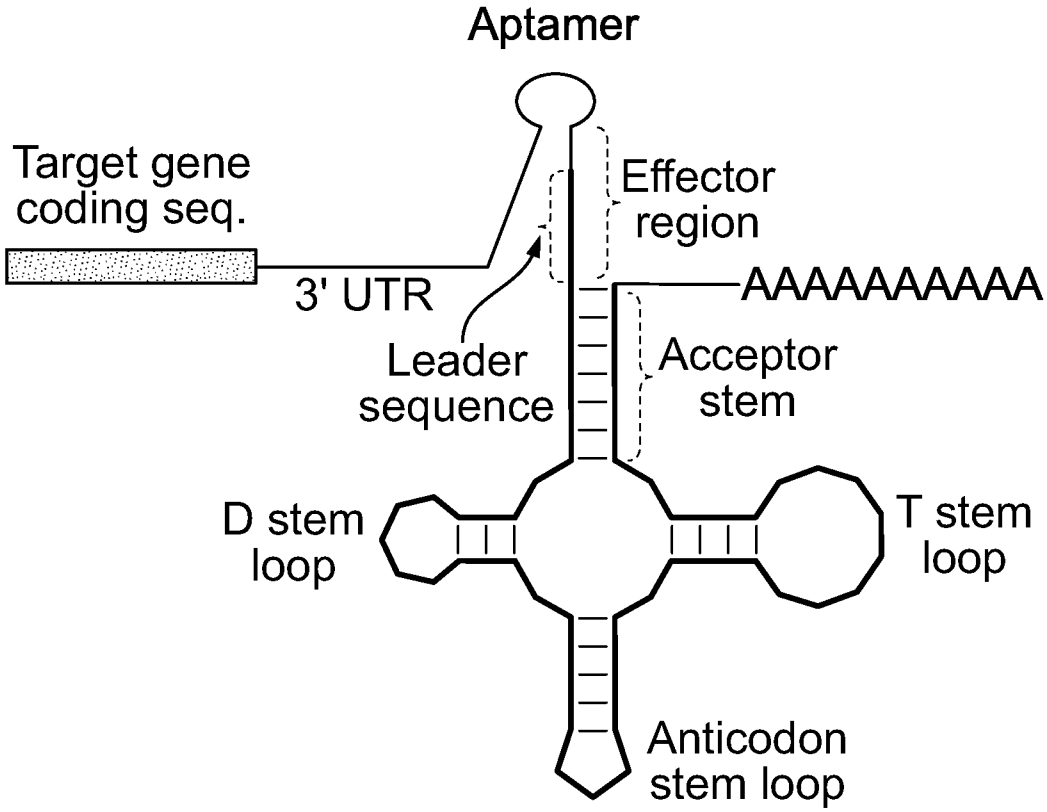

Aptamer
Target gene coding seq.
3' UTR
Leader sequence
Effector region
AAAAAAAAAA
Acceptor stem
D stem loop
T stem loop
Anticodon stem loop

Fig. 1a

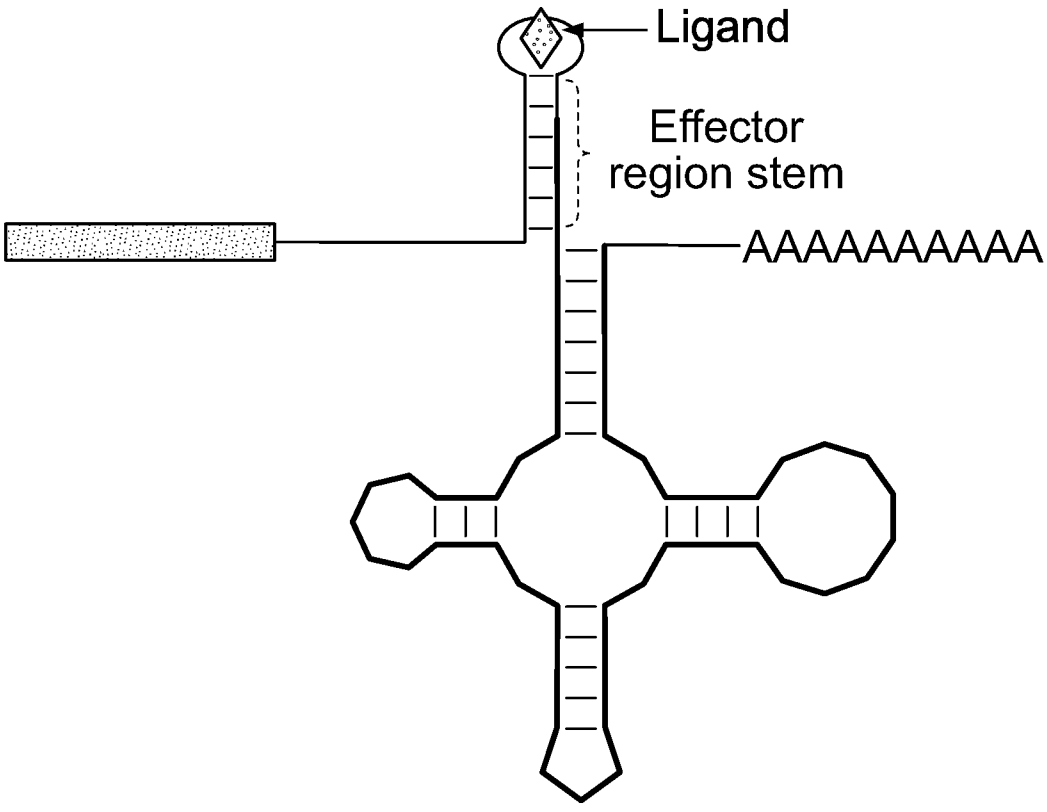

Ligand
Effector region stem
AAAAAAAAAA

Fig. 1b

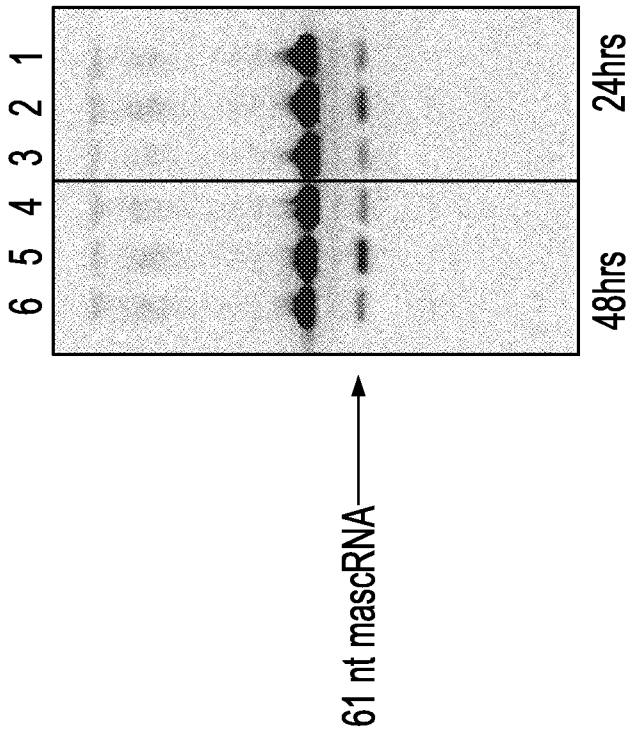

1. GFP
2. GFP-masc
3. GFP-mascRev
4. GFP
5. GFP-masc
6. GFP-mascRev
Probe: 5' DIG-all-masc-probe
6 5 4 3 2 1
48hrs
24hrs
61 nt mascRNA

Fig . 2a

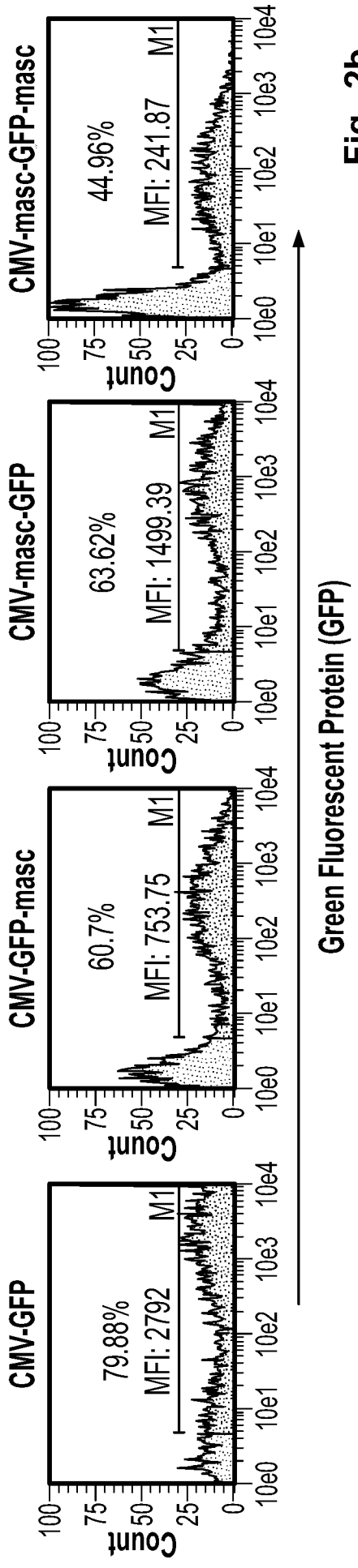
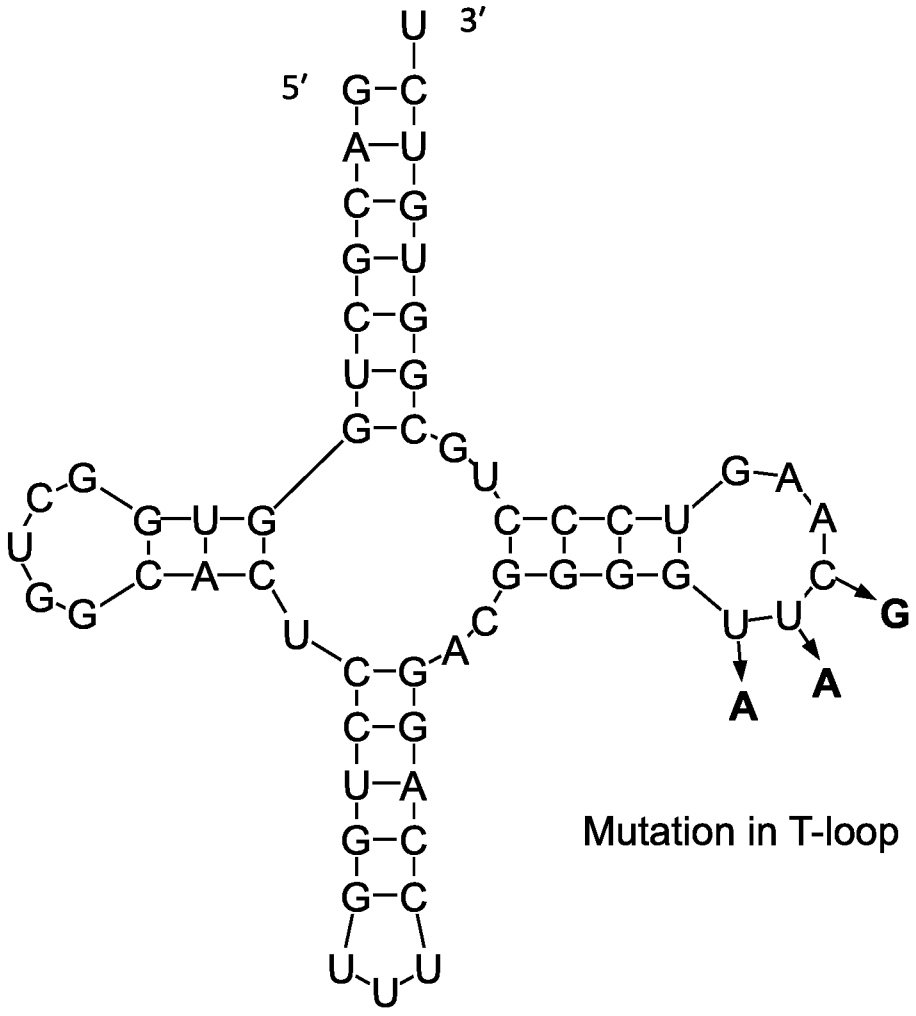

CMV-GFP
79.88%
MFI: 2792
M1
CMV-GFP-masc
60.7%
MFI: 753.75
M1
CMV-masc-GFP
63.62%
MFI: 1499.39
M1
CMV-masc-GFP-masc
44.96%
MFI: 241.87
M1
Count
100
75
50
25
0
10e0
10e1
10e2
10e3
10e4
Green Fluorescent Protein (GFP)

Fig . 2b


5′
3′
Mutation in T-loop

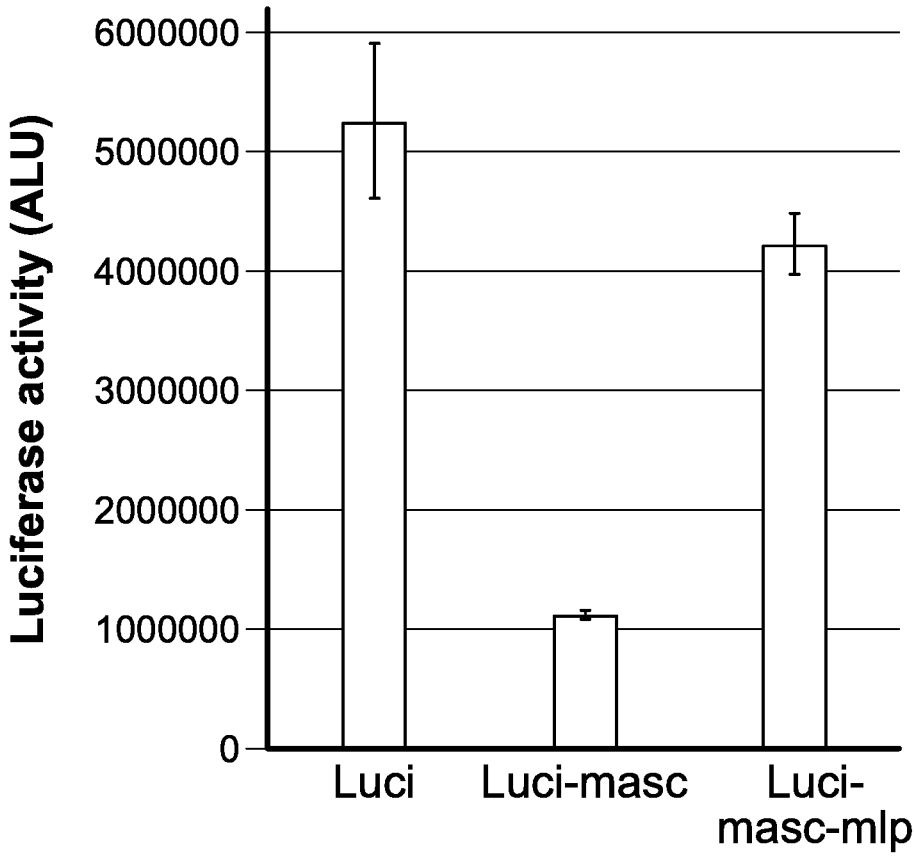
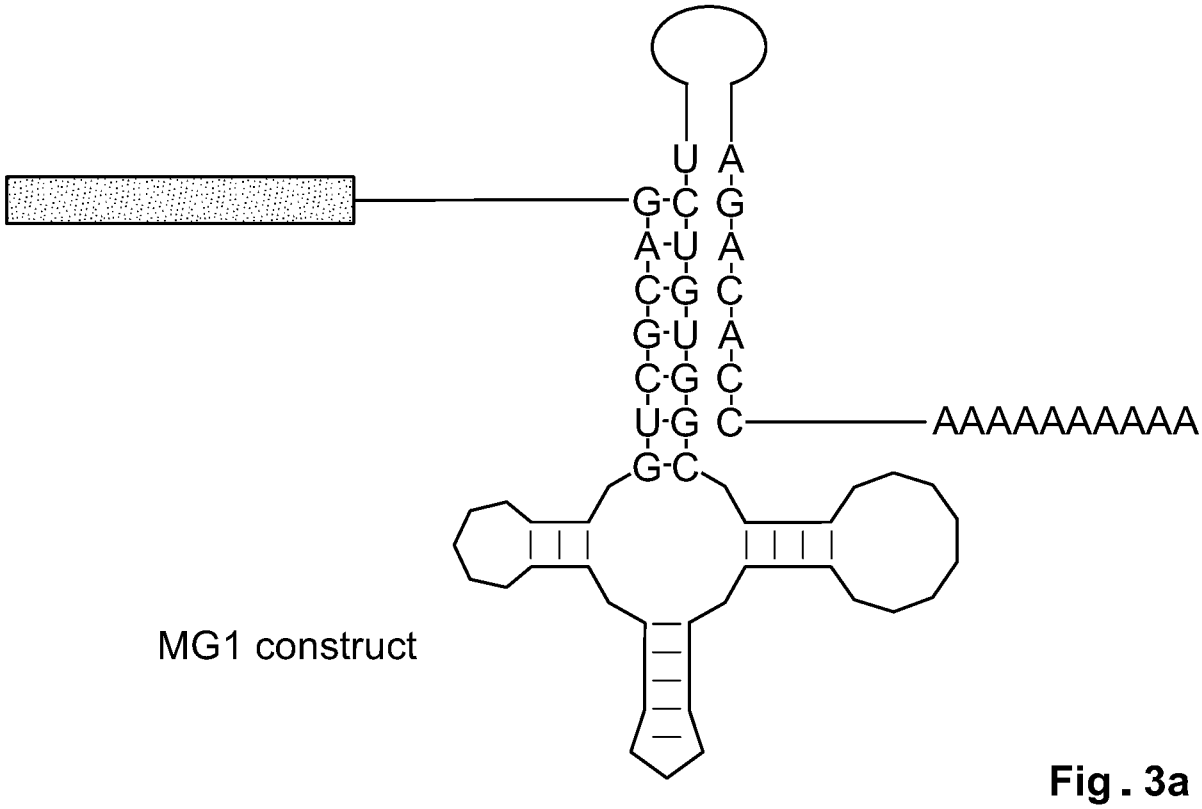
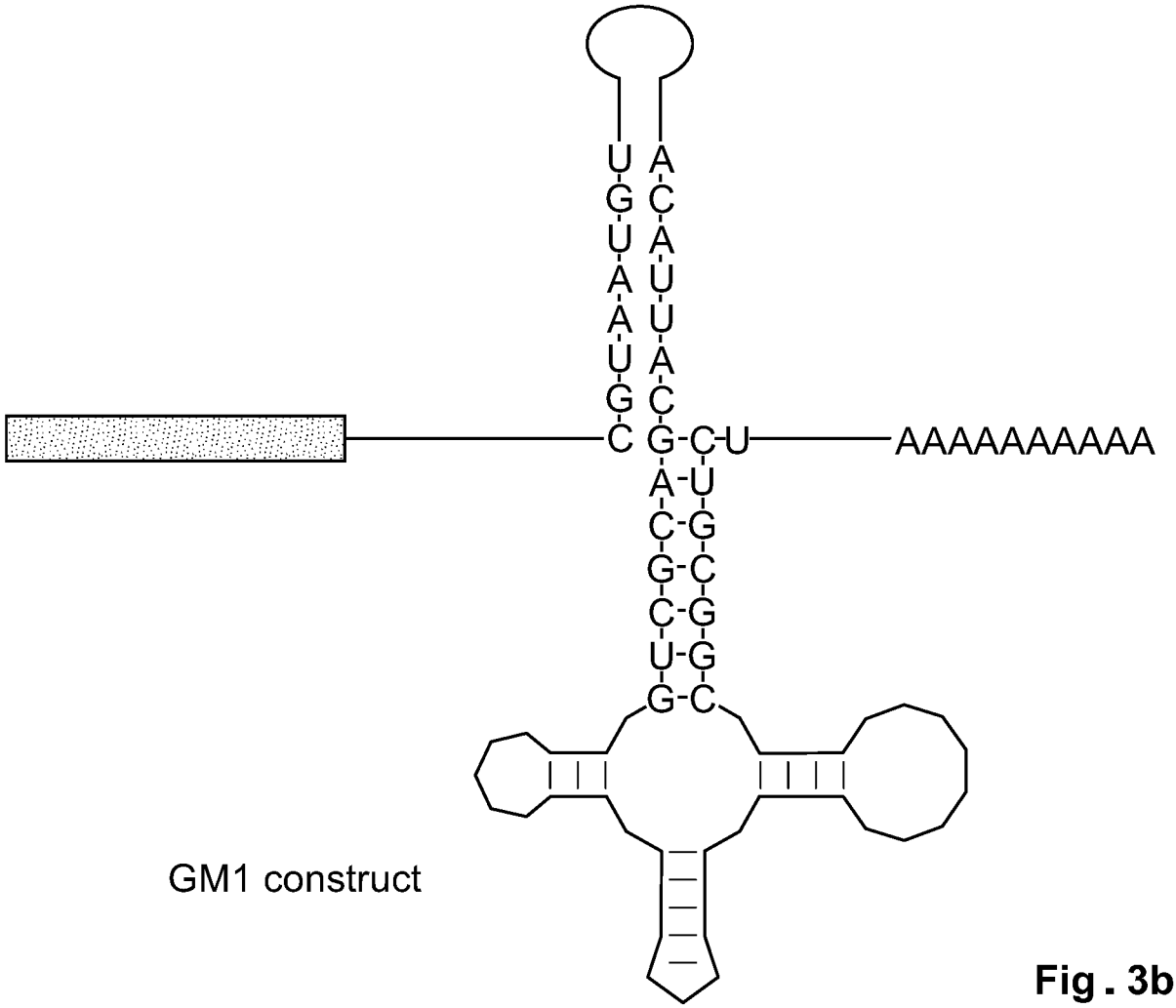

Luciferase activity (ALU)
6000000
5000000
4000000
3000000
2000000
1000000
0
Luci
Luci-masc
Luci-masc-mlp

Fig . 2c



MG1 construct

Fig . 3a



GM1 construct

Fig . 3b

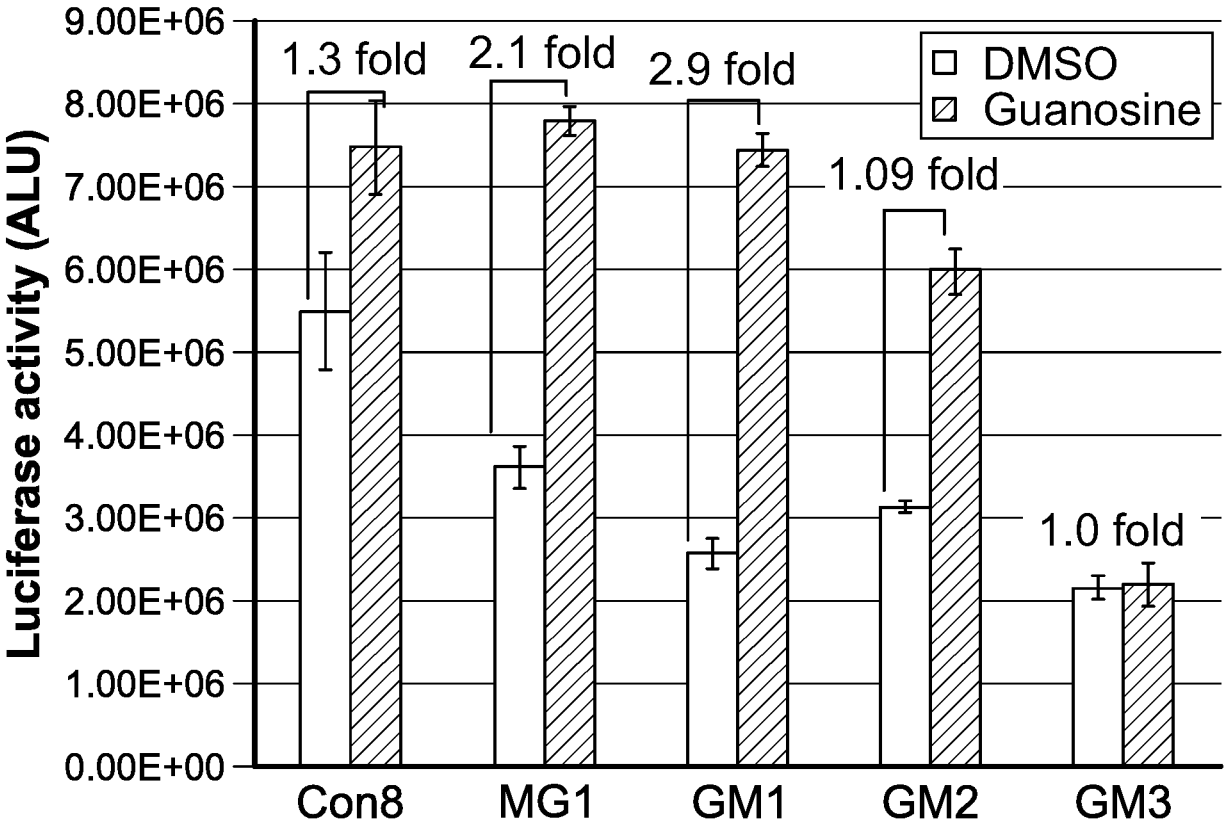

9.00E+06
8.00E+06
7.00E+06
6.00E+06
5.00E+06
4.00E+06
3.00E+06
2.00E+06
1.00E+06
0.00E+00
Luciferase activity (ALU)
1.3 fold
2.1 fold
2.9 fold
1.09 fold
1.0 fold
DMSO
Guanosine
Con8
MG1
GM1
GM2
GM3

Fig . 3c

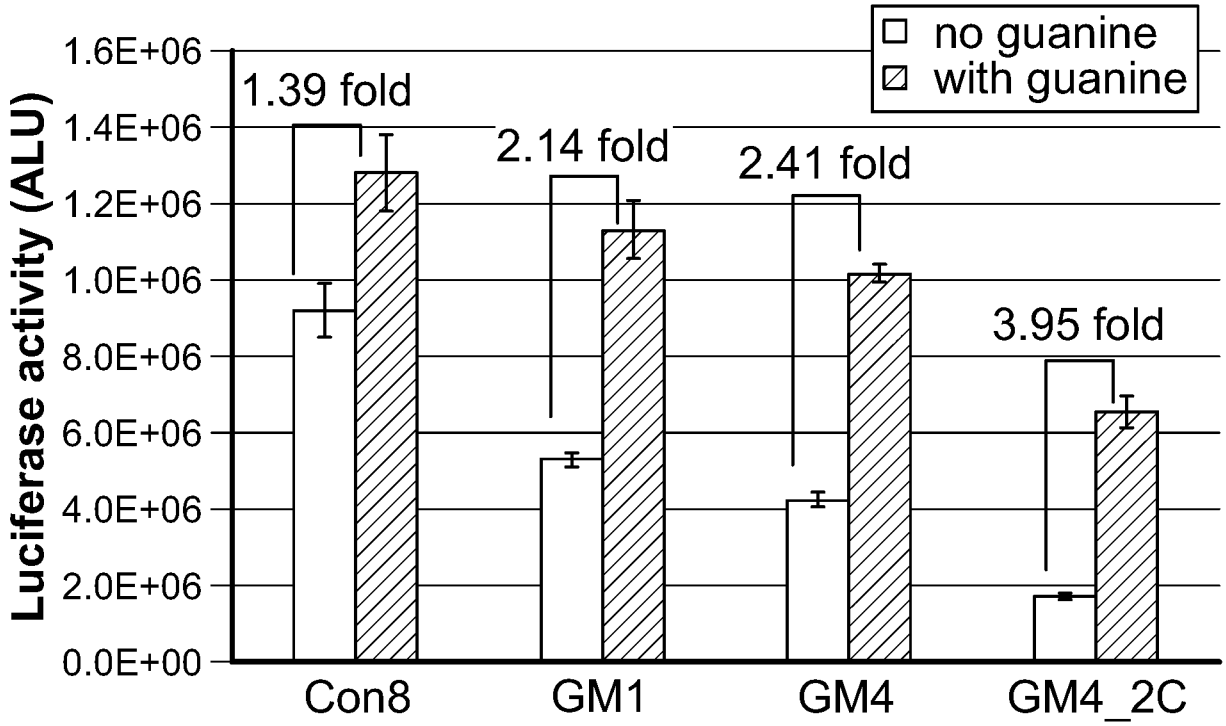

1.6E+06
1.4E+06
1.2E+06
1.0E+06
8.0E+06
6.0E+06
4.0E+06
2.0E+06
0.0E+00
Luciferase activity (ALU)
1.39 fold
2.14 fold
2.41 fold
3.95 fold
no guanine
with guanine
Con8
GM1
GM4
GM4_2C

Fig . 4a

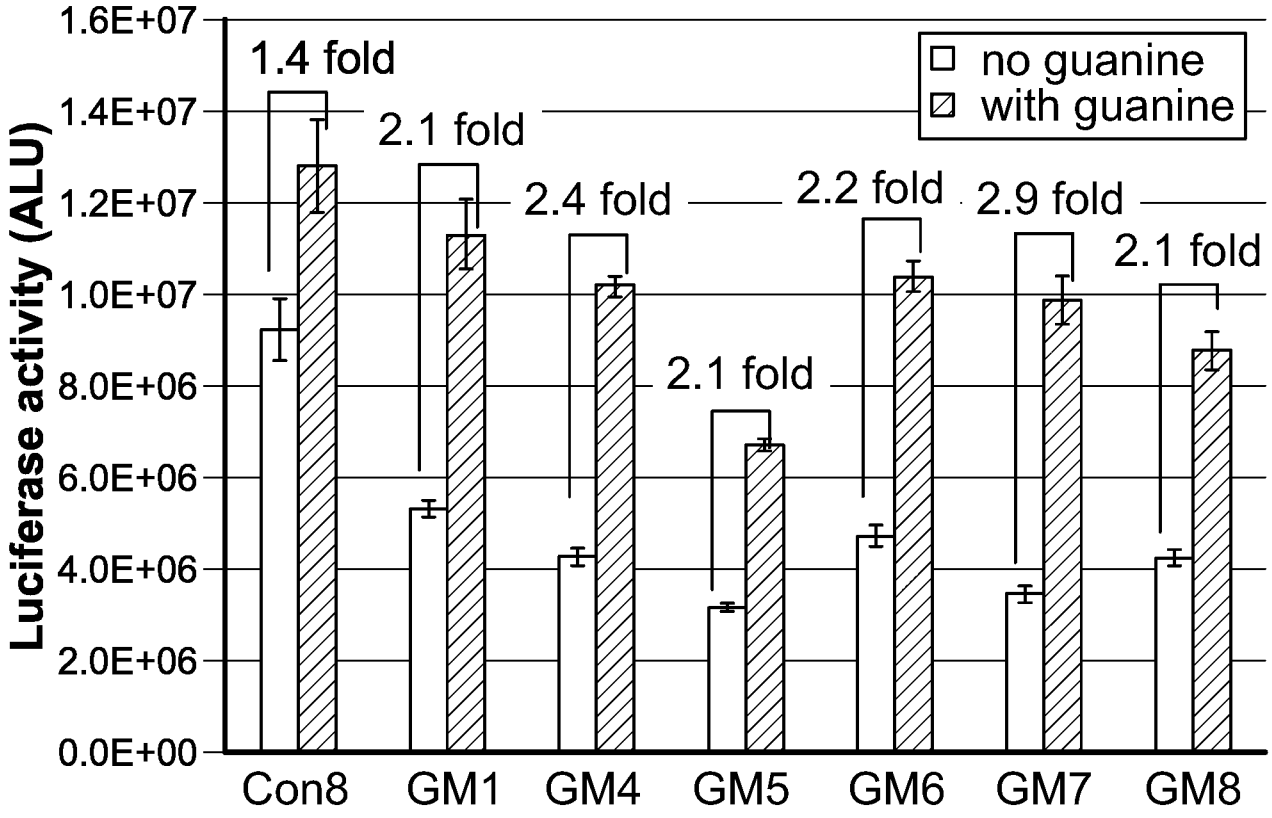

1.6E+07
1.4E+07
1.2E+07
1.0E+07
8.0E+06
6.0E+06
4.0E+06
2.0E+06
0.0E+00
Luciferase activity (ALU)
no guanine
with guanine
1.4 fold
2.1 fold
2.4 fold
2.1 fold
2.2 fold
2.9 fold
2.1 fold
Con8
GM1
GM4
GM5
GM6
GM7
GM8

Fig . 4b

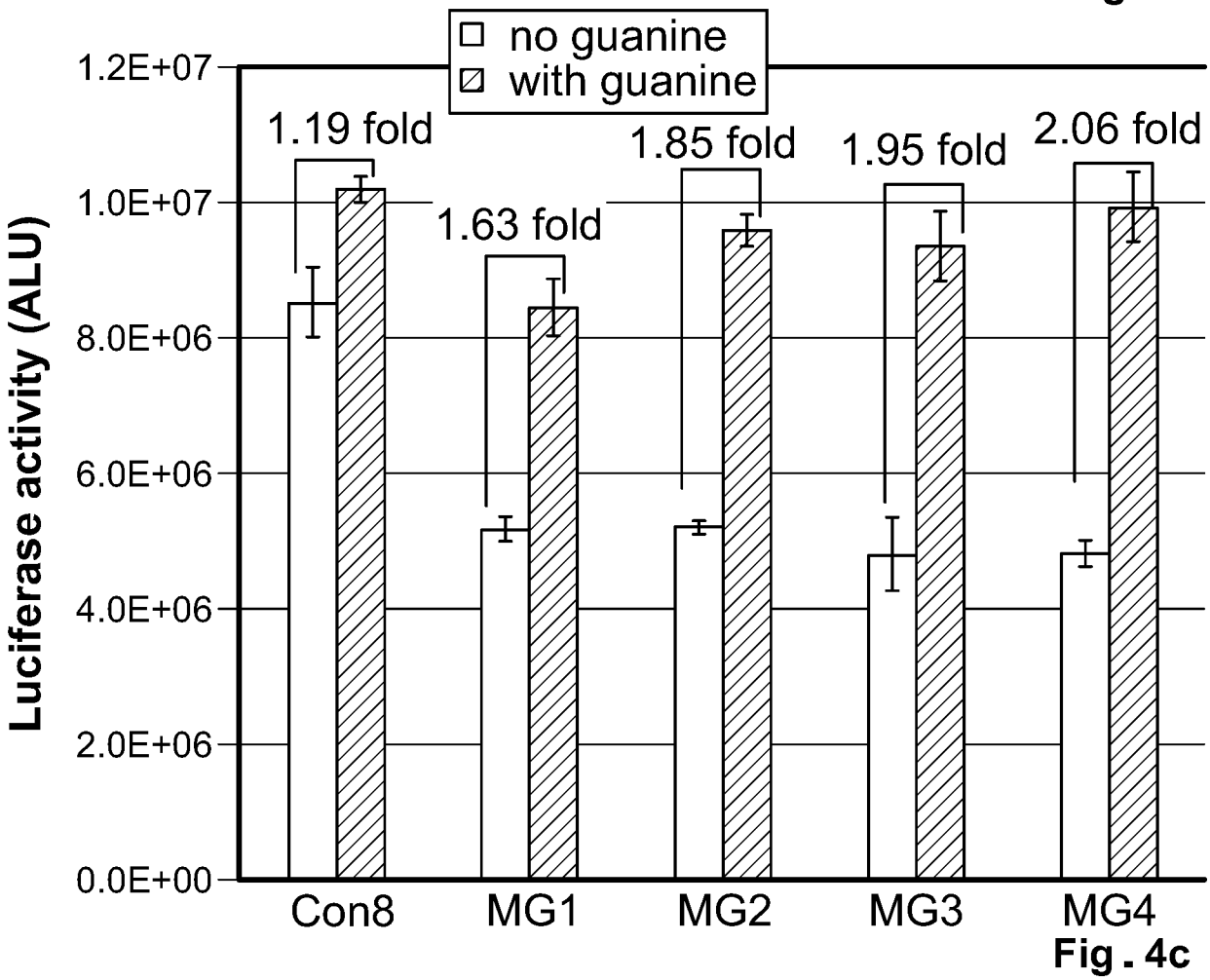

1.2E+07
1.0E+07
8.0E+06
6.0E+06
4.0E+06
2.0E+06
0.0E+00
Luciferase activity (ALU)
no guanine
with guanine
1.19 fold
1.63 fold
1.85 fold
1.95 fold
2.06 fold
Con8
MG1
MG2
MG3
MG4

Fig . 4c

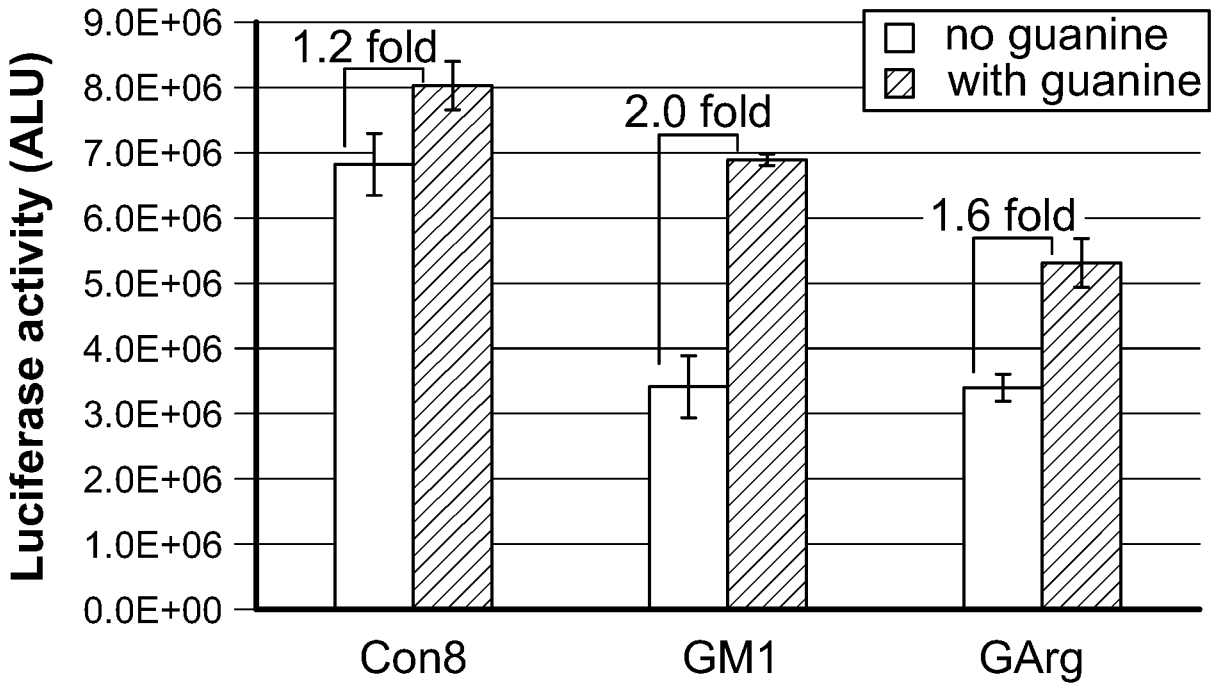

Luciferase activity (ALU)
9.0E+06
8.0E+06
7.0E+06
6.0E+06
5.0E+06
4.0E+06
3.0E+06
2.0E+06
1.0E+06
0.0E+00
1.2 fold
2.0 fold
1.6 fold
no guanine
with guanine
Con8
GM1
GArg

Fig. 5

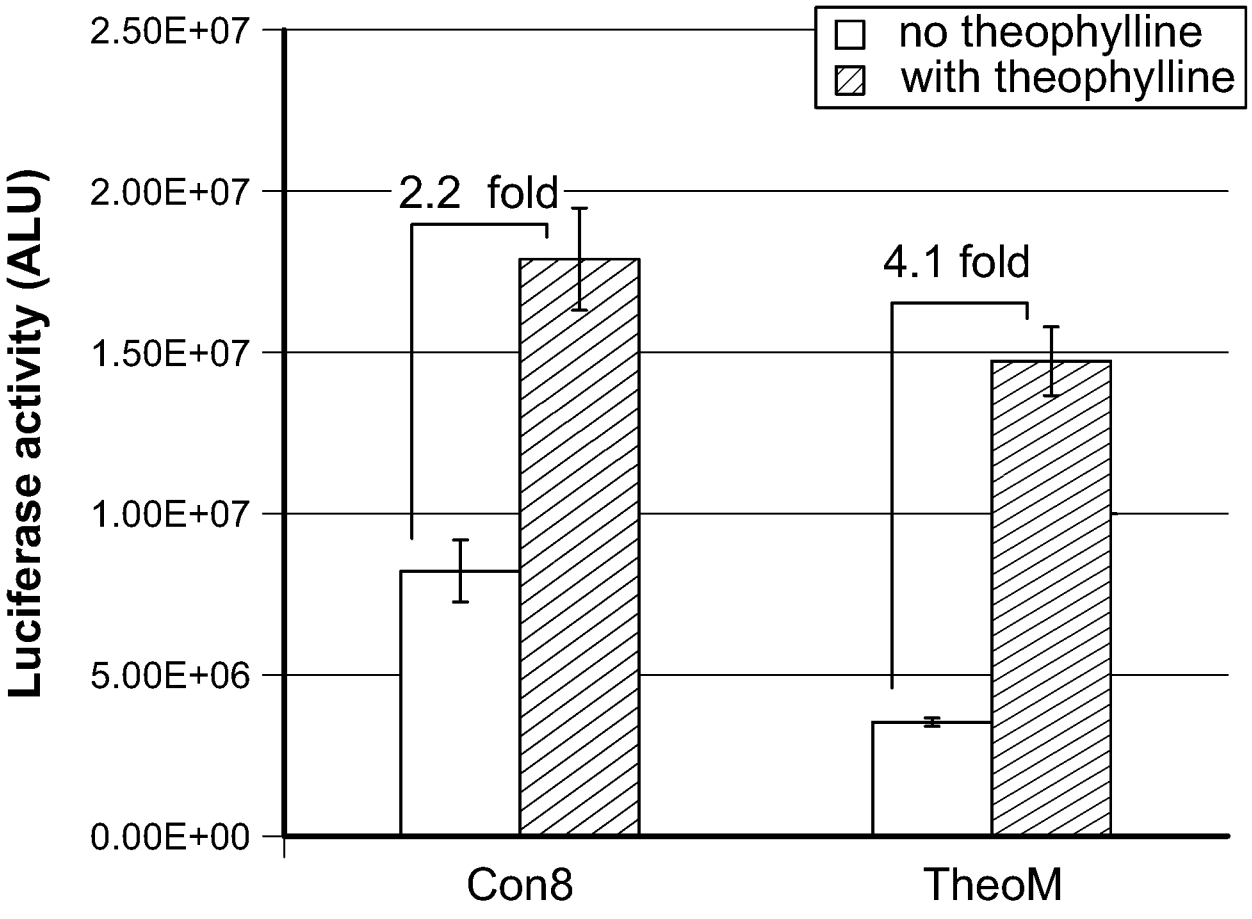

Luciferase activity (ALU)
2.50E+07
2.00E+07
1.50E+07
1.00E+07
5.00E+06
0.00E+00
2.2 fold
4.1 fold
no theophylline
with theophylline
Con8
TheoM

Fig. 6a

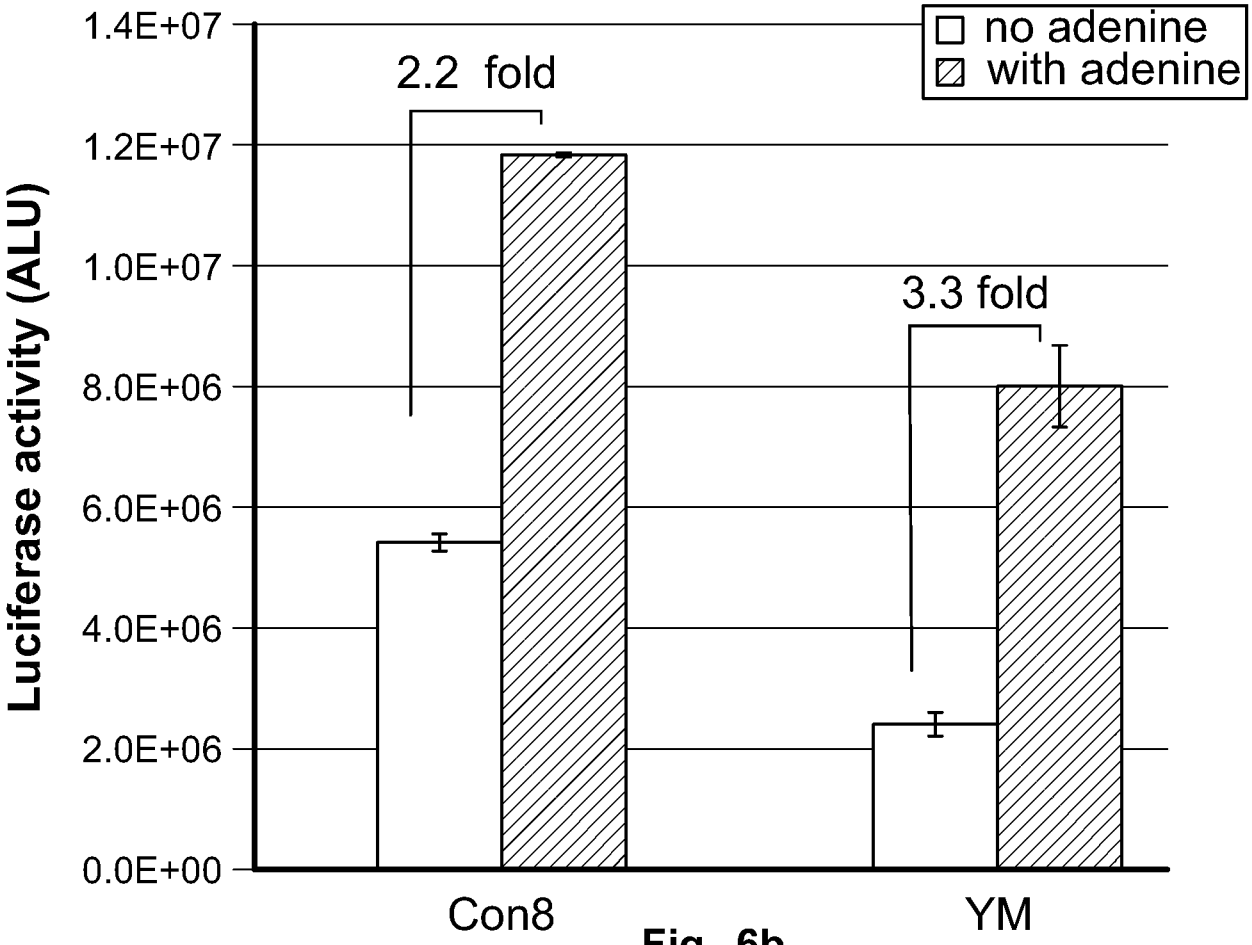

1.4E+07
1.2E+07
1.0E+07
8.0E+06
6.0E+06
4.0E+06
2.0E+06
0.0E+00
Luciferase activity (ALU)
no adenine
with adenine
2.2 fold
3.3 fold
Con8
YM

Fig . 6b

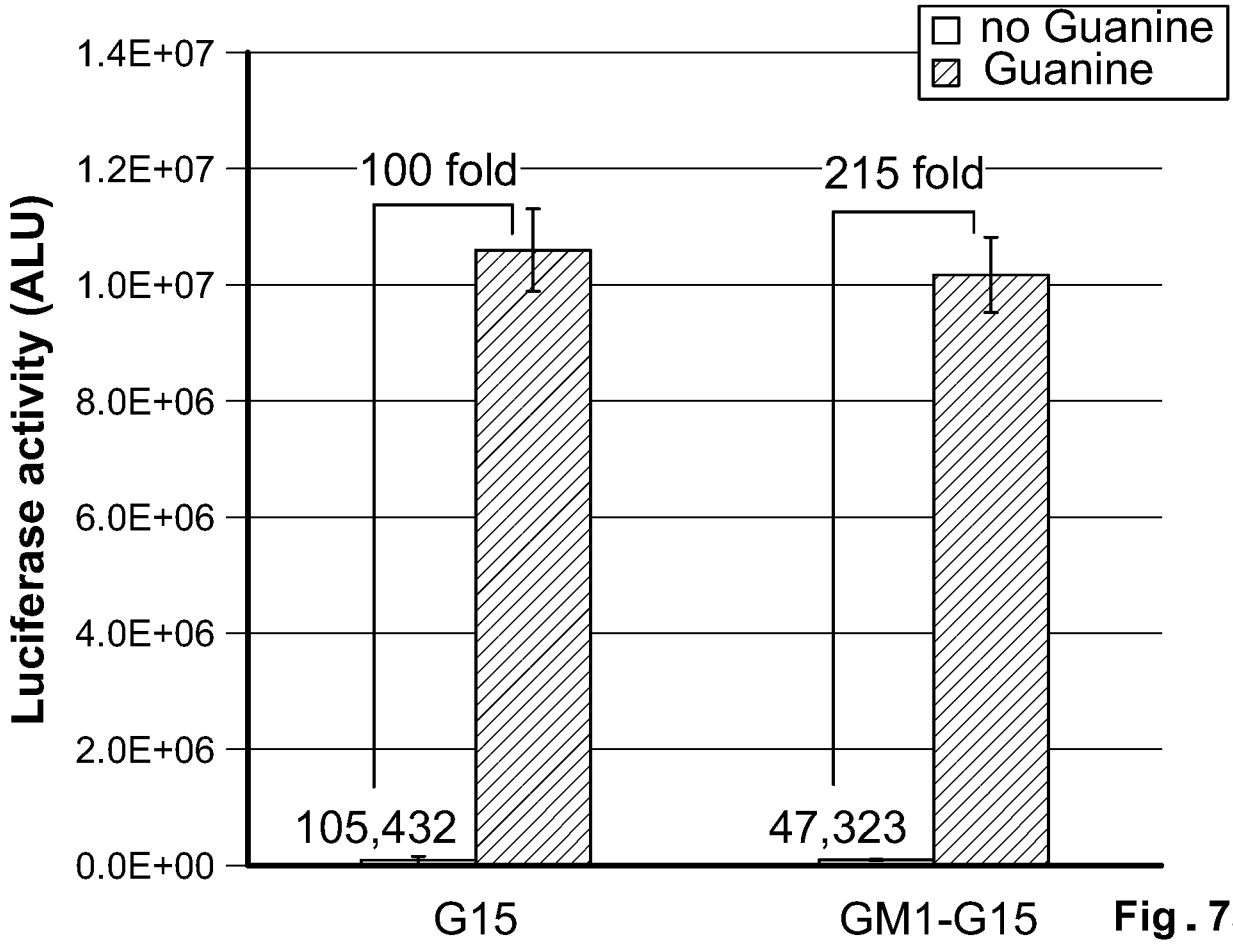

1.4E+07
1.2E+07
1.0E+07
8.0E+06
6.0E+06
4.0E+06
2.0E+06
0.0E+00
Luciferase activity (ALU)
no Guanine
Guanine
100 fold
215 fold
105,432
47,323
G15
GM1-G15

Fig . 7a

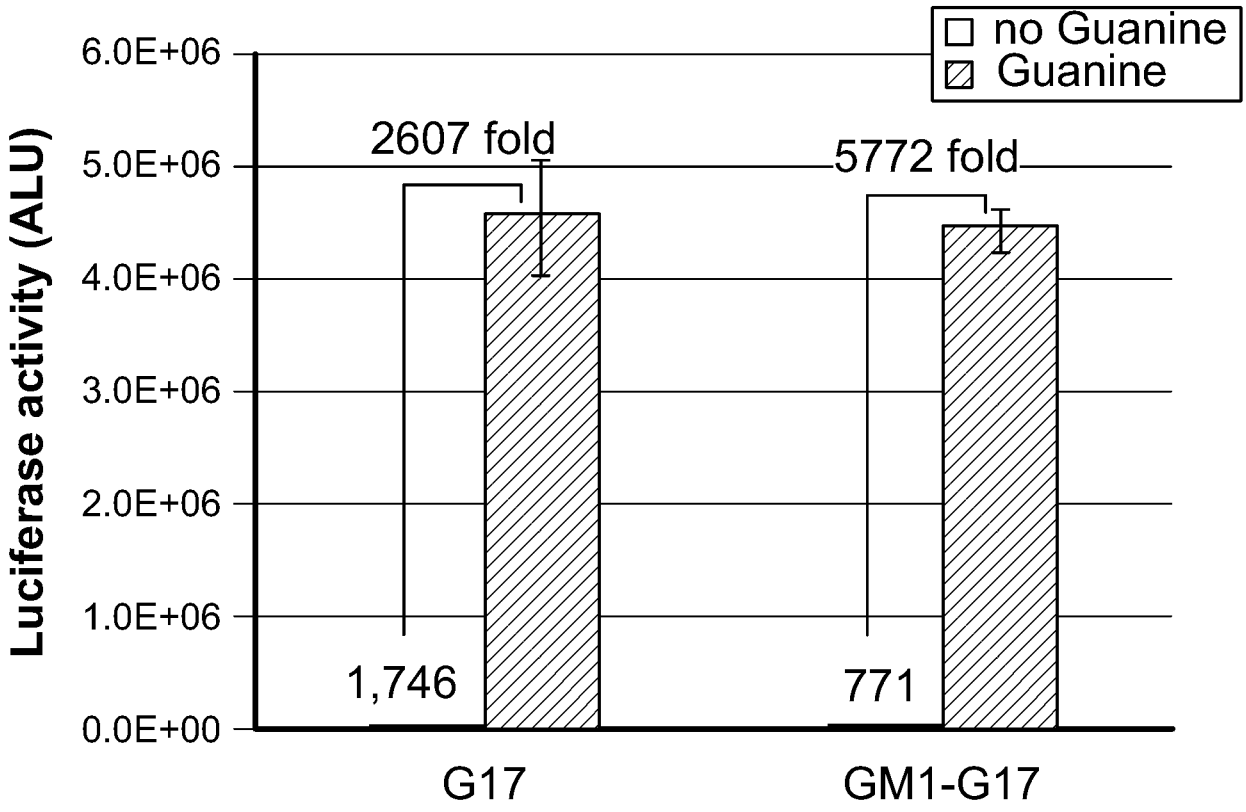

no Guanine
Guanine
Luciferase activity (ALU)
6.0E+06
5.0E+06
4.0E+06
3.0E+06
2.0E+06
1.0E+06
0.0E+00
2607 fold
5772 fold
1,746
771
G17
GM1-G17

Fig. 7b

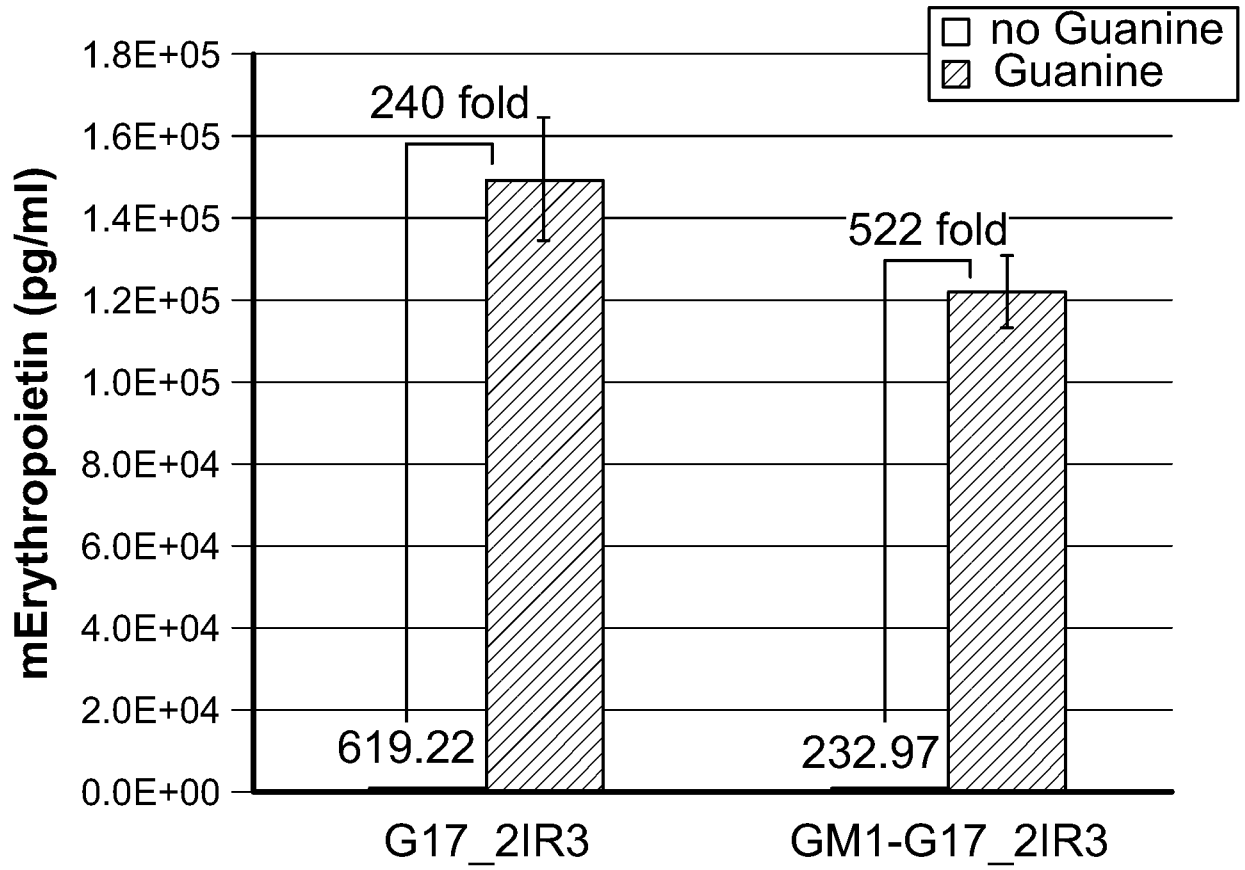

no Guanine
Guanine
mErythropoietin (pg/ml)
1.8E+05
1.6E+05
1.4E+05
1.2E+05
1.0E+05
8.0E+04
6.0E+04
4.0E+04
2.0E+04
0.0E+00
240 fold
522 fold
619.22
232.97
G17_2IR3
GM1-G17_2IR3

Fig. 7c

MG1 (SEQ ID NO: 1):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagcggccaattcggacaaaaacgagacgctggtggctggcactcctggtttccaggacgggggttcaagtccctgcggtgtcta
taatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactagacaccatctagagtcgacctgcaggcatgcaa
gcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

GM1 (SEQ ID NO: 2):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagcggccgtaatgtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactacattacgacgctggt
ggctggcactcctggtttccaggacgggggttcaagtccctgcggtgtcattgcttggatcggccgcgactctagagtcgacctgcagg
catgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

GM2 (SEQ ID NO: 3):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagcggccccgatcatataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactatggtcgacgctggt
ggctggcactcctggtttccaggacgggggttcaagtccctgcggtgtcattgcttggatcggccgcgactctagagtcgacctgcagg
catgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

GM3 (SEQ ID NO: 4):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagcggccggacaaaataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgacttttgtccaacgagcgac
gctggtggctggcactcctggtttccaggacgggggttcaagtccctgcggtgtcattgcttggatcggccgcgactctagagtcgacct
gcaggcatgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

GM4 (SEQ ID NO: 5):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagaagacgtaatgtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactacattacgacgctggt
ggctggcactcctggtttccaggacgggggttcaagtccctgcggtgtcattgcttggatcggccgcgactctagagtcgacctgcagg
catgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

Fig. 8

GM4_2C (SEQ ID NO: 6):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagaagacgtaatgtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactacattacgacgctggt
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catgcaagcttcagaagtaaagaagacgtaatgtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgact
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GM5 (SEQ ID NO: 7):

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TGTACAAGTAAAGaagagctaatgtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgacta
cattagcgacgctggtggctggcactcctggtttccaggacgggattcaagtccctgcggtgtcttgcttggatcggccgcgactcta
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GM6 (SEQ ID NO: 8):

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GM7 (SEQ ID NO: 9):

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GM8 (SEQ ID NO: 10):

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ctggtggctggcactcctggtttccaggacgggattcaagtccctgcggtgtcttgcttggatcggccgcgactctagagtcgacctg
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Fig. 8 (Cont.)

MG2 (SEQ ID NO: 11):

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agcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

MG3 (SEQ ID NO: 12):

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tataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactacagacaatctagagtcgacctgcaggcatgca
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MG4 (SEQ ID NO: 13):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatcCAAGACGAGC
TGTACAAGTAAAGCGGCCaattCGGACAAAAACGAgacgctggtggctggcactcctggtttccagga
cgggattcaagtccctgcggtgtctagtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactactaga
cttctagagtcgacctgcaggcatgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

GArg (SEQ ID NO: 14):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaAgacgagctgtaca
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YM (SEQ ID NO: 15):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatcCAAGACGAGC
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Fig. 8 (Cont.)

TheoM (SEQ ID NO: 16):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatcCAAGACGAGC
TGTACAAGTAAAGCGGCctaatgtgataccagccgaaaggcccttggcagcacattagacgctggtggctggcactc
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agctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

Fig. 8 (Cont.)