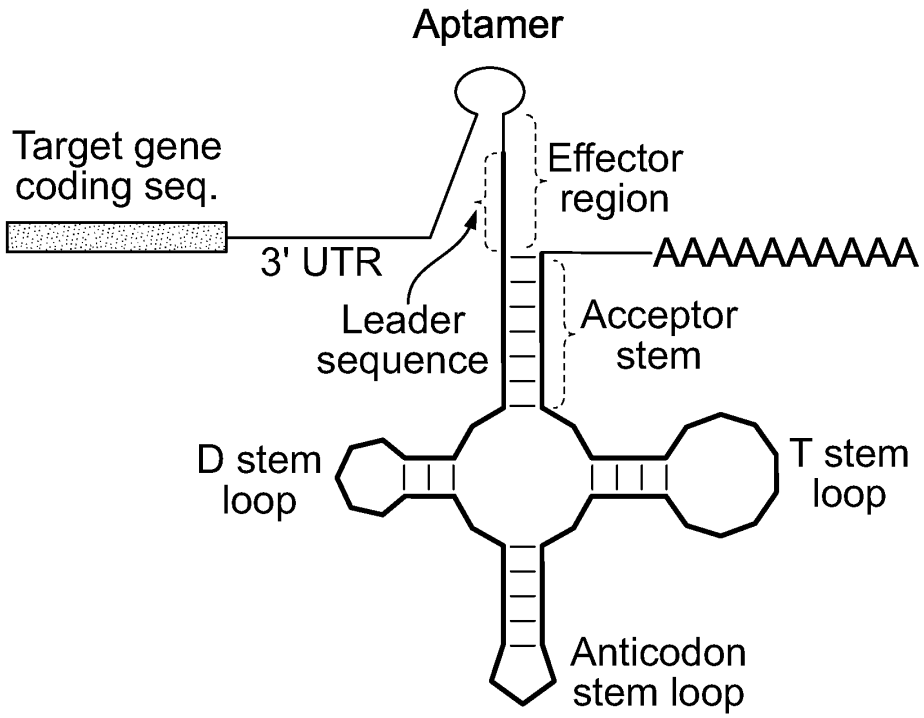

Aptamer
Target gene coding seq.
3' UTR
Leader sequence
Effector region
AAAAAAAAAA
Acceptor stem
D stem loop
T stem loop
Anticodon stem loop

Fig. 1a

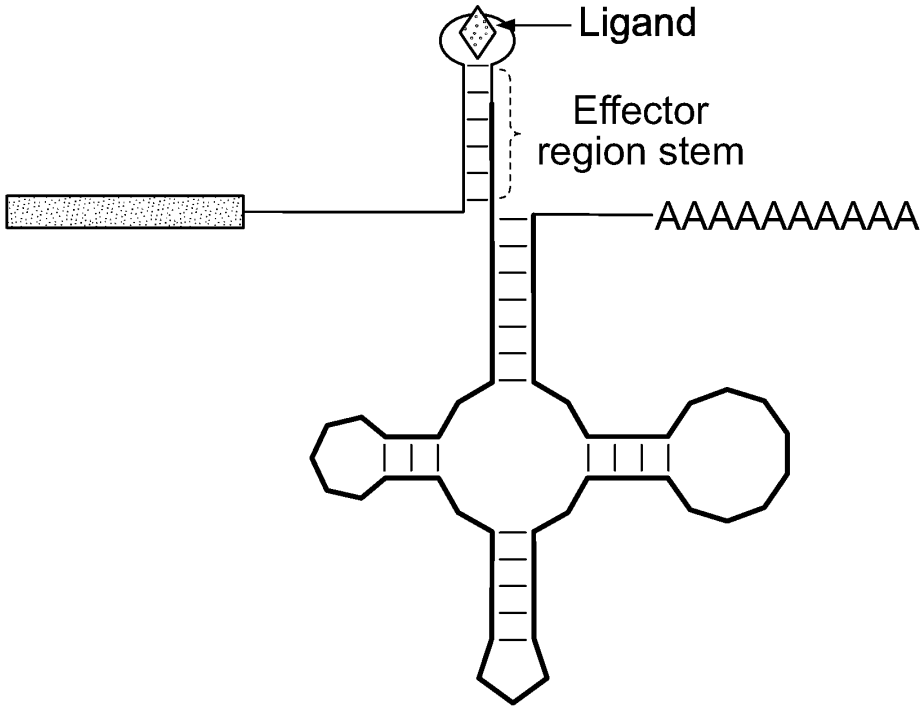

Ligand
Effector region stem
AAAAAAAAAA

Fig. 1b

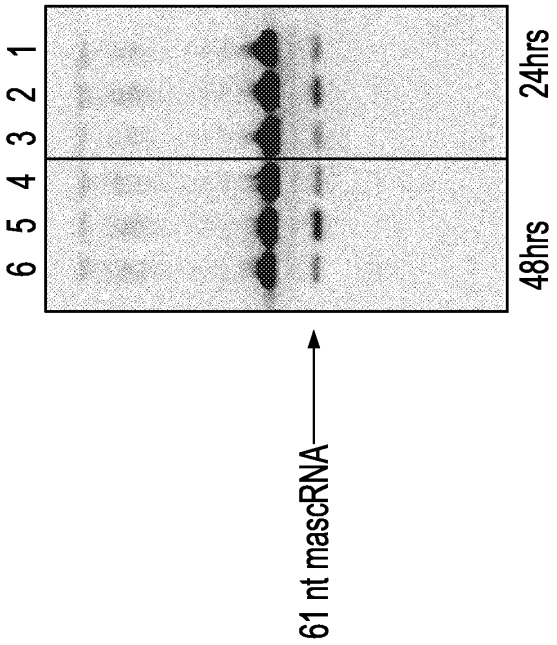

6 5 4 3 2 1
1. GFP
2. GFP-masc
3. GFP-mascRev
4. GFP
5. GFP-masc
6. GFP-mascRev
Probe: 5' DIG-all-masc-probe
61 nt mascRNA
48hrs
24hrs

Fig . 2a

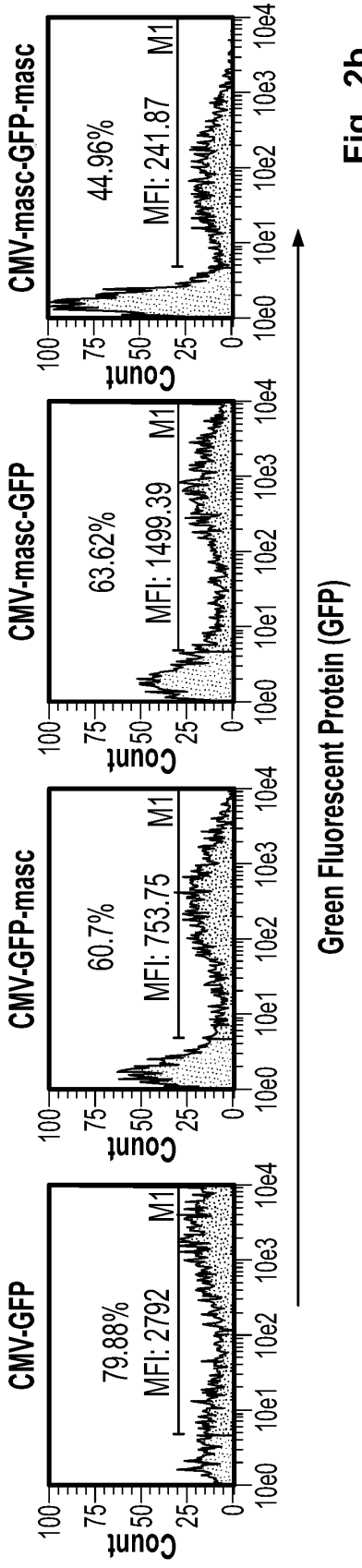
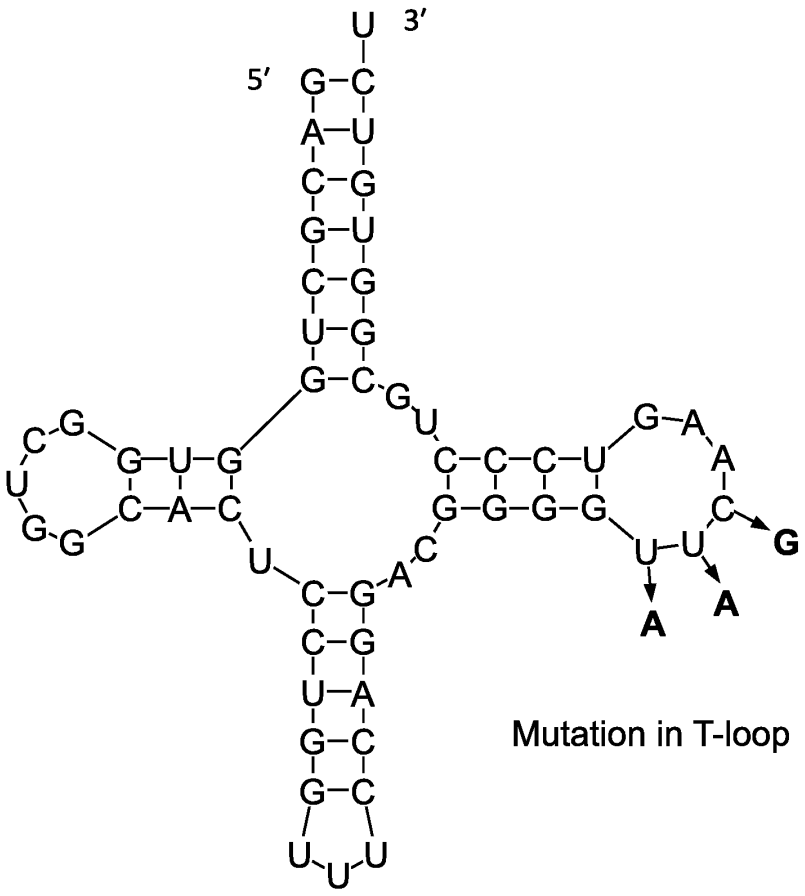

CMV-GFP
79.88%
MFI: 2792
M1
CMV-GFP-masc
60.7%
MFI: 753.75
M1
CMV-masc-GFP
63.62%
MFI: 1499.39
M1
CMV-masc-GFP-masc
44.96%
MFI: 241.87
M1
Count
100
75
50
25
0
10e0
10e1
10e2
10e3
10e4
Green Fluorescent Protein (GFP)

Fig . 2b


5′
3′
Mutation in T-loop

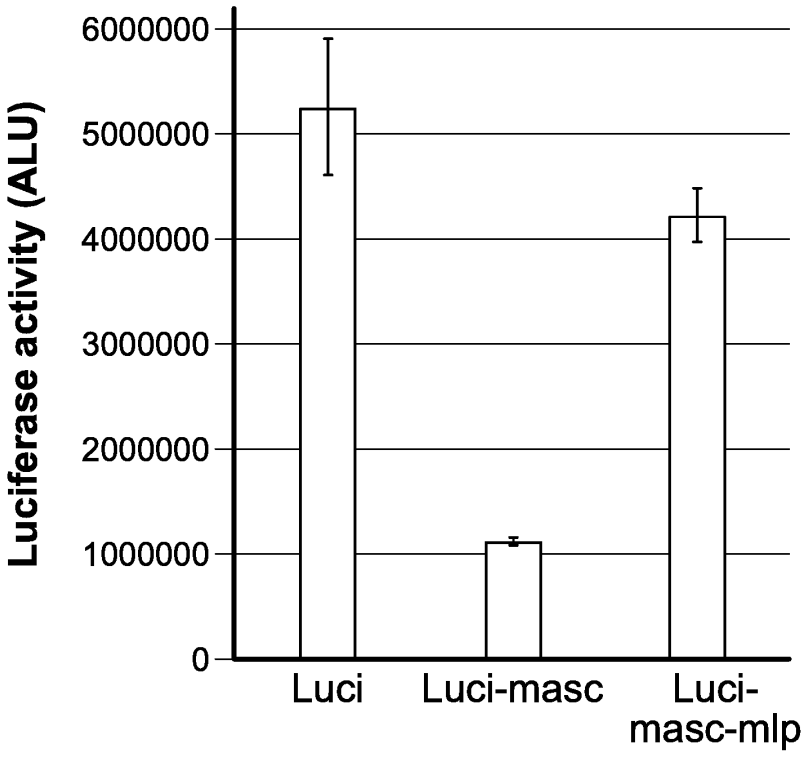

Luciferase activity (ALU)
6000000
5000000
4000000
3000000
2000000
1000000
0
Luci
Luci-masc
Luci-masc-mlp

Fig . 2c

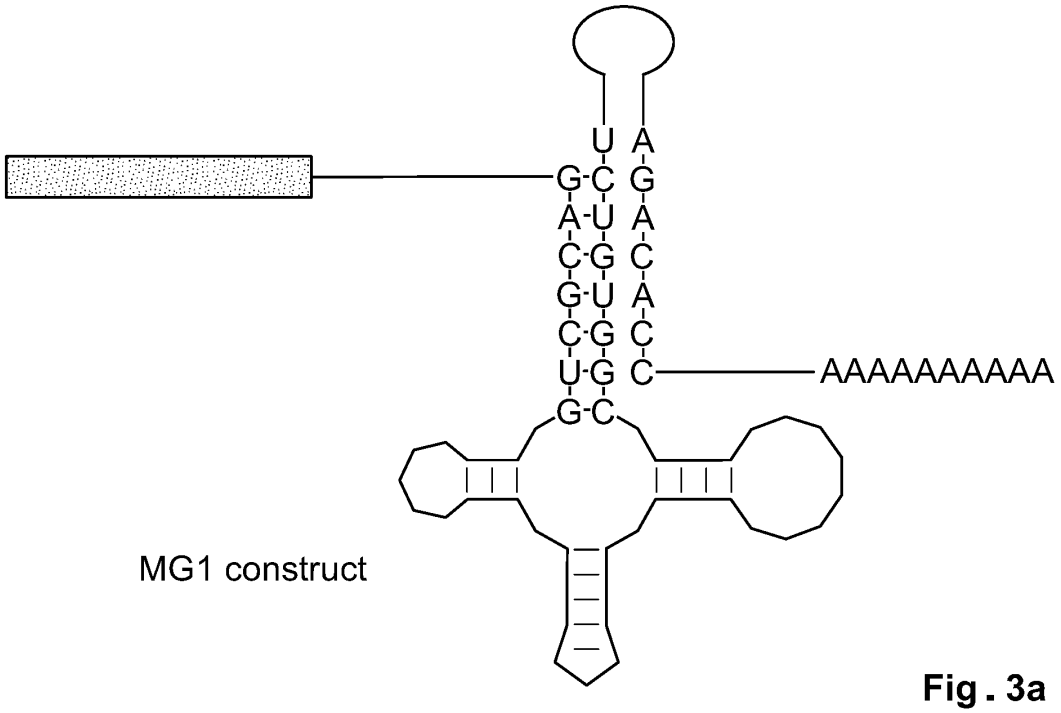


Fig. 3a

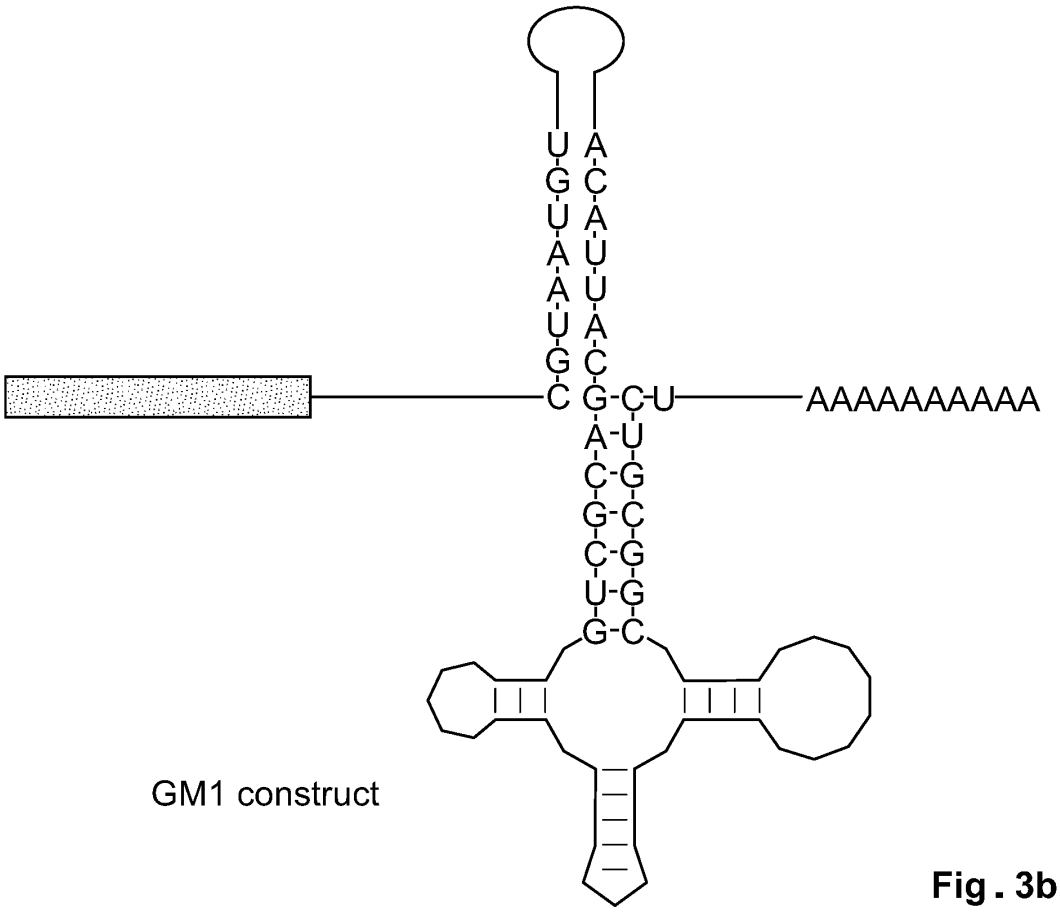


Fig. 3b

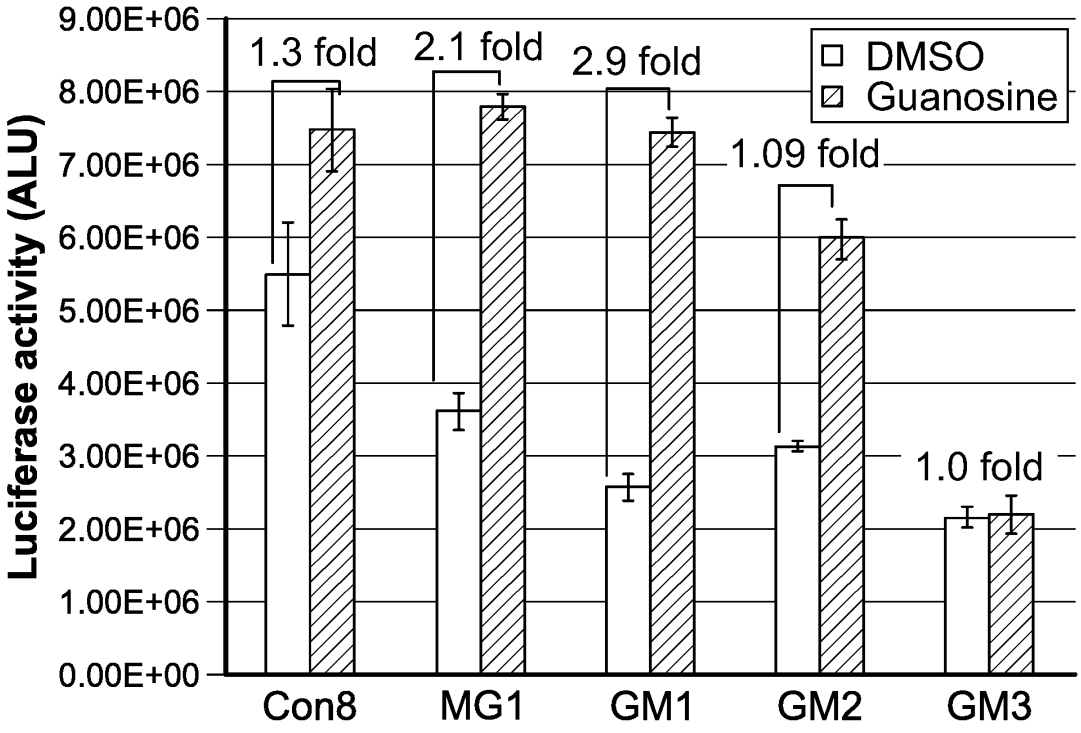

9.00E+06
8.00E+06
7.00E+06
6.00E+06
5.00E+06
4.00E+06
3.00E+06
2.00E+06
1.00E+06
0.00E+00
Luciferase activity (ALU)
1.3 fold
2.1 fold
2.9 fold
1.09 fold
1.0 fold
DMSO
Guanosine
Con8
MG1
GM1
GM2
GM3

Fig . 3c

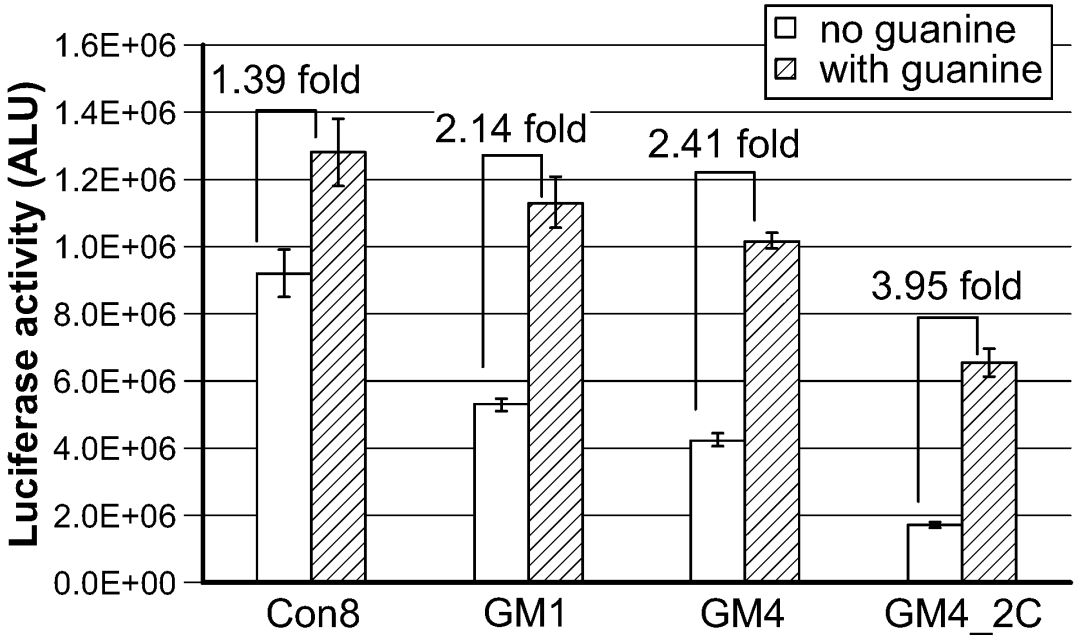

1.6E+06
1.4E+06
1.2E+06
1.0E+06
8.0E+06
6.0E+06
4.0E+06
2.0E+06
0.0E+00
Luciferase activity (ALU)
1.39 fold
2.14 fold
2.41 fold
3.95 fold
no guanine
with guanine
Con8
GM1
GM4
GM4_2C

Fig . 4a

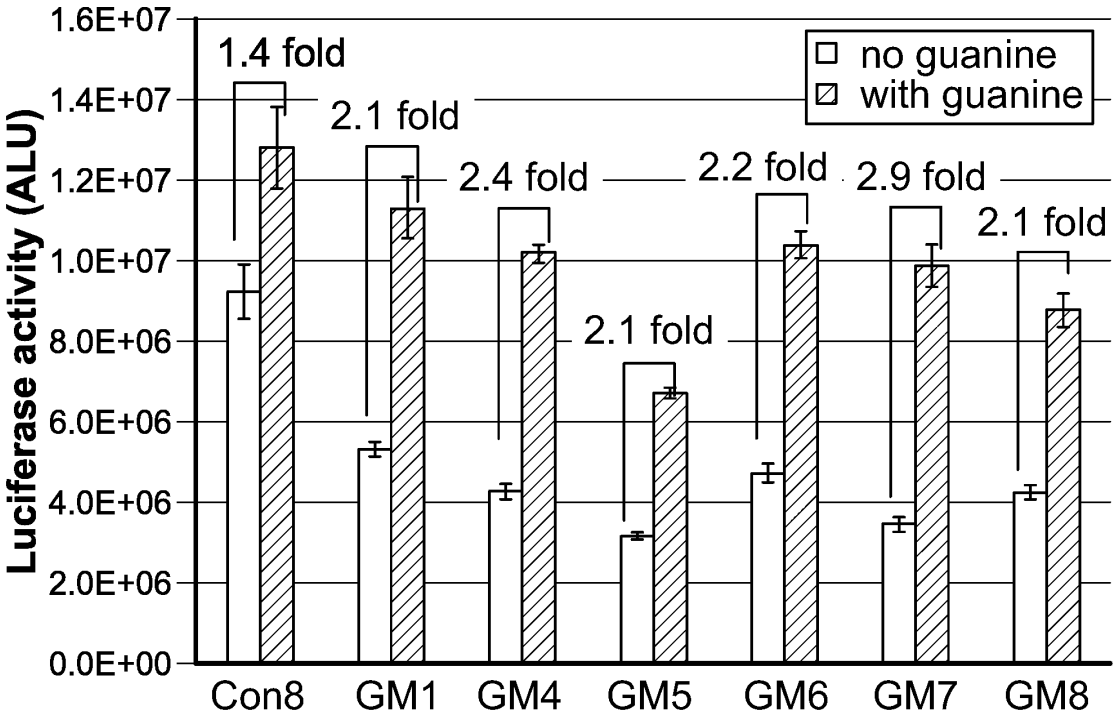

1.6E+07
1.4E+07
1.2E+07
1.0E+07
8.0E+06
6.0E+06
4.0E+06
2.0E+06
0.0E+00
Luciferase activity (ALU)
no guanine
with guanine
1.4 fold
2.1 fold
2.4 fold
2.1 fold
2.2 fold
2.9 fold
2.1 fold
Con8
GM1
GM4
GM5
GM6
GM7
GM8

Fig. 4b

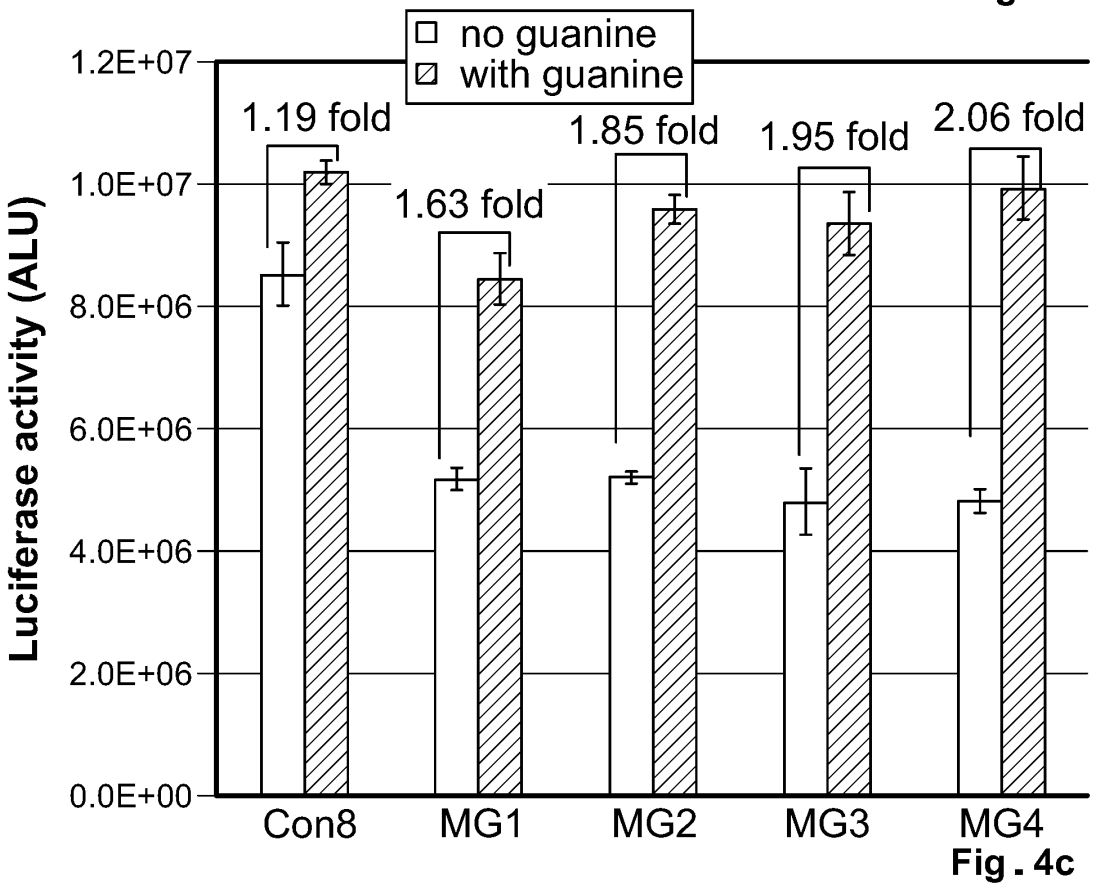

1.2E+07
1.0E+07
8.0E+06
6.0E+06
4.0E+06
2.0E+06
0.0E+00
Luciferase activity (ALU)
no guanine
with guanine
1.19 fold
1.63 fold
1.85 fold
1.95 fold
2.06 fold
Con8
MG1
MG2
MG3
MG4

Fig. 4c

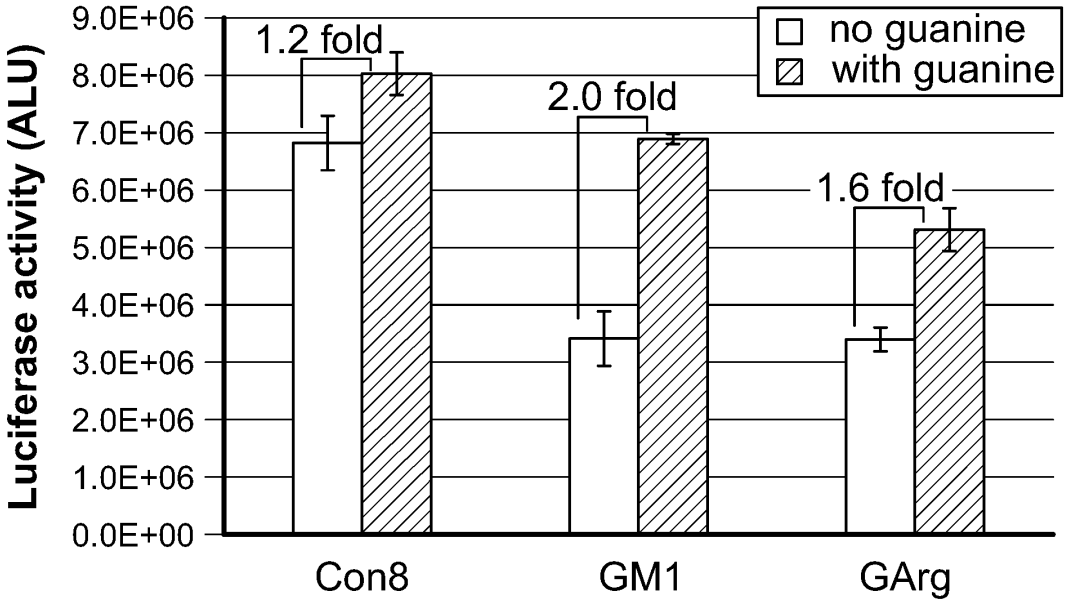

Luciferase activity (ALU)
9.0E+06
8.0E+06
7.0E+06
6.0E+06
5.0E+06
4.0E+06
3.0E+06
2.0E+06
1.0E+06
0.0E+00
1.2 fold
2.0 fold
1.6 fold
no guanine
with guanine
Con8
GM1
GArg

Fig. 5

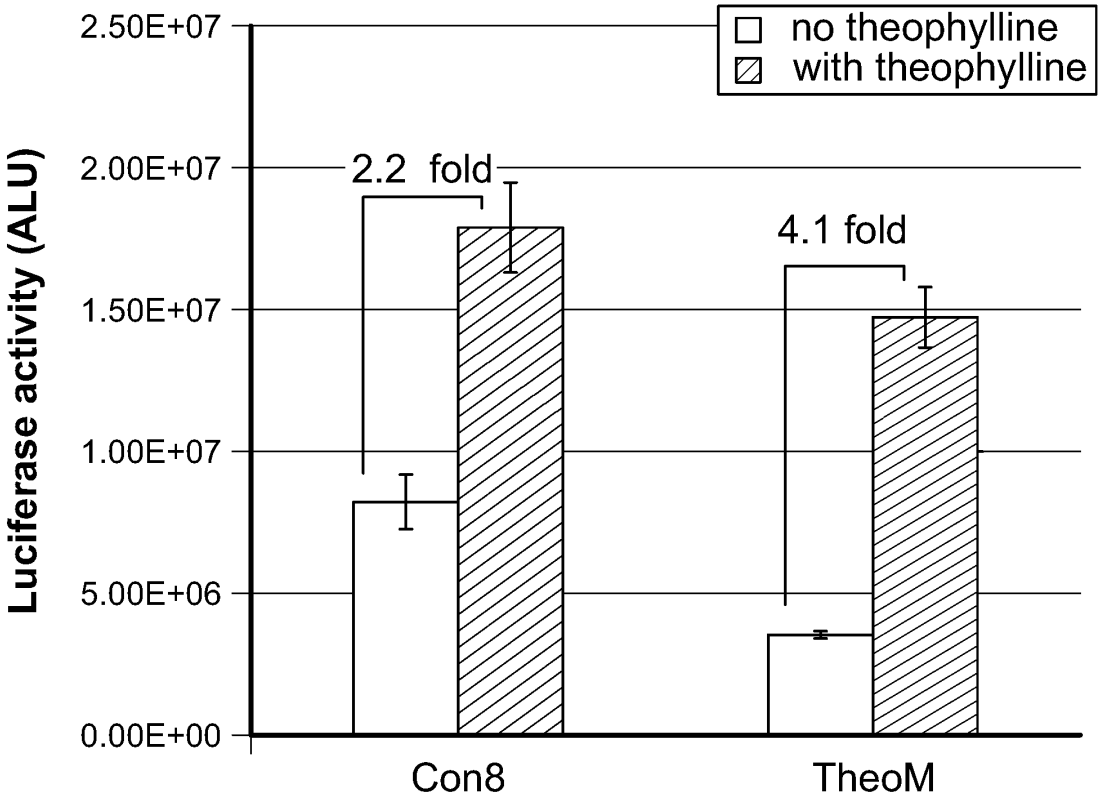

Luciferase activity (ALU)
2.50E+07
2.00E+07
1.50E+07
1.00E+07
5.00E+06
0.00E+00
2.2 fold
4.1 fold
no theophylline
with theophylline
Con8
TheoM

Fig. 6a

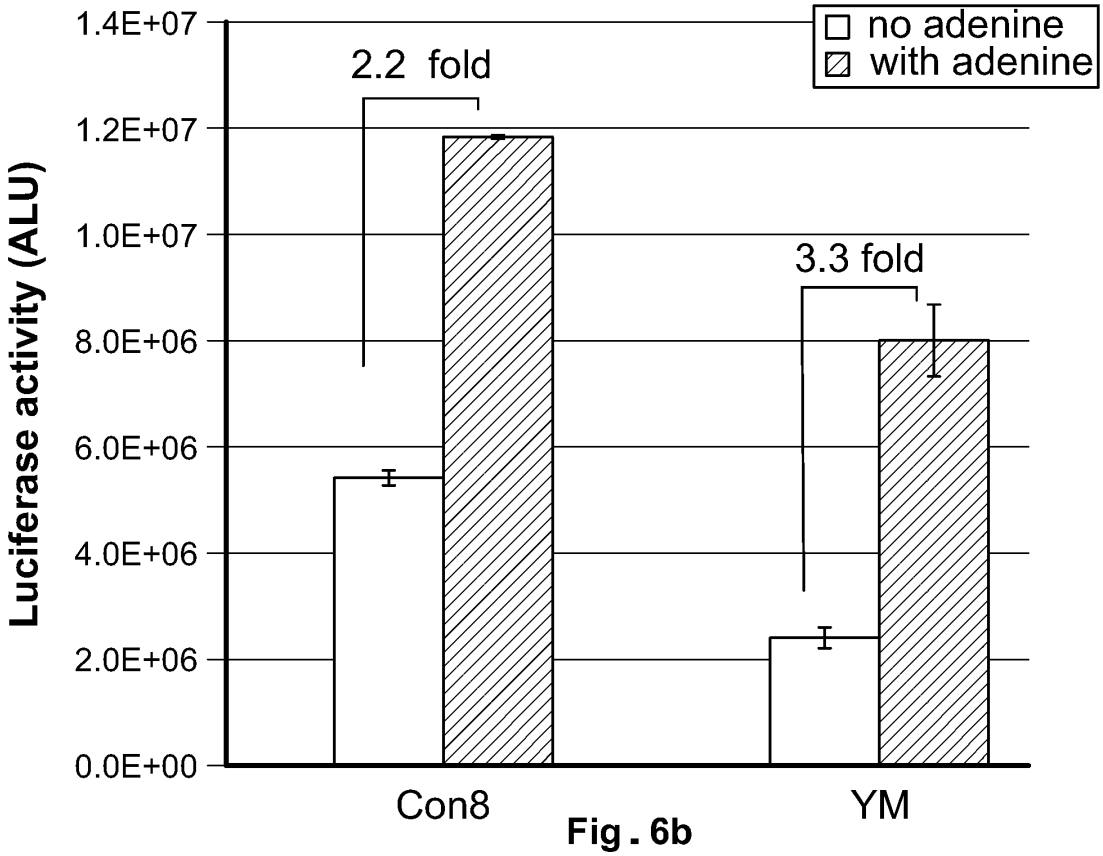

no adenine
with adenine
2.2 fold
3.3 fold
Luciferase activity (ALU)
1.4E+07
1.2E+07
1.0E+07
8.0E+06
6.0E+06
4.0E+06
2.0E+06
0.0E+00
Con8
YM

Fig . 6b

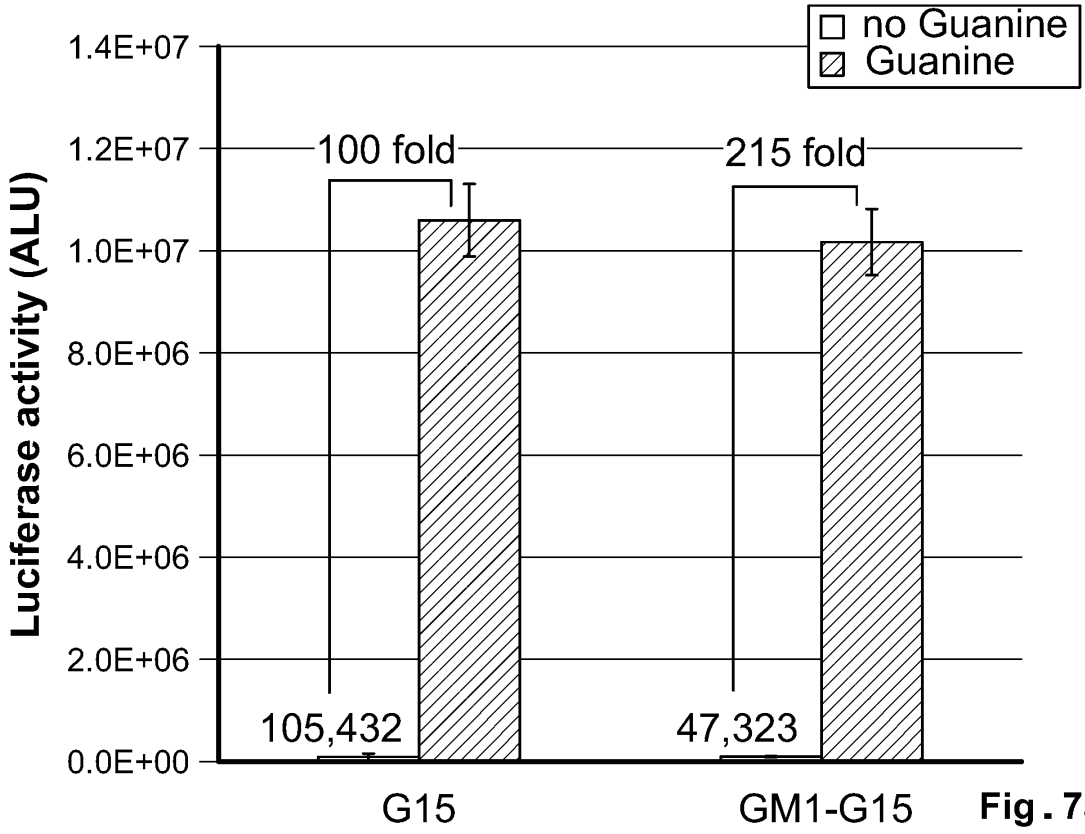

no Guanine
Guanine
100 fold
215 fold
Luciferase activity (ALU)
1.4E+07
1.2E+07
1.0E+07
8.0E+06
6.0E+06
4.0E+06
2.0E+06
0.0E+00
105,432
47,323
G15
GM1-G15

Fig . 7a

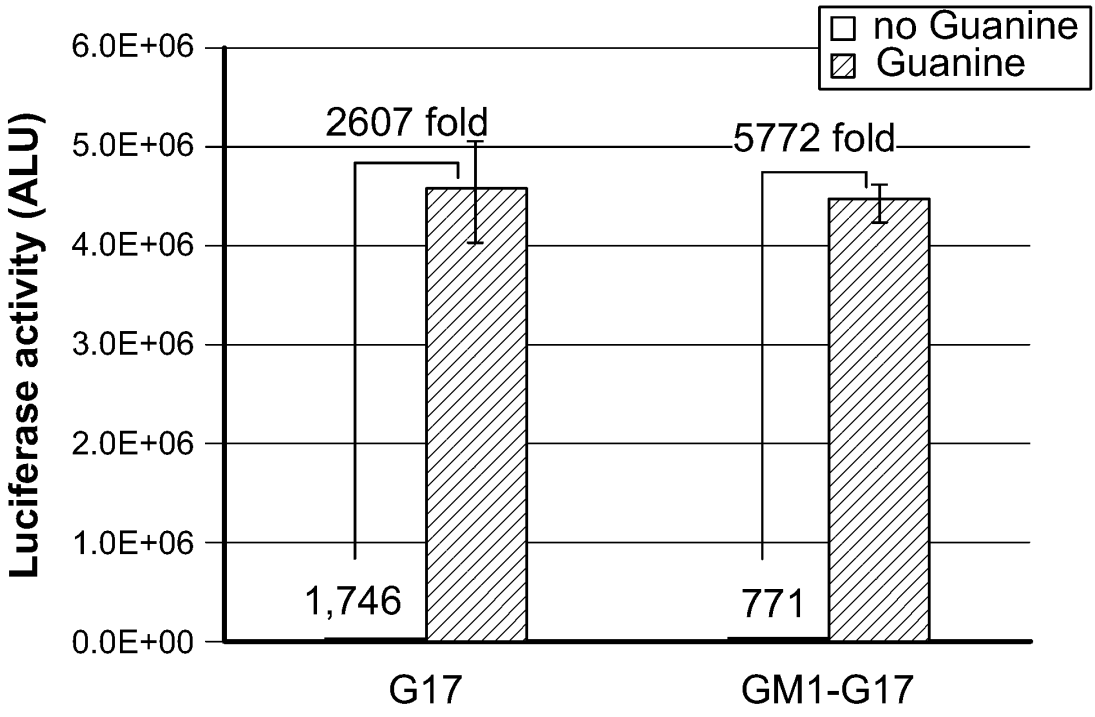

no Guanine
Guanine
Luciferase activity (ALU)
6.0E+06
5.0E+06
4.0E+06
3.0E+06
2.0E+06
1.0E+06
0.0E+00
2607 fold
5772 fold
1,746
771
G17
GM1-G17

Fig. 7b

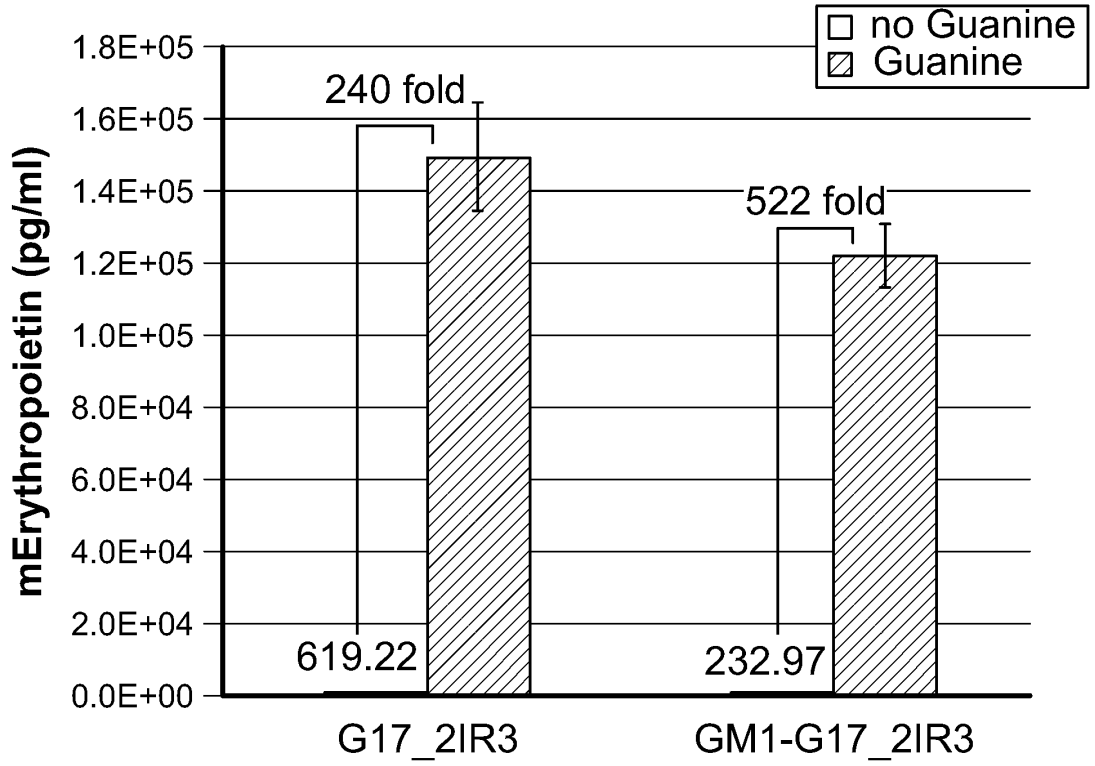

no Guanine
Guanine
mErythropoietin (pg/ml)
1.8E+05
1.6E+05
1.4E+05
1.2E+05
1.0E+05
8.0E+04
6.0E+04
4.0E+04
2.0E+04
0.0E+00
240 fold
522 fold
619.22
232.97
G17_2IR3
GM1-G17_2IR3

Fig. 7c

MG1 (SEQ ID NO: 1):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagcggccaattcggacaaaaacgagacgctggtggctggcactcctggtttccaggacgggggttcaagtccctgcgctgtcta
taatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactagacaccatctagagtcgacctgcaggcatgcaa
gcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

GM1 (SEQ ID NO: 2):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagcggccgtaatgtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactacattagacgctggt
ggctggcactcctggtttccaggacgggggttcaagtccctgcgctgtcttgcttggatcggccgcgactctagagtcgacctgcagg
catgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

GM2 (SEQ ID NO: 3):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagcggcccgatcatataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactatggtcgacgctggt
ggctggcactcctggtttccaggacgggggttcaagtccctgcgctgtcttgcttggatcggccgcgactctagagtcgacctgcagg
catgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

GM3 (SEQ ID NO: 4):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagcggccggacaaaataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgacttttgtccaacgagac
gctggtggctggcactcctggtttccaggacgggggttcaagtccctgcgctgtcttgcttggatcggccgcgactctagagtcgacct
gcaggcatgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

GM4 (SEQ ID NO: 5):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagaagacgtaatgtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactacattagacgctggt
ggctggcactcctggtttccaggacgggggttcaagtccctgcgctgtcttgcttggatcggccgcgactctagagtcgacctgcagg
catgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

Fig. 8

GM4_2C (SEQ ID NO: 6):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagaagacgtaatgtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactacattacgacgctggt
ggctggcactcctggtttccaggacgggggttcaagtccctgcggtgtctttgcttggatcggccgcgactctagagtcgacctgcagg
catgcaagcttcagaagtaaagaagacgtaatgtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgact
acattacgacgctggtggctggcactcctggtttccaggacgggggttcaagtccctgcggtgtctttgcttggatcggccgcgactcta
gagtcgacctgcaggcatgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

GM5 (SEQ ID NO: 7):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatcCAAGACGAGC
TGTACAAGTAAAGaagagctaatgtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactaca
cattagcgacgctggtggctggcactcctggtttccaggacgggggttcaagtccctgcggtgtctttgcttggatcggccgcgactcta
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GM6 (SEQ ID NO: 8):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
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GM7 (SEQ ID NO: 9):

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GM8 (SEQ ID NO: 10):

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gtaaagaagagctaatgtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactacattagccgagacg
ctggtggctggcactcctggtttccaggacgggggttcaagtccctgcggtgtctttgcttggatcggccgcgactctagagtcgacctg
caggcatgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

Fig. 8 (Cont.)

MG2 (SEQ ID NO: 11):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
gtaaagcggccaattcggacaaaaacgagacgctggtgctggcactcctggtttccaggacgggattcaagtccctgcggtgtctt
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agcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

MG3 (SEQ ID NO: 12):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaagacgagctgtacaa
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tataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactacagacaatctagagtcgacctgcaggcatgca
agcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

MG4 (SEQ ID NO: 13):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatcCAAGACGAGC
TGTACAAGTAAAGCGGCCaattCGGACAAAAACGAgacgctggtgctggcactcctggtttccaggac
gggattcaagtccctgcggtgtctagtataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactactaga
cttctagagtcgacctgcaggcatgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

GArg (SEQ ID NO: 14):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatccaAgacgagctgtaca
agtaaagaagactgcgacgataatcgcgtggatatggcacgcaagtttctaccgggcaccgtaaatgtccgactcgtcgcagggccct
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agtcgacctgcaggcatgcaagcttcagctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

YM (SEQ ID NO: 15):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatcCAAGACGAGC
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Fig. 8 (Cont.)

TheoM (SEQ ID NO: 16):

CCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTAAggatcCAAGACGAGC
TGTACAAGTAAAGCGGCctaatgtgataccagccgaaaggcccttggcagcacattagacgctgggtgcctggcactc
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agctgctcgagggcccagatctaattcaccccaccagtgcaggctgcctatcag

Fig. 8 (Cont.)