Figure 1

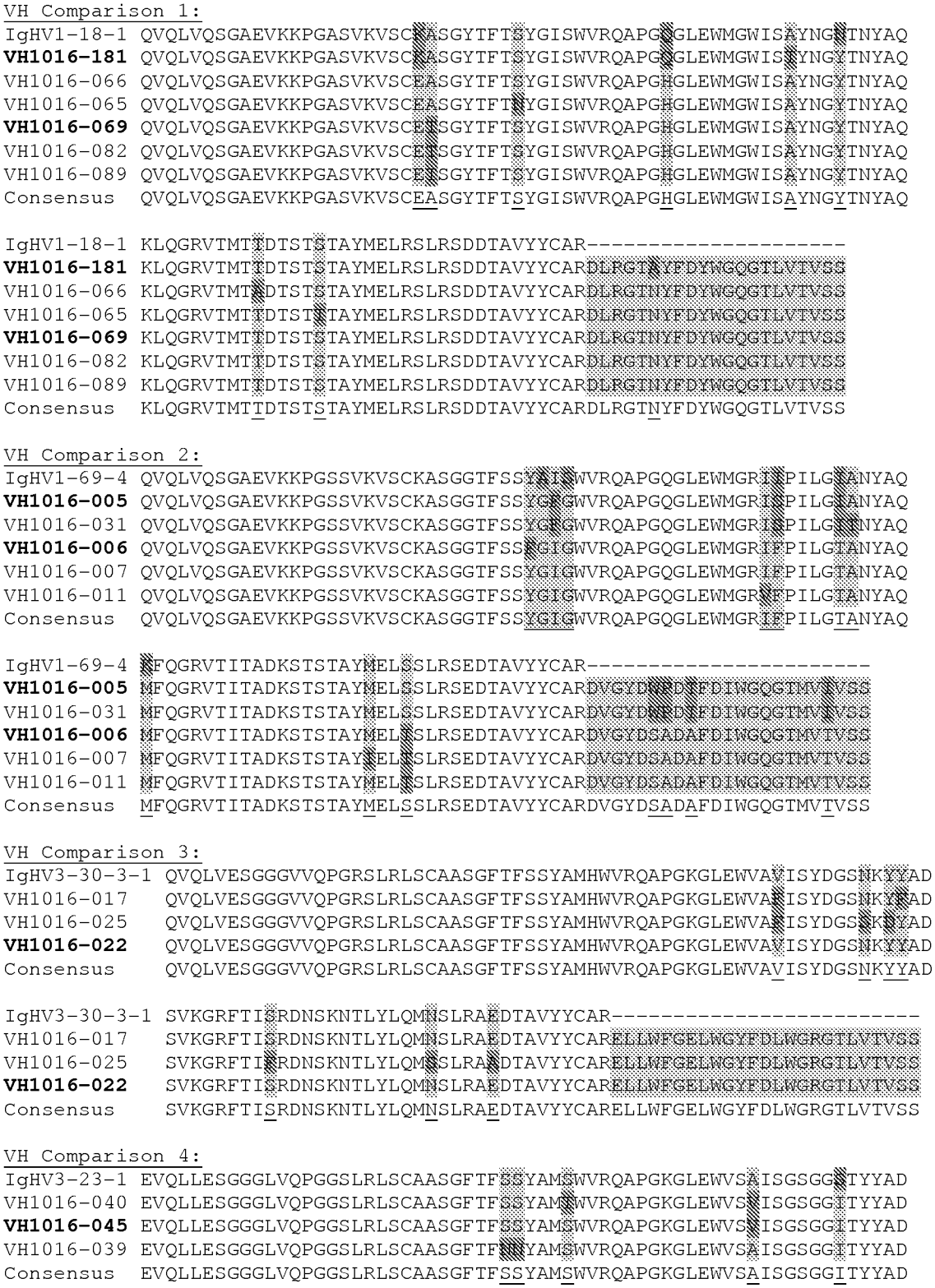

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VH1016-066 QVQLVQSGAEVKKPGASVKVSCEASGYTFTSYGISWVRQAPGHGLEWMGWISAYNGYTNYAQ
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VH1016-089 QVQLVQSGAEVKKPGASVKVSCETSGYTFTSYGISWVRQAPGHGLEWMGWISAYNGYTNYAQ
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IgHV1-18-1 KLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR----------
VH1016-181 KLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLRGTAYFDYWGQGTLVTVSS
VH1016-066 KLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLRGTNYFDYWGQGTLVTVSS
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VH1016-069 KLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLRGTNYFDYWGQGTLVTVSS
VH1016-082 KLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLRGTNYFDYWGQGTLVTVSS
VH1016-089 KLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLRGTNYFDYWGQGTLVTVSS
Consensus KLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDLRGTNYFDYWGQGTLVTVSS
VH Comparison 2:
IgHV1-69-4 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANYAQ
VH1016-005 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYGFGWVRQAPGQGLEWMGRISPILGIANYAQ
VH1016-031 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYGFGWVRQAPGQGLEWMGRISPILGIANYAQ
VH1016-006 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSFGIGWVRQAPGQGLEWMGRIFPILGTANYAQ
VH1016-007 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYGIGWVRQAPGQGLEWMGRIFPILGTANYAQ
VH1016-011 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYGIGWVRQAPGQGLEWMGRIFPILGTANYAQ
Consensus QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYGIGWVRQAPGQGLEWMGRIFPILGTANYAQ
IgHV1-69-4 KFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR----------
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VH1016-031 MFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARDVGYDWRDTFDIWGQGTMVTVSS
VH1016-006 MFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARDVGYDSADAFDIWGQGTMVTVSS
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VH1016-011 MFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARDVGYDSADAFDIWGQGTMVTVSS
Consensus MFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARDVGYDSADAFDIWGQGTMVTVSS
VH Comparison 3:
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VH1016-017 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAFISYDGSNKYYAD
VH1016-025 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAFISYDGSSKNYAD
VH1016-022 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYAD
Consensus QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYAD
IgHV3-30-3-1 SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR----------
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VH1016-025 SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELLWFGELWGYFDLWGRGTLVTVSS
VH1016-022 SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELLWFGELWGYFDLWGRGTLVTVSS
Consensus SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARELLWFGELWGYFDLWGRGTLVTVSS
VH Comparison 4:
IgHV3-23-1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYAD
VH1016-040 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSISGSGGITYYAD
VH1016-045 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSISGSGGITYYAD
VH1016-039 EVQLLESGGGLVQPGGSLRLSCAASGFTFNNYAMSWVRQAPGKGLEWVSAISGSGGITYYAD
Consensus EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGITYYAD

Figure 1 (continued)

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VH1016-045 SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGWGSDYWGQGTLVTVSS
VH1016-039 SEKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRGWGSDCWGQGTLVTVSS
Consensus  SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRGWGSDYWGQGTLVTVSS
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VH Comparison 5:

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VH1016-078   QLQLQESGSGLVKPSQTLSLTCAVSGGSISSGGHSWSWIRQPPGKGLEWIGCIYHSGNTYN
VH1016-084   QLQLQESGSGLVKPSQTLSLTCSVSGGSISSGGHSWSWIRQPPGKGLEWIGCIYHSGNTYN
VH1016-061   QLQLQESGSGLVKPSQTLSLTCAVSGGSISSGGHSWSWIRQPPGKGLEWIGCIYHSGNTYD
VH1016-062   QLQLQESGSGLVKPSQTLSLTCAVSGGSISSGGHSWSWIRQPPGKGLEWIGCIYHSGNTYD
VH1016-063   QLQLQESGSGLVKPSQTLSLTCAVSGGSISSGGHSWSWIRQPPGKGLEWIGCIYHSGNTYD
VH1016-064   QLQLQESGSGLVKPSQTLSLTCAVSGGSISSGGHSWSWIRQPPGKGLEWIGCIYHSGNTYD
VH1016-087   QLQLQESGSGLVKPSQTLSLTCAVSGGSISSGGHSWSWIRQPPGKGLEWIGCIYHSGNTYD
Consensus    QLQLQESGSGLVKPSQTLSLTCAVSGGSISSGGHSWSWIRQPPGKGLEWIGCIYHSGNTYD

IgHV4-30-2-1 NPSLKSRVTISVDRSKNQFSLKLSSVTAADTAVYYCAR--------------------
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VH1016-078   NPSLKSRVTISVDRSKNQFSLKLSSVTAADTAVYYCARSSYDILTDWGQGNLVTVSS
VH1016-084   NPSLKSRVTISVDRSKNQFSLKLSSVTAADTAVYYCARSSYDILTDWGQGTLVTVSS
VH1016-061   NPSLKSRVTIAVDRSKNQNSLKLSSVTAADTAVYYCARSSYDRLTDWGQGTLVTVSS
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VH1016-064   NPSLKSRVTISVDRSKNQNSLKLSSVTAADTAVYYCARSSYDILTDWGQGTLVTVSS
VH1016-087   NPSLKSRVTISVDRSKNQFSLKLSSVTAADTAVYYCARSSYDILTDWGQGTLVTVSS
Consensus    NPSLKSRVTISVDRSKNQFSLKLSSVTAADTAVYYCARSSYDILTDWGQGTLVTVSS
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VH Comparison 6:

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VH1016-028 EVQLVQSGSEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSD
VH1016-008 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSR
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VH1016-093 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSD
VH1016-096 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSD
VH1016-104 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSD
Consensus  EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSD

IgHV5-51-1 TRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR--------------------
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VH1016-008 TRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARQEITGRFDYWGQGTLVTVSS
VH1016-012 TRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARQEITGRFDYWGQGTLVTVSS
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VH1016-095 TRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARQEITGDFDYWGQGTLVTVSS
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VH1016-104 TRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARQEITGDFDYWGQGTLVTVSS
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Figure 2

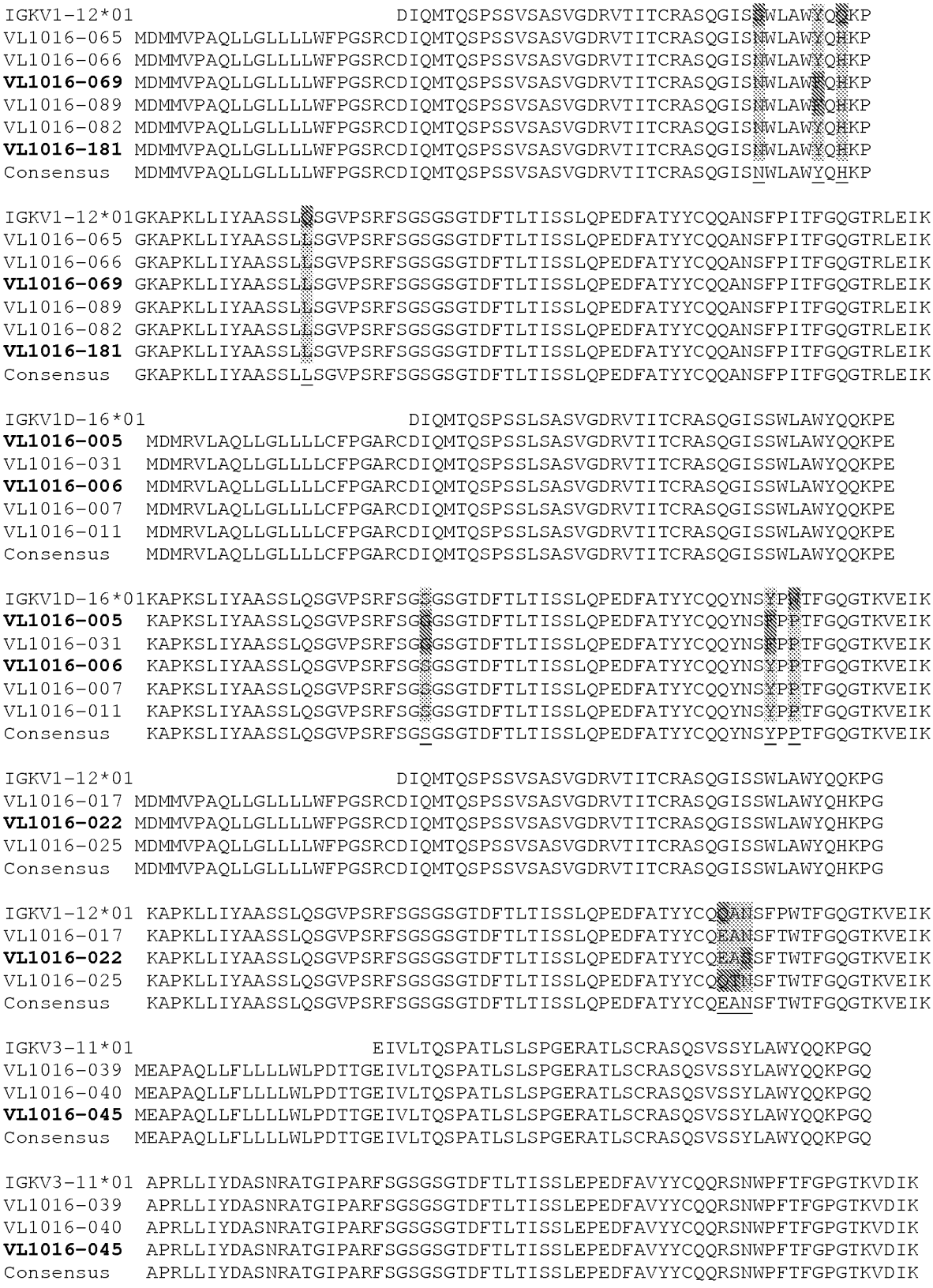

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VL1016-089 MDMMVPAQLLGLLLLWFPGSRCDIQMTQSPSSVSASVGDRVTITCRASQGISNWLAWFQHKP
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Consensus MDMMVPAQLLGLLLLWFPGSRCDIQMTQSPSSVSASVGDRVTITCRASQGISNWLAWYQHKP
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VL1016-089 GKAPKLLIYAASSLLSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPITFGQGTRLEIK
VL1016-082 GKAPKLLIYAASSLLSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPITFGQGTRLEIK
VL1016-181 GKAPKLLIYAASSLLSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPITFGQGTRLEIK
Consensus GKAPKLLIYAASSLLSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPITFGQGTRLEIK
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VL1016-031 MDMRVLAQLLGLLLLCFPGARCDIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPE
VL1016-006 MDMRVLAQLLGLLLLCFPGARCDIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPE
VL1016-007 MDMRVLAQLLGLLLLCFPGARCDIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPE
VL1016-011 MDMRVLAQLLGLLLLCFPGARCDIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPE
Consensus MDMRVLAQLLGLLLLCFPGARCDIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPE
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Consensus KAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPPTFGQGTKVEIK
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Consensus MDMMVPAQLLGLLLLWFPGSRCDIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQHKPG
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VL1016-025 KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQETNSFTWTFGQGTKVEIK
Consensus KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQEANSFTWTFGQGTKVEIK
IGKV3-11*01 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQ
VL1016-039 MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQ
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Consensus MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQ
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Figure 2 (continued)

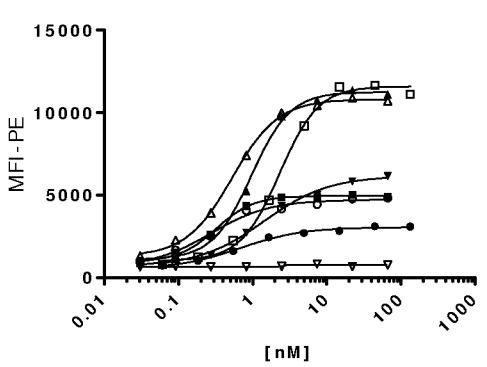
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Consensus   MDMMVPAQLLGLLLLWFPGSRCDIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQHKPG

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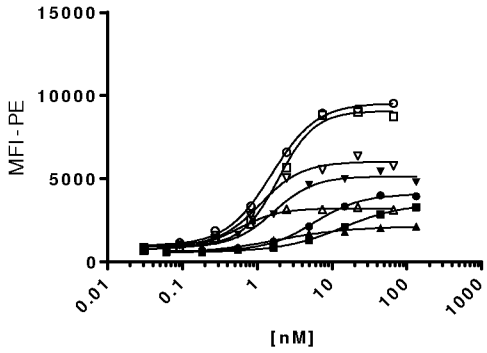
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Consensus   MDMRVPAQLLGLLLLWLPGARCAIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPG

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VL1016-028  KAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYPL-TFGGGTKVEIK
VL1016-095  KAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYPL-TFGGGTKVEIK
Consensus   KAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYPL TFGGGTKVEIK
```

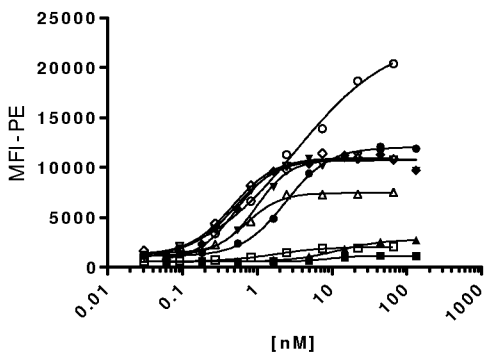
Figure 3



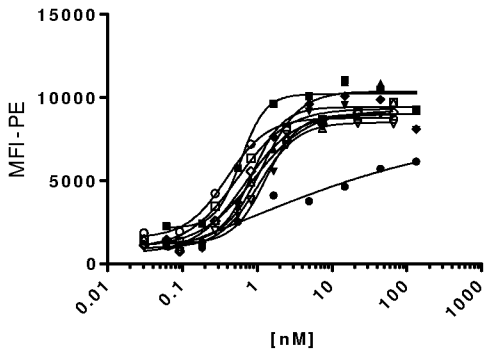
clone name	EC_{50}
Uni-058	0.670
IgG4-058	0.276
Uni-006-TE	0.323
IgG1-006	2.319
IgG4-5D5	0.966
IgG1-5D5	0.531
IgG1-G11-HZ	1.438
HuMab-KLH	ND



clone name	EC_{50}
Uni-005	5.797
IgG1-005	1.556
Uni-006	13.89
IgG1-006	1.918
Uni-008	1.848
IgG1-008	0.554
Uni-022	1.656
IgG1-022	1.097



clone name	EC_{50}
Uni-024	2.419
IgG1-024	~ 3.186
Uni-035-D09	9.319
IgG1-035-D09	1.783
Uni-045	12.20
IgG1-045	0.692
Uni-062	0.984
IgG1-062	0.503
Uni-064	0.519
IgG1-064	0.465



clone name	EC_{50}
Uni-068-TE	~ 0.605
IgG1-068	0.393
Uni-069	0.600
IgG1-069	0.547
Uni-098	1.157
IgG1-098	0.900
Uni-101	1.303
IgG1-101	1.035
Uni-181	0.847
IgG1-181	0.679

Figure 4

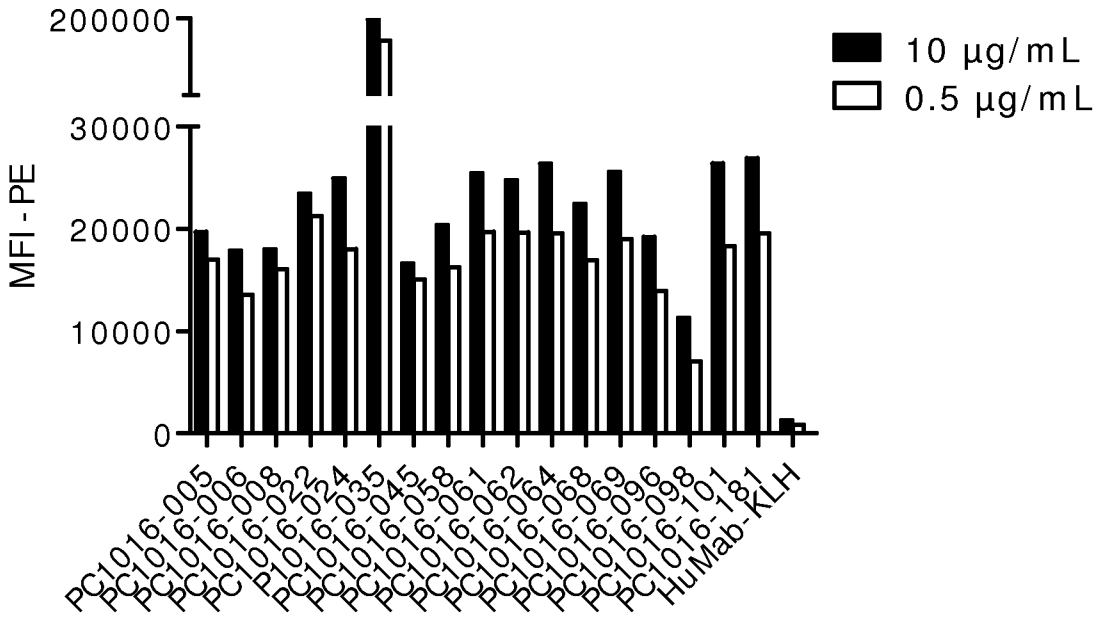
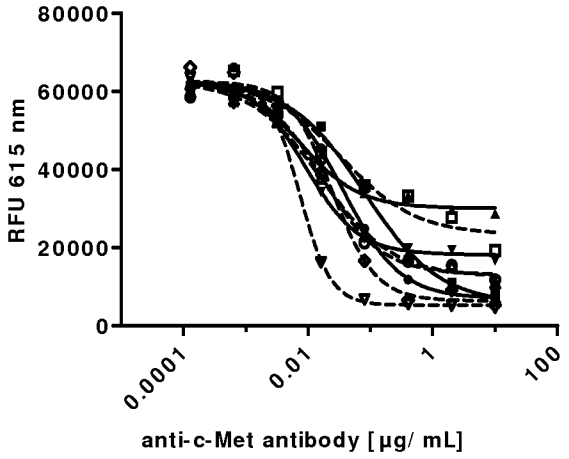
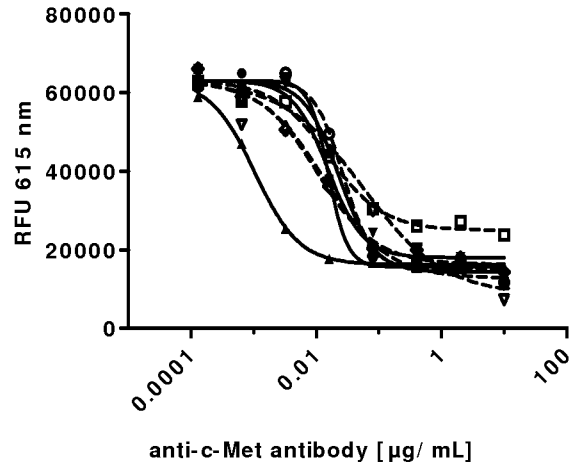

200000
30000
20000
10000
0
MFI-PE
10 µg/mL
0.5 µg/mL
PC1016-005
PC1016-006
PC1016-008
PC1016-022
PC1016-024
PC1016-035
PC1016-045
PC1016-058
PC1016-061
PC1016-062
PC1016-064
PC1016-068
PC1016-069
PC1016-096
PC1016-098
PC1016-101
PC1016-181
HuMab-KLH

Figure 5



	EC_{50}	Bottom
005	0.03616	6944
006	0.07994	5628
008	0.007878	30087
022	0.009265	18227
024	0.01684	13062
035	0.03484	23287
045	0.01646	12563
058	0.007270	5201
5D5	0.02435	6347

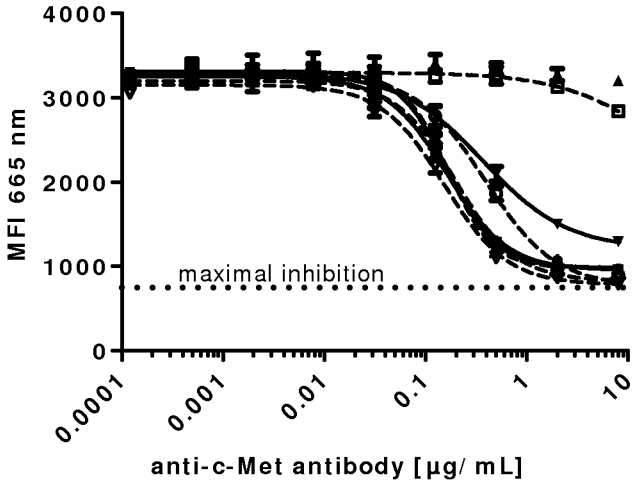
No HGF-Euopium $^{3+}$ ~ 600
No competing mAb ~ 66000



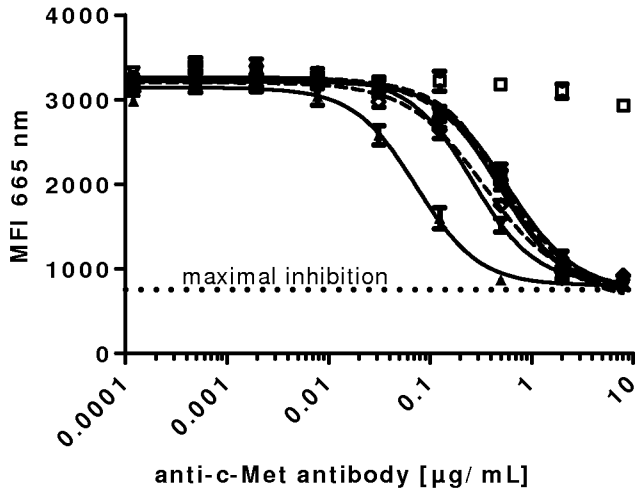
	EC_{50}	Bottom
061	0.01552	15583
062	0.02299	14276
064	0.001039	16172
068	0.01529	17943
069	0.02671	15028
096	0.01523	24849
098	0.01349	12699
101	0.05580	8380
181	0.01030	16255

No HGF-Euopium $^{3+}$ ~ 600
No competing mAb ~ 66000

Figure 6



	IC_{50}
005	0.1648
006	0.1619
008	ND
022	0.3687
024	0.3880
035	ND
045	0.1679
058	0.1534
5D5	0.1984



	IC_{50}
061	0.4882
062	0.5768
064	0.07363
068	0.2611
069	0.5360
096	ND
098	0.5526
101	0.5276
181	0.3368

Figure 7

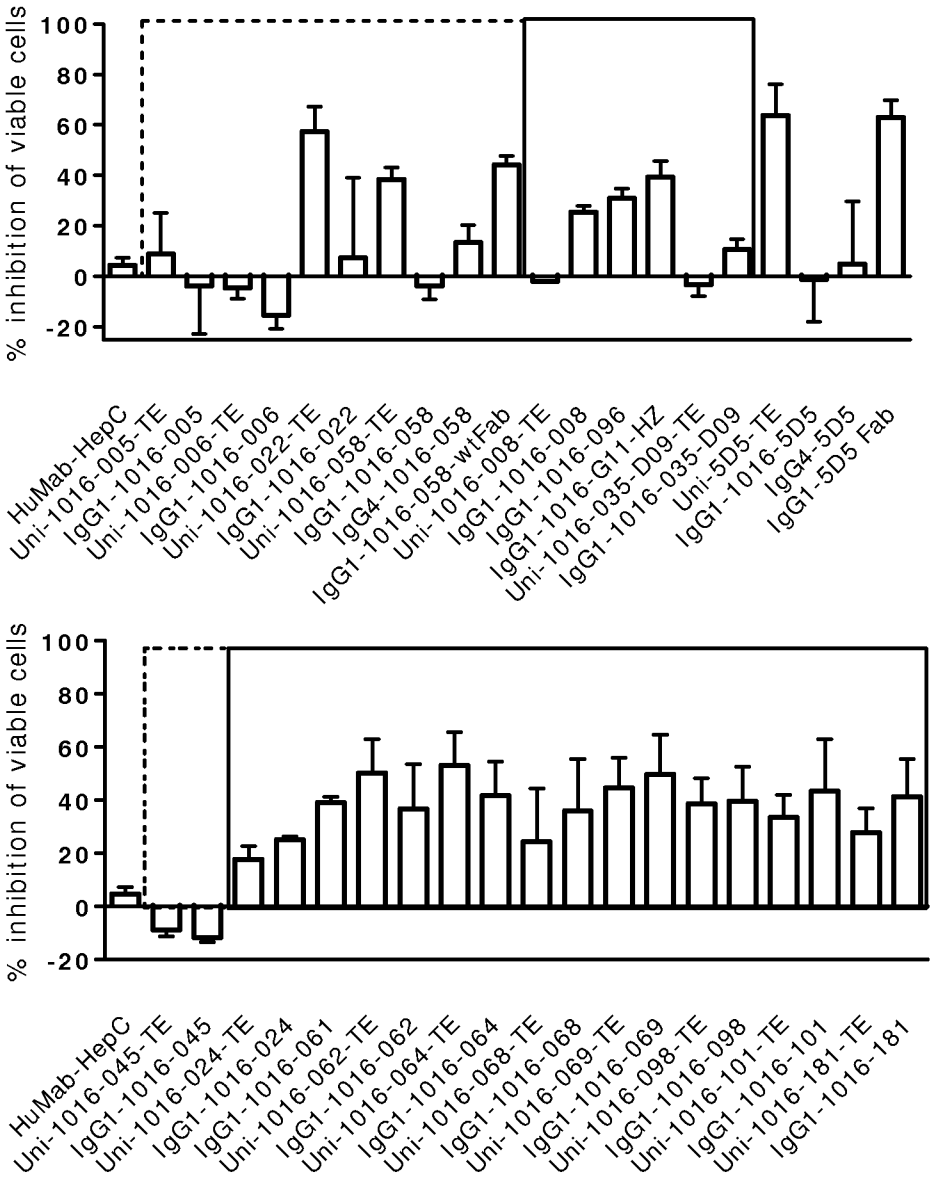

% inhibition of viable cells
100
80
60
40
20
0
-20
HuMab-HepC
Uni-1016-005-TE
IgG1-1016-005
Uni-1016-006-TE
IgG1-1016-006
Uni-1016-022-TE
IgG1-1016-022
Uni-1016-058-TE
IgG1-1016-058
IgG4-1016-058
IgG1-1016-058-wtFab
Uni-1016-008-TE
IgG1-1016-008
IgG1-1016-096
IgG1-1016-G11-HZ
Uni-1016-035-D09-TE
IgG1-1016-035-D09
Uni-5D5-TE
IgG1-1016-5D5
IgG4-5D5
IgG1-5D5 Fab
% inhibition of viable cells
100
80
60
40
20
0
-20
HuMab-HepC
Uni-1016-045-TE
IgG1-1016-045
Uni-1016-024-TE
IgG1-1016-024
IgG1-1016-061
Uni-1016-062-TE
IgG1-1016-062
Uni-1016-064-TE
IgG1-1016-064
Uni-1016-068-TE
IgG1-1016-068
Uni-1016-069-TE
IgG1-1016-069
Uni-1016-098-TE
IgG1-1016-098
Uni-1016-101-TE
IgG1-1016-101
Uni-1016-181-TE
IgG1-1016-181

Figure 8

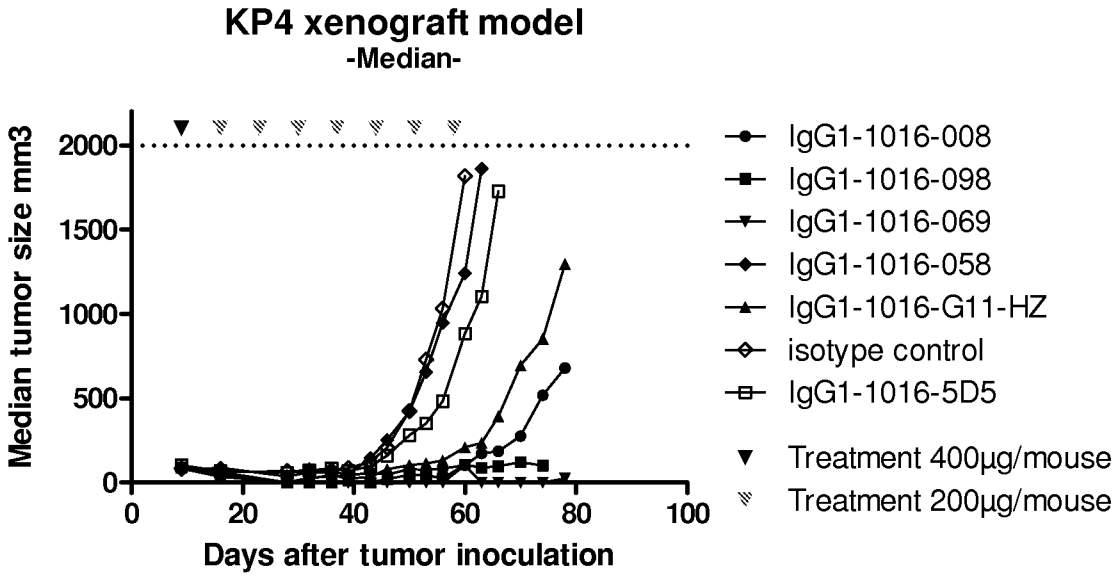

KP4 xenograft model
-Median-
Median tumor size mm3
2000
1500
1000
500
0
0
20
40
60
80
100
Days after tumor inoculation
IgG1-1016-008
IgG1-1016-098
IgG1-1016-069
IgG1-1016-058
IgG1-1016-G11-HZ
isotype control
IgG1-1016-5D5
Treatment 400µg/mouse
Treatment 200µg/mouse

Figure 9

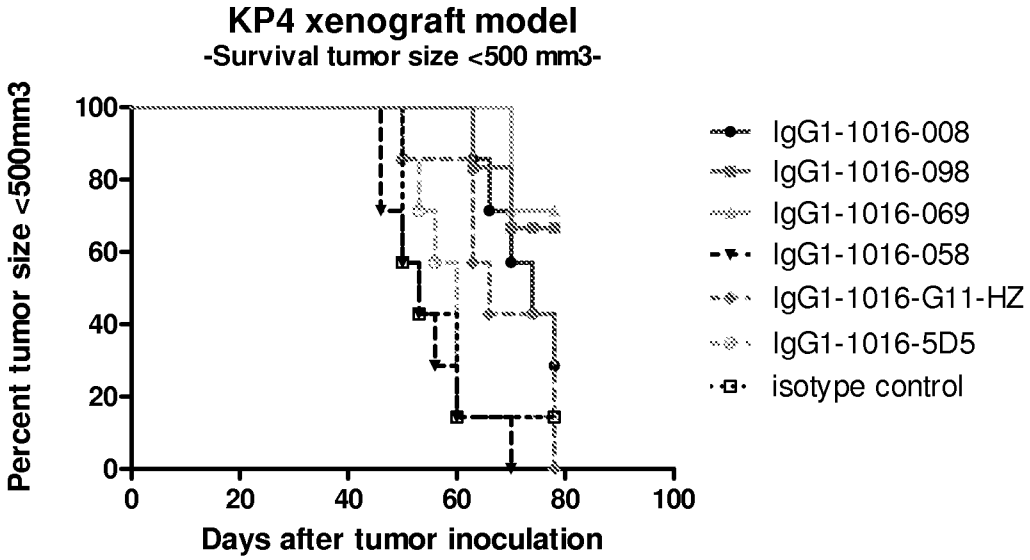

KP4 xenograft model
-Survival tumor size <500 mm3-
Percent tumor size <500mm3
100
80
60
40
20
0
0
20
40
60
80
100
Days after tumor inoculation
IgG1-1016-008
IgG1-1016-098
IgG1-1016-069
IgG1-1016-058
IgG1-1016-G11-HZ
IgG1-1016-5D5
isotype control

Figure 10

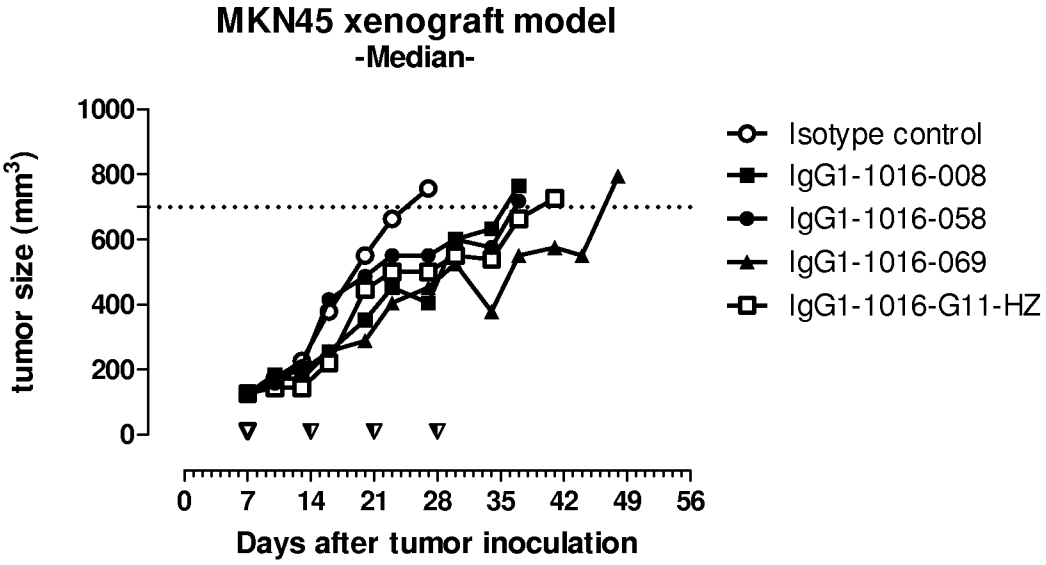

MKN45 xenograft model
-Median-
tumor size (mm3)
1000
800
600
400
200
0
0
7
14
21
28
35
42
49
56
Days after tumor inoculation
Isotype control
IgG1-1016-008
IgG1-1016-058
IgG1-1016-069
IgG1-1016-G11-HZ

Figure 11

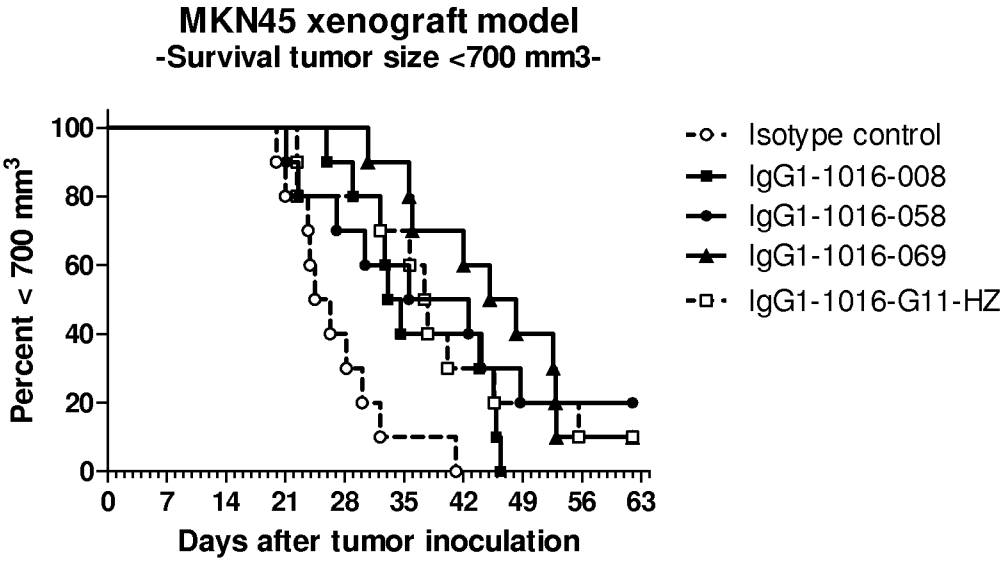

MKN45 xenograft model
-Survival tumor size <700 mm3-
Percent < 700 mm3
100
80
60
40
20
0
0 7 14 21 28 35 42 49 56 63
Days after tumor inoculation
Isotype control
IgG1-1016-008
IgG1-1016-058
IgG1-1016-069
IgG1-1016-G11-HZ

Figure 12

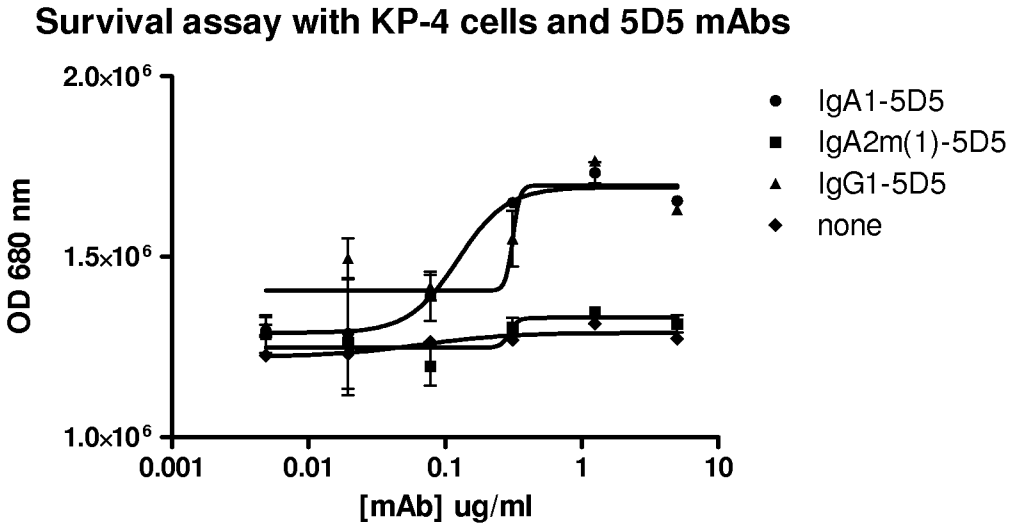

Survival assay with KP-4 cells and 5D5 mAbs
2.0x10^6
1.5x10^6
1.0x10^6
OD 680 nm
0.001
0.01
0.1
1
10
[mAb] ug/ml
IgA1-5D5
IgA2m(1)-5D5
IgG1-5D5
none

Figure 13

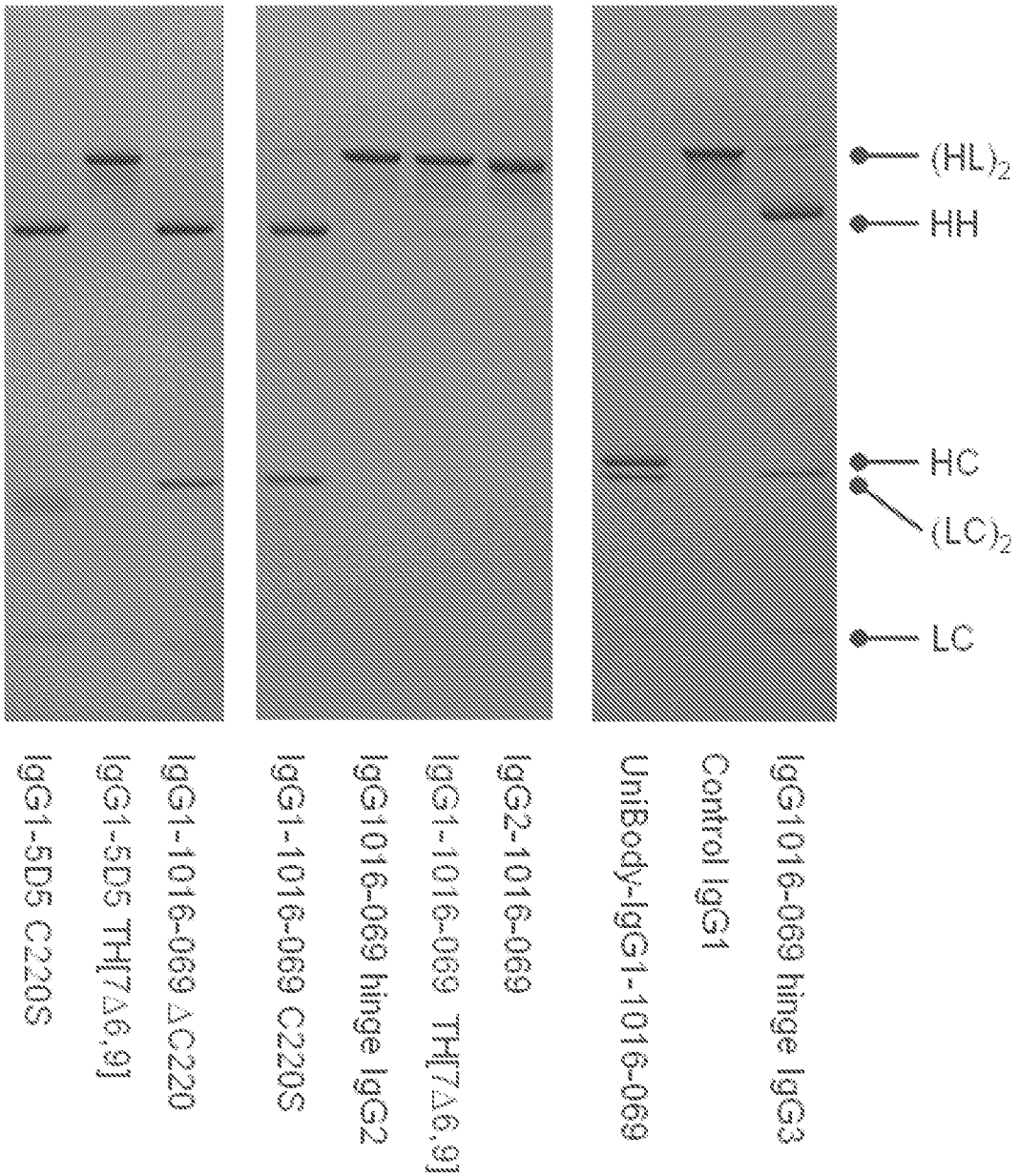

(HL)2
HH
HC
(LC)2
LC
IgG1-5D5 C220S
IgG1-5D5 THJ7Δ6,9]
IgG1-1016-069 ΔC220
IgG1-1016-069 C220S
IgG1016-069 hinge IgG2
IgG1-1016-069 THJ7Δ6,9]
IgG2-1016-069
UniBody-IgG1-1016-069
Control IgG1
IgG1016-069 hinge IgG3

Figure 14

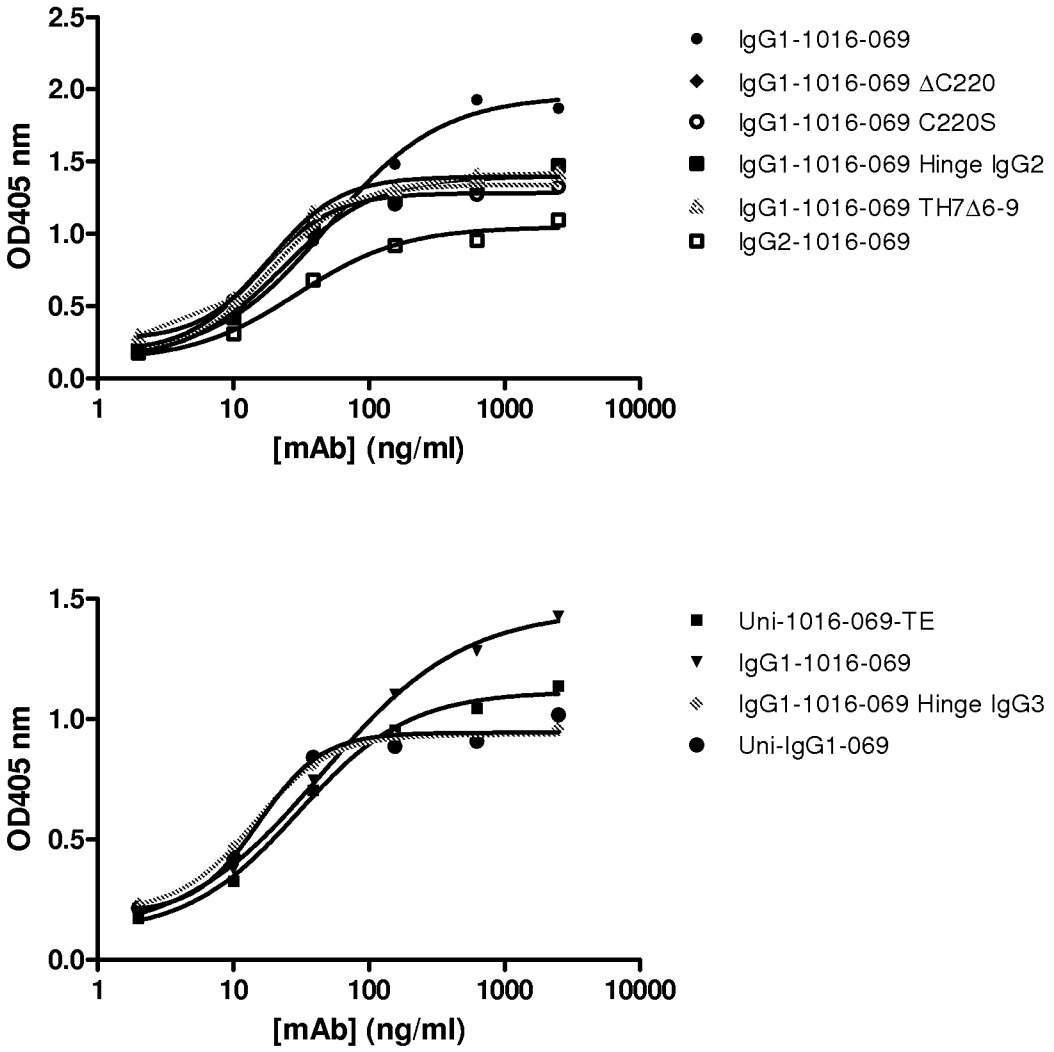

2.5
2.0
1.5
1.0
0.5
0.0
OD405 nm
1
10
100
1000
10000
[mAb] (ng/ml)
IgG1-1016-069
IgG1-1016-069 ΔC220
IgG1-1016-069 C220S
IgG1-1016-069 Hinge IgG2
IgG1-1016-069 TH7Δ6-9
IgG2-1016-069
1.5
1.0
0.5
0.0
OD405 nm
1
10
100
1000
10000
[mAb] (ng/ml)
Uni-1016-069-TE
IgG1-1016-069
IgG1-1016-069 Hinge IgG3
Uni-IgG1-069

Figure 15

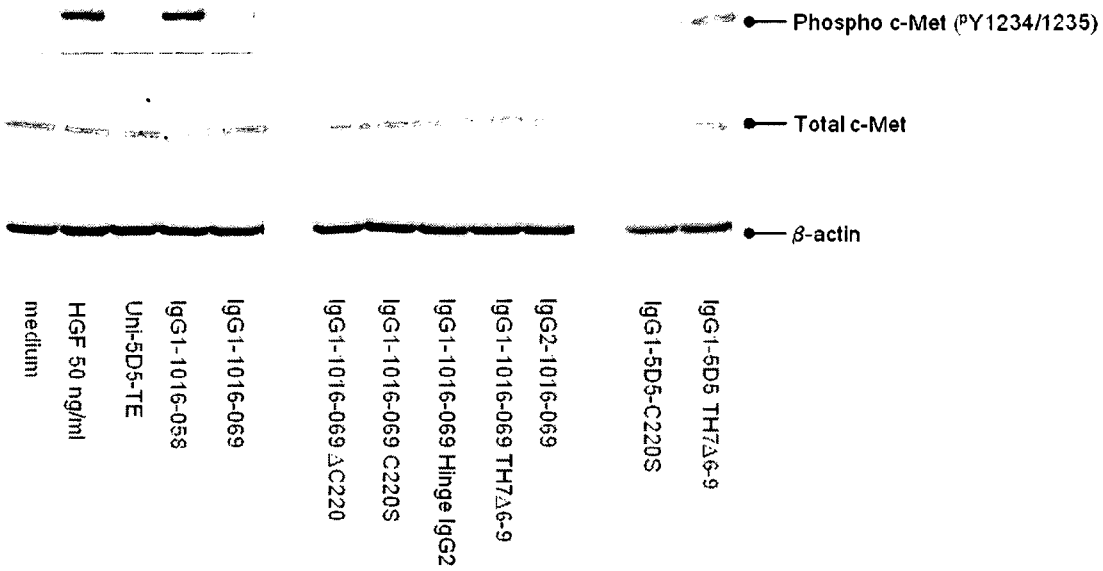

Phospho c-Met (PY1234/1235)
Total c-Met
β-actin
medium
HGF 50 ng/ml
Uni-5D5-TE
IgG1-1016-058
IgG1-1016-069
IgG1-1016-069 ΔC220
IgG1-1016-069 C220S
IgG1-1016-069 Hinge IgG2
IgG1-1016-069 TH7Δ6-9
IgG2-1016-069
IgG1-5D5-C220S
IgG1-5D5 TH7Δ6-9

Figure 16

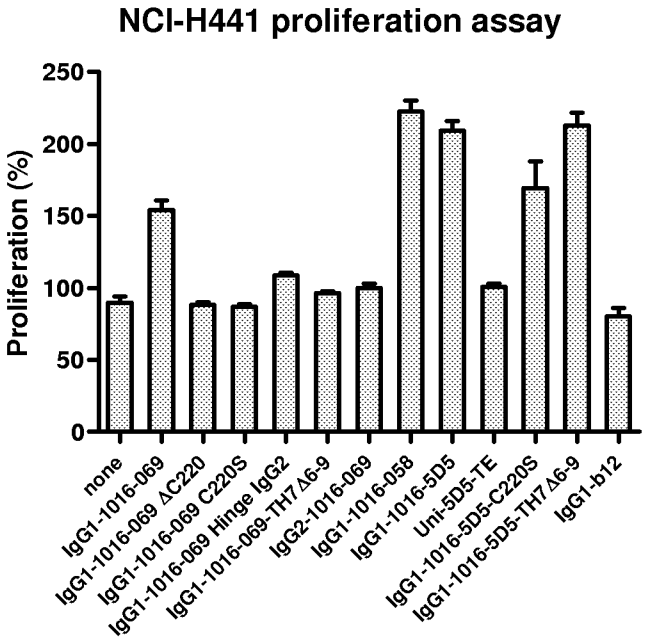

NCI-H441 proliferation assay
Proliferation (%)
250
200
150
100
50
0
none
IgG1-1016-069
IgG1-1016-069 ΔC220
IgG1-1016-069 C220S
IgG1-1016-069 Hinge IgG2
IgG1-1016-069-TH7Δ6-9
IgG2-1016-069
IgG1-1016-058
IgG1-1016-5D5
Uni-5D5-TE
IgG1-1016-5D5-C220S
IgG1-1016-5D5-TH7Δ6-9
IgG1-b12

Figure 17

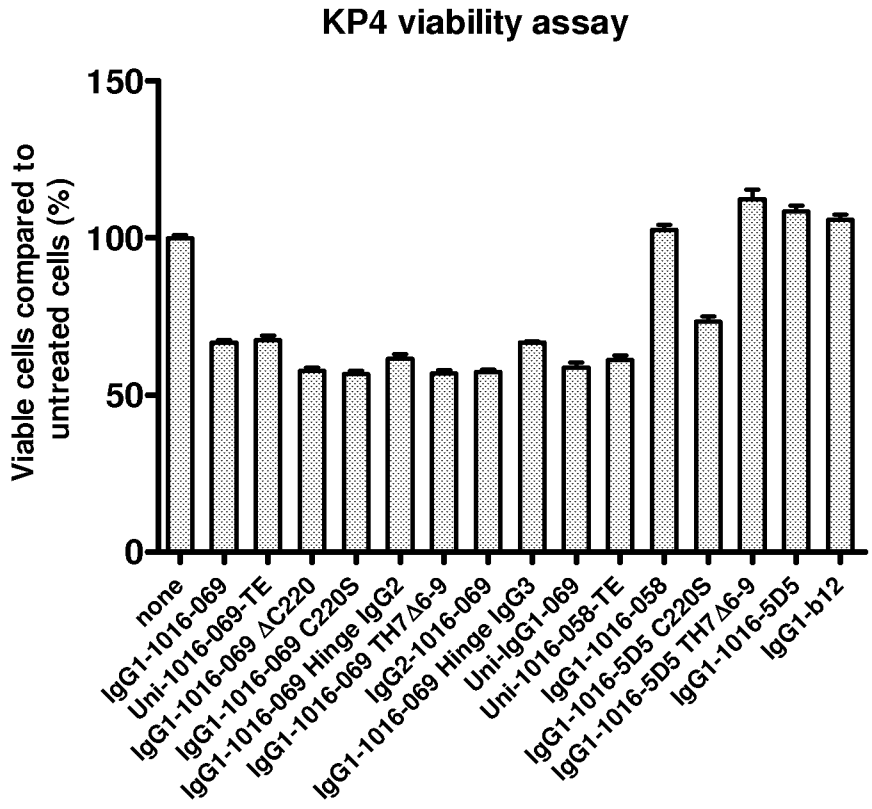

KP4 viability assay
Viable cells compared to untreated cells (%)
150
100
50
0
none
IgG1-1016-069
Uni-1016-069-TE
IgG1-1016-069 ΔC220
IgG1-1016-069 C220S
IgG1-1016-069 Hinge IgG2
IgG1-1016-069 TH7Δ6-9
IgG2-1016-069
IgG1-1016-069 Hinge IgG3
Uni-IgG1-069
Uni-1016-058-TE
IgG1-1016-058
IgG1-1016-5D5 C220S
IgG1-1016-5D5 TH7Δ6-9
IgG1-1016-5D5
IgG1-b12

Figure 18

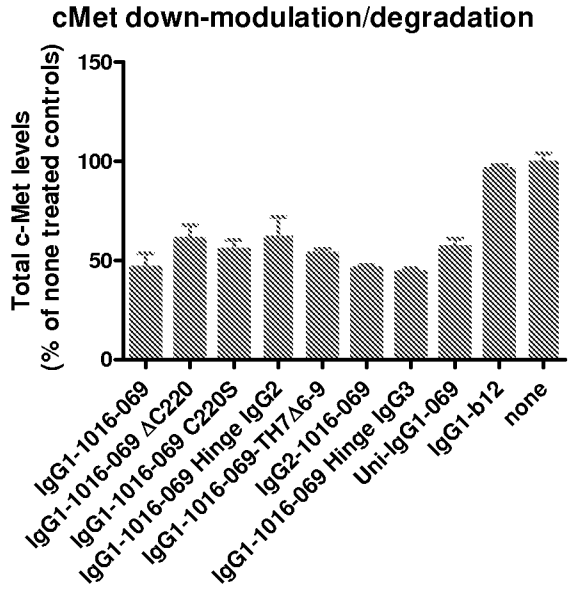

cMet down-modulation/degradation
Total c-Met levels
(% of none treated controls)
150
100
50
0
IgG1-1016-069
IgG1-1016-069 ΔC220
IgG1-1016-069 C220S
IgG1-1016-069 Hinge IgG2
IgG1-1016-069-TH7Δ6-9
IgG2-1016-069
IgG1-1016-069 Hinge IgG3
Uni-IgG1-069
IgG1-b12
none

Figure 19

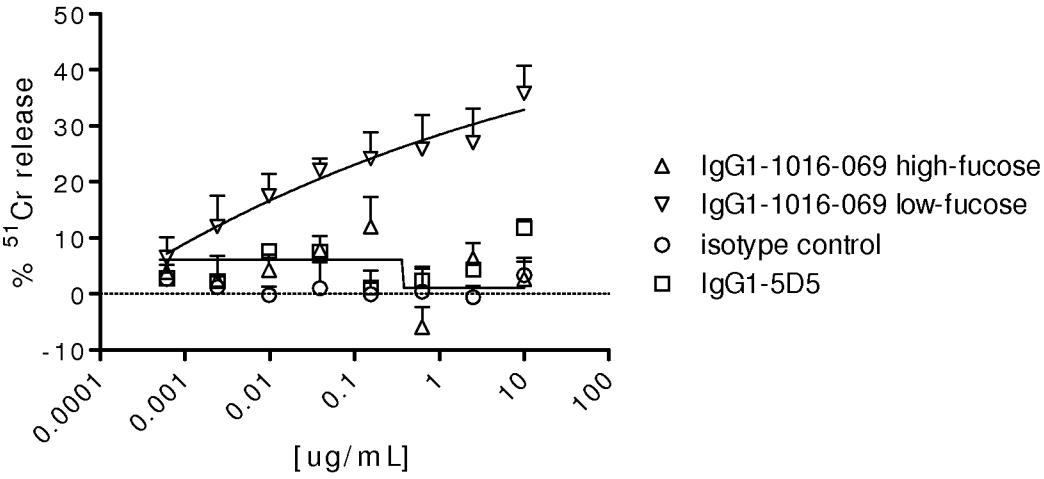
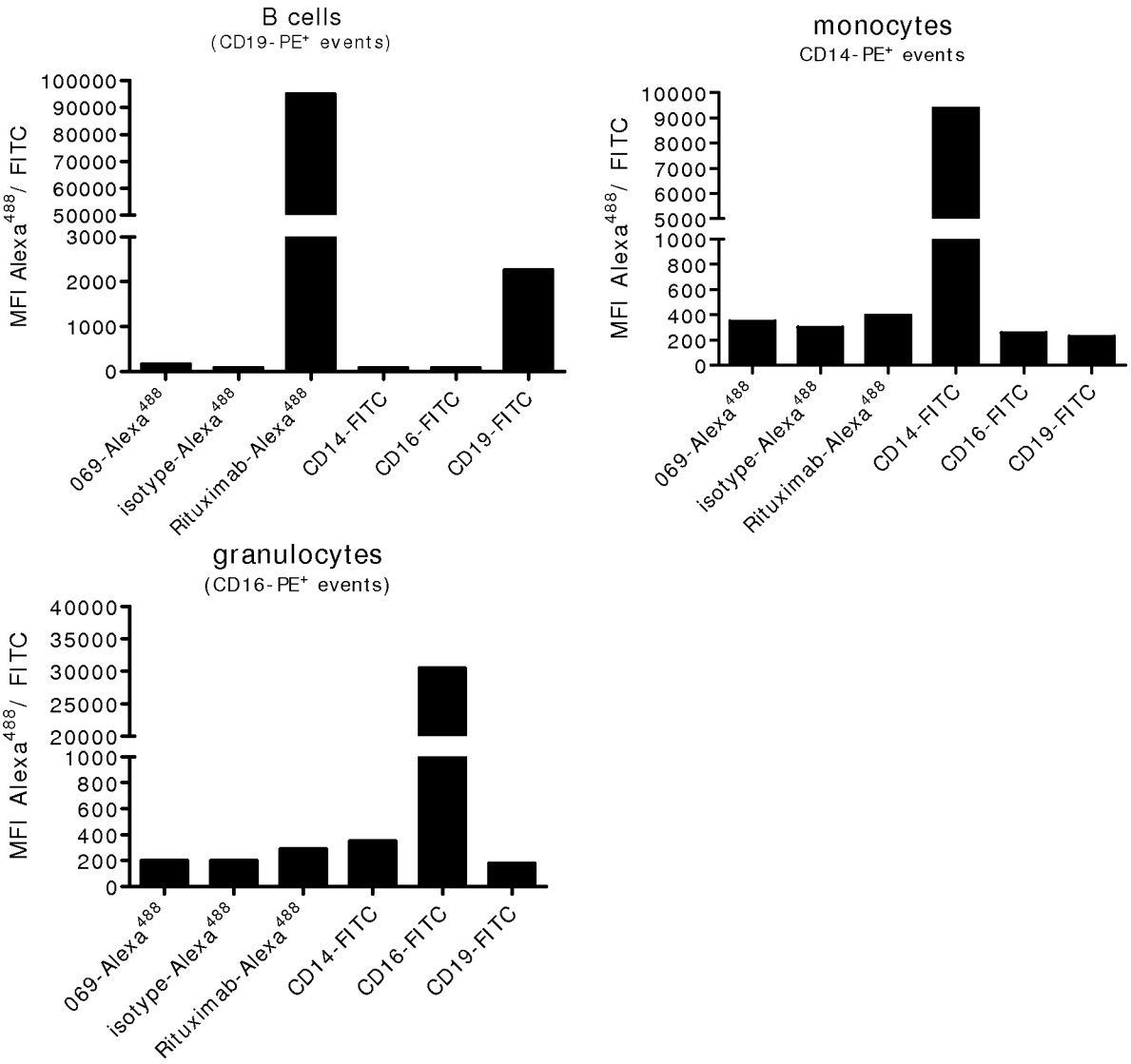

50
40
30
20
10
0
-10
% 51Cr release
0.0001
0.001
0.01
0.1
1
10
100
[ug/mL]
IgG1-1016-069 high-fucose
IgG1-1016-069 low-fucose
isotype control
IgG1-5D5

Figure 20


B cells
(CD19-PE+ events)
MFI Alexa488/ FITC
100000
90000
80000
70000
60000
50000
3000
2000
1000
0
069-Alexa488
isotype-Alexa488
Rituximab-Alexa488
CD14-FITC
CD16-FITC
CD19-FITC
monocytes
CD14-PE+ events
MFI Alexa488/ FITC
10000
9000
8000
7000
6000
5000
1000
800
600
400
200
0
069-Alexa488
isotype-Alexa488
Rituximab-Alexa488
CD14-FITC
CD16-FITC
CD19-FITC
granulocytes
(CD16-PE+ events)
MFI Alexa488/ FITC
40000
35000
30000
25000
20000
1000
800
600
400
200
0
069-Alexa488
isotype-Alexa488
Rituximab-Alexa488
CD14-FITC
CD16-FITC
CD19-FITC