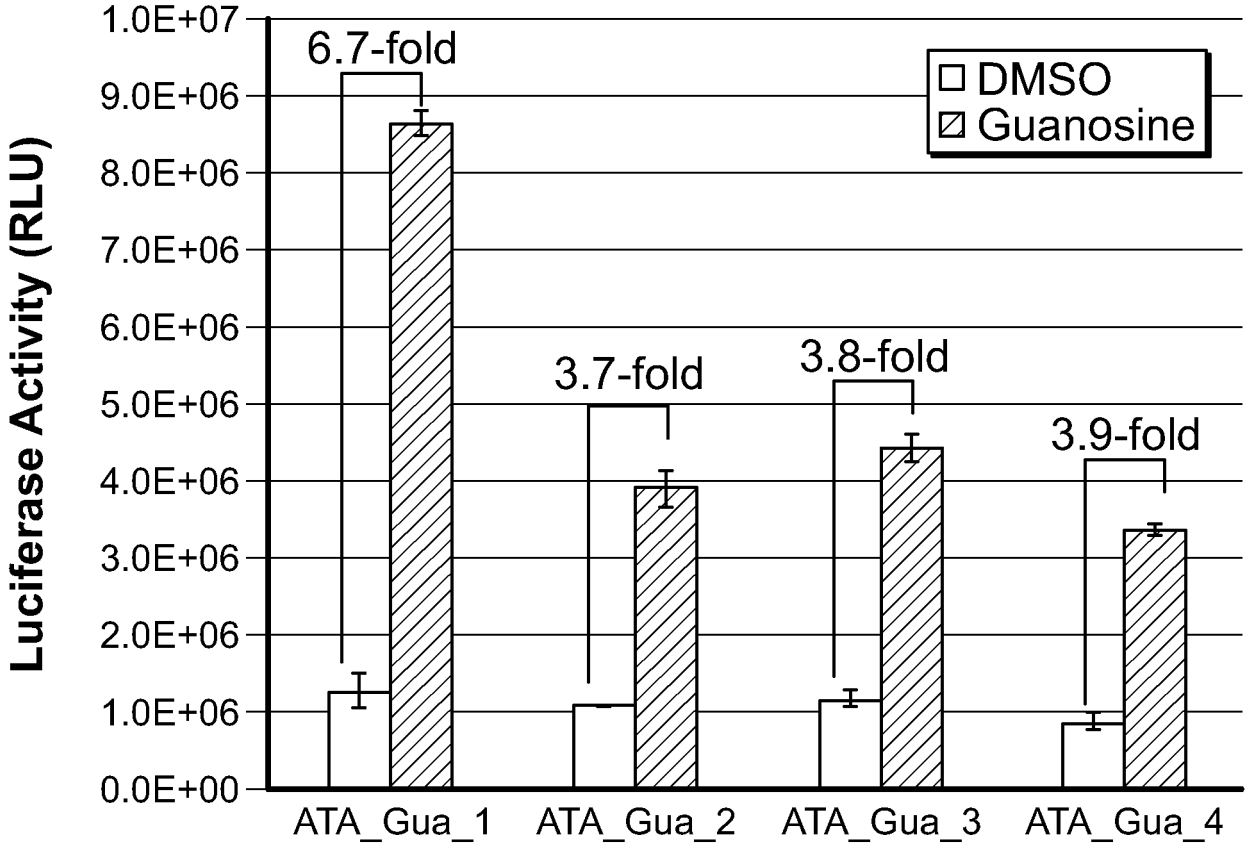

Luciferase Activity (RLU)
1.0E+07
9.0E+06
8.0E+06
7.0E+06
6.0E+06
5.0E+06
4.0E+06
3.0E+06
2.0E+06
1.0E+06
0.0E+00
6.7-fold
3.7-fold
3.8-fold
3.9-fold
DMSO
Guanosine
ATA_Gua_1
ATA_Gua_2
ATA_Gua_3
ATA_Gua_4

FIG. 1c

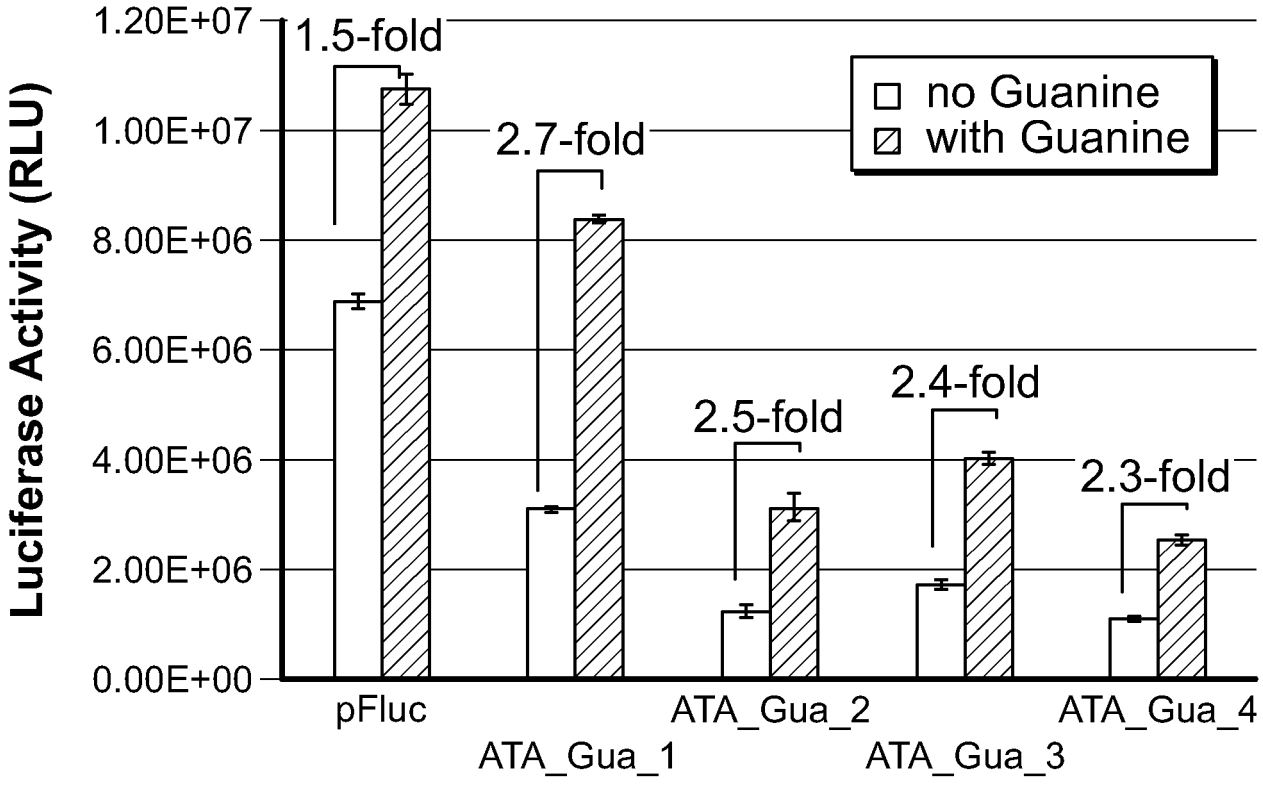

Luciferase Activity (RLU)
1.20E+07
1.00E+07
8.00E+06
6.00E+06
4.00E+06
2.00E+06
0.00E+00
1.5-fold
2.7-fold
2.5-fold
2.4-fold
2.3-fold
no Guanine
with Guanine
pFluc
ATA_Gua_1
ATA_Gua_2
ATA_Gua_3
ATA_Gua_4

FIG. 1d

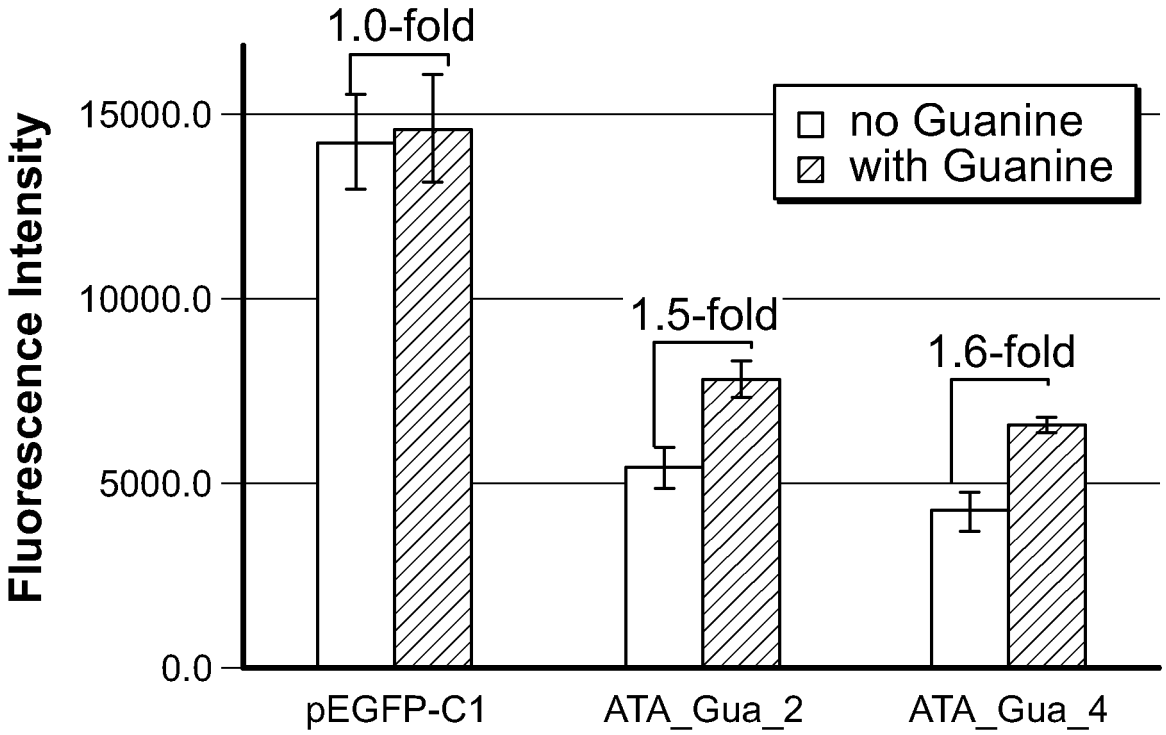

1.0-fold
15000.0
10000.0
5000.0
0.0
Fluorescence Intensity
no Guanine
with Guanine
1.5-fold
1.6-fold
pEGFP-C1
ATA_Gua_2
ATA_Gua_4

FIG. 1e

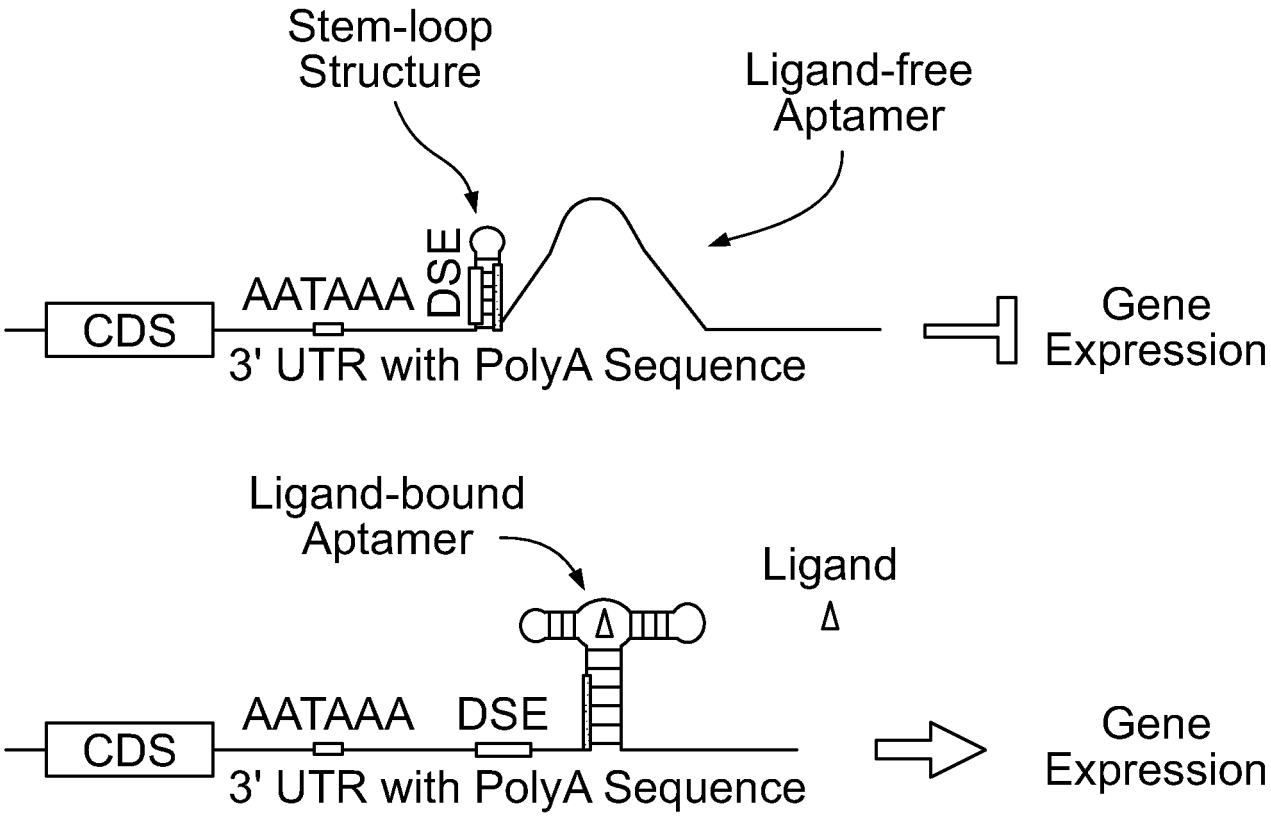

Stem-loop Structure
Ligand-free Aptamer
DSE
AATAAA
CDS
3' UTR with PolyA Sequence
Gene Expression
Ligand-bound Aptamer
Ligand
AATAAA
DSE
CDS
3' UTR with PolyA Sequence
Gene Expression

FIG. 2a

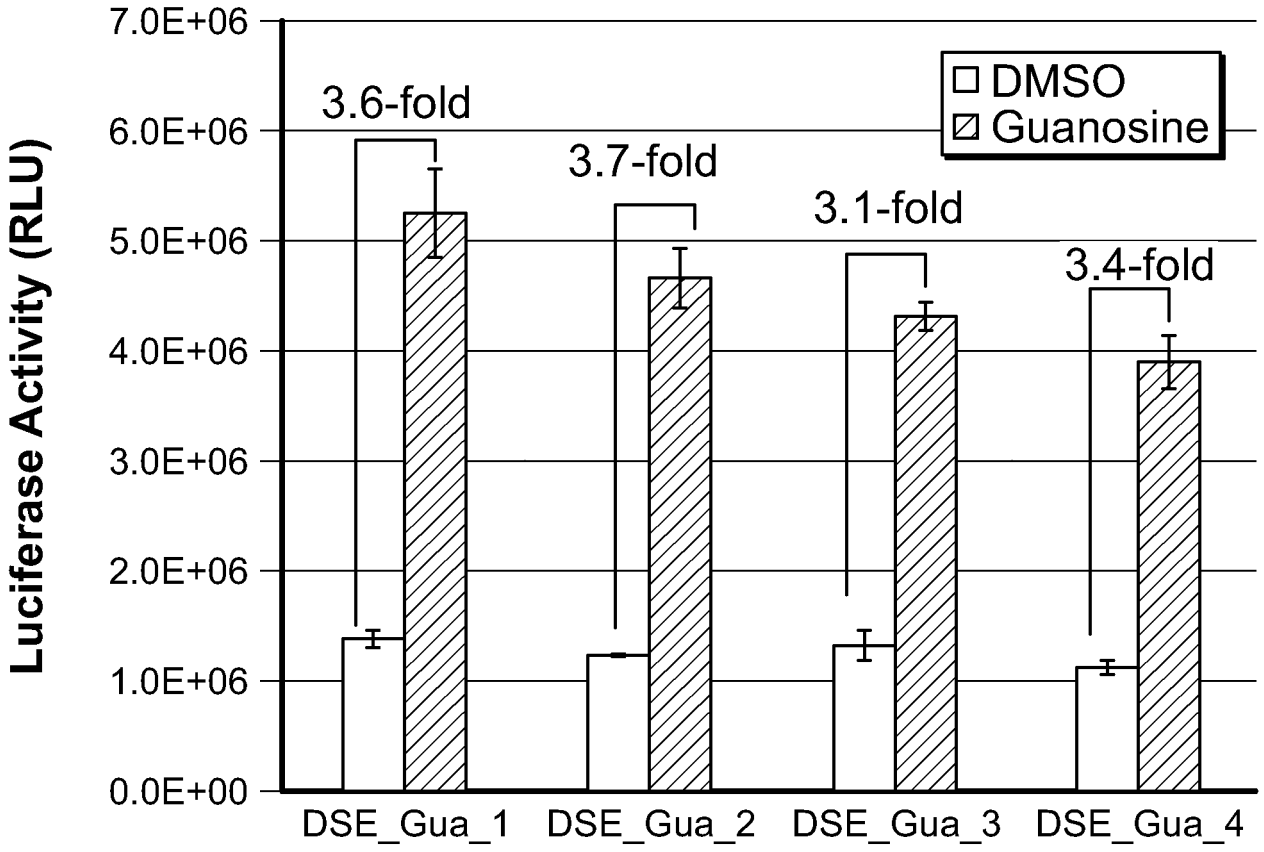

Luciferase Activity (RLU)
7.0E+06
6.0E+06
5.0E+06
4.0E+06
3.0E+06
2.0E+06
1.0E+06
0.0E+00
DMSO
Guanosine
3.6-fold
3.7-fold
3.1-fold
3.4-fold
DSE_Gua_1
DSE_Gua_2
DSE_Gua_3
DSE_Gua_4

FIG. 2b

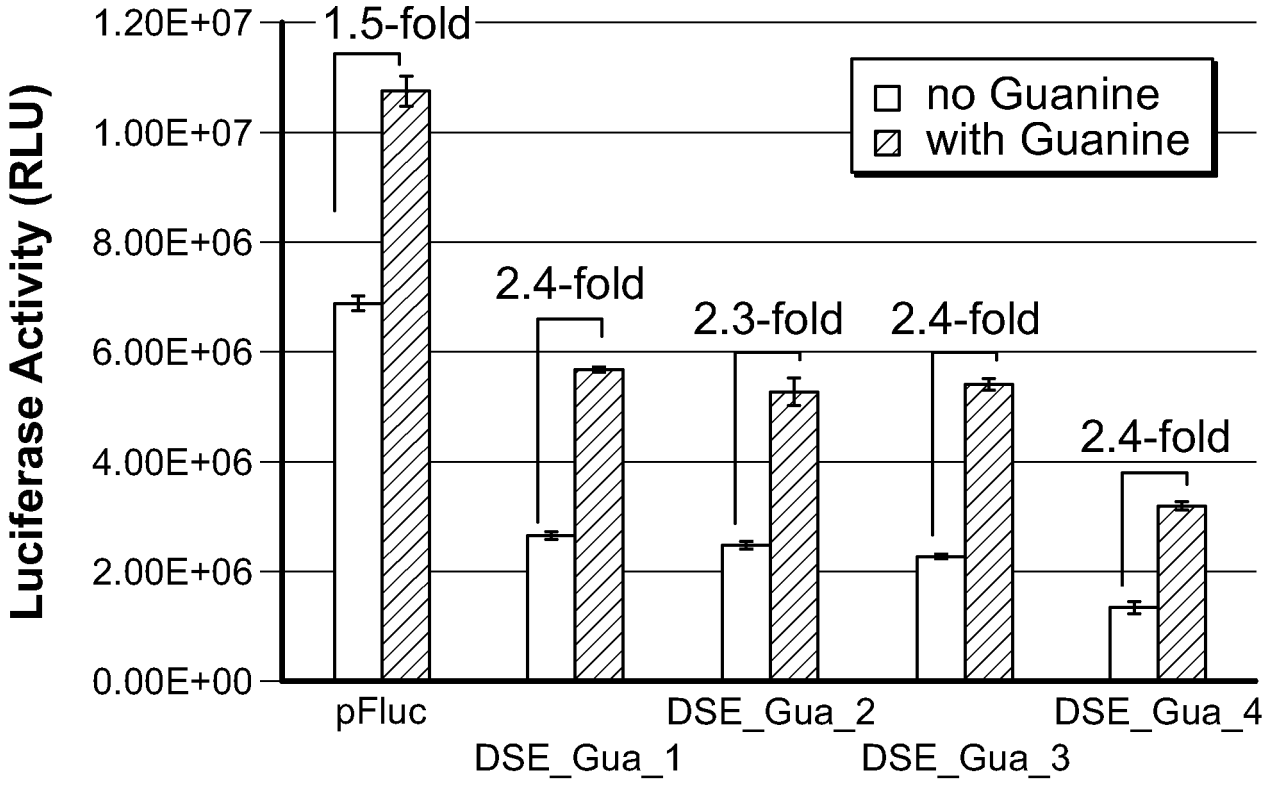

Luciferase Activity (RLU)
1.20E+07
1.00E+07
8.00E+06
6.00E+06
4.00E+06
2.00E+06
0.00E+00
no Guanine
with Guanine
1.5-fold
2.4-fold
2.3-fold
2.4-fold
2.4-fold
pFluc
DSE_Gua_1
DSE_Gua_2
DSE_Gua_3
DSE_Gua_4

FIG. 2c

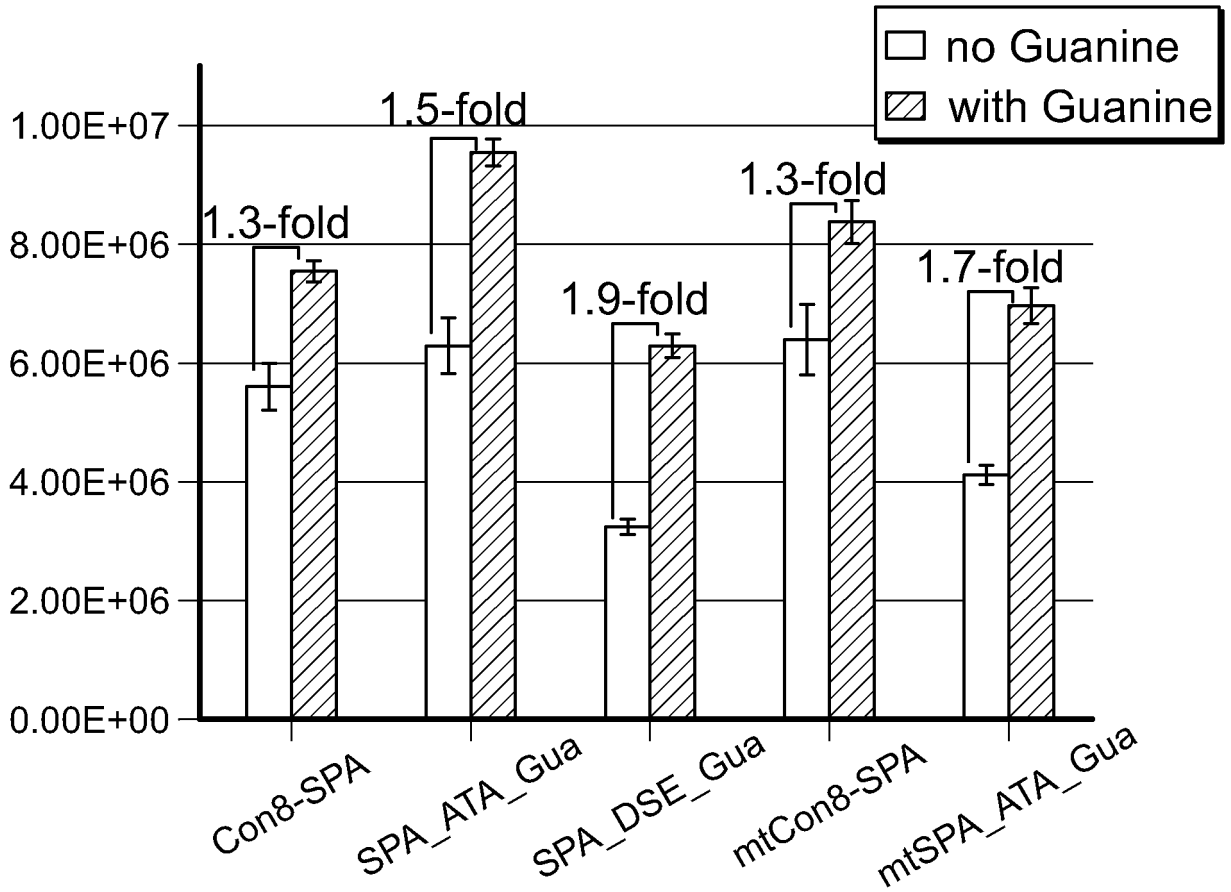

no Guanine
with Guanine
1.00E+07
8.00E+06
6.00E+06
4.00E+06
2.00E+06
0.00E+00
1.3-fold
1.5-fold
1.9-fold
1.3-fold
1.7-fold
Con8-SPA
SPA_ATA_Gua
SPA_DSE_Gua
mtCon8-SPA
mtSPA_ATA_Gua

FIG. 3

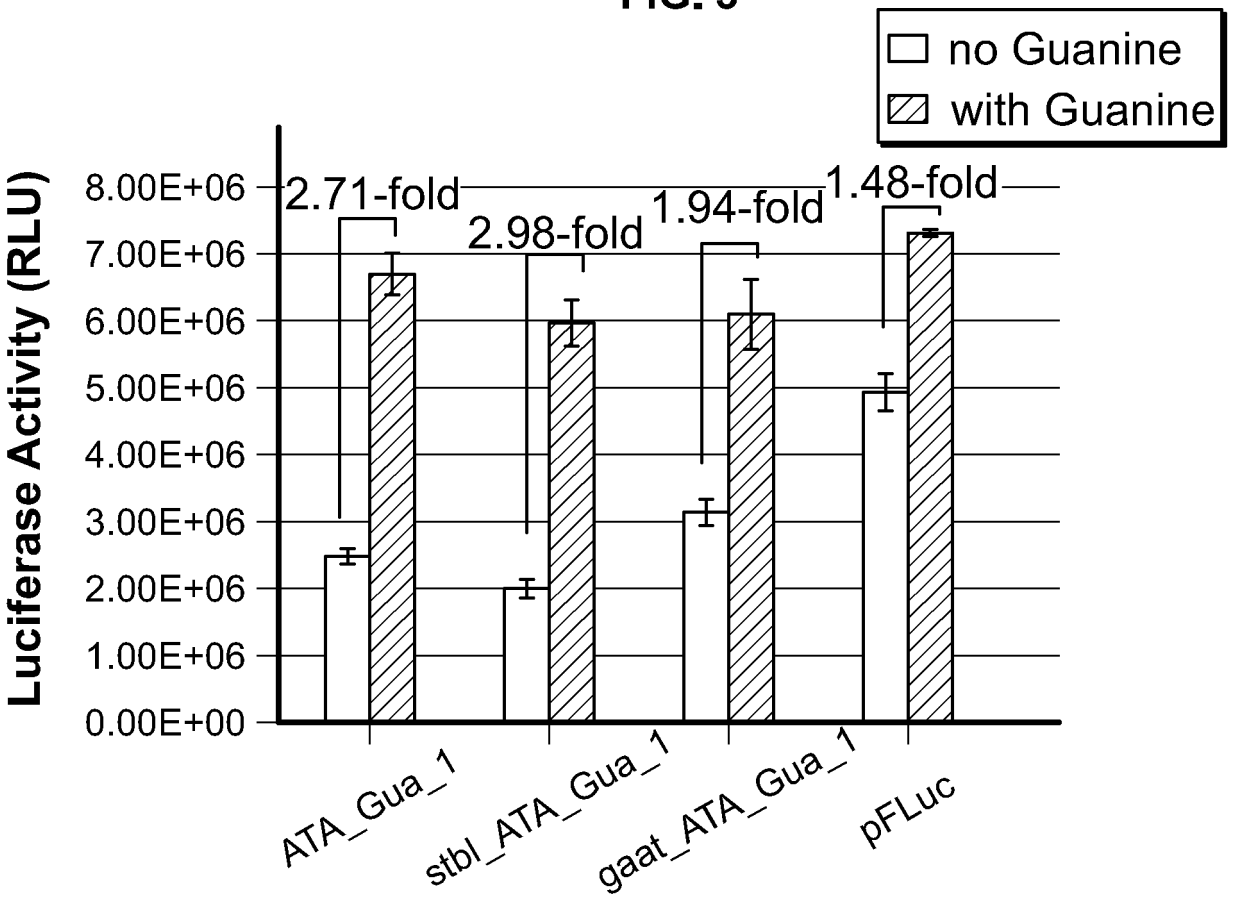

no Guanine
with Guanine
Luciferase Activity (RLU)
8.00E+06
7.00E+06
6.00E+06
5.00E+06
4.00E+06
3.00E+06
2.00E+06
1.00E+06
0.00E+00
2.71-fold
2.98-fold
1.94-fold
1.48-fold
ATA_Gua_1
stbl_ATA_Gua_1
gaat_ATA_Gua_1
pFLuc

FIG. 4

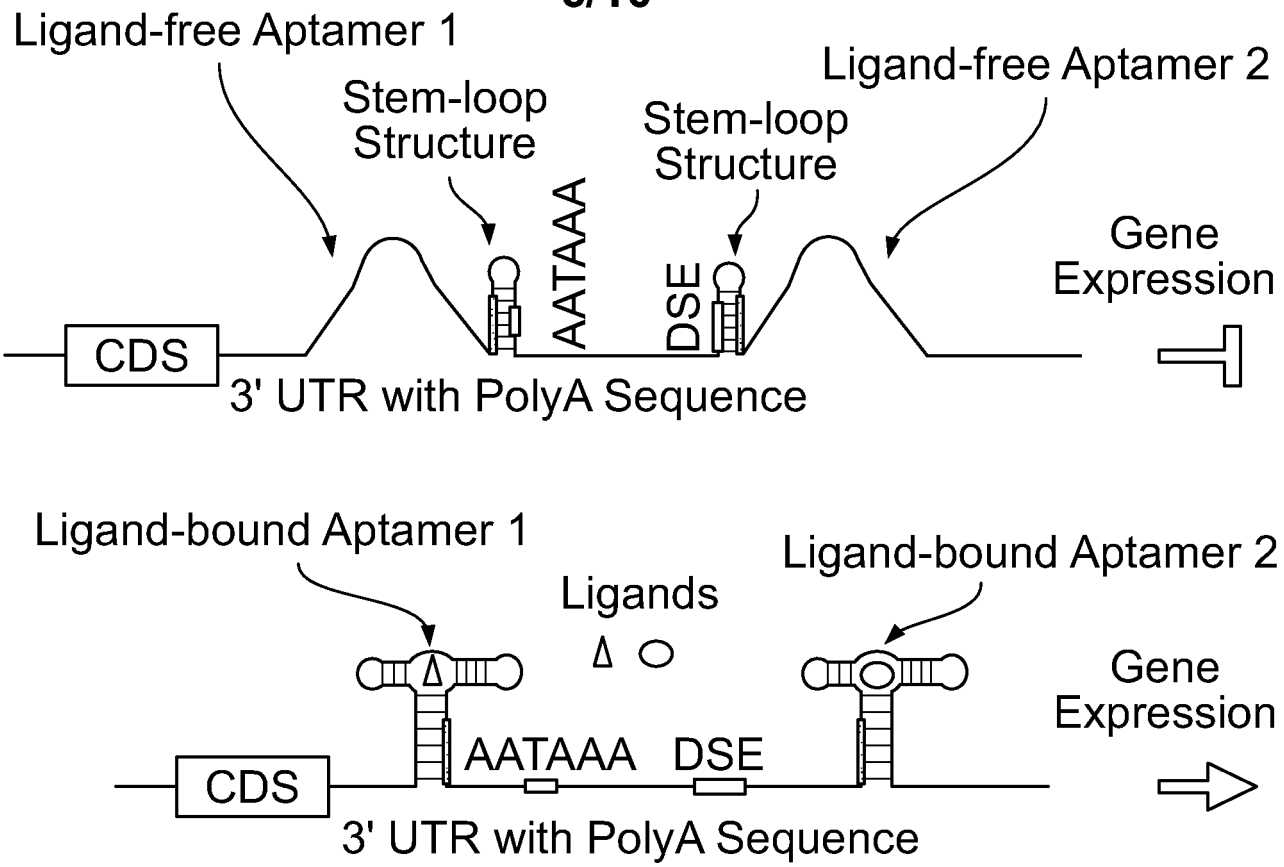

Ligand-free Aptamer 1
Stem-loop Structure
AATAAA
Stem-loop Structure
DSE
Ligand-free Aptamer 2
Gene Expression
CDS
3' UTR with PolyA Sequence
Ligand-bound Aptamer 1
Ligands
Ligand-bound Aptamer 2
Gene Expression
AATAAA DSE
CDS
3' UTR with PolyA Sequence

FIG. 5a

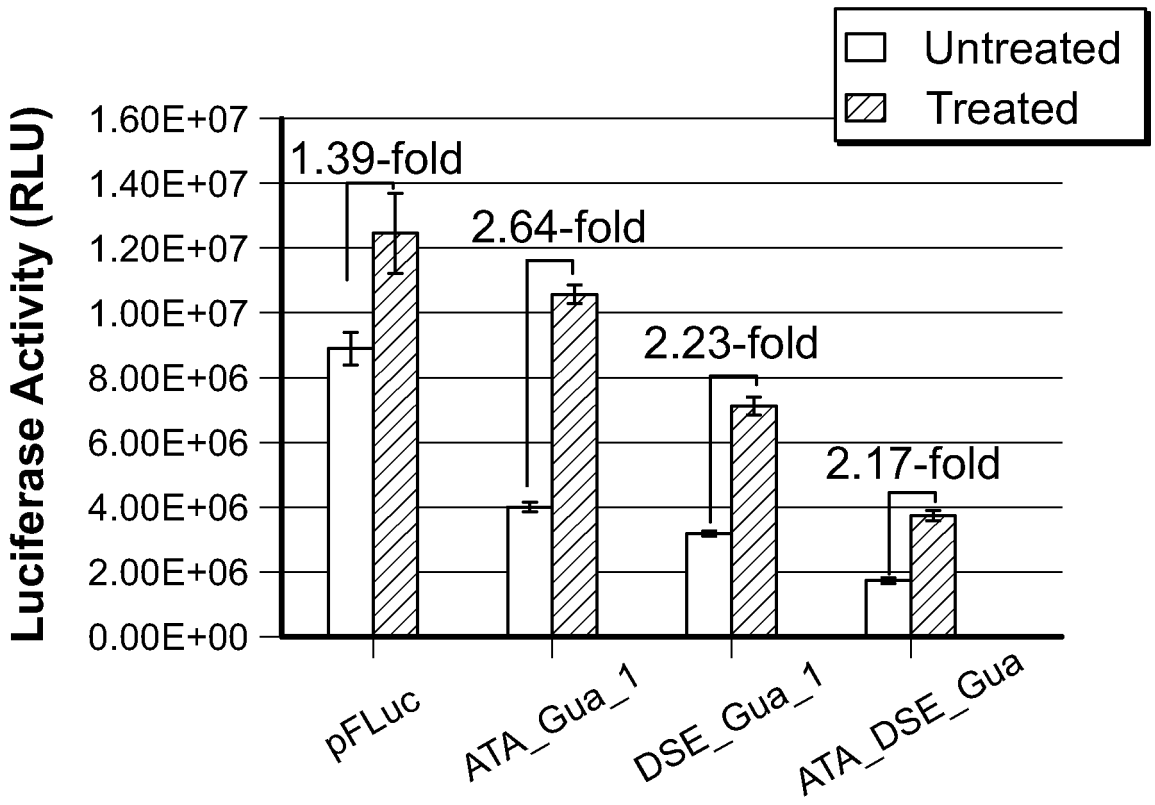
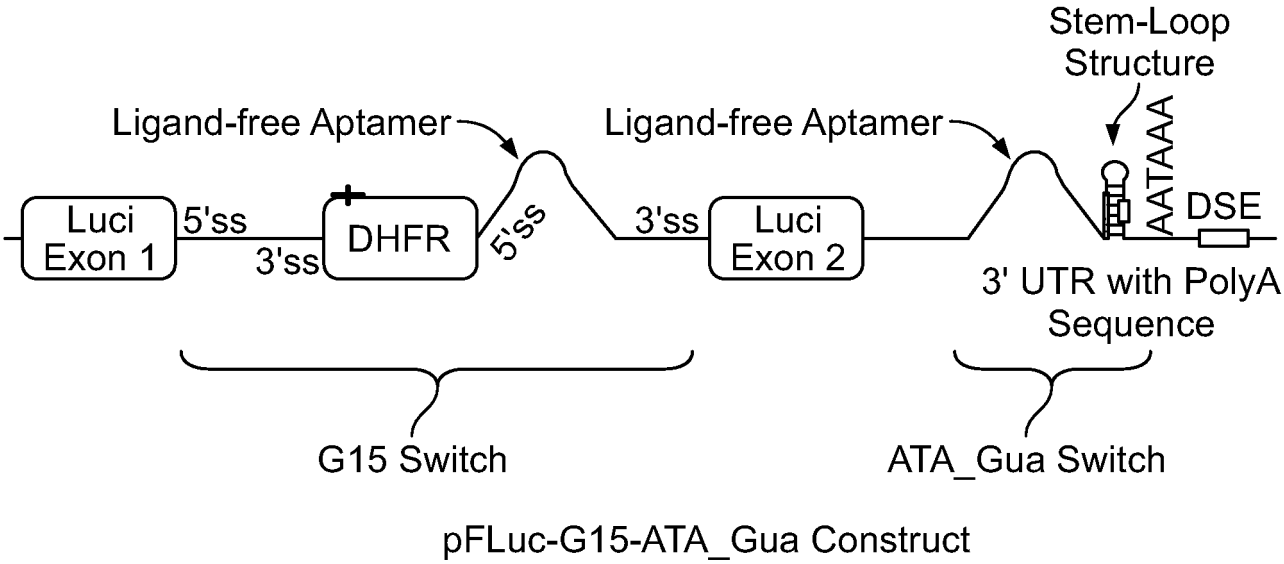

Untreated
Treated
Luciferase Activity (RLU)
1.60E+07
1.40E+07
1.20E+07
1.00E+07
8.00E+06
6.00E+06
4.00E+06
2.00E+06
0.00E+00
1.39-fold
2.64-fold
2.23-fold
2.17-fold
pFLuc
ATA_Gua_1
DSE_Gua_1
ATA_DSE_Gua

FIG. 5b



pFLuc-G15-ATA_Gua Construct

FIG. 6a

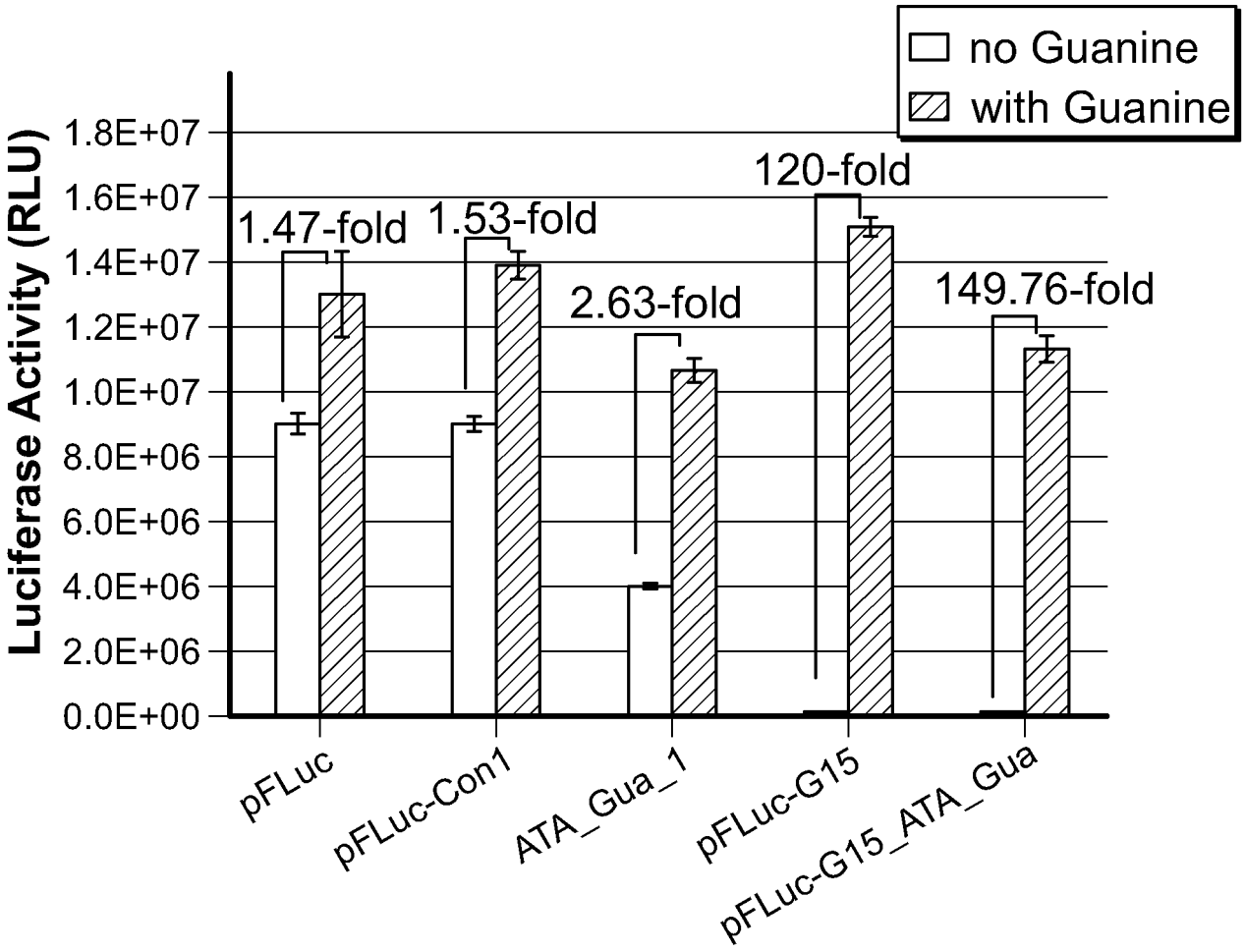


FIG. 6b

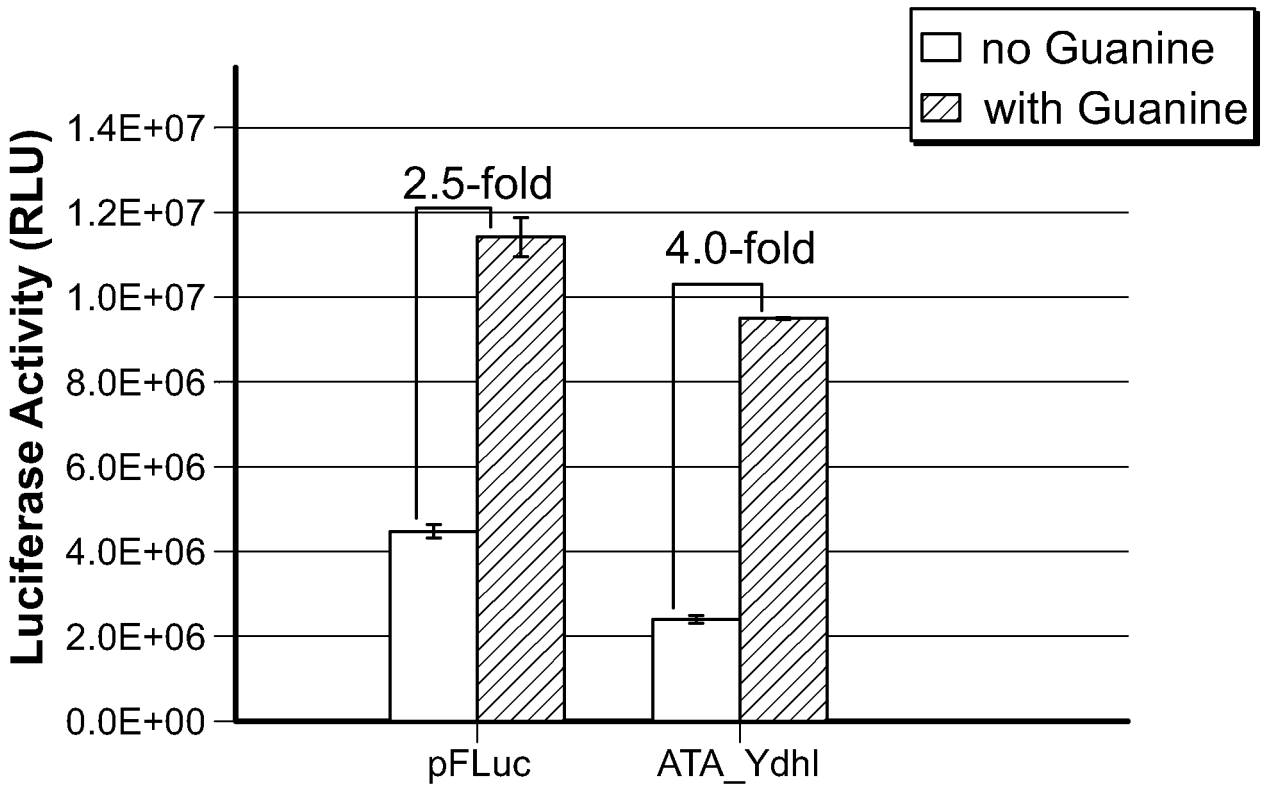

no Guanine
with Guanine
Luciferase Activity (RLU)
1.4E+07
1.2E+07
1.0E+07
8.0E+06
6.0E+06
4.0E+06
2.0E+06
0.0E+00
2.5-fold
4.0-fold
pFLuc
ATA_Ydhl

FIG. 7

ATA_Gua_1 (SEQ ID NO: 1):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAgccataccacatttgtagaggttttacttgctttaaa
aaacctcccacacctccccctgaacctgaaacataaaatgaatgcaattgttgttgttaacttgtttattgcagcttataatggttacaaataa
agcaatagcatcacaaatttc*taaaggta*taatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgac*taccttta*
tttcgaaaga[aataaa]gcatttttttcactgcattc[tagttgtggtttg]tccaaactcatcaatgtatcttaacgcgt

ATA_Gua_1 (SEQ ID NO: 2):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAgccataccacatttgtagaggttttacttgctttaaa
aaacctcccacacctccccctgaacctgaaacataaaatgaatgcaattgttgttgttaacttgtttattgcagcttataatggttacaaataa
agcaatagcatcacaaatttcac*ataaagca*taatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgac*tgcttt*
*att*tcgaaaga[aataaa]gcatttttttcactgcattc[tagttgtggtttg]tccaaactcatcaatgtatcttaacgcgt

ATA_Gua_3 (SEQ ID NO: 3):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAgccataccacatttgtagaggttttacttgctttaaa
aaacctcccacacctccccctgaacctgaaacataaaatgaatgcaattgttgttgttaacttgtttattgcagcttataatggttacaaataa
agcaatagcatcacaaattt*aataaaga*taatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgac*tctttattt*
gtgcgaaagcaca[aataaa]gcatttttttcactgcattc[tagttgtggtttg]tccaaactcatcaatgtatcttaacgcgt

ATA_Gua_4 (SEQ ID NO: 4):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAgccataccacatttgtagaggttttacttgctttaaa
aaacctcccacacctccccctgaacctgaaacataaaatgaatgcaattgttgttgttaacttgtttattgcagcttataatggttacaaataa
agcaatagcatcacaaattt*taaagcaa*taatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgac*ttgctttatt*
tgtgcgaaagcaca[aataaa]gcatttttttcactgcattc[tagttgtggtttg]tccaaactcatcaatgtatcttaacgcgt

DSE_Gua_1 (SEQ ID NO: 5):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAgccataccacatttgtagaggttttacttgctttaaa
aaacctcccacacctccccctgaacctgaaacataaaatgaatgcaattgttgttgttaacttgtttattgcagcttataatggttacaaataa
agcaatagcatcacaaatttcaca[aataaa]gcatttttttcactgcattc[tagttgtggtttg]tccgaaagg*acaaacca*taatcgcgtgga
tatggcacgcaagtttctaccgggcaccgtaaatgtccgac*tggtttgt*aaactcatcaatgtatcttaacgcgt

DSE_Gua_2 (SEQ ID NO: 6):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAgccataccacatttgtagaggttttacttgctttaaa
aaacctcccacacctccccctgaacctgaaacataaaatgaatgcaattgttgttgttaacttgtttattgcagcttataatggttacaaataa
agcaatagcatcacaaatttcaca[aataaa]gcatttttttcactgcattc[tagttgtggtttg]tccgaaagg*acaaaccaa*taatcgcgtgg
atatggcacgcaagtttctaccgggcaccgtaaatgtccgac*ttggtttg*aaactcatcaatgtatcttaacgcgt

DSE_Gua_3 (SEQ ID NO: 7):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAgccataccacatttgtagaggttttacttgctttaaa
aaacctcccacacctccccctgaacctgaaacataaaatgaatgcaattgttgttgttaacttgtttattgcagcttataatggttacaaataa
agcaatagcatcacaaatttcaca[aataaa]gcatttttttcactgcattc[tagttgtggtttg]tccgaaagg*acaaaccacaa*taatcgcgt
ggatatggcacgcaagtttctaccgggcaccgtaaatgtccgac*ttgtggttt*aaactcatcaatgtatcttaacgcgt

DSE_Gua_4 (SEQ ID NO: 8):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAgccataccacatttgtagaggttttacttgctttaaa
aaacctcccacacctccccctgaacctgaaacataaaatgaatgcaattgttgttgttaacttgtttattgcagcttataatggttacaaataa
agcaatagcatcacaaatttcaca[aataaa]gcatttttttcactgcattc[tagttgtggtttg]tccgaaaggacaaa*ccacaaca*taatcgc
gtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgac*tgttgtgg*aaactcatcaatgtatcttaacgcgt

FIG. 8

Con8-SPA (SEQ ID NO: 9):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagcttatcgataccgtcgacctcgagg
gcccagatctgcggccgcaataaaagatctttattttcattagatctgtgtgttggttttttgtgtgtctagaaataattcttactgtcat

SPA_ATA_Gua (SEQ ID NO: 10):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagcttatcgataccgtcgacctcgagg
gcccagatctgcggc*aaaaggta*taatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgac*tacctttt*attgg
aaacaataaaagatctttattttcattagatctgtgtgttggttttttgtgtgtctagaaataattcttact

SPA_DSE_Gua (SEQ ID NO: 11):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagcttatcgataccgtcgacctcgagg
gcccagatctgcggccgcaataaaagatctttattttcattagatctgtgtgttggttttttgtgtgtcgaaaga*cacacaata*taatcgcgt
ggatatggcacgcaagtttctaccgggcaccgtaaatgtccgac*tattgtgtg*gaaataattcttact

mtCon8-SPA (SEQ ID NO: 12):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagcttatcgataccgtcgacctcgagg
gcccagatctgcggccgcaataaaatatctttattttcattacatctgtgtgttggttttttgtgtgtctagaaataattcttact

mtSPA_ATA_Gua (SEQ ID NO: 13):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagcttatcgataccgtcgacctcgagg
gcccagatctgcgg*aaaaggta*taatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgac*tacctttt*attgcg
aaagcaataaaaatatctttattttcattacatctgtgtgttggttttttgtgtgtctagaaataattcttact

Stbl_ATA_GUA_1 (SEQ ID NO: 14):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAgccataccacatttgtagaggttttacttgctttaaa
aaacctcccacacctccccctgaacctgaaacataaaatgaatgcaattgttgttgttaacttgtttattgcagcttataatggttacaaataa
agcaatagcatcacaaatttc*taaaggta*taatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgac*tacctta*
tttcttcggaaataaagcatttttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttaacgcgt

gaat_ATA_Gua_1 (SEQ ID NO: 15):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAgccataccacatttgtagaggttttacttgctttaaa
aaacctcccacacctccccctgaacctgaaacataaaatgaatgcaattgttgttgttaacttgtttattgcagcttataatggttacaaataa
agcaatagcatcacaaatttc*taaaggta*taatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgac*tacctta*
tttcgaatgaaataaagcatttttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttaacgcgt

ATA_DSE_Gua (SEQ ID NO: 16):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAgccataccacatttgtagaggttttacttgctttaaa
aaacctcccacacctccccctgaacctgaaacataaaatgaatgcaattgttgttgttaacttgtttattgcagcttataatggttacaaataa
agcaatagcatcacaaatttc*taaaggta*taatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgac*tacctta*
tttcgaaagaaataaagcatttttttcactgcattctagttgtggtttgtccgaaagg*acaaacca*taatcgcgtggatatggcacgcaagt
ttctaccgggcaccgtaaatgtccgac*tggtttgt*aaactcatcaatgtatcttaacgcgt

ATA_ydhl (SEQ ID NO: 17):
AAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAgccataccacatttgtagaggttttacttgctttaaa
aaacctcccacacctccccctgaacctgaaacataaaatgaatgcaattgttgttgttaacttgtttattgcagcttataatggttacaaataa
agcaatagcatcacaaatttc*aataaaggta*taacctcaatatatggtttgagggtgtctaccaggaaccgtaaaatcctgat*tacctt*
*att*cttcggaaataaagcatttttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttaacgcgt

FIG. 8 (Cont.)