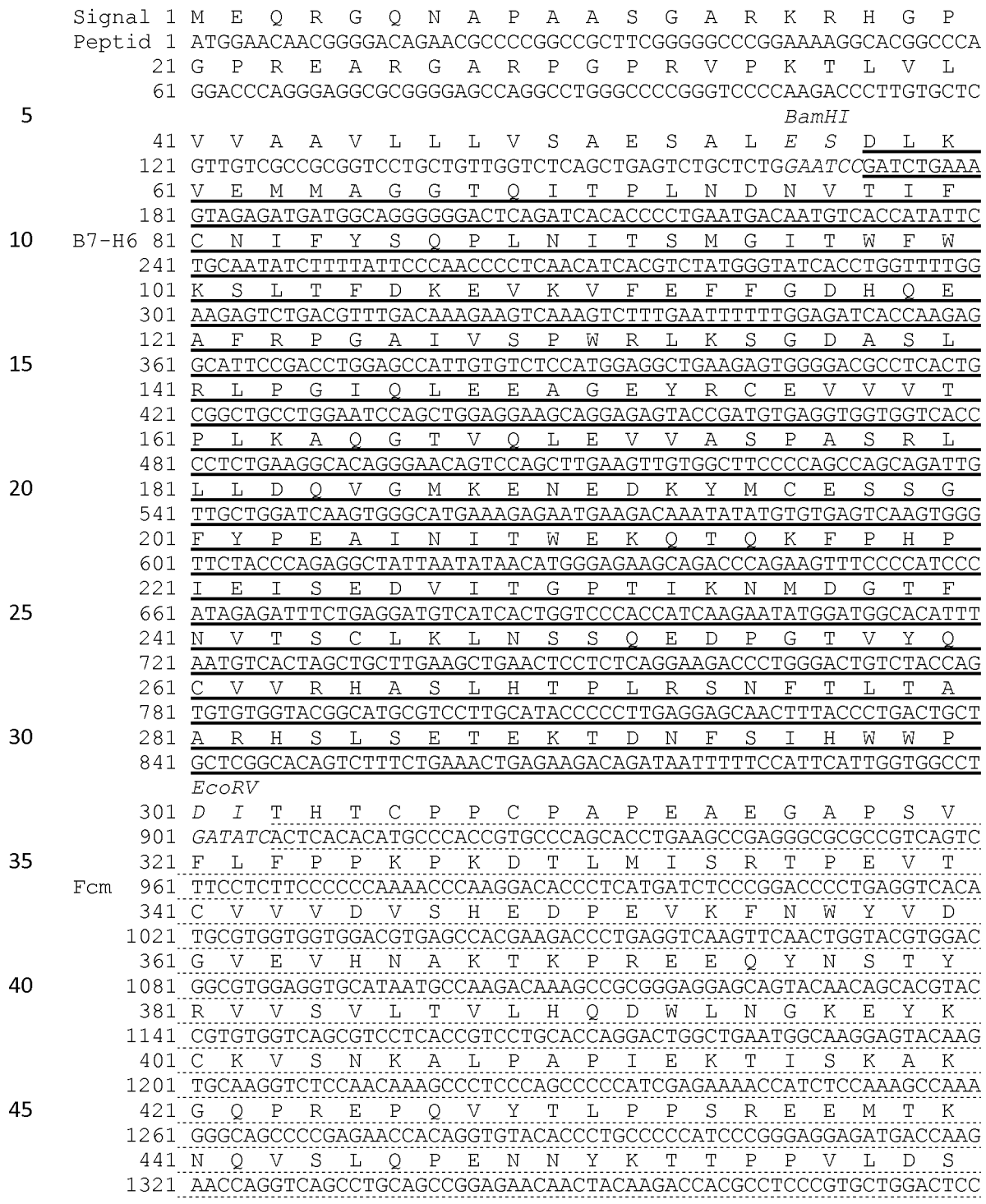

Signal 1 M E Q R G Q N A P A A S G A R K R H G P
Peptid 1 ATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCGGGGGCCCGGAAAAGGCACGGCCCA
21 G P R E A R G A R P G P R V P K T L V L
61 GGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGGCCCCGGGTCCCCAAGACCCTTGTGCTC
BamHI
41 V V A A V L L L V S A E S A L E S D L K
121 GTTGTCGCCGCGGTCCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGGAATCCGATCTGAAA
61 V E M M A G G T Q I T P L N D N V T I F
181 GTAGAGATGATGGCAGGGGGGACTCAGATCACACCCCTGAATGACAATGTCACCATATTC
B7-H6 81 C N I F Y S Q P L N I T S M G I T W F W
241 TGCAATATCTTTTATTCCCAACCCCTCAACATCACGTCTATGGGTATCACCTGGTTTTGG
101 K S L T F D K E V K V F E F F G D H Q E
301 AAGAGTCTGACGTTTGACAAAGAAGTCAAAGTCTTTGAATTTTTTGGAGATCACCAAGAG
121 A F R P G A I V S P W R L K S G D A S L
361 GCATTCCGACCTGGAGCCATTGTGTCTCCATGGAGGCTGAAGAGTGGGGACGCCTCACTG
141 R L P G I Q L E E A G E Y R C E V V V T
421 CGGCTGCCTGGAATCCAGCTGGAGGAAGCAGGAGAGTACCGATGTGAGGTGGTGGTCACC
161 P L K A Q G T V Q L E V V A S P A S R L
481 CCTCTGAAGGCACAGGGAACAGTCCAGCTTGAAGTTGTGGCTTCCCCAGCCAGCAGATTG
181 L L D Q V G M K E N E D K Y M C E S S G
541 TTGCTGGATCAAGTGGGCATGAAAGAGAATGAAGACAAATATATGTGTGAGTCAAGTGGG
201 F Y P E A I N I T W E K Q T Q K F P H P
601 TTCTACCCAGAGGCTATTAATATAACATGGGAGAAGCAGACCCAGAAGTTTCCCCATCCC
221 I E I S E D V I T G P T I K N M D G T F
661 ATAGAGATTTCTGAGGATGTCATCACTGGTCCCACCATCAAGAATATGGATGGCACATTT
241 N V T S C L K L N S S Q E D P G T V Y Q
721 AATGTCACTAGCTGCTTGAAGCTGAACTCCTCTCAGGAAGACCCTGGGACTGTCTACCAG
261 C V V R H A S L H T P L R S N F T L T A
781 TGTGTGGTACGGCATGCGTCCTTGCATACCCCCTTGAGGAGCAACTTTACCCTGACTGCT
281 A R H S L S E T E K T D N F S I H W W P
841 GCTCGGCACAGTCTTTCTGAAACTGAGAAGACAGATAATTTTTCCATTCATTGGTGGCCT
EcoRV
301 D I T H T C P P C P A P E A E G A P S V
901 GATATCACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGAGGGCGCGCCGTCAGTC
321 F L F P P K P K D T L M I S R T P E V T
Fcm 961 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
341 C V V V D V S H E D P E V K F N W Y V D
1021 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC
361 G V E V H N A K T K P R E E Q Y N S T Y
1081 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC
381 R V V S V L T V L H Q D W L N G K E Y K
1141 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG
401 C K V S N K A L P A P I E K T I S K A K
1201 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA
421 G Q P R E P Q V Y T L P P S R E E M T K
1261 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
441 N Q V S L Q P E N N Y K T T P P V L D S
1321 AACCAGGTCAGCCTGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC

Fig. 1

```
      461 D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q  G
     1381 GACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG
      481 N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  K  S
     1441 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC
                              NdeI
      501 L  S  L  S  P  G  K  H  M  G  G  D  E  K  T  T  G  W  R  G
     1501 CTCTCCCTGTCTCCGGGTAAACATATGGGAGGTGACGAAAAGACCACCGGCTGGCGCGGC
SBP   521 G  H  V  V  E  G  L  A  G  E  L  E  Q  L  R  A  R  L  E  H
     1561 GGCCACGTGGTGGAAGGCCTGGCCGGCGAACTGGAACAGCTGCGCGCCCGCCTGGAACAC
                                    XhoI
      541 H  P  Q  G  Q  R  E  P  *  L  E
     1621 CACCCACAGGGCCAGCGCGAACCATGACTCGAG
```

Fig. 1 (continued)

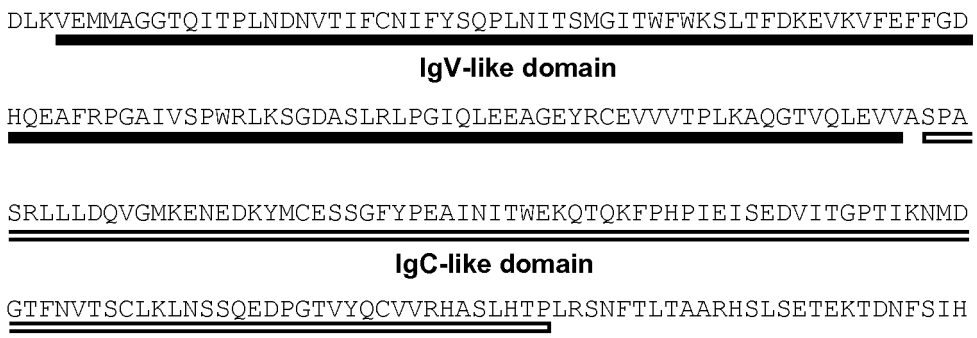

1 DLKVEMMAGGTQITPLNDNVTIFCNIFYSQPLNITSMGITWFWKSLTFDKEVKVFEFFGD
IgV-like domain
61 HQEAFRPGAIVSPWRLKSGDASLRLPGIQLEEAGEYRCEVVVTPLKAQGTVQLEVVASPA
121 SRLLLDQVGMKENEDKYMCESSGFYPEAINITWEKQTQKFPHPIEISEDVITGPTIKNMD
IgC-like domain
181 GTFNVTSCLKLNSSQEDPGTVYQCVVRHASLHTPLRSNFTLTAARHSLSETEKTDNFSIH
241 WWP

Fig. 2

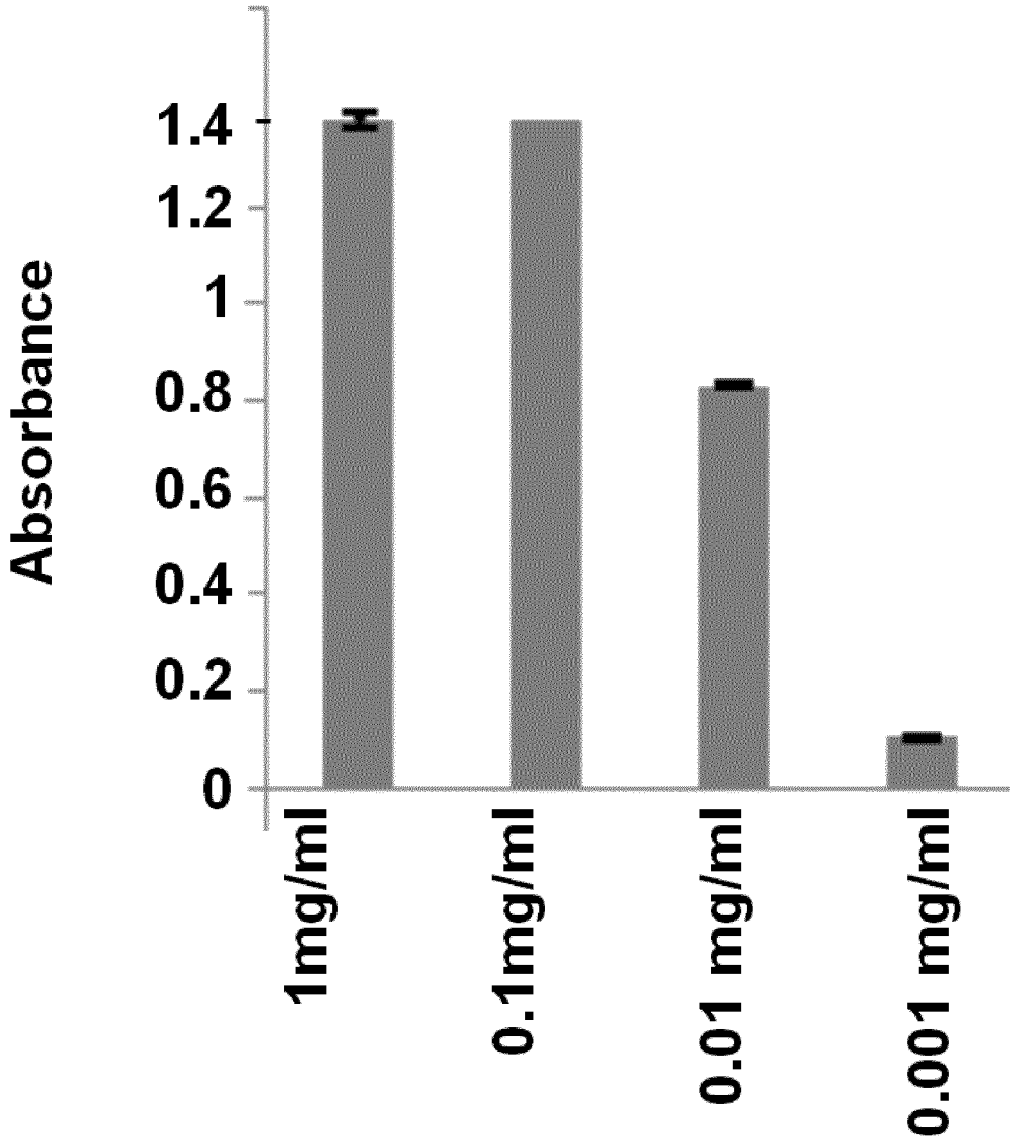

Absorbance
1.4
1.2
1
0.8
0.6
0.4
0.2
0
1mg/ml
0.1mg/ml
0.01 mg/ml
0.001 mg/ml

Fig. 3

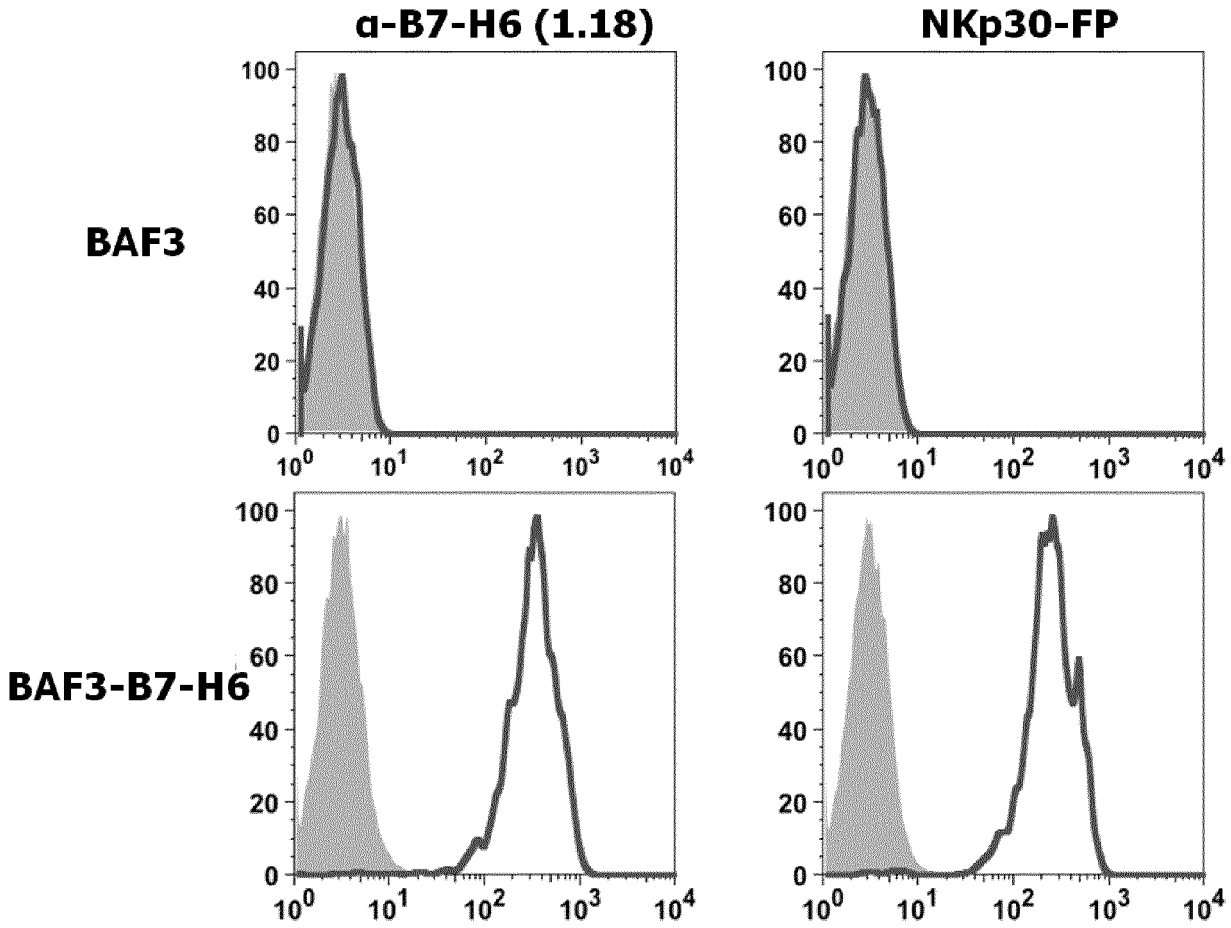

α-B7-H6 (1.18)
NKp30-FP
BAF3
BAF3-B7-H6
100
80
60
40
20
0
10^0
10^1
10^2
10^3
10^4

Fig. 4a

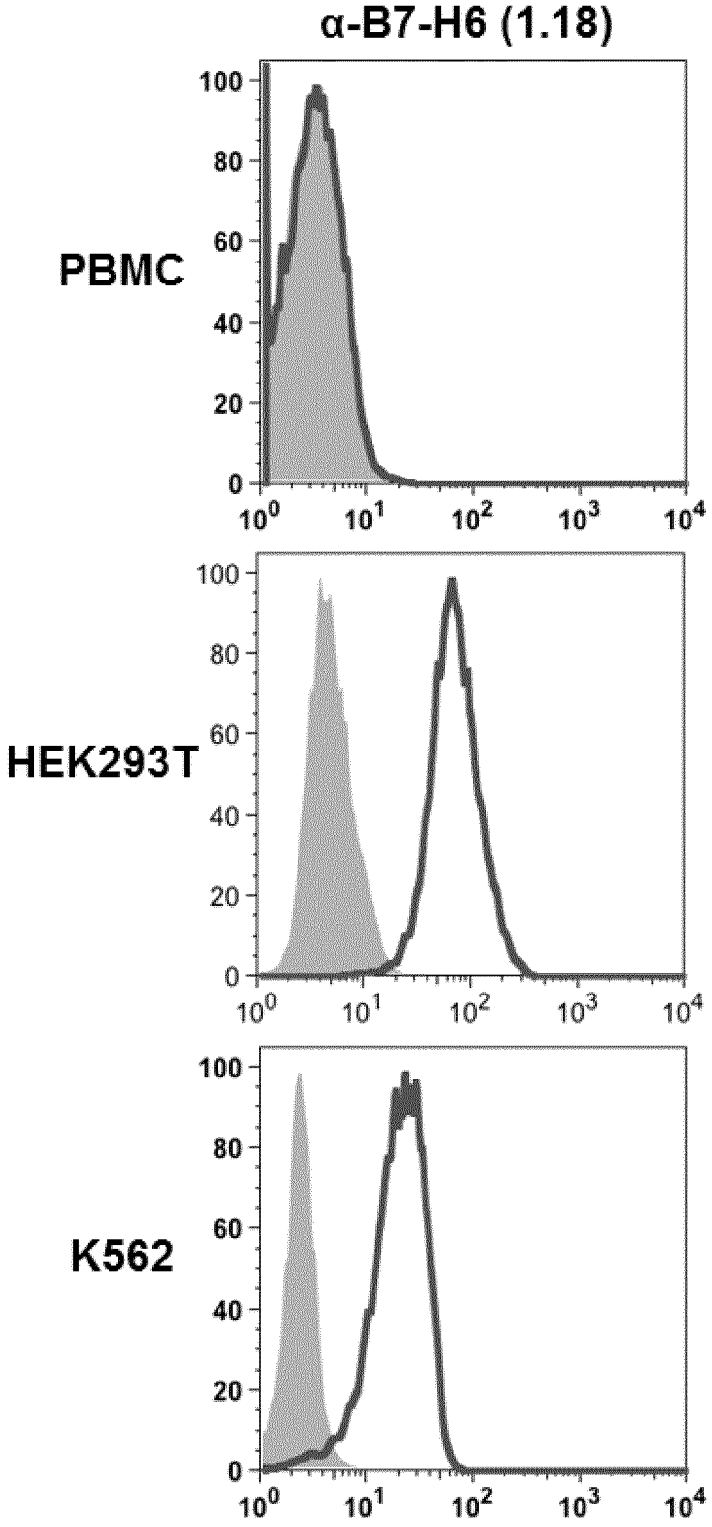

α-B7-H6 (1.18)
PBMC
HEK293T
K562
100
80
60
40
20
0
10^0
10^1
10^2
10^3
10^4

Fig. 4b

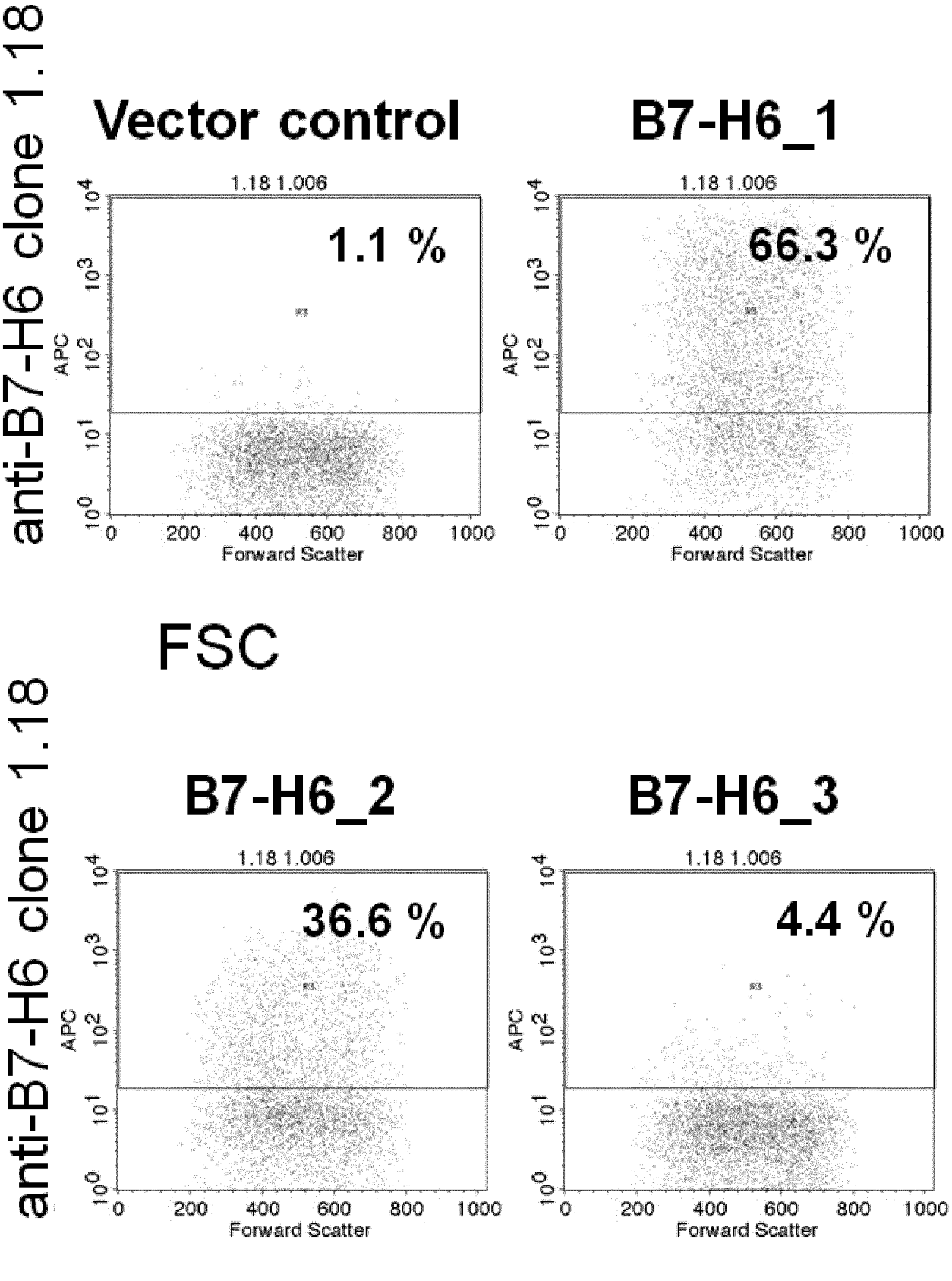
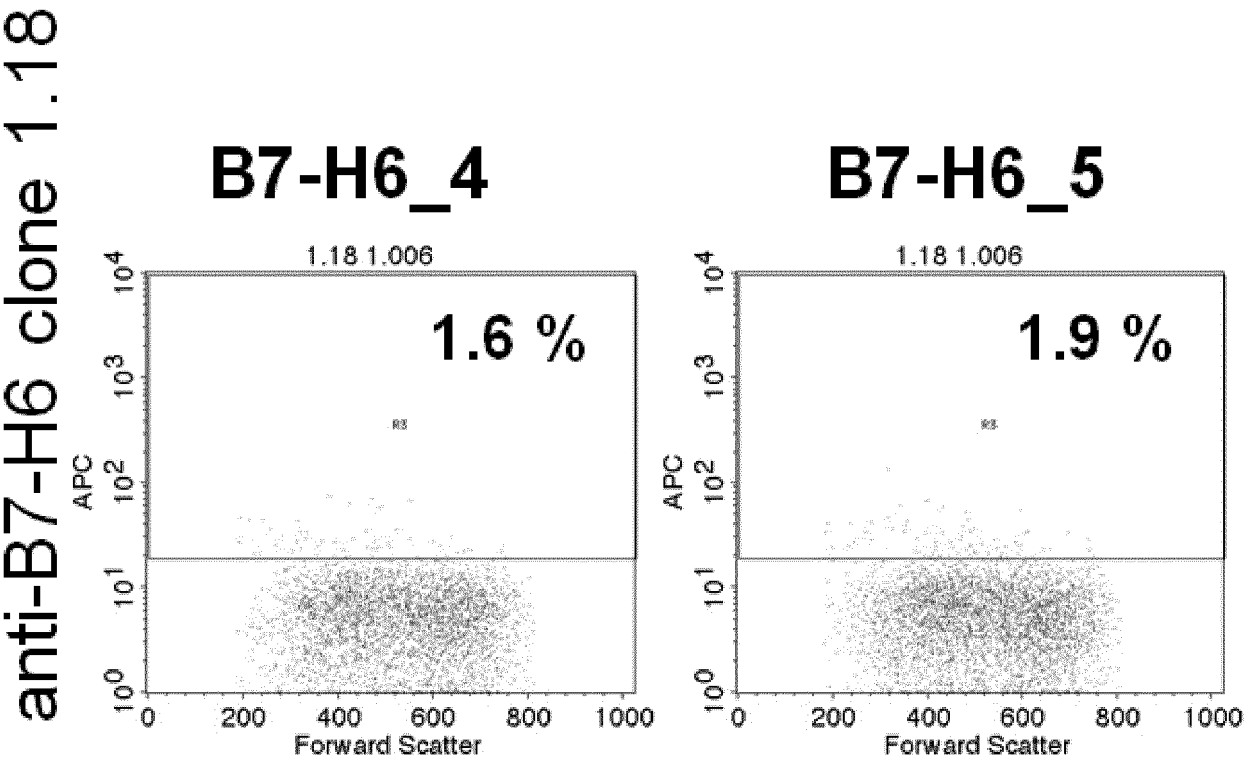

anti-B7-H6 clone 1.18
Vector control
B7-H6_1
B7-H6_2
B7-H6_3
1.18 1.006
1.1 %
66.3 %
36.6 %
4.4 %
APC
Forward Scatter
FSC

Fig. 5



B7-H6_1 (amino acids 24-454)
B7-H6_2 (amino acids 83-454)
B7-H6_3 (amino acids 141-454)
B7-H6_4 (amino acids 190-454)
B7-H6_5 (amino acids 239-454)

Fig. 5 (continued)

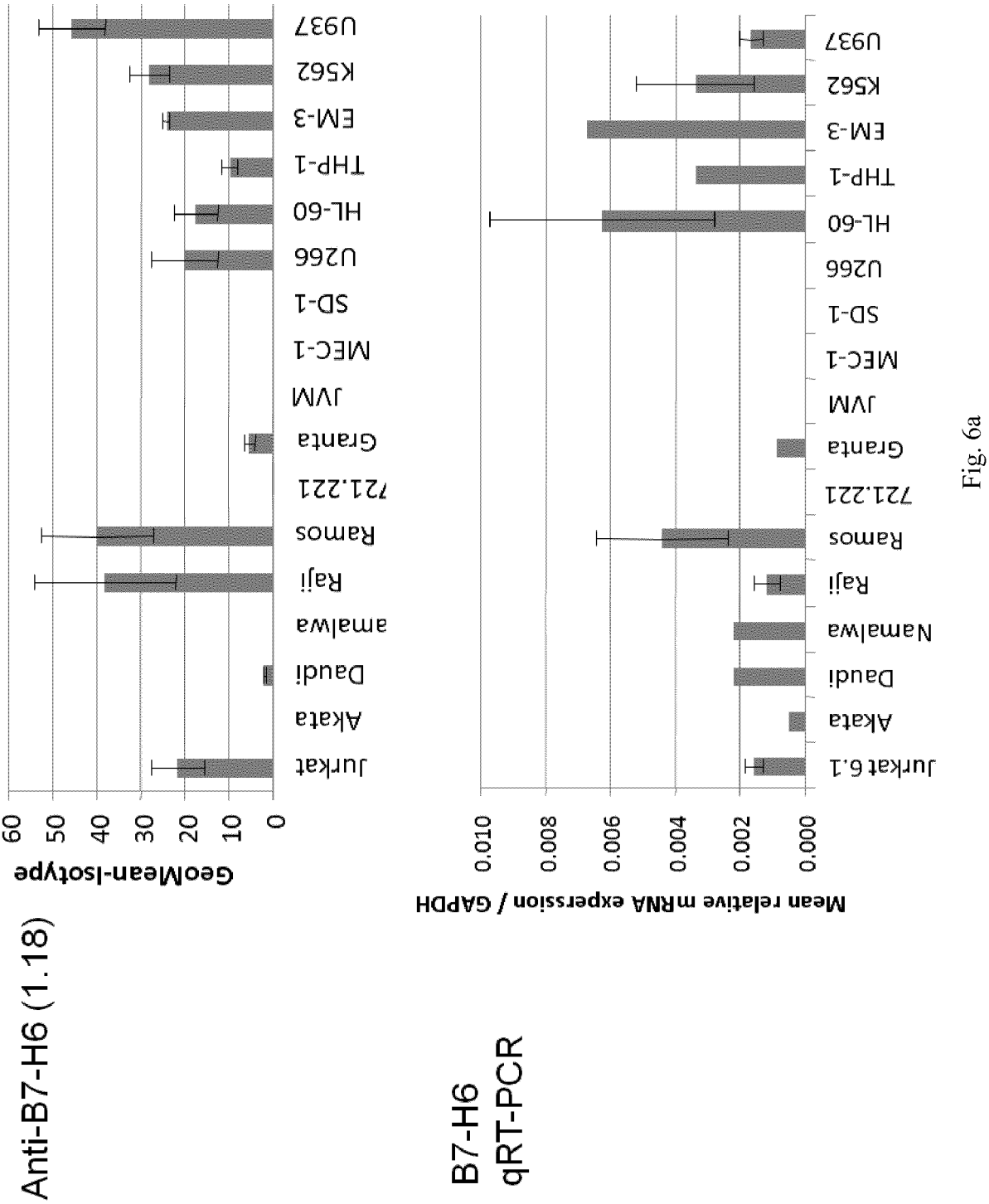

Anti-B7-H6 (1.18)
GeoMean-Isotype
60
50
40
30
20
10
0
Jurkat
Akata
Daudi
amalwa
Raji
Ramos
721.221
Granta
JVM
MEC-1
SD-1
U266
HL-60
THP-1
EM-3
K562
U937
B7-H6
qRT-PCR
Mean relative mRNA expression / GAPDH
0.010
0.008
0.006
0.004
0.002
0.000
Jurkat 6.1
Akata
Daudi
Namalwa
Raji
Ramos
721.221
Granta
JVM
MEC-1
SD-1
U266
HL-60
THP-1
EM-3
K562
U937

Fig. 6a

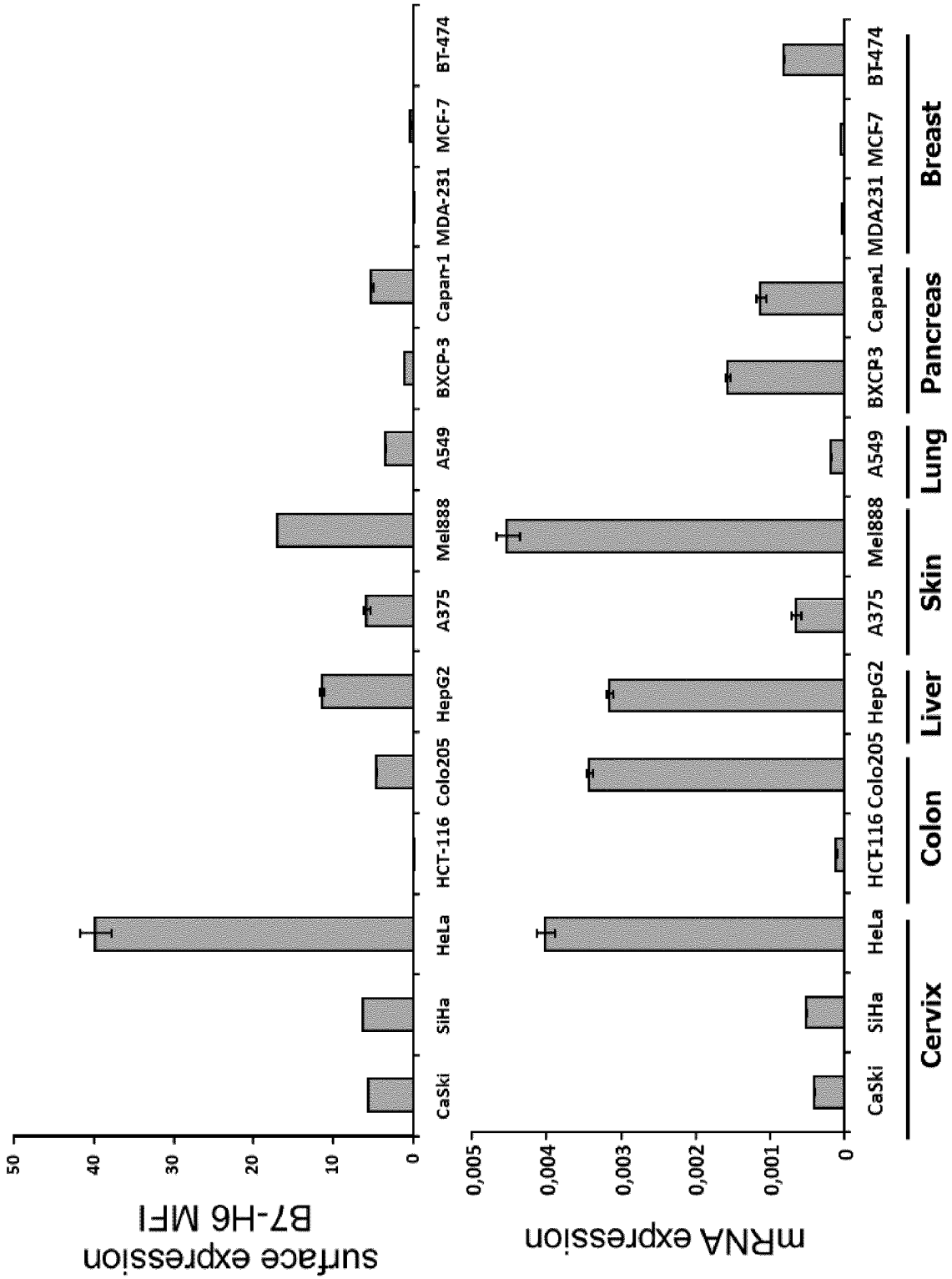

surface expression
B7-H6 MFI
50
40
30
20
10
0
CaSki
SiHa
HeLa
HCT-116
Colo205
HepG2
A375
Mel888
A549
BXCP-3
Capan-1
MDA-231
MCF-7
BT-474
mRNA expression
0,005
0,004
0,003
0,002
0,001
0
CaSki
SiHa
HeLa
HCT116
Colo205
HepG2
A375
Mel888
A549
BXCP3
Capan1
MDA231
MCF7
BT-474
Cervix
Colon
Liver
Skin
Lung
Pancreas
Breast

Fig. 6b

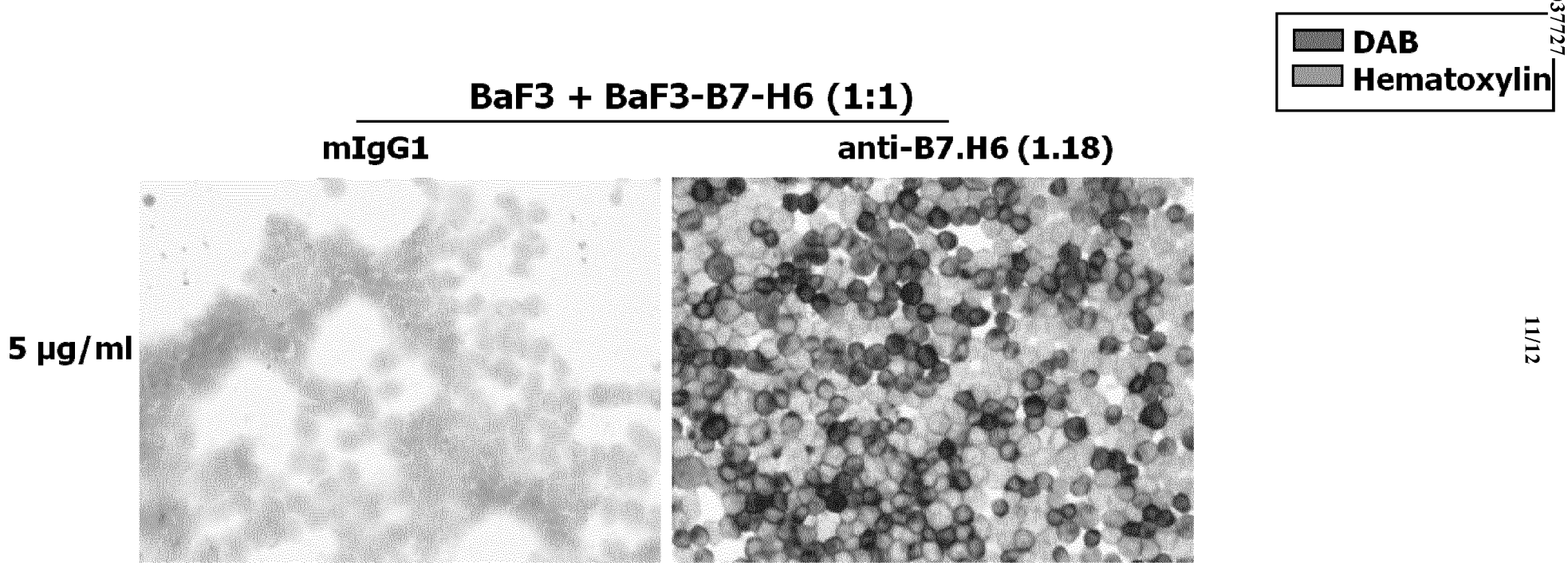


Fig. 7

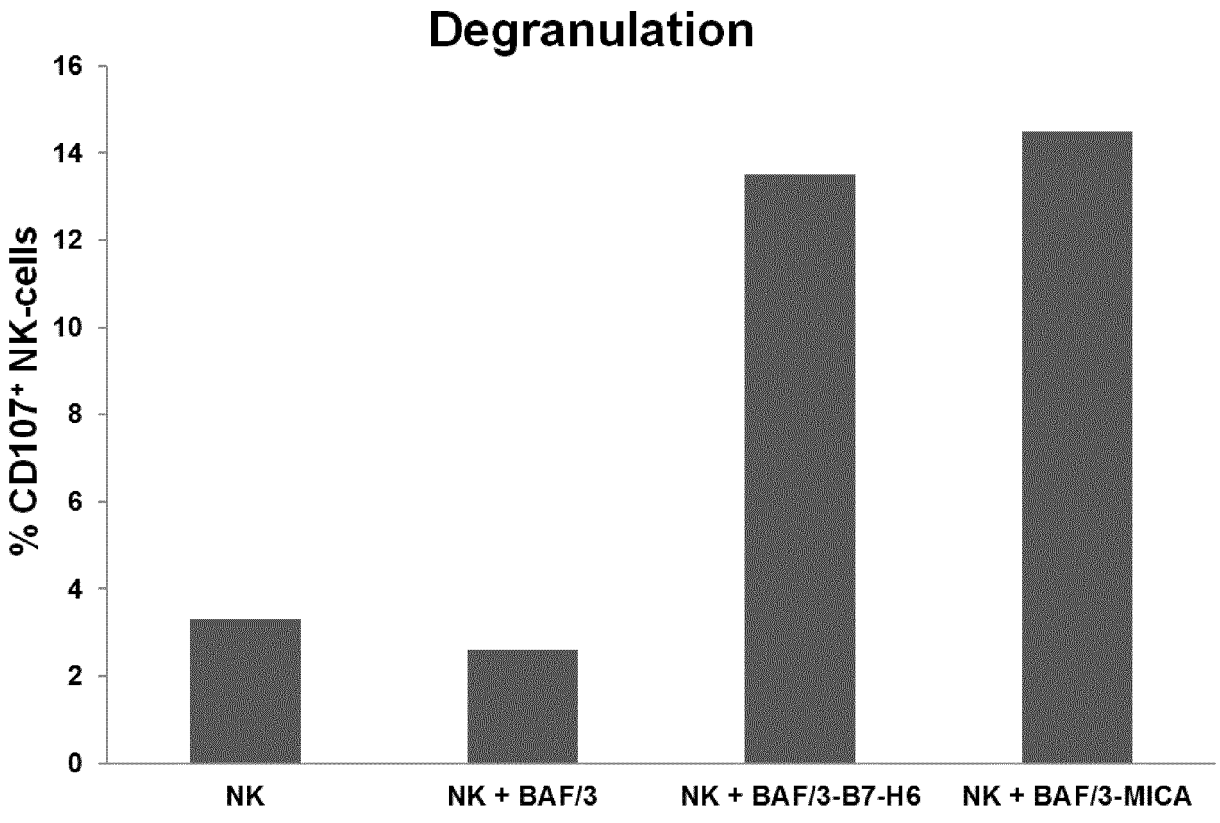

Degranulation
% CD107+ NK-cells
16
14
12
10
8
6
4
2
0
NK
NK + BAF/3
NK + BAF/3-B7-H6
NK + BAF/3-MICA

Fig. 8