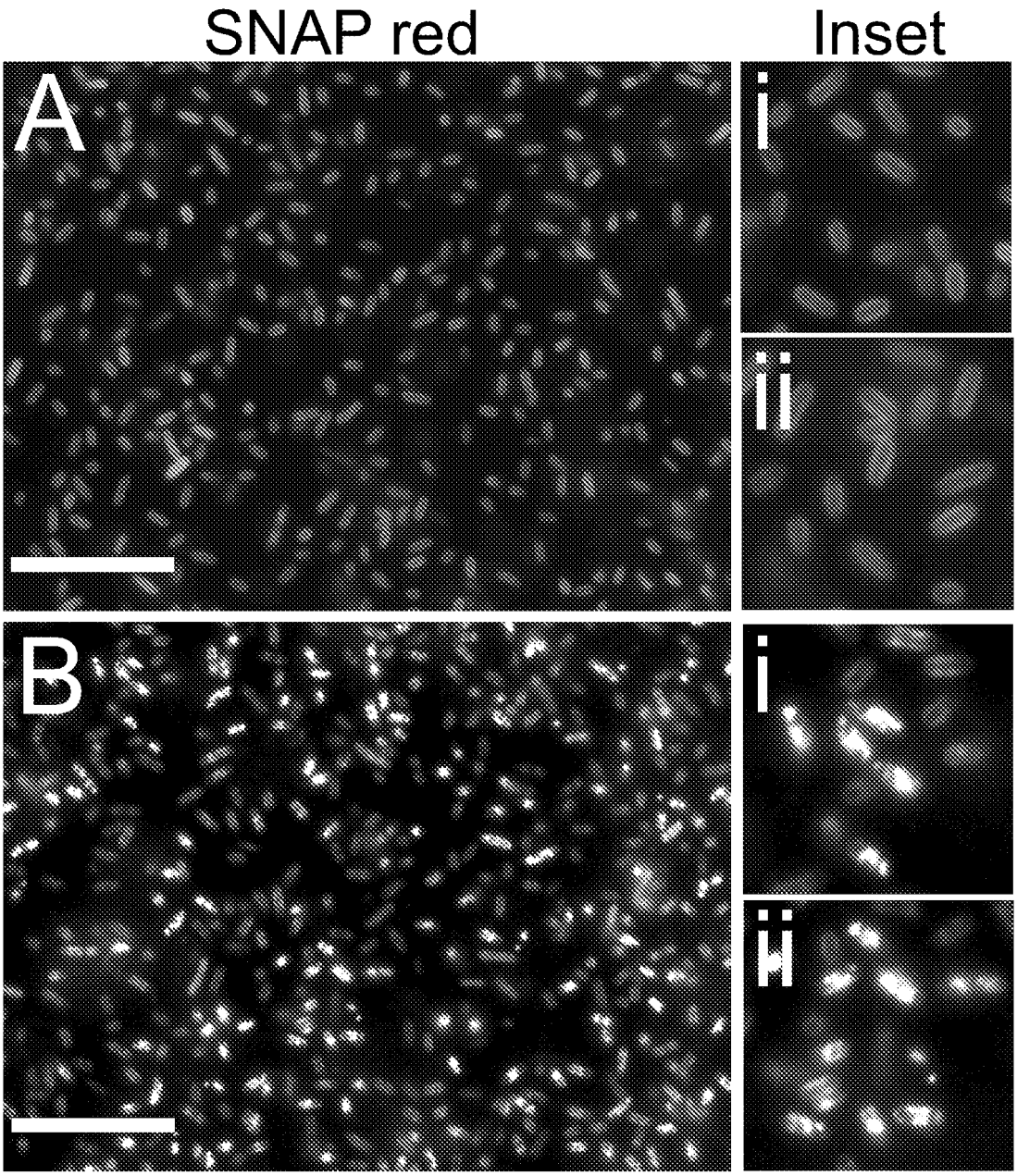


Figure 1

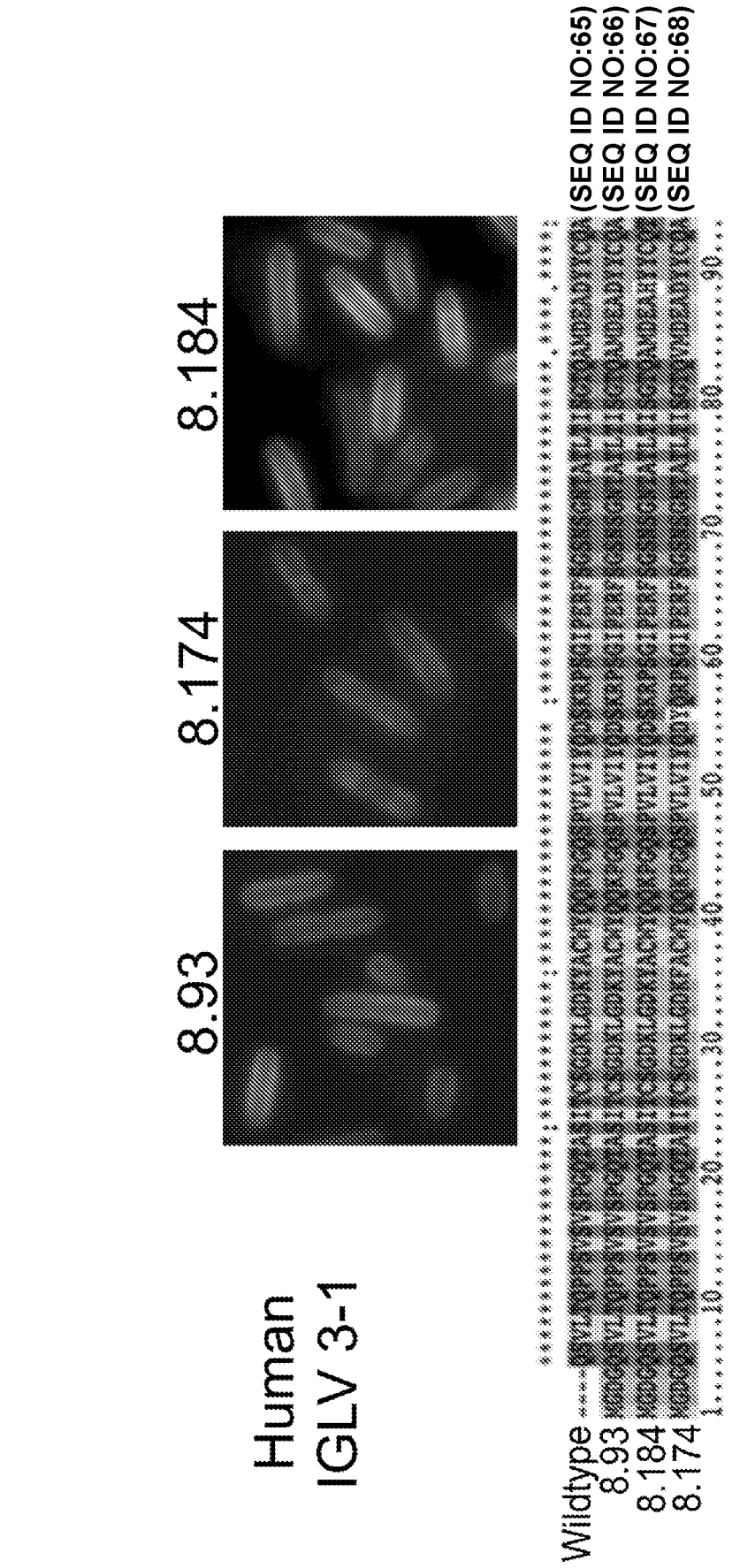

Human
IGLV 3-1
8.93
8.174
8.184
Wildtype
8.93
8.184
8.174
(SEQ ID NO:65)
(SEQ ID NO:66)
(SEQ ID NO:67)
(SEQ ID NO:68)

Figure 2

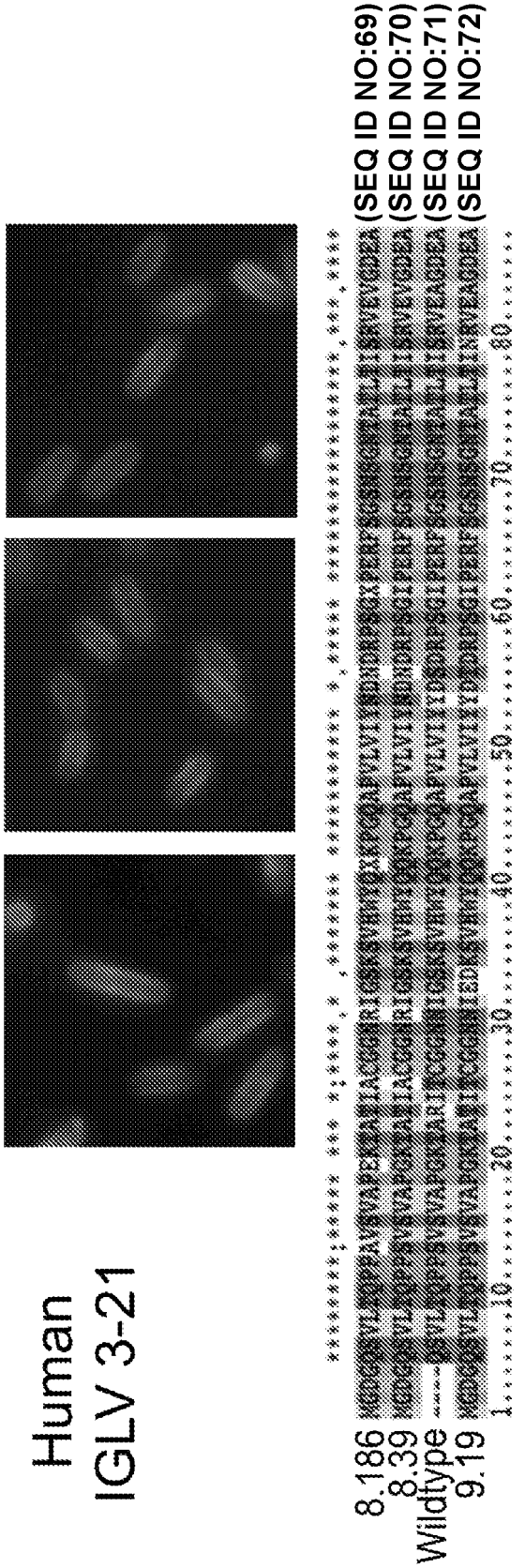


Figure 2 (continued)

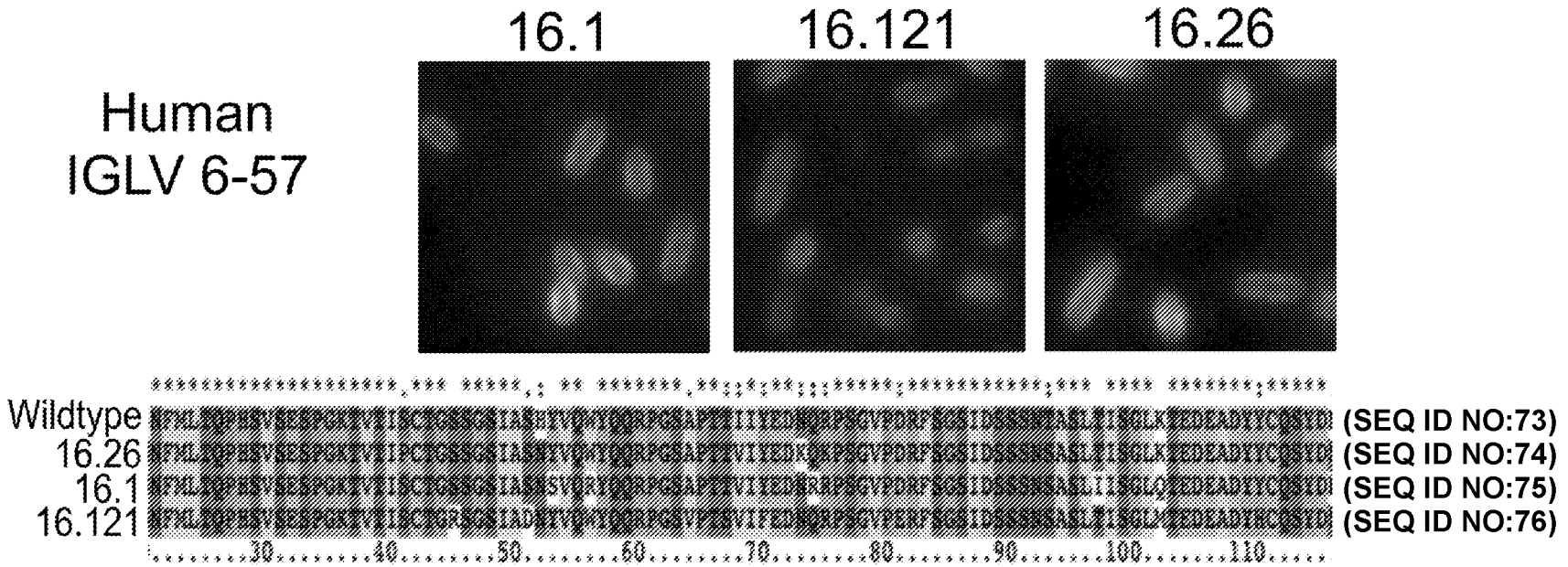


Figure 2 (continued)

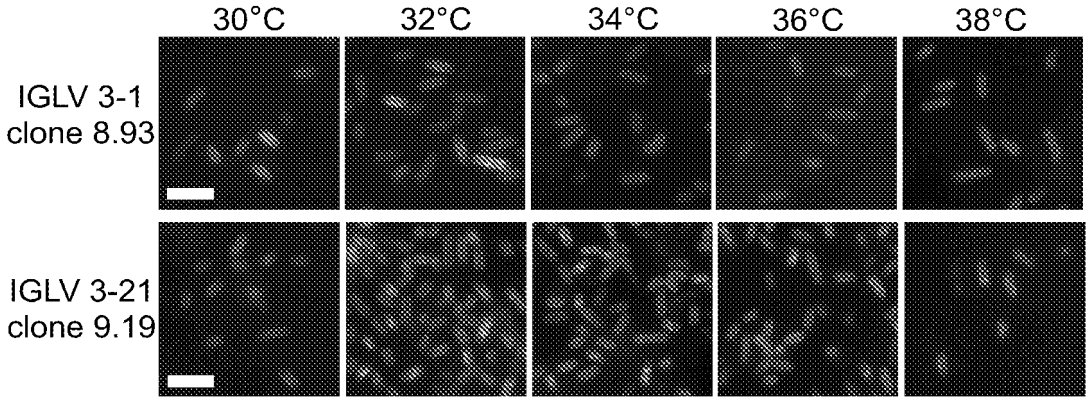


Figure 3

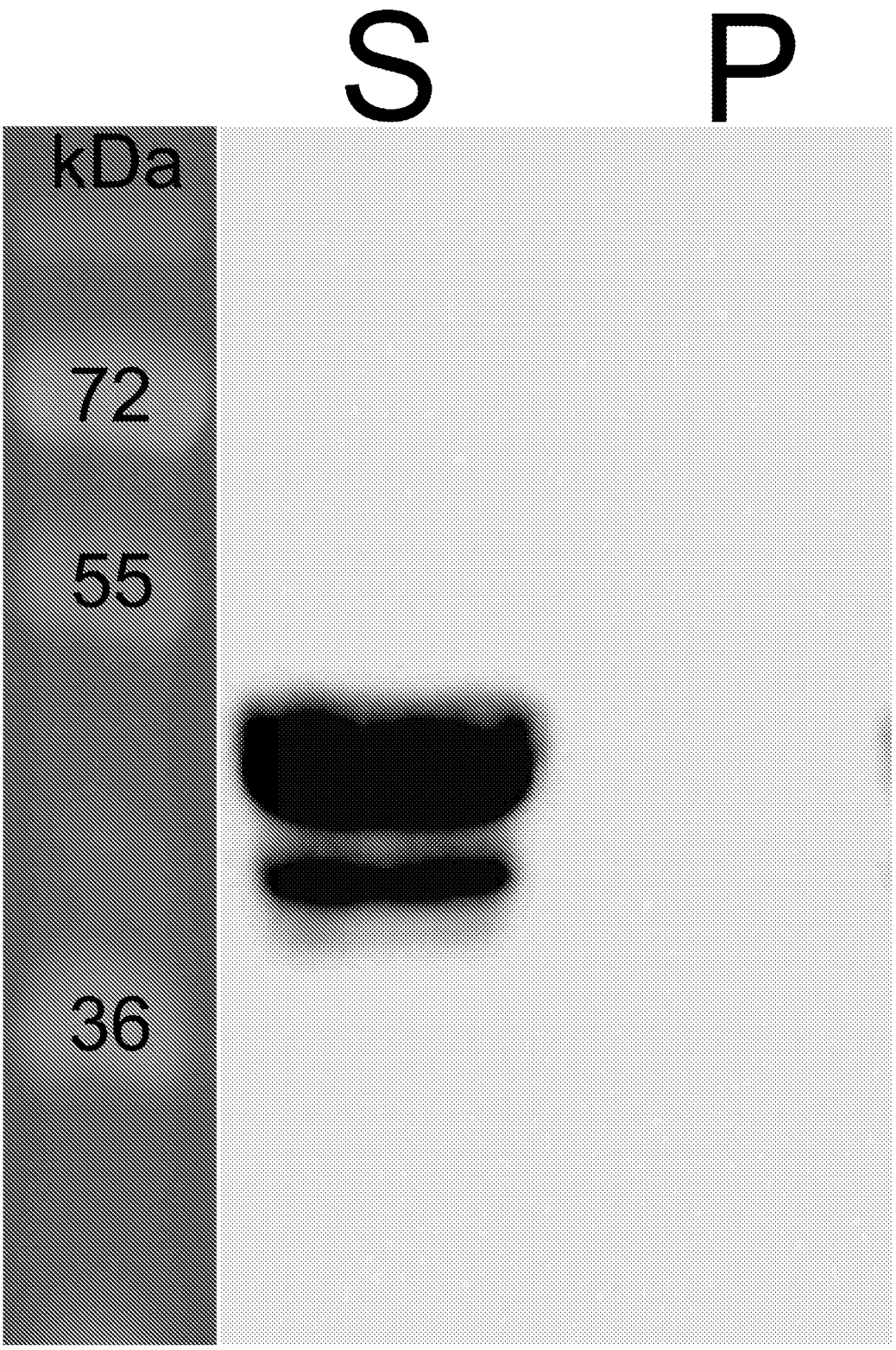


Figure 4

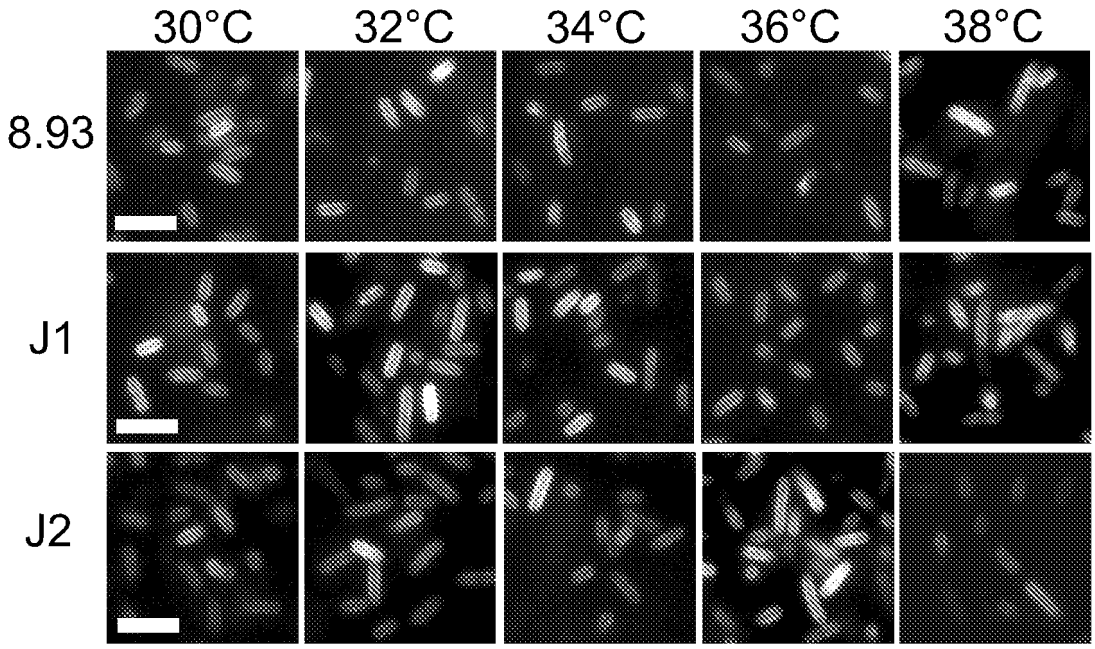


Figure 5

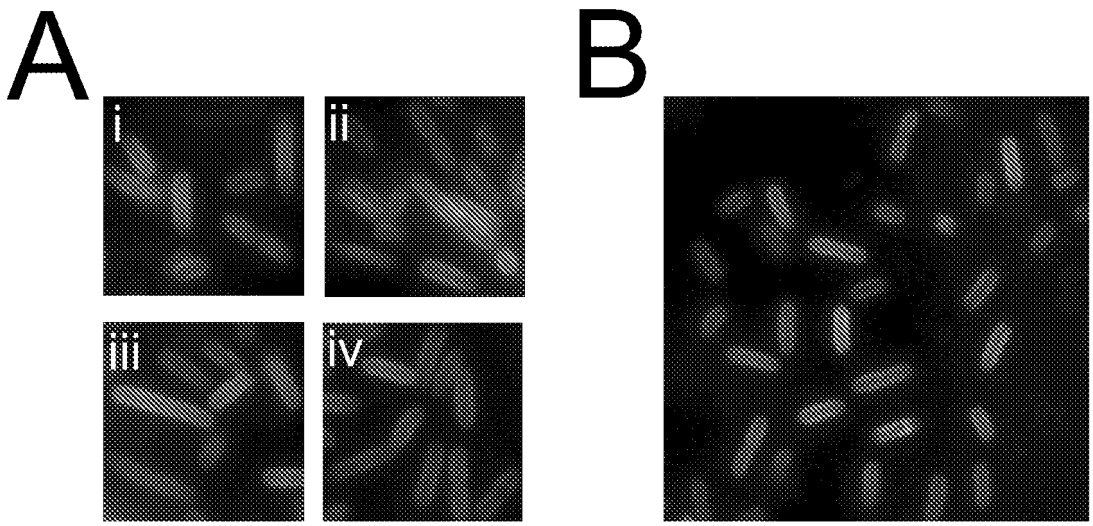


Figure 6

IGLV1-51(aka DPL5) (SEQ ID NO: 15)
QSVLTQPPSVSAAPGQKVTISCS**GSSSNIGNNY**VSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGT**WDSSLSAG**

IGLV1-40 (aka DPL6) (SEQ ID NO: 18)
QSVLTQPPSVSGAPGQRVTISCT**GSSSNIGAGYD**VHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQS**YDSSLSGS**

IGLV1-44 (aka DPL2) (SEQ ID NO: 21)
QSVLTQPPSASGTPGQRVTISCS**GSSSNIGSNT**VNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAA**WDDSLNGP**

IGV1-47 (aka DPL3) (SEQ ID NO: 24)
QSVLTQPPSASGTPGQRVTISCS**GSSSNIGSNY**VYWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAA**WDDSLSGP**

IGLV3-1 (aka DPL23) (SEQ ID NO: 6)
QSVLTQPPSVSVSPGQTASITCS**GDKLGDKY**ACWYQQKPGQSPVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQA**WDSSTA**

IGLV3-19 (SEQ ID NO: 27)
SSELTQDPAVSVALGQTVRITCQ**GDSLRSYY**ASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS**RDSSGNHL**

IGLV3-21 (SEQ ID NO: 9)
QSVLTQPPSVSVAPGQTARITCG**GNNIGSKS**VHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQV**WDSSSDHP**

IGLV6-57 (SEQ ID NO: 12)
NFMLTQPHSVSESPGKTVTISCT**GSSGSIASNY**VQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQS**YDSSN**

IGHV3-23 (aka DP47) (SEQ ID NO: 3)
EVQLLESGGGLVQPGGSLRLSCAAS**GFTFSSY**AMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK

Figure 7

IGLV3-1::IGHV3-23 scaffold with variable CDR3 regions (SEQ ID NO: 42)

ATG GGA GAC GGT CAG TCT GTG CTG ACT CAG CCA CCC
TCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGAT
AAATTGGGGGATAAATATGCTTGCTGGTATCAGCAGAAGCCAGGCCAGTCC
CCTGTGCTGGTCATCTATCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGG
ACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAC
NNTNNTNNTGGAGGTNNTNNTNNT
ACTGTGGTGTTCGGCACGGGCACCAAGCTCATCATTTCGTCT
CAGACCGGTGGTTCTGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGT GGTGGATCC
GAAGTCCAACTGCTGGAGTCCGGCGGTGGCCTGGTGCAGCCAGGTGGCAGC
CTGCGCCTGAGCTGCGCCGCATCCGGTTTTACTTTCAGCAGCTACGCGATGT
CGTGGGTGCGCCAGGCACCGGGCAAGGGCCTGGAGTGGGTCAGCGCCATC
AGCGGTAGCGGCGGTTCTACGTATTATGCGGACAGCGTCAAGGGCCGTTTC
ACCATCAGCCGTGACAATTCCAAAAACACCCTGTACTTGCAGATGAACAGC
TTGCGTGCGGAAGATACGGCTGTTTACTACTGTGCGAAA
NNTNNTNNTGGANNTNNTNNT
GCCTTTGATATTTGGGGTCAAGGTACCATGGTTACCGTGAGC AGC

Translation (SEQ ID NO: 43):

MGDGQSVLTQPPSVSVSPGQTASITCSGDKLGDKYACWYQQKPGQSPVLVIYQDSKRPSG
IPERFSGSNSGNTATLTISGTQAMDEADYYCQAWD **NNNGGNNN** TVVFGTGTKVTVSS ***QTGGSGGGG SGGGGSGGGGS*** EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVS
AISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK **NNNGNNN**
AFDIWGQGTMVTVSS

Figure 8

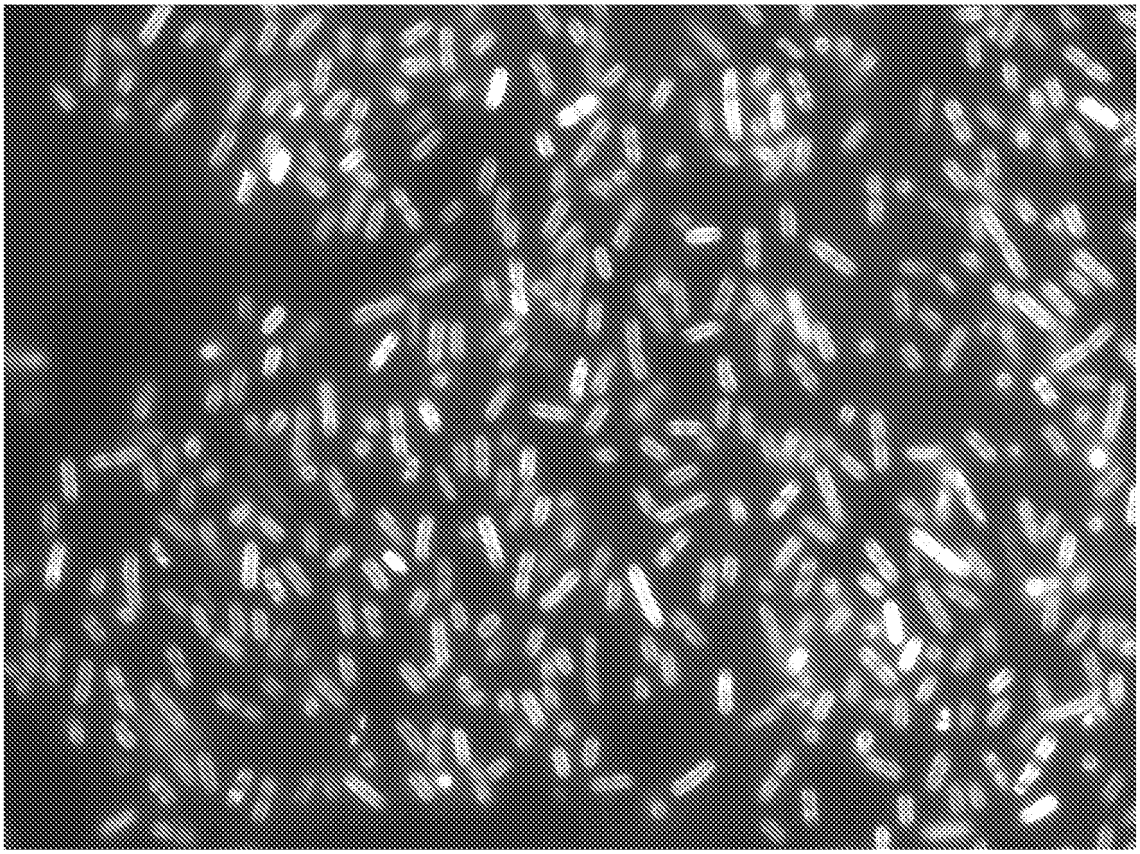


Figure 9

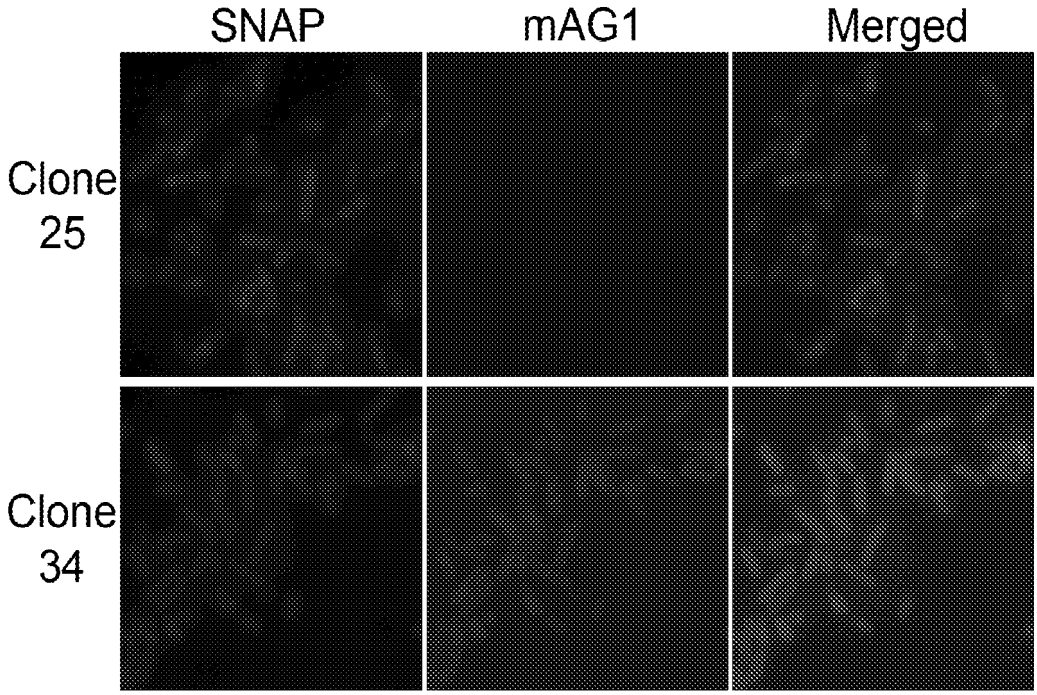


Figure 10

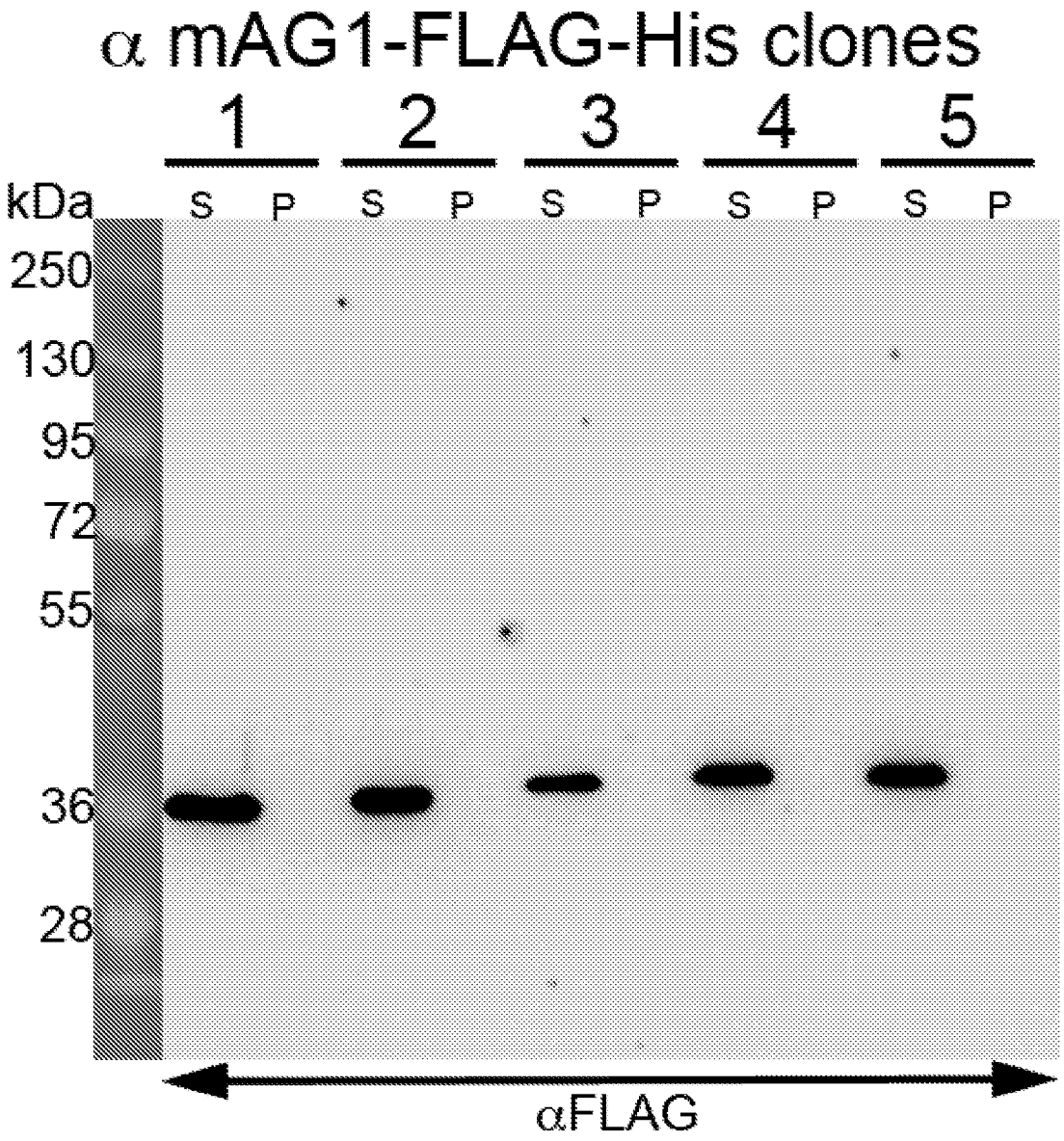

α mAG1-FLAG-His clones
1
2
3
4
5
kDa
S P S P S P S P S P
250
130
95
72
55
36
28
αFLAG

Figure 11

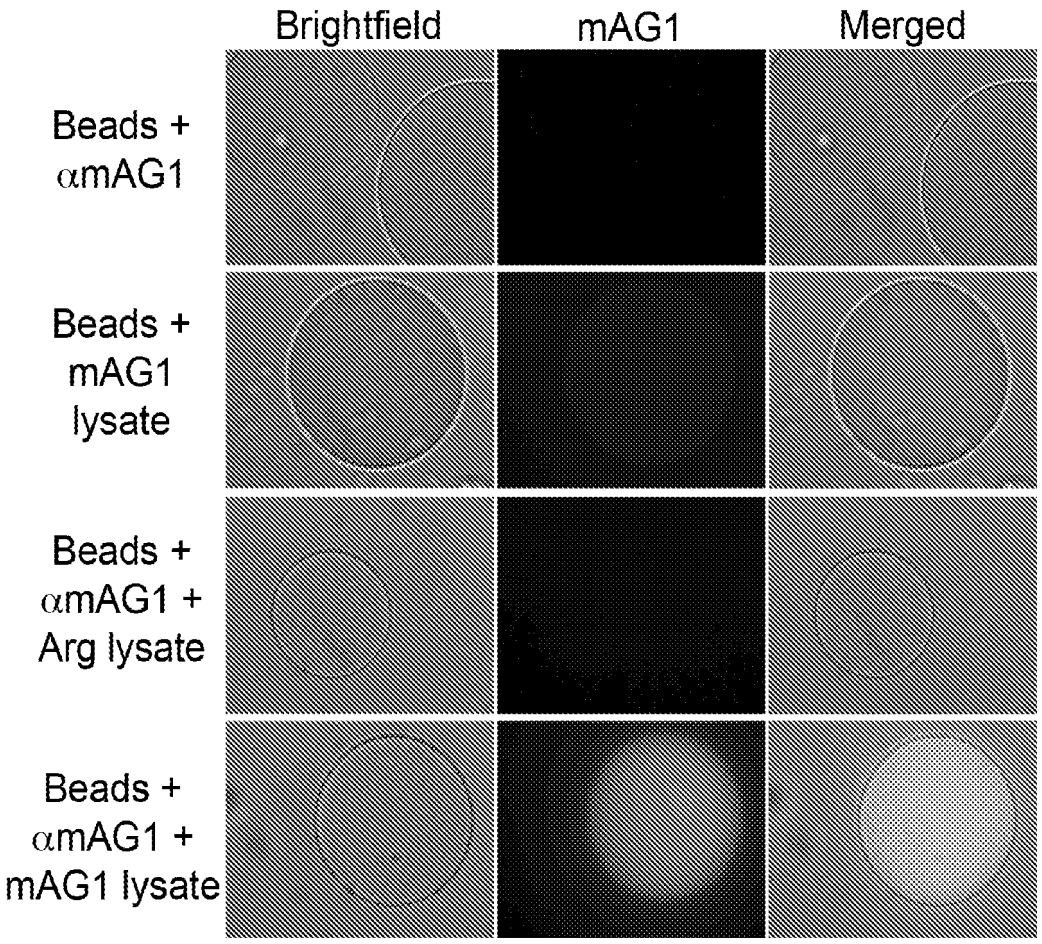

Brightfield
mAG1
Merged
Beads + αmAG1
Beads + mAG1 lysate
Beads + αmAG1 + Arg lysate
Beads + αmAG1 + mAG1 lysate

Figure 12

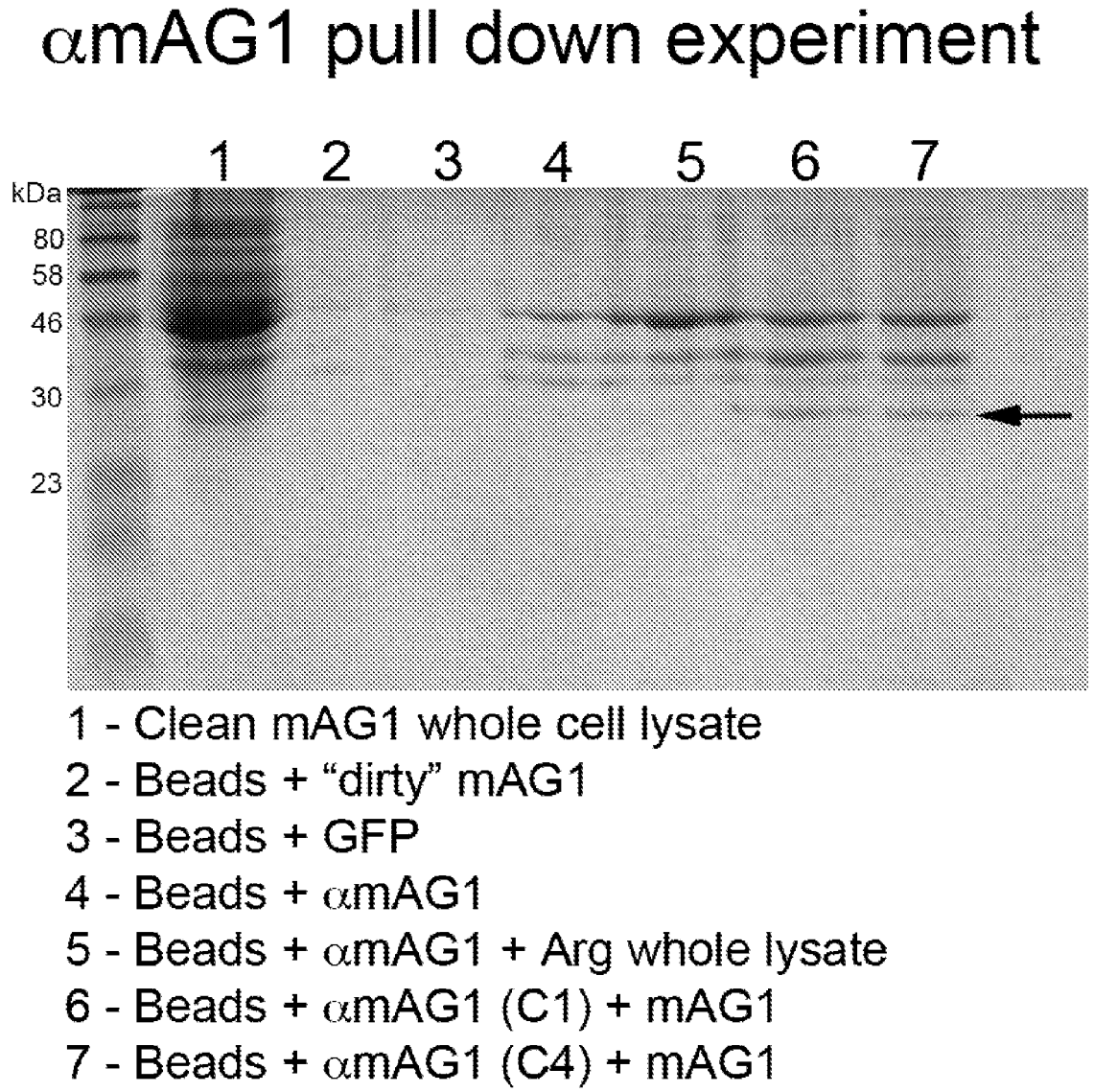

αmAG1 pull down experiment
1 2 3 4 5 6 7
kDa
80
58
46
30
23
1 - Clean mAG1 whole cell lysate
2 - Beads + "dirty" mAG1
3 - Beads + GFP
4 - Beads + αmAG1
5 - Beads + αmAG1 + Arg whole lysate
6 - Beads + αmAG1 (C1) + mAG1
7 - Beads + αmAG1 (C4) + mAG1

Figure 13

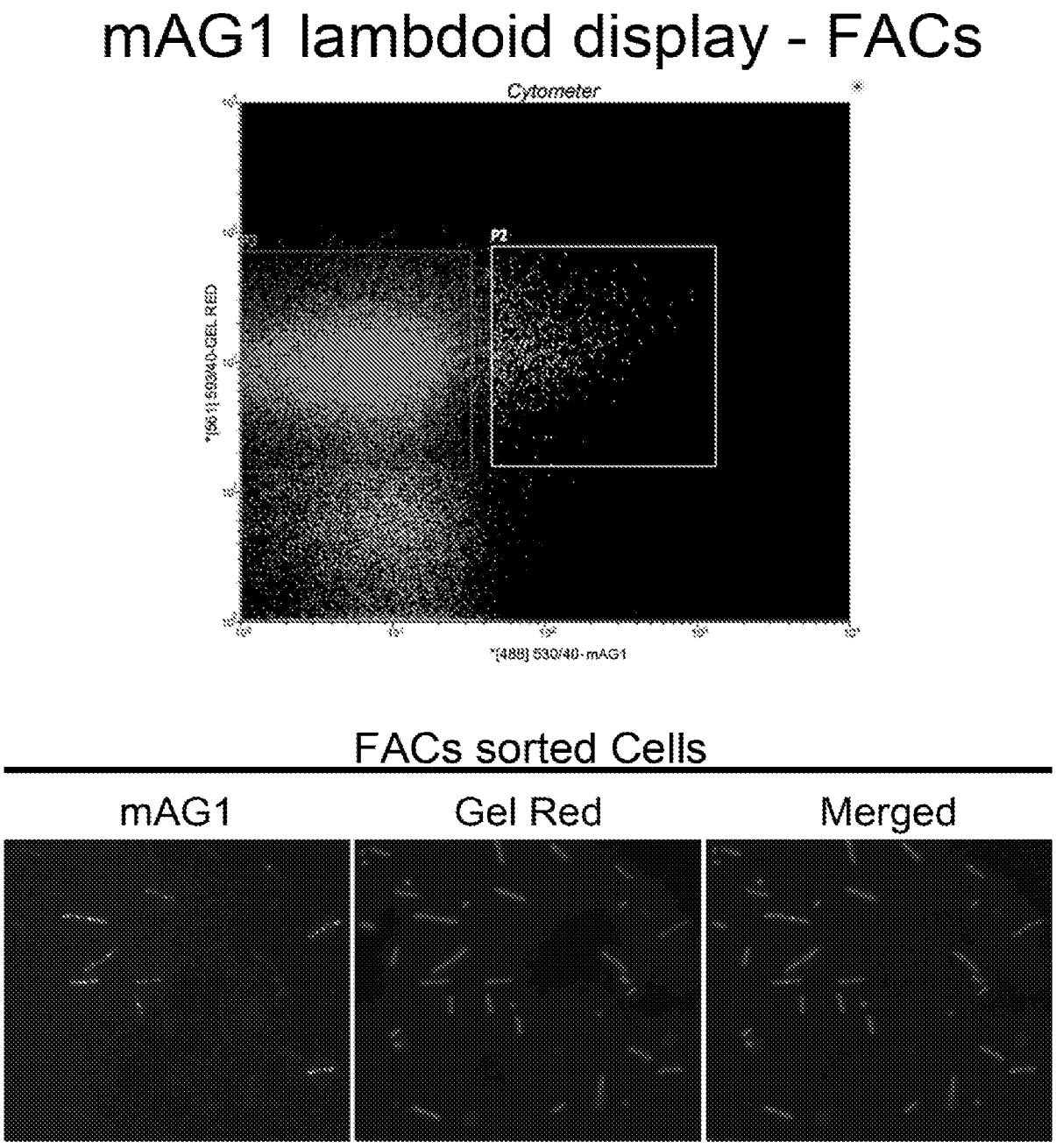

mAG1 lambdoid display - FACs
Cytometer
P2
*[561] 593/40-CEL RED
*[488] 530/40 - mAG1
FACs sorted Cells
mAG1
Gel Red
Merged

Figure 14

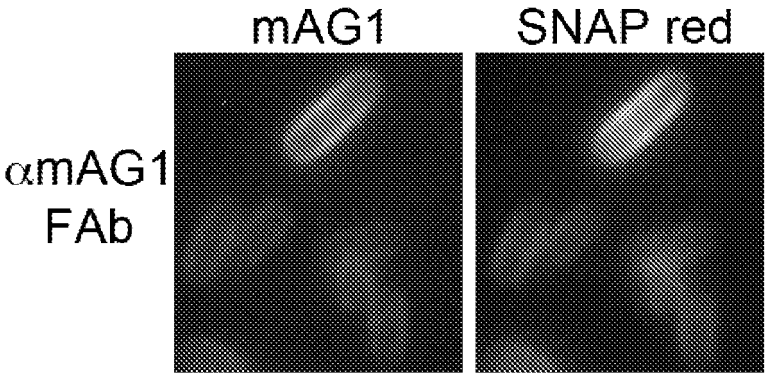


Figure 15

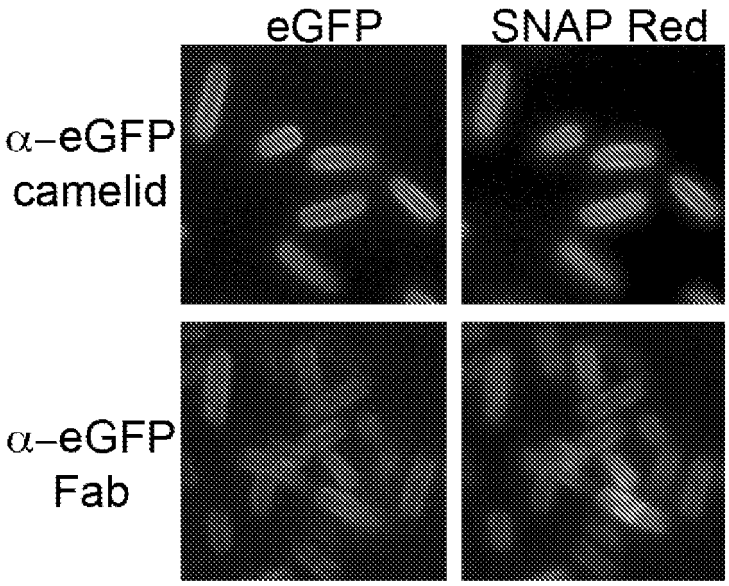


Figure 16

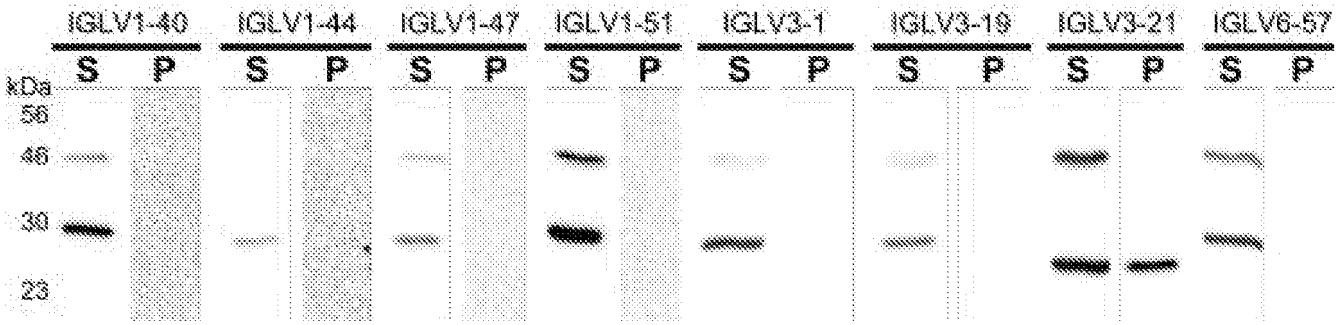

IGLV1-40
IGLV1-44
IGLV1-47
IGLV1-51
IGLV3-1
IGLV3-19
IGLV3-21
IGLV6-57
S P S P S P S P S P S P S P S P
kDa
56
46
30
23

Figure 17

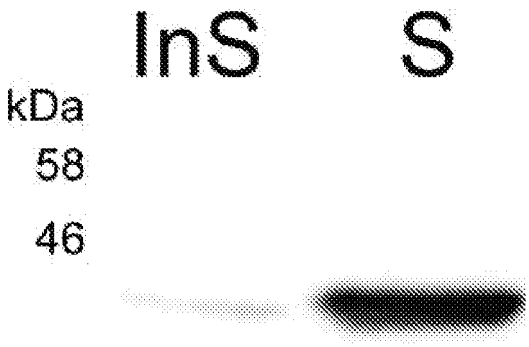


Figure 18