

Figure 1

MF nr.	Specificity:	Germline:	VH sequence:
1337	IT	IGH1-08	EVQLVETGAEVKKPGASVKASDYLFTKYLINWVRQAPGGGLEWMGMSANTGNVGYAQKPGQRTMTTRFISINAYMELSSITSCDTAVYFCARSSLEKTTETAPYVHEPALDVMGQGTTLTVSS
3125	HER3	IGH3-30	QVQLVESGGGVQVQPGHSLRLSCAASGFTSSYGMHWVRQAPEGKLEWVAIVSYDGSNKYIADSVKGRFTIISRDNSKNTLYLQMNSLRAEDTAVYYCARGSGMPSSYNWGFYWGQGTTLTVSS
3176	HER3	IGH3-23	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPEGKLEWVAISLGGSGSYIADSVKGRFTIISRDNSKNTLYLQMNSLRAEDTAVYYCARDWYIPEYXWGFYWGQGTTLTVSS
3178	HER3	IGH1-2	QVQLVQSGAEVKKPGASVKASGYTFTGVMHWVRQAPQGQLEWGWINPNSGGIN YAQKPGQRTMTTRDTSISTAYMELSRILSDTAVYYCARDGSRHFWSYWGFYWGQGTTLTVSS
4863	HER3	IGH7-4-1	EVQLVQSGSELKPKPGASVAVSCKASGYTSIRYALNWVRQAPEGKLEWLGWINNTNCTNCTYARGFTGRTVFSLDTSVSTAYLQISLKAEDTAVYYCARDYDSTGYNLWPFYWGQGTTLTVSS
3370	EGFR	IGH1-18	QVQLVQSGAEVKKPGASVAVSCKASGYTFTSISGI SNVRQAPEGKLEWGWISAVXNGNIN YAQKLGQRVTMTTDTSTAYMELSRILSDTAVYYCARDRHWHWLDADFYGQGTTLTVSS
3755	EGFR	IGH7-4-1	QVQLVQSGSELKPKPGASVKISCKASGYDTFN YAMNWVRQAPEGHLEWGW INANTGDPT YAGGFTGRFVFSLDTSVSTAYLQISLKAEDSAVYYCTRETFLEWLHFDYWGQGTTLTVSS
4280	EGFR	IGH1-24	QVQLVQSGAEVKKPGASVAVSCKVSGYTTILTELMEHWVRQAPGKLEWGGDFEYKGTFFAQNPGQRTVMTEDTSAUTAYMELSLRS EDTAVYYCATEGYETTTYYINLFDWQGTTLTVSS
4289	EGFR	IGH7-4-1	QVQLVQSGSELKPKPGASVAVSCKTSCYTFTDYAMTWVRQAPEGKLEWGWITTTNTGDTYARGFTGRTVFSLDTSVSTAYLQISLKAEDTAVYYCARVYVHWIRGPEFWGQGTTLTVSS
5777	LGR4	IGH7-4-1	QVQLVQSGSELKPKPGASVAVSCKASGYTFTFN YMNWVRQAPEGKLEWGW INNTNCTNCTYAGGFTGRTVFSLDTSVSTAYLQISLKAEDTAVYYCARWELLDYWGQGTTLTVSS
5781	LGR4	IGH3-23	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPEGKLEWVSVISGSGGTTYIADSVKGRFTIISRDNSKNTLYLQMNSLRAEDTAVYYCAKGAGELDYWGQGTTLTVSS
5790	LGR5	IGH4-39	QVQLQESGPELVKPSPTLSITCTVSCGSESSSSYWGWIROPPEKGI LEWISGFYYSCKTYNPSLKSPTVLS EDTSKNPFSLKLSSTVAADTAVYYCARQTYSSNDGVILYYEDYWGQGTTLTVSS
5803	LGR5	IGH4-59	QVQLQESGPELVKPSPTLSITCTVSNGLSISTYYWSWIRQPPGKLEWIECYVYTGRTKYNPSLKSRTVTSVDTSKNPFSLNLS SVTAAADTAVYYCARGGIVVPAARDYYIYMDVMWCKETTVTVSS
5805	LGR5	IGH5-51	EVQLVQSGAEVKKPGESLKLACKGSGFTSISHWI CNVRQKPGKLEWGW IYPGSDTRYSFSPFQGVTVSADKSIINTAYLQNSLKASDPAIYYCARPNSGSPRPFEFWGRGTLTVSS
5808	LGR5	IGH4-39	QVQLQESGPELVKPSPTLSITCTVSCGSSISSSSY YWGWIRQPPGKLEWISGFYYSCKTYNPSLKSRTVTSVDTSKNPFSLKLSSTVAADTAVYYCARQEYYXGSGSPSYIEDYWGQGTTLTVSS
5809	LGR5	IGH5-51	EVQLVQSGAEVKKPGESLKLISCKGSGDSISLISHWI AWRQMPKPGKLEWGW IYVPGSDTRYSFSPFQGVTVTSADKSIITTAYLQNSLKASDPAIYYCARHWEILIGLIFDYWGQGTTLTVSS
5814	LGR5	IGH1-69	EVQLVQSGAEVKKPGSSVAVSCKASGDTSTNDALSNVRQTPGQLEWGW IIPILDTTDHAQKPGQRTVITADKSTNTAYMELNLSRSDTAVYYCAREHIAARQDYEDYWGQGTTLTVSS
5816	LGR5	IGH7-4-1	EVQLVQSGSLKPKPGASVAVSCKASGYTFTSYTMNWVRQAPEGKLEWGW INTDGDTPT YAGGFTGRTVFSLDTSVSTAFILQINSLKAEDTAVYYCARGDCDSTCYSYGYEDYWGQGTTLTVSS
5817	LGR5	IGH1-69	QVQLVQSGAEVKKPGSSVAVSCKVSGGTSPRSVAISNVRQAPEGKLEWGW IIPILDTTN YAQILQGRVTITADLSTSTAYMELNLSRSEDPAIYYCARGSDEGWEDPWGQGTTLTVSS
5818	LGR5	IGH1-69	EVQLVQSGTEVTRKPGSSVAVSCKASGGTFESNVAISNVRQAPEGKLEWGW IIPILGTTDHAQKQDQRTVITITADKSSNTTYMELSLRSDDTAVYYCAREYIAARLDYEDFSWGQGTTLTVSS
5832	RNF3	IGH3-13	EVQLVESGGGLVQPGGSLRLSCVVGSGFTSSYYDMHWVRQVTCGKLEWVAISATAGATYYPGSVKGRFTISRENARNSLYLQMNSLRAGDTAVYYCARDRGYSGYDAYYDFWQGTTLTVSS
5836	RNF3	IGH4-39	QVQLQESGPELVKPSPTLSITCTVSCGSSISSSNYWGWIROPPEKGI LEWIGNIYYRGTYNPSLKSPTVTSVDTSKNPFSLTSSSVTAAADTAMYYCARSGSDXGVVGAFDWDGQGTTLTVSS
5839	RNF3	IGH3-13	EVQLVQSGGGLVQPGGSLRLSCAASGFTSSYYDMHWVRQVTCGKLEWVSTTICATGDTPTYSDSVKGRFTISRQNAKNSLYLQINSLRAGDTAVYYCYVRDRGTYGDSYDFDNGQGTTLTVSS
5850	ZNF3	IGH7-4-1	QVQLVQSGSELKPKPGASVKASGYTFTTRYPNNWVRQAPGGGLEWMGWINNTNNTGNPT YAGGFTGRTVFSLDTSVSTAFIQISLKAEDTAVYYCAREFTNFYDAFDWQGTTLTVSS
5853	ZNF3	IGH7-4-1	QVQLVQSGSELKPKPGASVKASGYTENS YAMDWVRQAPEGKLEWGW INNTNNTGNPT YAGGFTGRTVFSLDTSVSTAFIEISLKAEDTAVYYCARPHGYFEAFDWDGQGTTLTVSS
5855	ZNF3	IGH7-4-1	QVQLVQSGSELKPKPGASVKASGYTFTTKYNNWVRQAPEGKLEWGW INNTNNTGNPT YAGGFTGRTVFSLDTSVSTAYLQVSSLRAEDTALYYCARESNWNVDYDFWQGTTLTVSS
5862	ZNF3	IGH5-51	QVQLVQSGTEVTRKPGESLKLISCKSGSYSTFTTWI CNVRQMPKPGKLEWGW IYPGSDITRYSFSPFQGVTVTSADKSI STAYLQISLKAEDTAMYYCARGLSNRPLSNFDFWQGTTLTVSS
5882	ZNF3	IGH7-4-1	QVQLVQSGSELKPKPGASVKASGYTFTTR YAMNWVRQAPEGKLEWGW INNTNNTGNPT YAGGFTGRTVFSLDTSVSTAYLQISLKAEDTAVYYCARDRGYSYDAFDWQGTTLTVSS
5884	ZNF3	IGH7-4-1	EVQLVQSGSELKPKPGASVKASGYTFTTKYAMNWVRQVPGGKLEWGW INNTNNTGNPT YAGGFTGRTVFSLDTSVSTAYLQISLKAEDTAVYYCARGGSSYYDWDFWQGTTLTVSS
5887	ZNF3	IGH7-4-1	QVQLVQSGSELKPKPGASVKASGYTFTTR YAMNWVRQAPEGKLEWGW INNTNNTGNPT YAGGFTGRTVFSLDTSVSTAYLQISLKAEDTAVYYCAPDKGYNWNYMGAFDWQGTTLTVSS
5888	ZNF3	IGH7-4-1	QVQLVQSGSELKPKPGSMKVASGYTFTTR YAMNWVRQAPEGKLEWGW INNTNNTGNPT YAGGFTGRTVFSLDTSVSTAYLQISLKAEDTAVYYCARGSGSYDYDFWQGTTLTVSS

MF nr.	Specificity:	Germline:	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
1337	TT	IGH1-08	EYQLIVETGAELVKPGASVKVSCRASDIYFT	KYDIN	WYRQAPGGGLEWMG	WNSANTGNTGYAQKFTQG	RVTMTSDTSLNTAYMELSLHSITSGDTAVYFCAR	SSLFKIETAPYYHEALDV	WGQGTILVTYSS
3125	HER3	IGH3-30	QVQLVDSGGGVQPGGSLRISCAASGFTFS	SYGMH	WYRQAPGKGLIEWA	VIYDGSNRYKYNADSVKRG	RFTI BRUNSKNTLYIQMNSLRADDTAVYYCAR	GSSGNSPSYNGEDY	WGQGTILVTSS
3176	HER3	IGH3-23	EYQLLESGGGLVQPGGSLRLSCAASGFTFS	SYAMS	WYRQAPGKGLIEWA	AIISGGSGTYYADSVKRG	RFTISRDNSKNTLYIQMNSLRADDTAVYYCAR	DWNYPPYYWGFY	WGQGTILVTYSS
3178	HER3	IGH1-2	QVQLVDSGAEVKPKPGASVKVSCKASGYTFT	GYVMH	WYRQAPGGGLEWMG	WINPNSGGTNYAQKFTQG	RVTMTSDTSLNTAYMELSLRSDDTAVYYCAR	DHGSRHFWSYWGFY	WGQGTILVTYSS
4863	HER3	IGH7-4-1	EYQLVDSGSEELKPKGASVKVSCKASGYTSL	RYALN	WYRQAPGGGLEWLG	WINTNTGNPTIYARGFTG	RFVFSLDTSVSTAYLQISSLKAEADTAVYYCAR	DTYDSTGYLWFDY	WGQGTILVTYSS
3370	EGFR	IGH1-18	QVQLVDSGAEVKPKPGASVKVSCKASGYTFT	SYGIS	WYRQAPGGGLEWMG	WISAYNGNTNYAQKFTQG	RVTMTTDTSTSTAYMELSLRSDDTAVYYCAR	DRHWHWLDADFY	WGQGTILVTYSS
3755	EGFR	IGH7-4-1	QVQLVDSGSEELKPKGASVKVSCKASGYTFT	NYAMN	WYRQAPGGGLEWMG	WINATGDPPTYAQGFTG	RFVFSLDTSVSTAYLQISSLKAEADTAVYYCTR	BSFLWHLHEDY	WGQGTILVTYSS
4280	EGFR	IGH1-24	QVQLVDSGAEVKPKPGASVKVSCKASGYTFT	ELSMH	WYRQAPGKGLIEWG	GFDPFKGTFEAKNTFG	RVTMTEDTSADTAYMELSLRSDDTAVYYCAT	EGYETTTTYYTNLFDS	WGQGTILVTYSS
4289	EGFR	IGH7-4-1	QVQLVDSGSEELKPKGASVKVSCKASGYTFT	DYAMT	WYRQAPGGGLEWMG	WINTNTGDPPTYAQGFTG	RFVFSLDTSVSTAYLQISSLKAEADTAVYYCAR	VYHMI RGEFF	WGQGTILVTYSS
5777	LGR4	IGH7-4-1	QVQLVDSGSEELKPKGASVKVSCKASGYTFT	NYVMN	WYRQAPGGGLEWMG	WINTNTGNPTIYAQGFTG	RFVFSLDTSVSTAYLQISSLKAEADTAVYYCAR	WELLIDY	WGQGTILVTYSS
5781	LGR4	IGH3-23	EYQLVDSGGGLVQPGGSLRLSCAASGFTFS	SYAMS	WYRQAPGKGLIEWA	VIISGGGTYYADSVKRG	RFTISRDNSKNTLYIQMNSLRADDTAVYYCAR	GAGELDY	WGQGTILVTYSS
5790	LGR5	IGH4-39	QVQLQESGPGIVPKPSETLSITCTVSGGSES	SSSYWG	WIROPKPGKGLIEWIG	SFYSGNTYYNPSLKS	RVTISBDTSKNQFSLKLSSTVTAADTAVYYCAR	QTYSSMDGVLYYFEDY	WGQGTILVTYSS
5803	LGR5	IGH4-59	QVQLQESGPGIVPKPSETLSITCTVSGSGIS	TYTWS	WIROPKPGKGLIEWIG	VYVYTGRTKYNPSLKS	RVTISVDTSKNQFSLNLSSTVTAADTAVYYCAR	GGLVVPAAARDYYYMDV	WGKGTILVTYSS
5805	LGR5	IGH5-51	EYQLVDSGAEVKPKPGESLKIACKSGSFST	SHWIG	WIROPKPGKGLIEWIG	VIYPGSDTRYSPSTQG	QVTVSADKSLNTAYLIQMSLRKASDTAVYYCAR	PNSGSPRYEFT	WGKGTILVTYSS
5808	LGR5	IGH4-39	QVQLQESGPGIVPKPSETLSITCTVSGGSGIS	SSSYWG	WIROPKPGKGLIEWIG	SFYSGNTYYNPSLKS	RVTISVDTSKNQFSLKLSSTVTAADTAVYYCAR	QYVYYGSGSPSYIEDY	WGQGTILVTYSS
5809	LGR5	IGH5-51	EYQLVDSGAEVKPKPGESLKIACKSGSDSTI	SHWIA	WIROPKPGKGLIEWIG	VIYPGSDTRYSPSTQG	QVTVSADKSLNTAYLIQMSLRKASDTAVYYCAR	HEWELLGPEFY	WGQGTILVTYSS
5814	LGR5	IGH1-69	EYQLVDSGAEVKPKPGSSVKVSCKASGGTST	NDALIS	WYRQTPPGGLEWMG	SIIPILDTTTHAQKFTQG	RVTITADKSLNTAYMELSLRSDDTAVYYCAR	BHIAARQDYEDY	WGQGTILVTYSS
5816	LGR5	IGH7-4-1	EYQLVDSGSKLKPKGASVKVSCKASGYTFT	SYTMN	WYRQAPGGGLEWMG	WINTNTGDPPTYAQGFTG	RFVFSLDTSVSTAFLOINSLRKAEADTAVYYCAR	GCDCSTSCYRISYGYEDY	WGQGTILVTYSS
5817	LGR5	IGH1-69	QVQLVDSGAEVKPKPGSSVKVSCKASGGTFR	SYALIS	WYRQAPGGGLEWMG	GIIPIFDTRYAQKFTQG	RVTITADLSSTAYMELSLRSDDTAVYYCAR	GSDGDMWFDY	WGQGTILVTYSS
5818	LGR5	IGH1-69	EYQLVDSGTEVYRKPSSVKVSCKASGGTFS	NYALIS	WYRQAPGGGLEWMG	SIIPILGTTTHAQKFTQD	RVTITADKSLNTAYMELSLRSDDTAVYYCAR	BYIAARLDYFDS	WGQGTILVTYSS
5832	RNF43	IGH3-13	EYQLVDSGGGLVQPGGSLRLSCVVSQFTFS	YXDMH	WYRQVTKGKLEHWIS	AICTAGATYYPGSVKRG	RFVTSRENAKNSLYIQMNSLRAGDTAVYYCAR	DHGSYGYDAYYFDE	WGQGTILVTYSS
5836	RNF43	IGH4-39	QVQLQESGPGIVPKPSETLSITCTVSGGSGIS	SSSYWG	WIROPKPGKGLIEWIG	NIYYRGTYTYYNPSLKS	RVTISVDTSKNQFSLKLSSTVTAADTAVYYCAR	EGSDYGDYVGAFDI	WDQGTIMVTYSS
5839	RNF43	IGH3-13	EYQLVDSGGGLVQPGGSLRLSCAASGFTFS	YXDMH	WYRQVTKGKLEHWIS	TIIGATGDTYYSDSVKRG	RFTISRQNAKNSLYIQMNSLRAGDTAVYYCVR	DHGYIGYDSYYFDN	WGQGTILVTYSS
5850	ZNR3	IGH7-4-1	QVQLVDSGSEELKPKGASVKVSCKASGYTFT	RYPMN	WYRQAPGGGLEWMG	WINTNTGNPTIYAQGFTG	RFVFSLDTSVSTAFLOISSLKAEADTAVYYCAR	RPTNFYDAFDI	WGQGTIMVTYSS
5853	ZNR3	IGH7-4-1	QVQLVDSGSEELKPKGASVKVSCKASGYTFT	SYAMD	WYRQAPGGGLEWMG	WINTNTGNPTIYAOAFTG	RFVFSLDTSVSTAYLQISSLKAEADTAVYYCAR	BRHGYFEAFDI	WGQGTIMVTYSS
5855	ZNR3	IGH7-4-1	QVQLVDSGSEELKPKGASVKVSCKASGYTFT	KYVMN	WYRQAPGGGLEWMG	WINTNTGNPTIYAOAFTG	RFVFSLDTSVSTAYLQISSLKAEADTAVYYCAR	ESNMWYDYEDY	WGQGTIMVTYSS
5862	ZNR3	IGH5-51	QVQLVDSGTEVYRKPGEESLKIACKSGSFST	TYWIG	WYRQMPKGLIEWIG	IIYPGSDTRYSPSTQG	QVTVSADKSLNTAYLIQMSLRKASDTAVYYCAR	RGLSHVRLSADFV	WGQGTILVTYSS
5882	ZNR3	IGH7-4-1	QVQLVDSGSEELKPKGASVKVSCKASGYTFT	RYAMN	WYRQAPGGGLEWMG	WINTNTGNPTIYAOAFTG	RFVFSLDTSVSTAYLQISSLKAEADTAVYYCAR	DHGSYDYDAFDI	WGQGTIMVTYSS
5884	ZNR3	IGH7-4-1	EYQLVDSGSEELKPKGASVKVSCKASGYTFT	KYAMN	WYRQVPGGLEWMG	WINTNTGNPTIYAOAFTG	RFVFSLDTSVSTAYLQISSLKAEADTAVYYCAR	KGGSYYDMWFDY	WGQGTILVTYSS
5887	ZNR3	IGH7-4-1	QVQLVDSGSEELKPKGASVKVSCKASGYTFT	RYAMN	WYRQAPGGGLEWMG	WINTNTGKPTIYAOGFTG	RFVFSLDTSVSTAYLQISSLKAEADTAVYYCAR	DHGYNMWNGAFDI	WGQGTIMVTYSS
5888	ZNR3	IGH7-4-1	QVQLVDSGSEELKPKGSSMKVSCKASGYTFT	RYAMN	WYRQAPGGGLEWMG	WINTNTGNPTIYAOGFTG	RFVFSLDTSVSTAYLQISSLKAEADTAVYYCAR	RSGSYYDYEDY	WGQGTILVTYSS

Figure 2

MF1337:

gaggtgcagctggtggagactggggctgaggtgaagaagccggggcctcagtgaaggtctcctgcaagg
cttctgactacatcttcaccaaataatgacatcaactgggtgcgcagggccctggacaagggcttgatg
gatgggatggatgagcgctaacttgaaacacgggctatgcacagaagttccagggcagagtcaccatg
accagggacacgtccataaacacagcctacatggagctgagcagcctgacatctggtgacacggccgtt
atttctgtgcgaggagtagtcttttcaagacagagacggcgccctactatcacttcgctctggacgtctg
ggccaagggaccacgggtcacgtctccagt

MF3755:

caggtgcagctggtgcagctctgggtctgagttgaagaagcctggggcctcagtgaagatttcctgcaagg
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gatgggatggatcaacgccaacactggggacccaacgtatgccagggcttcacaggacgggttcttct
tccttggacacctctgtcagcacggcatatctgcagatcagcagtttaaggctgaggactctgccgtgt
attactgtacgagagagcgatTTTTGGAGTGGTTACACTTTGACTACTGGGGCCAGGGAACCCTGGTCAC
CGTCTCCAGT

MF3178:

caggtgcagctggtgcagctctggggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
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MF5790:

caggtgcagctgcaggagtcggggccaggactggtgaagccttcggagaccctgtccctcacctgcactg
tctctgggtggctccttcagcagtagtagttcctactggggctggatccgccagcccccagggaaggggct
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tgtattactgtgcgagacagacgtatagcagcagctgggacggggctcctgtactactttgactactgggg
ccagggaaccctggtcaccgtctccagt

MF5816:

gaggtgcagctggtgcagctctgggtctaaattgaagaagcctggggcctcagtgaaggtttcctgcaagg
cttctggatacaccttcactagctatactatgaattgggtgcgcagggccctggacaagggcttgatg
gatgggatggatcaacaccgacactggggacccaacgtatgccagggcttcacaggacgggttcttct
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MF3125:

caggtgcagctggtggagctctgggggaggcgtggtccagcctgggaggtccctgagactctcctgtgcag
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taccctggtcaccgtctccagt

MF3176:

gaggtgcagctgttggagctctgggggaggccttggtacagcctgggggggtccctgagactctcctgtgcag
cctctggattcaccttttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtg
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ggtcaccgctctccagt

MF4863:

gaggtgcagctggtgcagctctgggtctgagttgaagaagcctggggcctcagtgaaaggtttcctgcaagg
cttctggatacacctccattagatatgctttgaactgggtgcgacaggcccttgacaaggccttgagt
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tcttggaacacctctgtcagcacggcatatctgcagatcagcagcctaaaggtgaggacactgccgtgt
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ggtcaccgctctccagt

MF3370:

caggttcagctggtgcagctctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
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accacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggctgtgt
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gtcaccgtctccagt

MF4280:

cagggtgcagctggtgcagctctgggctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg
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gatgggaggctttgatcctgagtatggtaaaacattcttcgcacagaacttccagggcagagtcaccatg
accgaggacacatctgcagacacagcctacatggagctaagcagcctgagatctgaggacacggccgtgt
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gggaaccttggtcaccgtctccagt

MF4289:

caggtgcagctggtgcaatctgggtctgaattgaagaagcctggggcctcagtgaaggtttcctgcaaga
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gatgggatggatcaccaccaacactggggaccacaacgtatgccccgggcttcacaggacggtttgtcttc
tccttggacacctctgtgcagcagggcatatctgcagatcagcagcctaagggccgaggacactgccgtat
attactgtgcgagagtgtatcattggatacggggatttgagttttggggccagggaaccctggtcaccgt
ctccagt

MF5777:

caggtgcagctggtgcaatctgggtctgagttgaagaagcctggggcctcagtgaaggtttcctgcaagg
cttctggatacaccttcactaactatgttatgaattgggtgcgacaggccctggacaagggttgagtg
gatgggatggatcaacaccaacactggaacccaacgtatgccagggttcacaggacggtttgtcttc
tccttgacacctctgtcagcacggcatatctgcagatcagcagcctaaaggctgaggacactgccgtgt
attactgtgcgaggtgggagctactagactactggggccagggaaccctggtcaccgtctccagt

MF5781:

gaggtgcagctggtggagtctgggggaggcttggtacagcctggggggtccctgagactctcctgtgcag
cctctggattcaccttagcagctatgccatgagctgggtccgccaggctccagggaaggggctggagtg
ggtctcagttattagtggtagtgggtgggaccacatactacgcagactccgtgaagggccgggttcaccatc

tccagagacaattccaagaacacgctgtatctgcaaataaacagcctgagagccgaggacacggccgtat
attactgtgcgaaaggggctggggagcttgactactggggccagggaaccctggtcaccgtctccagt

MF5803:

caggtgcagctgcaggagtcggggccaggactggtgaagccttcggagaccctgtccctcacctgcactg
tctctaattggctccatcagtagtacttactactggagctggatccggcagccccaggggaaggggctggagtg
gattggatatgtctattacactggggcgaccaagtacaacccctccctcaagagtcgagtcaccatatca
gtagacacgtccaagaaccagttctccctgaacctgagttctgtgaccgctgcggacacggccgtgtatt
actgtgagaggggggtattgtagtagtcccagctgcgcgggactattactactacatggacgtctgggg
caaagggaccacgggtcaccgtctccagt

MF5805:

gaggtgcaactggtgcagctctggagcagaggtgaaaaagcccggggagttctctgaagatcgctgttaagg
gttctggattcagttttaccagccactggatcggtctgggtgcgccagaagcccgggagaggcctggagtg
gatgggggtcatctatcctgggtgactctgataccagatacagccgtccttccaagggcagggtcaccgtc
tcagccgacaagtccatcaataccgcctacctgcagtggaacagcctgaaggcctcggaacccgccatat
attactgtgagagaccgaacagtgaggagtcgccgggtacttcgagttctggggccgtggcaccctggtcac
cgtctccagt

MF5808:

caggtgcagctgcaggagtcggggccaggactggtgaagccttcggagaccctgtccctcacctgcactg
tctctgggtggctccatcagcagtagtagttactactggggctggatccggcagccccaggggaaggggct
ggagtggattgggagtttctattatagtggggaacacctactacaacccgtccctcaagagtcgagtcacc
atatccgtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgcagacacggctg
tgtattactgtgagagacaggagtattactatgggttcggggagtccttcgtactactttgactactgggg
ccagggaaaccctggtcaccgtctccagt

MF5809:

gaggtgcagctggtgcagctctggagcagaggtgaaaaagcccggggagttctctgaagatctcctgttaagg
gttctggagacagttttatcagccactggatcgctctgggtgcgccagatgcccggaagggcctggagtg
gatggggatcgtctatcctgggtgactctgataccagatacagccgtccttccaagggcagggtcaccatc
tcagccgacaagtccatcaccaccgcctacttgcagtgaggagcagcctgaaggcctcggaacccgccatgt
attactgtgagagacagagtgggaaactacttggccctttgactactggggccagggaaccctggtcac
cgtctccagt

MF5814:

gaggtgcagctggtgcagctctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaagg
cttctggaggcaccttcactaacgatgctatcagttgggtgcgacagaccctggacaagggcttgagtg
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accgcggaacaaatccacgaacacagcctacatggagctgaacagcctgagatctgatgacacggccgtgt
attactgtgagagagcatatagcagctcgtcaggactactttgactattggggccagggaaccctggtcac
caccgtctccagt

MF5817:

caggtgcagctggtgcagctctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaagg
tttctggaggcaccttcaggagctatgctatcagctgggtgcgacagggccctggacaagggcttgagtg
gatgggagggatcatccctatctttgatacaagaaactacgcacagattcttcagggcagagtcacgatt
accgcggaacttatccacgagcacagcctacatggagctgaacagctctgagatctgaggacacggccat
attactgtgagaggggagcgacgaggggggactgggttcgaccctggggccaaggaaccctggtcaccgt
ctccagt

MF5818:

gaggtgcagctggtgcagctctgggactgaggtgaggaagcctgggtccctcggtgaaggtctcctgcaagg
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gatgggaagtatcatccctatccttggaaacaacagaccacgcacagaagttccaggacagagtcacgatt
accgcggacaaatcctcgaacacaacctacatggagctgagcagcctgagatctgatgacacggccgtat
attactgtgcgagagagtatatagcagctcgtctggactactttgactcttggggccagggaaccctggt
cacctctccagt

MF5832:

gaggtgcagctggtggagtctgggggaggcttggtacagcctgggggggtccctgagactctcctgtgtag
tctctggattcaccttcagttactacgacatgcactgggtccgccaagtacaggaaaaggctctggagtg
ggtctcagctattggcactgctggtgccacatactatccaggctccgtgaagggccgattcacctatctcc
agagaaaatgccagaactccttgtatcttcaaataaatagcctgagagccggggacacggctgtgtatt
actgtgcaagagatcgtggatatagtggctacgatgcgtactactttgacttctggggccagggaaccct
ggtcacctctccagt

MF5836:

caggtgcagctgcaggagtcggggccaggactggtgaagccttcggagaccctgtccctcacctgcactg
tctctgggtggctccatcagcagtagtaattactactggggctggatccgccagccccagggaaggggct
ggagtggattgggaatatctattatagaggggtacacctattataaccctgccctcaagagtcgagtcacc
atatccgtagacacgtccaagaagcagttctccctgacgctgagctctgtgaccgccgcagacacggcta
tgtattactgtgcgagagaggggagtgactacggtgactacgtaggagcttttgatatctgggaccaagg
gacaatggtcacctctccagt

MF5839:

gaggtgcagctggtgcagctctgggggaggcttggtacagcctgggggggtccctgagactctcctgtgcag
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ggtctcaactattggtgctactggtgacacatactattcagactccgtgaagggccgatttacctatctcc
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actgtgtaagagatcgtggatatattggctacgattcgtactactttgacaactggggccagggaaccct
ggtcacctctccagt

MF5850:

caggtgcagctggtgcagctctgggtctgagttgaagaagcctggggcctcagtgaaggtttcctgcaagg
cttctggatacaccttcactaggtatcctatgaattgggtgcgacaggccctggacaagggcttgagtg
gatgggatggatcaacaccaactggtgaacccaacatattgccagggttcacaggacgggtttgtcttc
tccttggacacctctgtcagcacggcattttctgcagatcagcagcctaaaggctgaggacactgccgtgt
attactgtgcgagagagaggactaacttttatgatgcttttgatatctggggccaagggaacatggtcac
cgtctccagt

MF5853:

caggtgcagctggtgcaatctgggtctgagttgaagaagcctggggcctcagtgaaggtttcctgcaagg
cttctggatataccttcaatagctatgctatggattgggtgcgacaggccctggacaagggcttgagtg
gatgggatggatcaacaccaatactgggaacccaacgtatgccaggccttcacaggacgggtttgtcttc
tccttggacacctctgtcagcacggcatatctggagatcagcagcctaaaggctgaggacactgccgtgt
attactgtgcgagagagaggcatggatatatttgaaagcttttgatatctggggccaagggaacacggtcac
cgtctccagt

MF5855:

caggtgcagctggtgcaatctgggtctgagttgaagaagcctggggcctcagtgaaggtttcctgcaagg
cttctggatacaccttcactaagtatgttatgaattgggtgcgacaggccctggacaagggcttgagtg

gatgggatggatcaacaccaacactgggaacccaacgtatgccagggttcacaggacgggtttgtcttc
tccttggacacctctgtcagcacggcataatctgcaggtcagcagtcctaagggtgaggacactgccctgt
attactgtgcgagagagtctaactggaactacgactactttgactactggggccaggggcaccctggtcac
cgtctccagt

MF5862:

caggtgcagctgggtgcagtcctggaacagaggtgaaaaagcccgagggtctctgaagatctcctgtaagg
gttctggatacagctttaccacctaactggatcgggtgggtgcgcagatgcccggaaggcctggagtg
gatgggaatcatctatcctgggtgactctgataccagatacagccgtccttccaaggccaggtcaccatc
tcagccgacaagtccatcagcacccgctacctgcagttgagcagcctgaaggcctcggacaccgccatgt
attactgtgcgagacgggggtcttagtatgggttcgggtgagcgttttgatgtctggggccaaggaaccct
ggtcaccgtctccagt

MF5882:

caggtgcagctgggtgcaatctgggtctgagttgaagaagcctggggcctcagtgagggtttcctgcaagg
cttctggatacacccttcactagatatgctatgaattgggtgcgacaggccctggacaagggttgagtg
gatgggatggatcaacaccaaactgggaacccaacgtatgccagggttcacaggacgggtttgtcttc
tccttggacacctctgtcagcacggcataatctgcagatcagcagcctaaaggctgaggacactgccgtgt
attactgtgcgagagatcgtgggagctactatgatgcttttgatatctggggccaagggaacaatggtcac
cgtctccagt

MF5884:

gaggtgcagctgggtgcagtcctgggtctgaattgaagaagcctggggcctcagtgagggtttcctgcaagg
cttctggatacacccttcactaagtatgctatgaattgggtgcgacaggccctggacaagggttgagtg
gatgggatggatcaacaccaacactgggaacccaacgtatgccagggttcacaggacgggtttgtcttc
tccttggacacctctgtccgcacggcataatctgcagatcagcagcctaaaggctgaggacactgccgtgt
attactgtgcgagaaaaggggggagctactacgactgggttcgacccctggggccagggaaccctggtcac
cgtctccagt

MF5887:

caggtgcagctgggtgcagtcctgggtctgagttgaagaagcctggggcctcagtgagggtttcctgcaagg
cttctggatacacccttcactcgctatgctatgaattgggtgcgacaggccctggacaagggttgagtg
gatgggatggatcaacaccaacactgggaacccaacgtatgccagggttcacaggacgggtttgtcttc
tccttggacacctctgtcagcacggcataatctgcagatcagcagcctgaaggctgaggacactgccgtgt
attactgtgcgagagataagggctataactggaactacatgggtgcttttgatatctggggccaagggaac
cacggtcaccgtctccagt

MF5888:

caggtgcagctgggtgcagtcctgggtctgagttgaagaagcccgggggctcaatgaagggtttcctgcaagg
cttctggatacacccttcactagatatgctatgaattgggtgcgacaggccctggacaagggttgagtg
gatgggatggatcaacaccaacactgggaacccaacgtatgccagggttcacaggacgggtttgtcttc
tccttggacacctctgtcagcacggcataatctgcagatcagcagcctaaaggctgaggacactgccgtct
attattgtgcgagacggagtgaggagctactacgactactttgactactggggccagggaaccctggtcac
cgtctccagt

Figure 3

Common Light Chain amino acid (A.A.) sequence

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCQSYSTPPTFGQGTKVEIK
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Annotated sequence:

VL:

gacatccagatgacccagtcctccatcctccctgtctgcatctgtaggagacagagtcacc
D I Q M T Q S P S S L S A S V G D R V T
atcacttgccgggcaagtcagagcatttagcagctacttaaattggatcagcagaaacca
I T C R A S Q S I S S Y L N W Y Q Q K P
gggaaagcccctaagctcctgatctatgctgcatccagtttgcaaagtgggtcccatca
G K A P K L L I Y A A S S L Q S G V P S
aggttcagtgaggcagtgatctgggacagatttcactctcaccatcagcagtcctgcaacct
R F S G S G S G T D F T L T I S S L Q P
gaagattttgcaacttactactgtcaacagagttacagtaccctccaacgttcggccaa
E D F A T Y Y C Q Q S Y S T P P T F G Q
gggaccaaggtggagatcaaa
G T K V E I K

CL:

cgaactgtggctgcaccatctgtcttcatcttcccgccatctgatgagcagttgaaatct
R T V A A P S V F I F P P S D E Q L K S
ggaactgcctctgttgtgtgcctgctgaataacttctatcccagagaggccaaagtacag
G T A S V V C L L N N F Y P R E A K V Q
tggaaggtggataacgccctccaatcgggtaactcccaggagagtggtcacagagcaggac
W K V D N A L Q S G N S Q E S V T E Q D
agcaaggacagcacctacagcctcagcagcaccctgacgctgagcaaagcagactacgag
S K D S T Y S L S S T L T L S K A D Y E
aaacacaaagtctacgcctgcgaagtcacccatcagggcctgagctcgcccgtcacaaag
K H K V Y A C E V T H Q G L S S P V T K
agcttcaacaggggagagtgtag
S F N R G E C -

Figure 4

VH: dependent on the MF (target): Figures 1 and 2.

CH1:

```
gctagcaccaagggcccatcggtcttccccctggcaccctcctccaagagcacctctggg
A S T K G P S V F P L A P S S K S T S G
ggcacagcgccctgggctgcttggtcaaggactacttccccgaaccggtgacggtgtcg
G T A A L G C L V K D Y F P E P V T V S
tggaactcaggcgccctgaccagcggtgcacaccttcccggtgtcctacagtcctca
W N S G A L T S G V H T F P A V L Q S S
ggactctactccctcagcagcgctgacggtgccctccagcagcttgggcacccagacc
G L Y S L S S V V T V P S S S L G T Q T
tacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagtt
Y I C N V N H K P S N T K V D K R V
```

Hinge:

```
gagcccaaattctgtgacaaaactcacacatgcccaccgtgcca
E P K S C D K T H T C P P C P
```

CH2:

```
gcacctgaactcctggggggacggtcagtccttcttccccccaaaaccaaggacacc
A P E L L G G P S V F L F P P K P K D T
ctcatgatctcccggaacctgaggtcacatgctggtggtggacgtgagccacgaagac
L M I S R T P E V T C V V V D V S H E D
cctgaggtcaagttcaactggtacgtggacggcggtggaggtgcataatgccaagacaaag
P E V K F N W Y V D G V E V H N A K T K
ccgcgaggagcagtagacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcac
P R E E Q Y N S T Y R V V S V L T V L H
caggactgggtgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcc
Q D W L N G K E Y K C K V S N K A L P A
cccatcgagaaaaccatctccaaagccaaa
P I E K T I S K A K
```

CH3: KK of DEKK

```
gggcagccccgagaaccacaggtgtacaccaagcccccatcccgaggagatgaccaag
G Q P R E P Q V Y T K P P S R E E M T K
aaccaggtcagcctgaagtgcctgggtcaaaggcttctatcccagcgacatcgccgtggag
N Q V S L K C L V K G F Y P S D I A V E
tgggagagcaatgggcagccggagaacaactacaagaccacgcctcccggtgctggactcc
W E S N G Q P E N N Y K T T P P V L D S
gacggctccttcttctctatagcaagctcaccgtggacaagagcaggtggcagcagggg
D G S F F L Y S K L T V D K S R W Q Q G
aacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagc
N V F S C S V M H E A L H N H Y T Q K S
ctctccctgtctccgggttga
L S L S P G -
```

CH3: DE of DEKK

gggcagccccgagaaccacaggtgtacaccgaccccccatcccgggaggagatgaccaag
G Q P R E P Q V Y T D P P S R E E M T K
aaccaggtcagcctgacctgcgaggtcaaaggcttctatcccagcgacatcgccgtggag
N Q V S L T C E V K G F Y P S D I A V E
tgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactcc
W E S N G Q P E N N Y K T T P P V L D S
gacggctccttcttctctatagcaagctcaccgtggacaagagcaggtggcagcagggg
D G S F F L Y S K L T V D K S R W Q Q G
aacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagc
N V F S C S V M H E A L H N H Y T Q K S
ctctccctgtctccgggttga
L S L S P G -

Figure 5

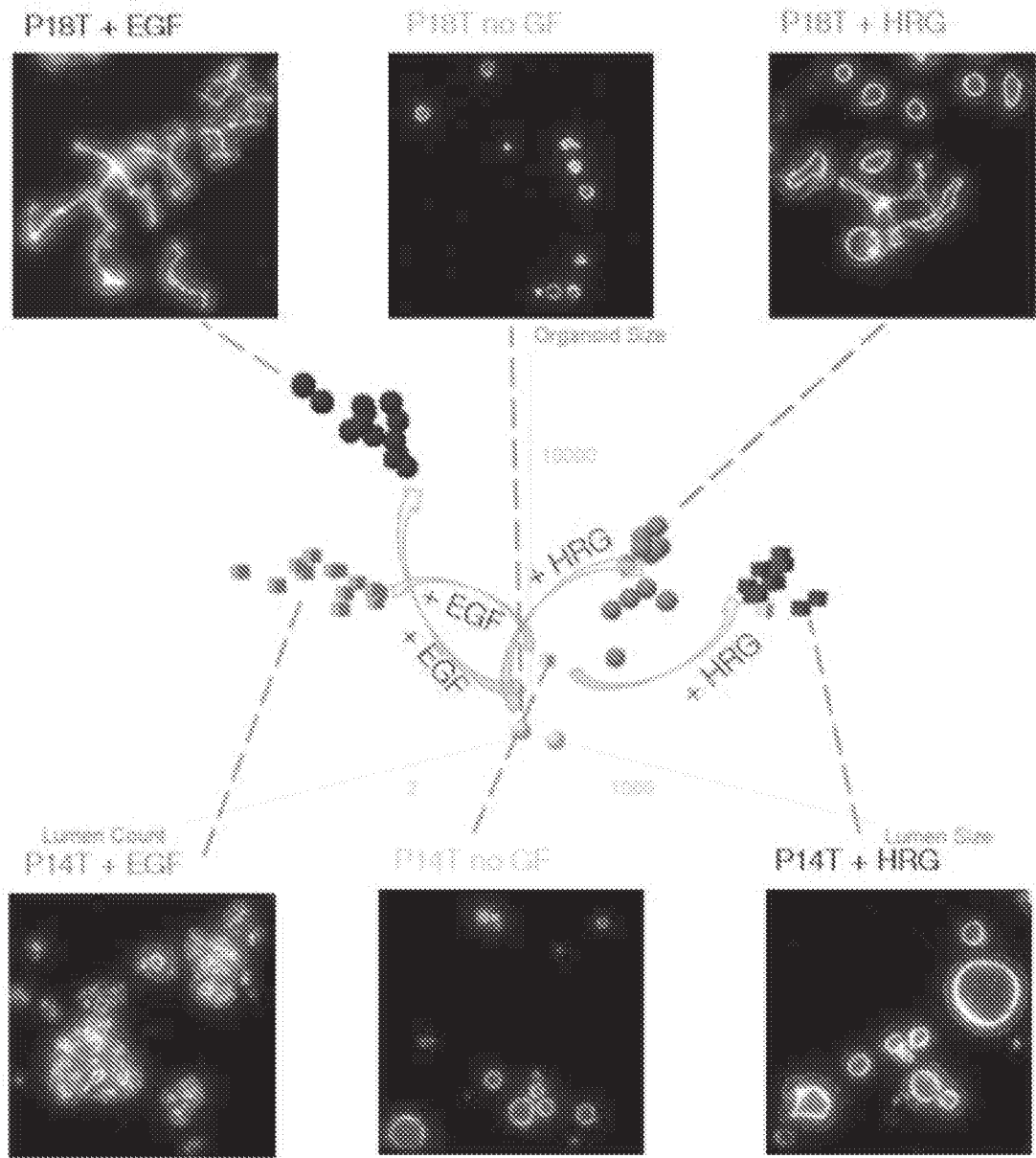


Figure 6

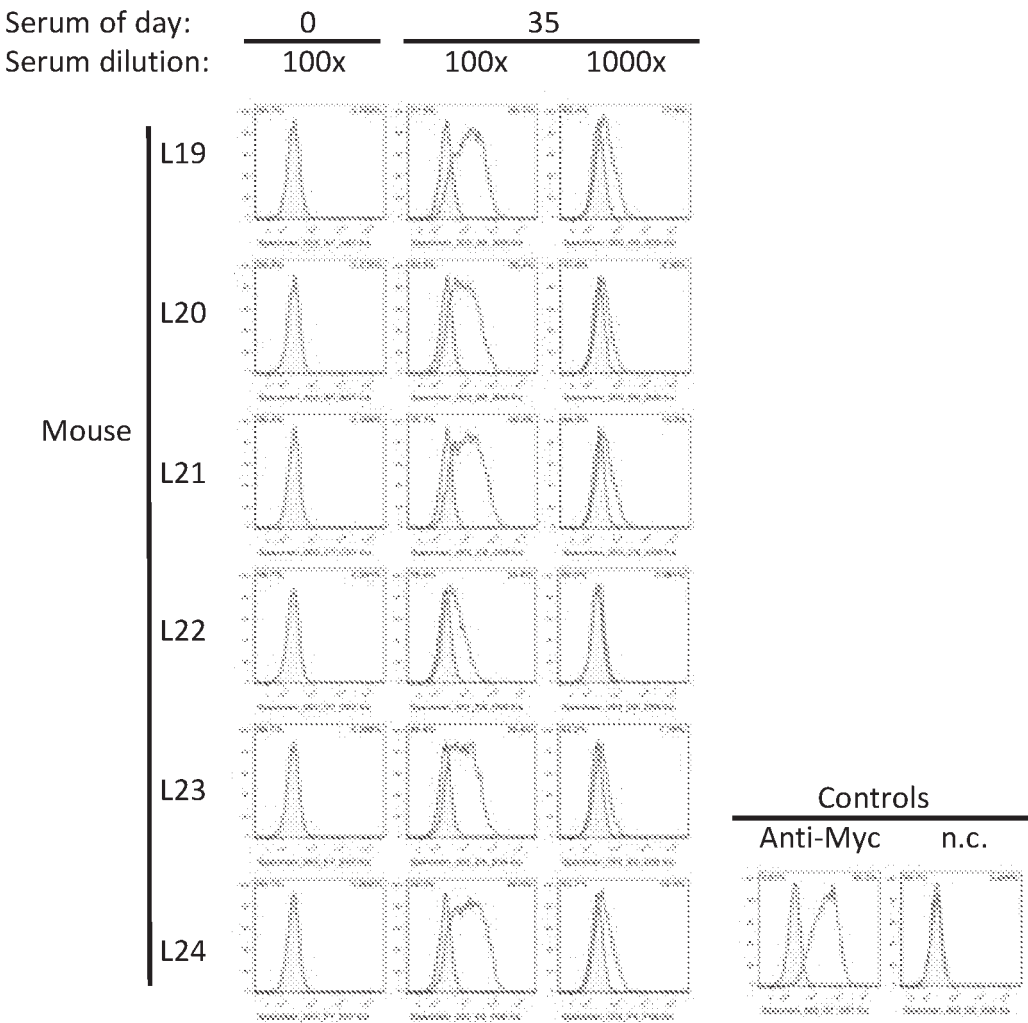
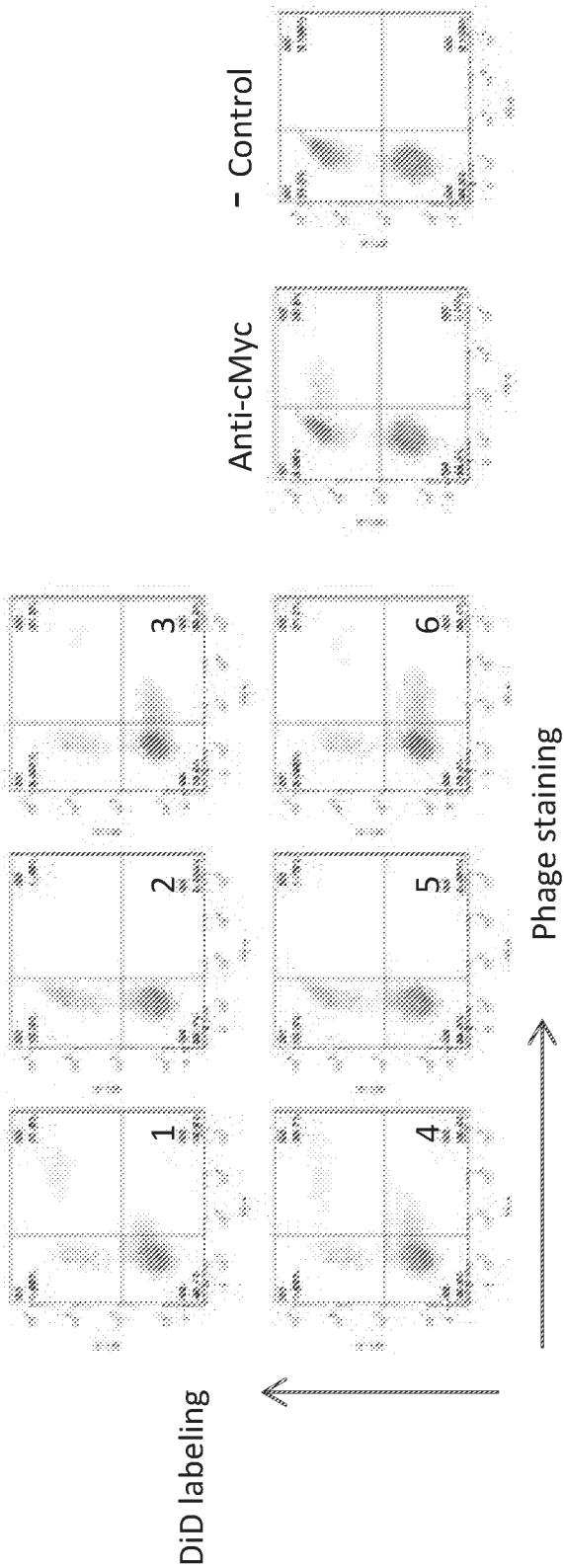


Figure 7



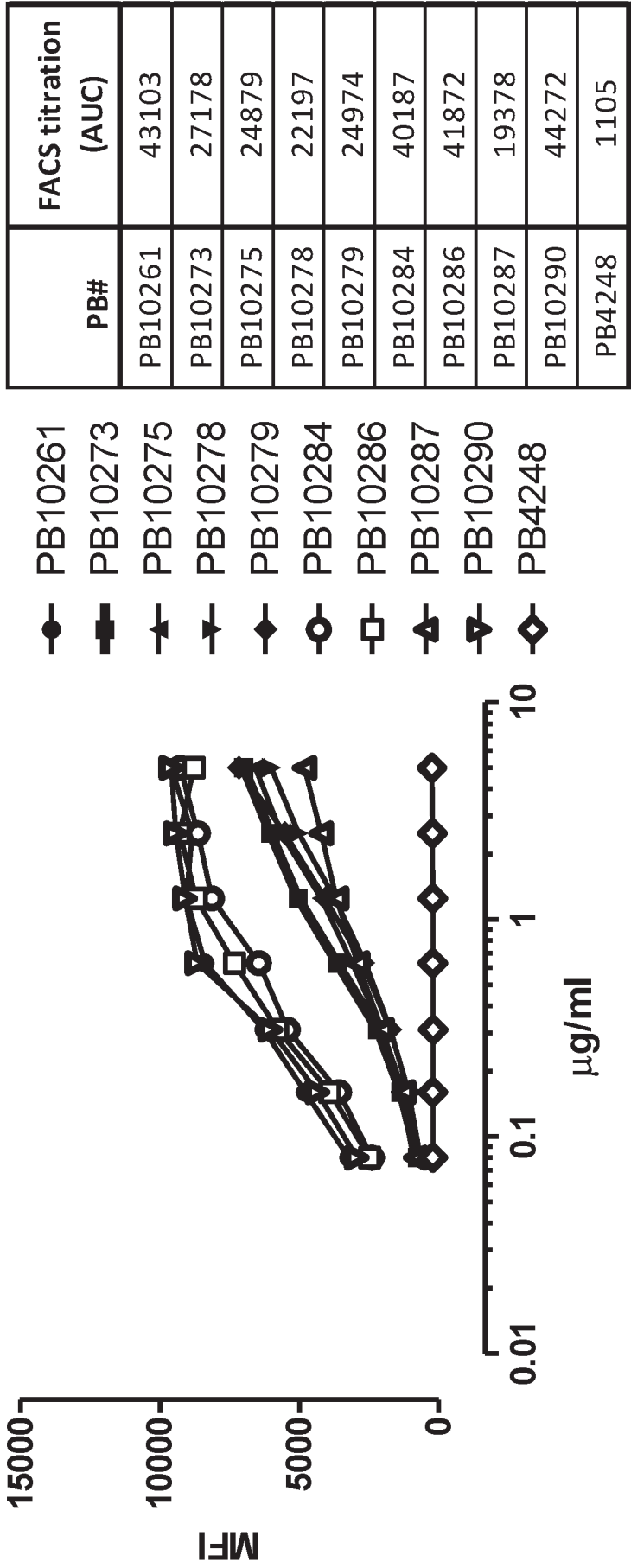


Figure 8

Figure 9

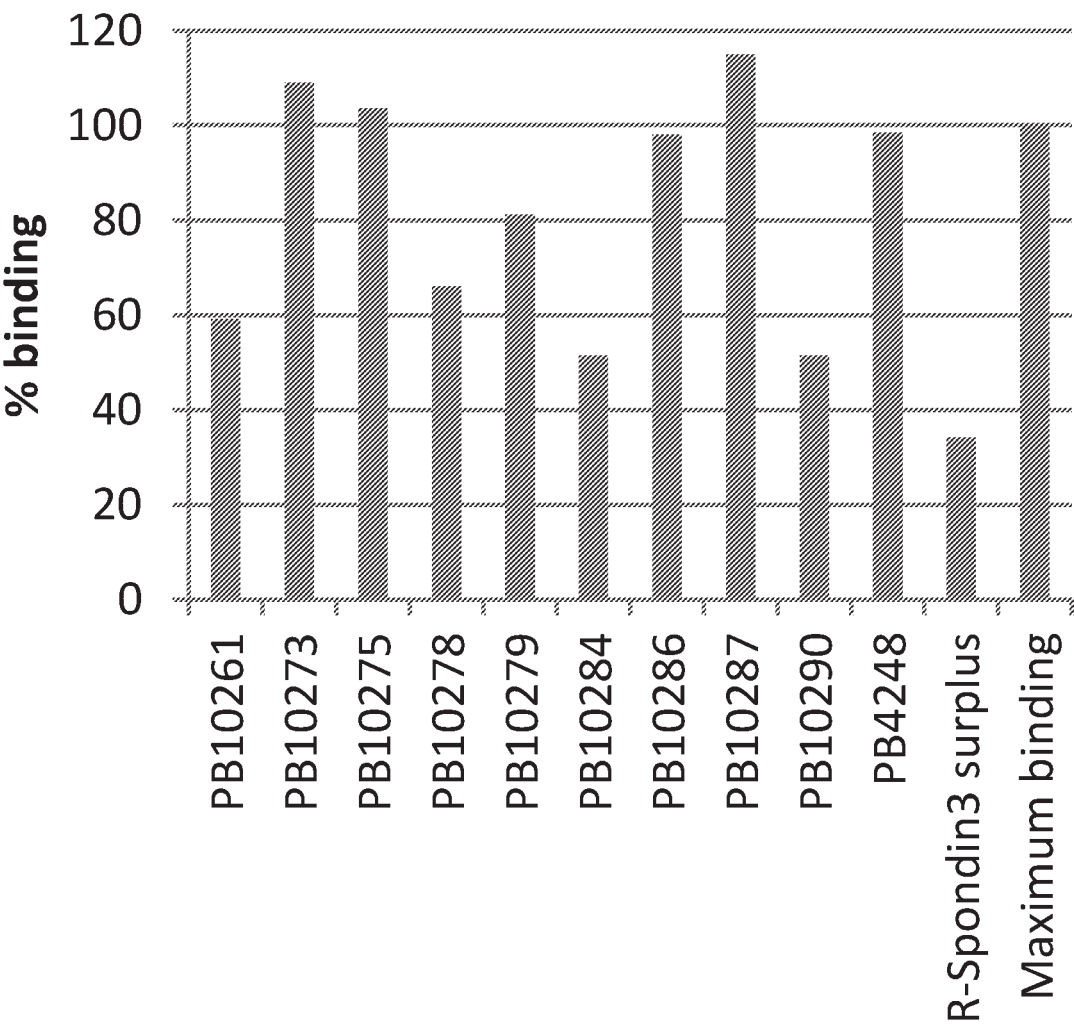


Figure 11

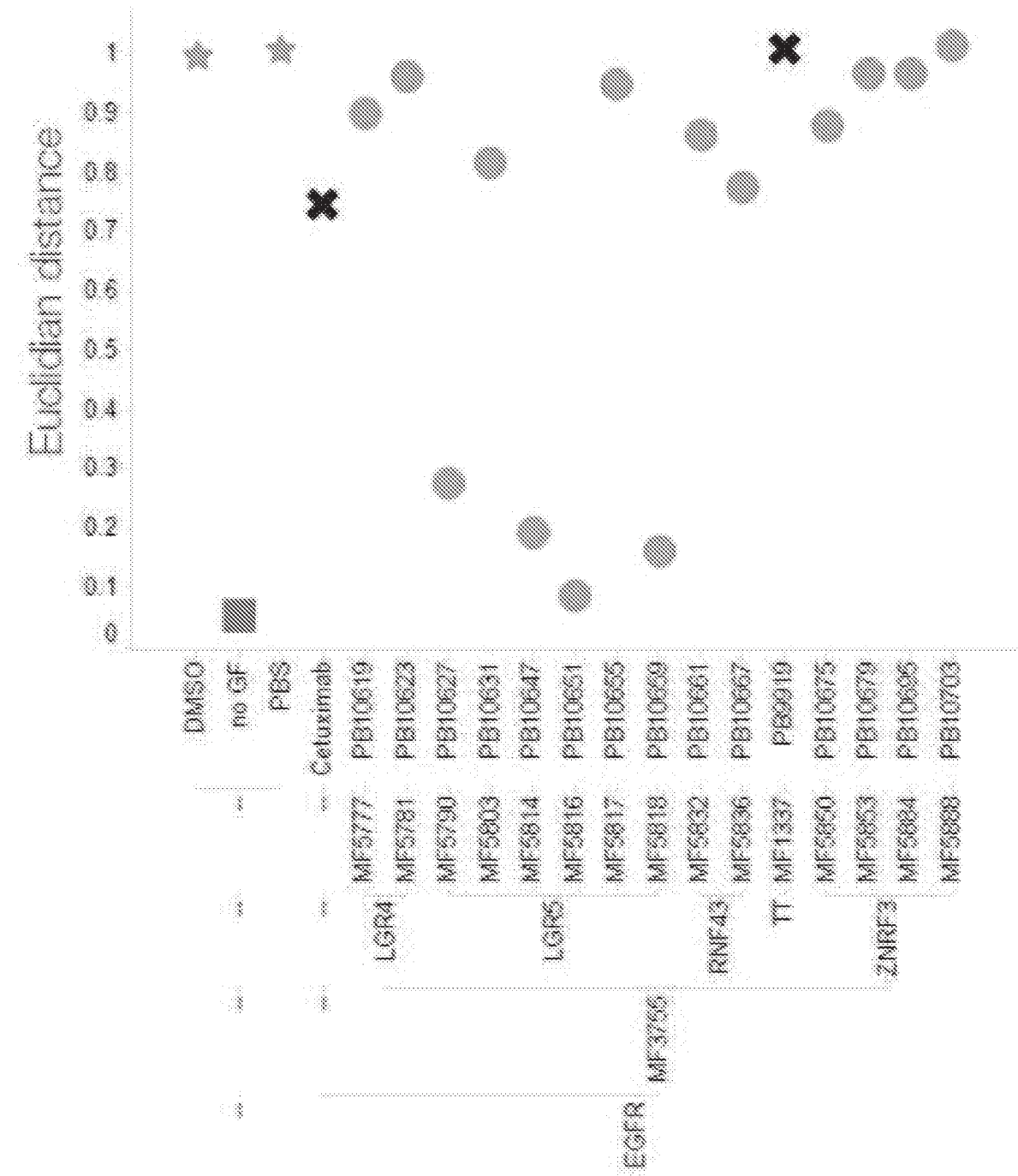


Figure 12

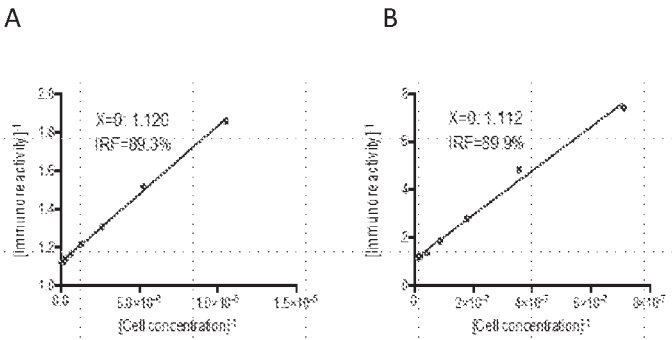


Figure 13

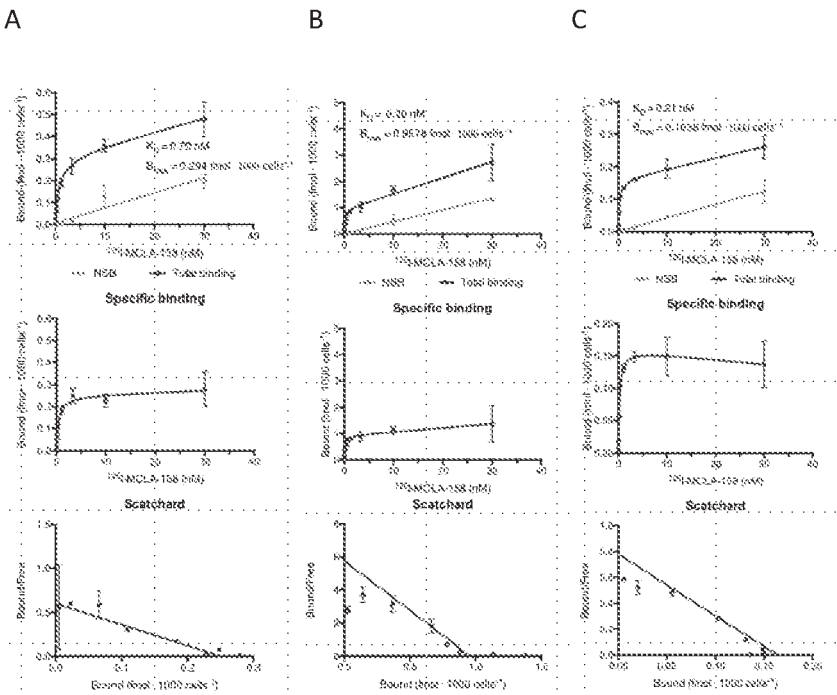


Figure 14

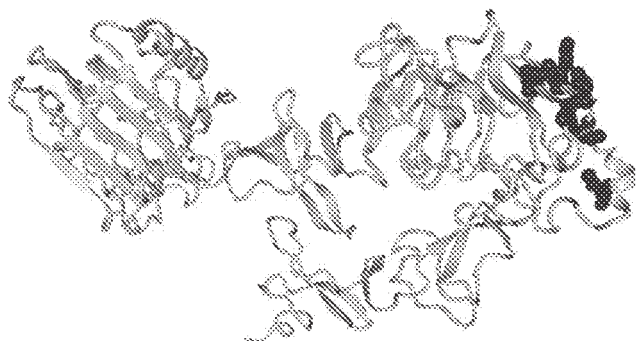


Figure 15

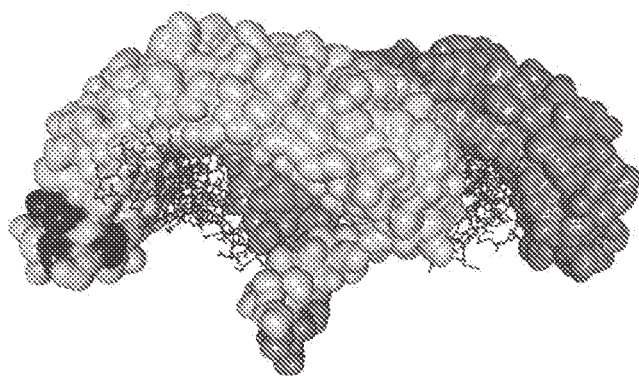


Figure 16

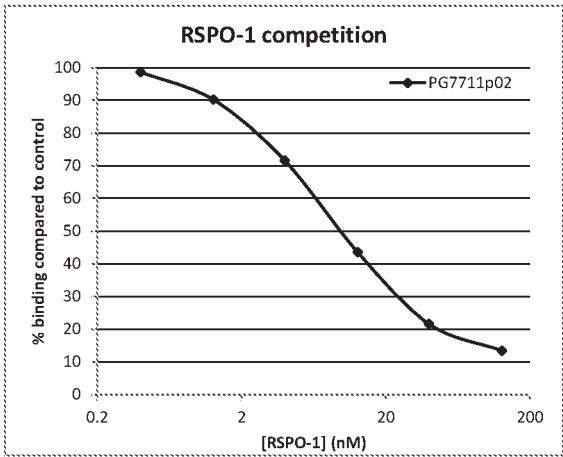


Figure 17

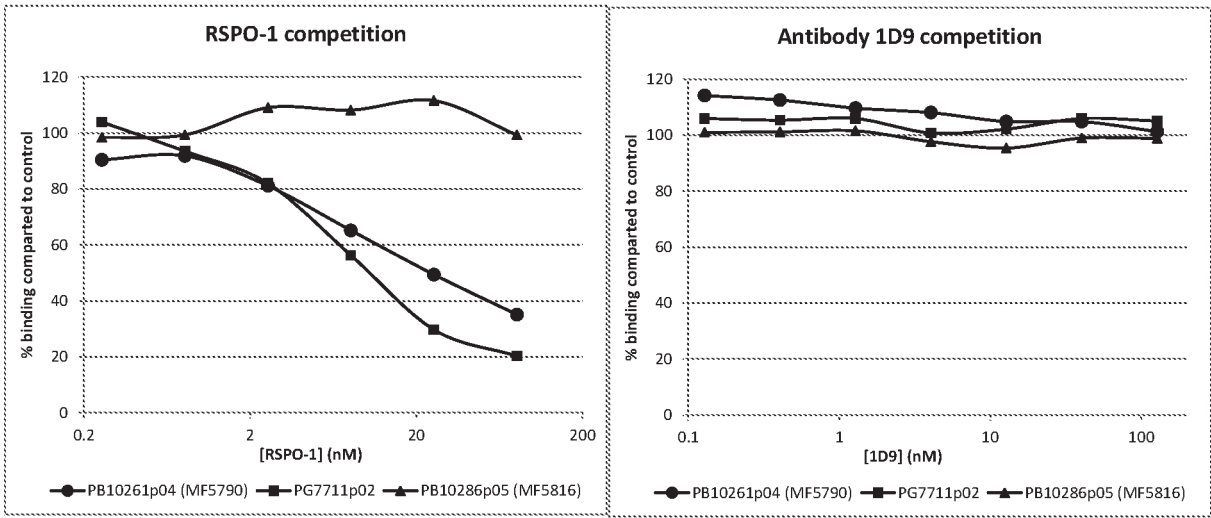


Figure 18

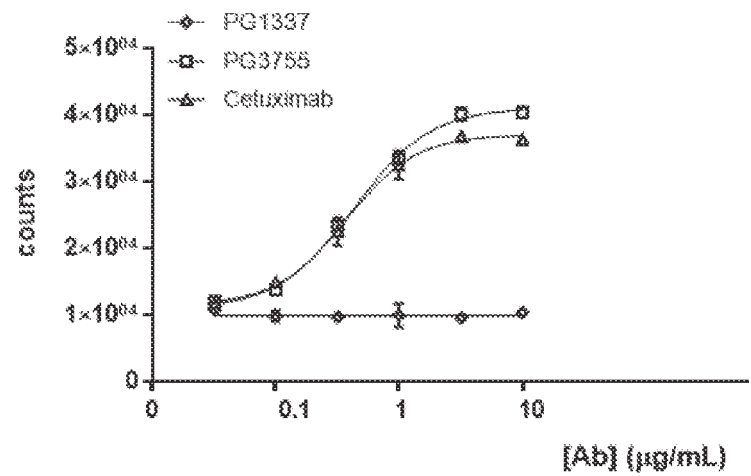


Figure 19

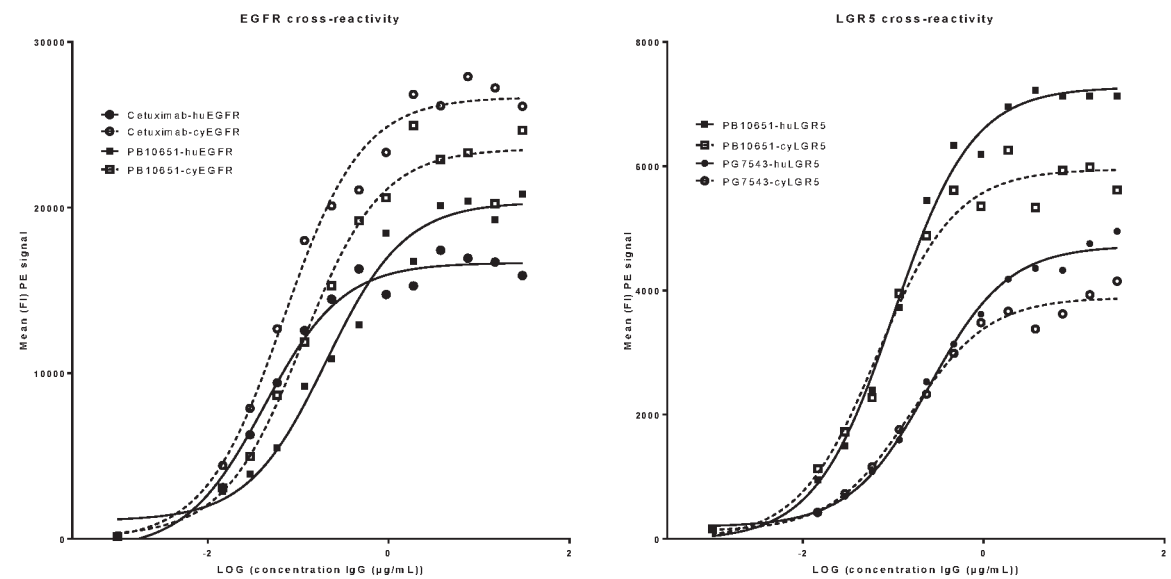
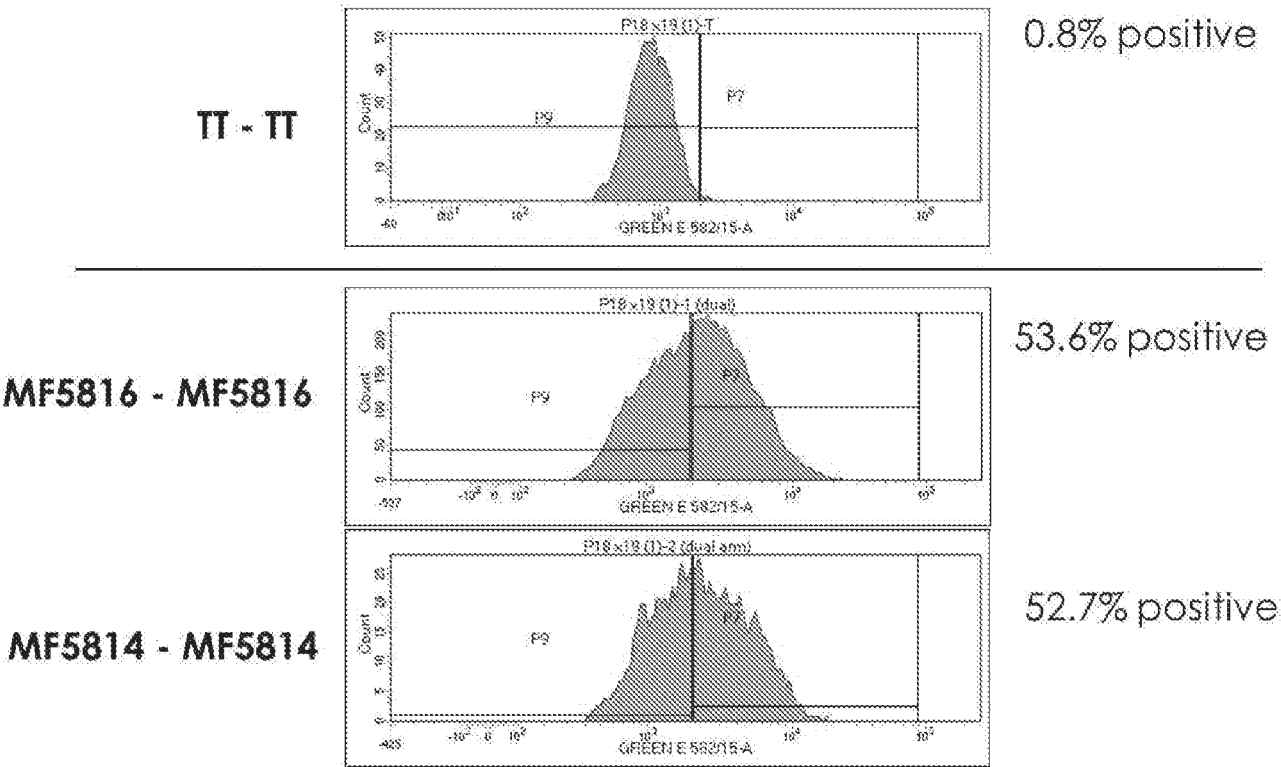


Figure 20



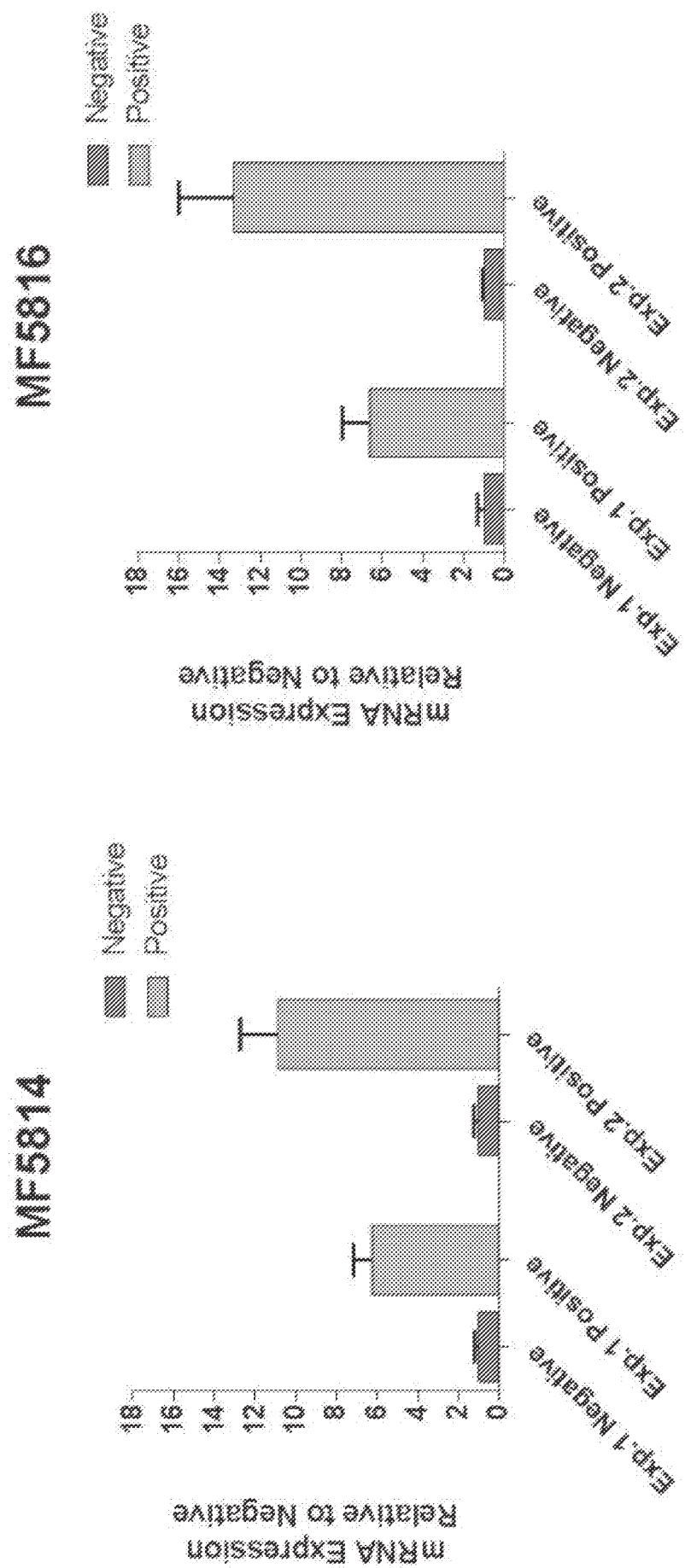


Figure 21

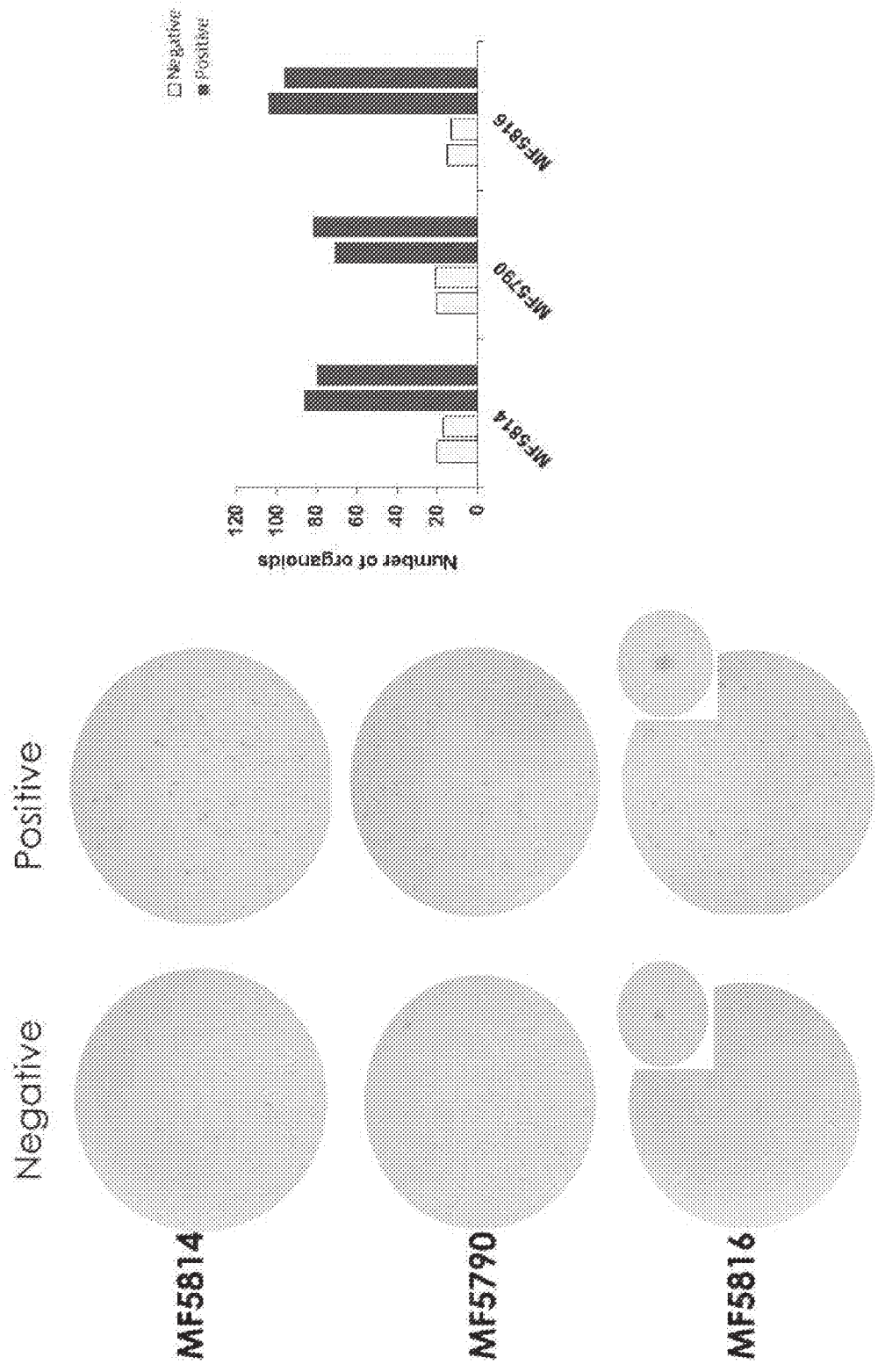


Figure 22

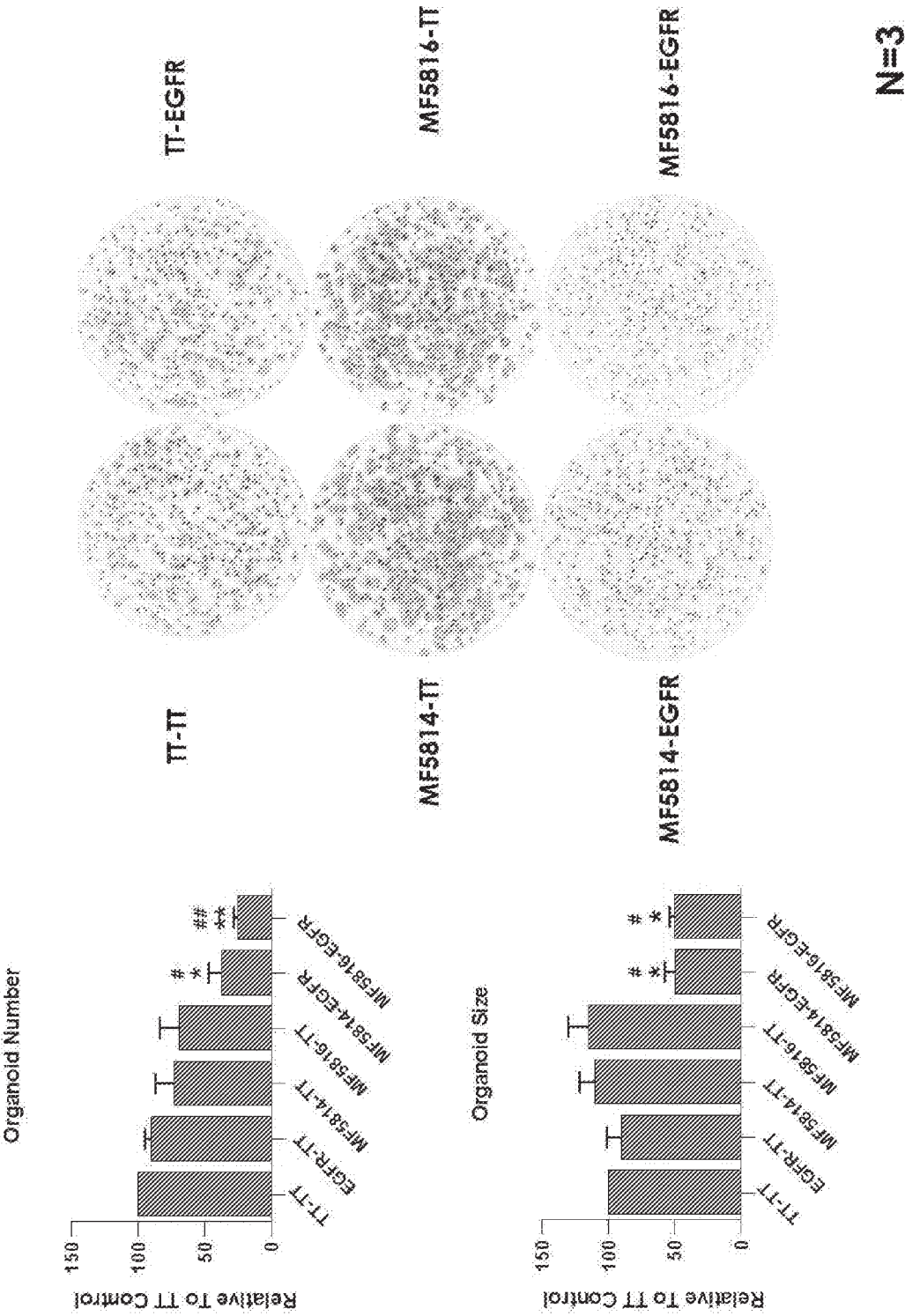


Figure 23

Figure 24

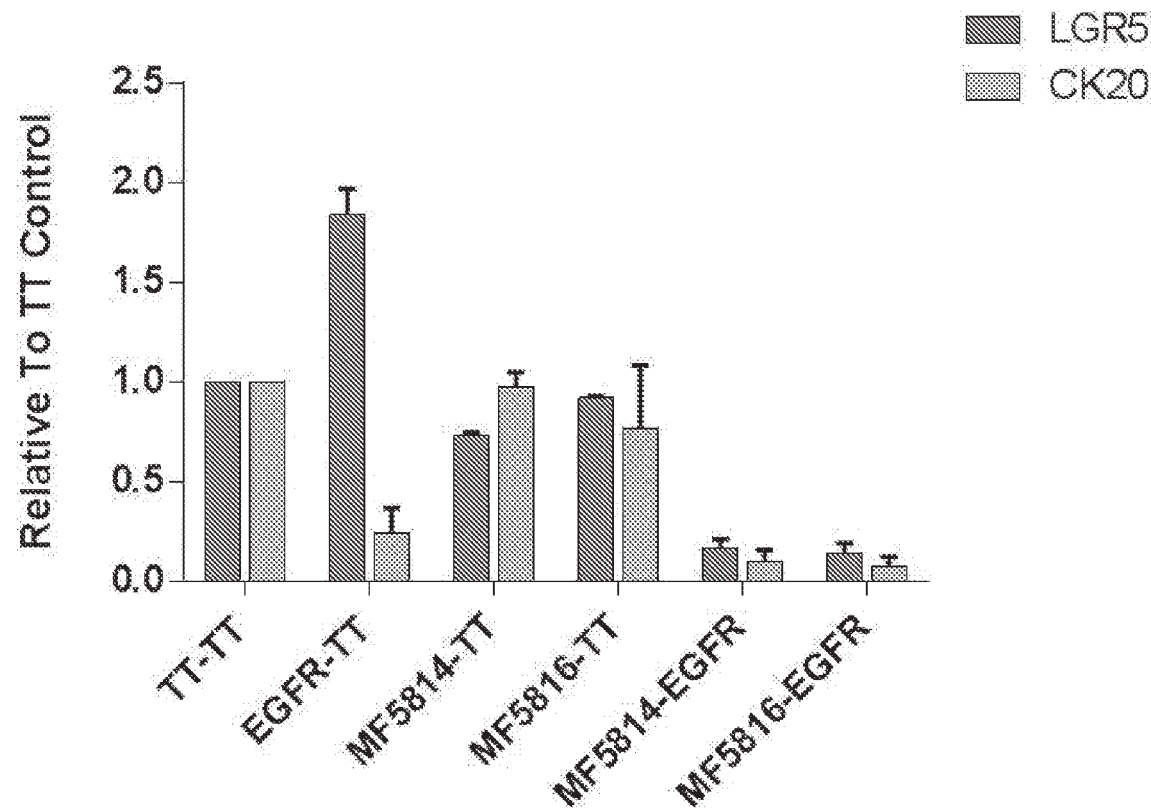


Figure 25

Figure 25A

Supercluster 1 (MF5814 and MF5818)

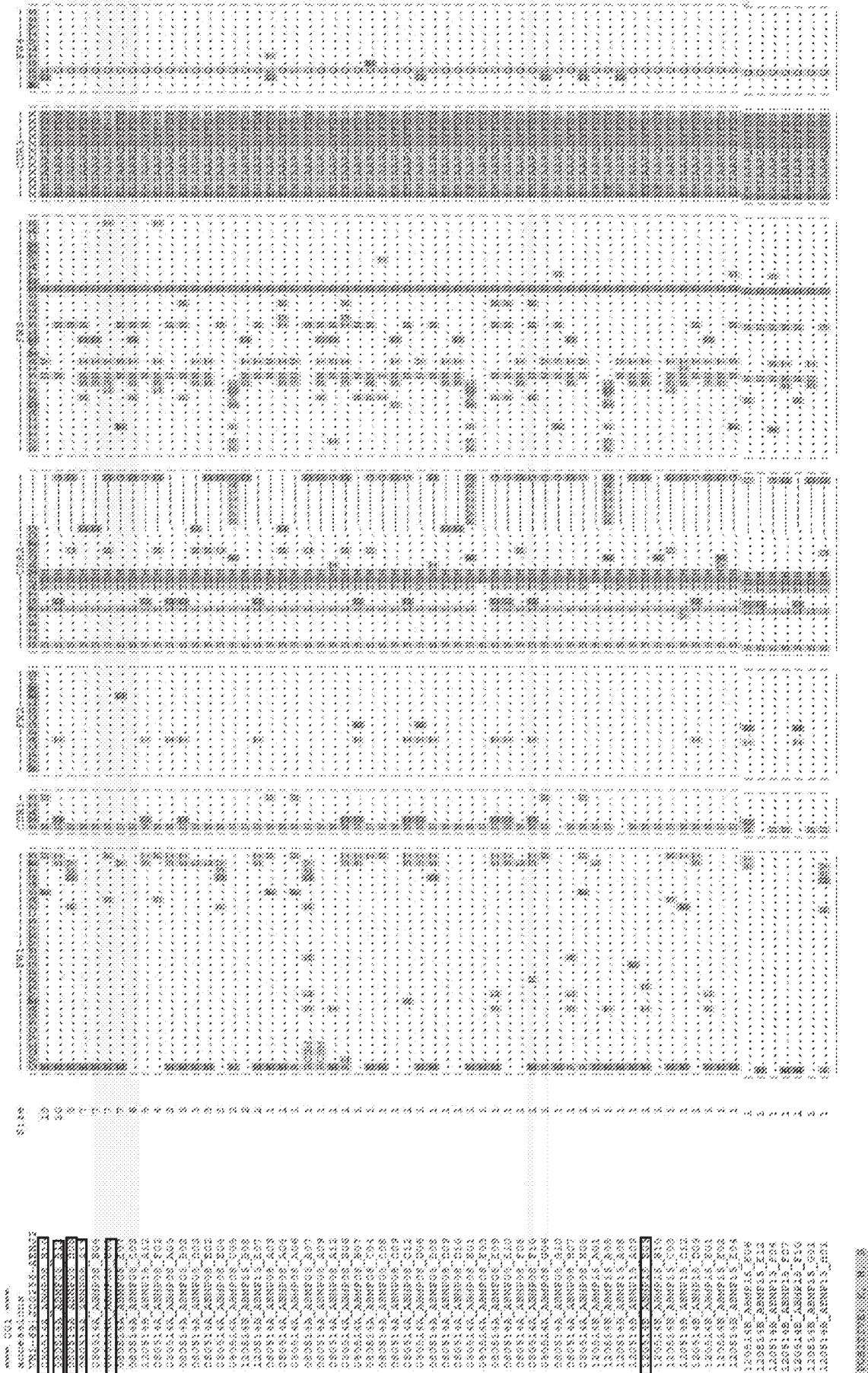


Figure 25B

Supercluster 8 (MF5790)

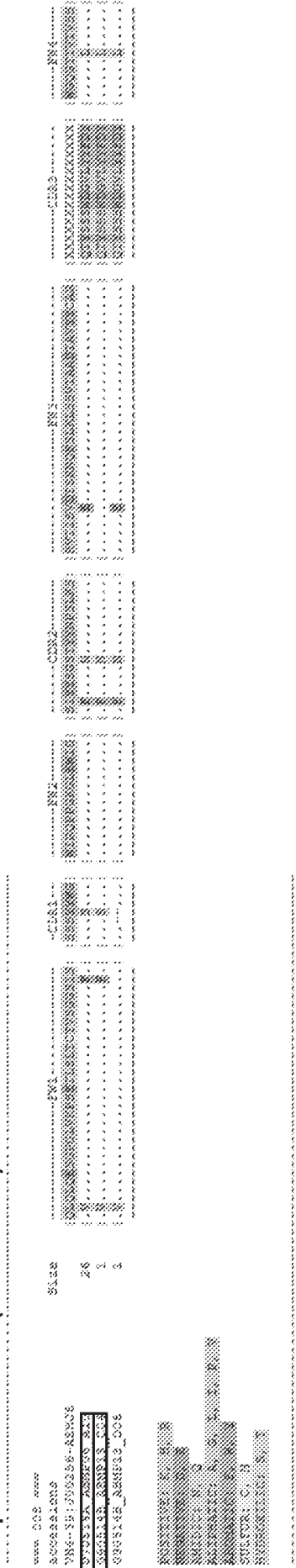


Figure 25C

Supercluster 10 (MF5816)

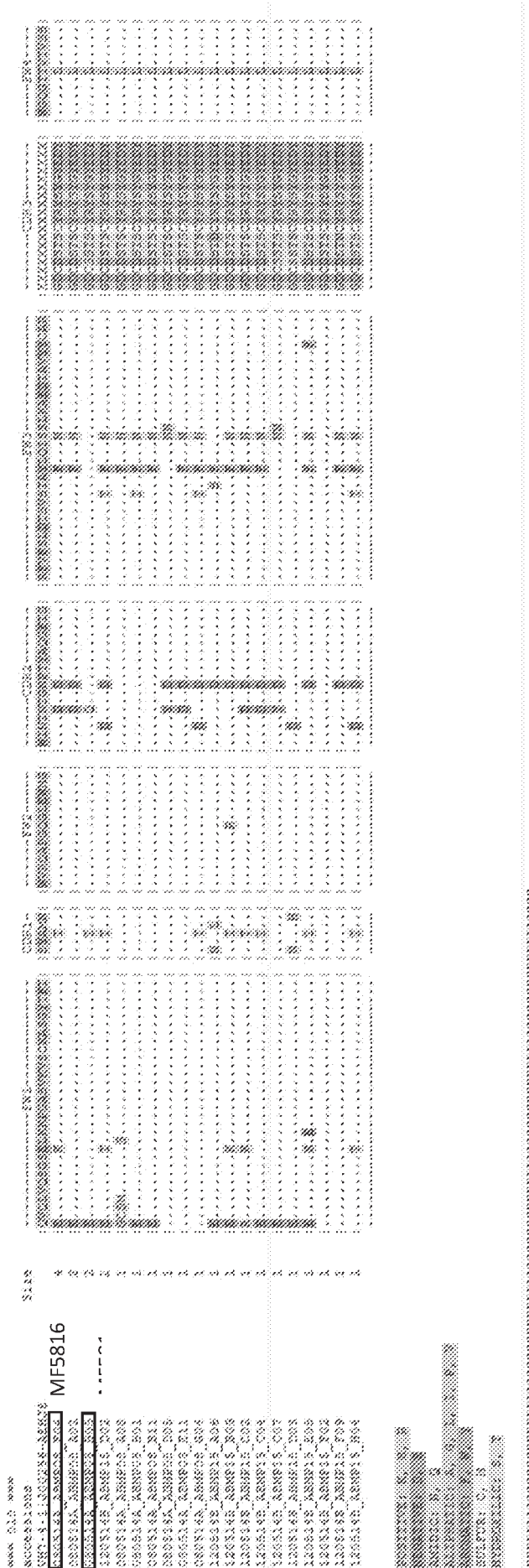


Figure 26
Figure 26A

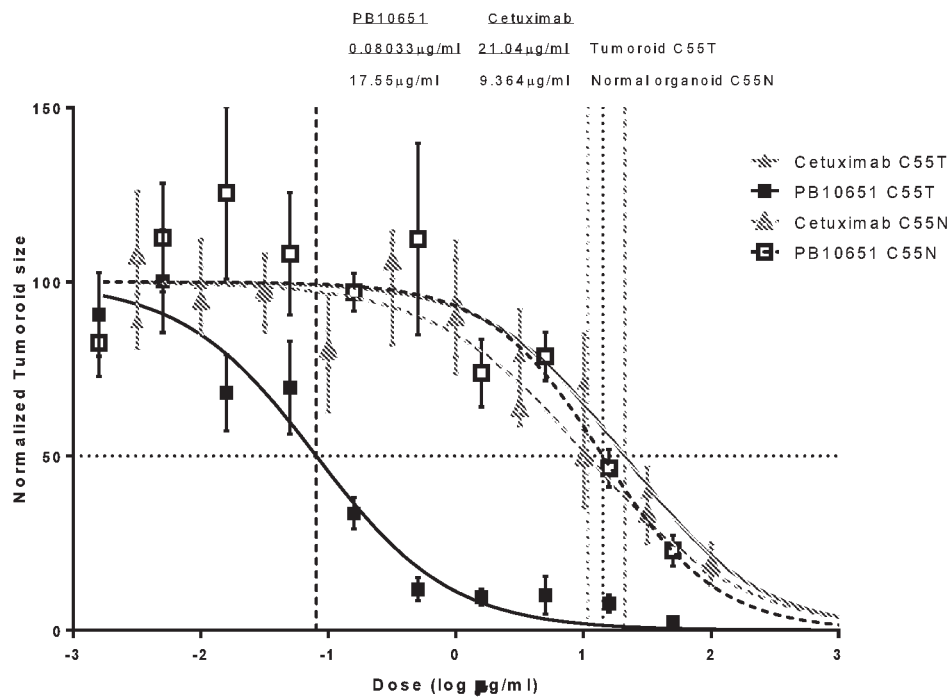


Figure 26B

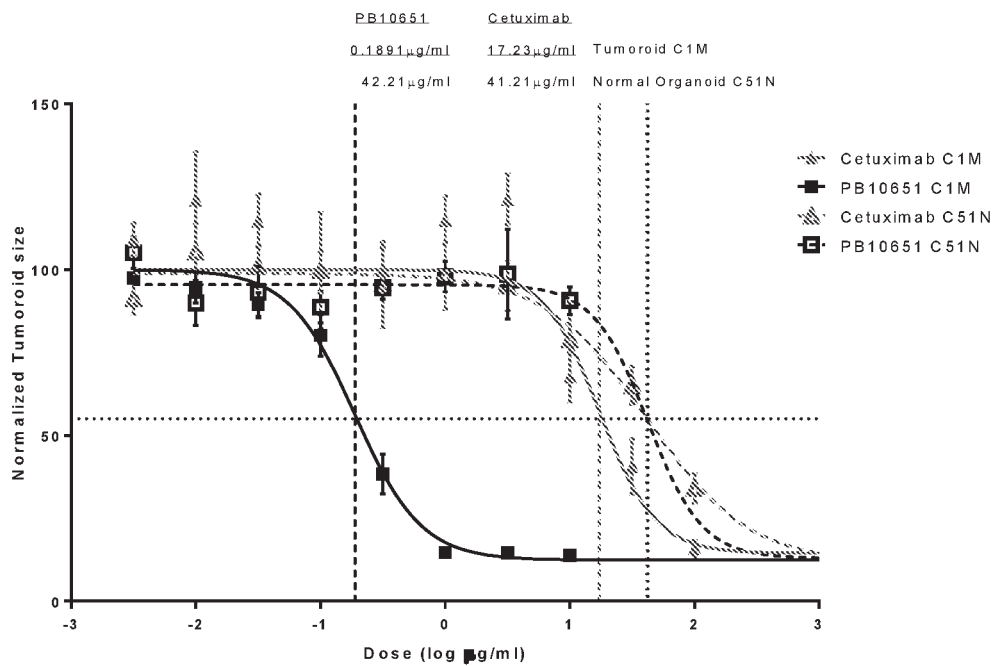


Figure 26C

		IC50 (µg/ml)		
Organoid type	Name	Cetuximab	PB10651	Ratio
Normal	C7N	13.43	19.05	0.7
Normal	C51N	52	67.45	0.8
Normal	C71N	1.37	3.09	0.4
Normal	C57N	1.08	4.52	0.2
Normal	C55N	11.17	14.86	0.8
Tumoroid	C55T	19.63	0.08	245
Tumoroid	C57T	22.75	1.25	18.2
Tumoroid	C0M	10.12	0.39	25.9
Tumoroid	C1M	24.21	0.25	96.8
Tumoroid	C65M	18.92	0.99	19.1
Tumoroid	P18T	5.17	0.25	20.7

Figure 27

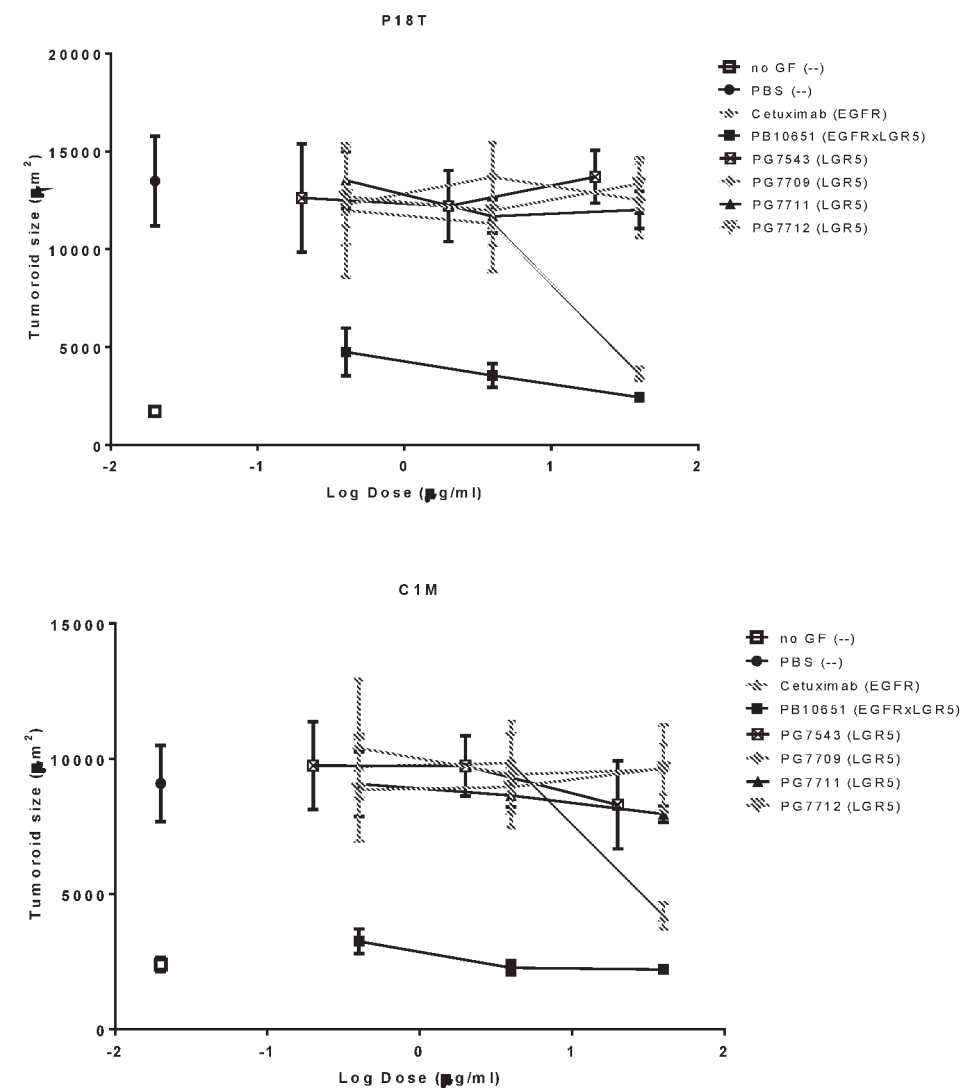


Figure 28
Figure 28A

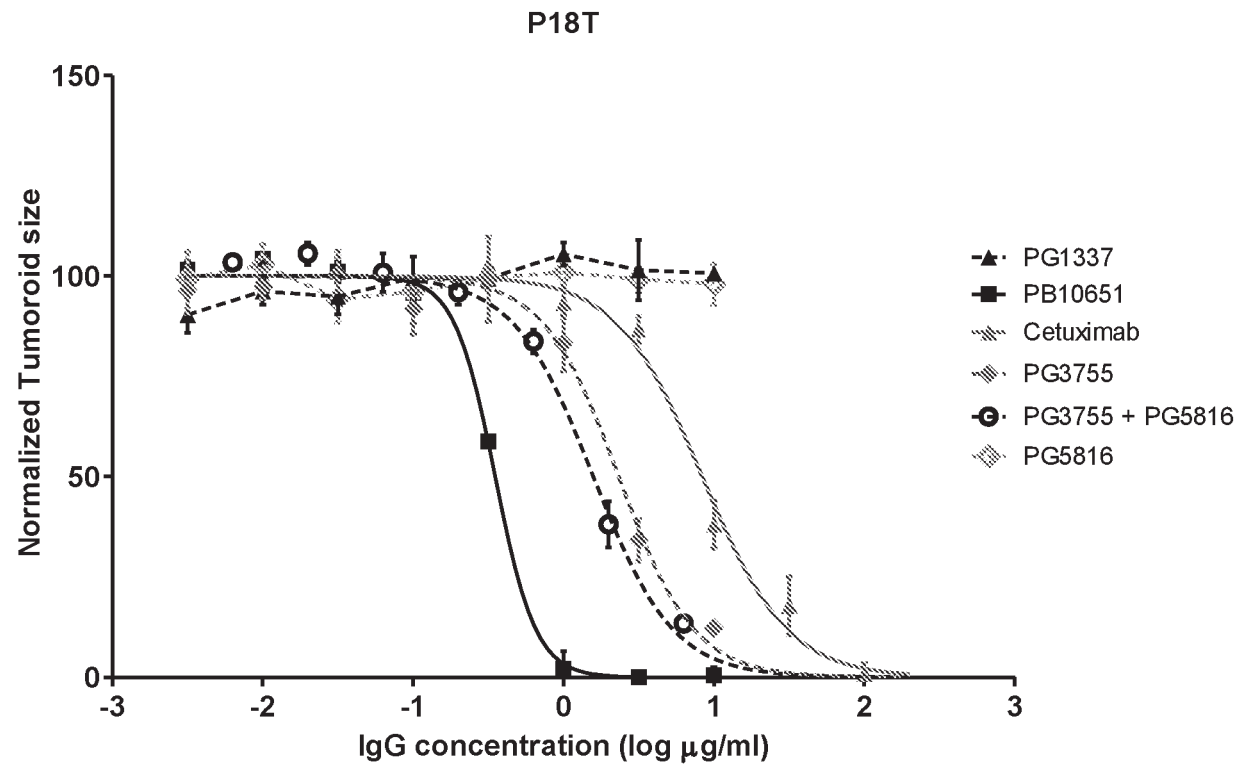
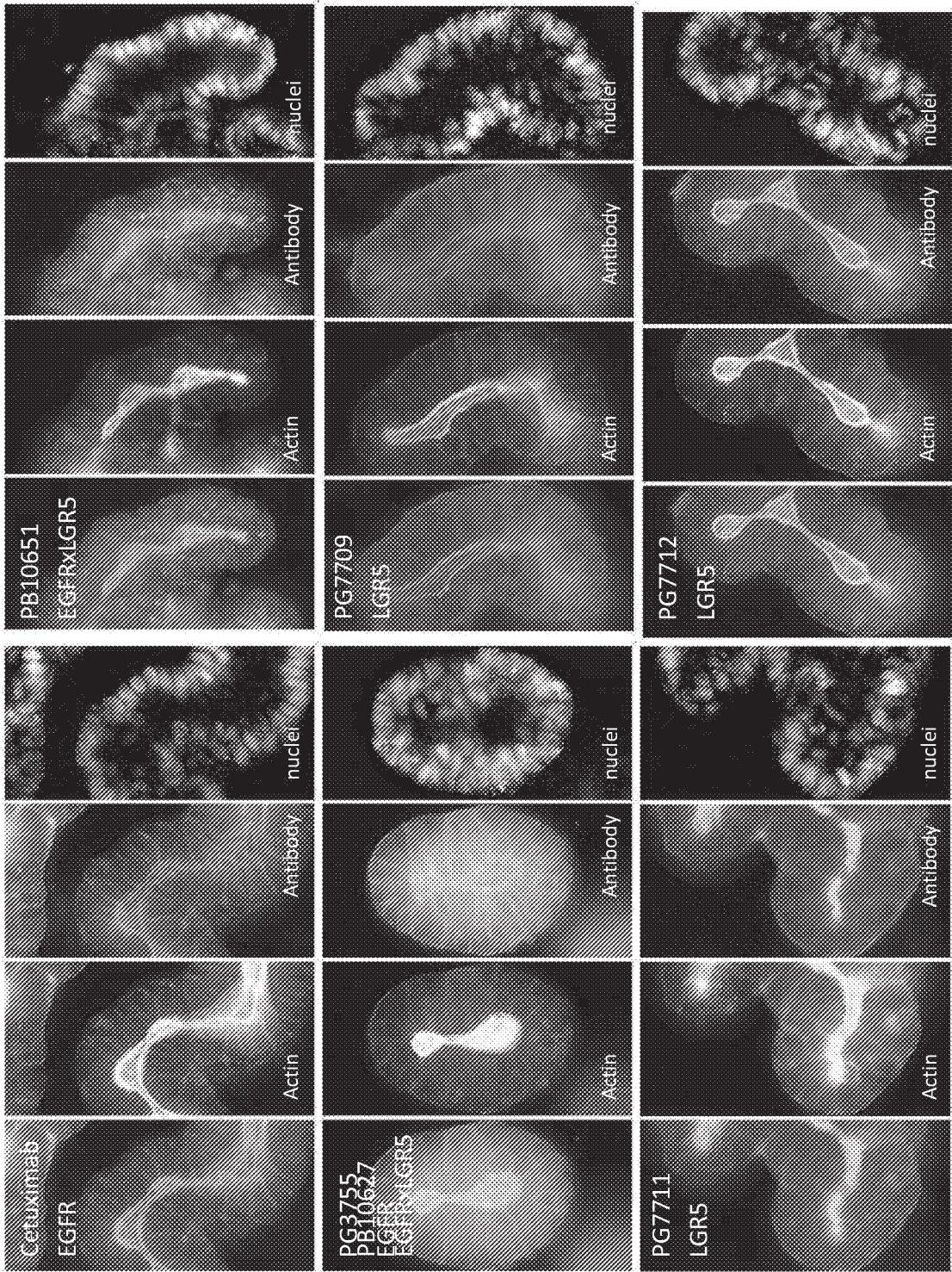


Figure 28B

IC ₅₀ table (µg/ml)		Primary tumour			Metastasis			Normal				
		P18T	C55T	C57T	C65M	C1M	C0M	C51N	C7N	C71N	C55N	C57N
EGFR		IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀
	Cetuximab	8.39	28.51	15.63	15.70	17.10	3.35	26.36	16.11	3.14	2.18	4.80
EGFRxLGR5	PB10651	0.35	0.11	1.20	3.57	0.19	0.14	53.83	17.51	4.77	6.03	8.24
EGFR + LGR5	PG3755 +PG5816	1.59	7.87	16.94	8.89	2.58	1.36	2.17	2.39	0.32	0.47	1.32

Figure 29



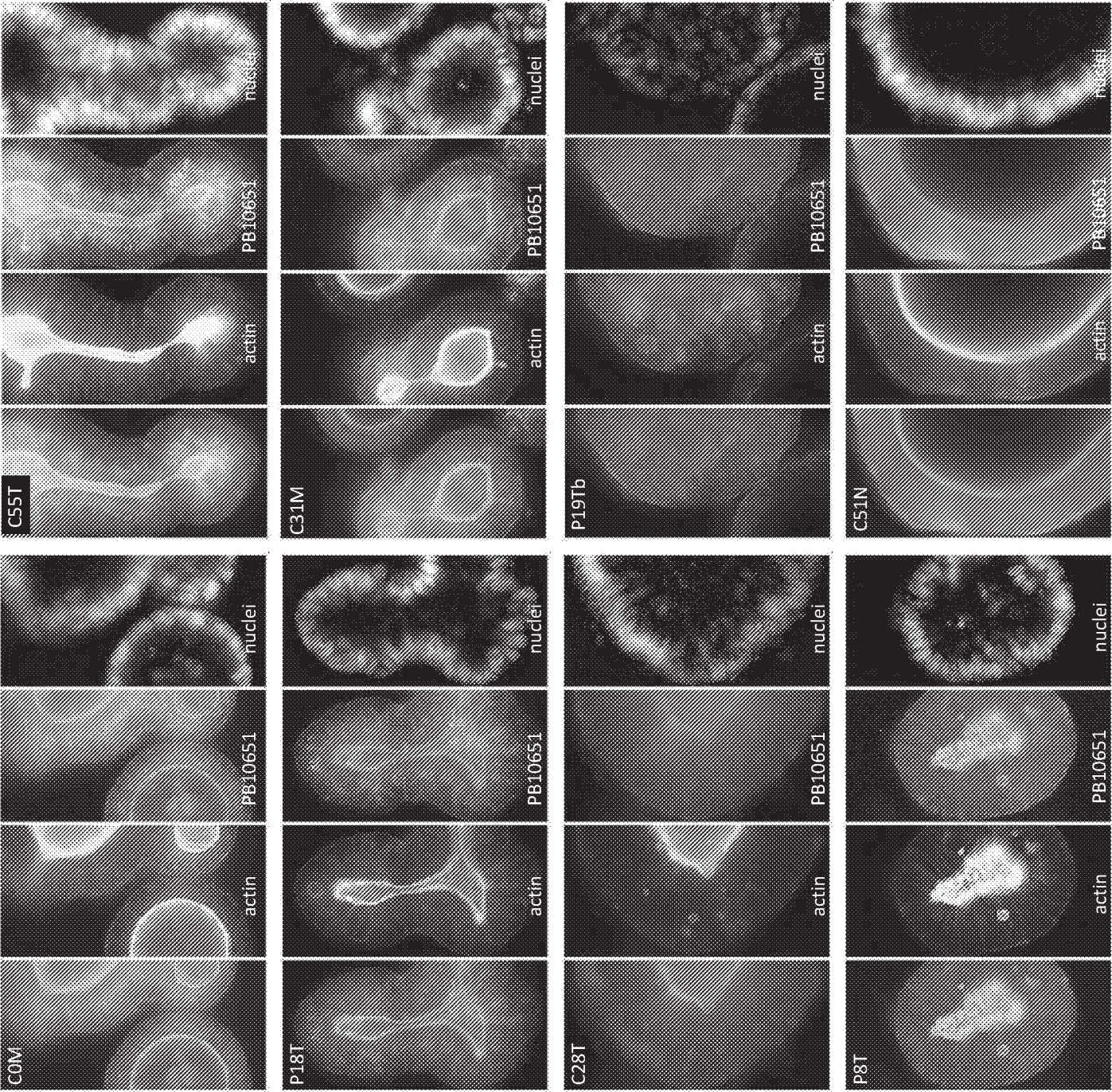


Figure 30

Figure 31

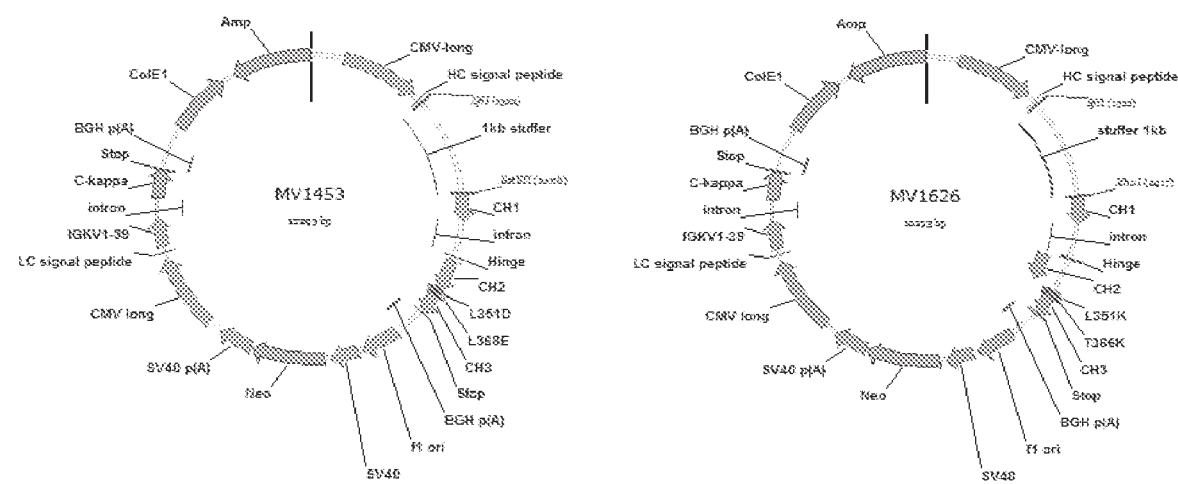


Figure 32

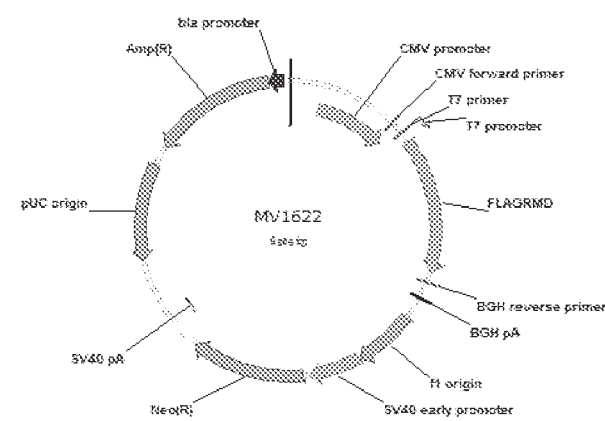


Figure 33

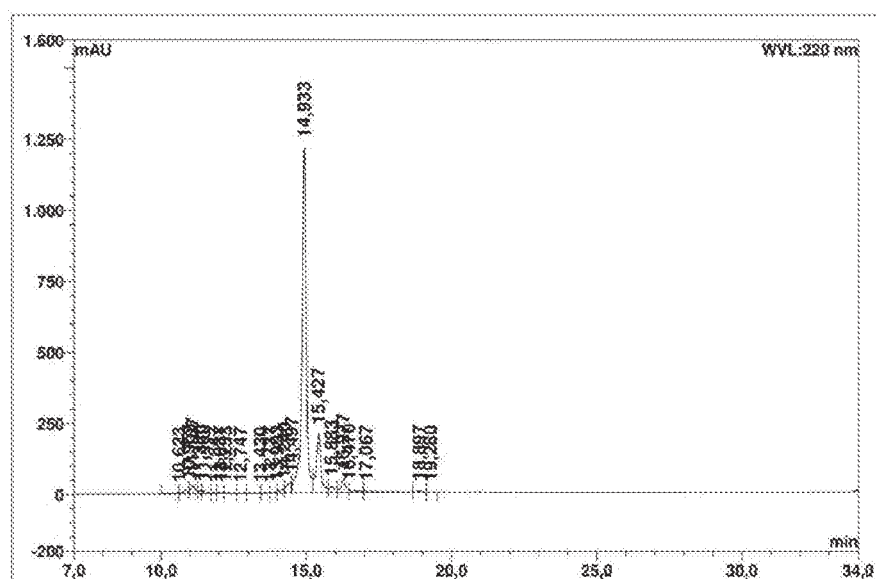


Figure 34

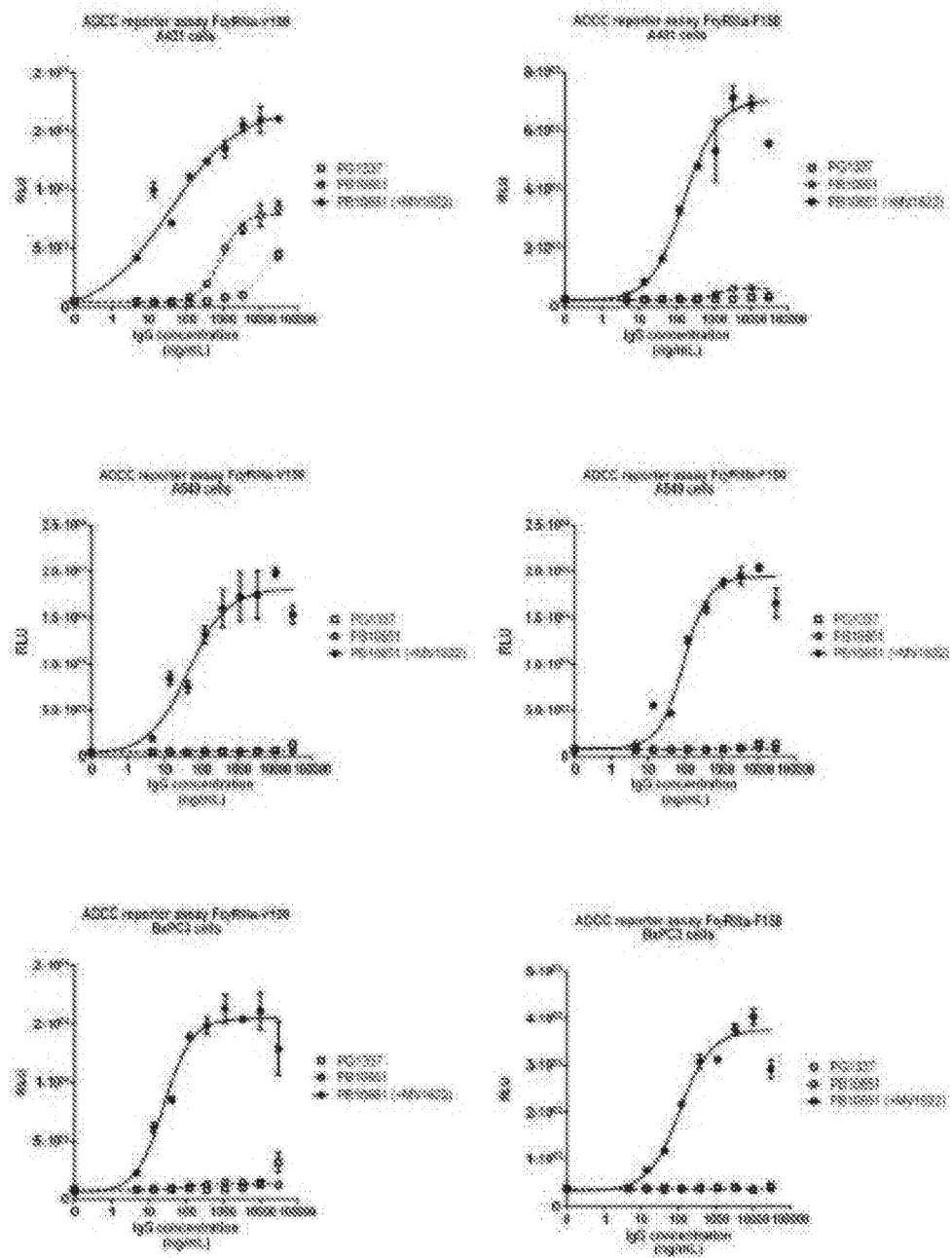


Figure 35

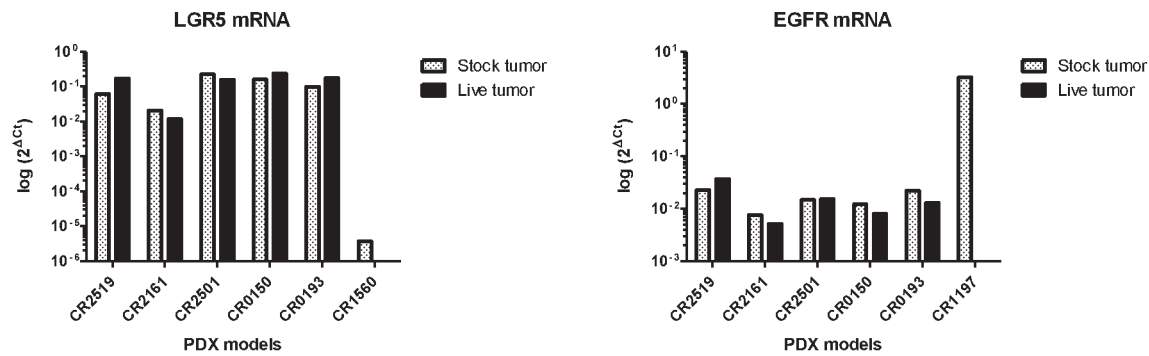


Figure 36

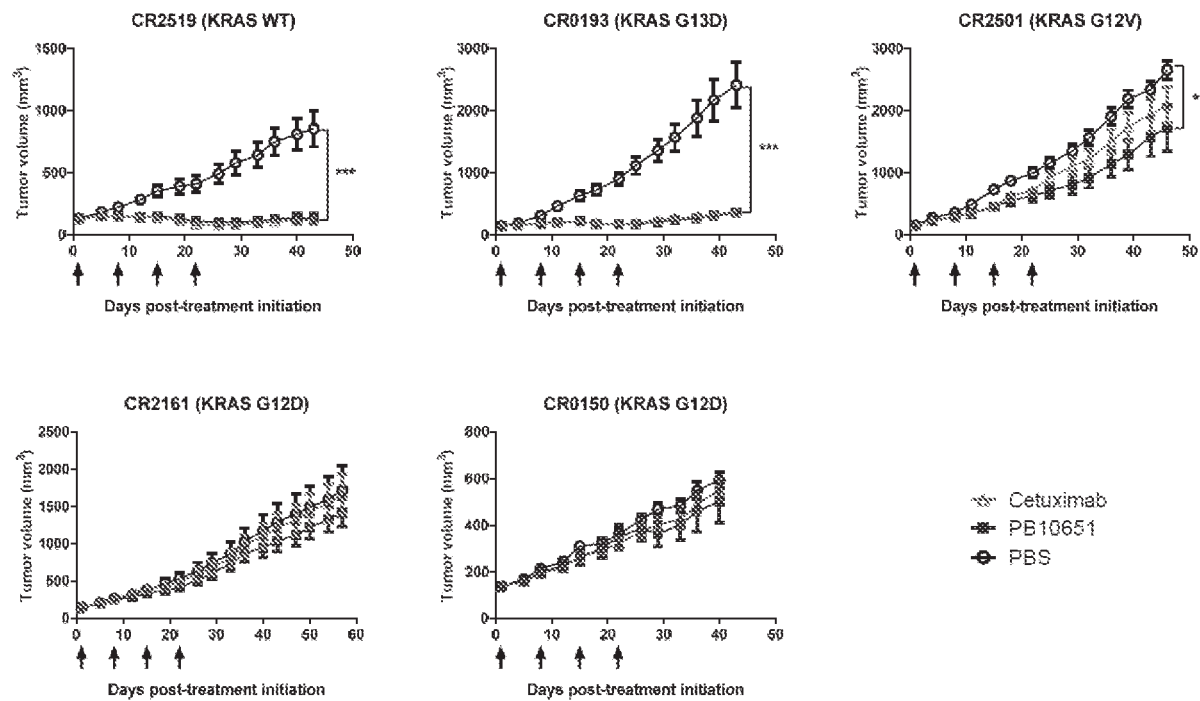


Figure 37

48hrs After Addition of Antibodies

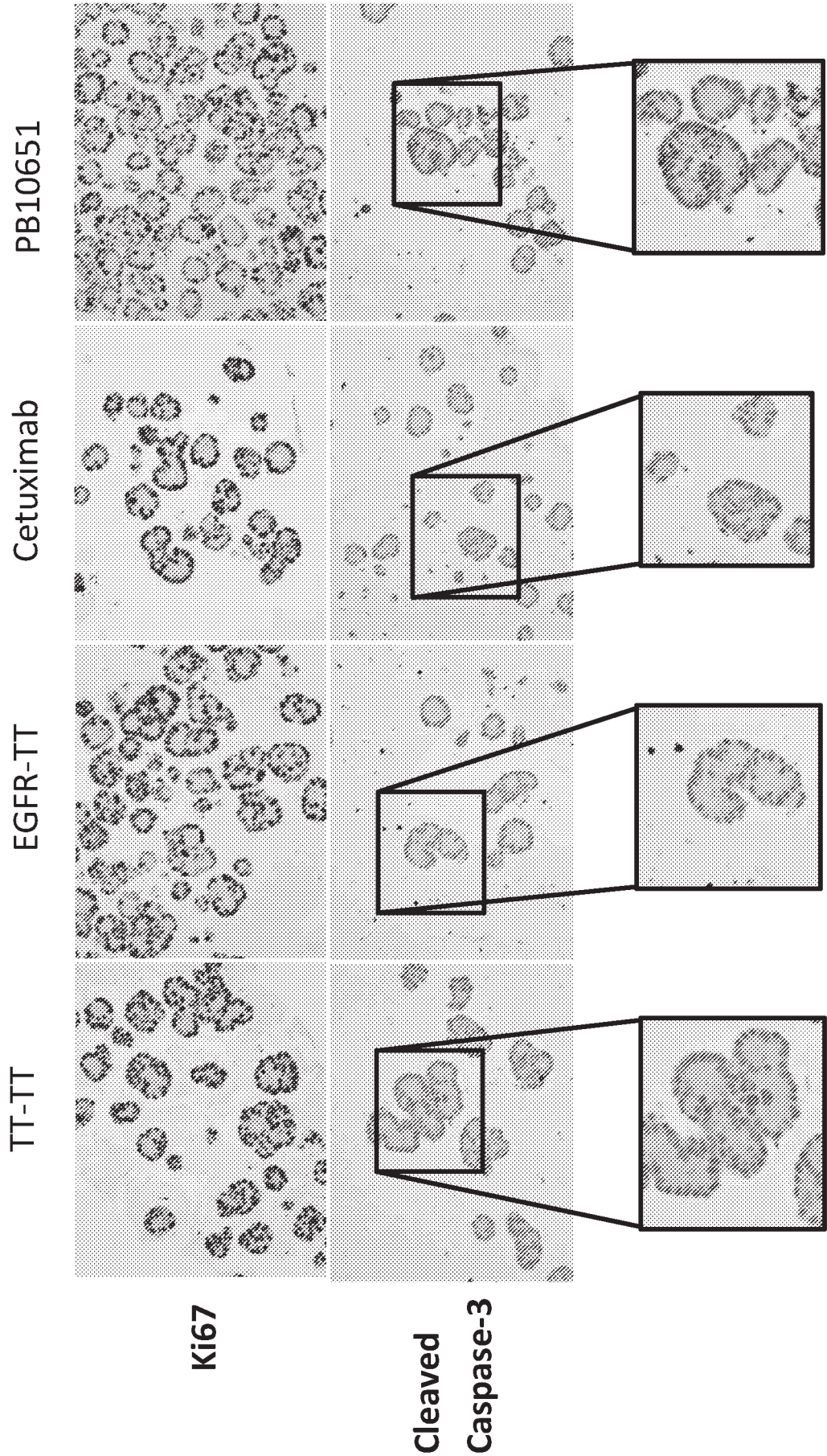


Figure 38

Figure 38A

Average Tumor Volume on Day 0

	Day 0
PBS	46.9
PB10651	47.3
CET	44.3

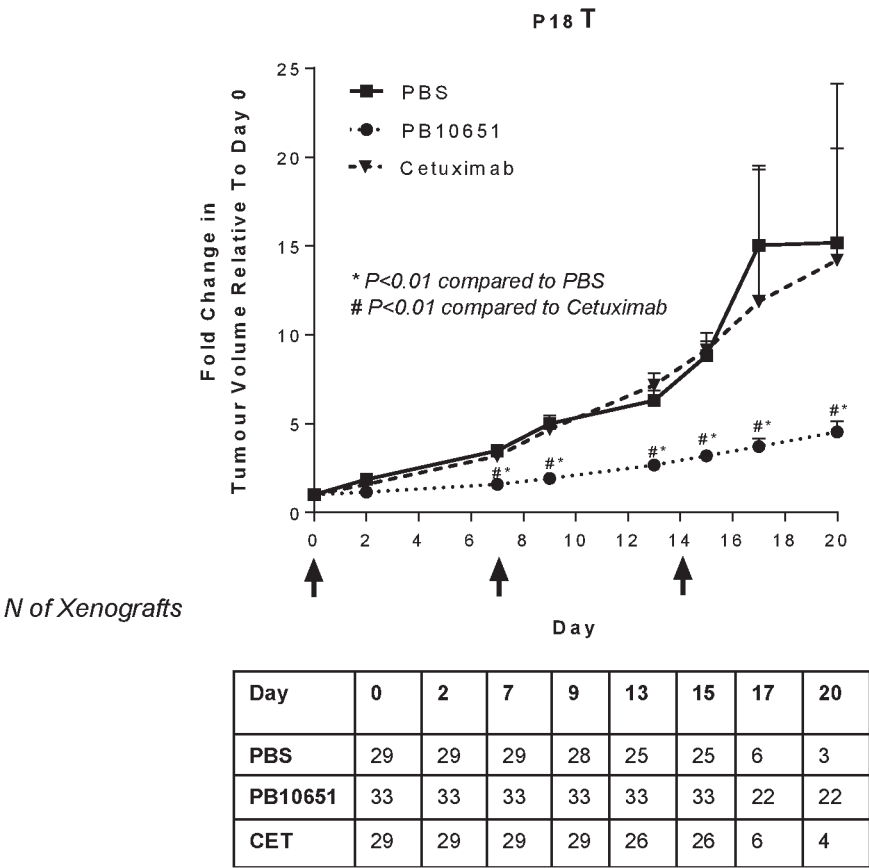
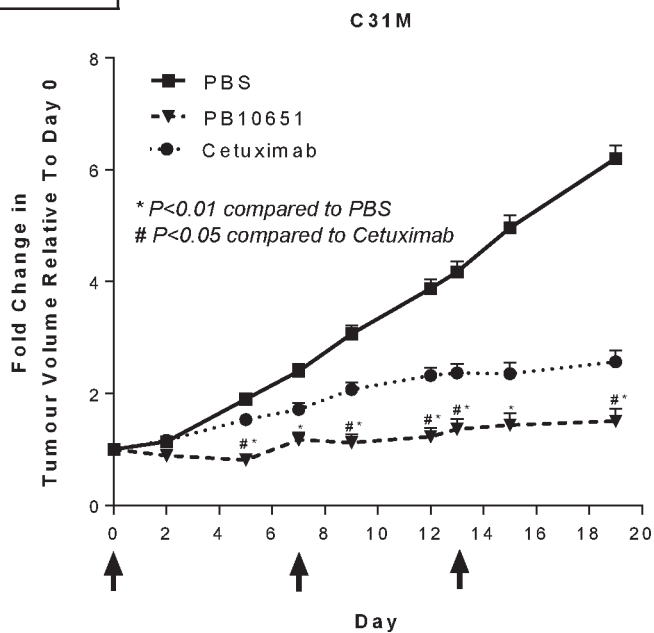


Figure 38B

Average Tumor Volume on Day 0

	Day 0
PBS	29.1
PB10651	29.6
CET	31.2



N of Xenografts

[illegible]

Figure 39

SEQ ID NO:1

MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPHCHCEPDGRMLLRVDCSDLGLSELPSNLSVFTSYLDL
 SMNNISQLLPNPLPSLRFLEELRLAGNALTYPKGAFGLYSLKVLMLQNNQLRHVPTEALQNLRLSLQSLRLD
 ANHISYVPPSCFSGLHSLRHLWDDNALTEIPVQAFRSLALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHN
 NRIHSLGKKCFDGLHSLETLDLNYNNLDEFPTAIRTLNLKELGFHSNNIRSIPEKAFVGNPSLITHFYDNPIQ
 FVGRSAFQHLPELRTLTLNGASQITEFPDLTG TANLES LTLTGAQISSLPQTVCNQLPNLQVLDLSYNLLEDLP
 SFSVCQKLQKIDLRHNEIYEIKVDTFQQLSLRSLNLAWN KIAIHPNAFSTLPSLIKLDLSSNLLSSFPITGLHG
 LTHLKL TGNHALQSLISSENFPELKVIEMPYAYQCCAFGVCENAYKISNQWNKGDNSSMDDLHKKDAGMFQ
 AQDERDLEDLDFEEDL KALHSVQCSPSPGPFKCEHLLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYI
 SPIKLLIGVIAAVNMLTGVS SA VLAGVDAFTFGSFARHGAWWENG VGVIGFLSIFASESSVFLTLAALERG
 FSVKYS AKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEPTMGYMVALILLNSLCFL
 MMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNCPVAFLSFSSLINLTFISPEVIK FILLVVVPLPA
 CLNPLLYILFNPHFKEDLVSLRKQTYVWTRSKHPSLMSINSDDVEKQSCDSTQALVTFTSSSITYDLPPSSVPSP
 AYPVTESCHLSSVAFVPCL

Annotated sequence No1:

Mdtsrlgvllslpvllqlat **Signal peptide**

GgssprsgvllrgcpthchcepdgrmllrvdcSDLGLSELPSNLSVFTSY **N-region**

Idlsmnnisqllpnplpslrflee	LRR1
Lrlagnaltypkgafglyslqv	LRR2
Lmlqnnqlrhvptealqnlrslqs	LRR3
Lrldanhisvppscfsglhlrh	LRR4
Lwddnalteipvqafsrslsalqa	LRR5
mtlalnkiihipdyafgnlsslvv	LRR6
Lhlhnnrihslgkkcfddlhlsl	LRR7
Dlnynnldefptairtlsl	LRR8
Lkelgfhsnnirsipekafvgnpslit	LRR9
Ihfydnpiqfvgrsafqhlpelrt	LRR10
Ltlngasqitefpdltgtanles	LRR11
Ltlgtaqisslpqtvclpnlqv	LRR12
Idlsynlledlpsfsvcqlqk	LRR13
Idlrhneiyeikvdtfqqlslr	LRR14
Slnlawnkiaiihpnaftlpslik	LRR15
Ldlssnllssfpitglhglthlk	LRR16
Ltgnhalqslissenfpelkvem	LRR17

pyayqccafgvcenaykisanqwnkgnssmddlhkkdagmfqaqderd

Ledflldfeedlkalhsvqcspspgpfkpcelhldgwlir

CRL region

igvwtiavlaltcnaIvtstvf

predicted TM1

rsplyispi

klllgviaavnmltgvsavlagvda

predicted TM2

ftfgsfarhgawwengvgchv

igflsifasessvflItlaaler

predicted TM3

gfsvkysakfetkapfss

lkviillcallaltmaavpllggsk

predicted TM4

ygasplclplpfgepstm

gymvalillnslcflmmtiaytkly

predicted TM5

cnldkgdleniwdcsmvk

hialllftncilncpvaflsfssl

predicted TM6

inltfispevi

kfillvvvplpacInpllyilfnp

predicted TM7

hfkedlvslrkqtyvwtrskhpslmsinsddvekqscdstqalvtft

sssitydlppssvpaspaypvteschlssvafvpcl

C-terminal tail

Figure 40

SEQ ID NO: 2

MRPSGTAGAALLALLAALCPASRALEEKKVCQGTSNKLTQLGTFEDHFLS
LQRMFNNEEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIP
LENLQIIRGNMYYENSALAVLSNYDANKTGLKELPMRNLQEILHGAVRF
SNNPALCNVESIQWRDIVSSDFLSNMSMDFQNLHLSGSCQKCDPSCPNGSCW
GAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGPRESCLV
CRKFRDEATCKDTCPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYV
VTDHGSCVRACGADSYEMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDSLS
INATNIKHFKNCTSIGDLHILPVAFRGDSFTHTPPLDPQELDILKTVKE
ITGFLLIQAWPENRTDLHAFENLEIIRGRKQHGQFSLAVVSLNITSLGL
RSLKEISDGDVLIISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSCK
ATGQVCHALCSPEGCWGPEPRDCVSCRNVSRGRECVDKCNLLEGEPREFV
ENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVM
GENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLEGCPNGPKIPSIATGM
VGALLLLLVALGIGLFMRRRHIVRKRTLRLRLQERELVEPLTPSGEAPN
QALLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREA
TSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPFGCLLD
YVREHKDNIGSQYLLNWCVQIAKGMNYLEDRLVHRDLAARNVLVKTPQH
VKITDFGLAKLLGAEKEYHAEGGKVPKWMMALESILHRIYTHQSDVWSY
GVTWELMTFGSKPYDGIPASEISSILEKGERLPQPPICTIDVYMIMVKC
WMIDADSRPKFRELIIEFSKMARDPQRYLVIQDERMHLPSPDTSNFYRA
LMDEEDMDVDVDADEYLIPOQGFSSPSTSRTPLLSSLSATSNNSTVACI
DRNGLQSCPIKEDSFLQRYSSDPTGALTEDSIDDTFLPVPEYINQSVPKR
PAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLNTVQPTCVNST
FDSPAHWAKGSHQISLDNPDYQQDFFPKEAKPNGIFKGSTAENAEYLRV
APQSSEFIGA

Annotated seq. No: 2

MRPSGTAGAALLALLAALCPASRA **signal peptide**

LEEKKVCQGTSNKLTQLGTFEDHFLS
LQRMFNNEEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIP
LENLQIIRGNMYYENSALAVLSNYDANKTGLKELPMRNLQEILHGAVRF
SNNPALCNVESIQWRDIVSSDFLSNMSMDFQNLHLSGSCQKCDPSCPNGSCW
GAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGPRESCLV
CRKFRDEATCKDTCPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYV
VTDHGSCVRACGADSYEMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDSLS
INATNIKHFKNCTSIGDLHILPVAFRGDSFTHTPPLDPQELDILKTVKE
ITGFLLIQAWPENRTDLHAFENLEIIRGRKQHGQFSLAVVSLNITSLGL
RSLKEISDGDVLIISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSCK
ATGQVCHALCSPEGCWGPEPRDCVSCRNVSRGRECVDKCNLLEGEPREFV
ENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVM
GENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLEGCPNGPKIPSIAT

Extra-cellular domainGMVGALLLLLVALGI **predicted transmembrane domain**

GLFMRRRHIVRKRTLRLRLQERELVEPLTPSGEAPN

QALLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREA
TSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPFGCLLD
YVREHKDNIGSQYLLNWCVQIAKGMNYLEDRLVHRDLAARNVLVKTPQH
VKITDFGLAKLLGAEKEYHAEGGKVPIKWMALESILHRIYTHQSDVWSY
GVTVWELMTFGSKPYDGIPASEISSILEKGERLPQPPICTIDVYMIMVKC
WMIDADSRPKFRELIIEFSKMARDPQRYLVIQGDERMHLPSPDTSNFYRA
LMDEEDMDDVVDADAYLIPQQGFFSSPSTSRTPLSSLSATSNNSTVACI
DRNGLQSCPIKEDSFLQRYSSDPTGALTEDSIDDTFLPVPEYINQSVPKR
PAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLNTVQPTCVNST
FDSPAHWQAQKGSHQISLDNPDYQQDFFPKEAKPNGIFKGSTAENAEYLRV
APQSSEFIGA

Intra-cellular tyrosine kinase and C-terminal tail