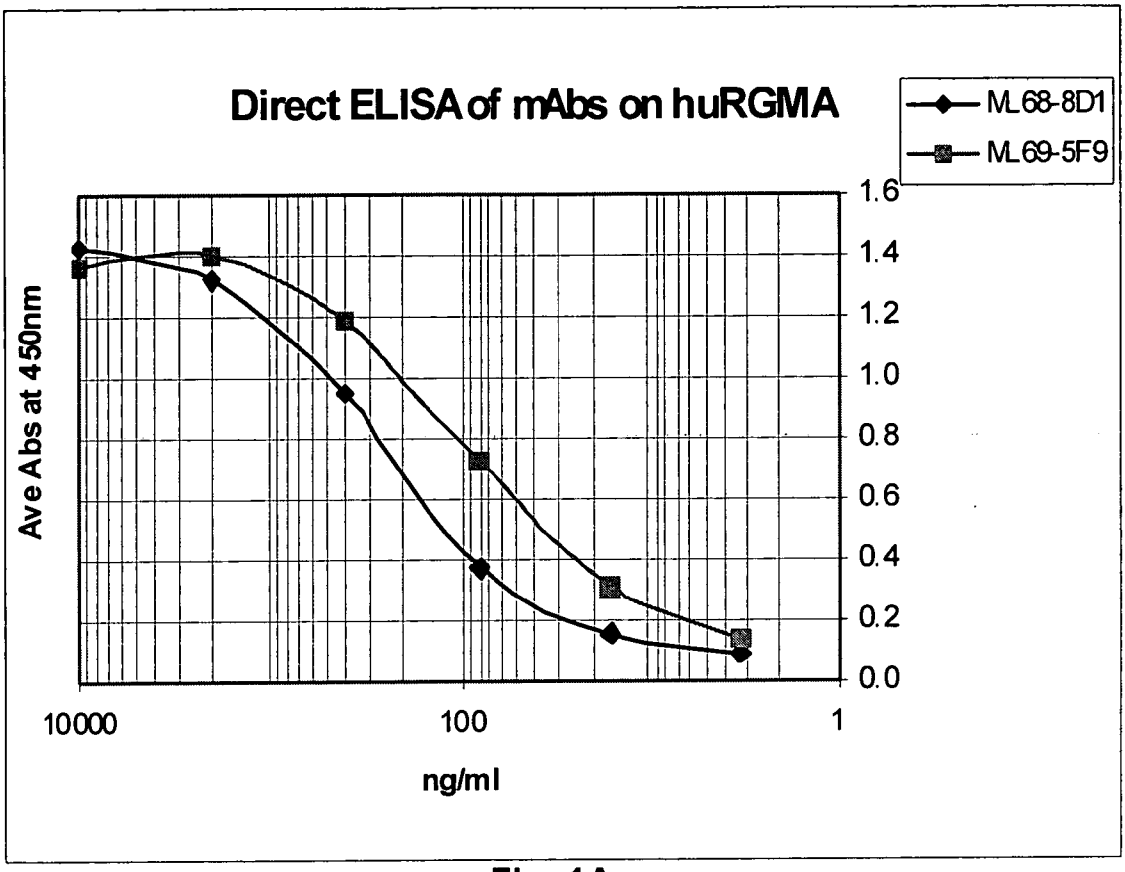

Direct ELISA of mAbs on huRGMA
ML68-8D1
ML69-5F9
Ave Abs at 450nm
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
10000
100
1
ng/ml

Fig. 1A

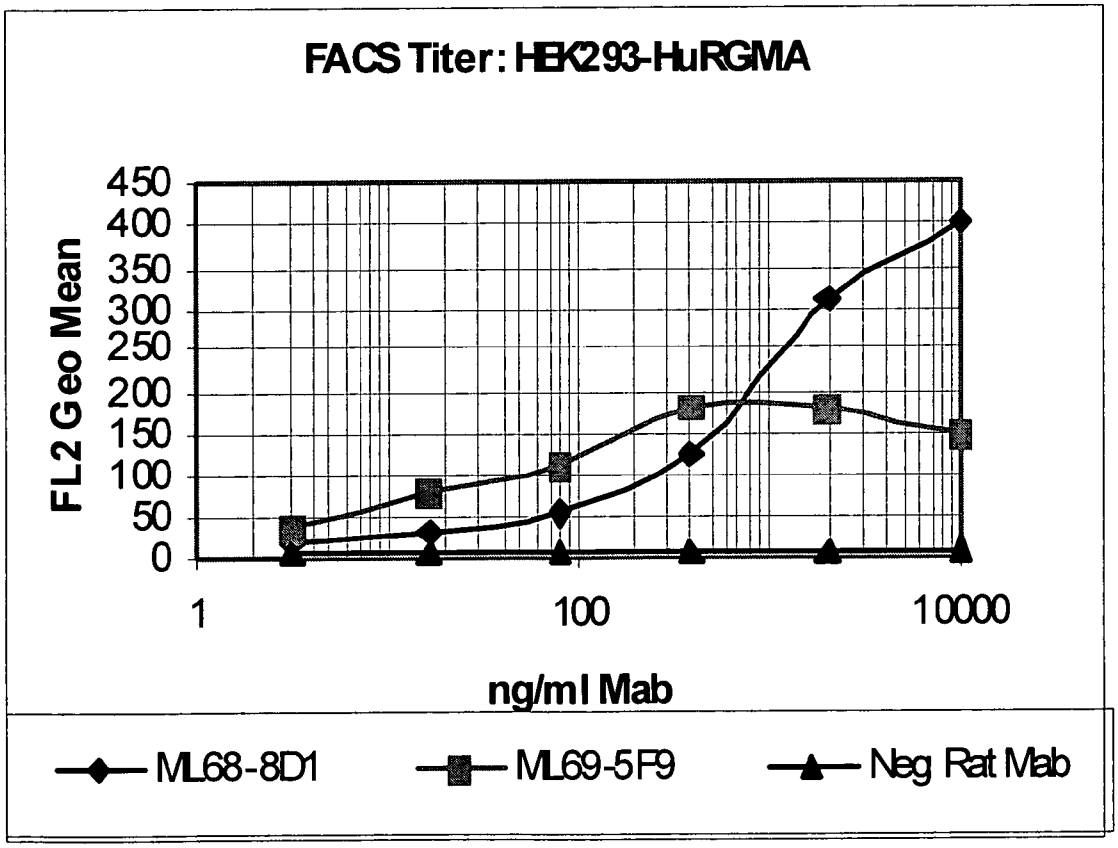

FACS Titer: HEK293-HuRGMA
FL2 Geo Mean
450
400
350
300
250
200
150
100
50
0
1
100
10000
ng/ml Mab
ML68-8D1
ML69-5F9
Neg Rat Mab

Fig. 1B

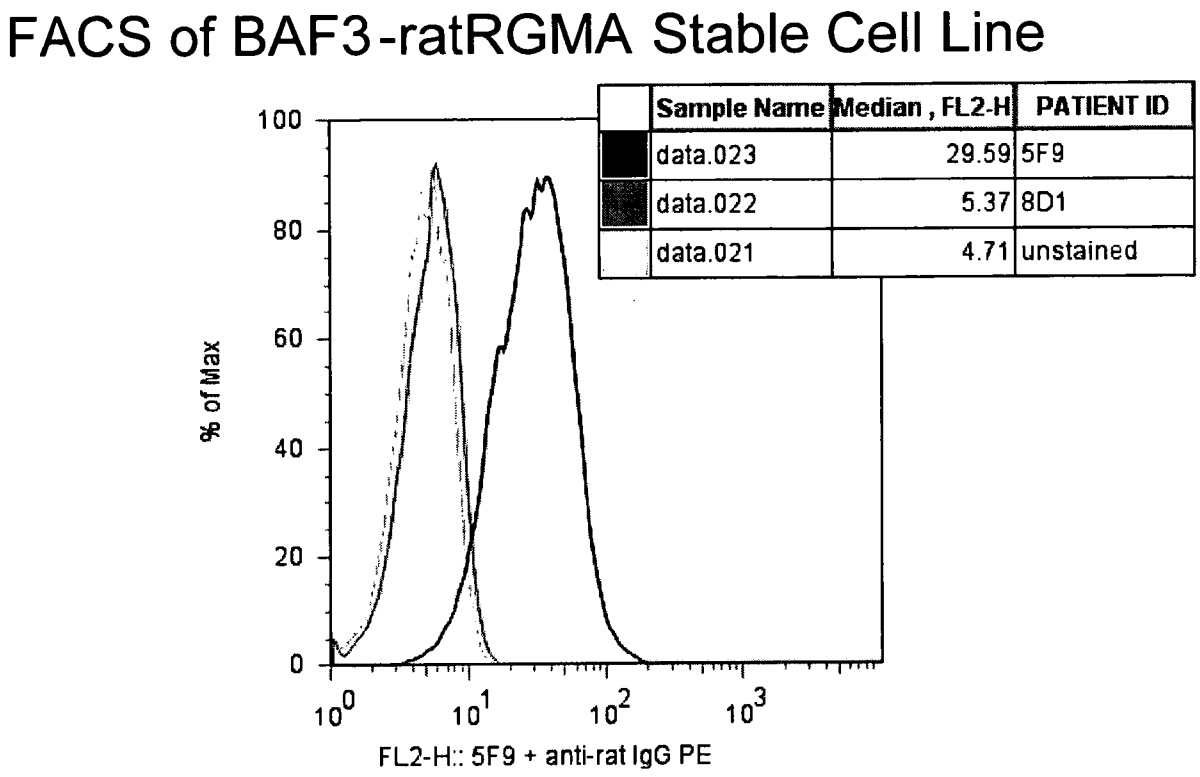

FACS of BAF3-ratRGMA Stable Cell Line
Sample Name
Median , FL2-H
PATIENT ID
data.023
29.59
5F9
data.022
5.37
8D1
data.021
4.71
unstained
100
80
60
40
20
0
% of Max
10^0
10^1
10^2
10^3
FL2-H:: 5F9 + anti-rat IgG PE

Fig. 1C

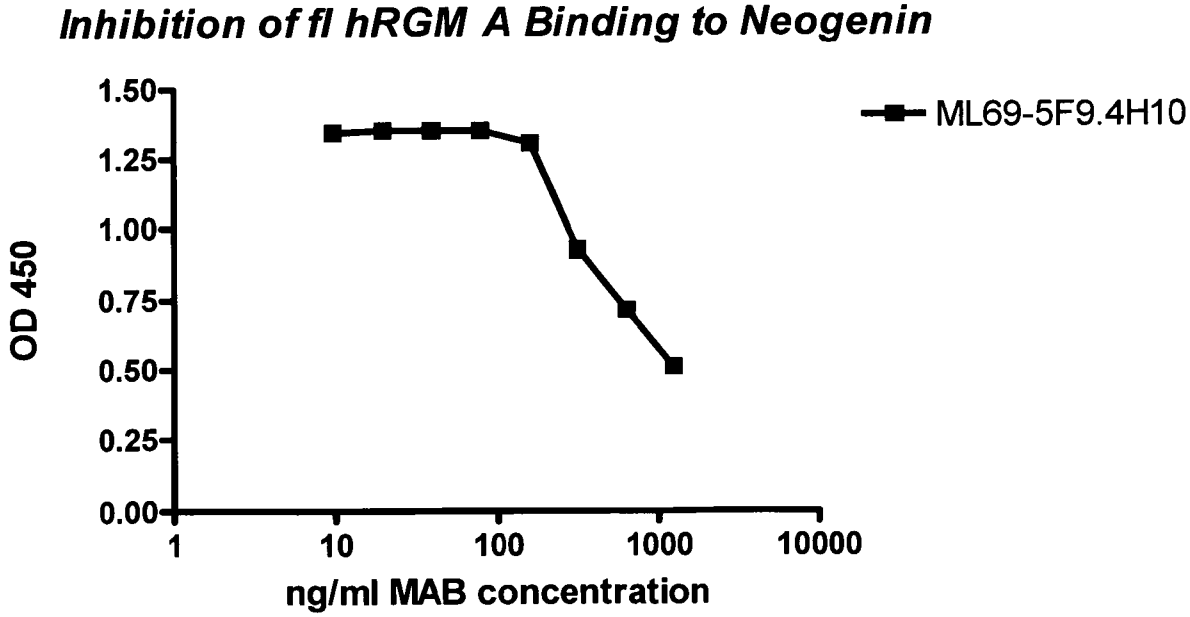

Inhibition of fl hRGM A Binding to Neogenin
ML69-5F9.4H10
1.50
1.25
1.00
0.75
0.50
0.25
0.00
OD 450
1
10
100
1000
10000
ng/ml MAB concentration

Fig. 2

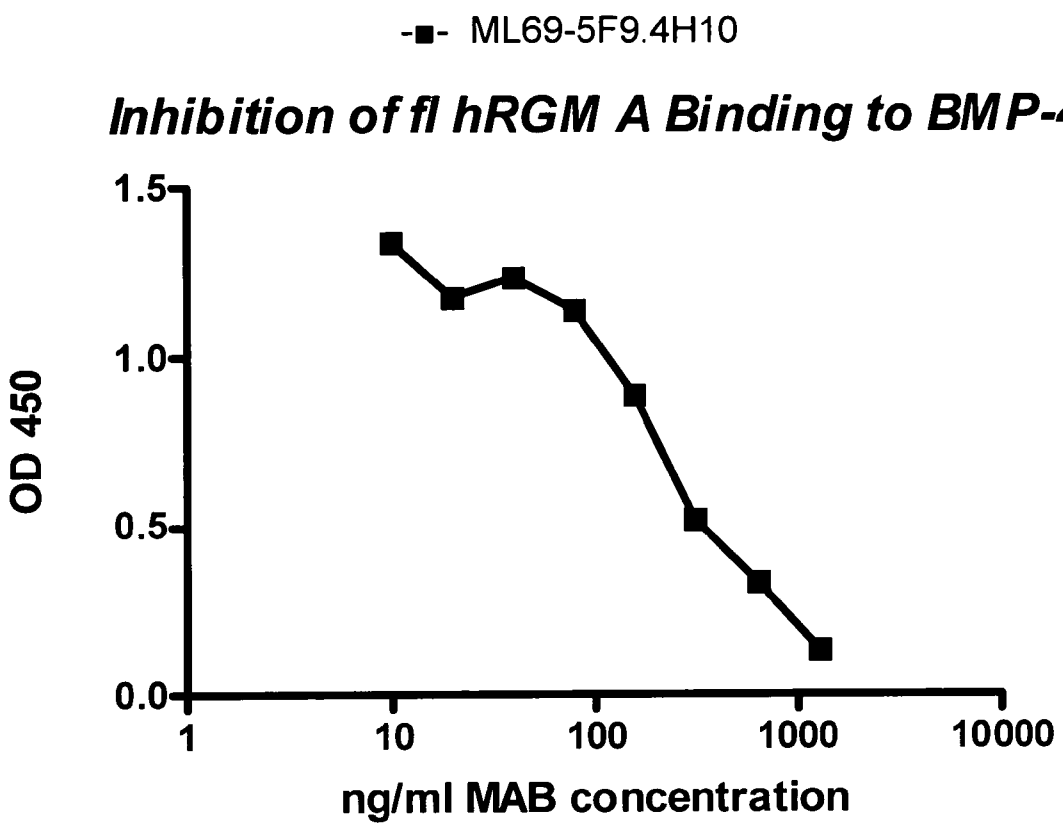

-■- ML69-5F9.4H10
Inhibition of fl hRGM A Binding to BMP-4
OD 450
1.5
1.0
0.5
0.0
1
10
100
1000
10000
ng/ml MAB concentration

Fig. 3

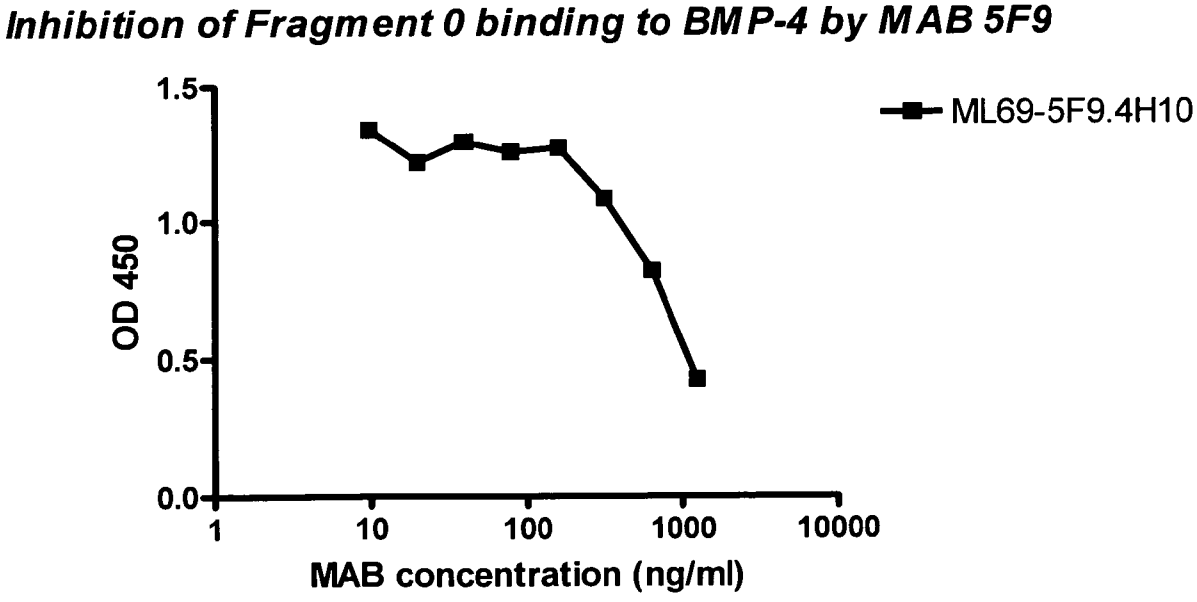

Inhibition of Fragment 0 binding to BMP-4 by MAB 5F9
ML69-5F9.4H10
OD 450
1.5
1.0
0.5
0.0
1
10
100
1000
10000
MAB concentration (ng/ml)

Fig. 4

Inhibition of binding of fc-conjugated, full length hRGM A to BMP-2

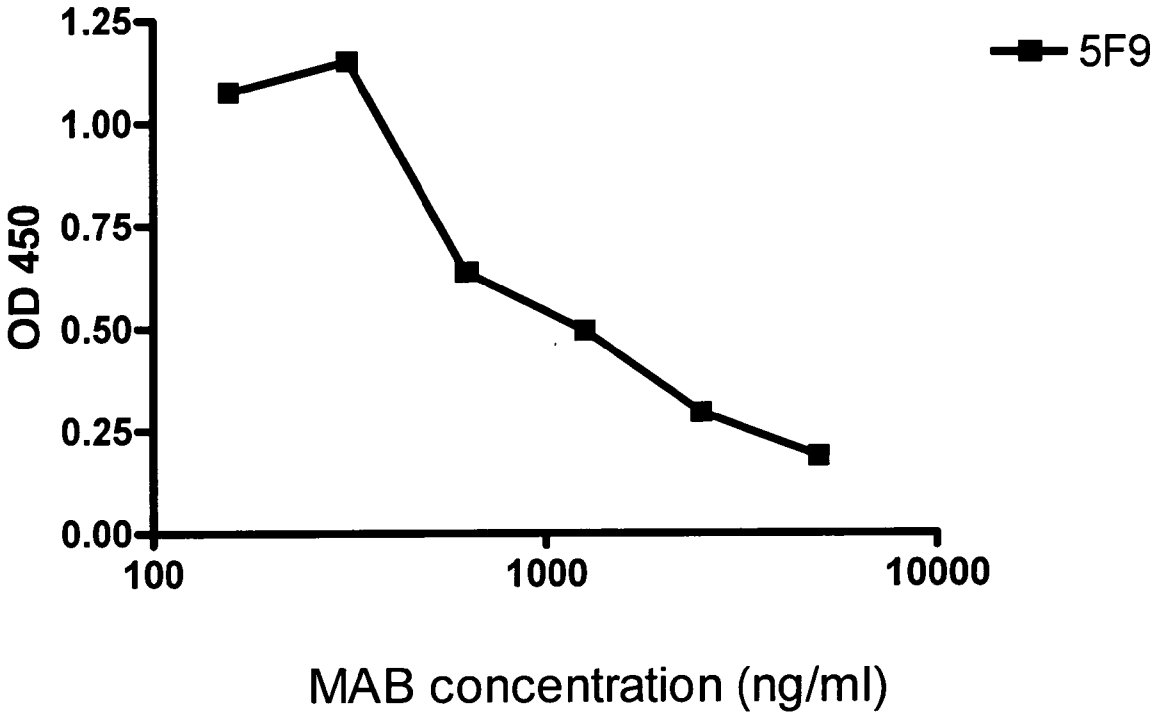


Fig. 5

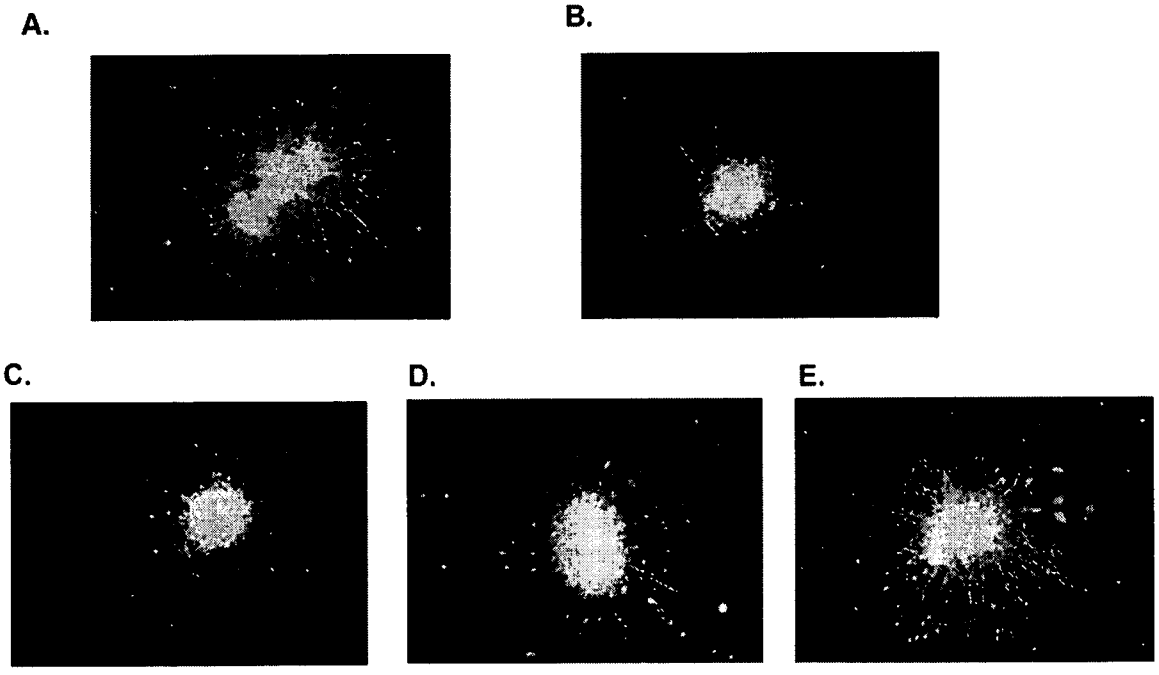


Fig. 6

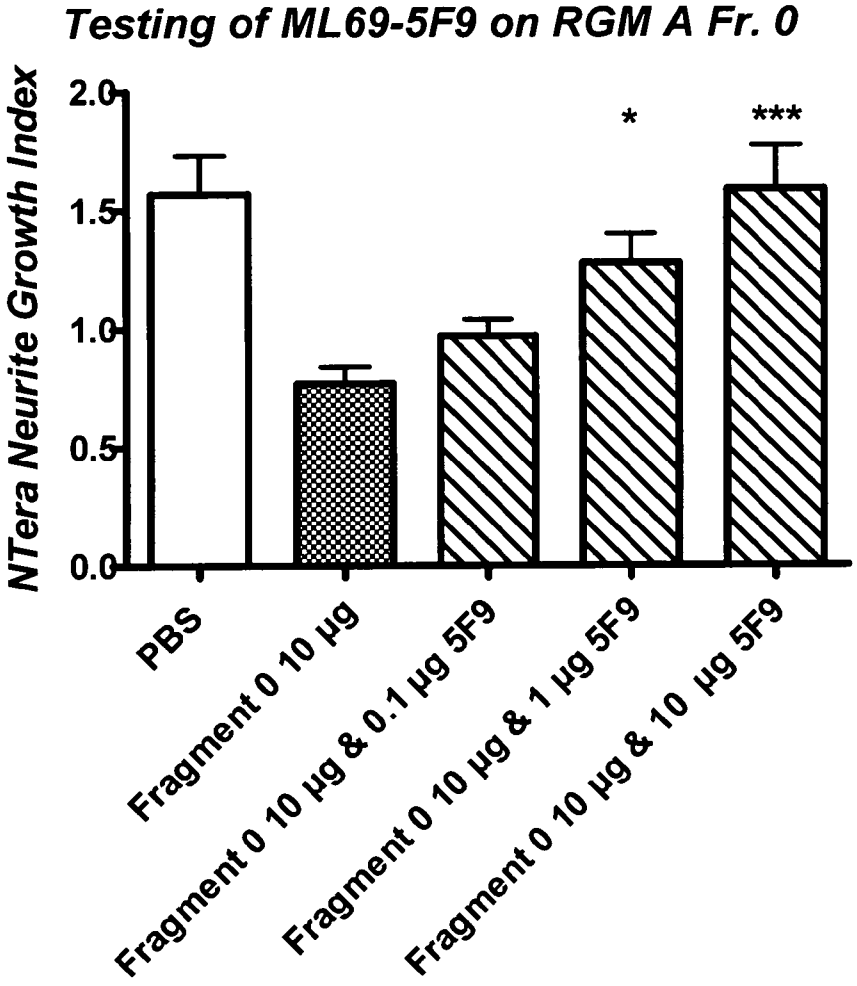

Testing of ML69-5F9 on RGM A Fr. 0
NTera Neurite Growth Index
2.0
1.5
1.0
0.5
0.0
*
***
PBS
Fragment 0 10 µg
Fragment 0 10 µg & 0.1 µg 5F9
Fragment 0 10 µg & 1 µg 5F9
Fragment 0 10 µg & 10 µg 5F9

Fig. 7

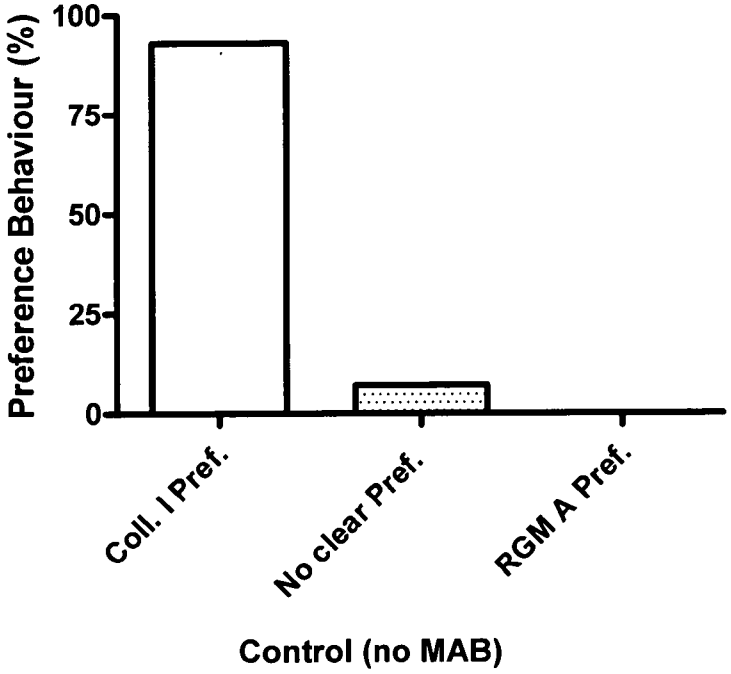

Preference Behaviour (%)
100
75
50
25
0
Coll. I Pref.
No clear Pref.
RGM A Pref.
Control (no MAB)

Fig. 8A

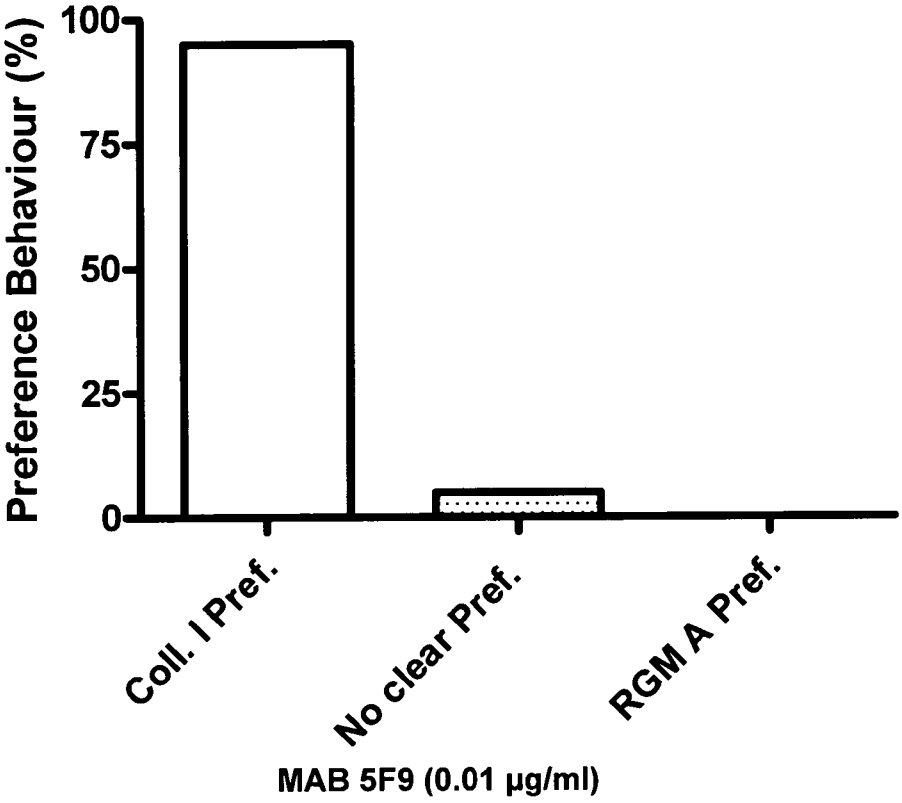

Preference Behaviour (%)
100
75
50
25
0
Coll. I Pref.
No clear Pref.
RGM A Pref.
MAB 5F9 (0.01 µg/ml)

Fig. 8B

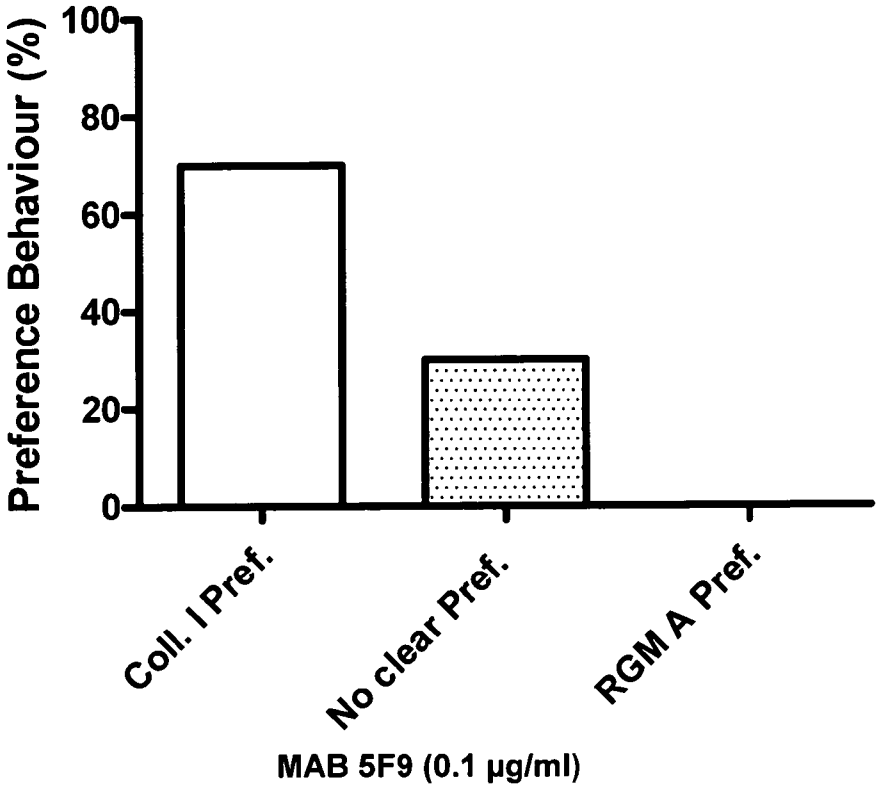

Preference Behaviour (%)
100
80
60
40
20
0
Coll. I Pref.
No clear Pref.
RGM A Pref.
MAB 5F9 (0.1 µg/ml)

Fig. 8C

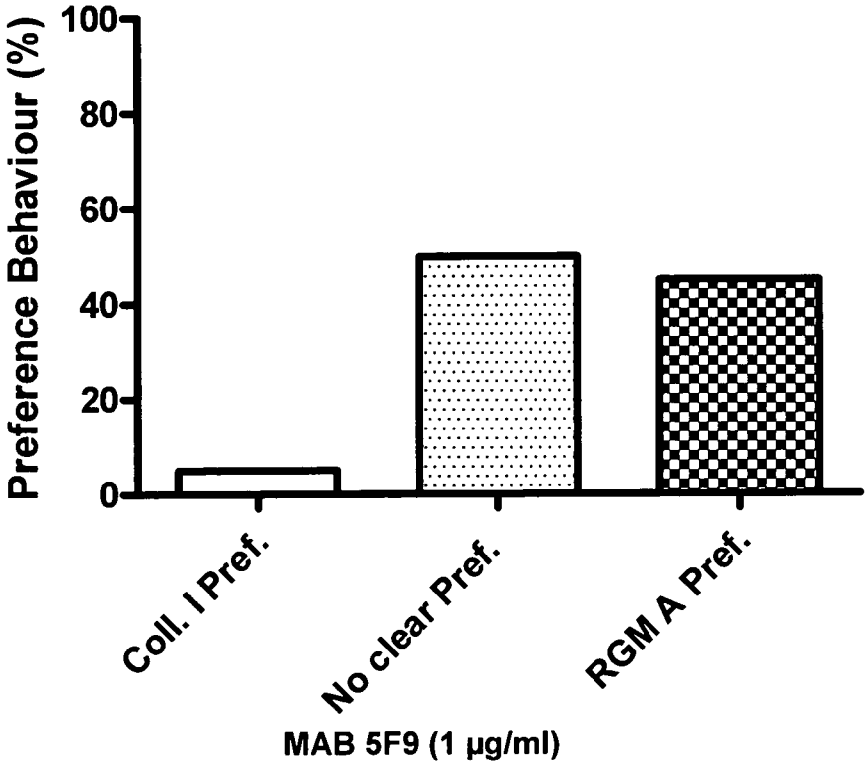

Preference Behaviour (%)
100
80
60
40
20
0
Coll. I Pref.
No clear Pref.
RGM A Pref.
MAB 5F9 (1 µg/ml)

Fig. 8D

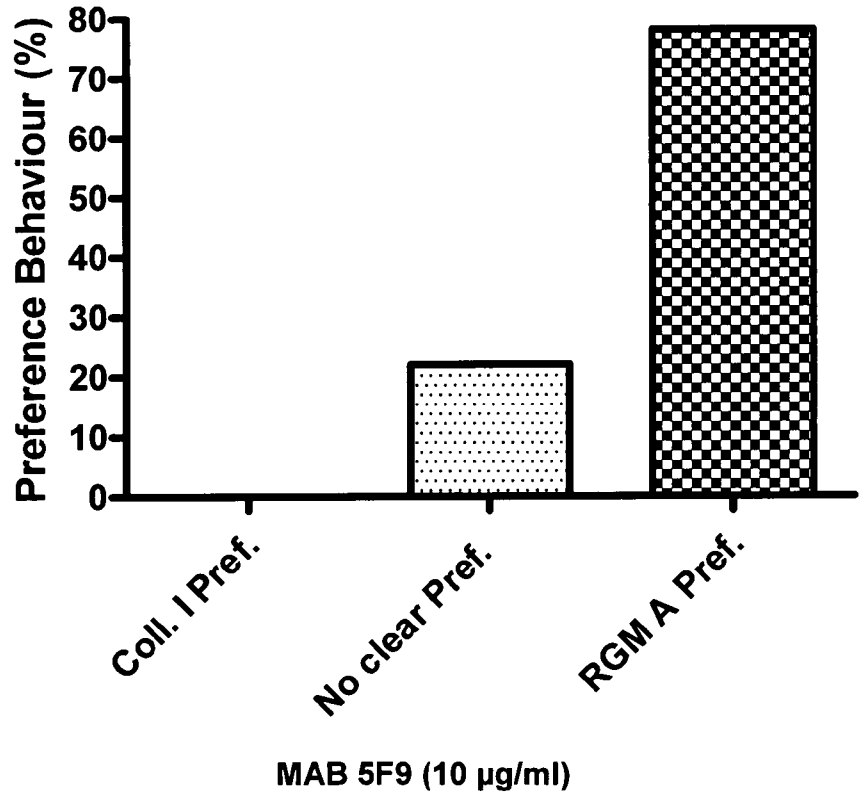

Preference Behaviour (%)
80
70
60
50
40
30
20
10
0
Coll. I Pref.
No clear Pref.
RGM A Pref.
MAB 5F9 (10 µg/ml)

Fig. 8E

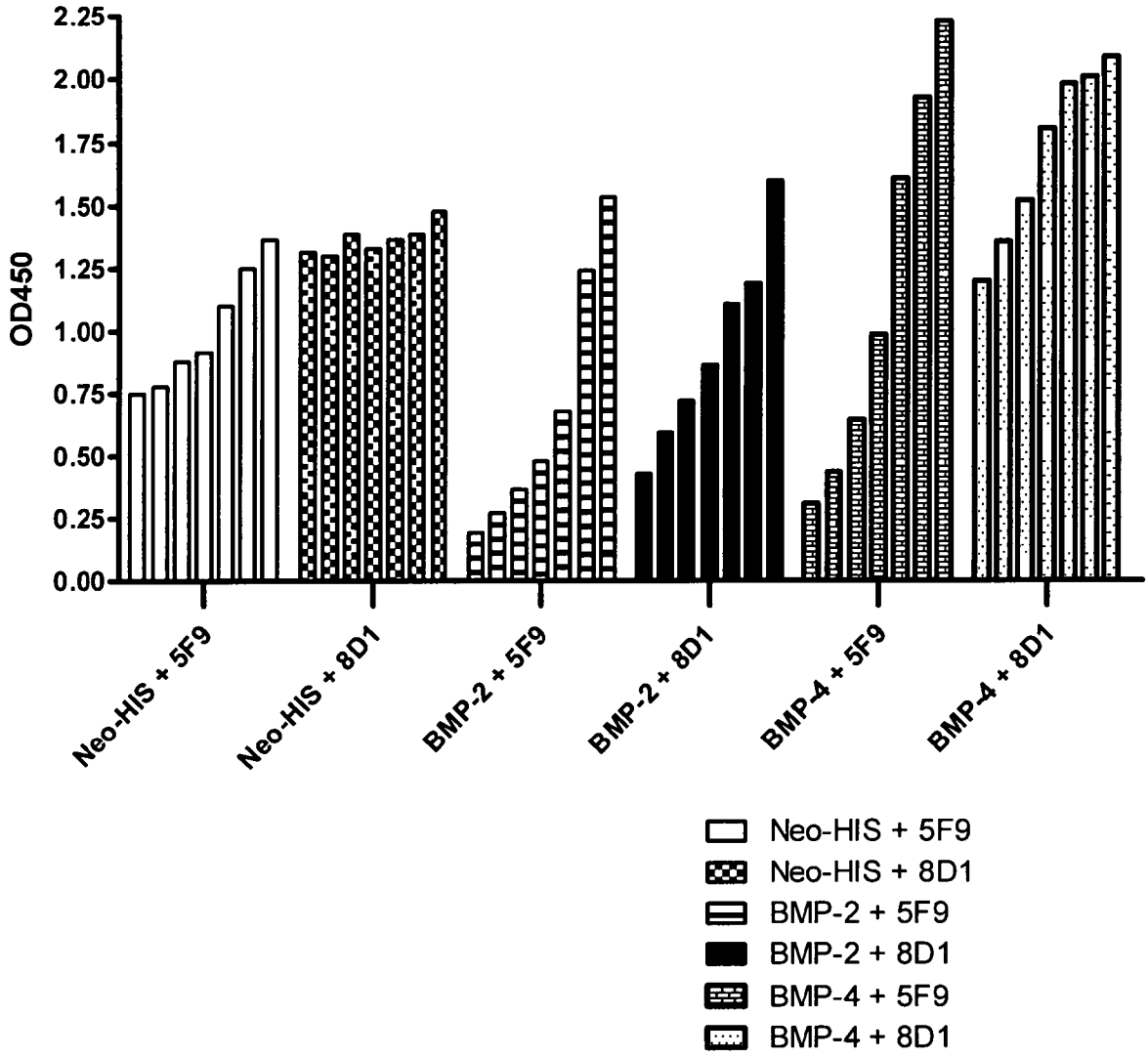
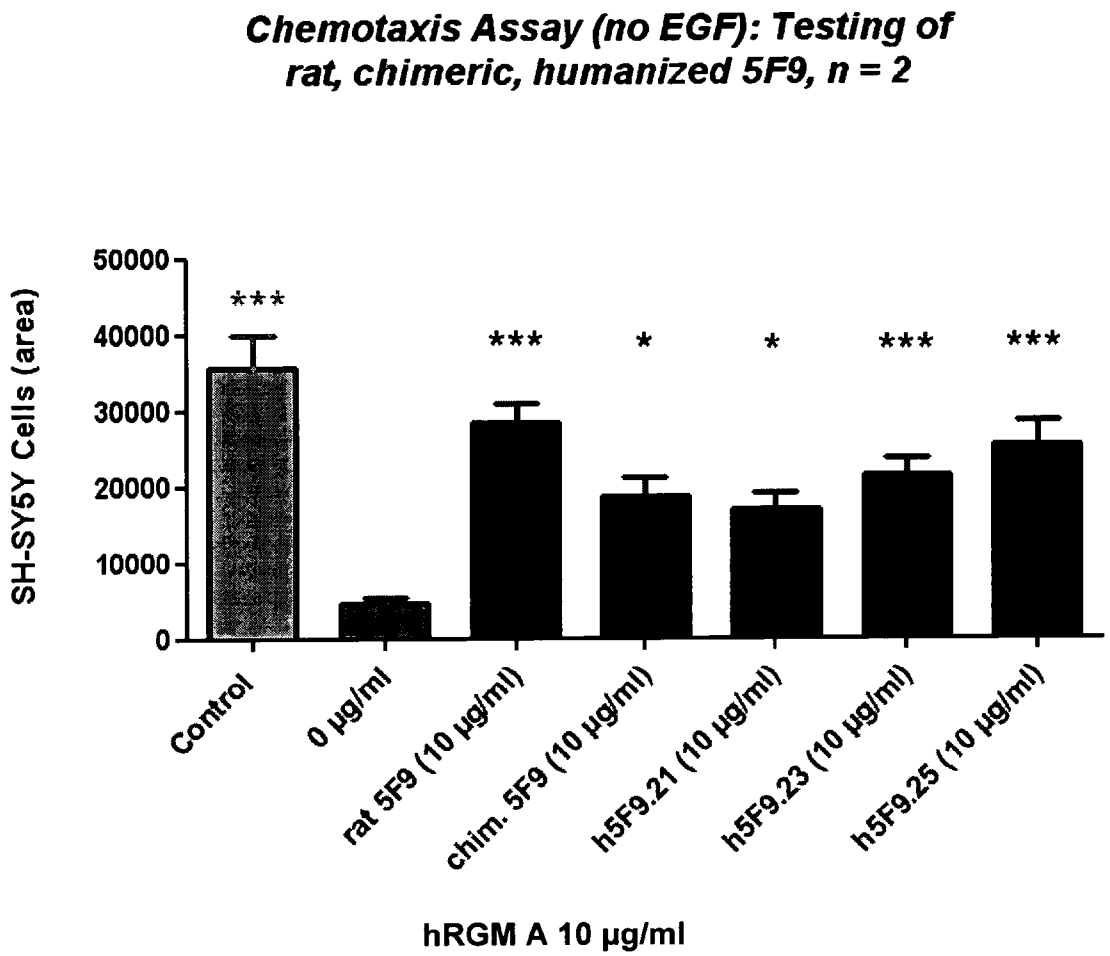

2.25
2.00
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0.00
OD450
Neo-HIS + 5F9
Neo-HIS + 8D1
BMP-2 + 5F9
BMP-2 + 8D1
BMP-4 + 5F9
BMP-4 + 8D1
Neo-HIS + 5F9
Neo-HIS + 8D1
BMP-2 + 5F9
BMP-2 + 8D1
BMP-4 + 5F9
BMP-4 + 8D1

Fig. 9



* p < 0.05: significance vs. 5F9 0 µg/ml
*** p < 0.001: significance vs. 5F9 0 µg/ml
*** p < 0.001: significance vs. 5F9 0 µg/ml

Fig. 10

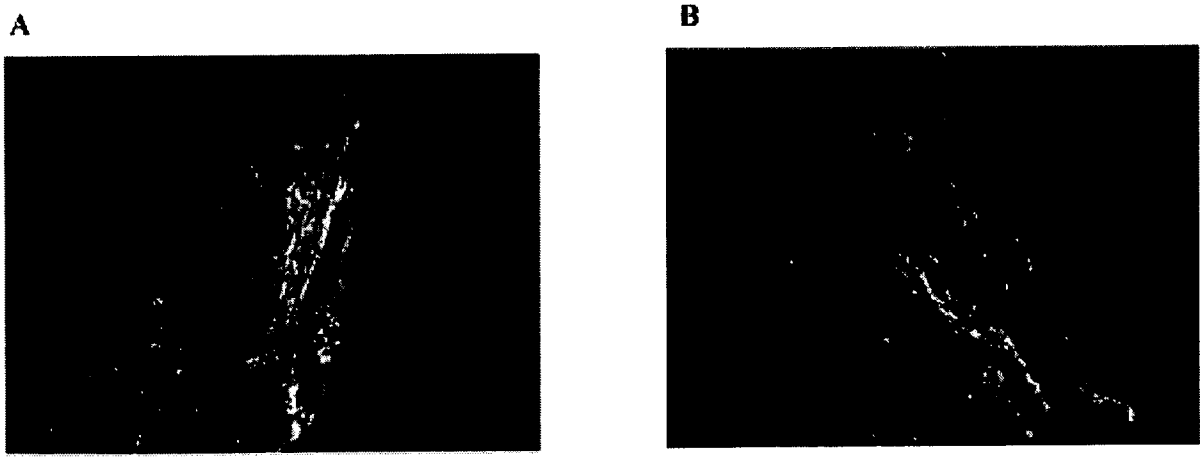
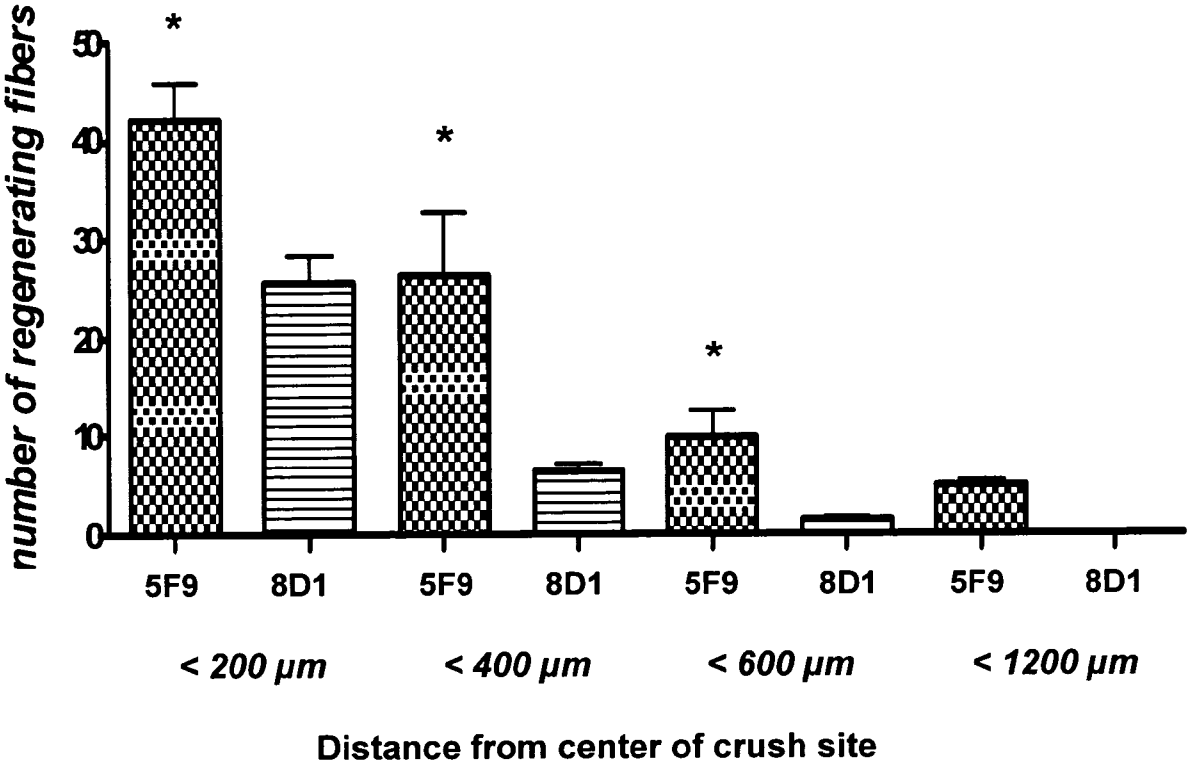


Fig. 11


number of regenerating fibers
50
40
30
20
10
0
*
*
*
5F9
8D1
5F9
8D1
5F9
8D1
5F9
8D1
< 200 µm
< 400 µm
< 600 µm
< 1200 µm
Distance from center of crush site

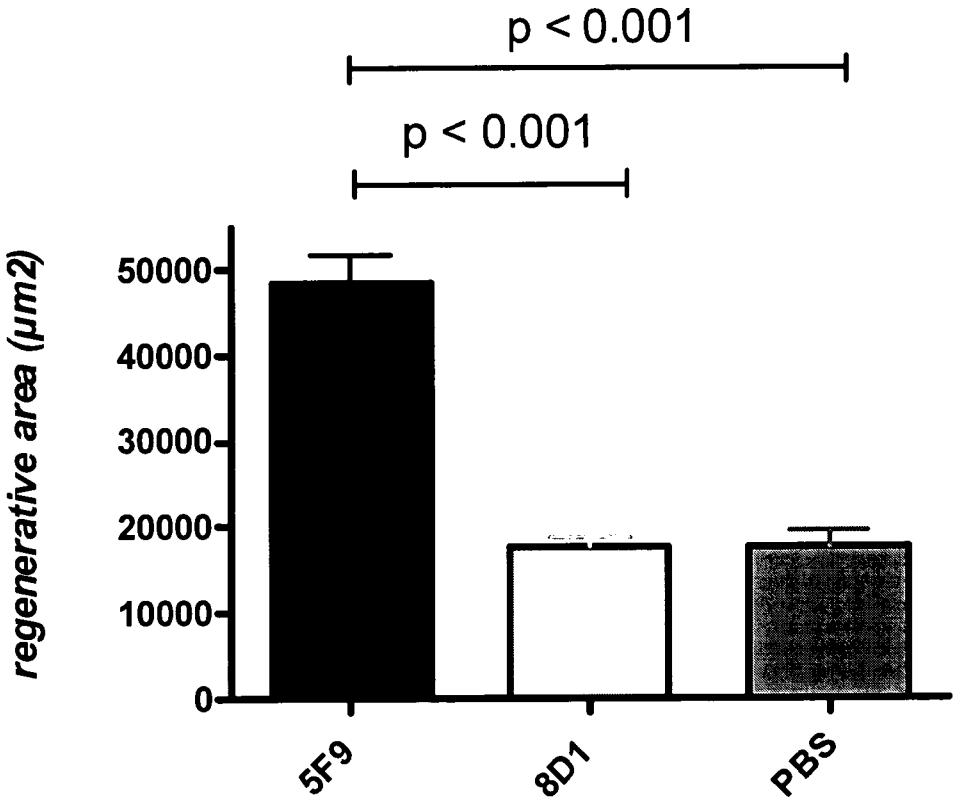

p < 0.001
p < 0.001
regenerative area (µm2)
50000
40000
30000
20000
10000
0
5F9
8D1
PBS

Fig. 12

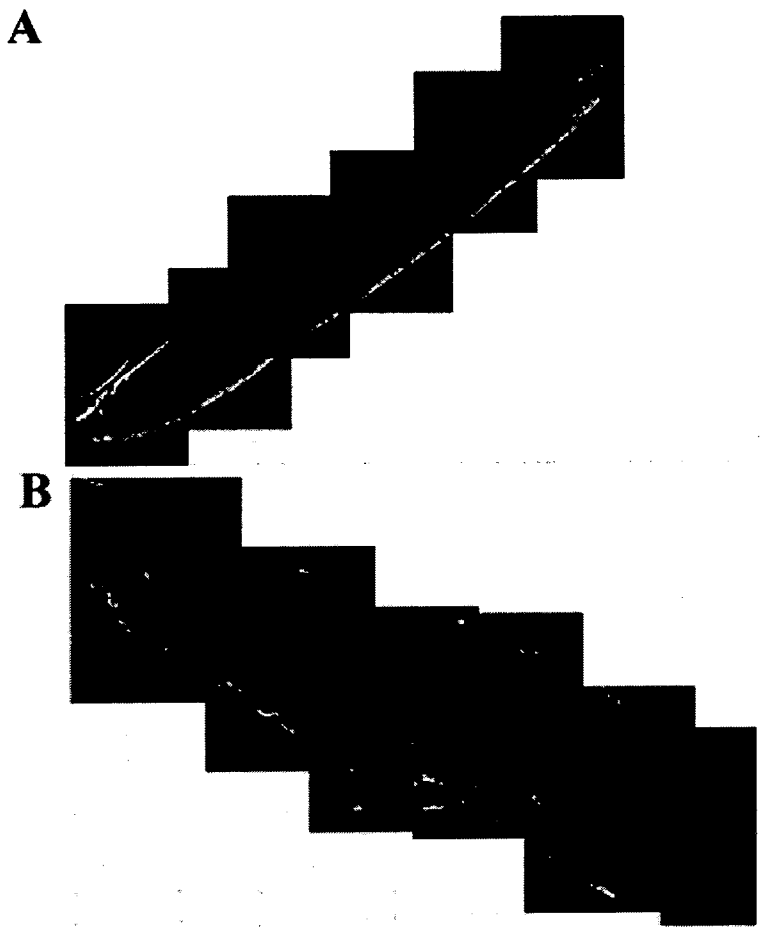


Fig. 13

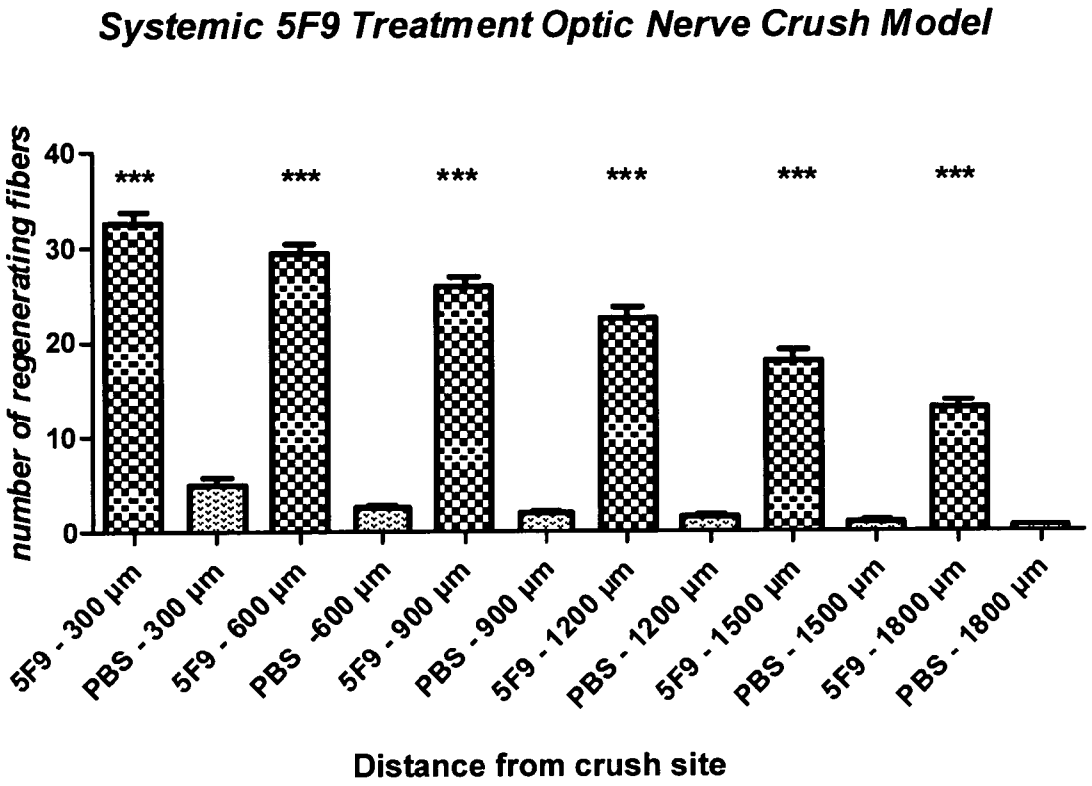


Fig. 14A

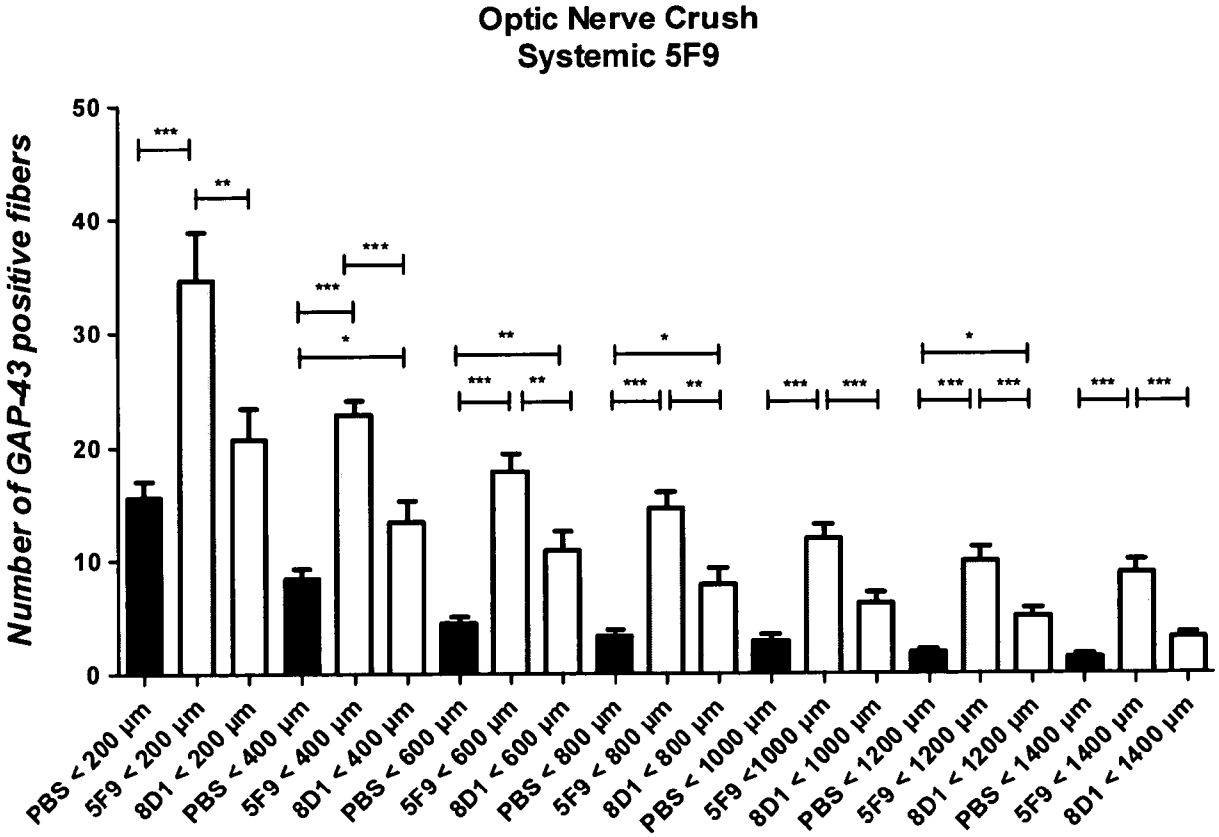


Fig. 14B

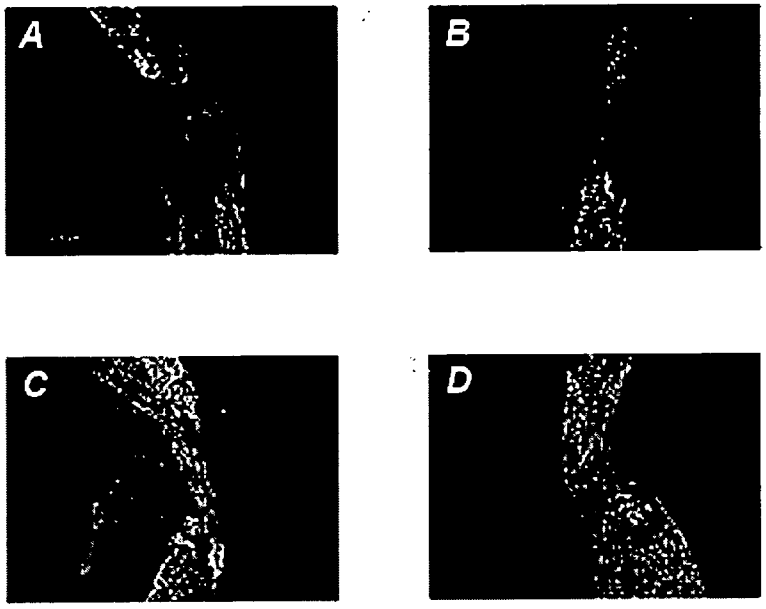

A
B
C
D

Fig. 15

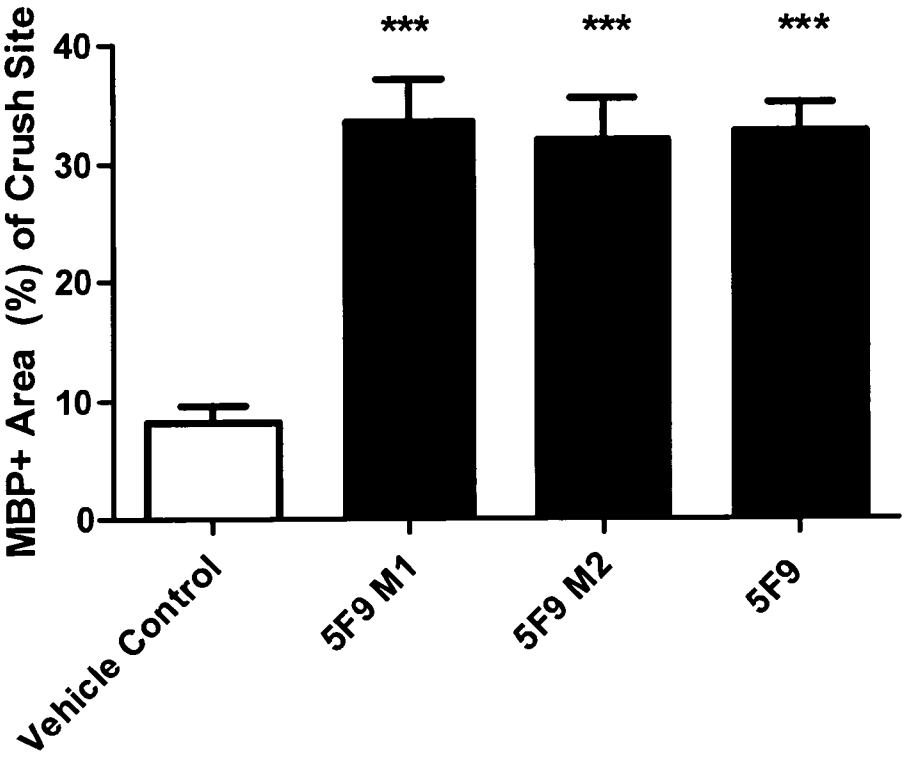

MBP+ Area (%) of Crush Site
40
30
20
10
0
***
***
***
Vehicle Control
5F9 M1
5F9 M2
5F9

Fig. 16