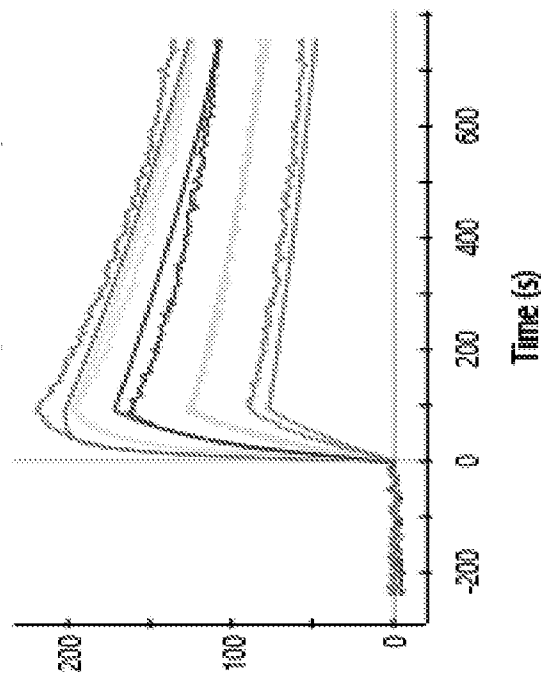


D11 - 4.1nM

L1 - 11_EM3-TyrD Cycle1

ka:1.72E+05 1/Ms kd:7.14E-04 1/s KD:4.14E-09 M



D7 - 3.8nM

L1 - 18_EM3-TyrD Cycle2

ka:7.07E+04 1/Ms kd:2.70E-04 1/s KD:3.82E-09 M

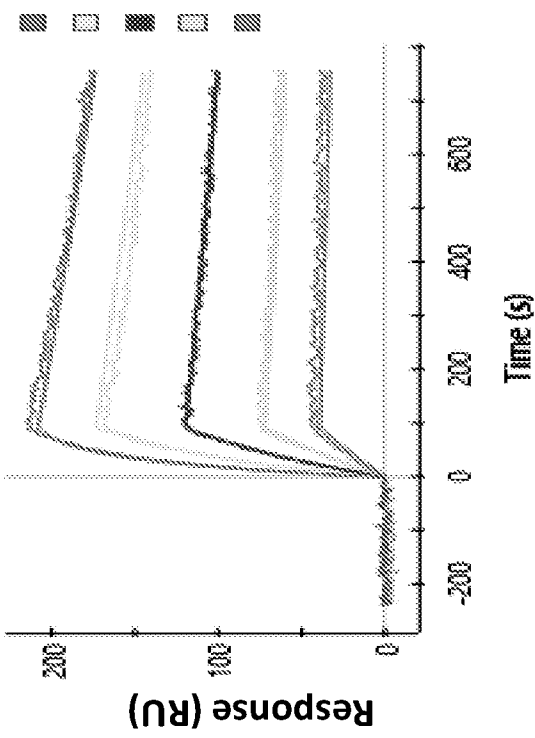
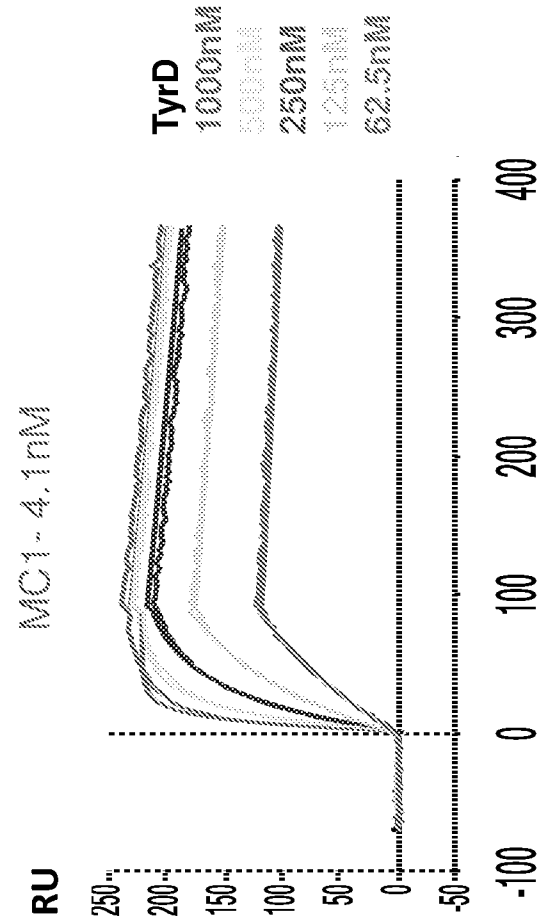
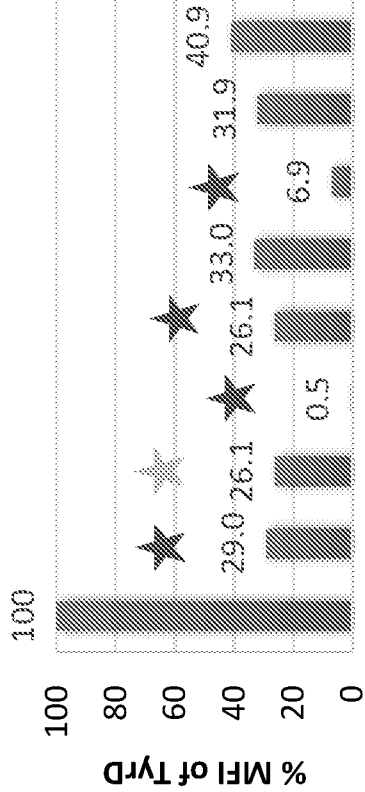


Figure 1

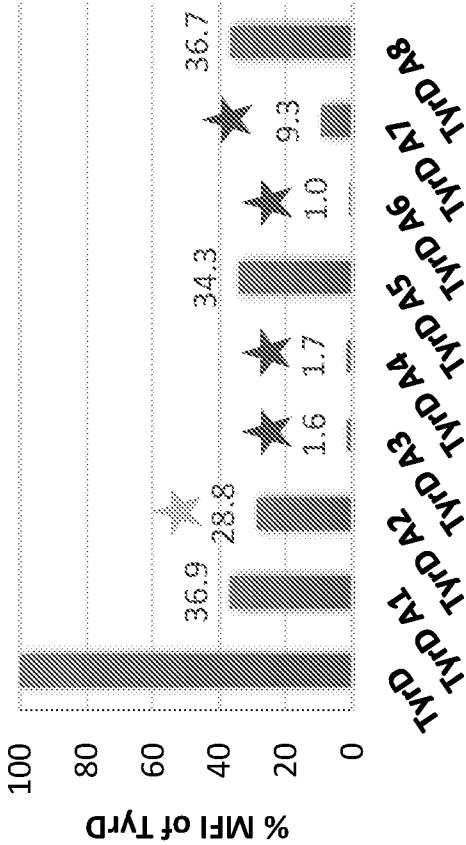
TyrD	YMDGTMSQV
TyrD A1	AMDGTMSQV
TyrD A2 anchor position	YADGTMSQV
TyrD A3	YMAGTMSQV
TyrD A4	YMDATMSQV
TyrD A5	YMDGAMSQV
TyrD A6	YMDGTASQV
TyrD A7	YMDGTMAQV
TyrD A8	YMDGTMSAV

Alanine scanning D11B10 10µg/ml



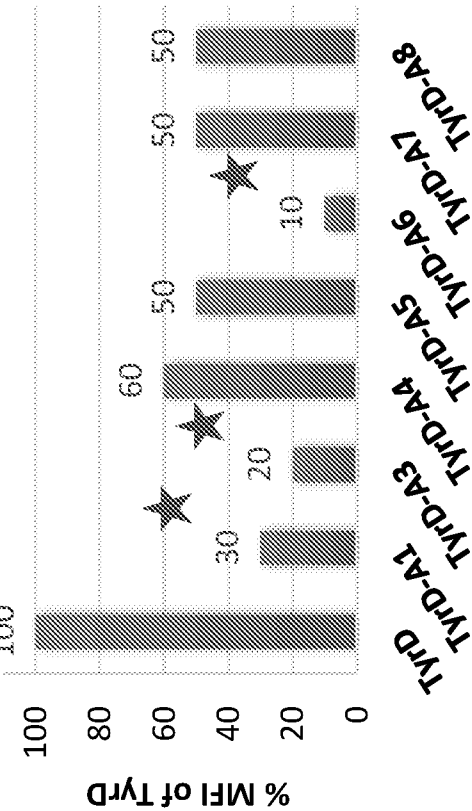
- Decrease of >90% at two positions # 3, 6
- Decrease of > 70% in five positions # 1, 2, 3, 4, 6

Alanine scanning D7C2 10µg/ml



- Decrease of >90% at four positions # 3, 4, 6, 7
- Decrease of > 70% in five positions # 2, 3, 4, 6, 7

Alanine scanning MC1 10µg/ml



- Decrease of 90% at one position # 6
- Decrease of > 70% in three positions # 1, 3, 6

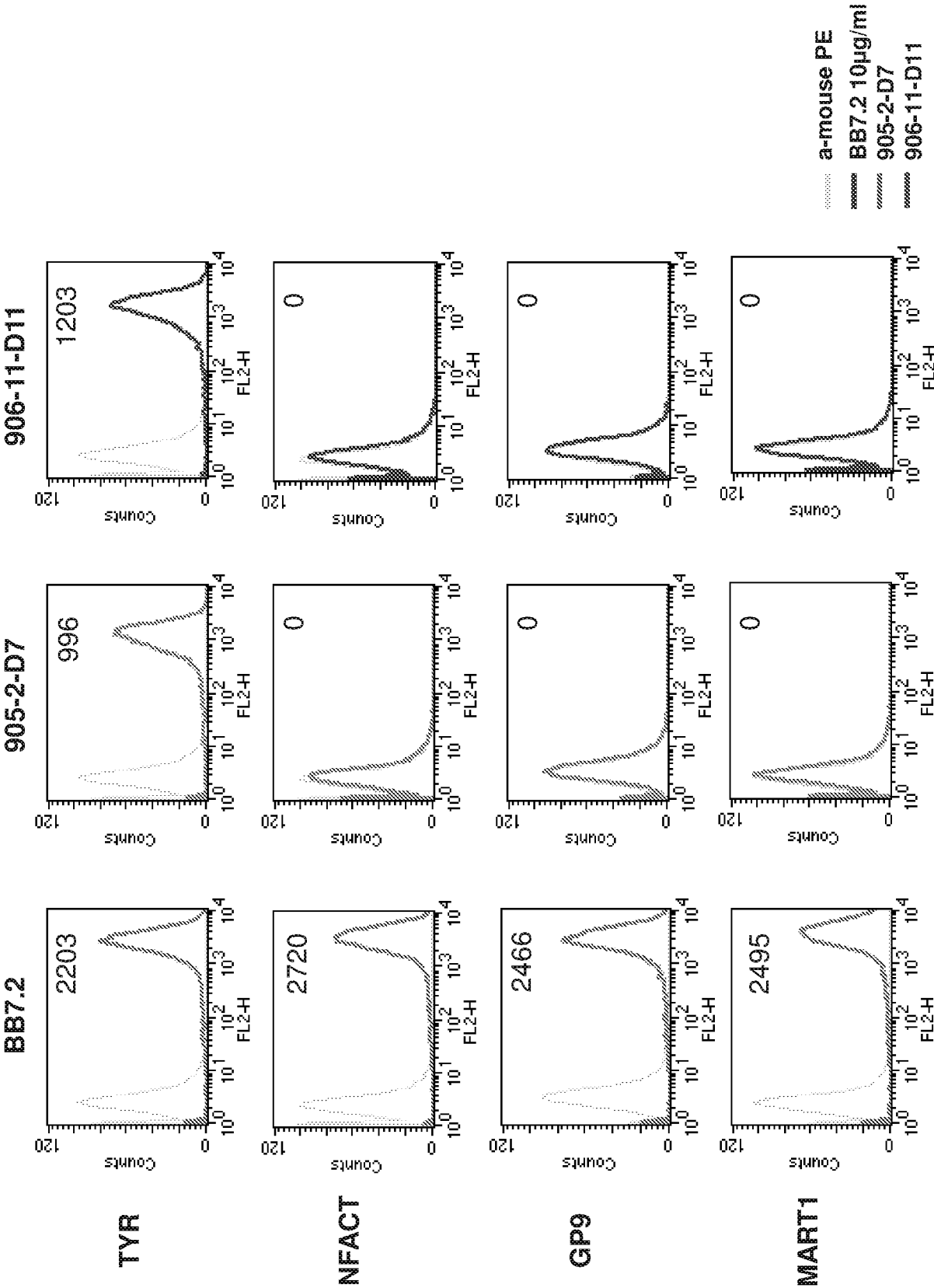


Figure 3

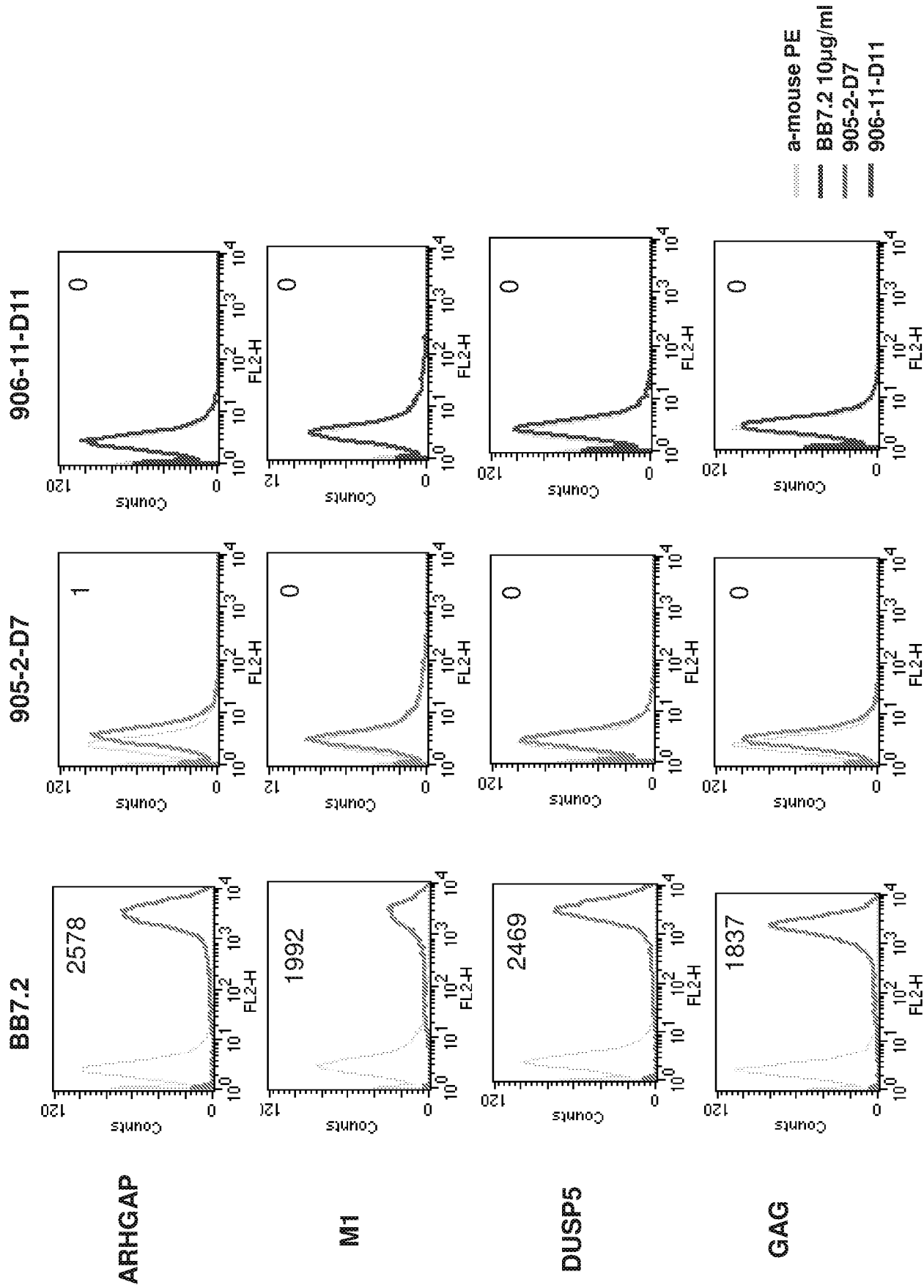


Figure 3 - continued

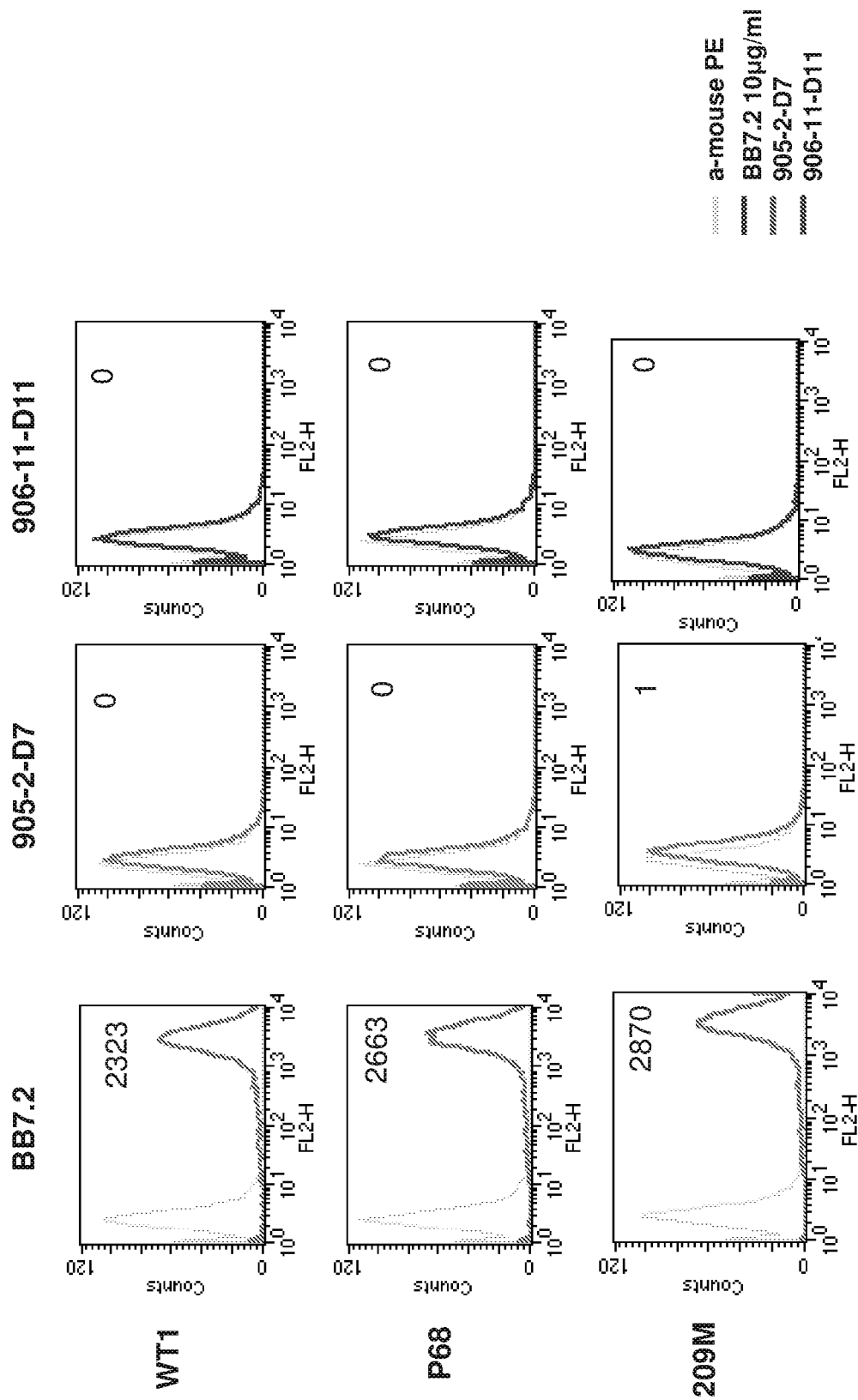


Figure 4

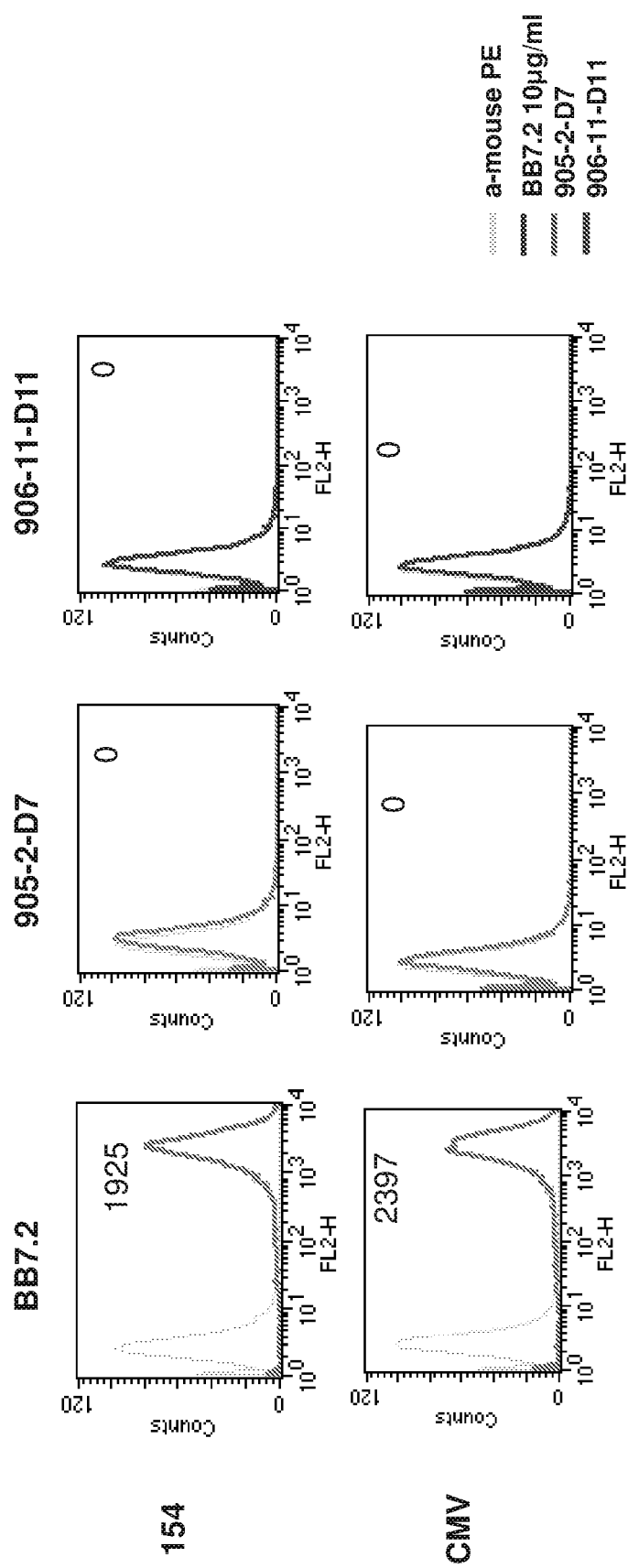
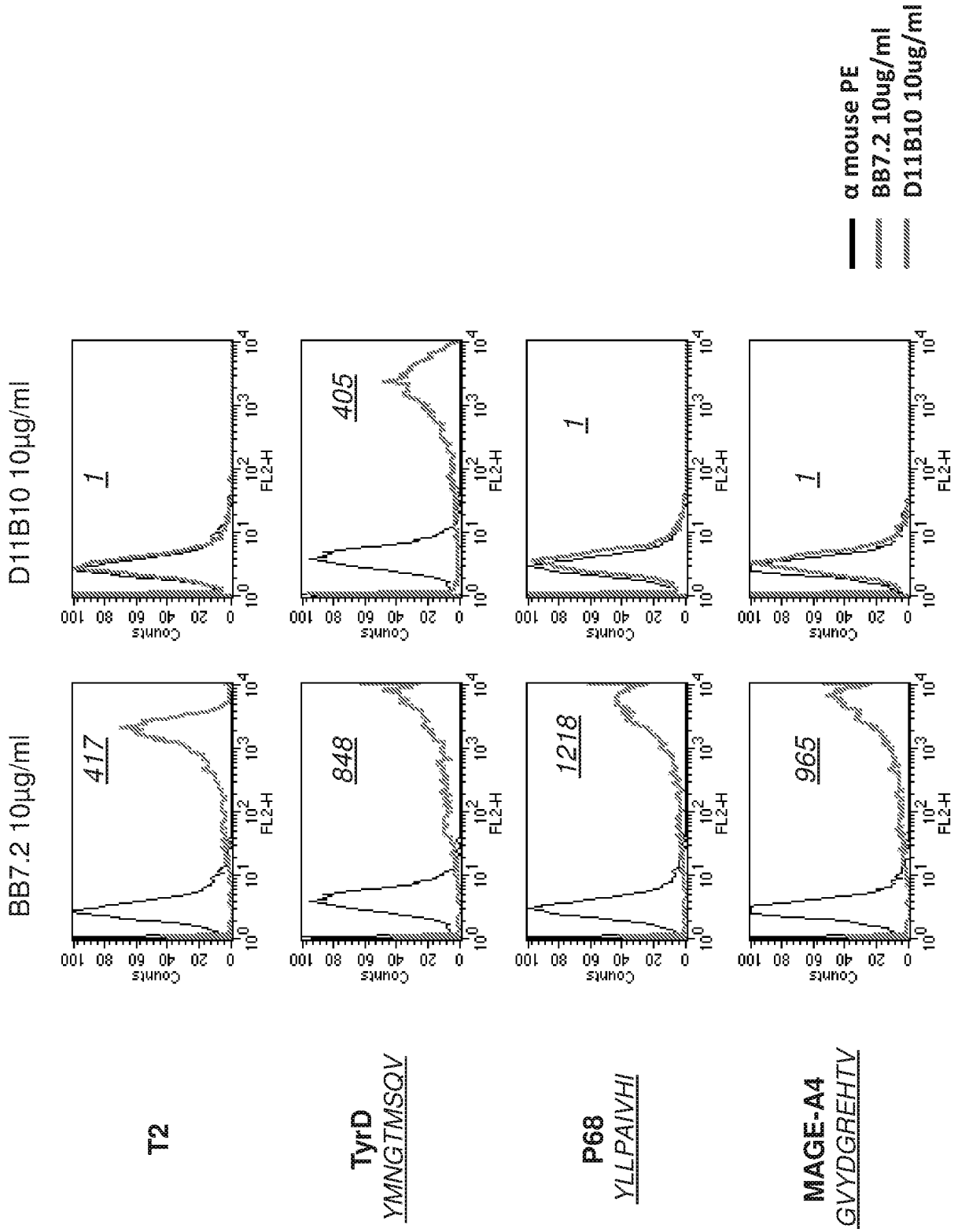
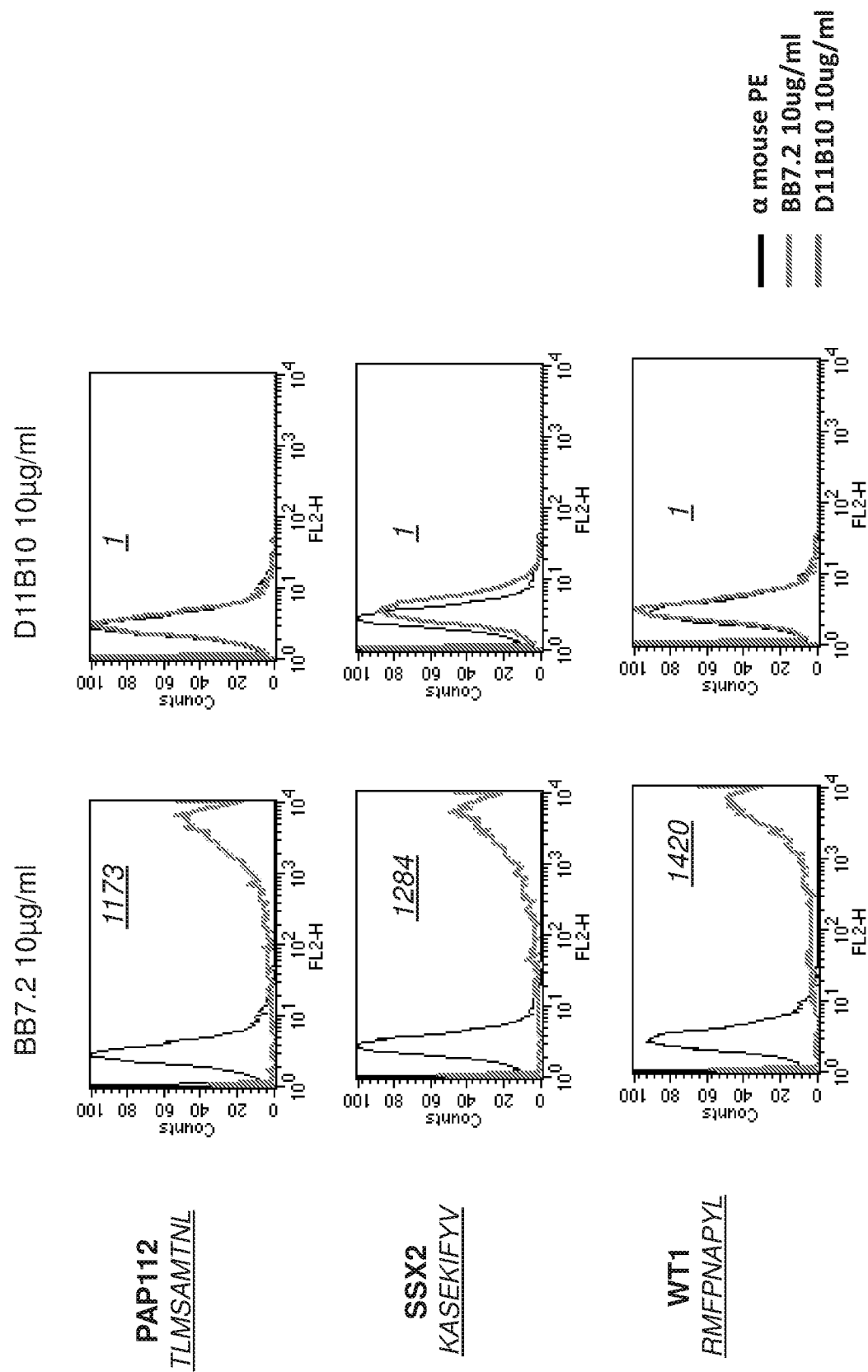


Figure 4 - continued



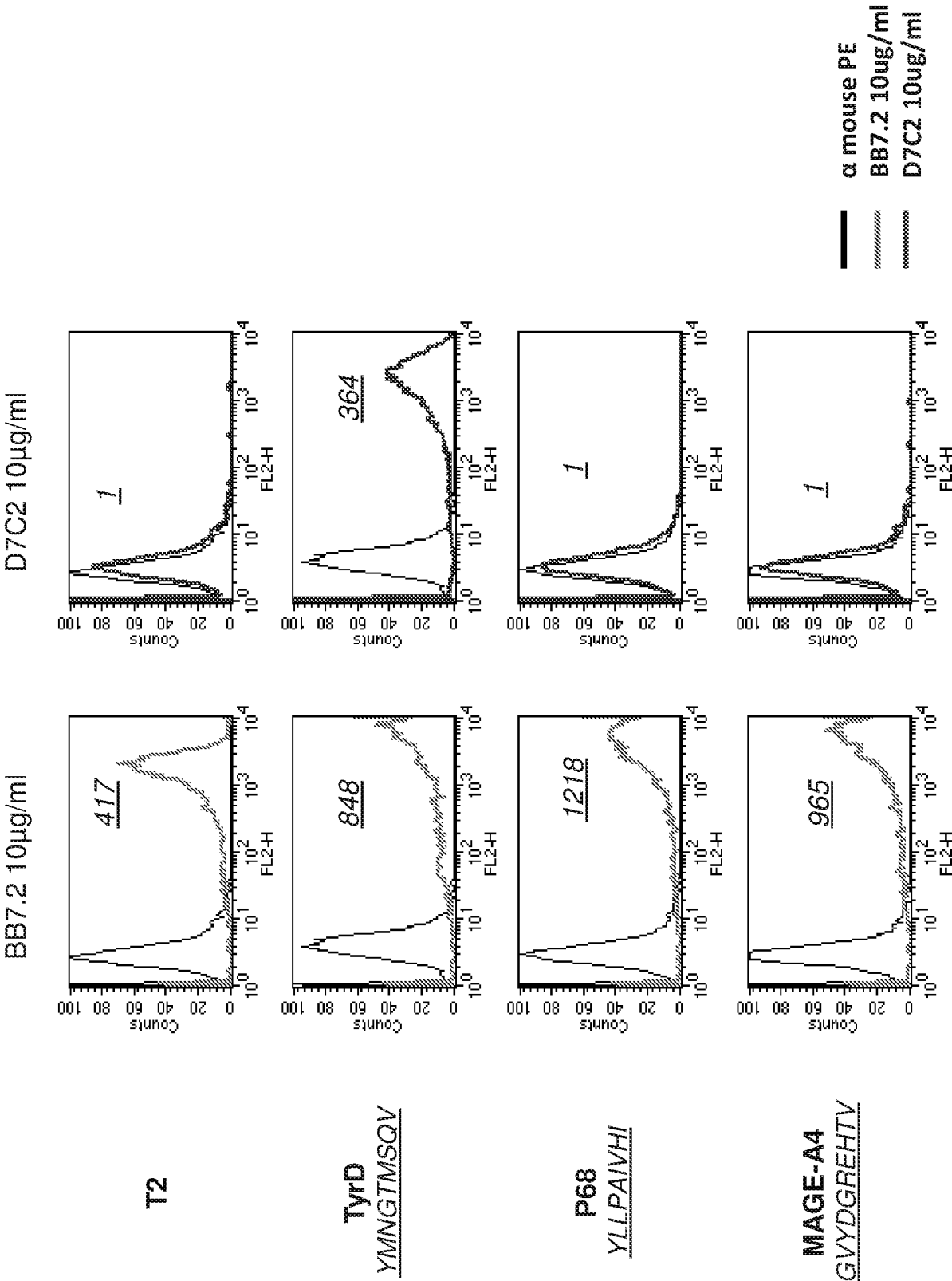
MFI values are relative to background. Value of `1` means no binding

Figure 5



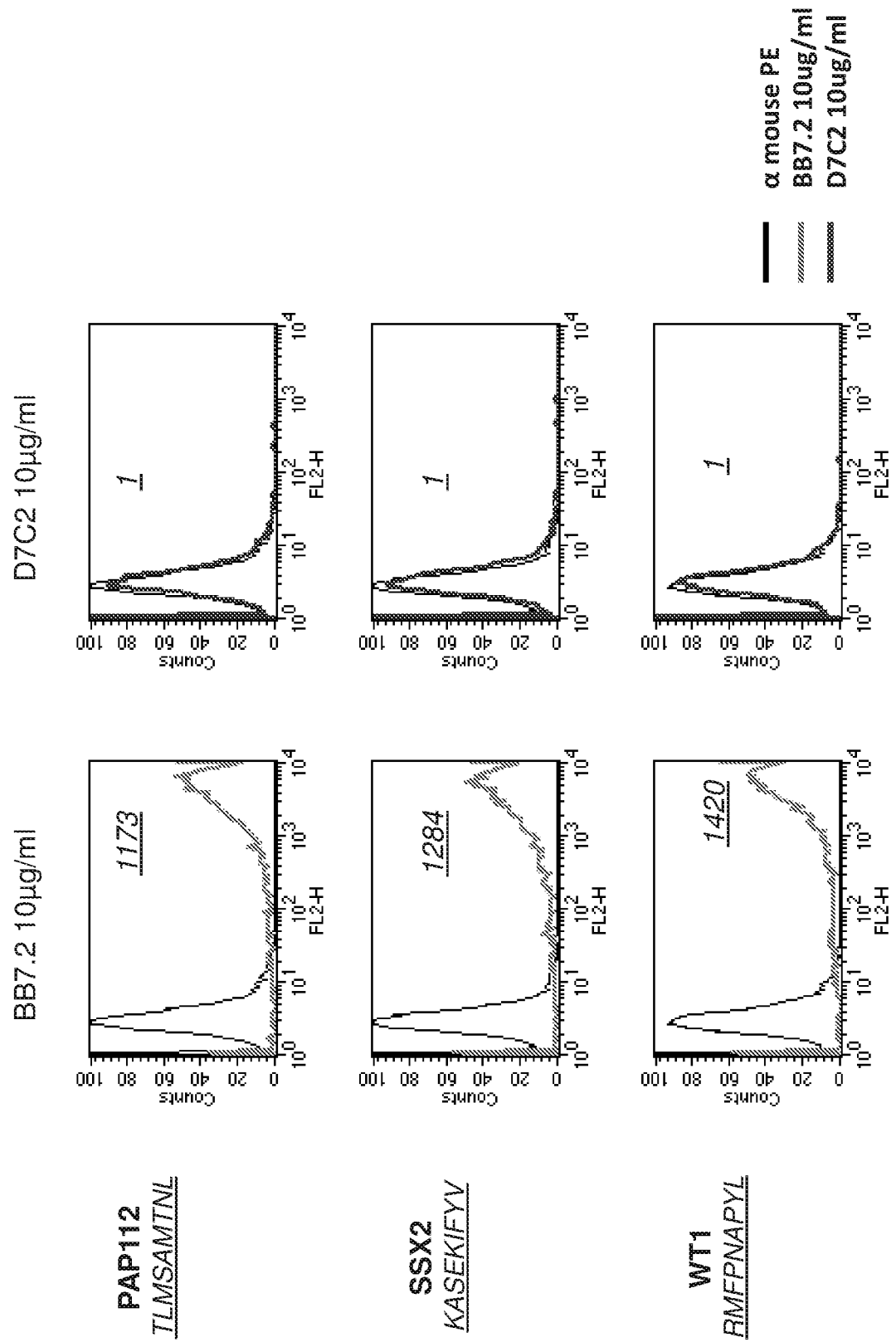
MFI values are relative to background. Value of `1` means no binding

Figure 5 - continued



MFI values are relative to background. Value of `1` means no binding

Figure 6



MFI values are relative to background. Value of 1 means no binding

Figure 6 - continued

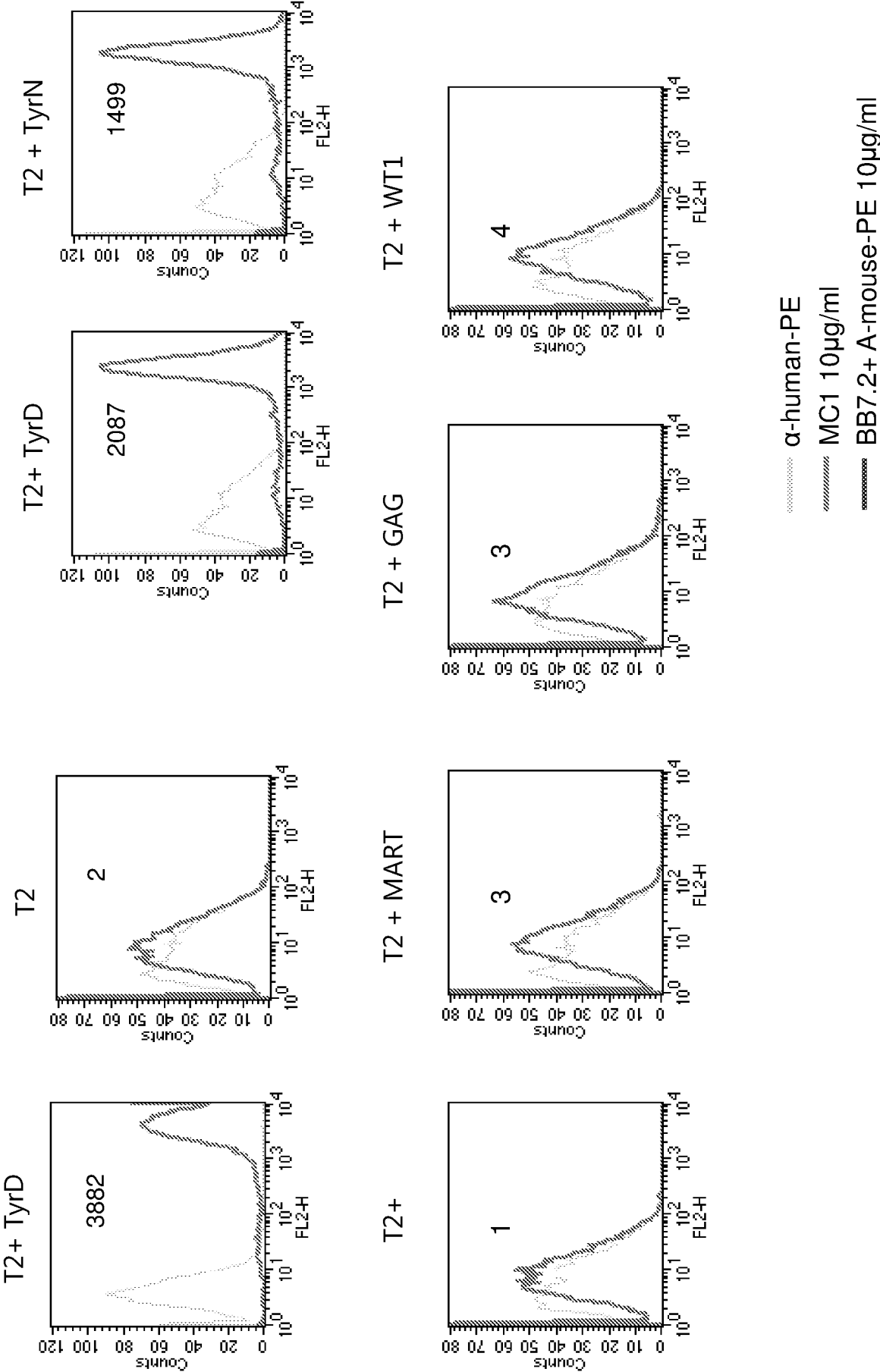
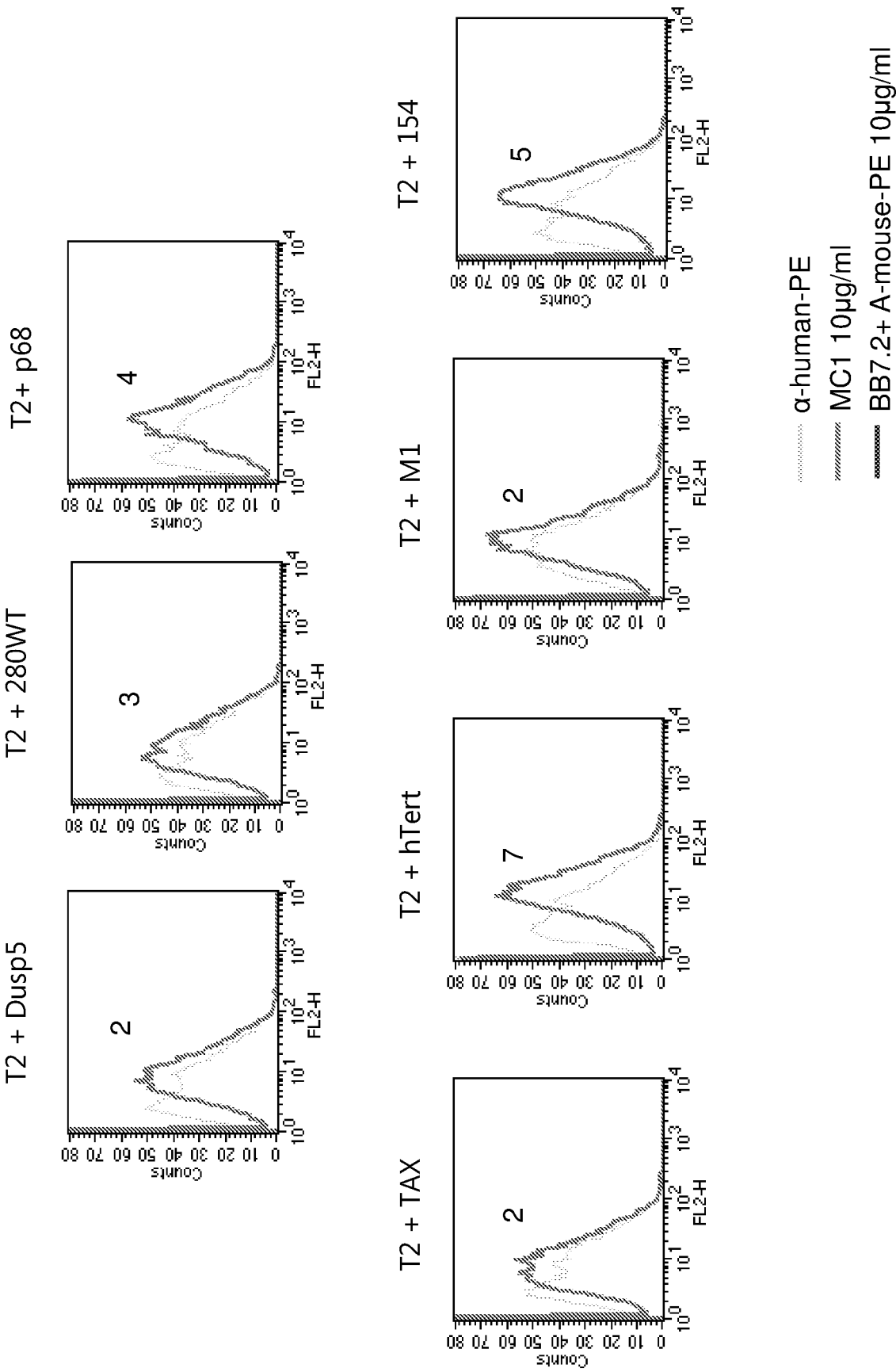


Figure 7



BB7.2 on A2+ Melanoma cells

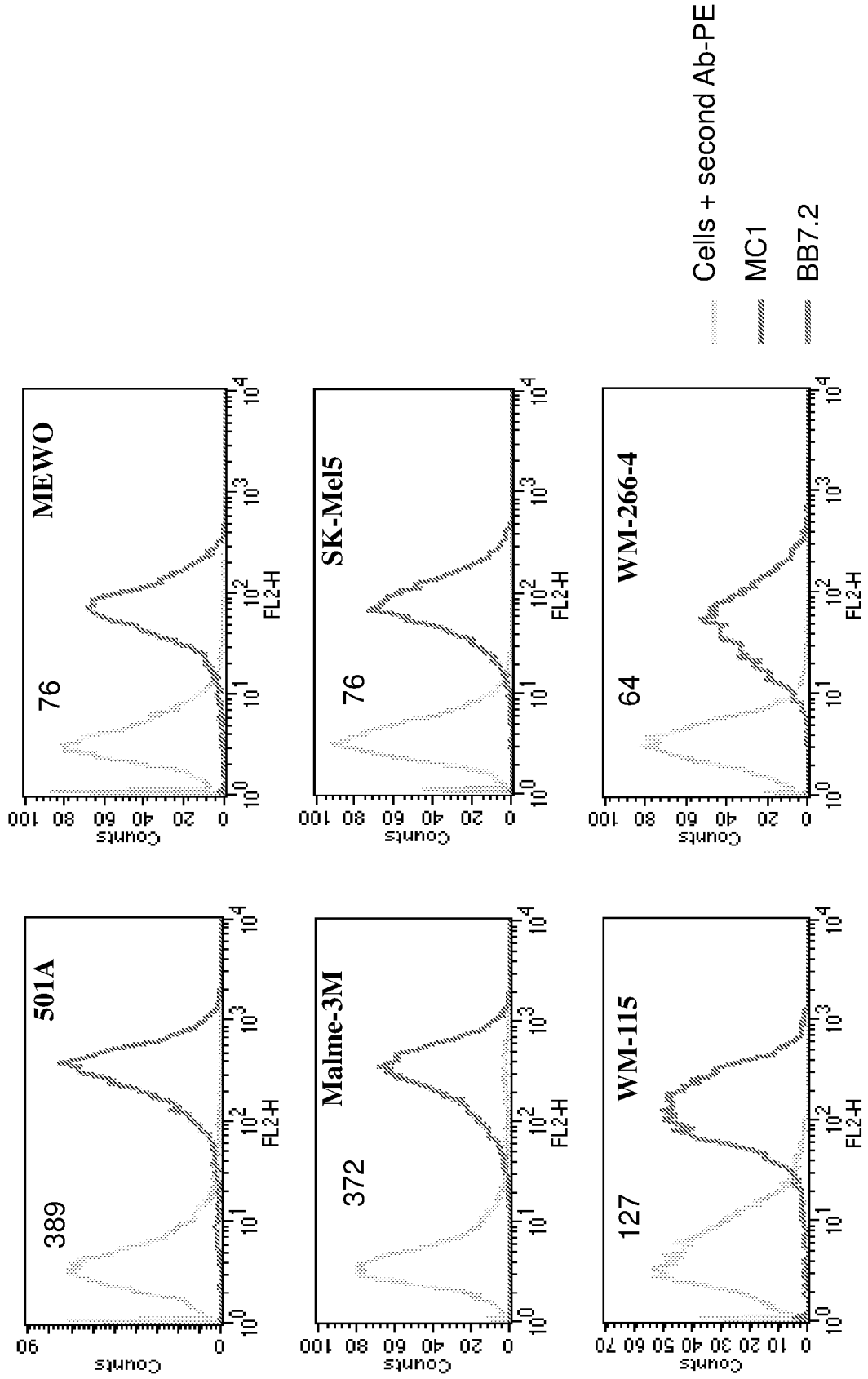


Figure 8

MC1 on A2+ Melanoma cells

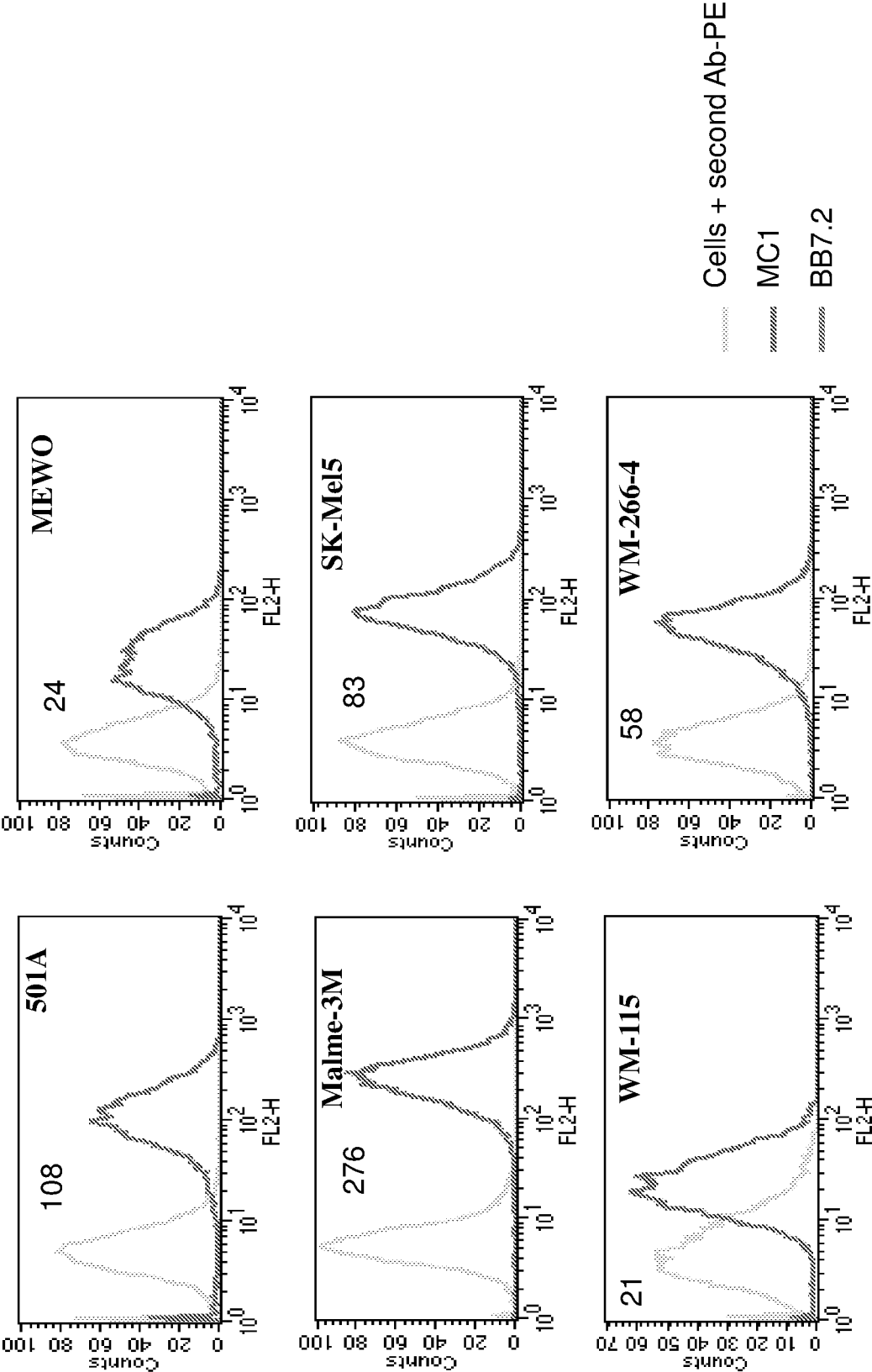
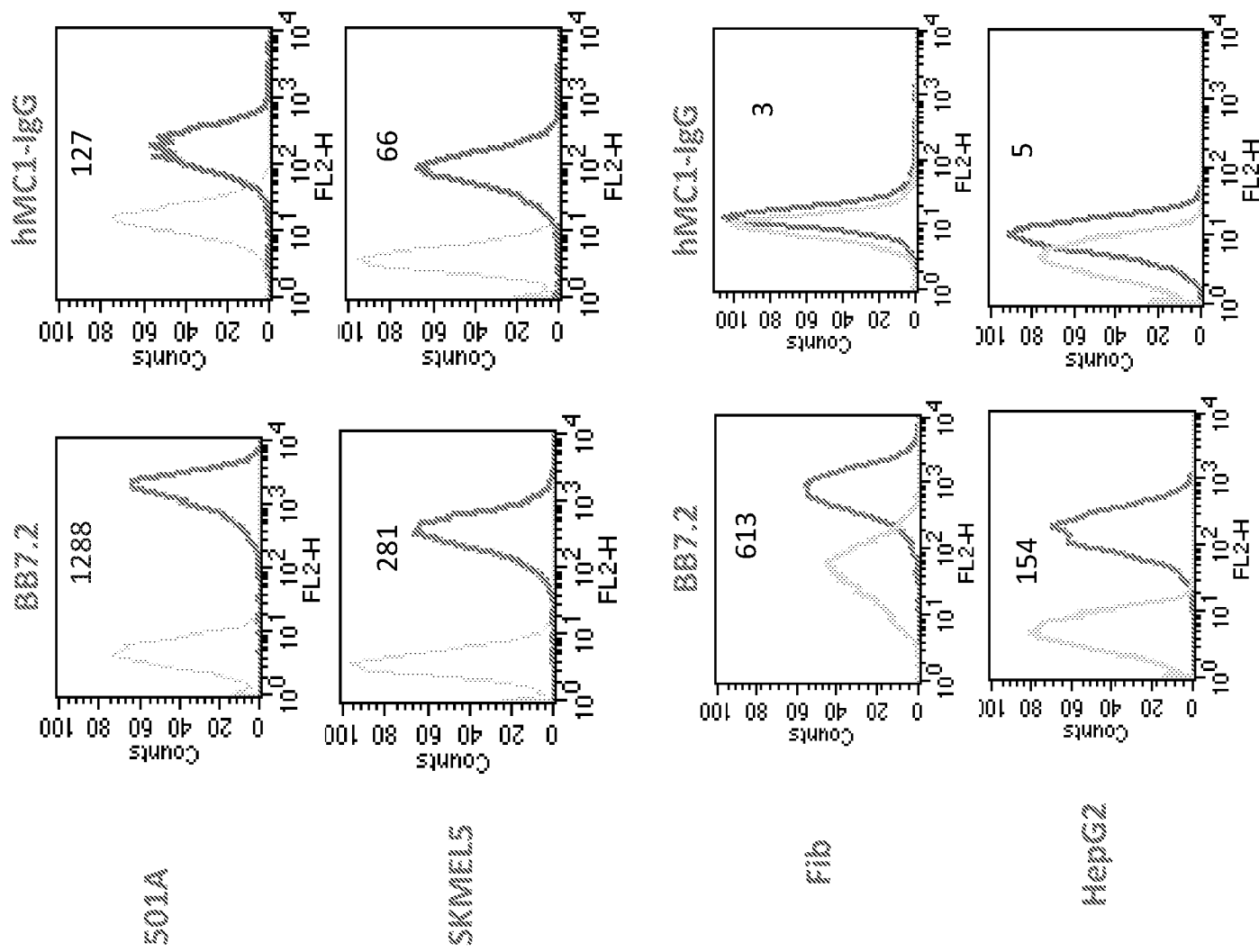


Figure 8 - continued



GeoMean number indicated

Figure 9

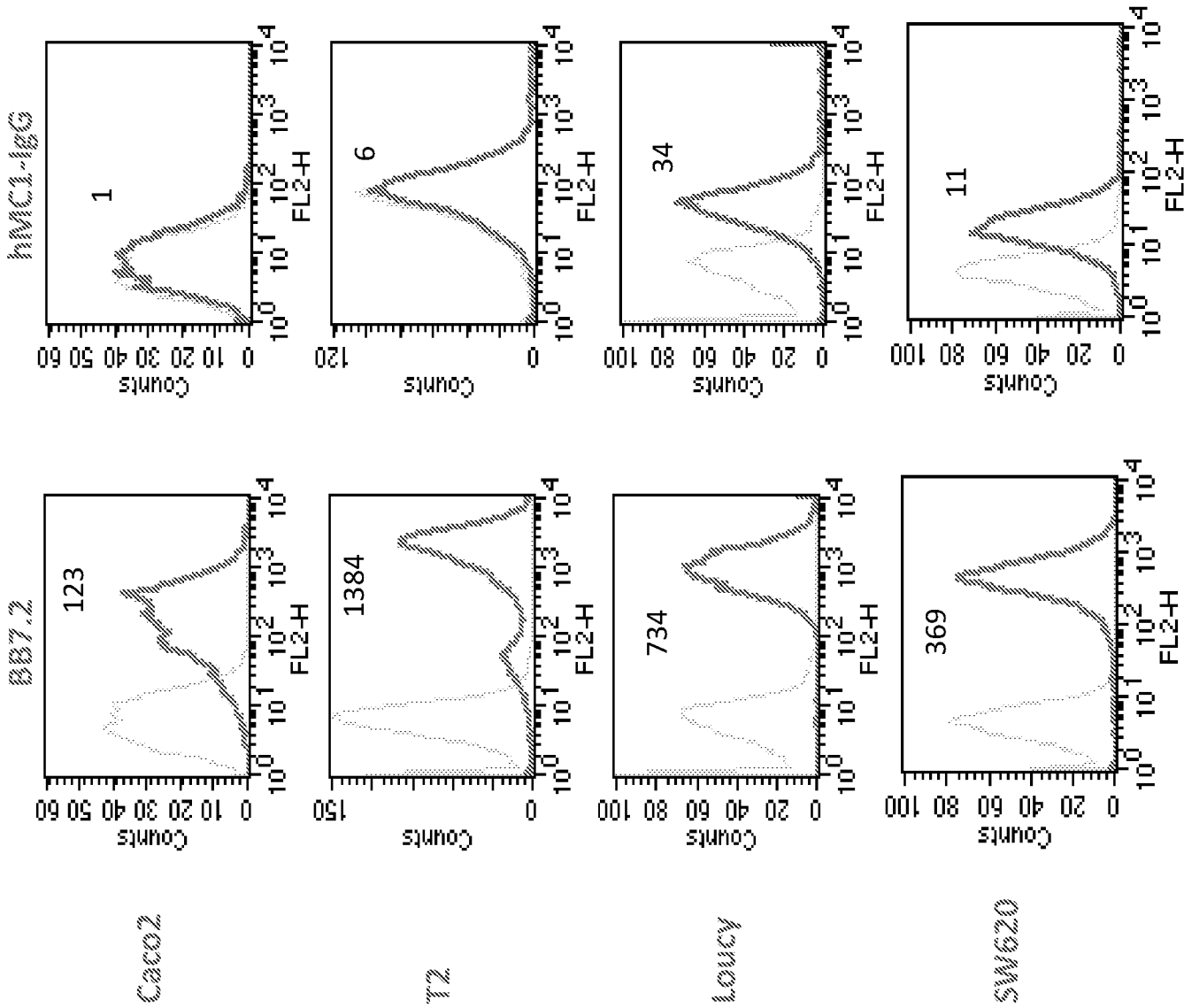
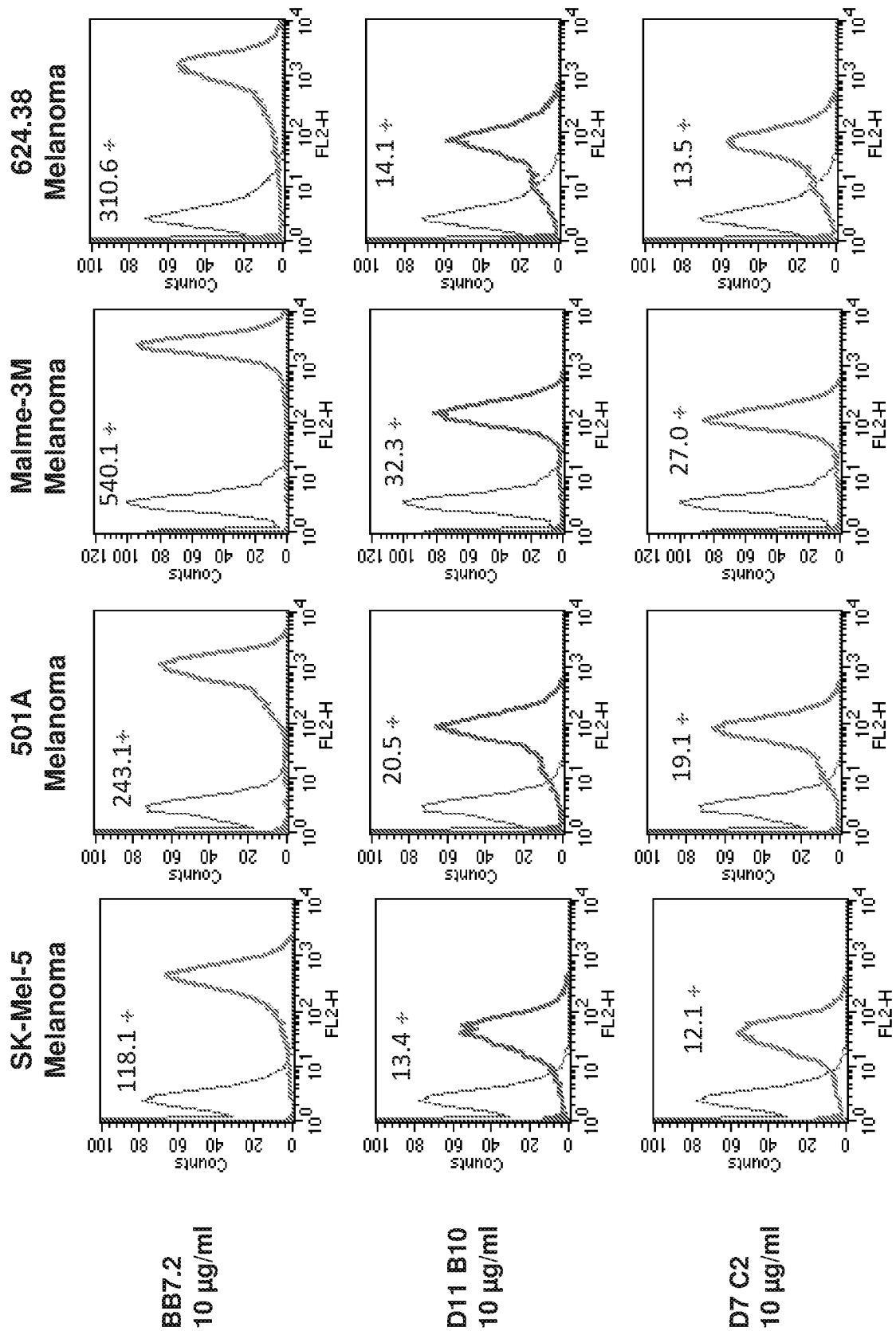


Figure 9 - continued

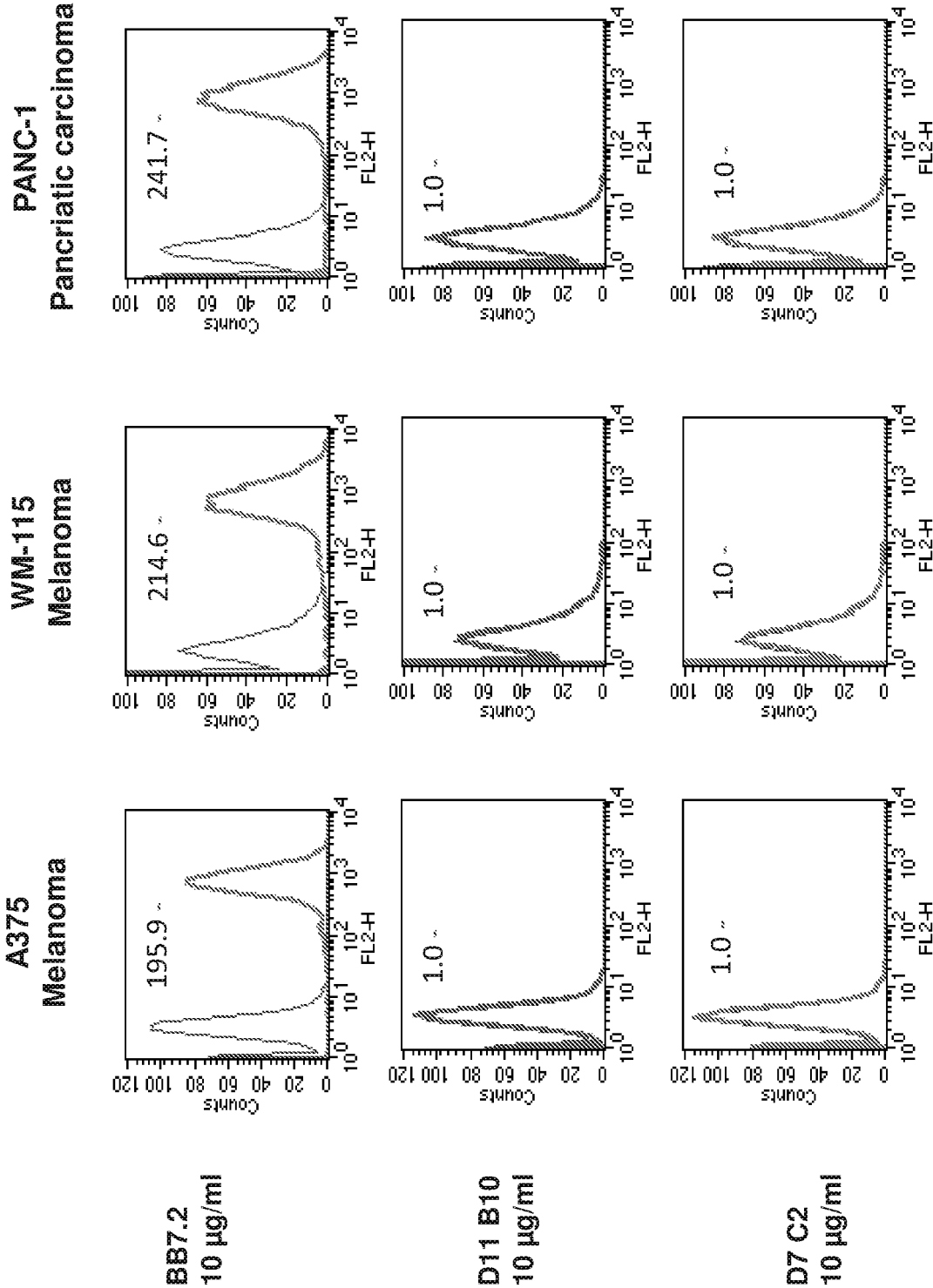
Antigen positive Melanoma cells



-/- in the right upper corner indicates the presence or absence of relevant mRNA in the tested cells

Figure 10

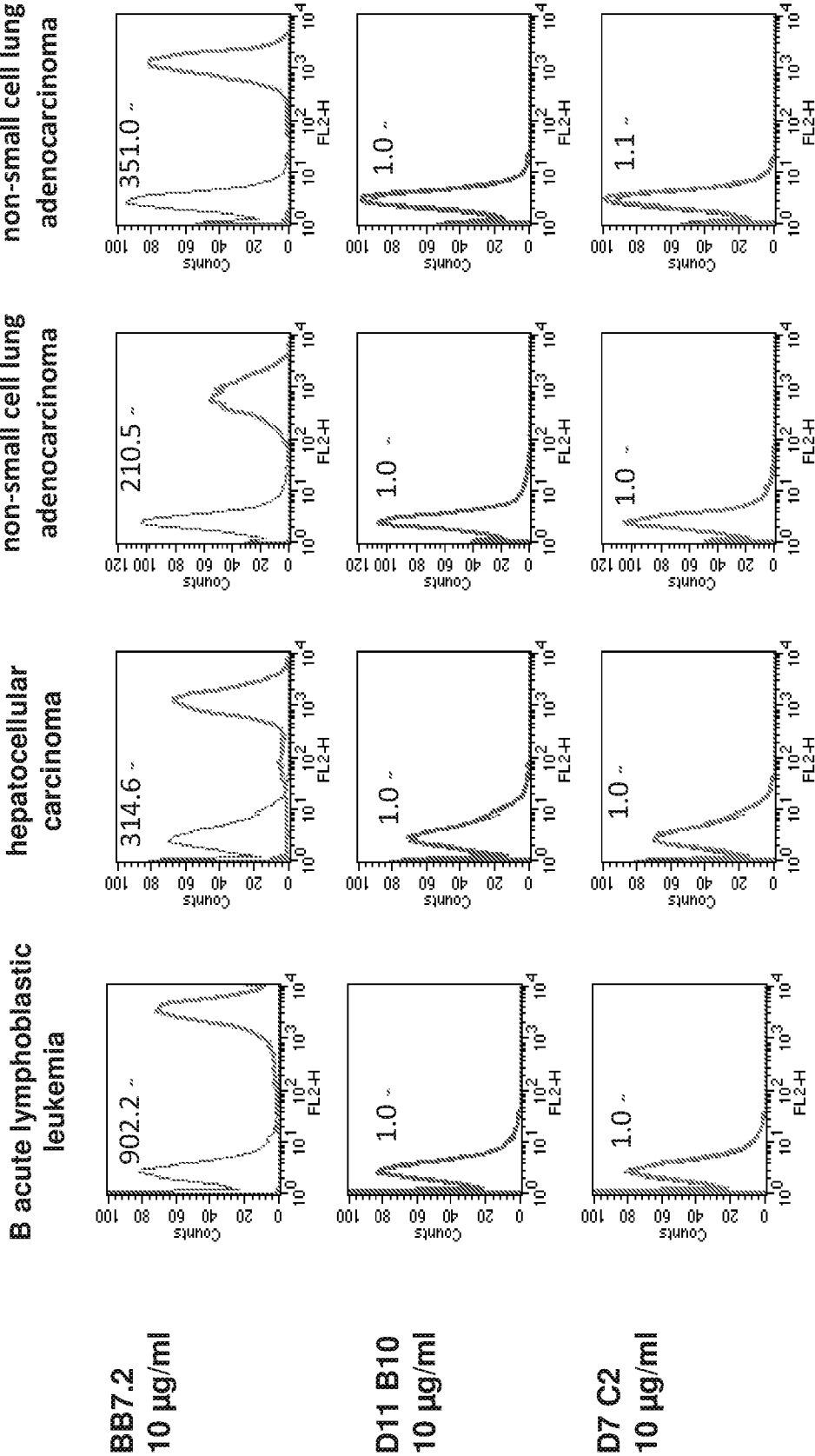
Antigen negative cell lines



1.0 in the right upper corner indicates the presence or absence of relevant mRNA in the tested cells

Figure 10 - continued

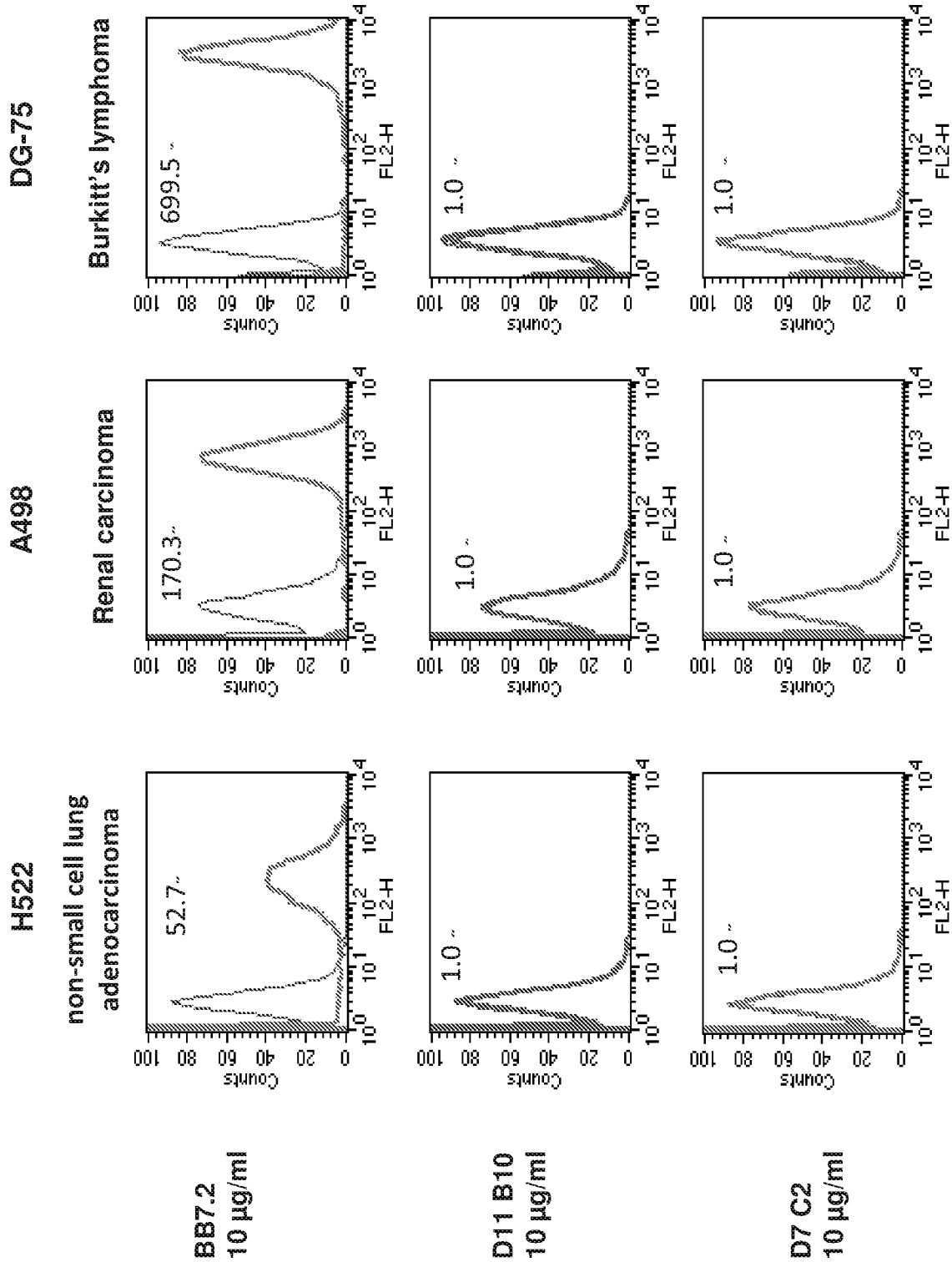
Antigen negative cell lines



in the right upper corner indicates the presence or absence of relevant mRNA in the tested cells

Figure 10 - continued

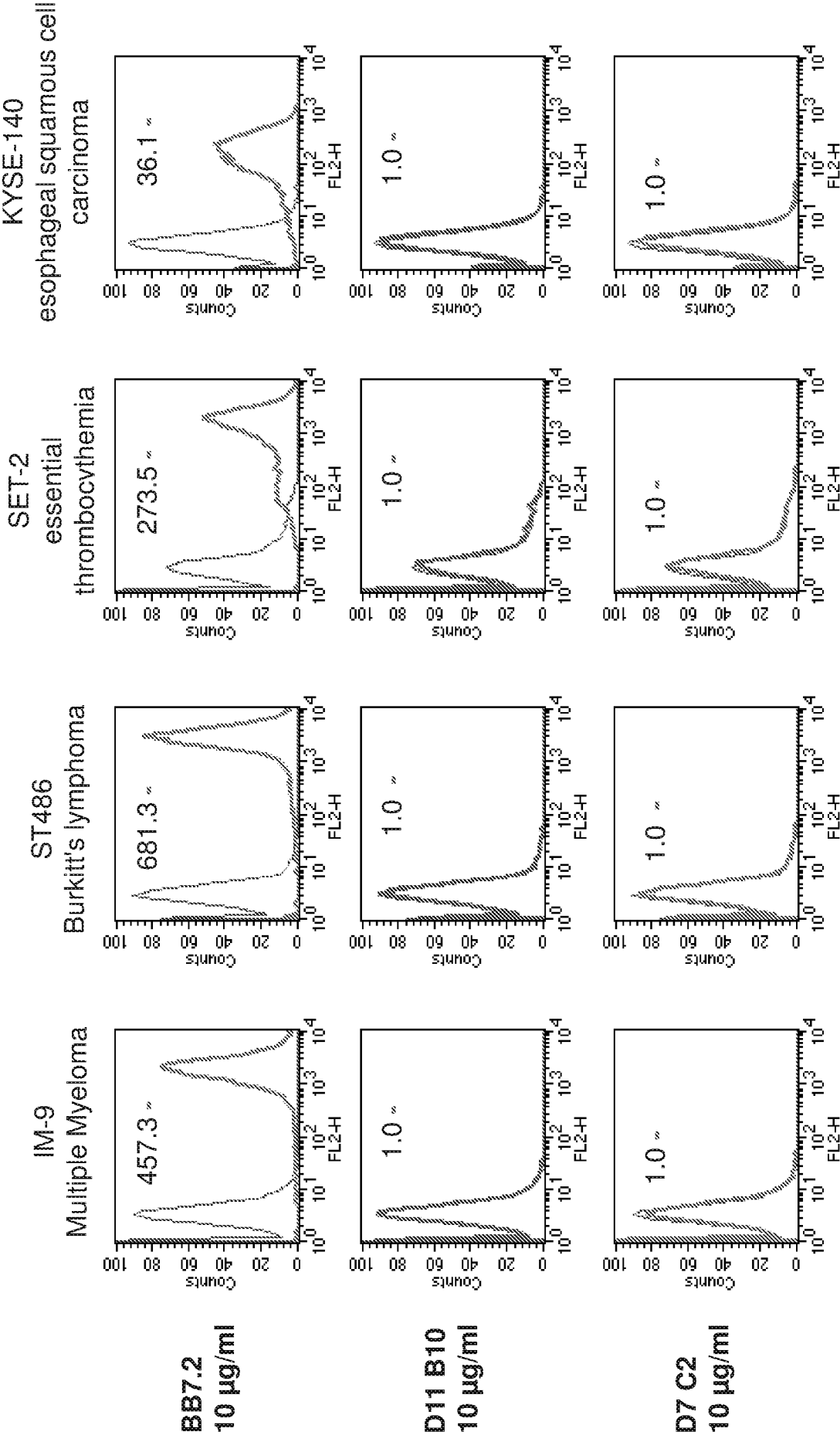
Antigen negative cell lines



+/+ in the right upper corner indicates the presence or absence of relevant mRNA in the tested cells

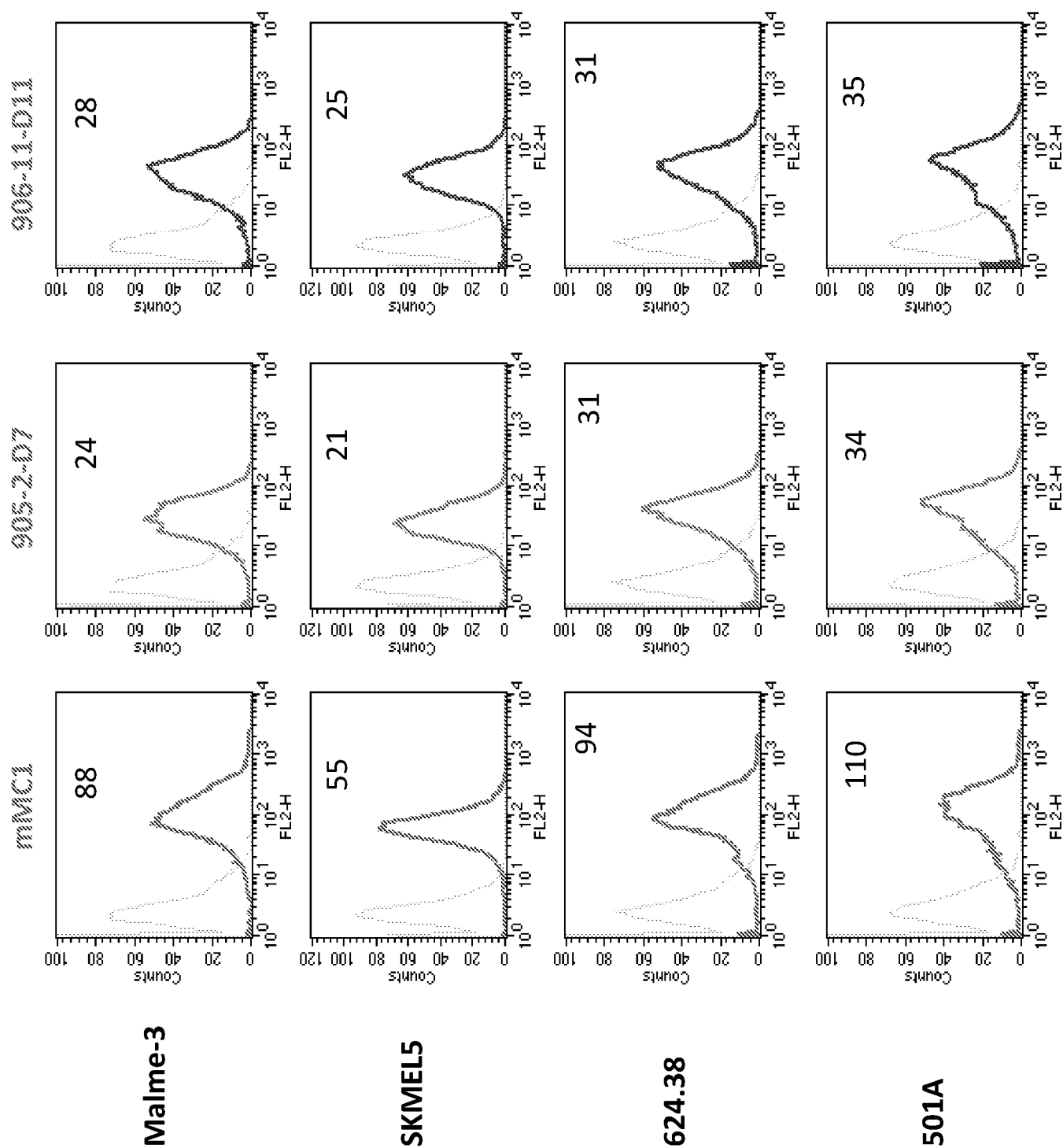
Figure 10 - continued

Antigen negative cell lines



+/+ in the right upper corner indicates the presence or absence of relevant mRNA in the tested cells

Figure 11



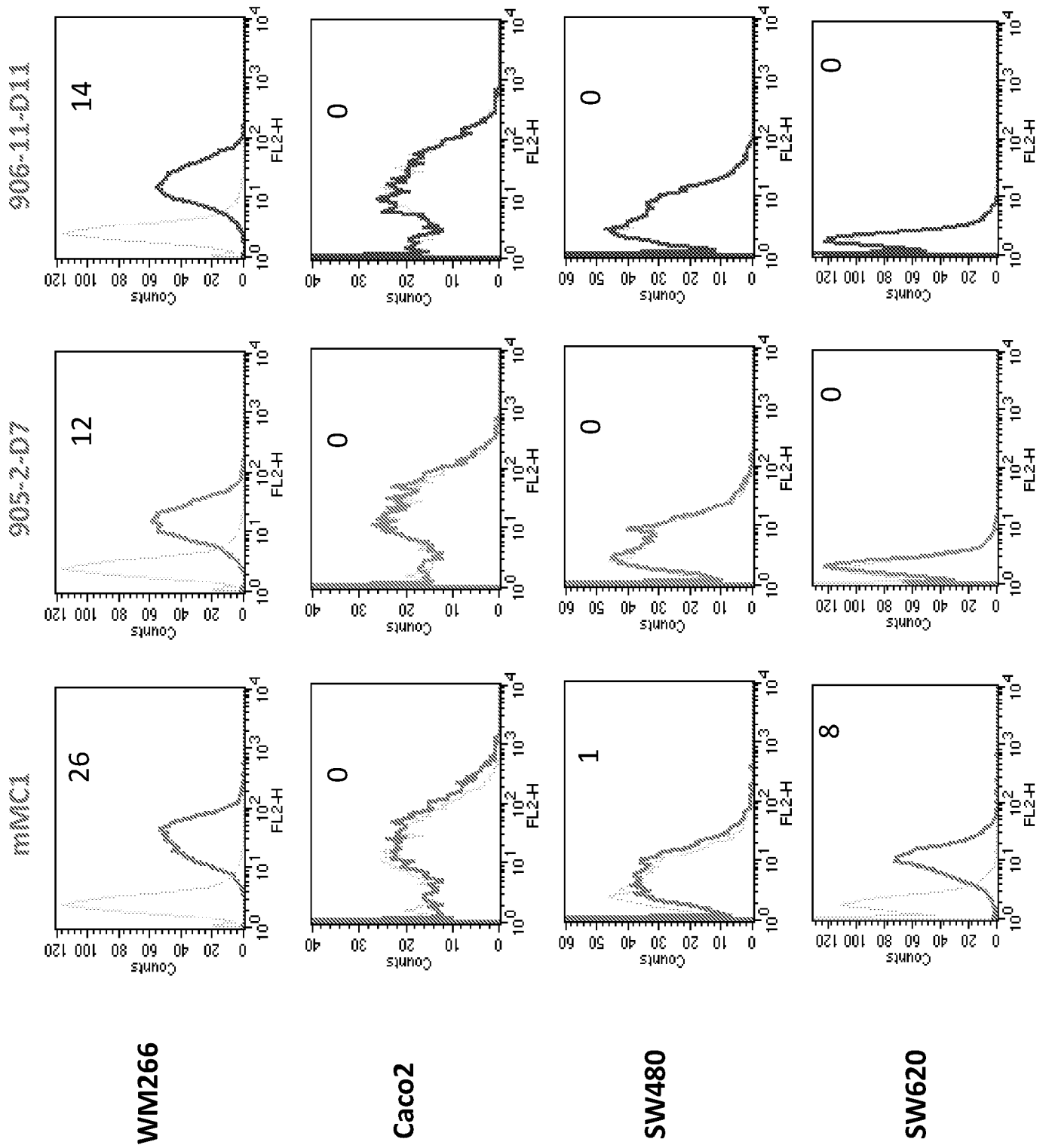


Figure 12 - continued

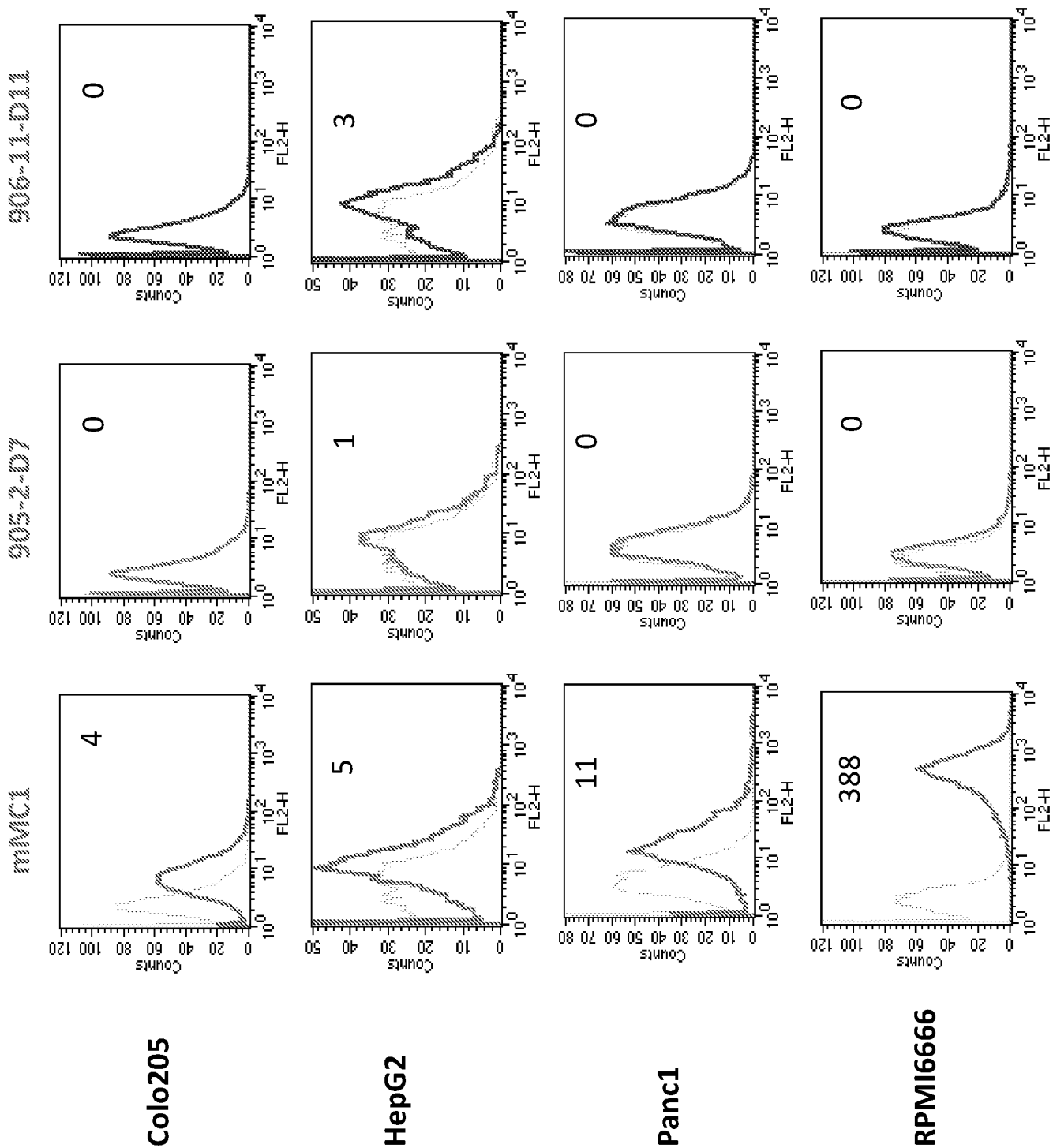


Figure 12 - continued

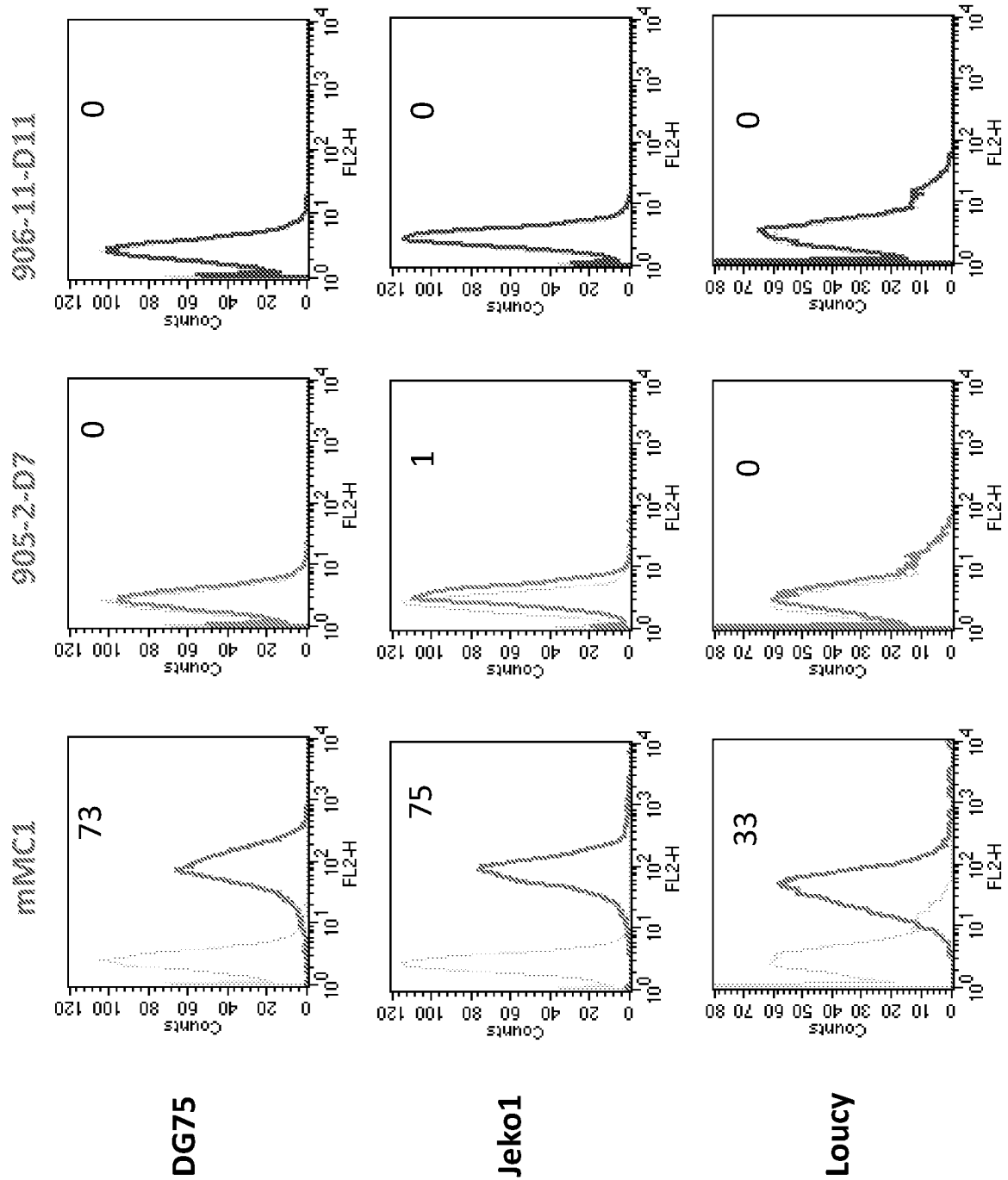


Figure 12 - continued

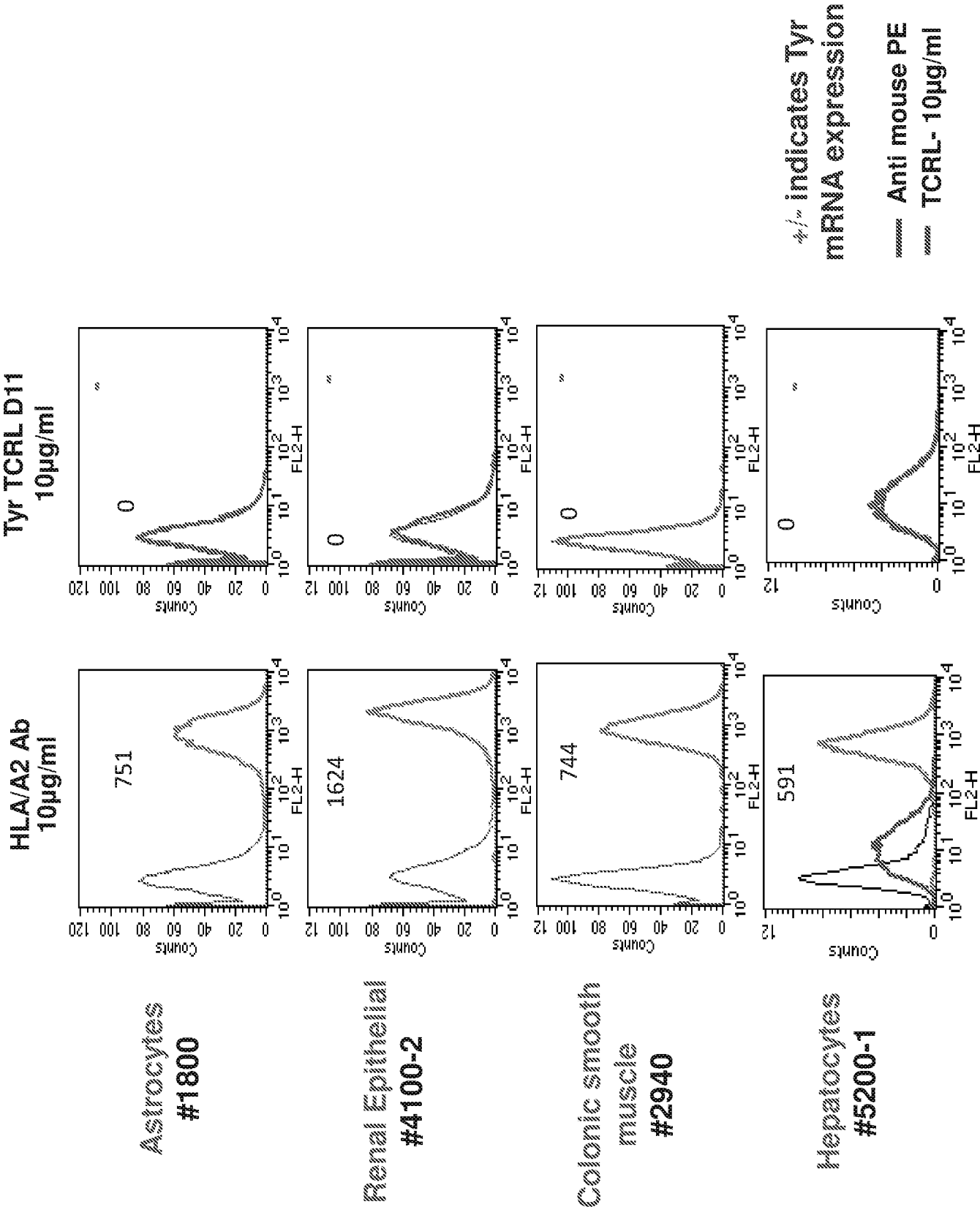


Figure 13

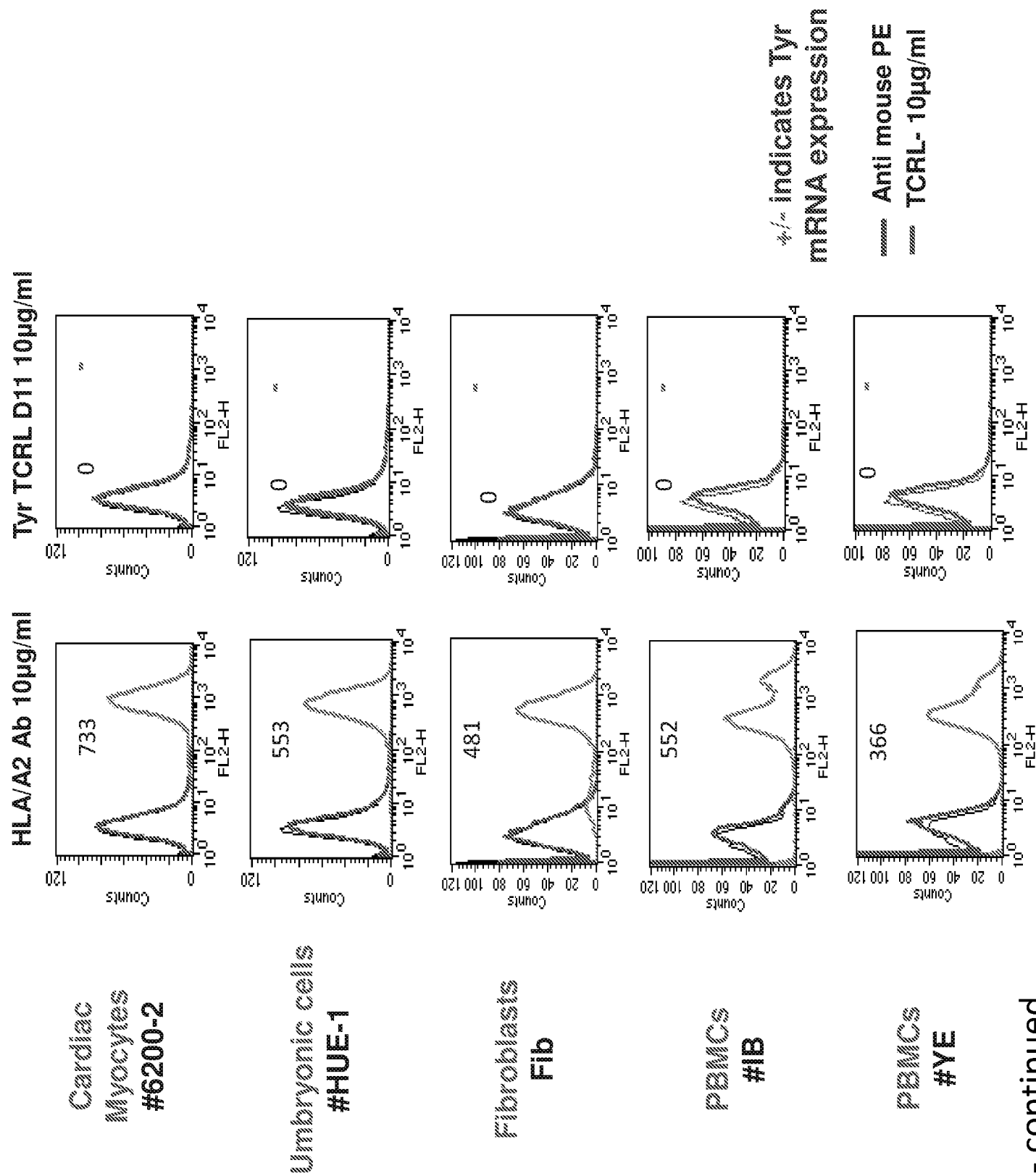


Figure 13 - continued

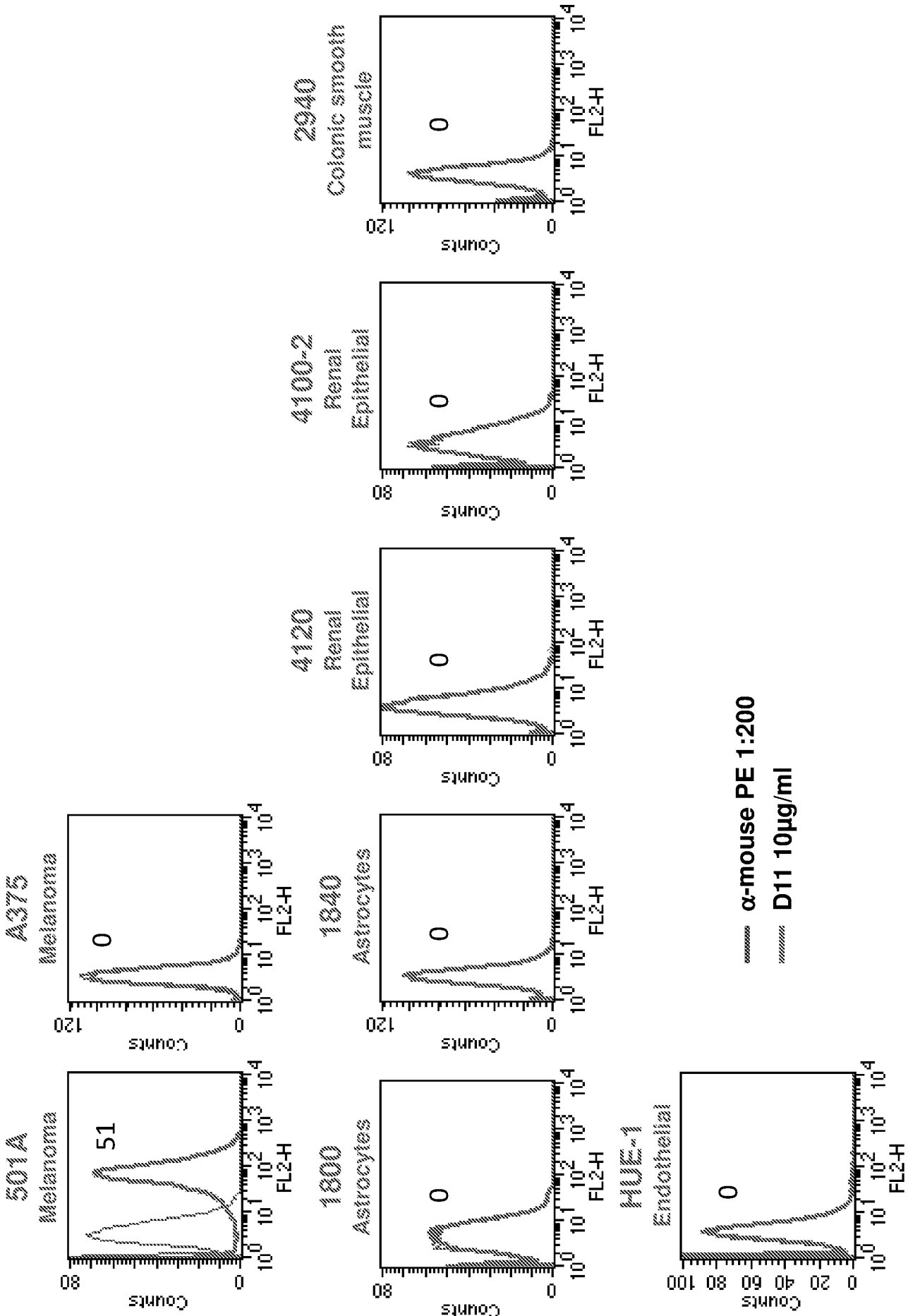


Figure 14

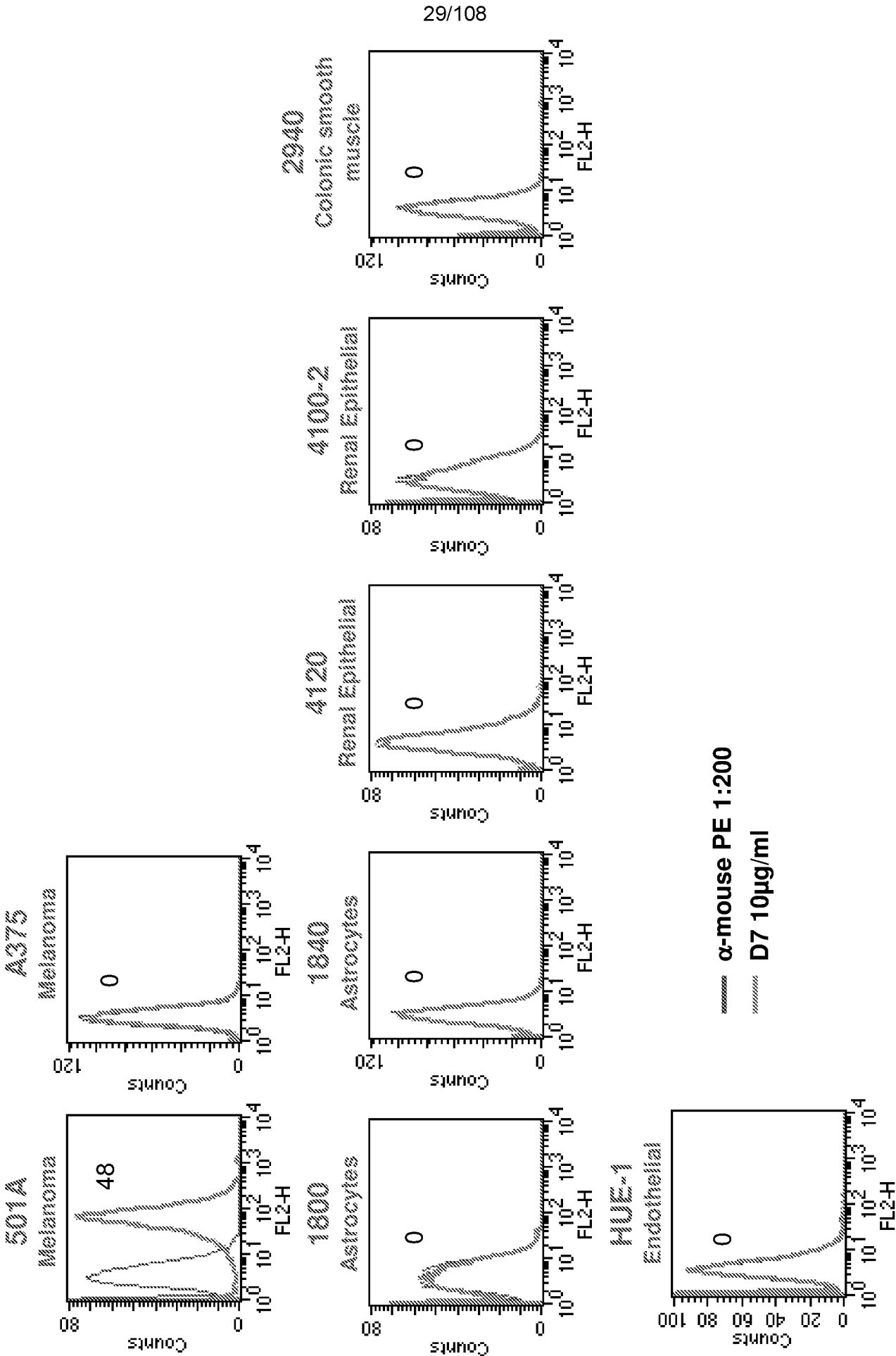


Figure 15

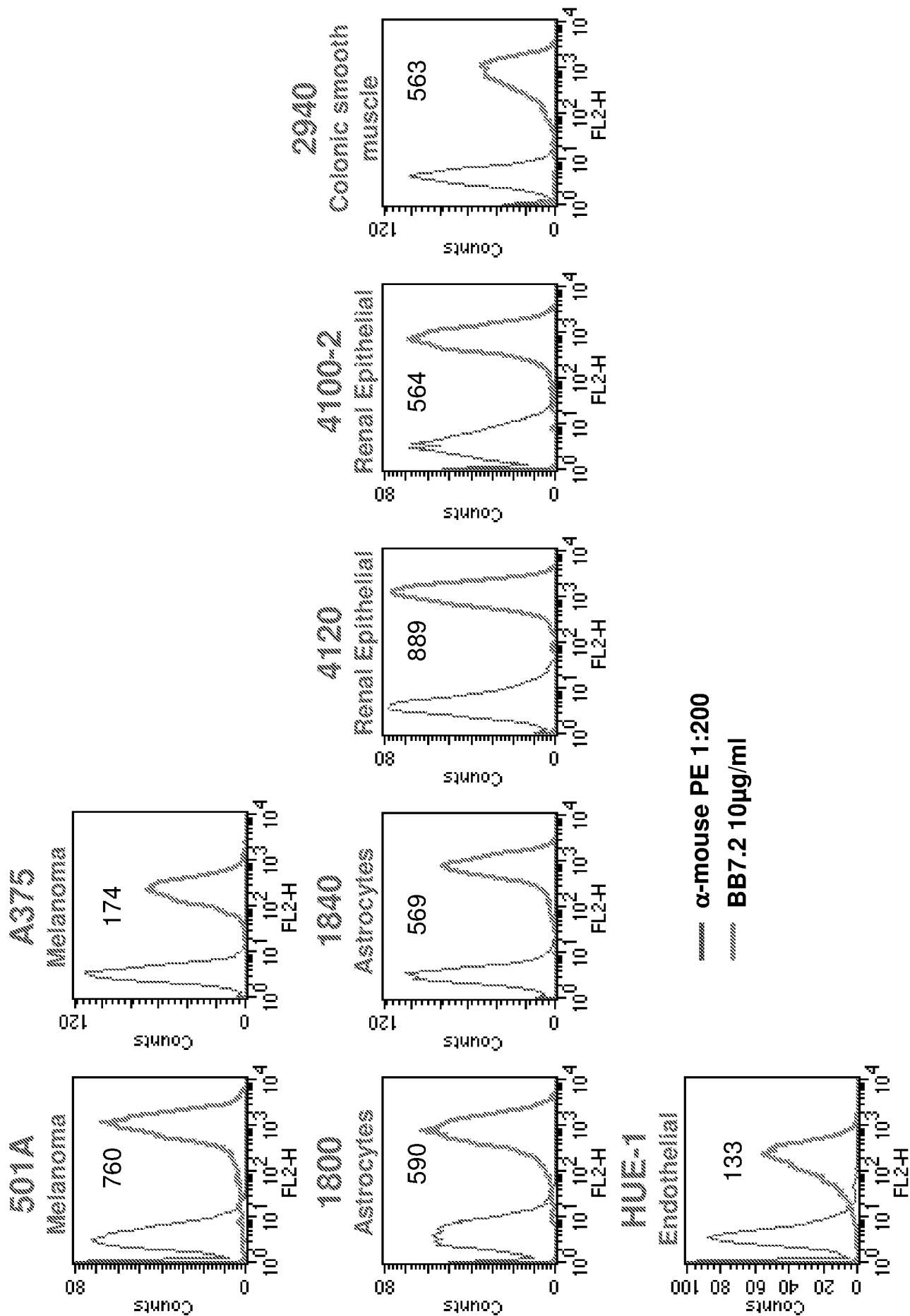


Figure 16

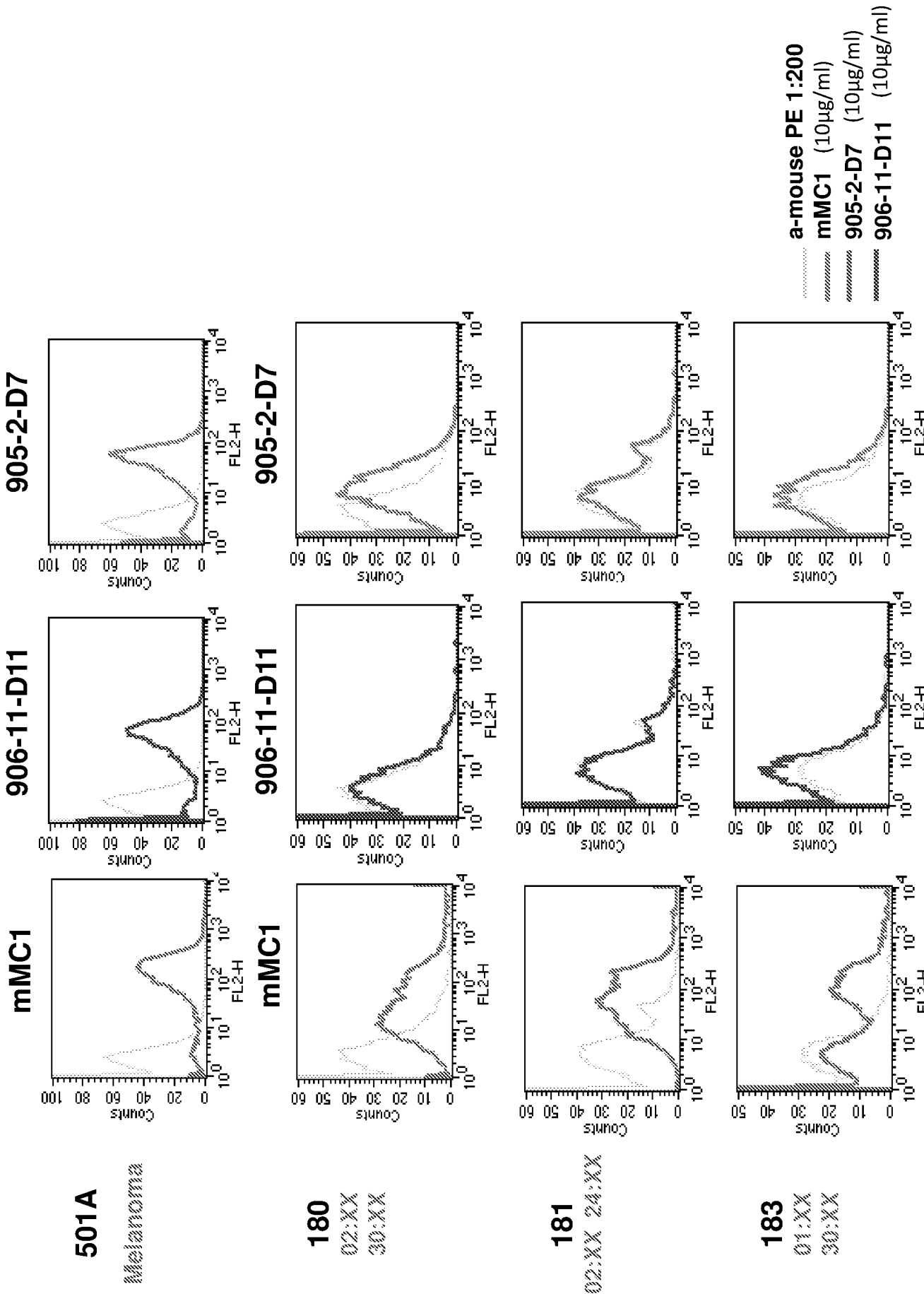


Figure 17

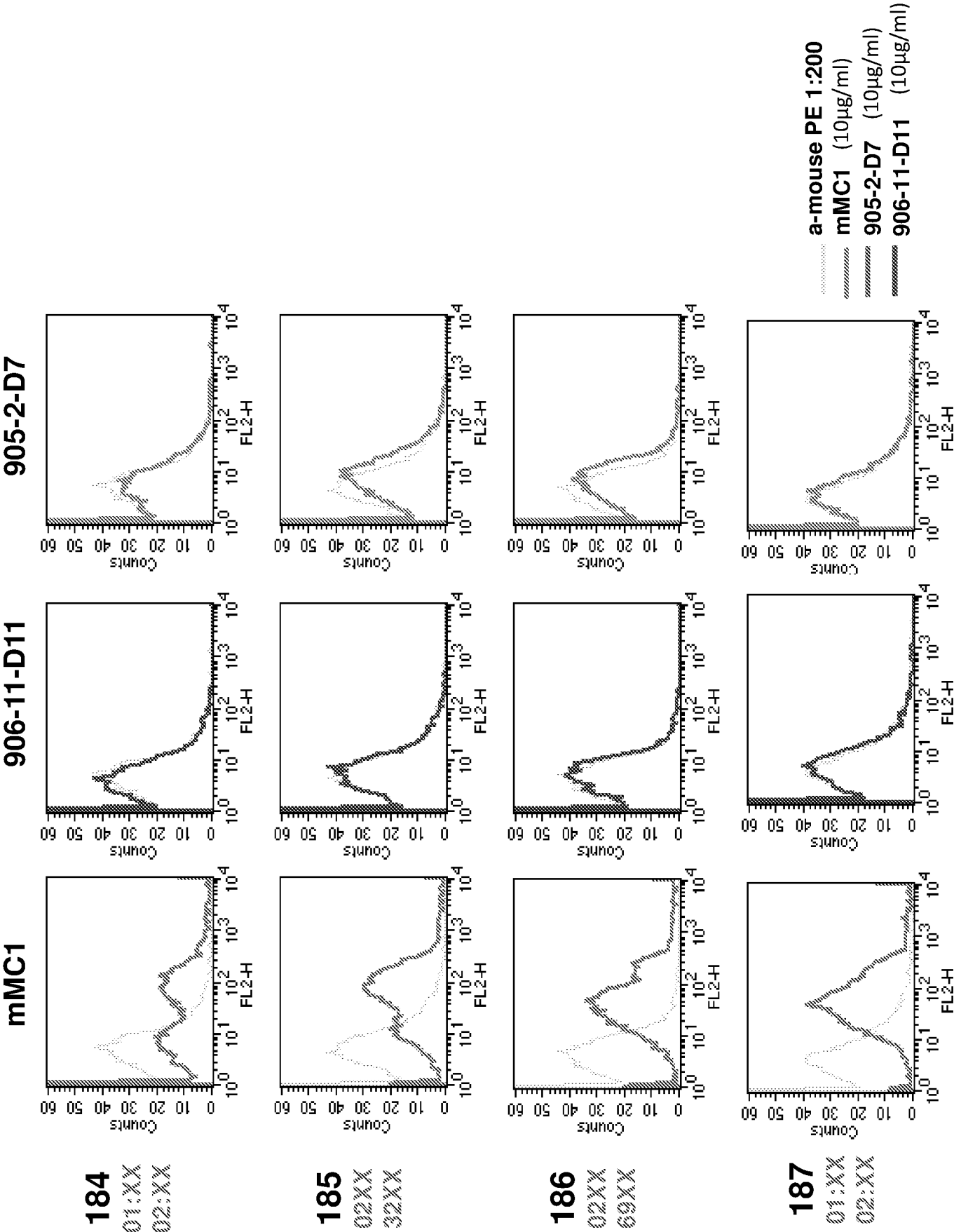
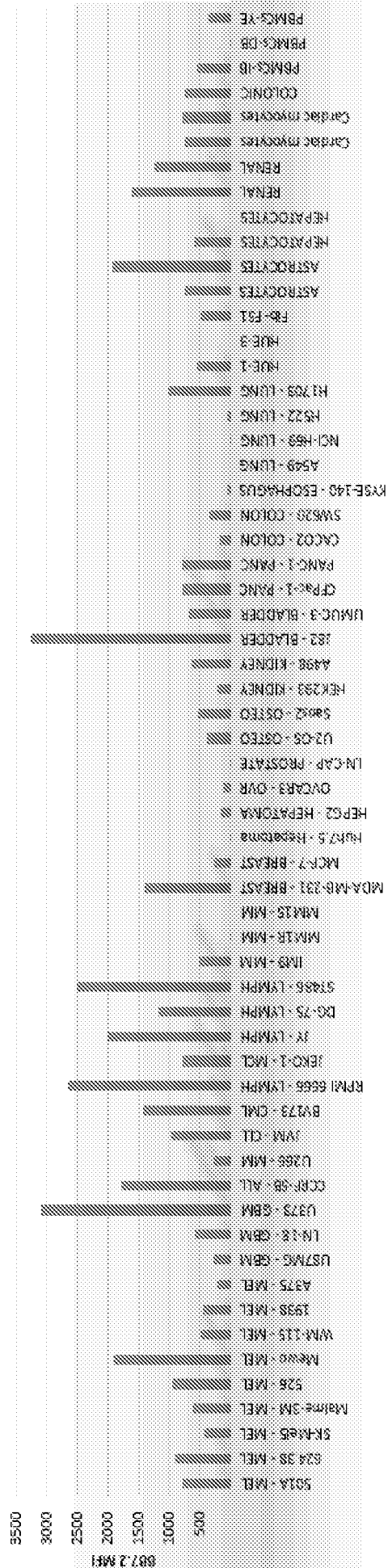
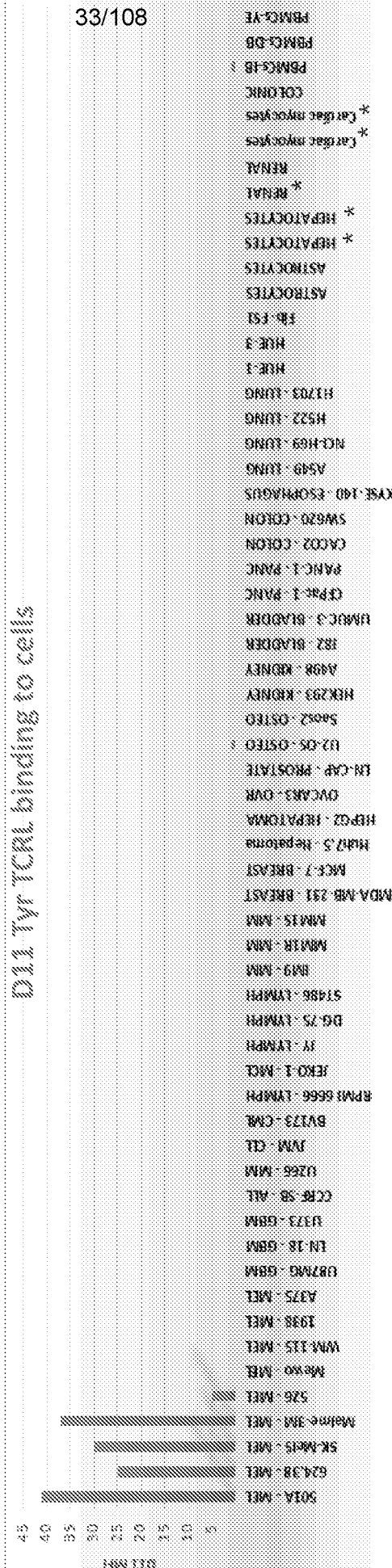


Figure 17 - continued



Don't forget to



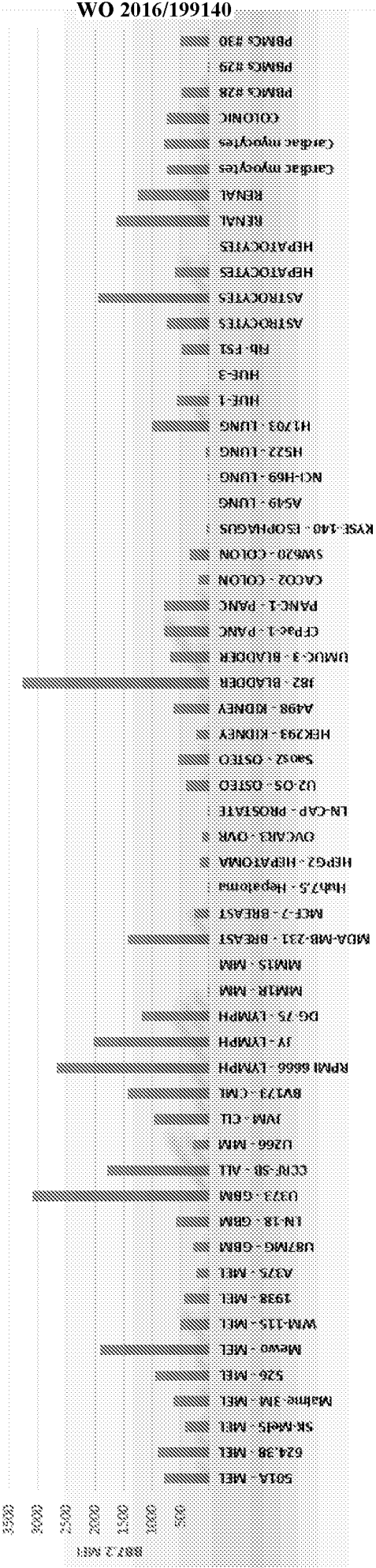
Primary normal cells

Cancer cell lines

[illegible]

Figure 18

HLA-A2 (BB7.2 binding)



D7 Tyr TCRL binding to cells



		Melanoma				GBM		Hematological				Breast		Hep	Ovi	pro	oste	Kidney	Bladder	Panc	Colon	Eso	Lung	HUE	HE	AST	HEP	RCC	CRD	Col	PBMCs
mRNA	protein	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
		+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+

Cancer cell lines

Primary normal cells

PCT/IL2016/050599

Figure 19

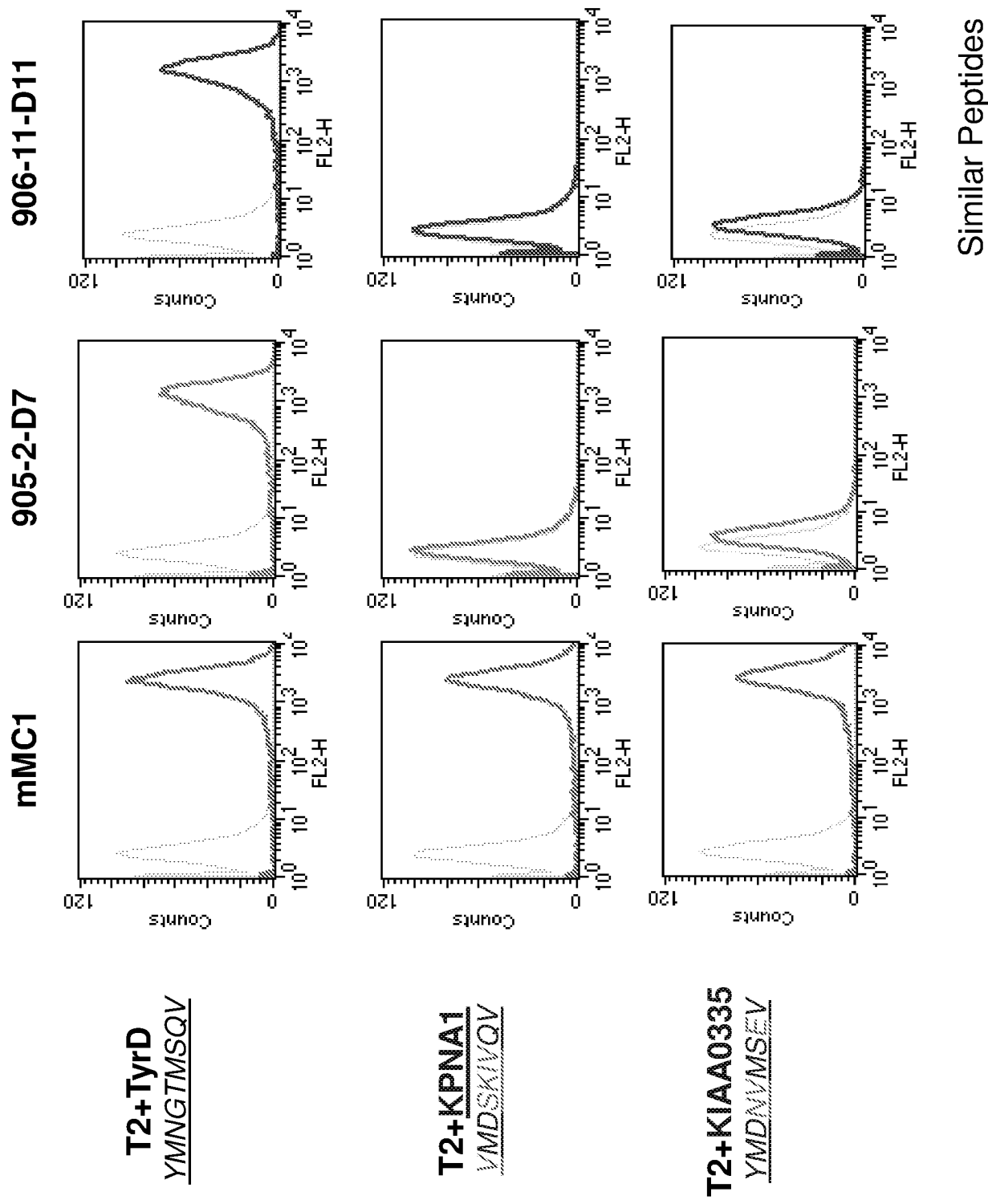
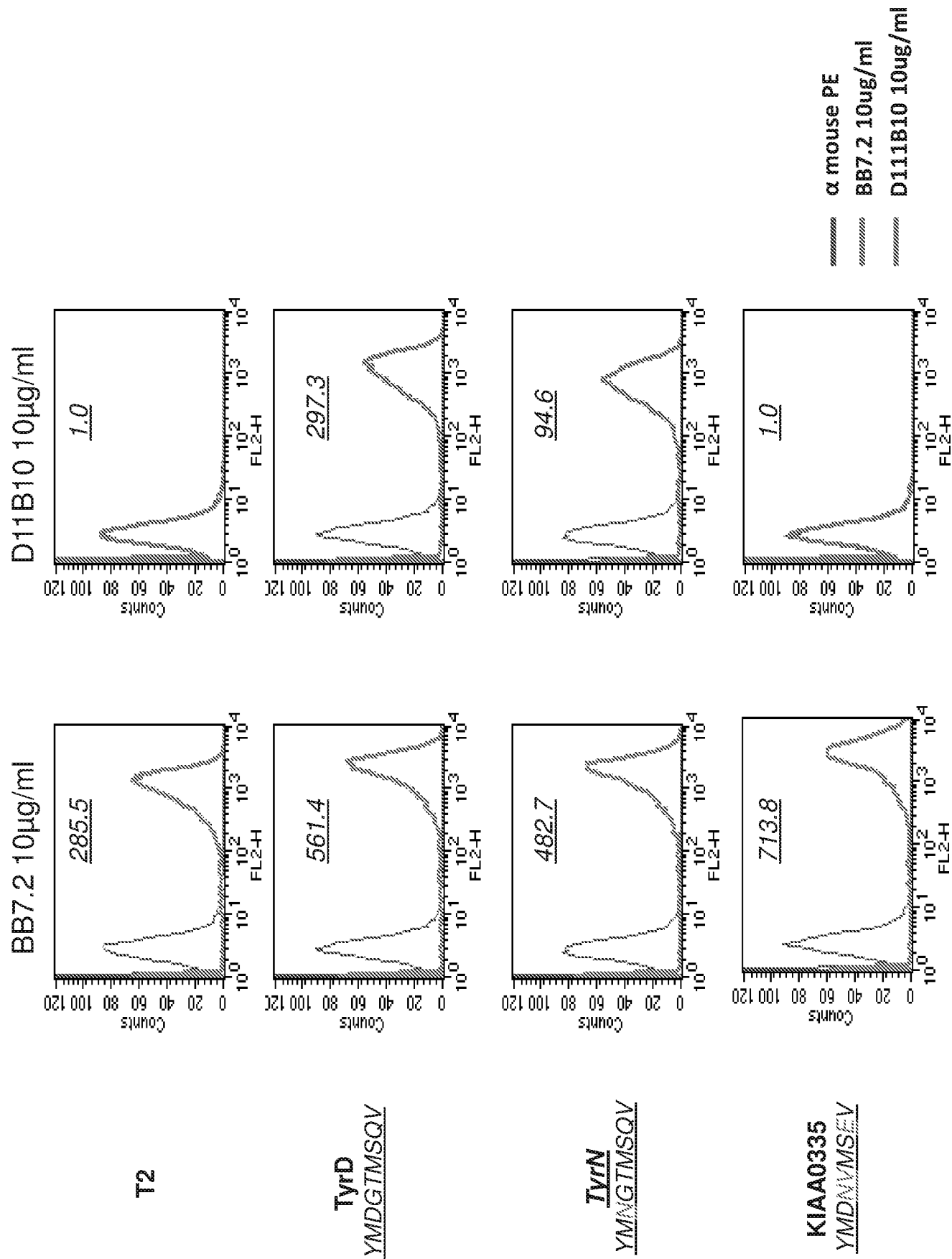


Figure 20



MFI values are relative to background. Value of `1` means no binding

Figure 21

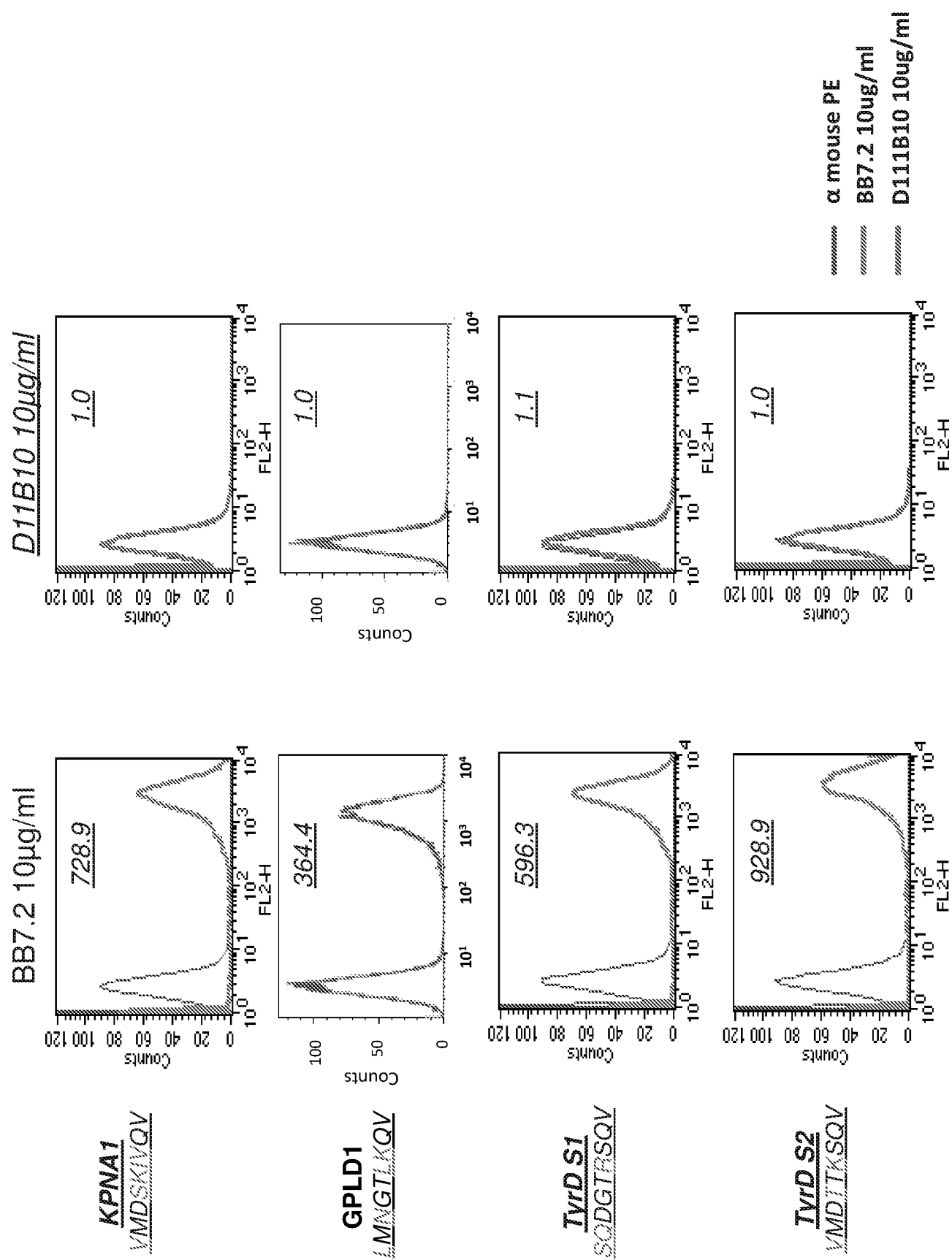
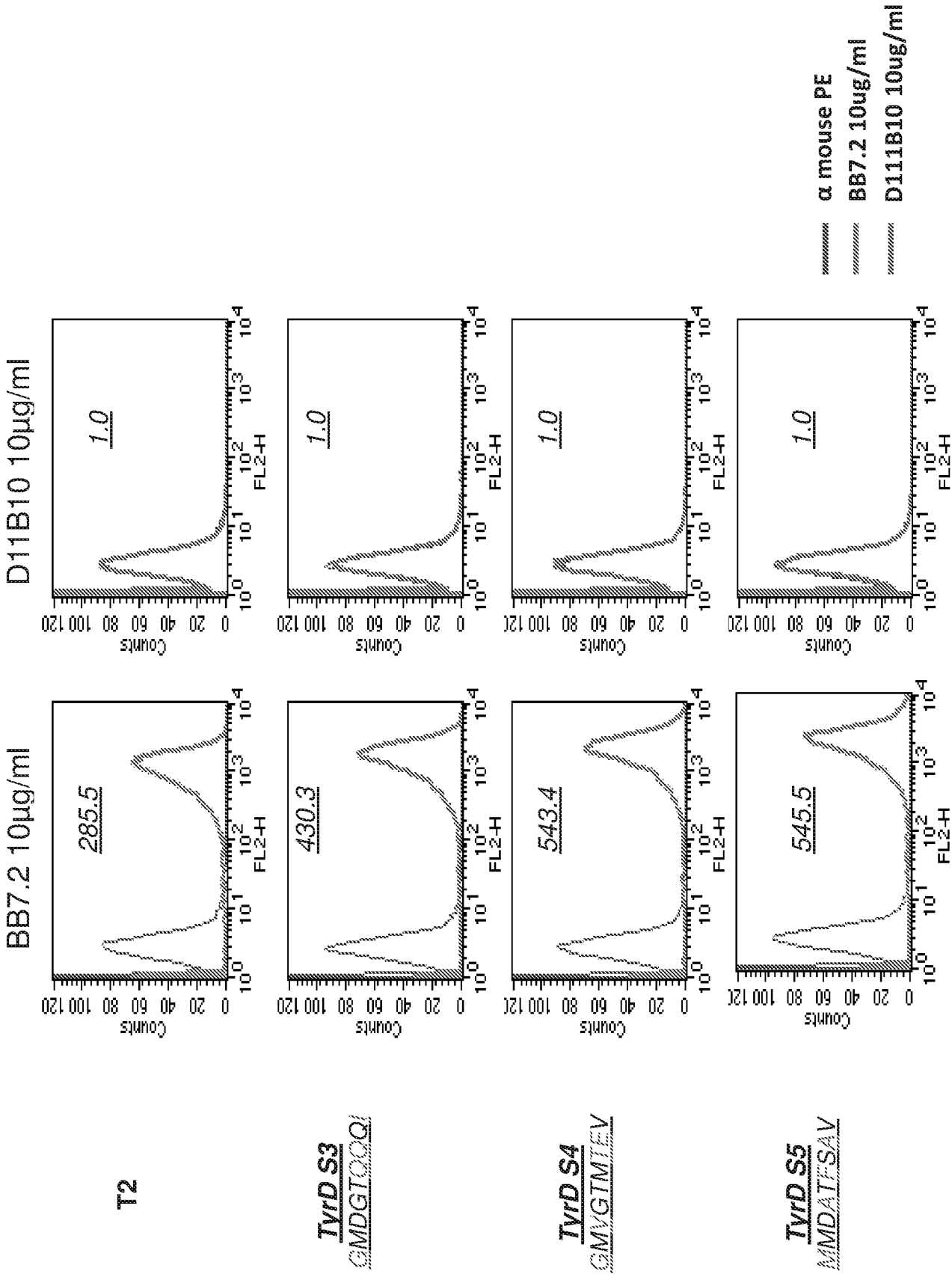
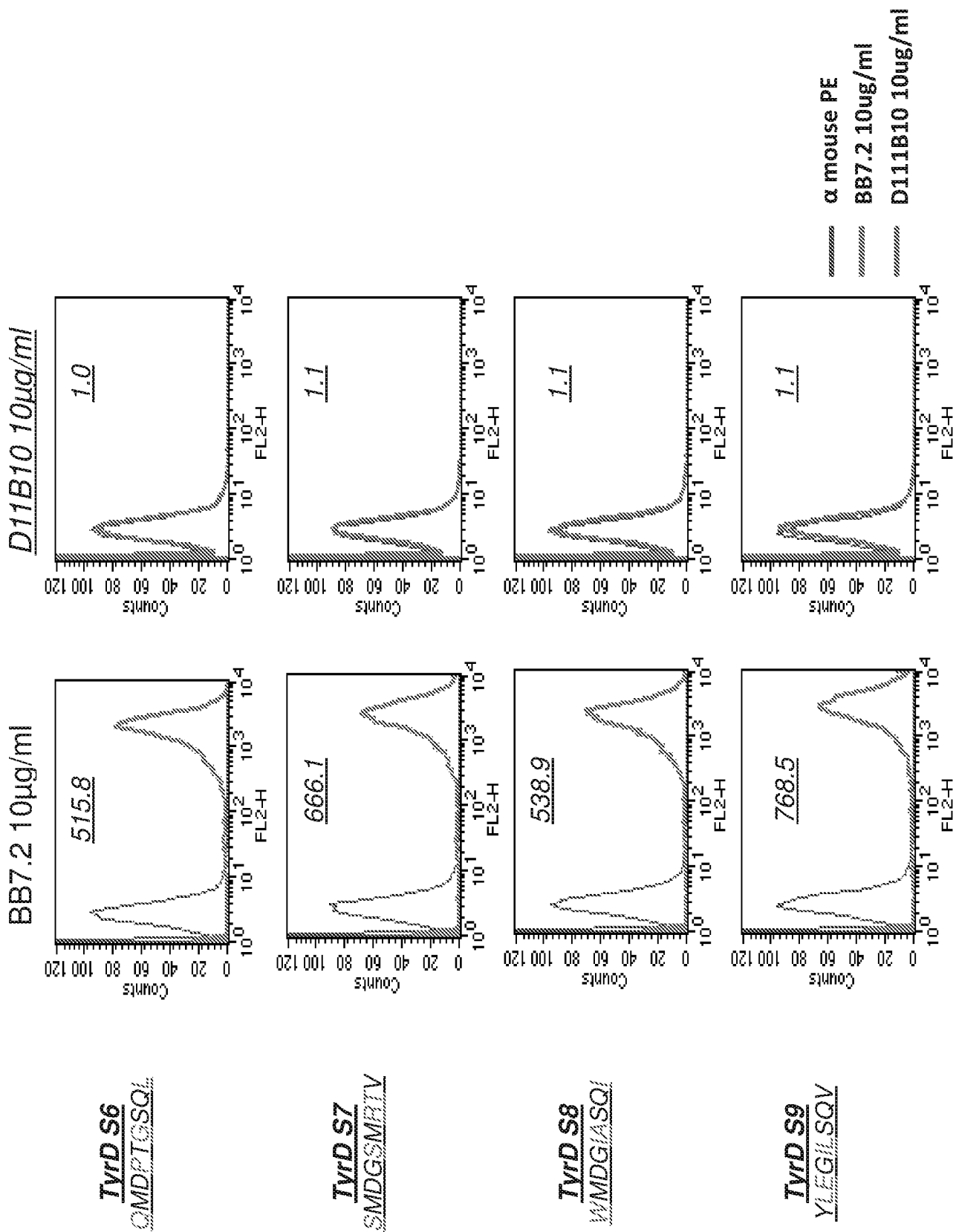


Figure 21 - continued



MFI values are relative to background. Value of `1` means no binding

Figure 22



MFI values are relative to background. Value of `1` means no binding

Figure 22 - continued

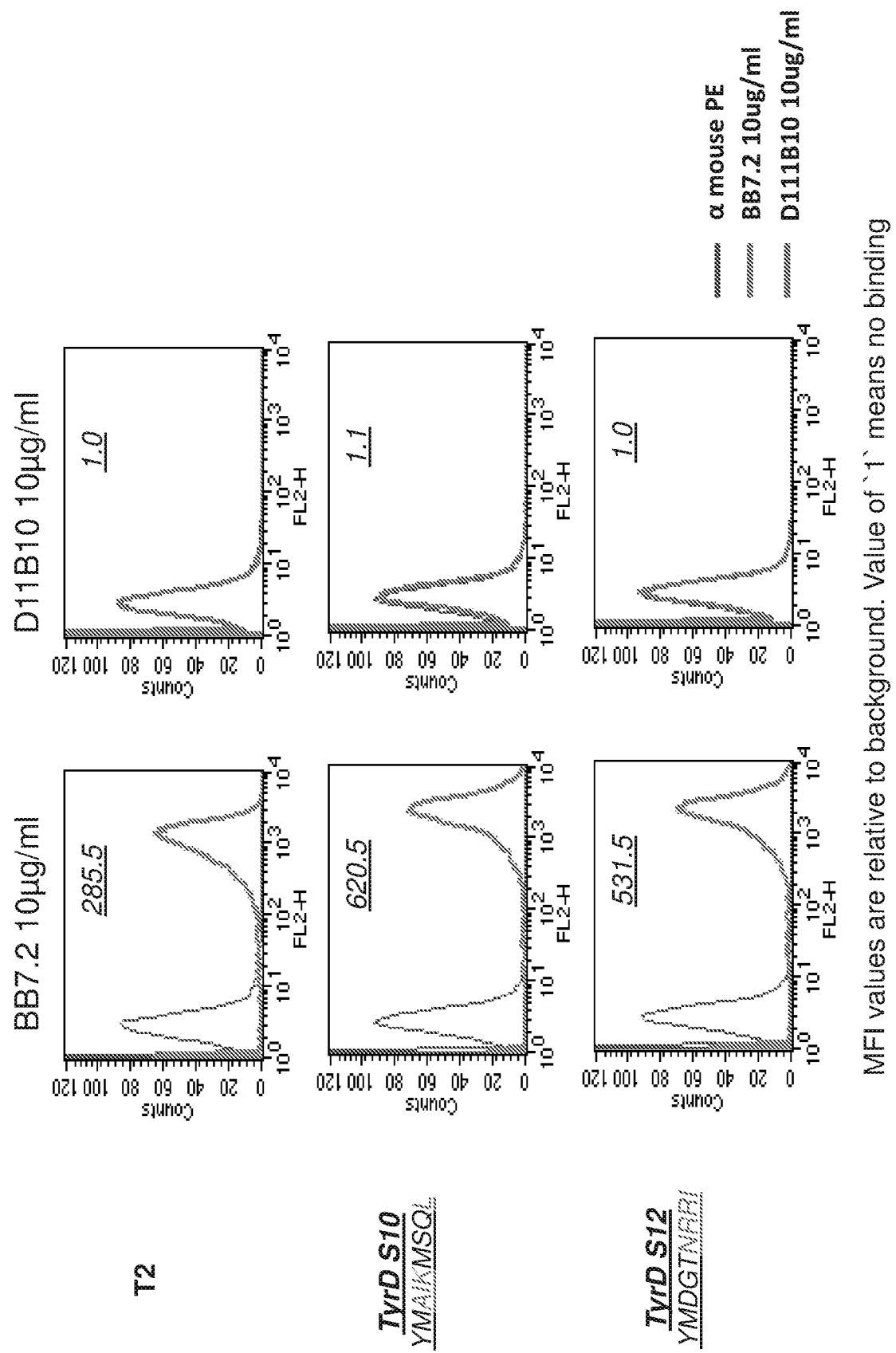
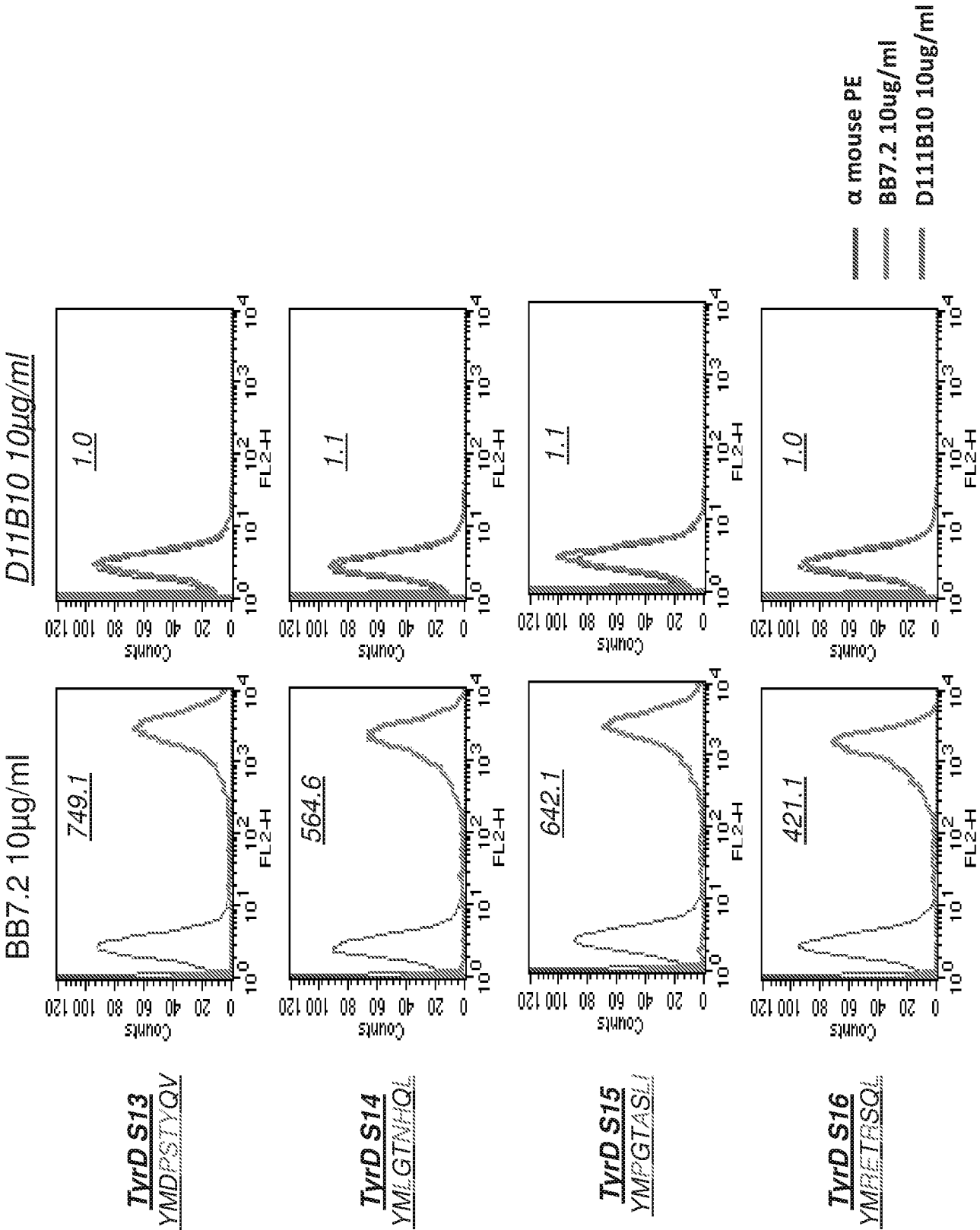


Figure 23



MFI values are relative to background. Value of `1` means no binding

Figure 23 - continued

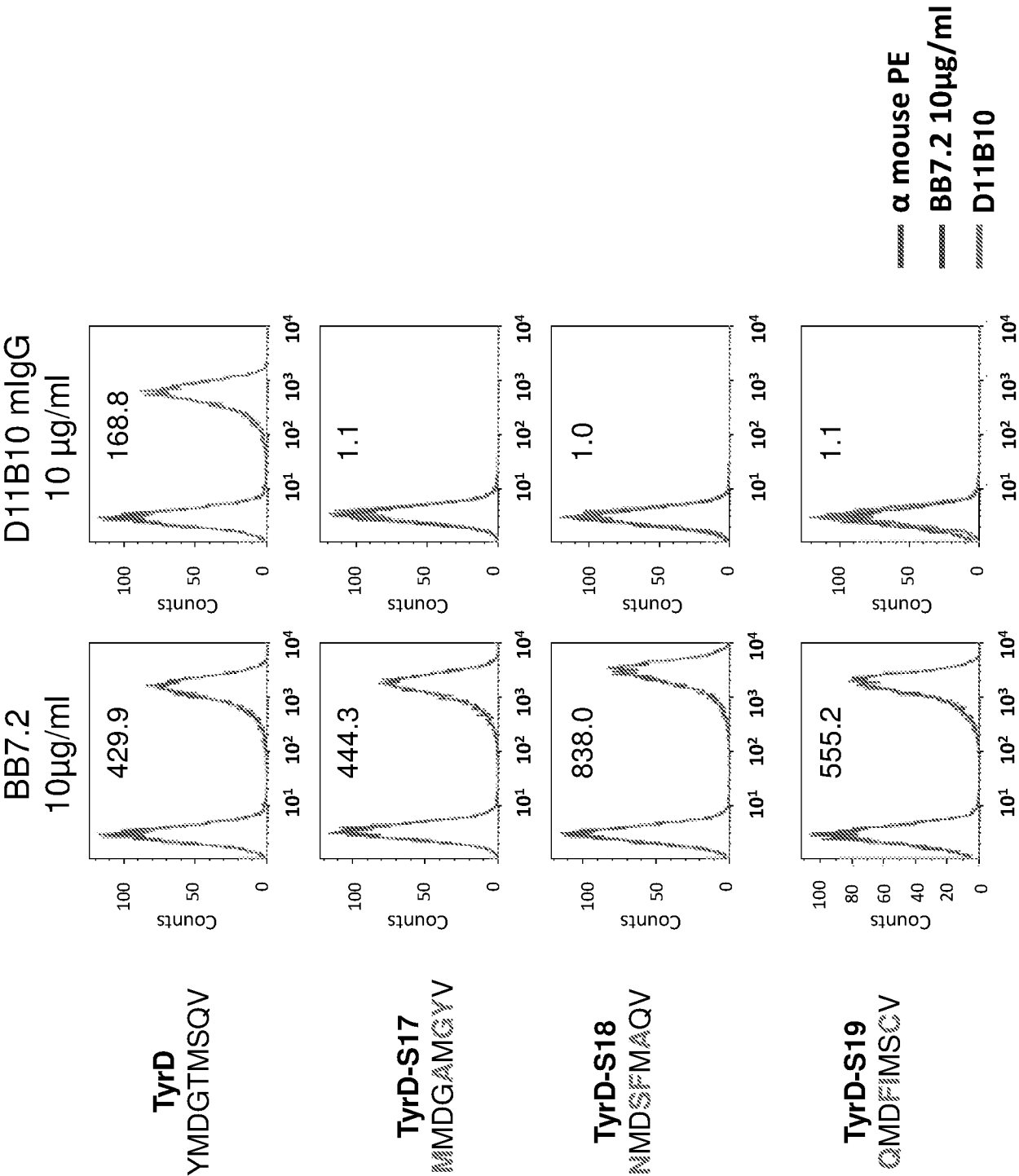
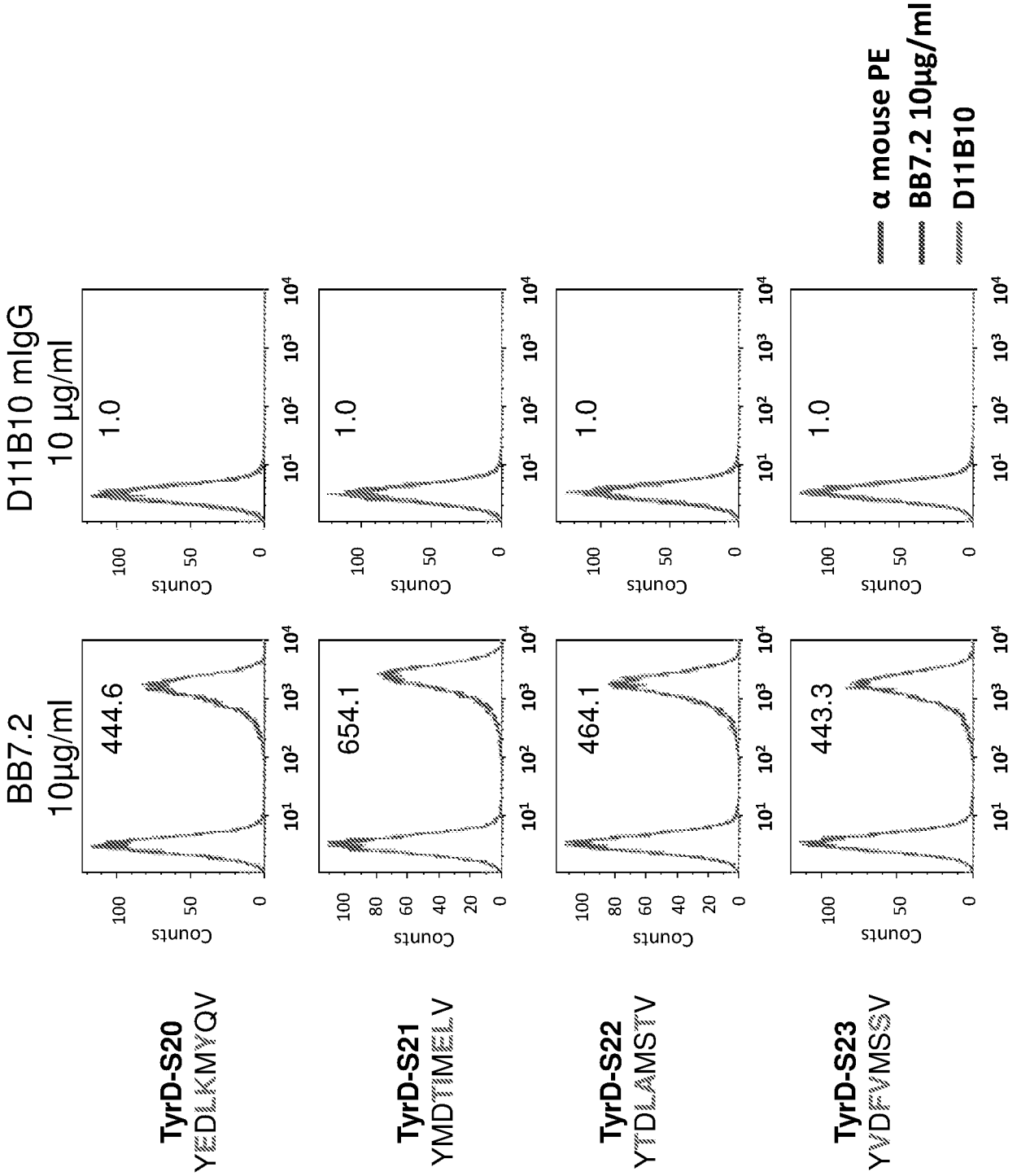
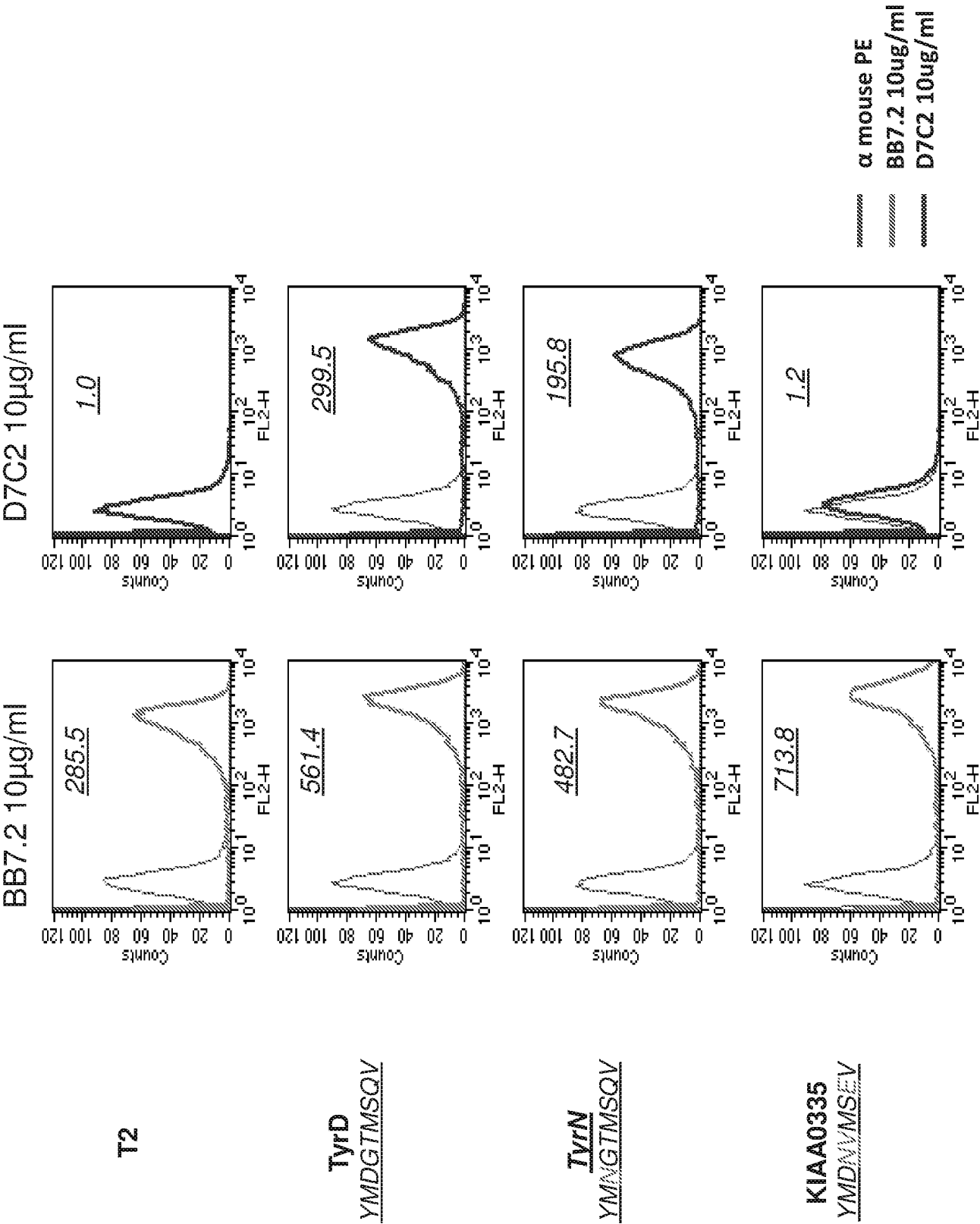


Figure 24



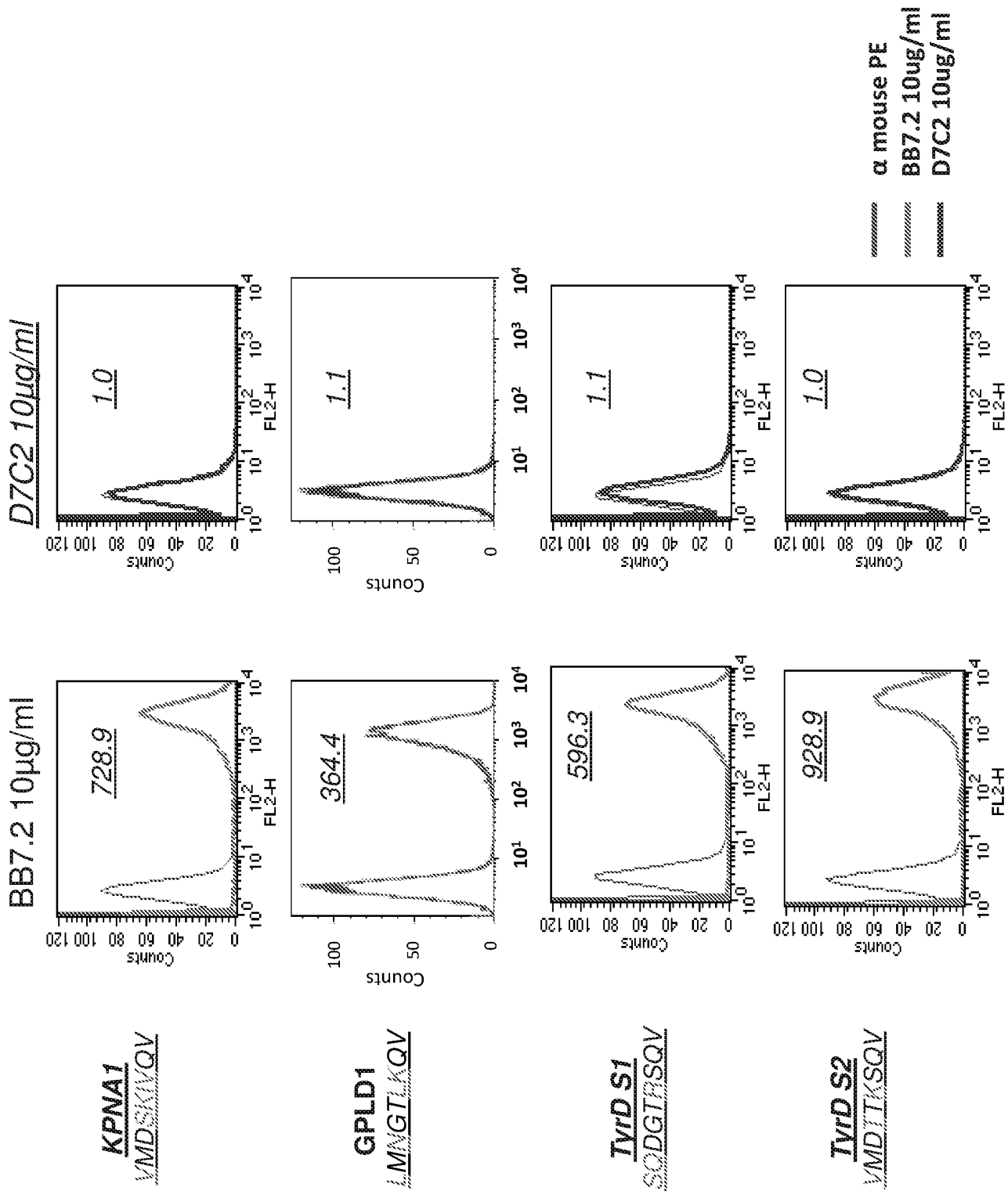
MFI values are relative to background. Value of `1` means no binding

Figure 24 - continued



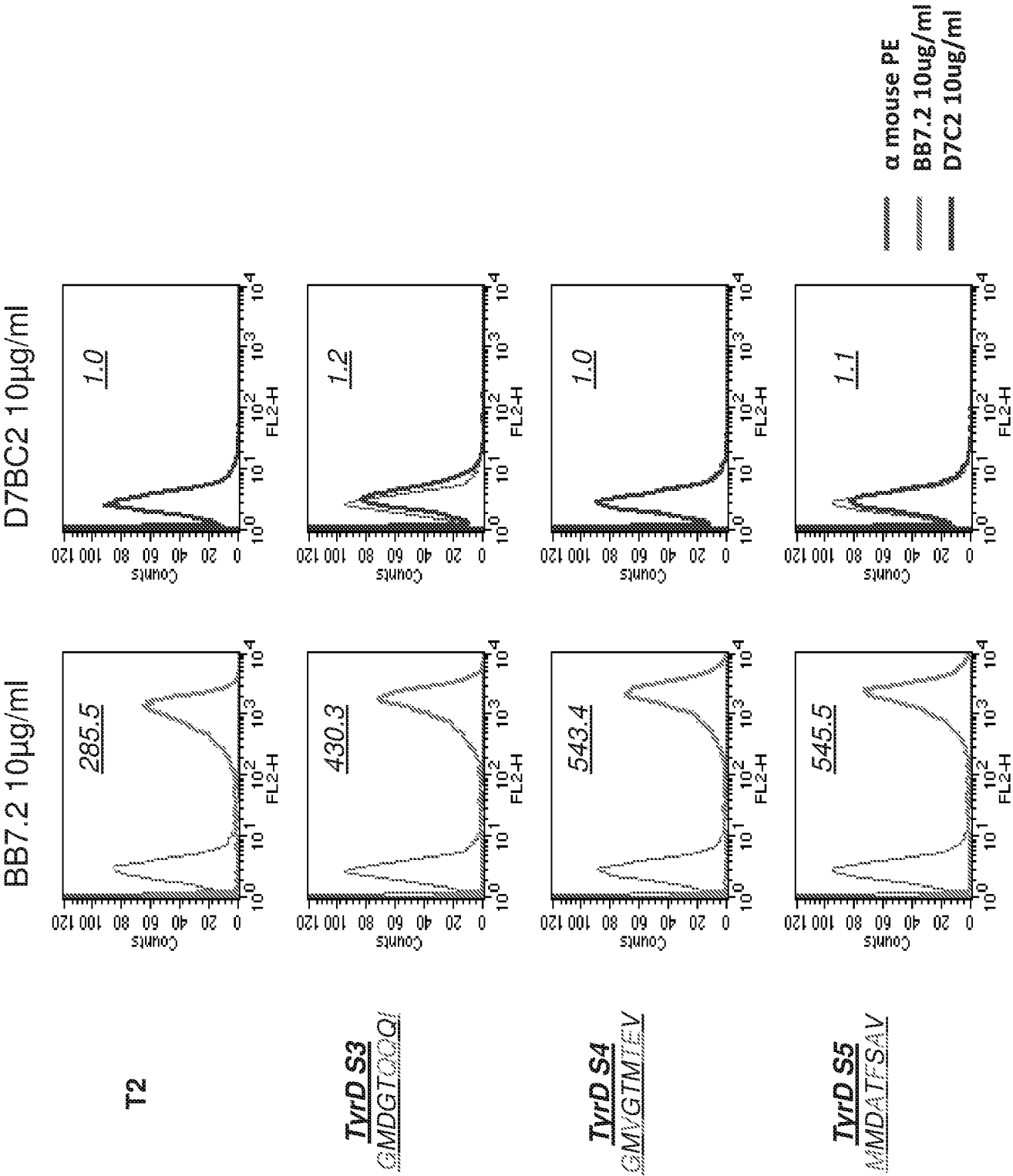
MFI values are relative to background. Value of `1` means no binding

Figure 25



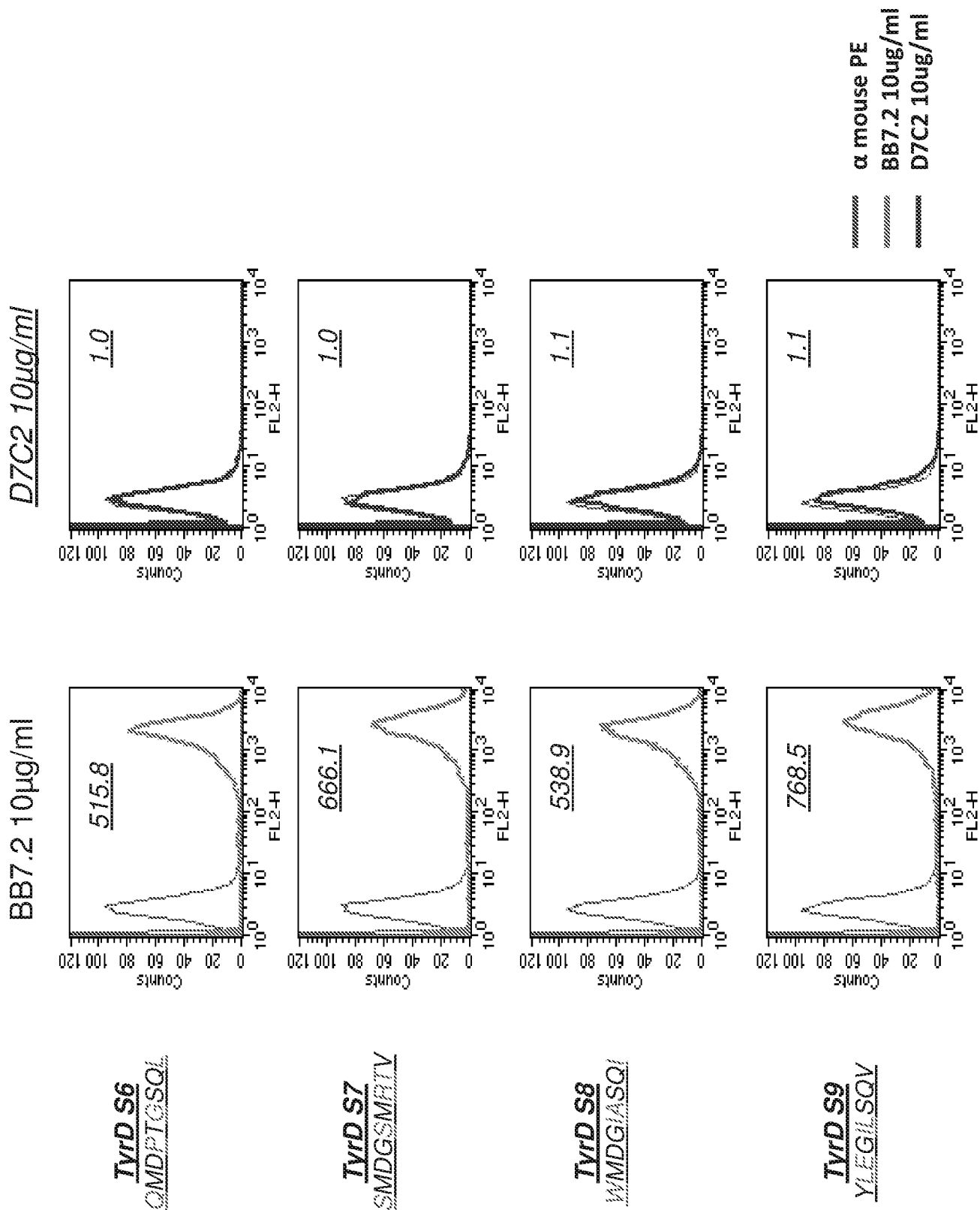
MFI values are relative to background. Value of `1` means no binding

Figure 25 - continued



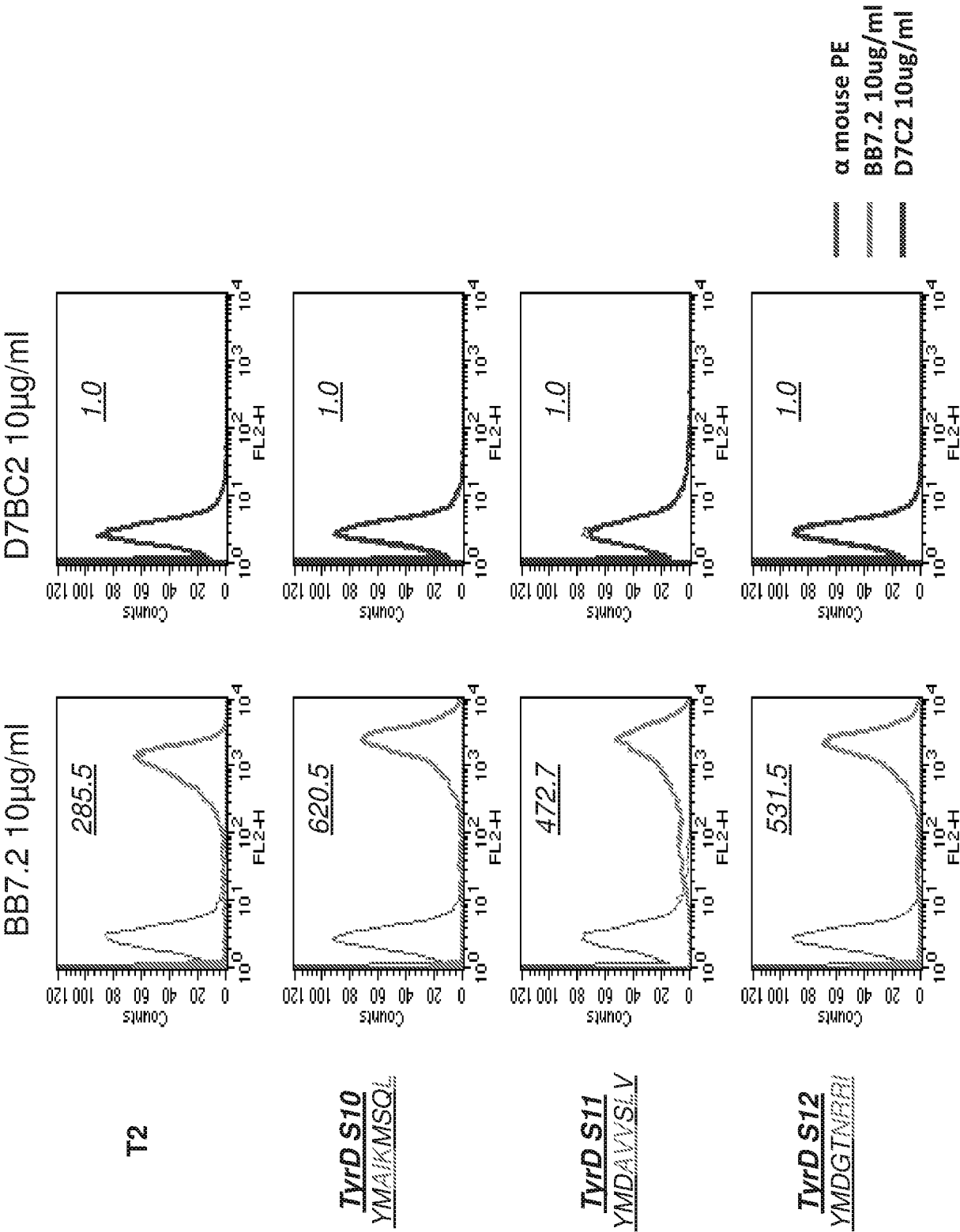
MFI values are relative to background. Value of 1 means no binding

Figure 26



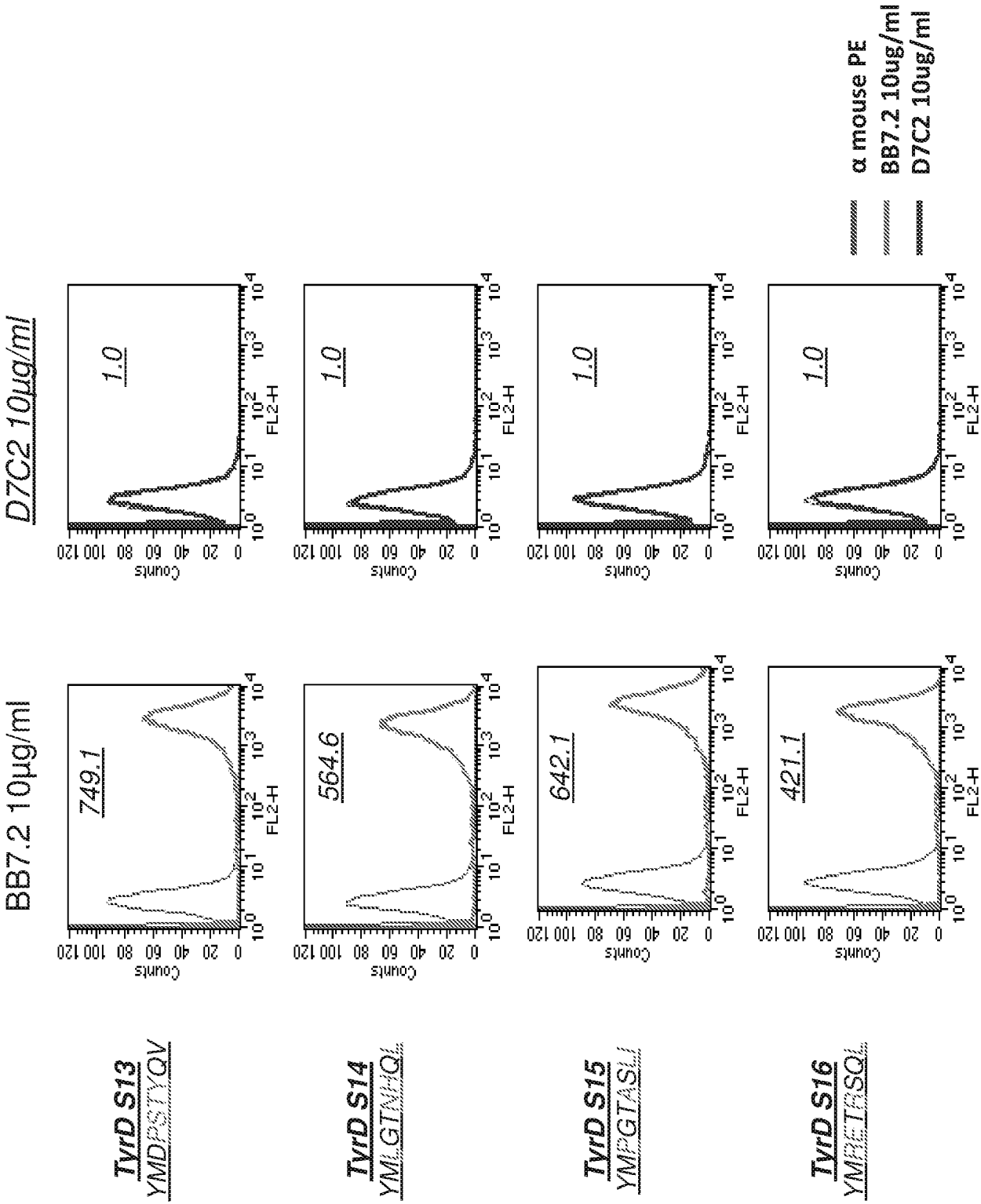
MFI values are relative to background. Value of 1` means no binding

Figure 26 - continued



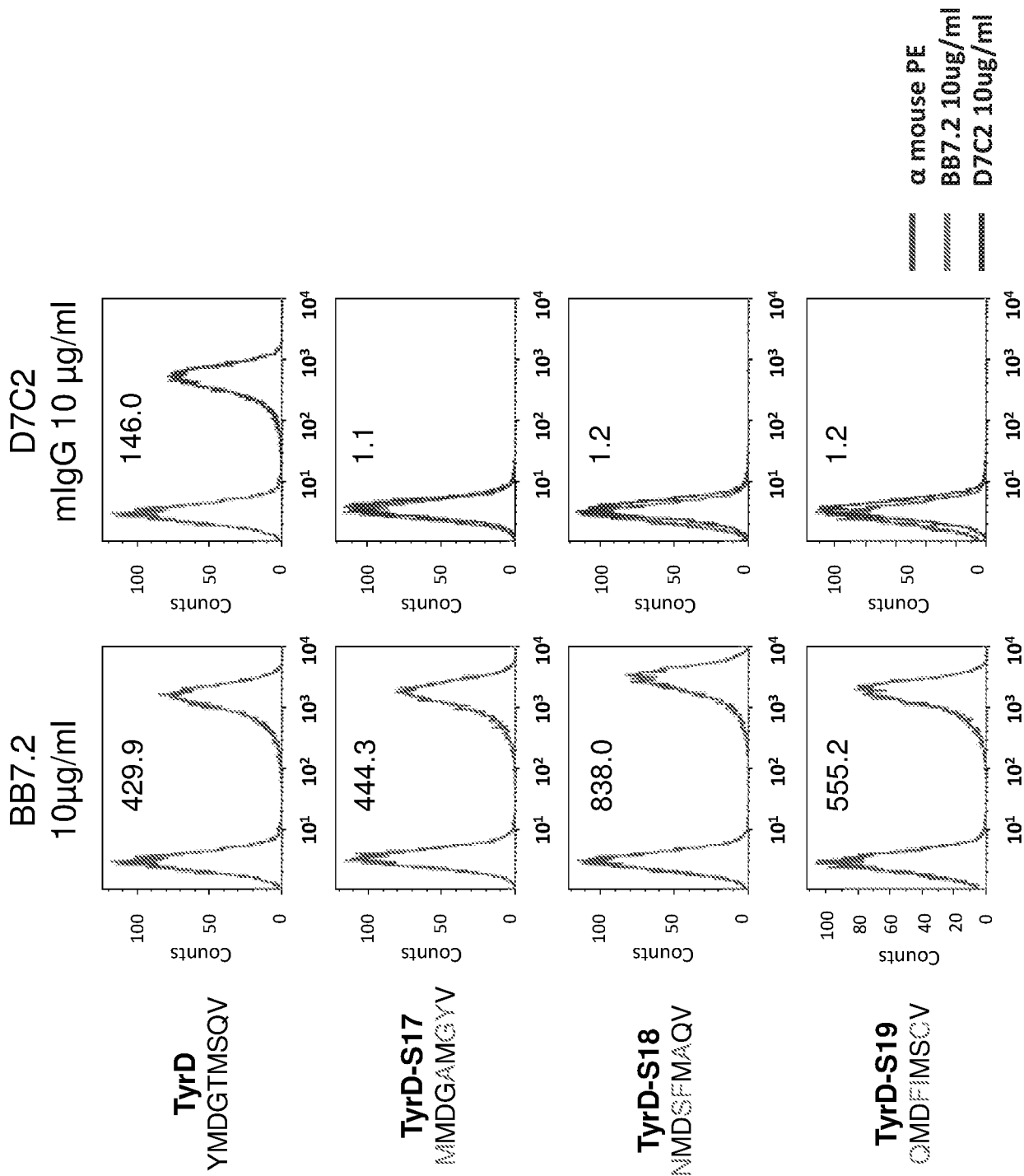
MFI values are relative to background. Value of `1` means no binding

Figure 27



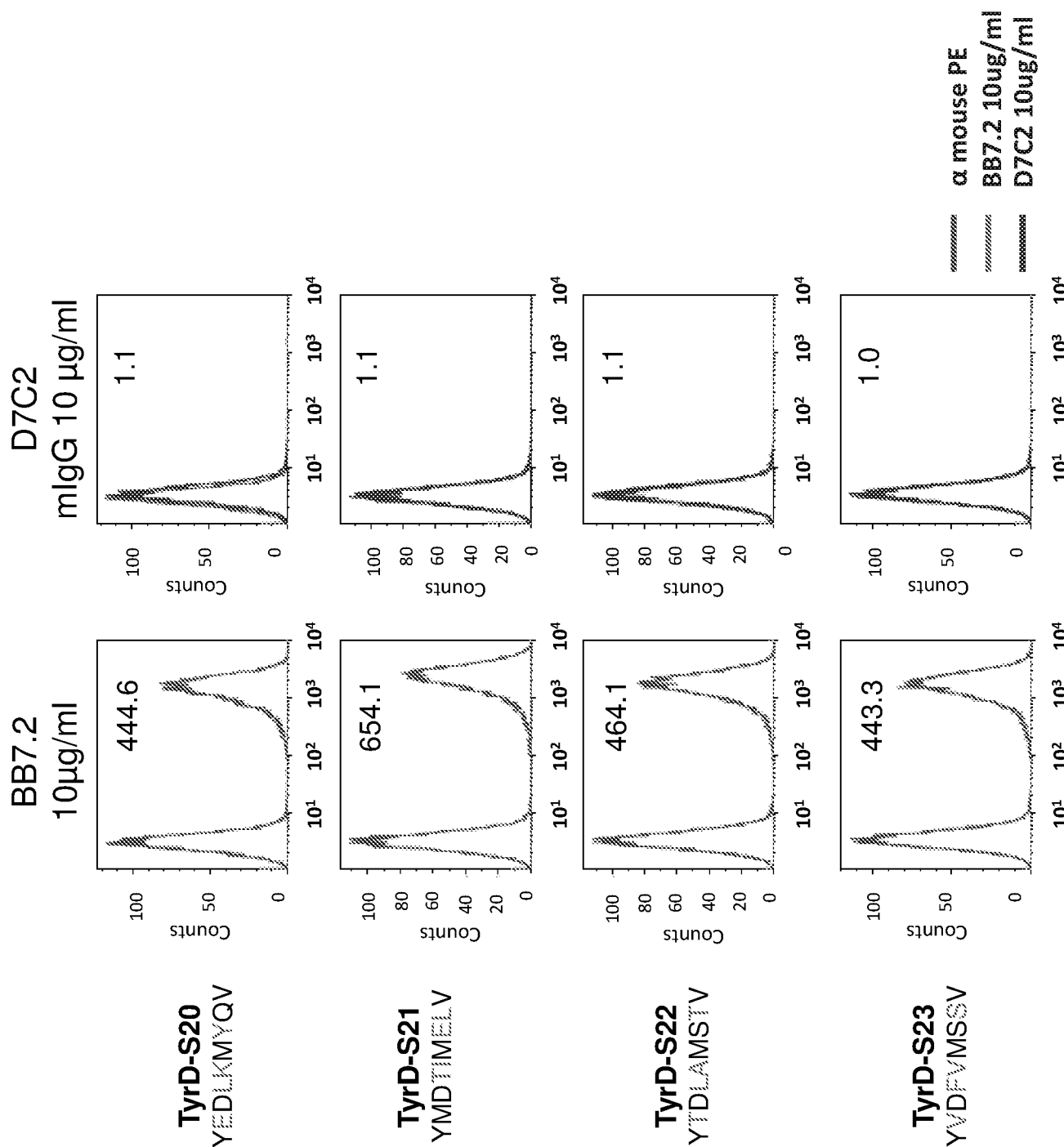
MFI values are relative to background. Value of `1` means no binding

Figure 27 - continued



MFI values are relative to background. Value of 1 means no binding

Figure 28



MFI values are relative to background. Value of `1` means no binding

Figure 28 - continued

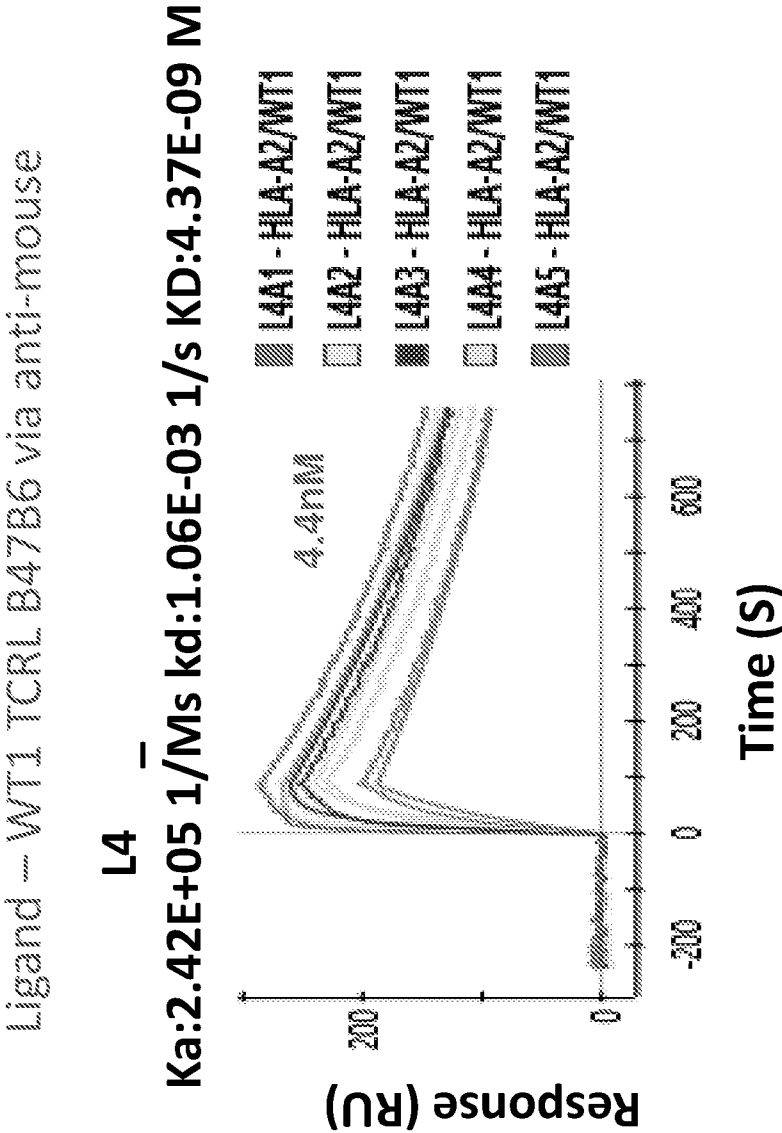


Figure 29

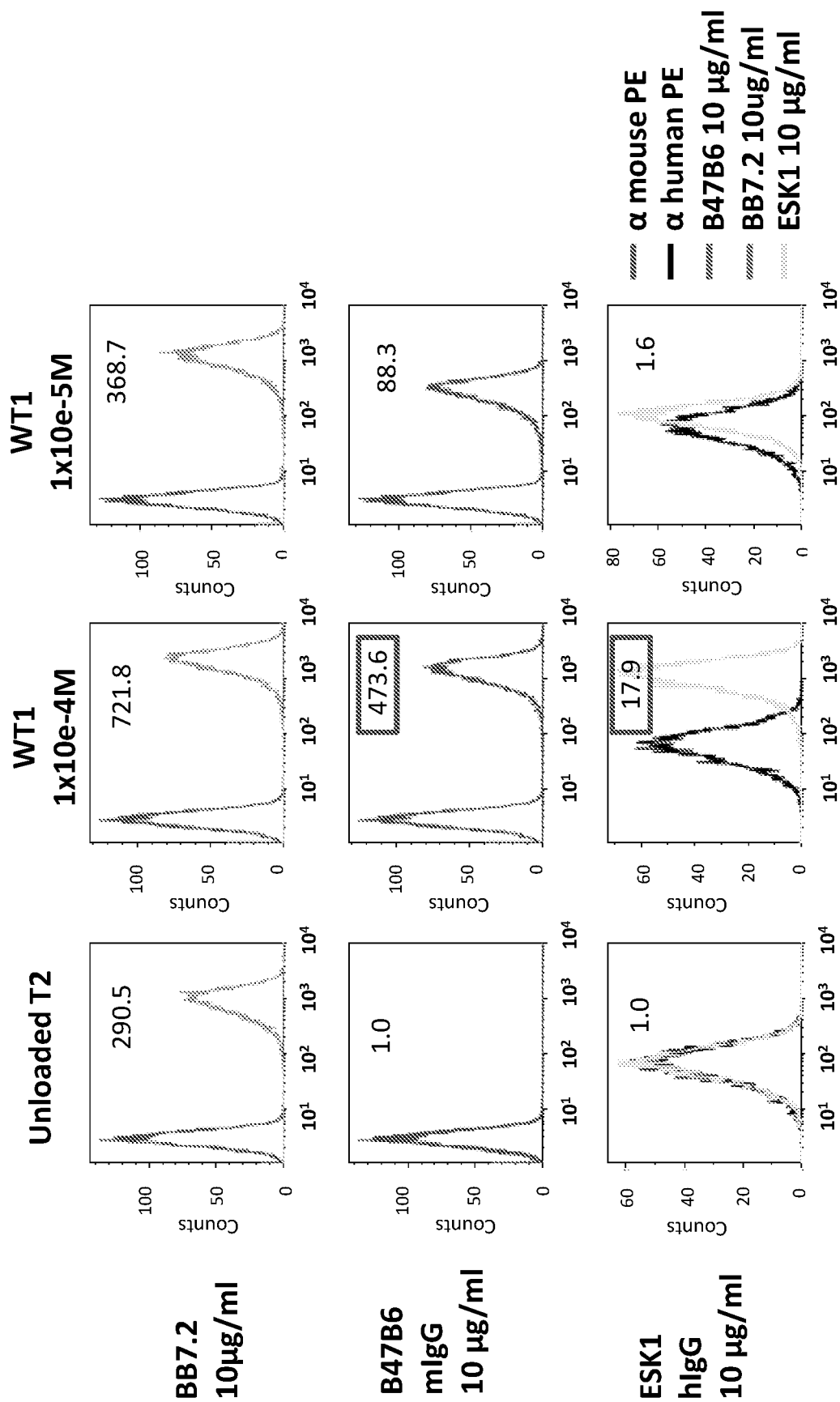
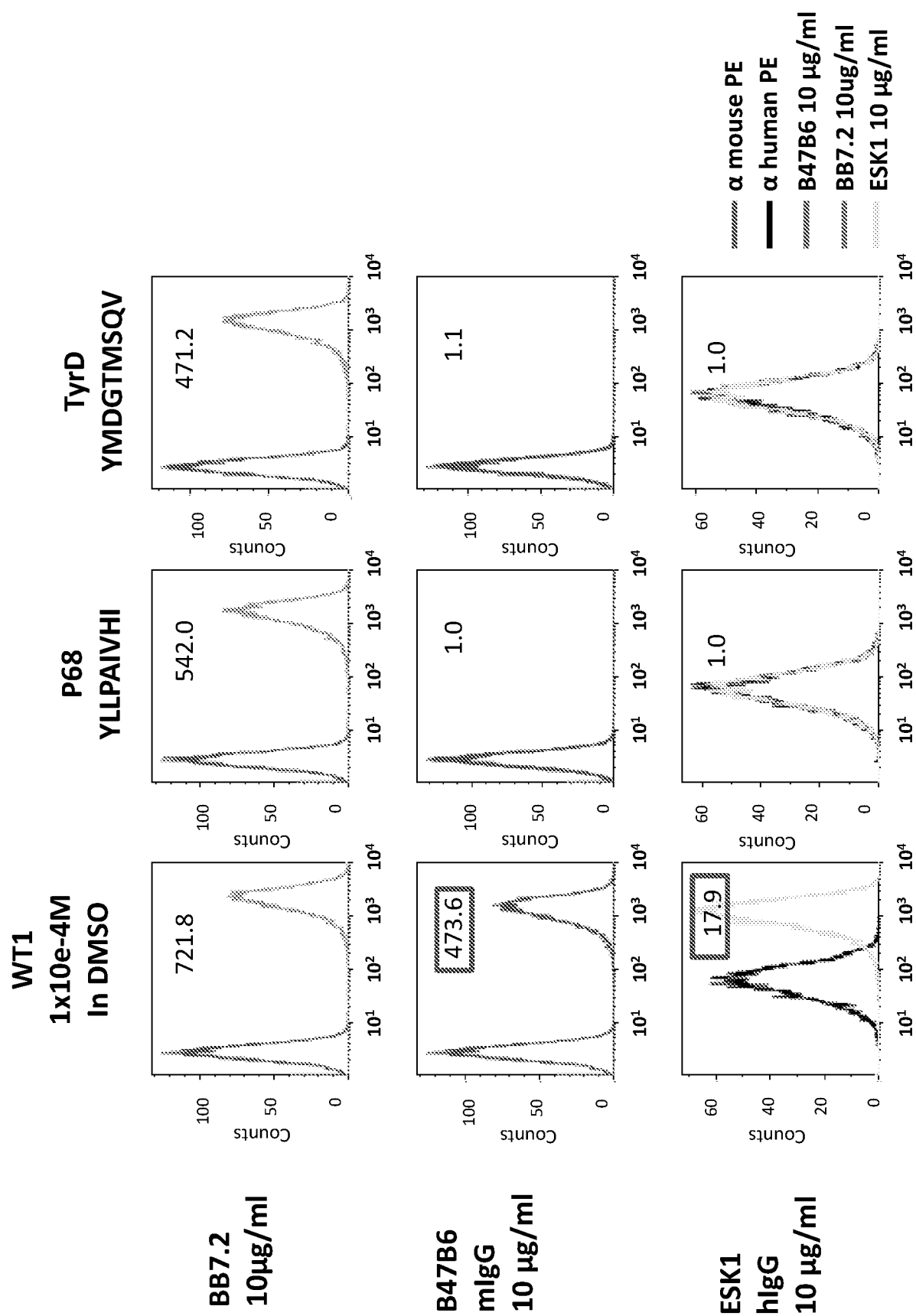


Figure 30



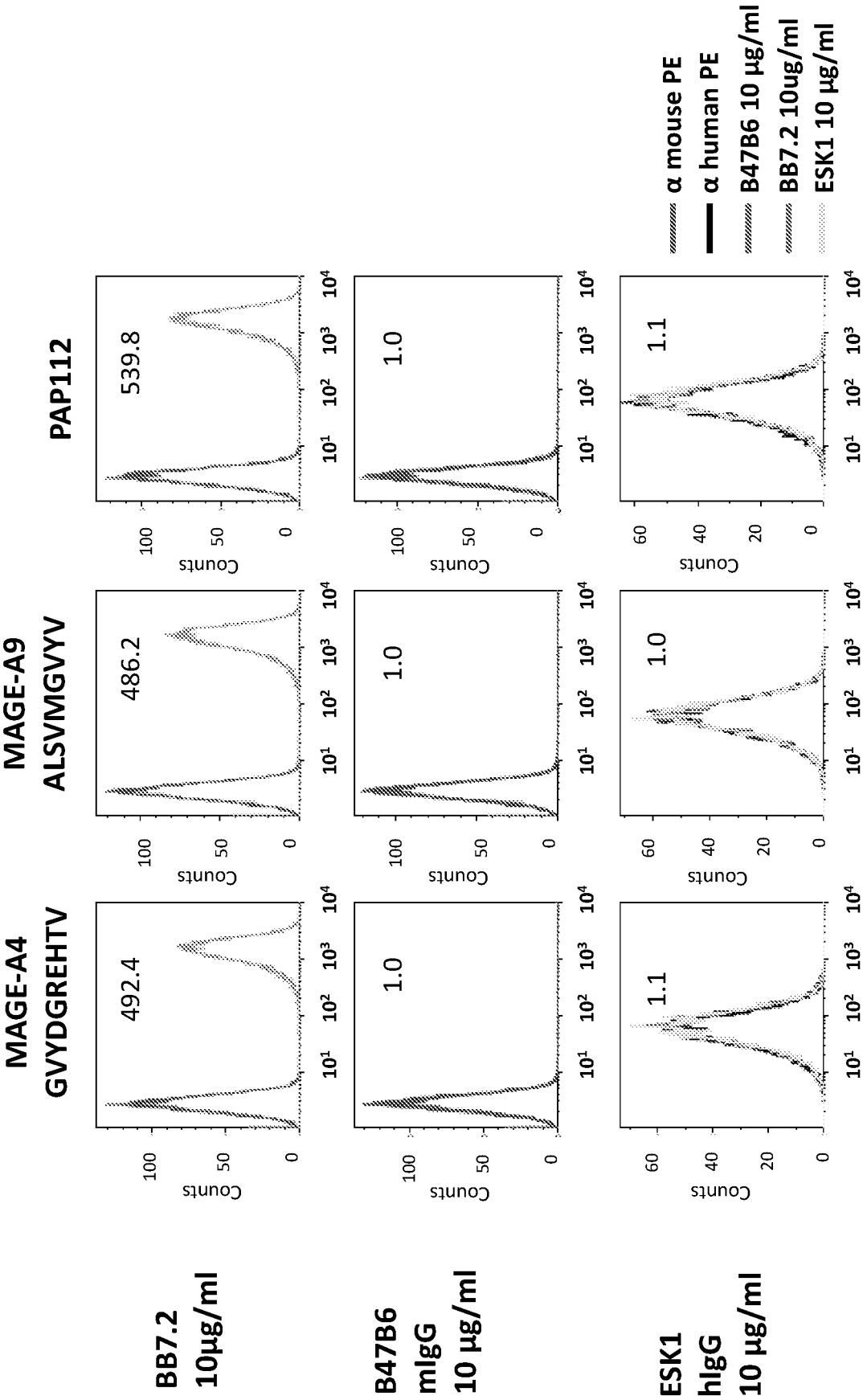


Figure 31 - continued

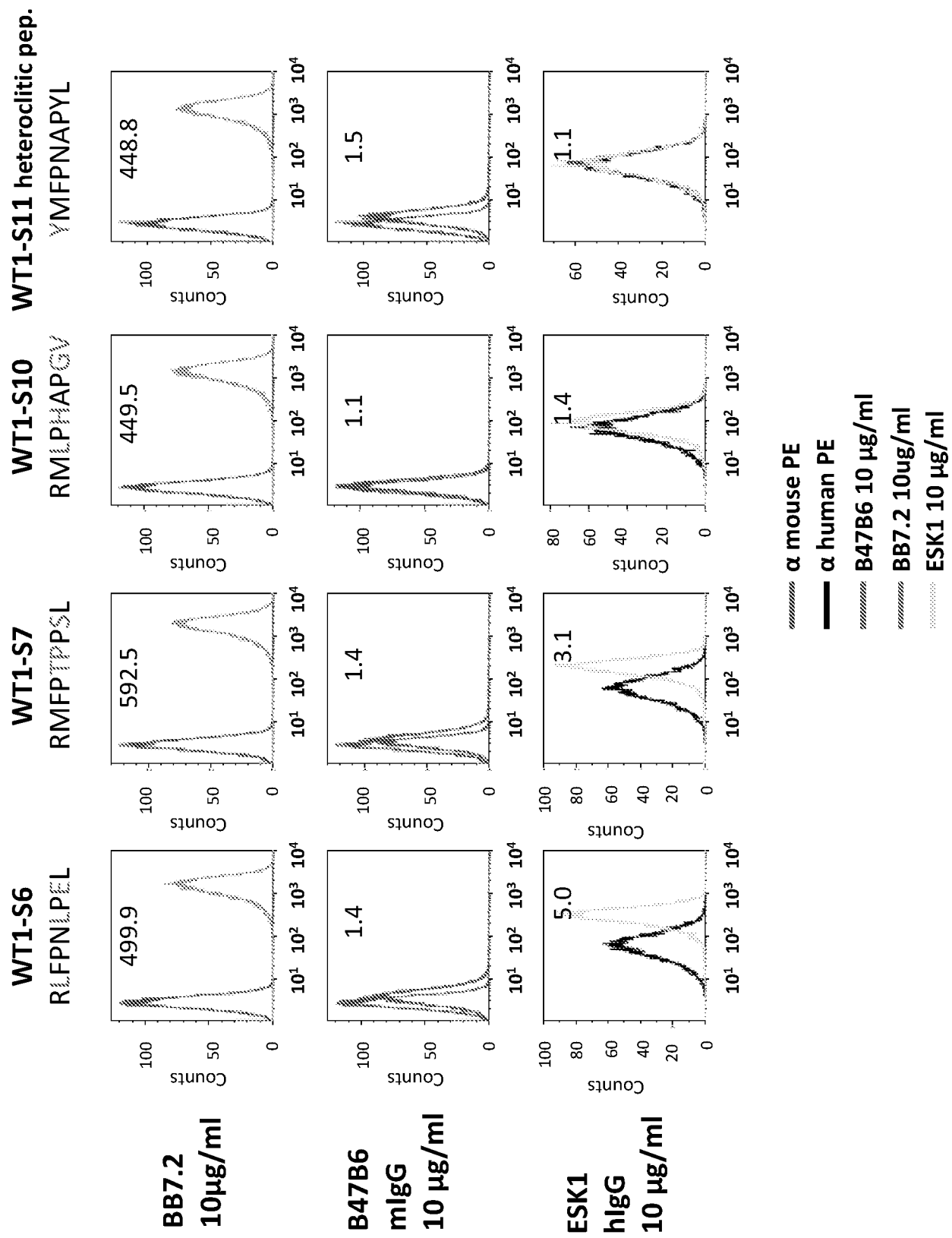


Figure 32

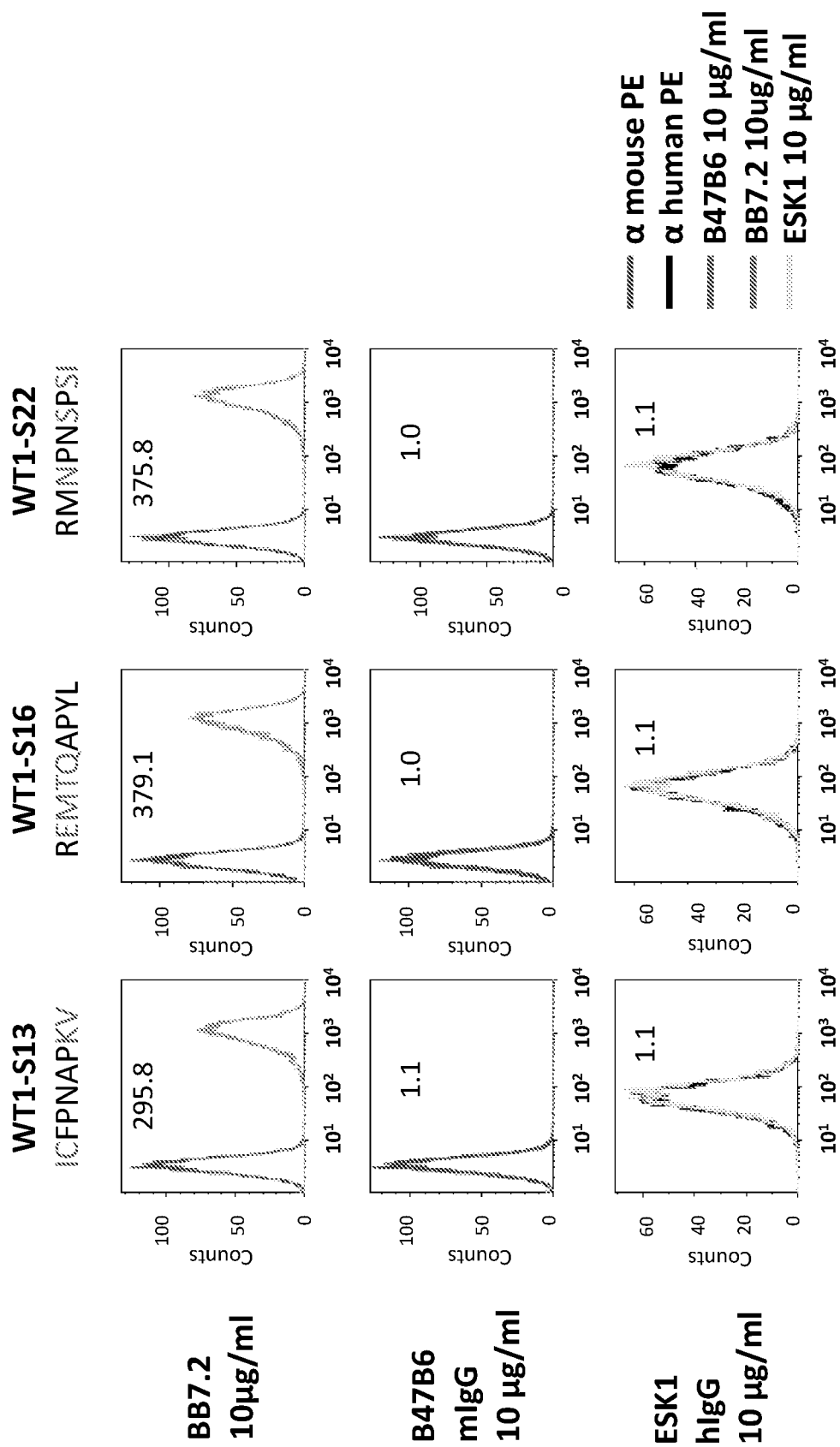
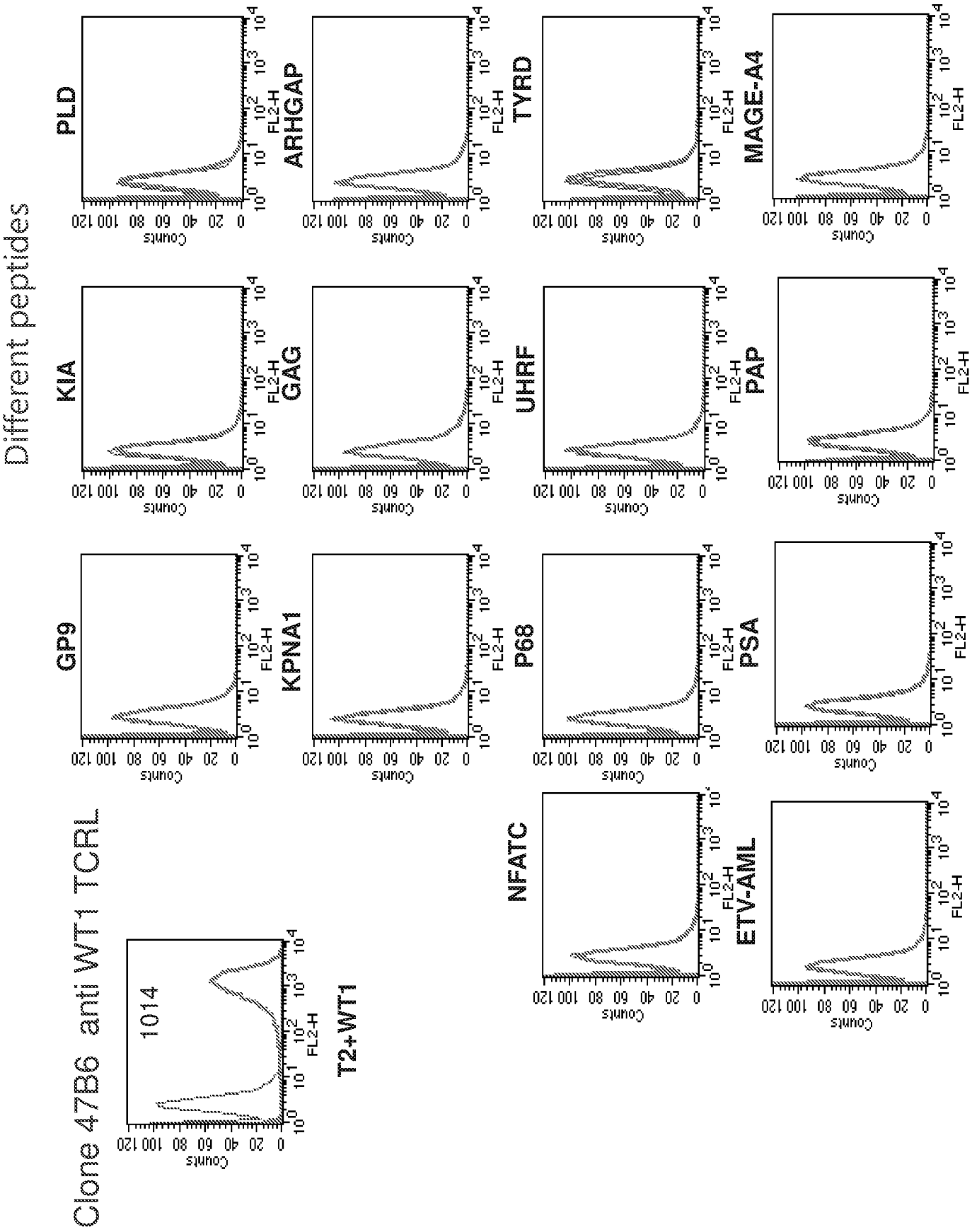
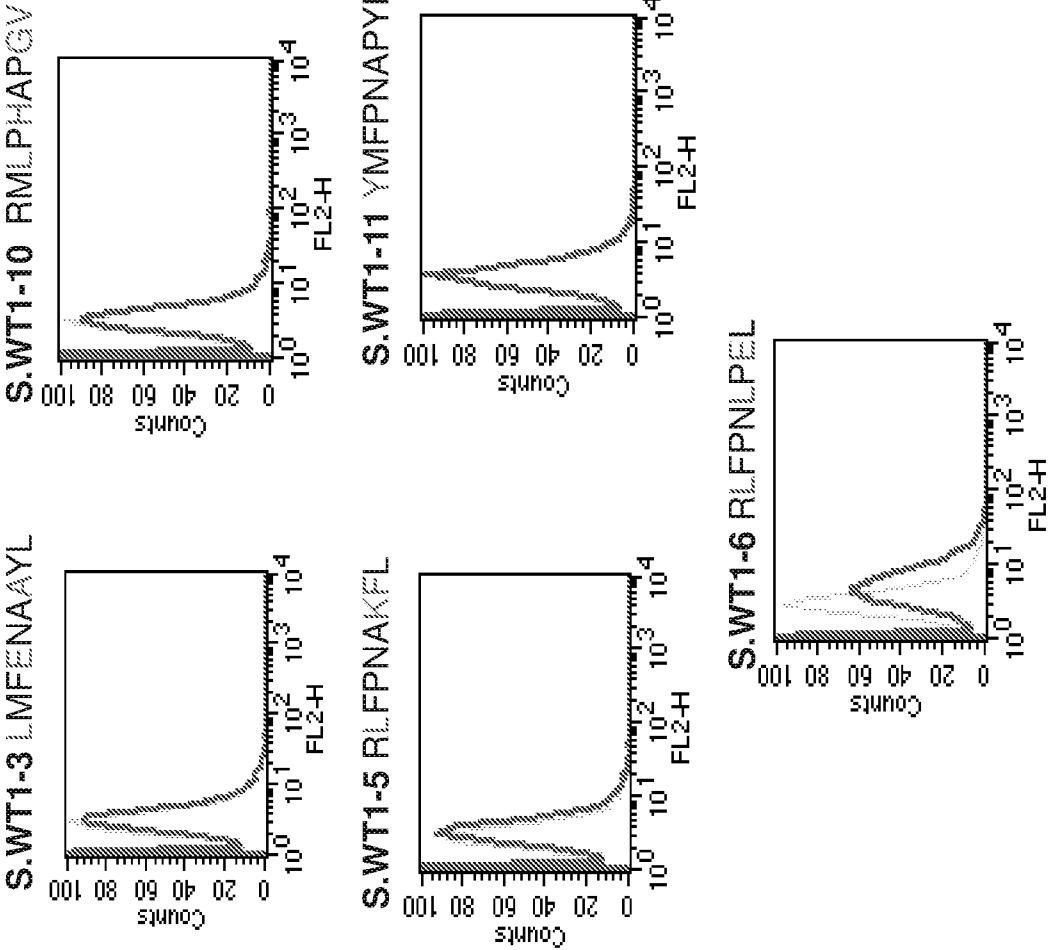


Figure 32 - continued



WT1 Similar peptides



Anti-WT1 TCRL binds only WT1 loaded cells. It didn't bind other peptides (14 different peptides+5 similar peptides were analyzed)

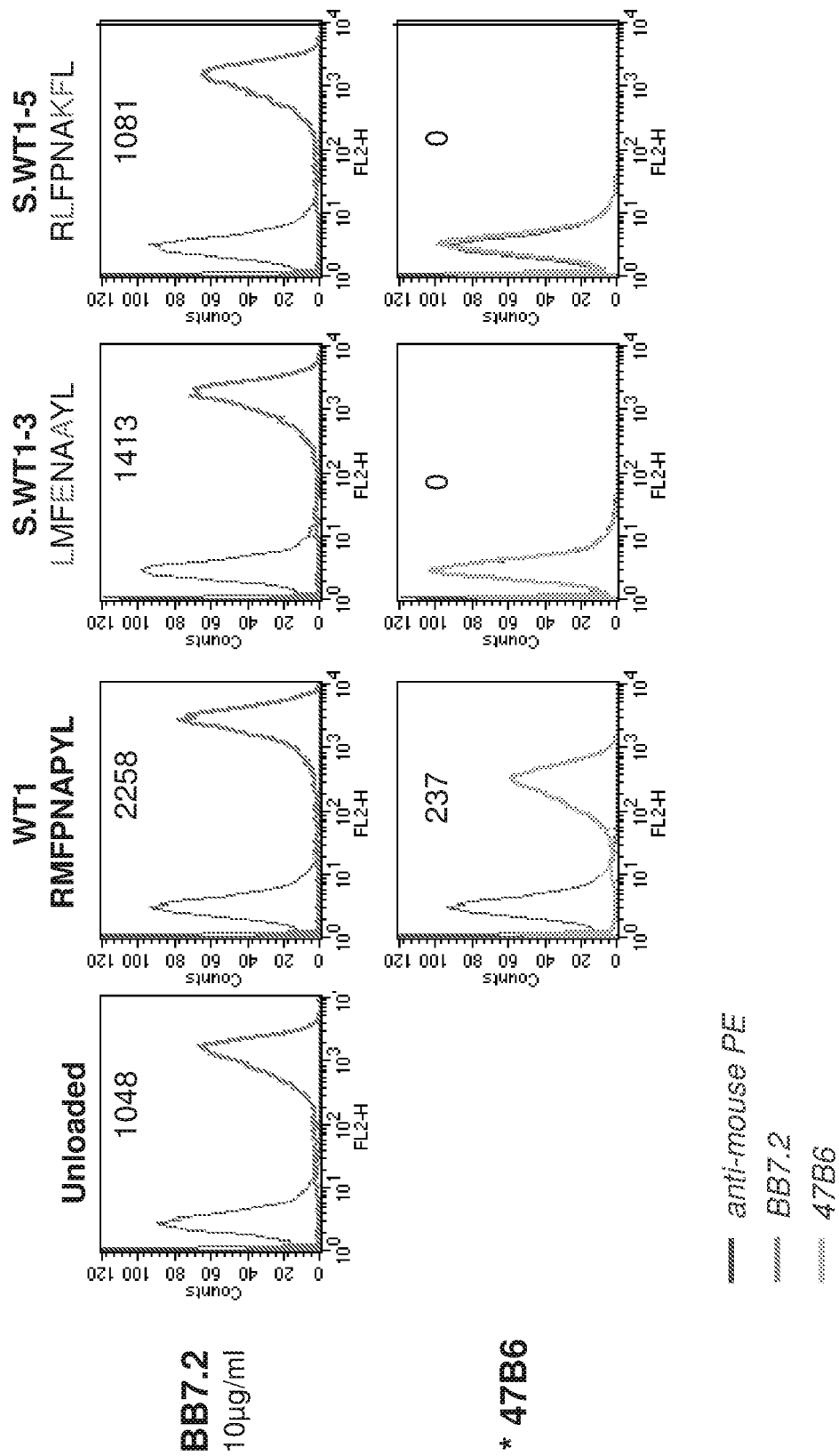


Figure 34

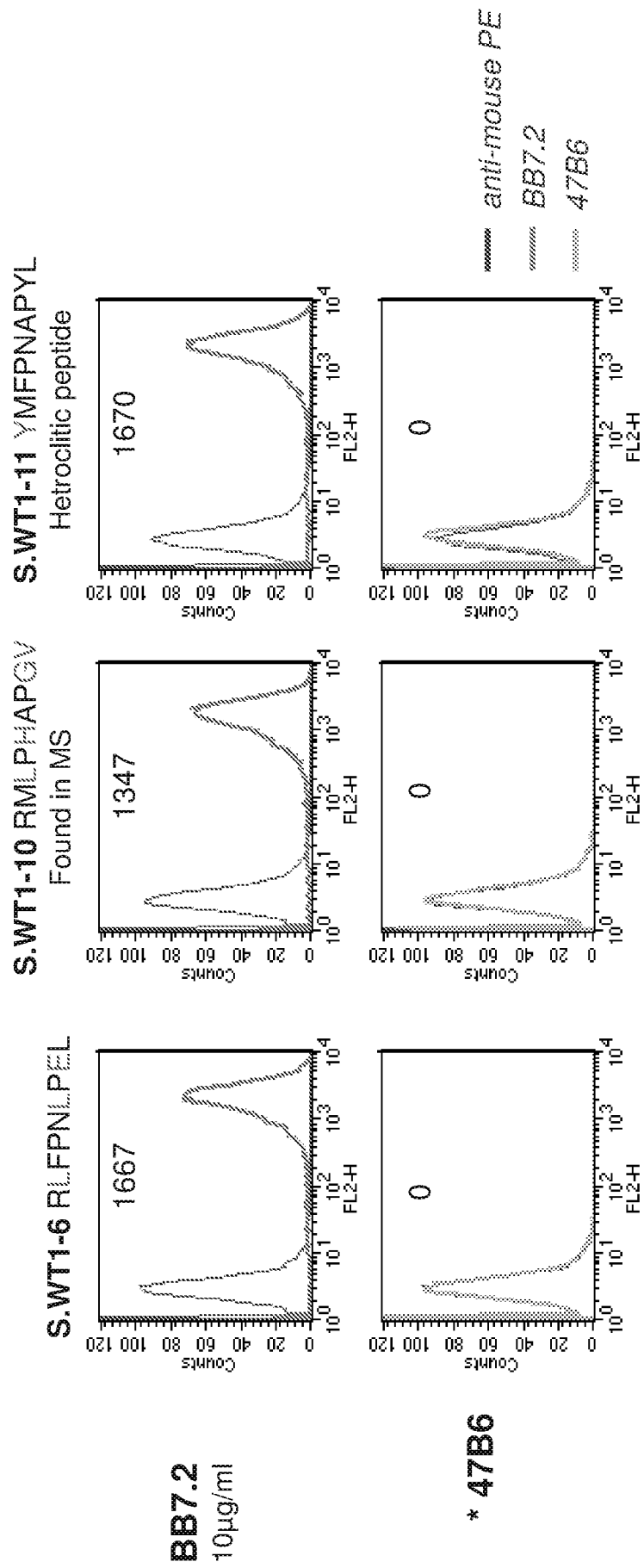
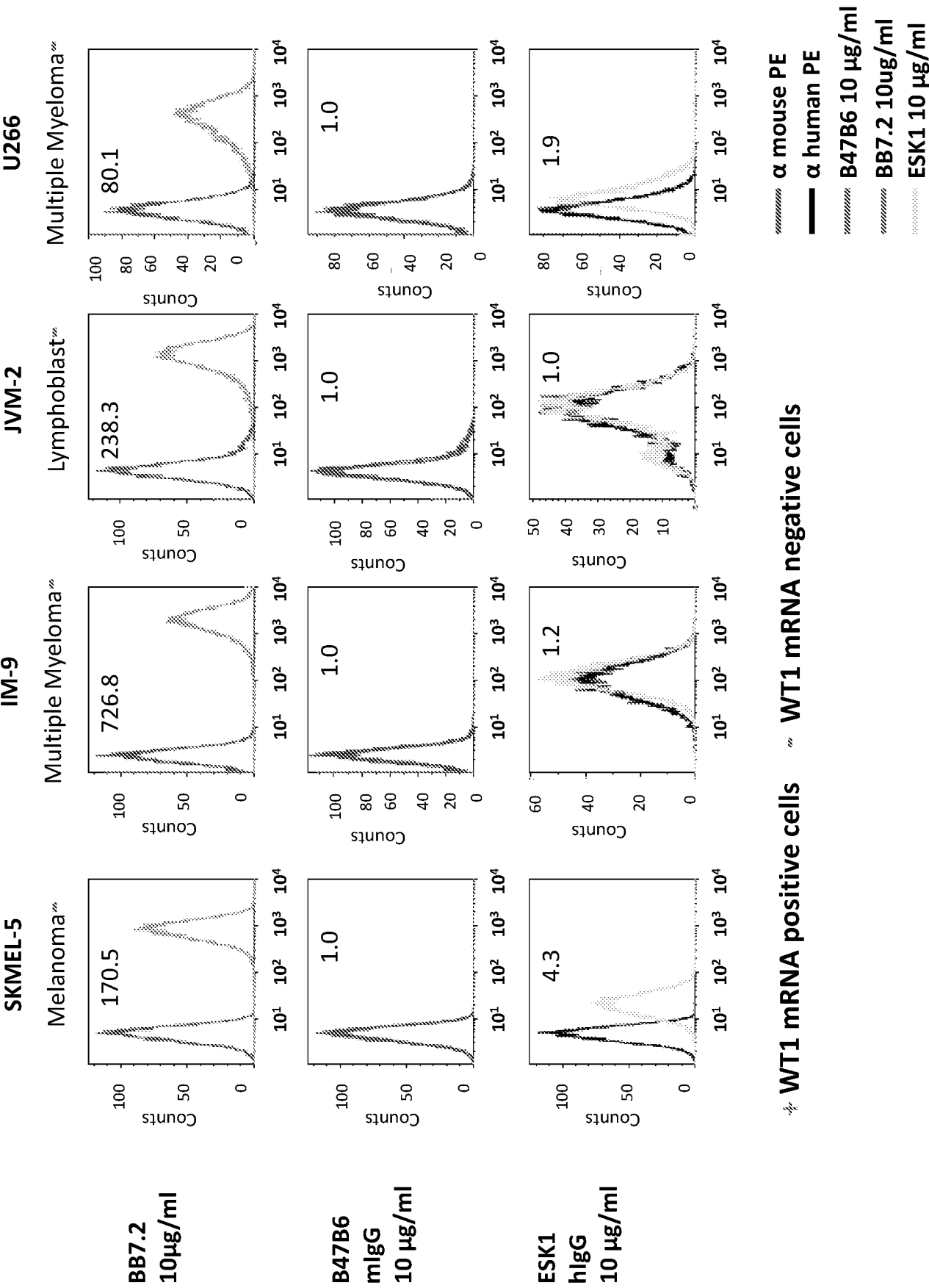


Figure 34 - continued



Figure 35



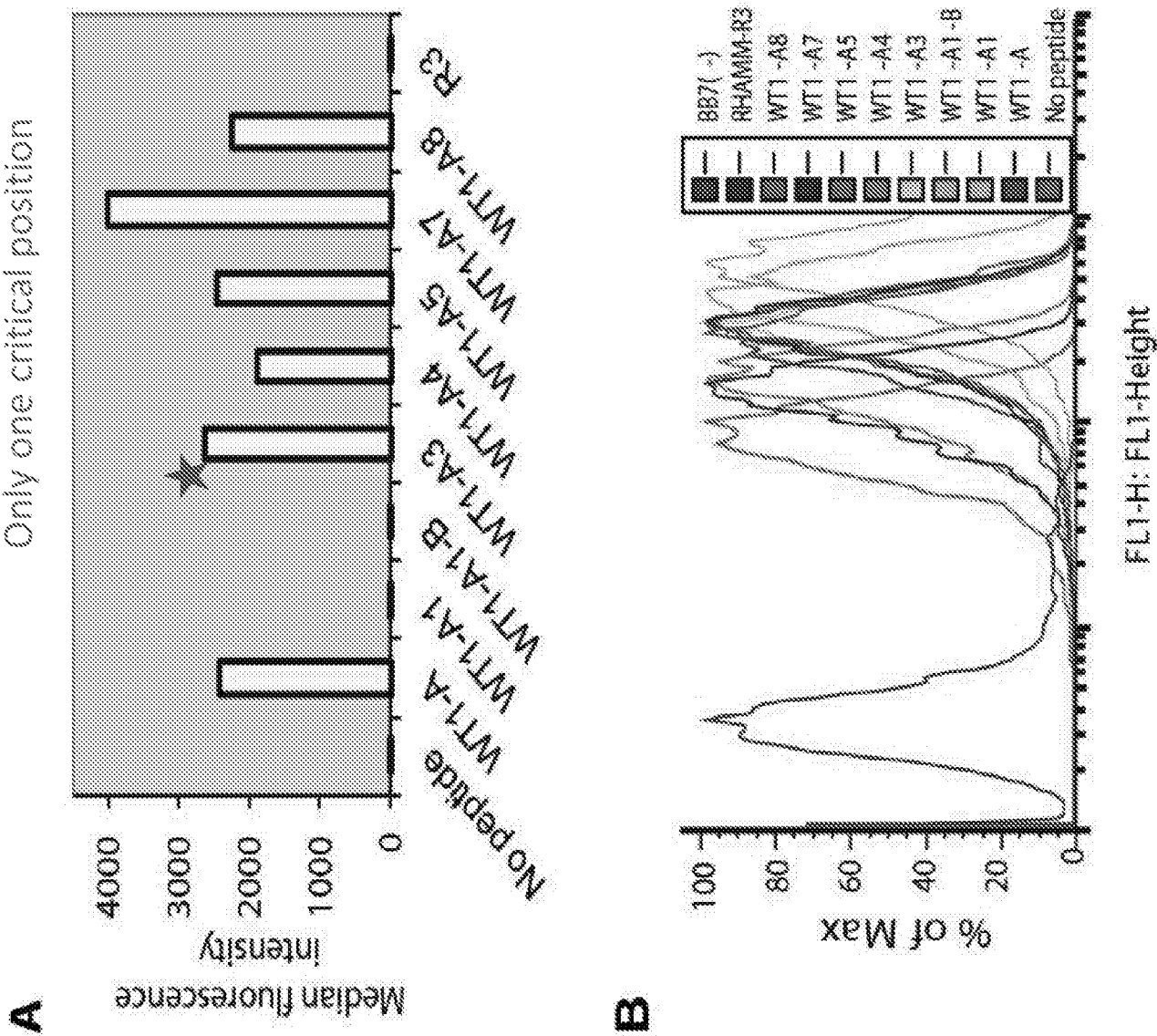


47B6 MFI

Cancer cell lines

** WT1-loaded T2 serve as positive control. Actual MFI reaches 1300.

Figure 36



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Figure 37

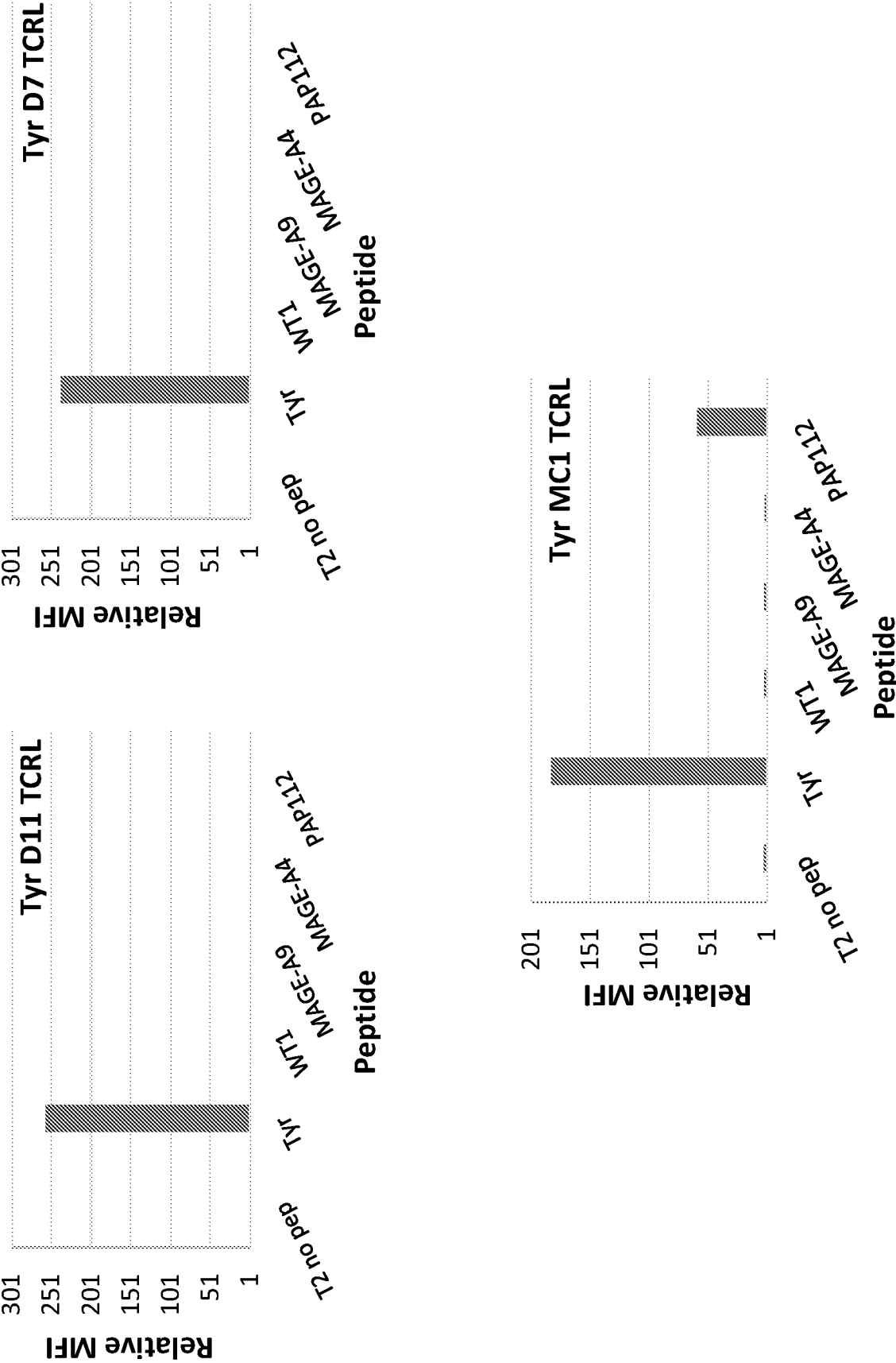
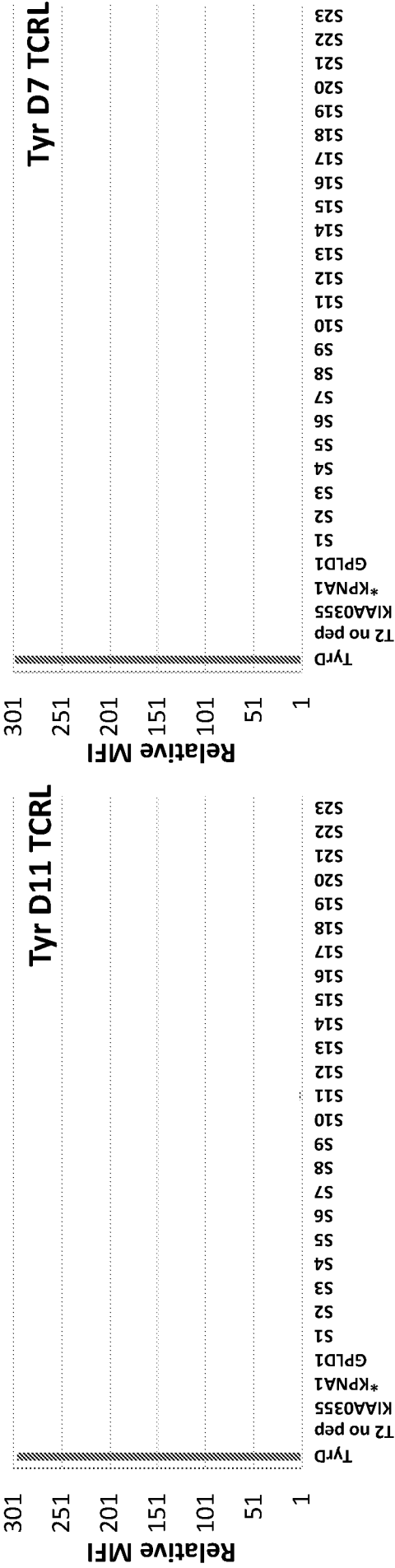
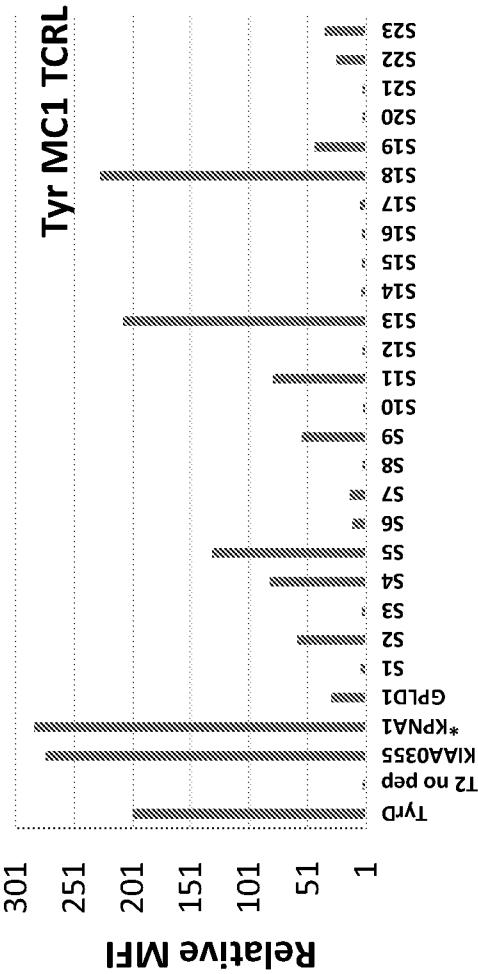


Figure 38



* Found by MS in normal tissues

Figure 39

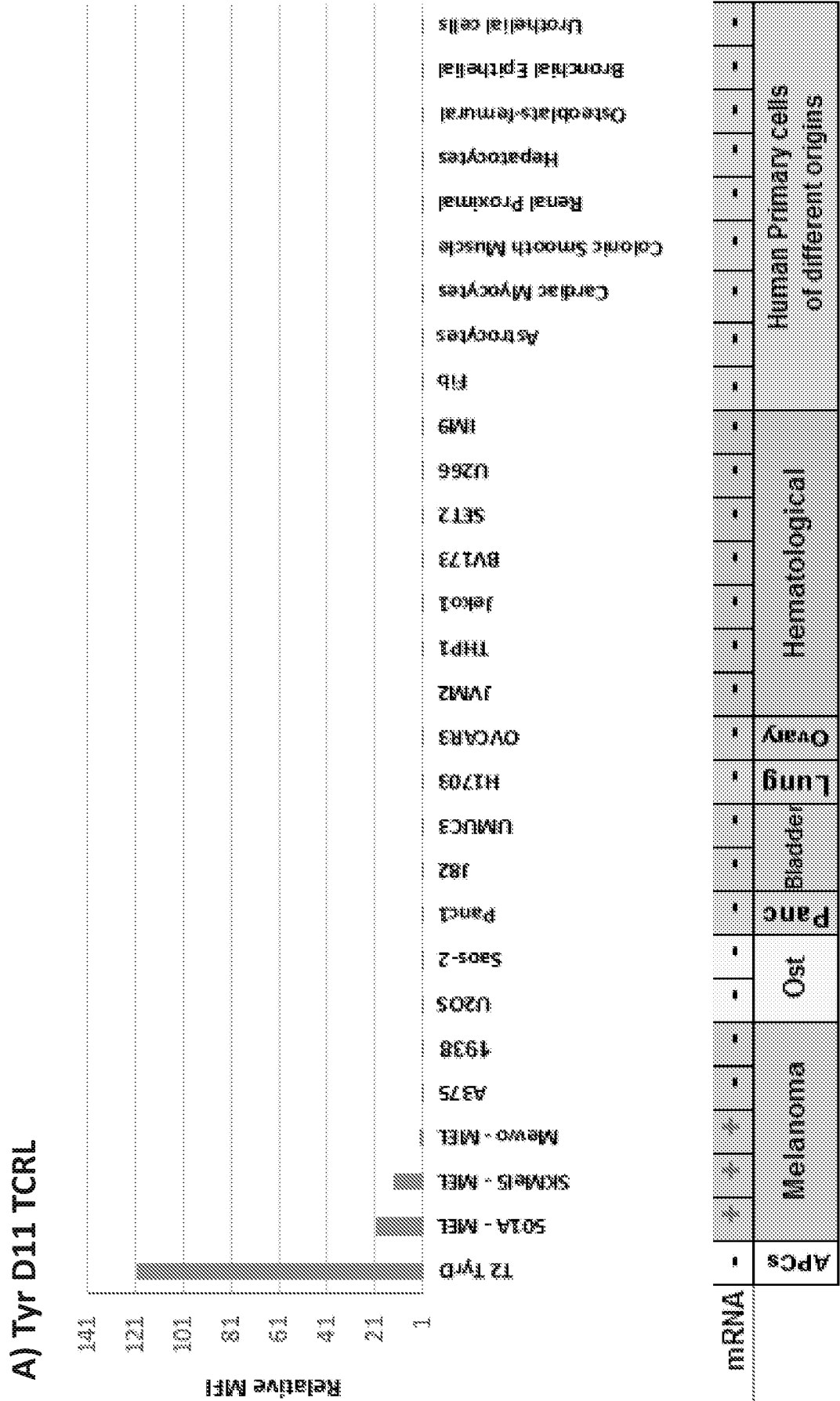


Figure 40A

B) Tyr D7 TCRL



mRNA	Melanoma				Ost		Panc		Bladder		Lung	Ovary	Hematological						Human Primary cells of different origins					
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Figure 40B

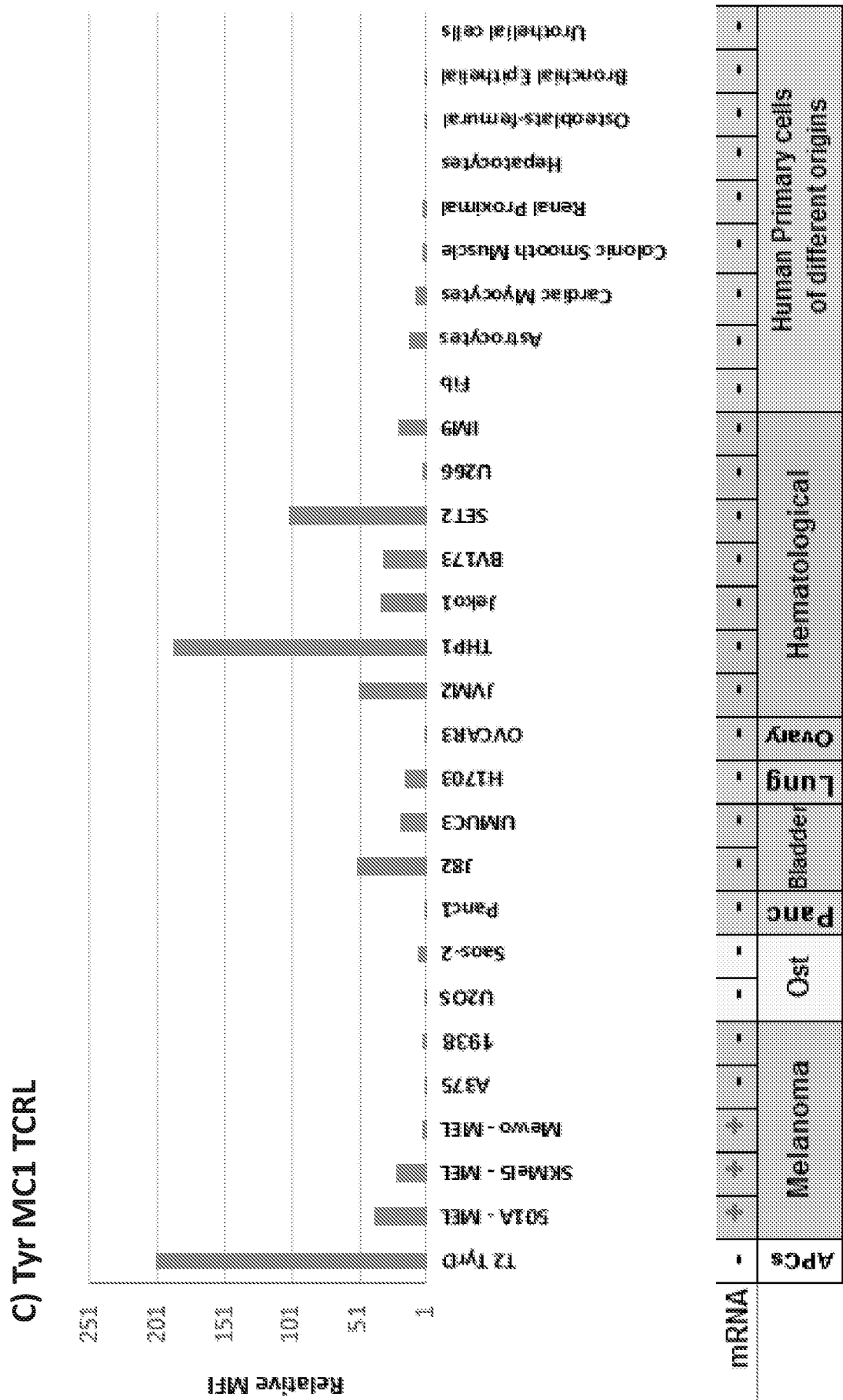


Figure 40C

Tyr D11 BS TCRL - killing assay on cell lines

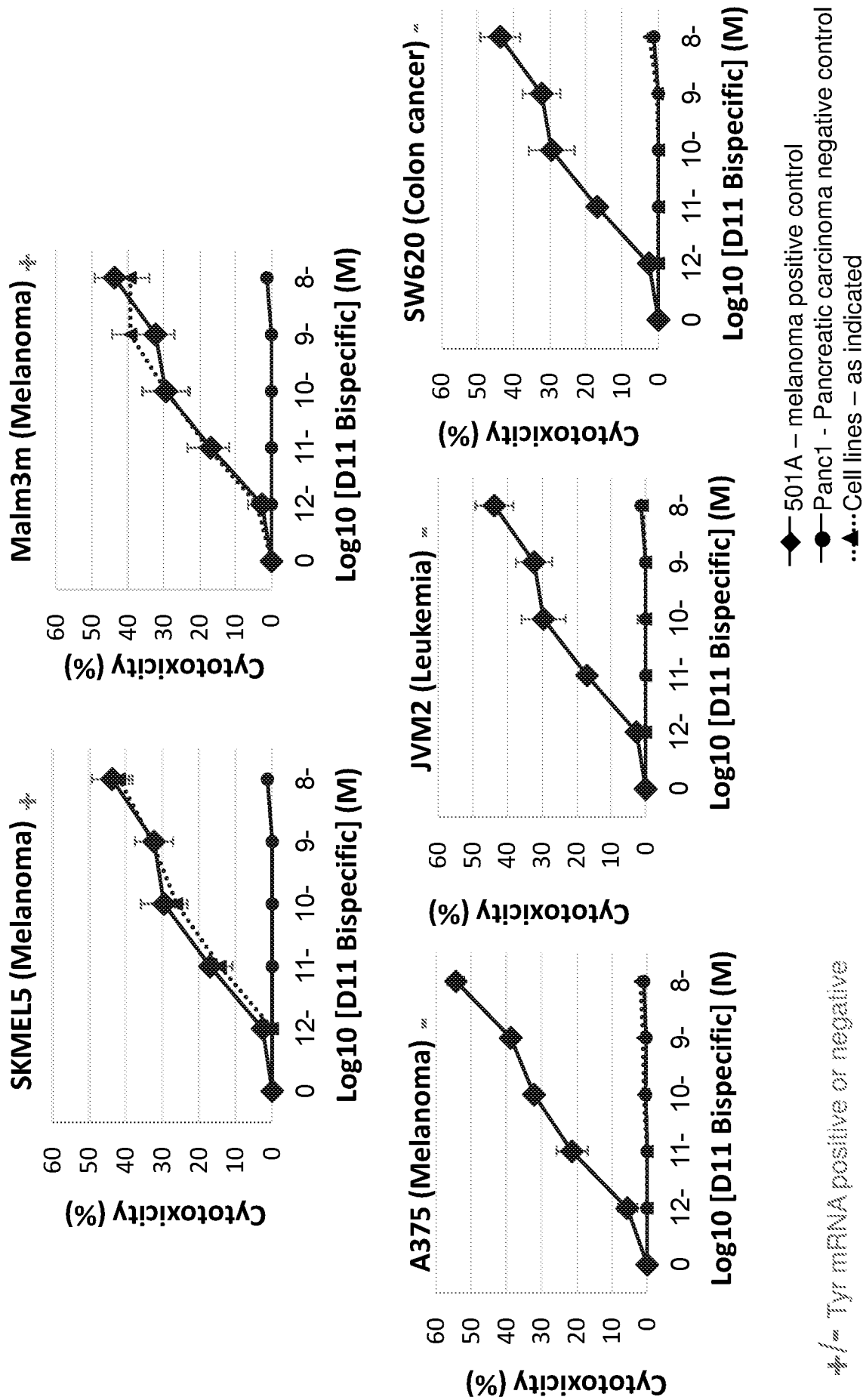


Figure 41

Tyr D11 BS TCRL - killing assay on normal primary cells

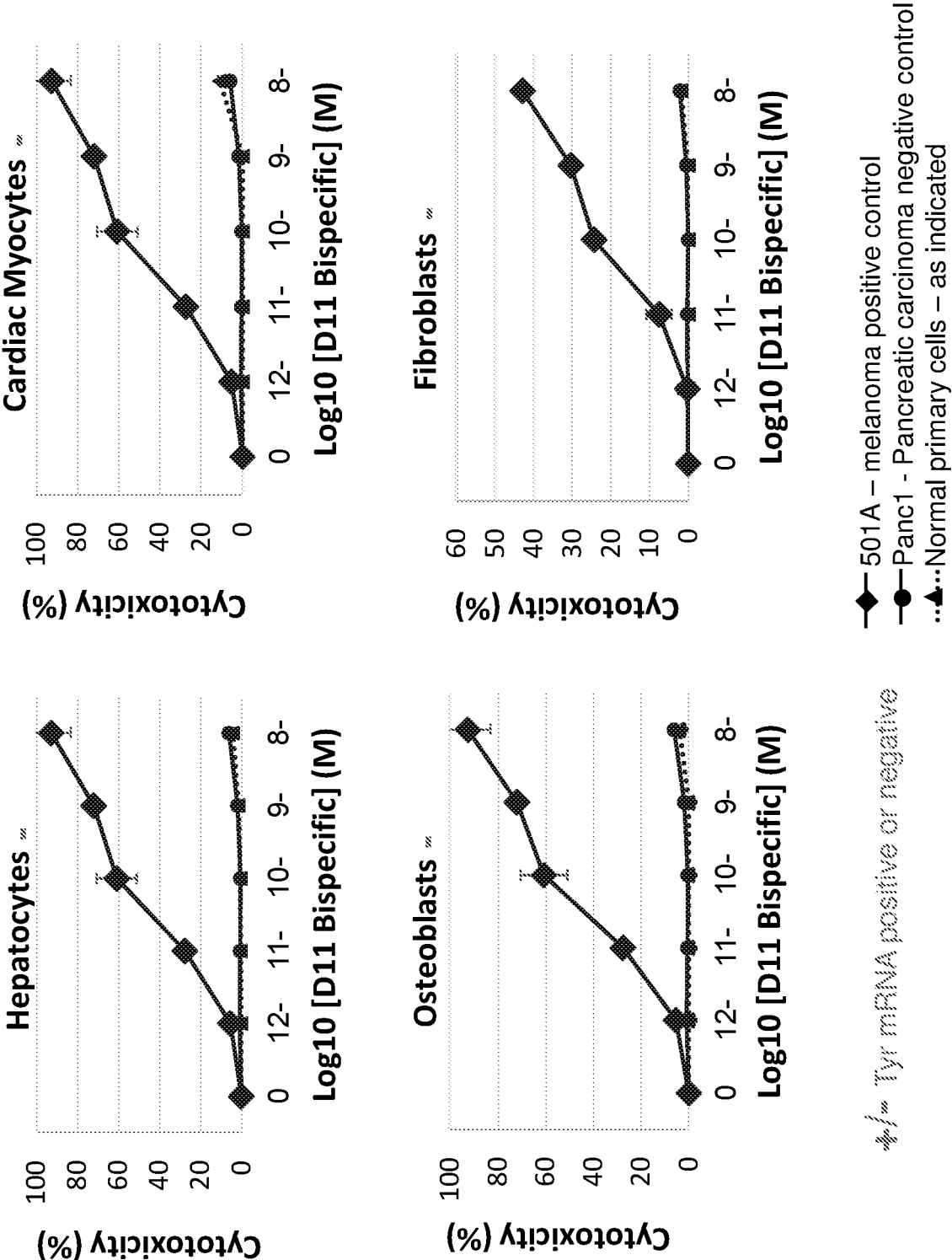


Figure 42

Tyr D7 BS TCRL - killing assay on cell lines

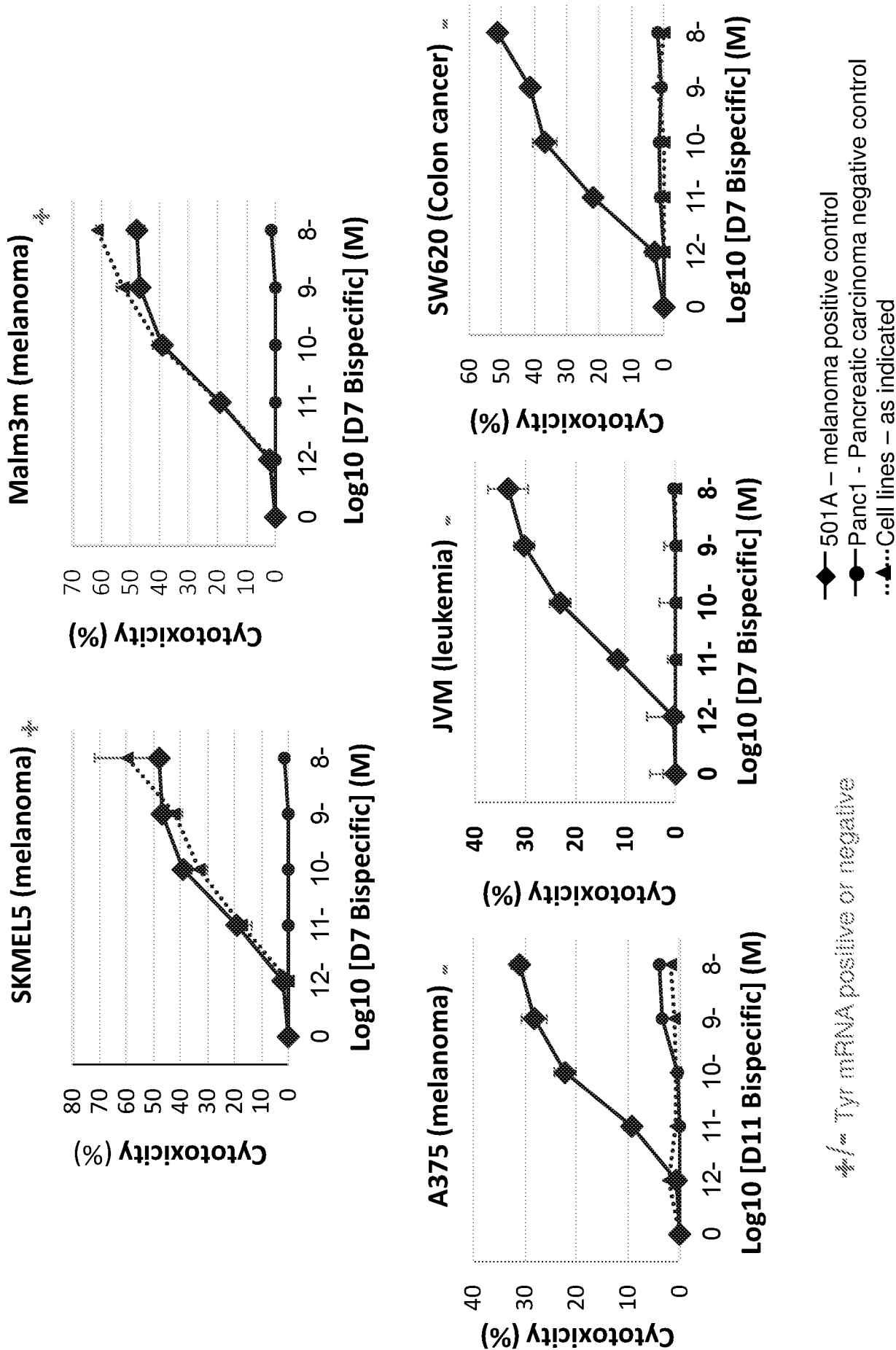


Figure 43

Tyr D7 BS TCRL - killing assay on normal primary cells

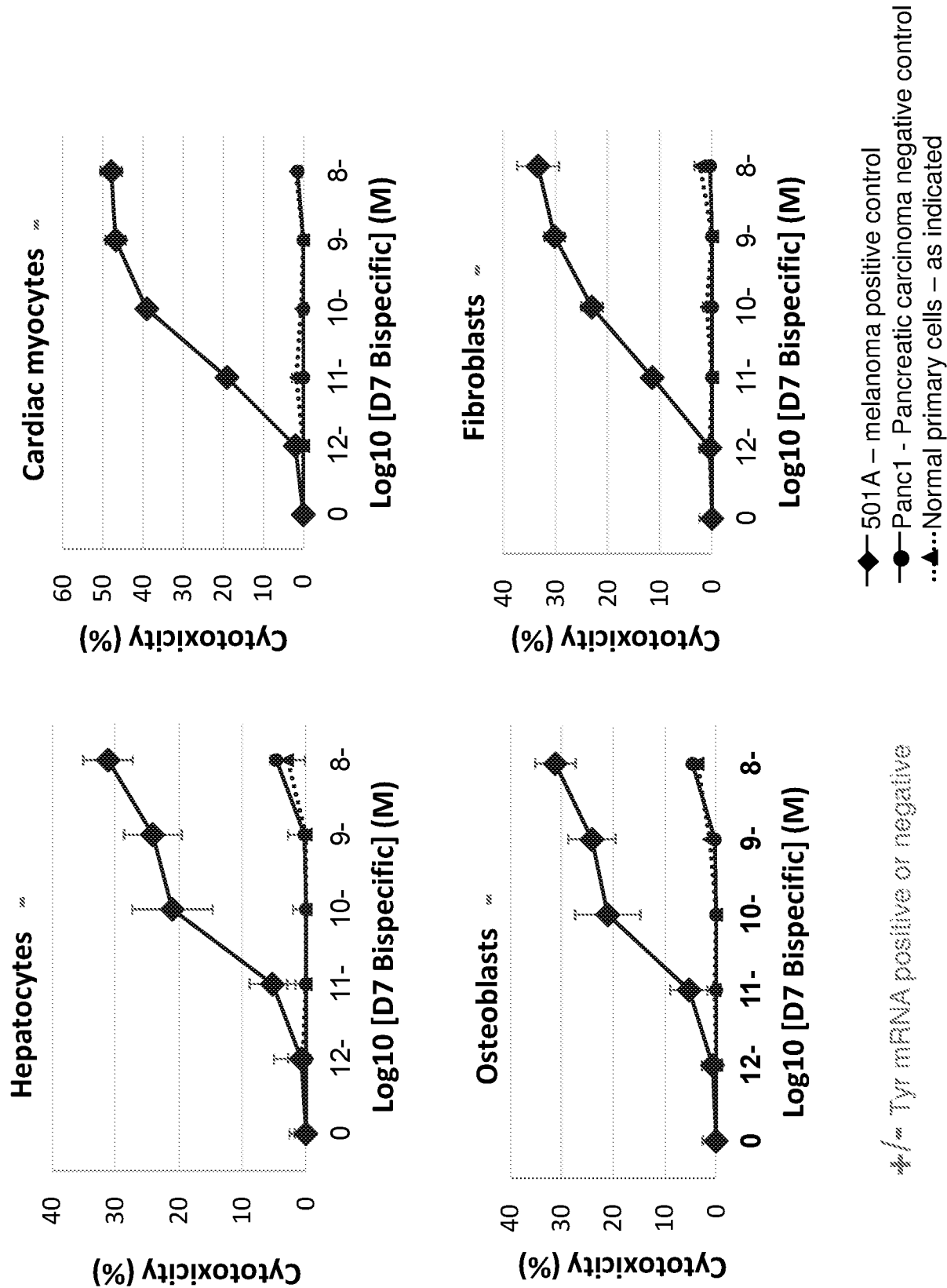


Figure 44

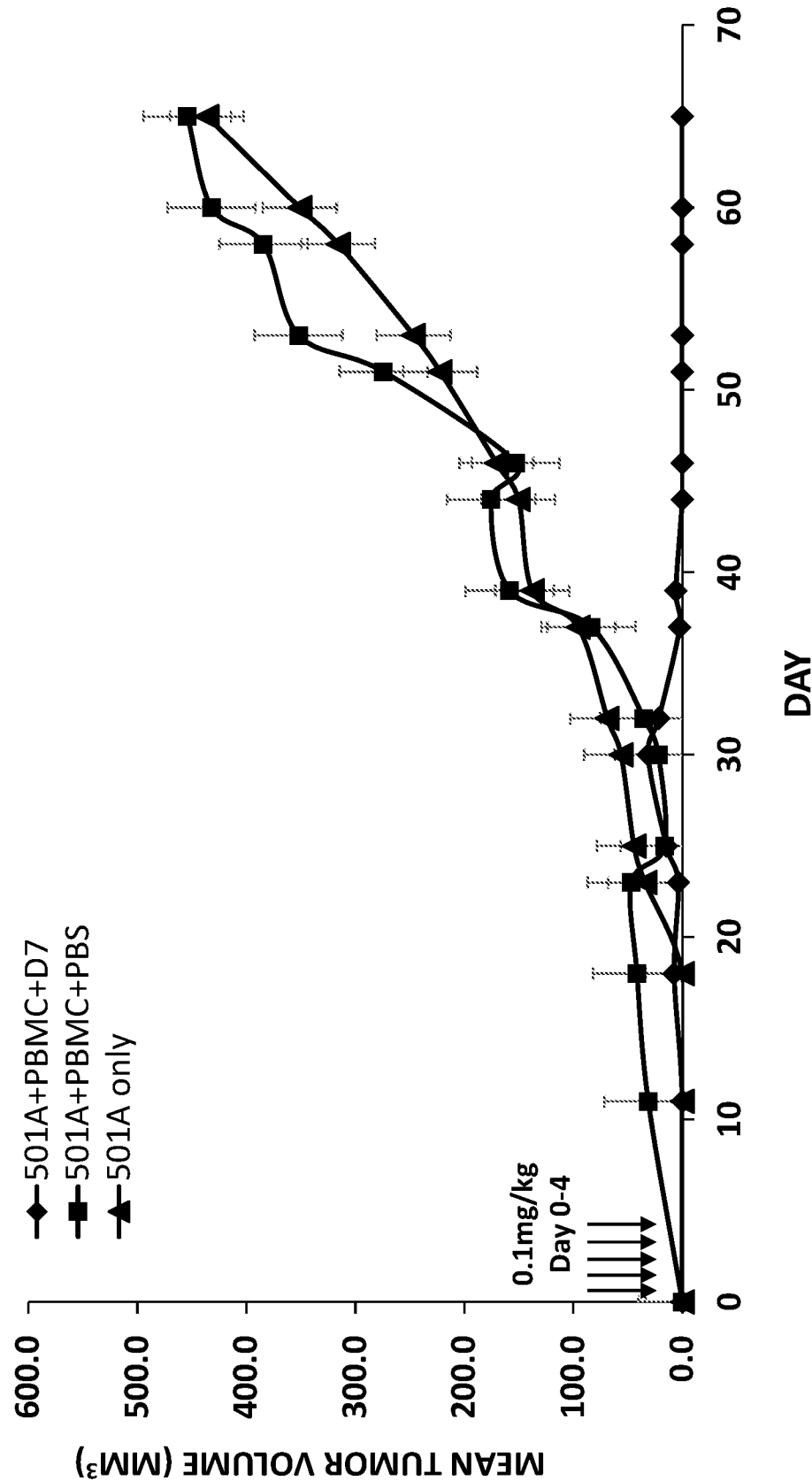


Figure 45

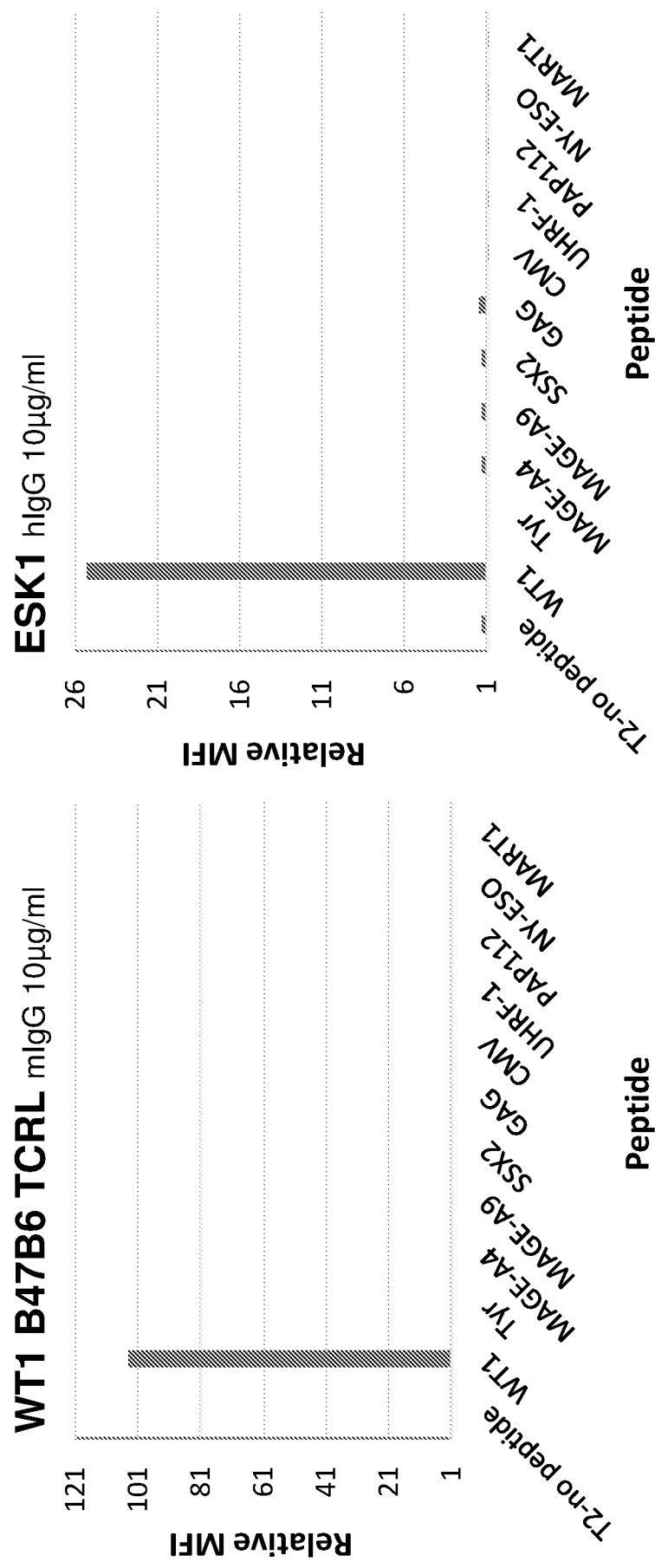


Figure 46

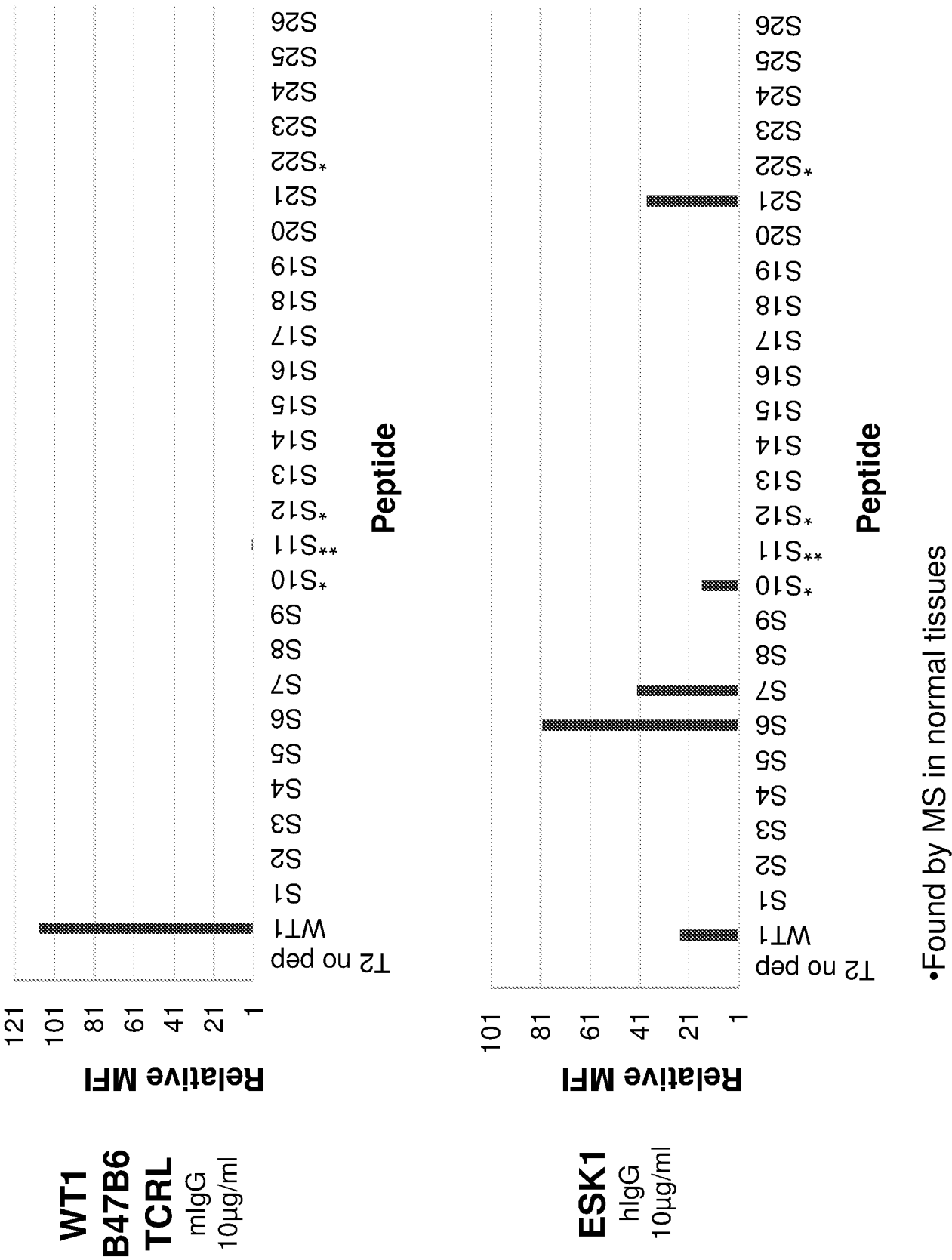
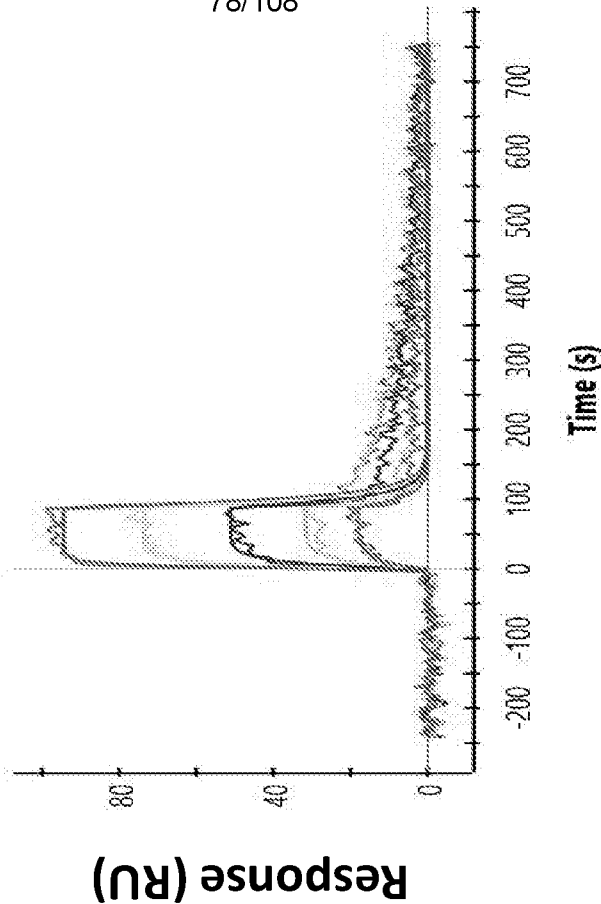


Figure 47

ESK1 – 200nM



B47B6 – 5nM

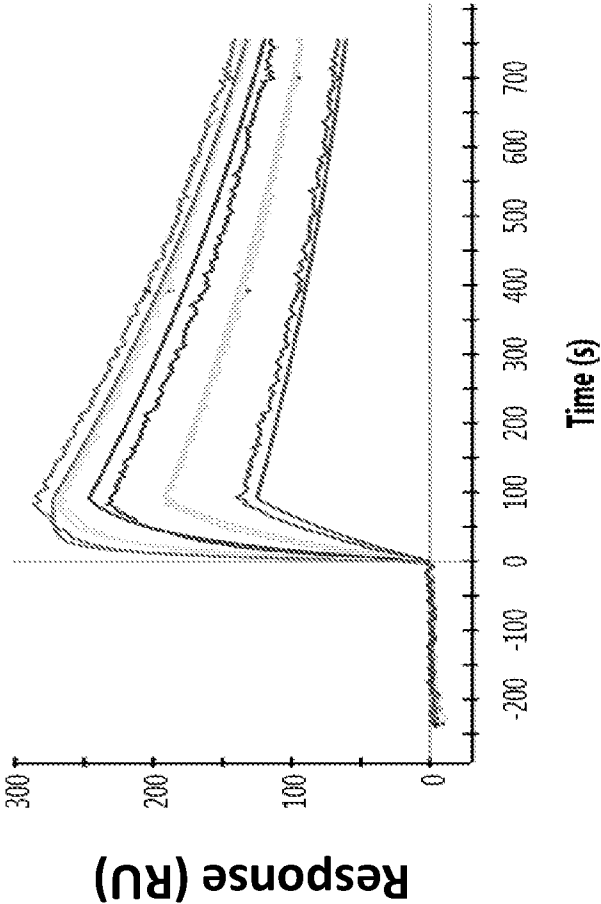


Figure 48

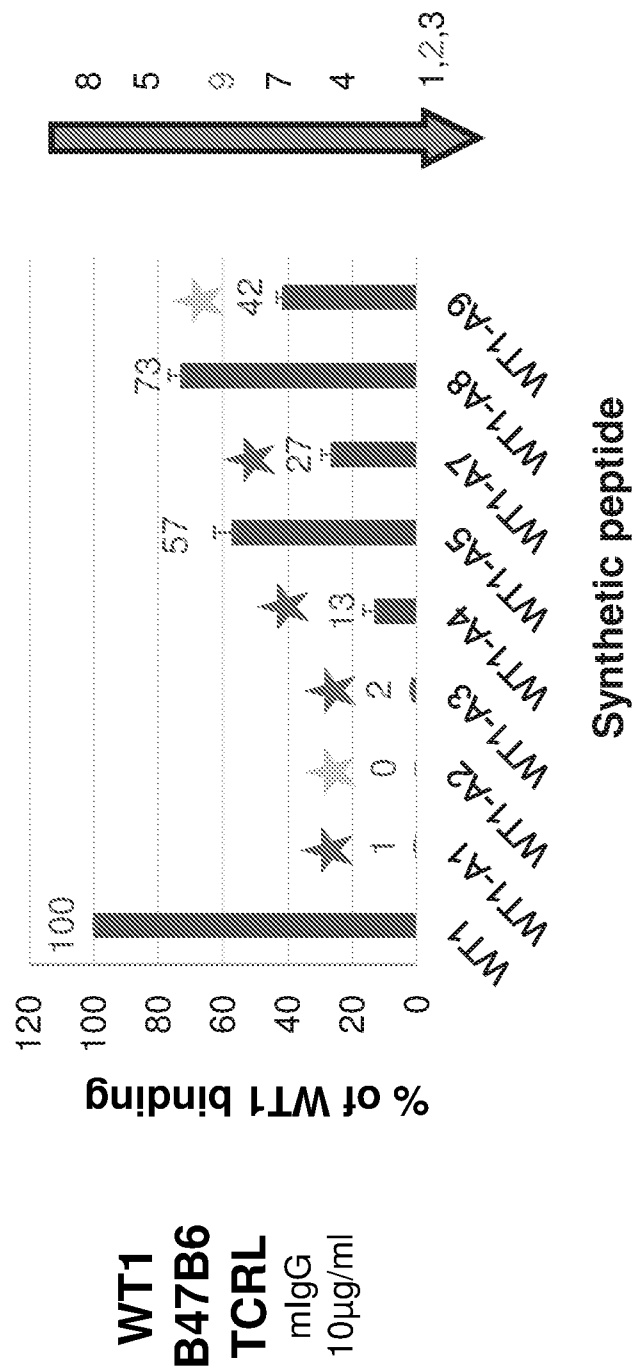
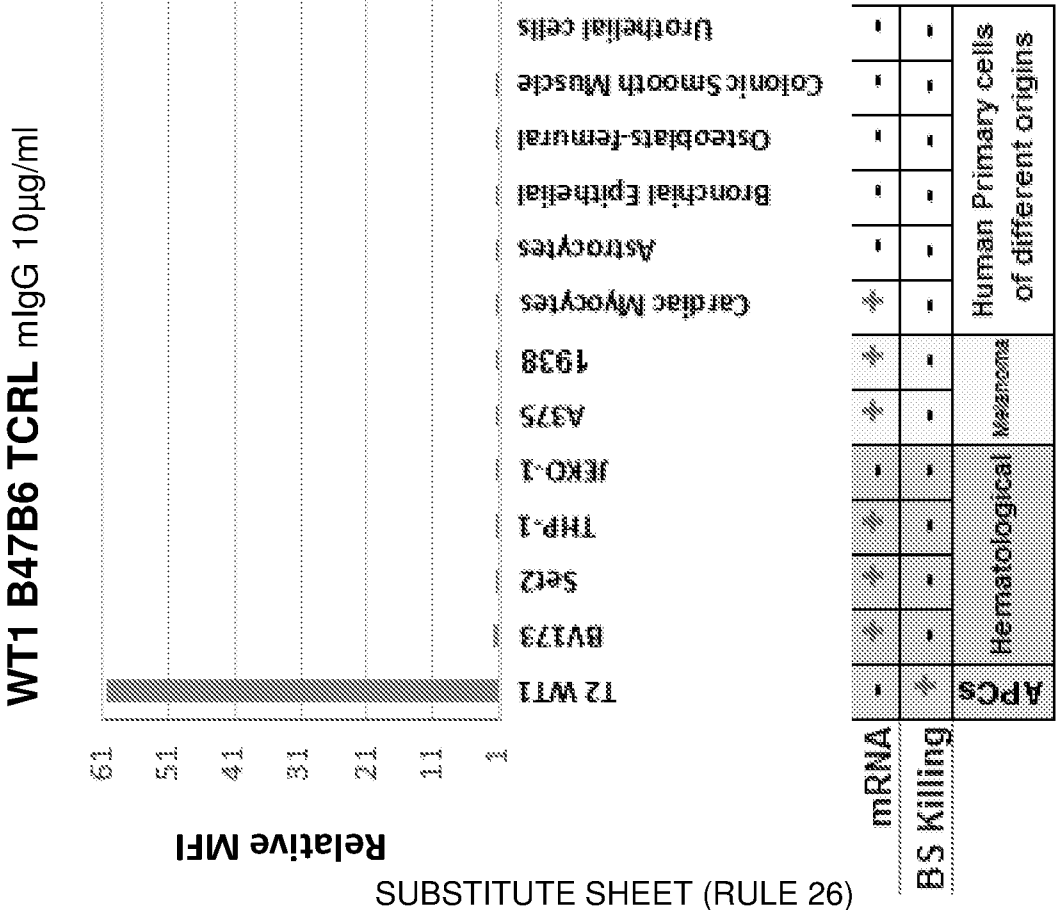
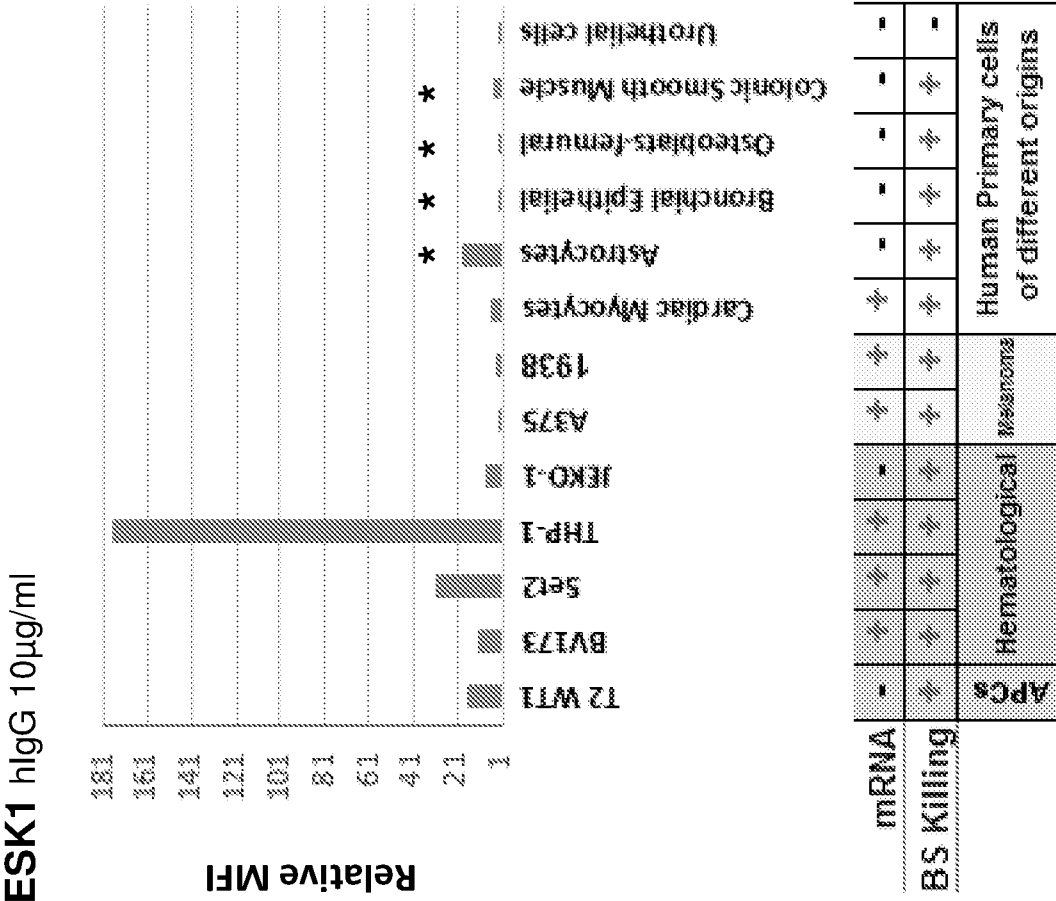


Figure 49



* ESK1-BS mediates killing of WT1-mRNA negative cell lines

Figure 50

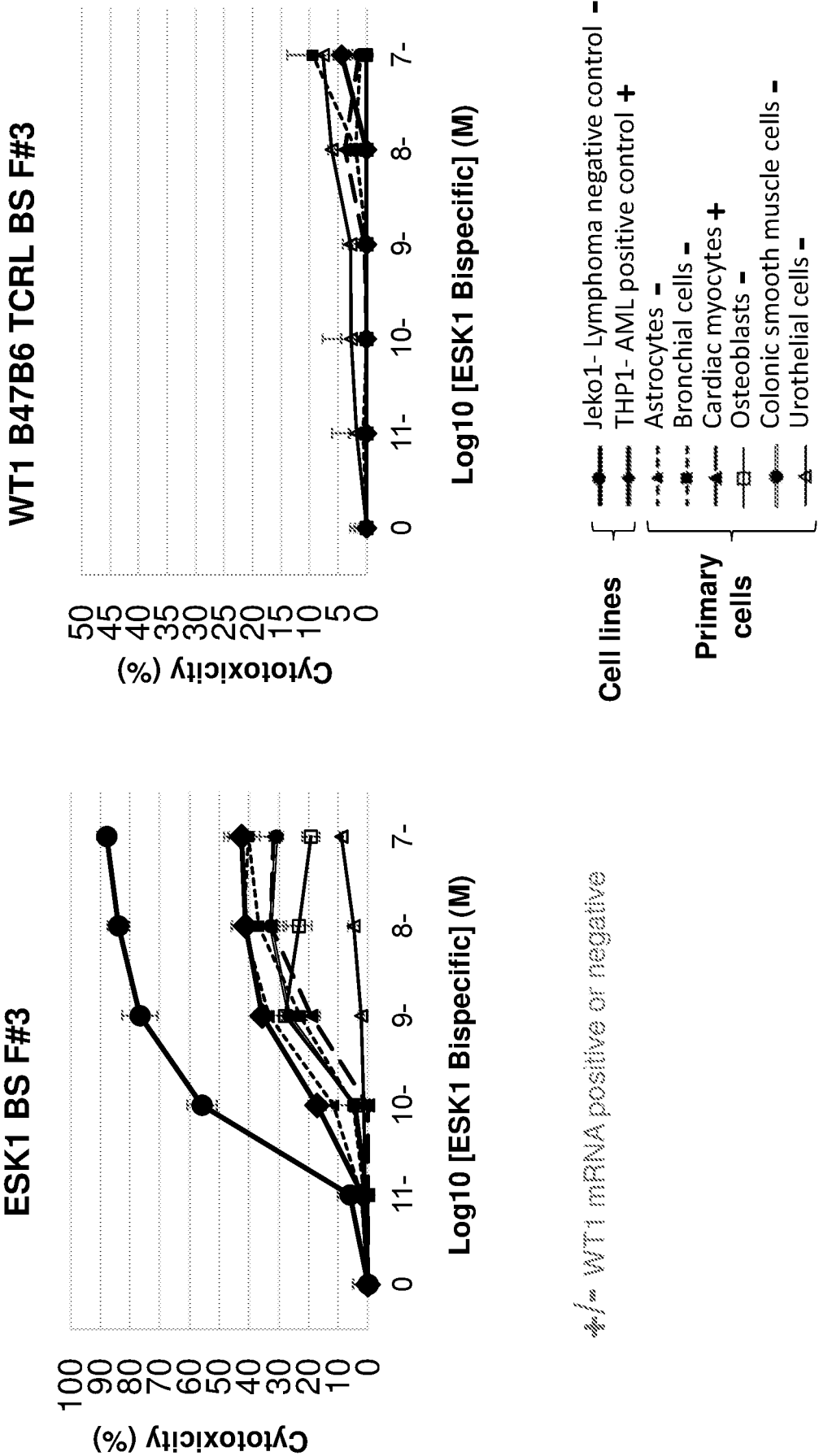
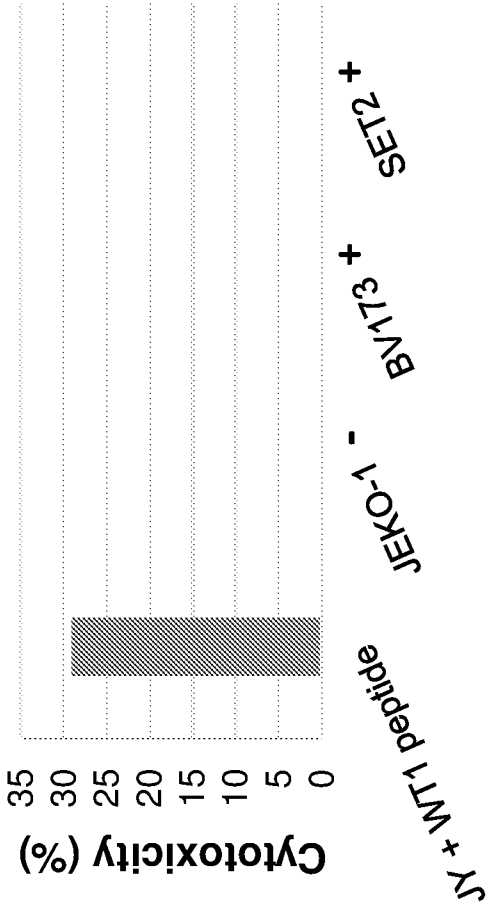
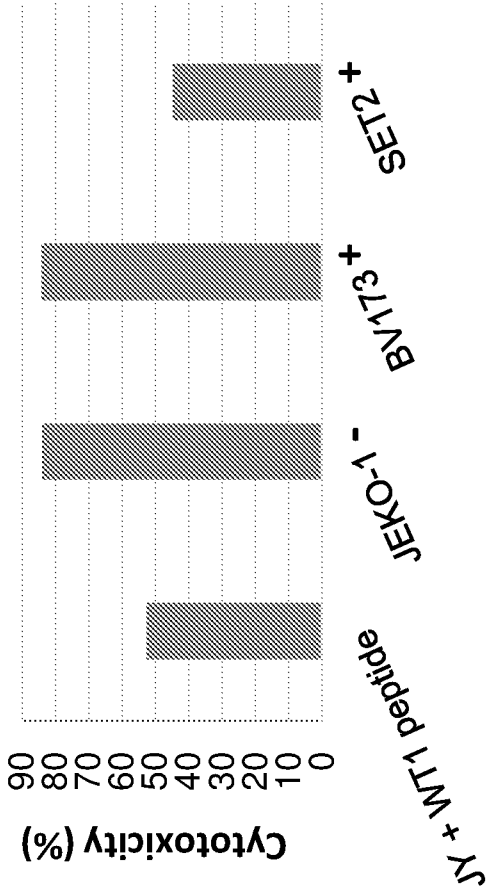


Figure 51A

WT1 B47B6 TCRL BS F#3



WT1 ESK1 BS F#3



+/- WT1 mRNA positive or negative

Figure 51B

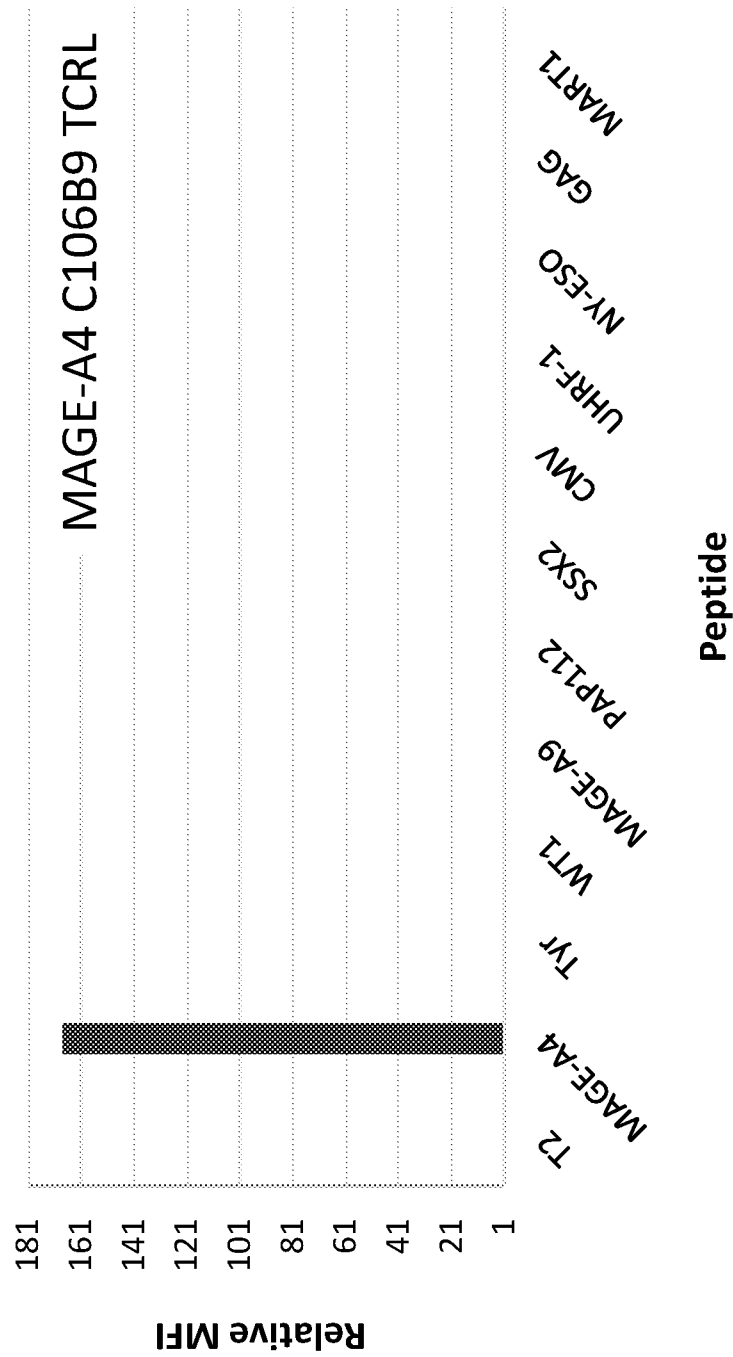
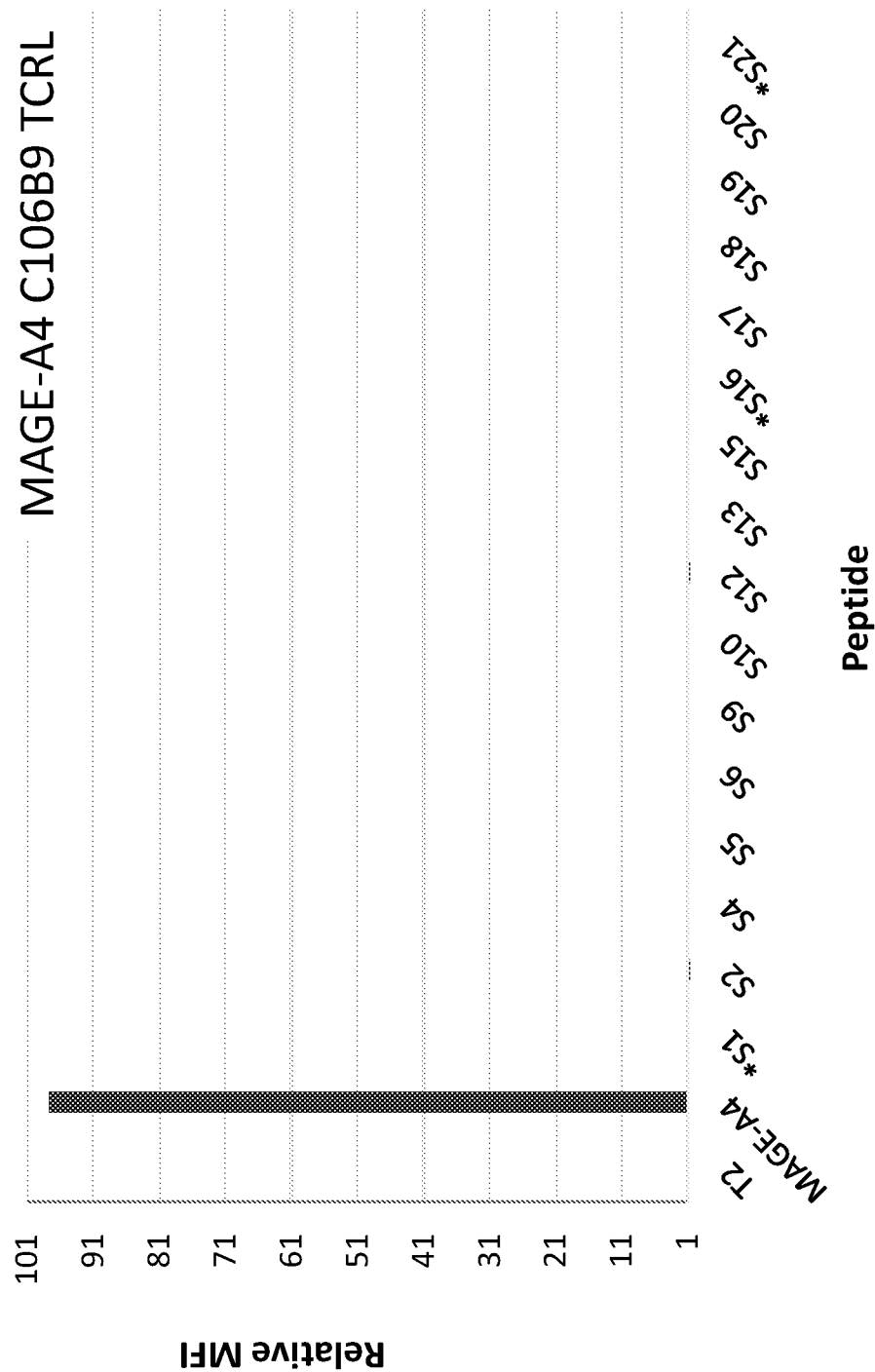


Figure 52



* Found by MS in normal tissues

Figure 53

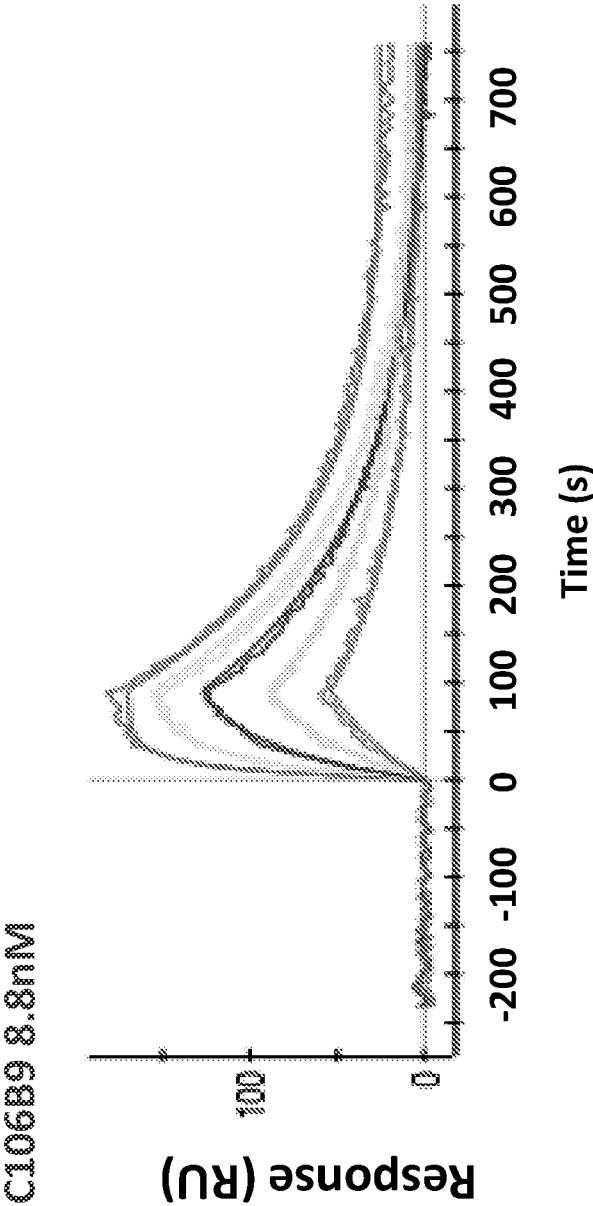


Figure 54

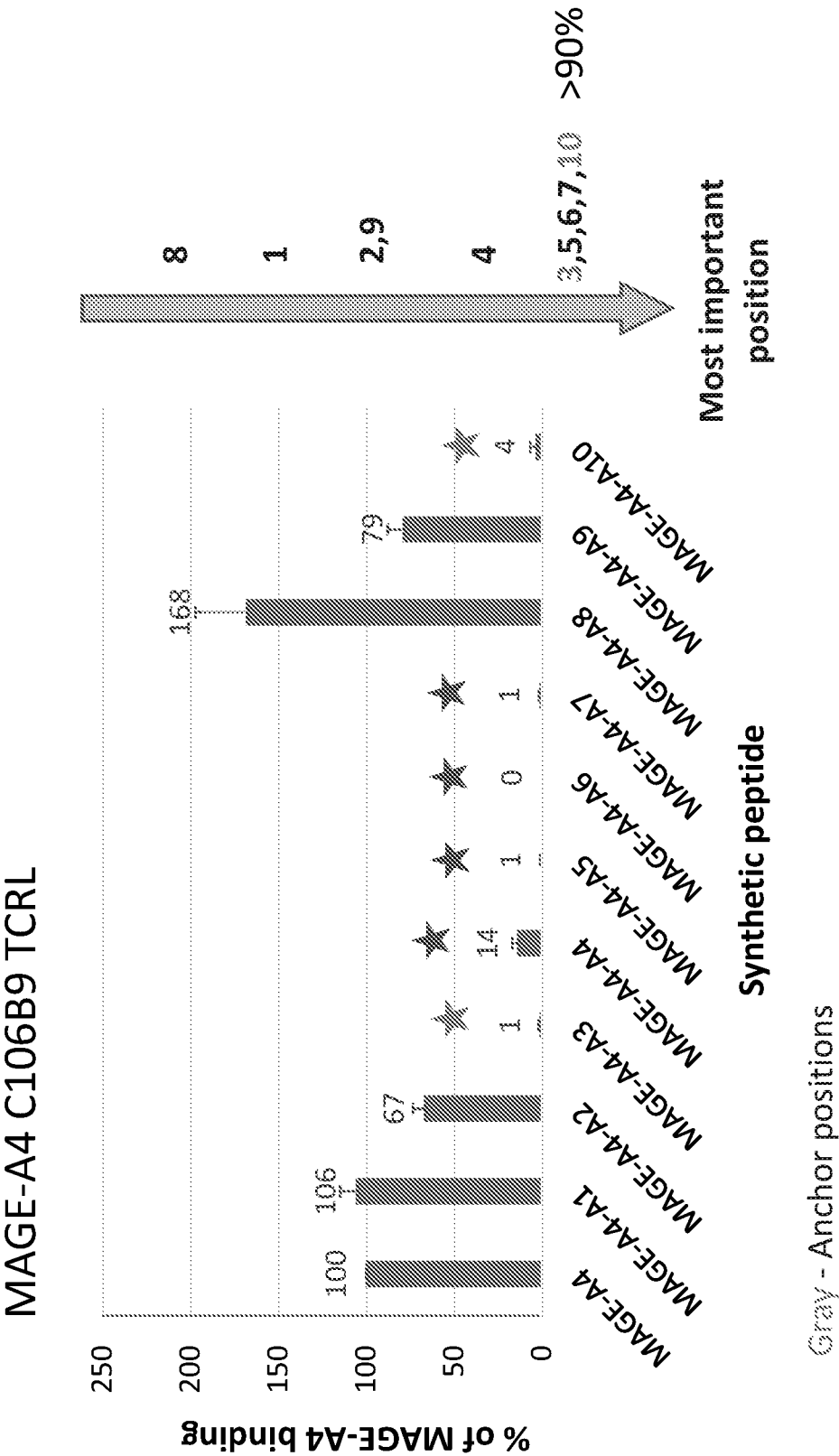


Figure 55

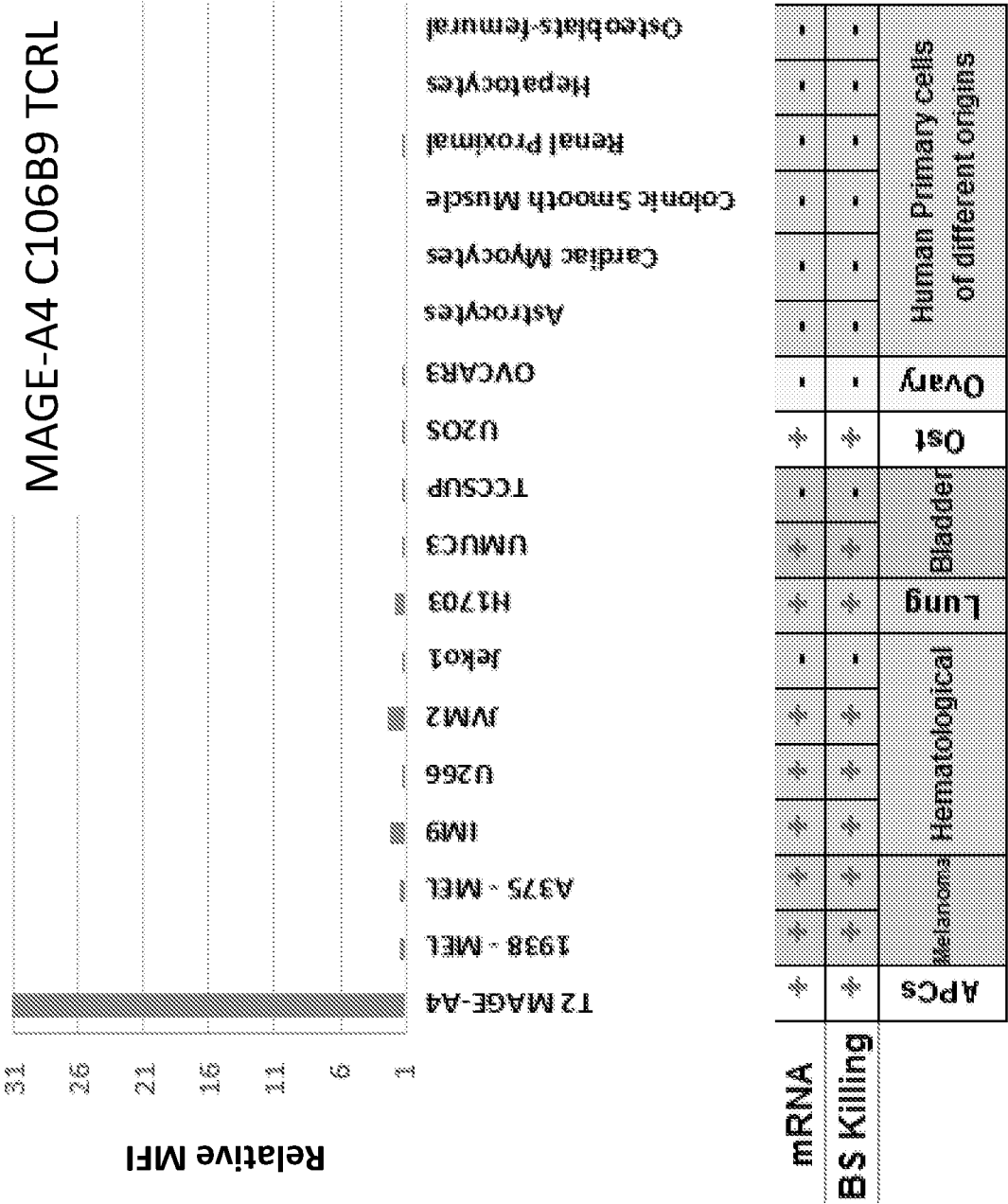


Figure 56

MAGE-A4 C106B9 BS TCRL - killing assay on cell lines

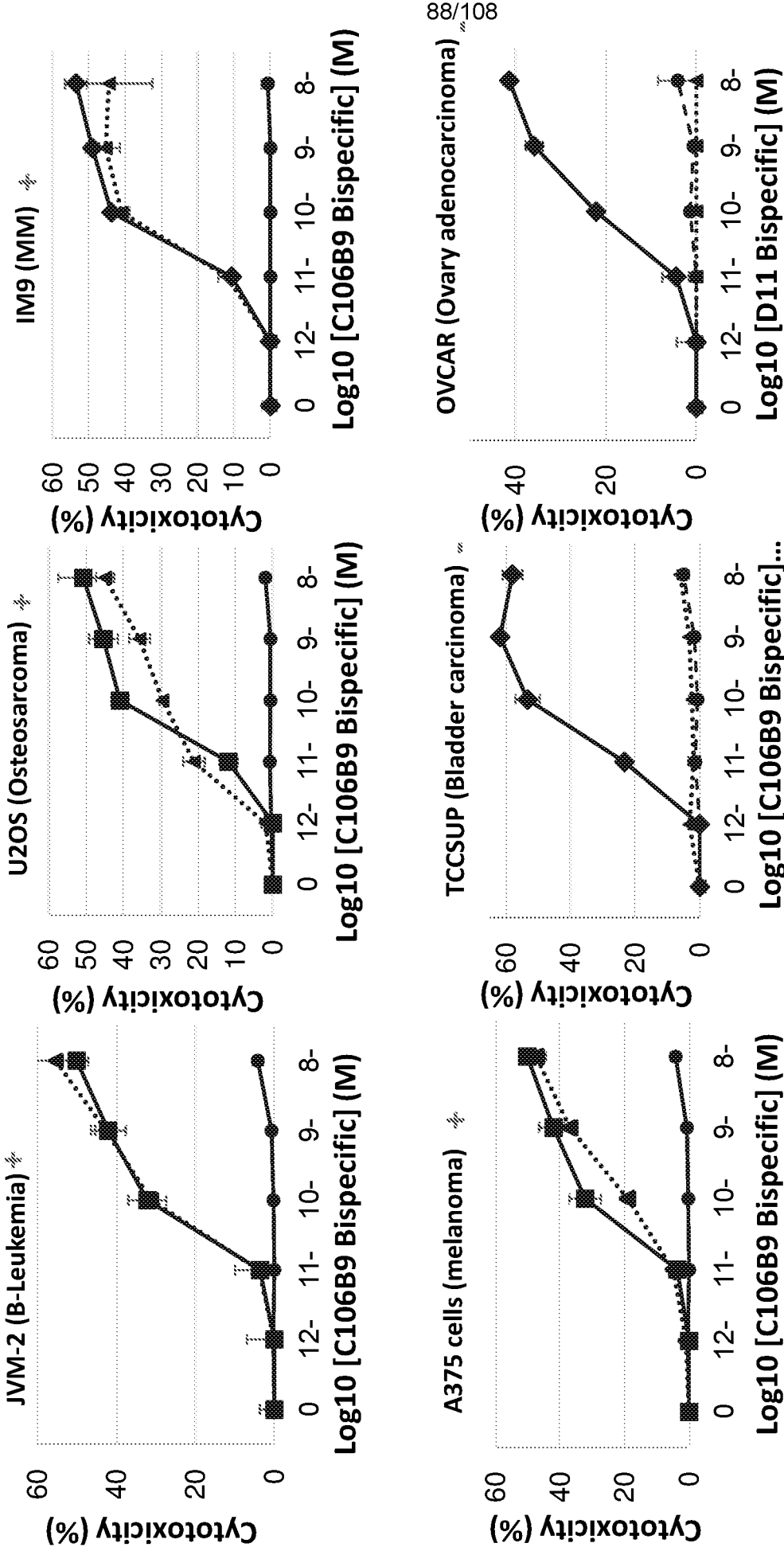


Figure 57

MAGE-A4 C106B9 BS TCRL - killing assay on normal primary cells

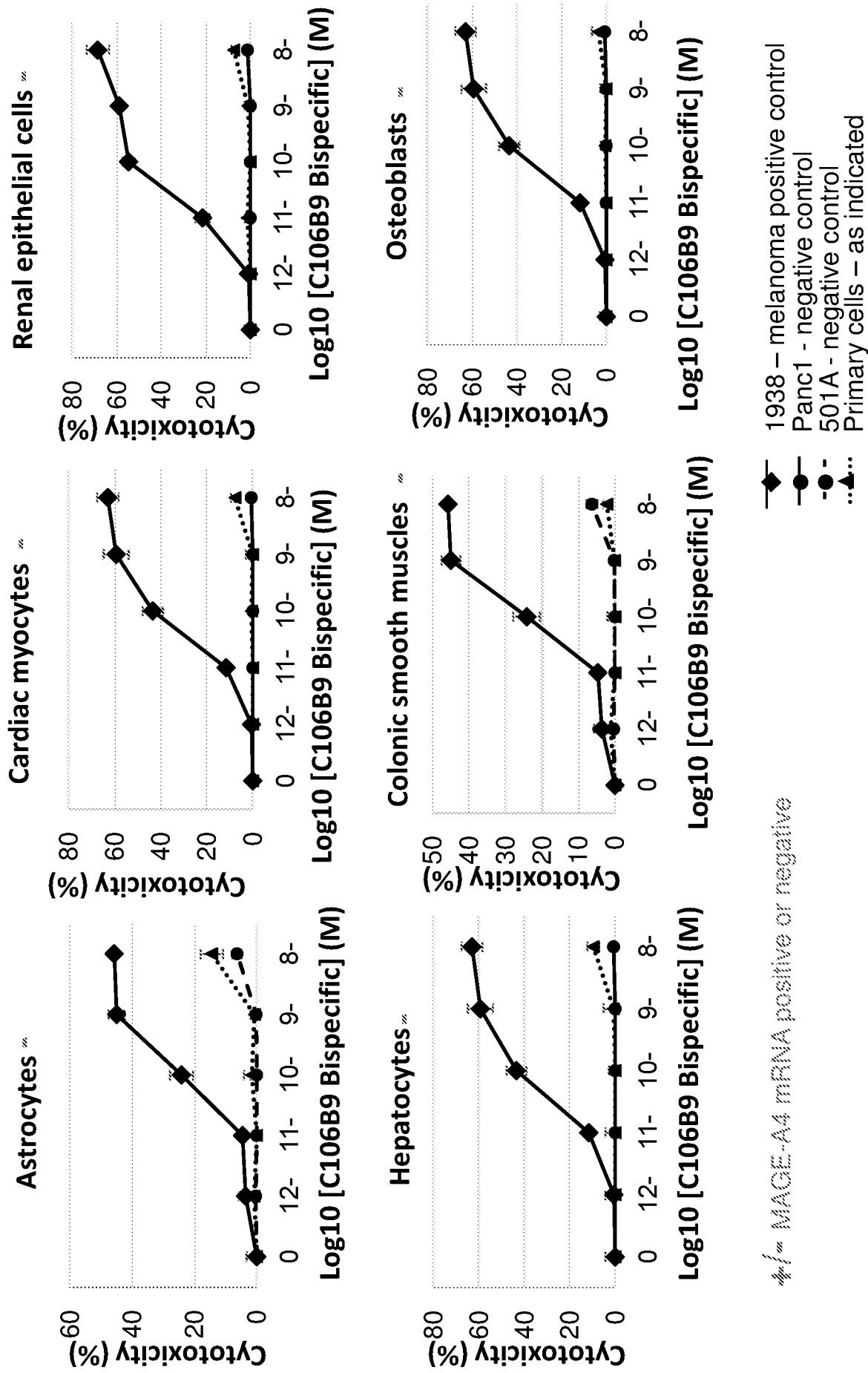


Figure 58

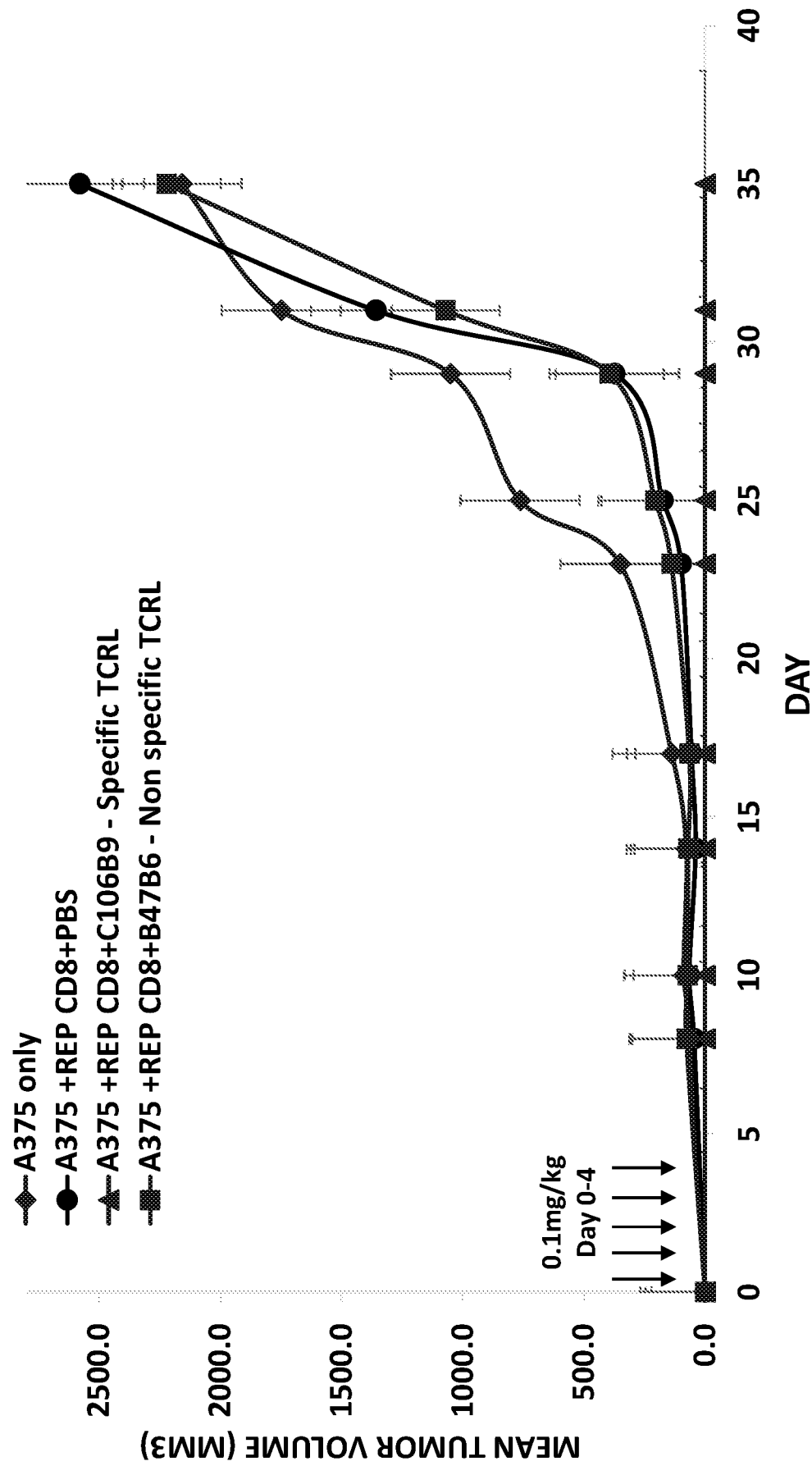


Figure 59

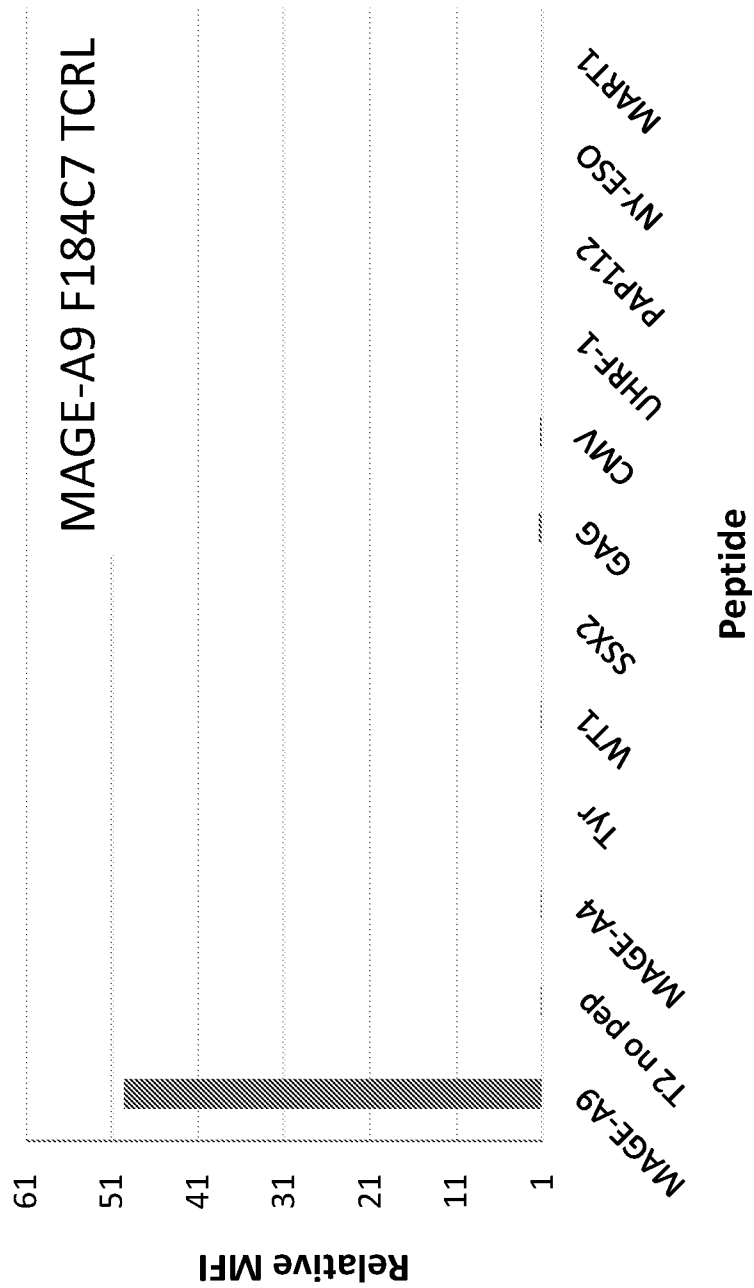
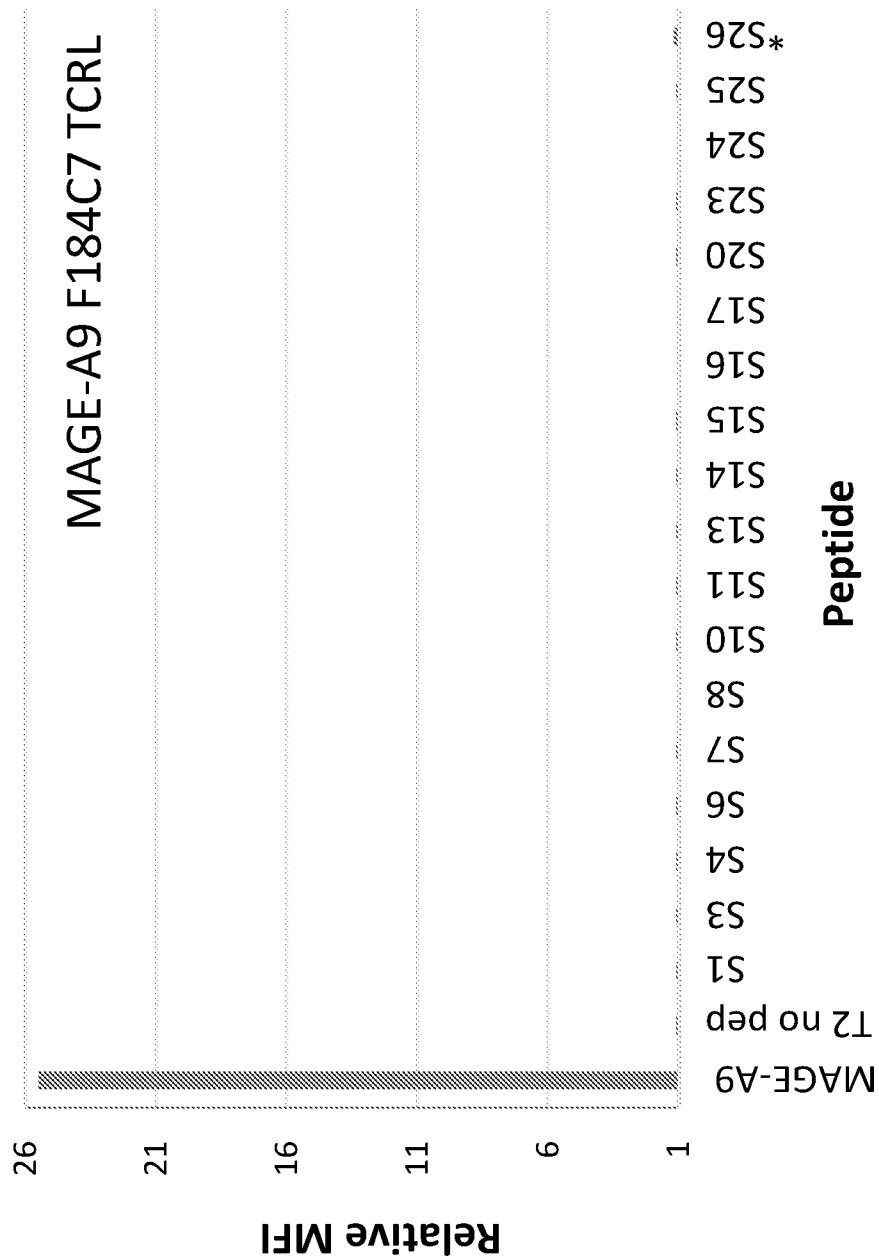


Figure 60



* Found by MS in normal tissues

Figure 61

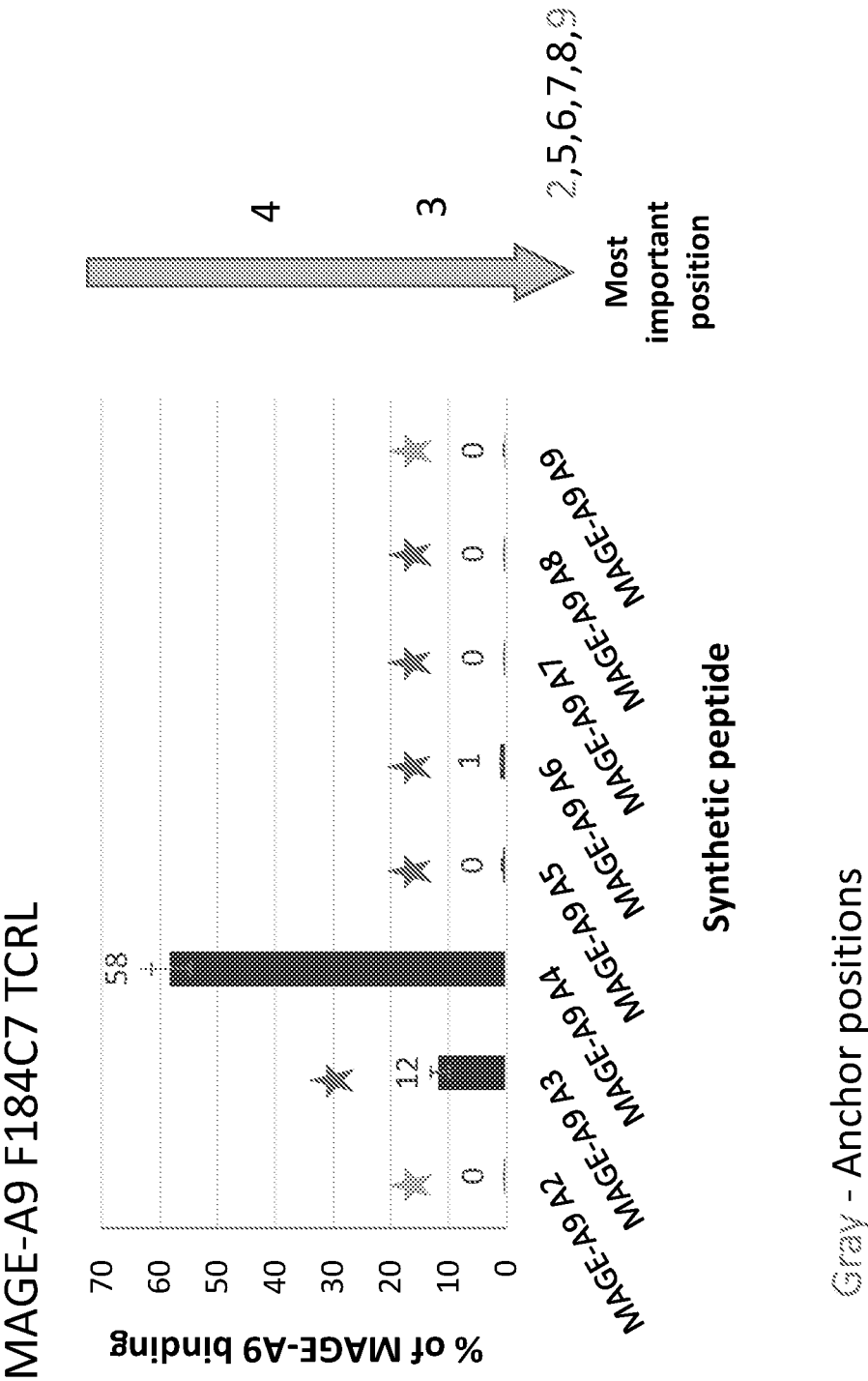


Figure 62

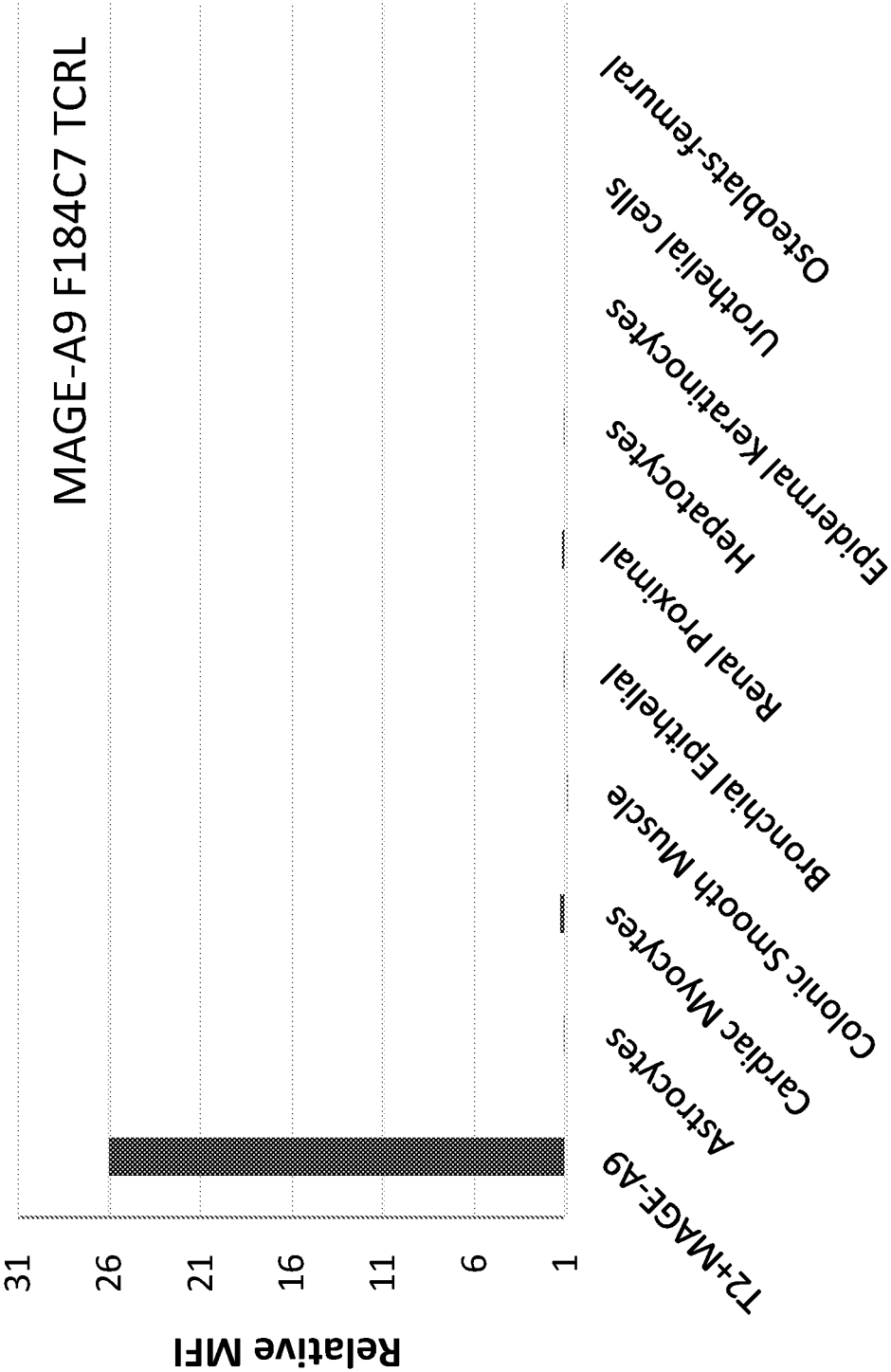


Figure 63

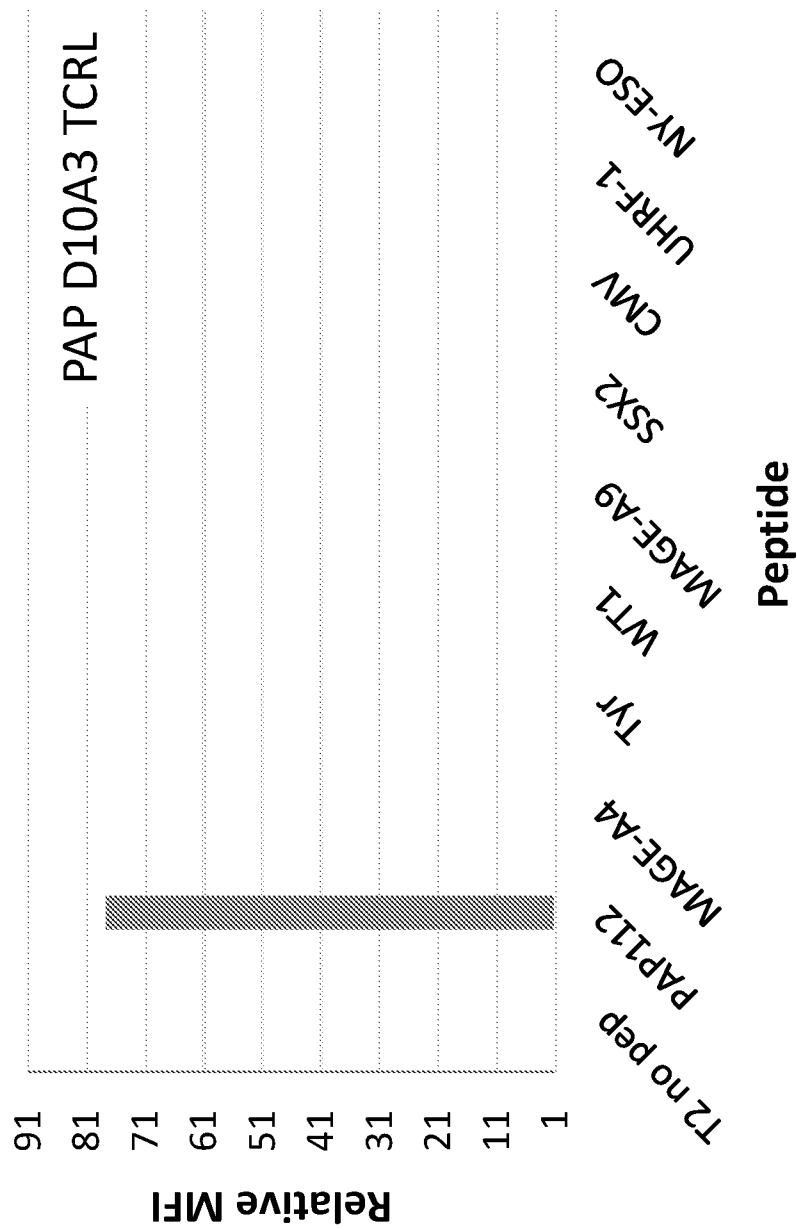
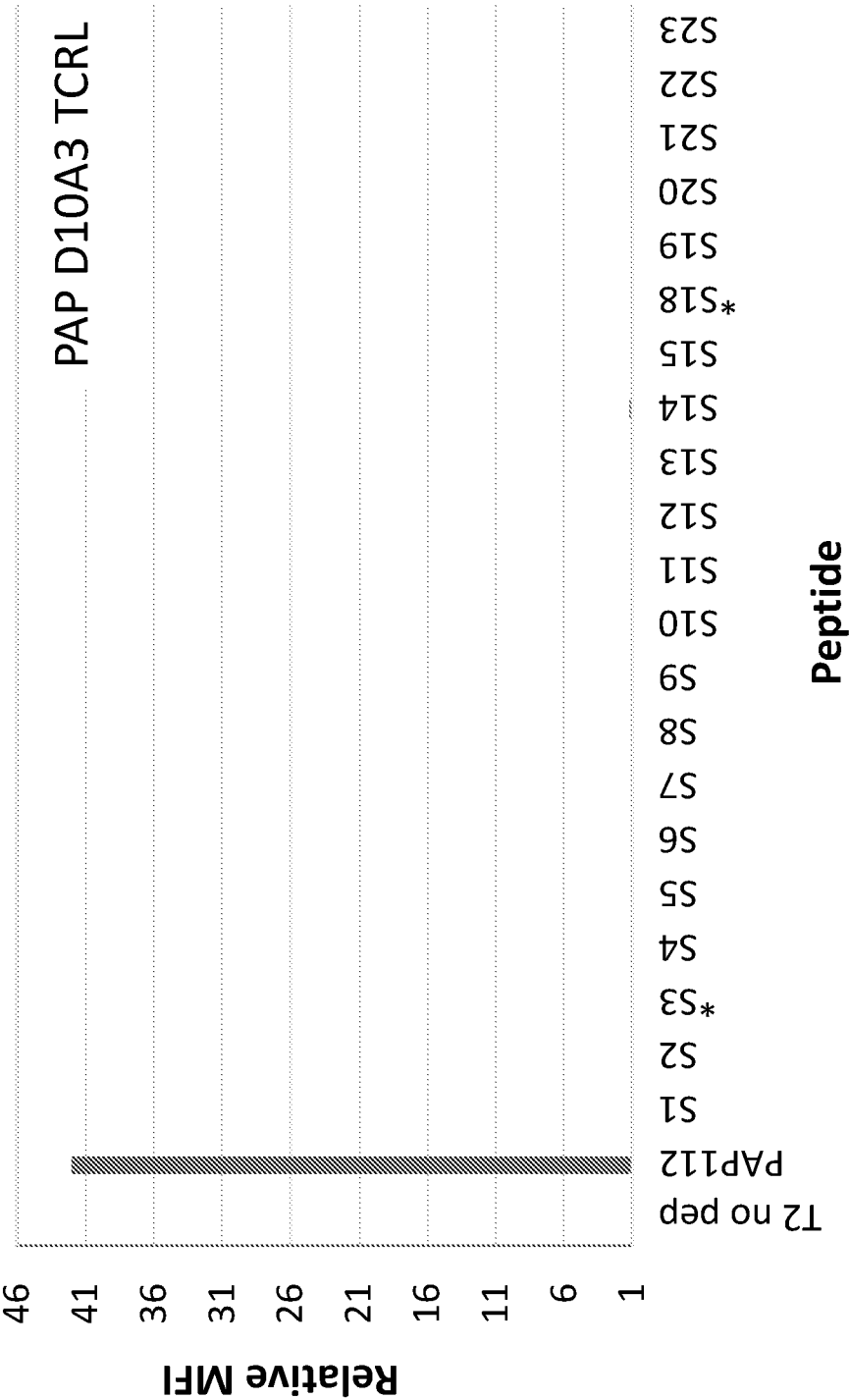


Figure 64



* Found by MS in normal tissues

Figure 65

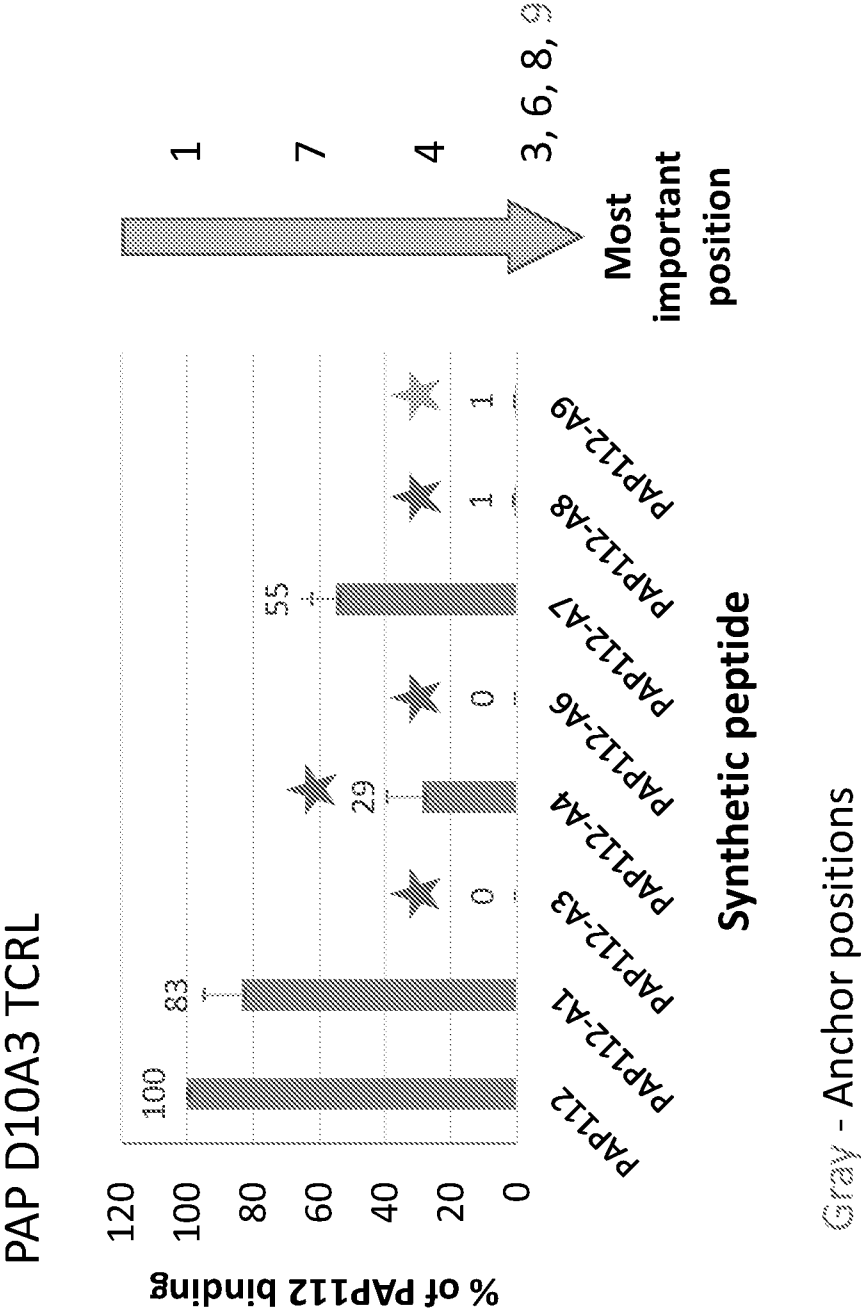


Figure 66

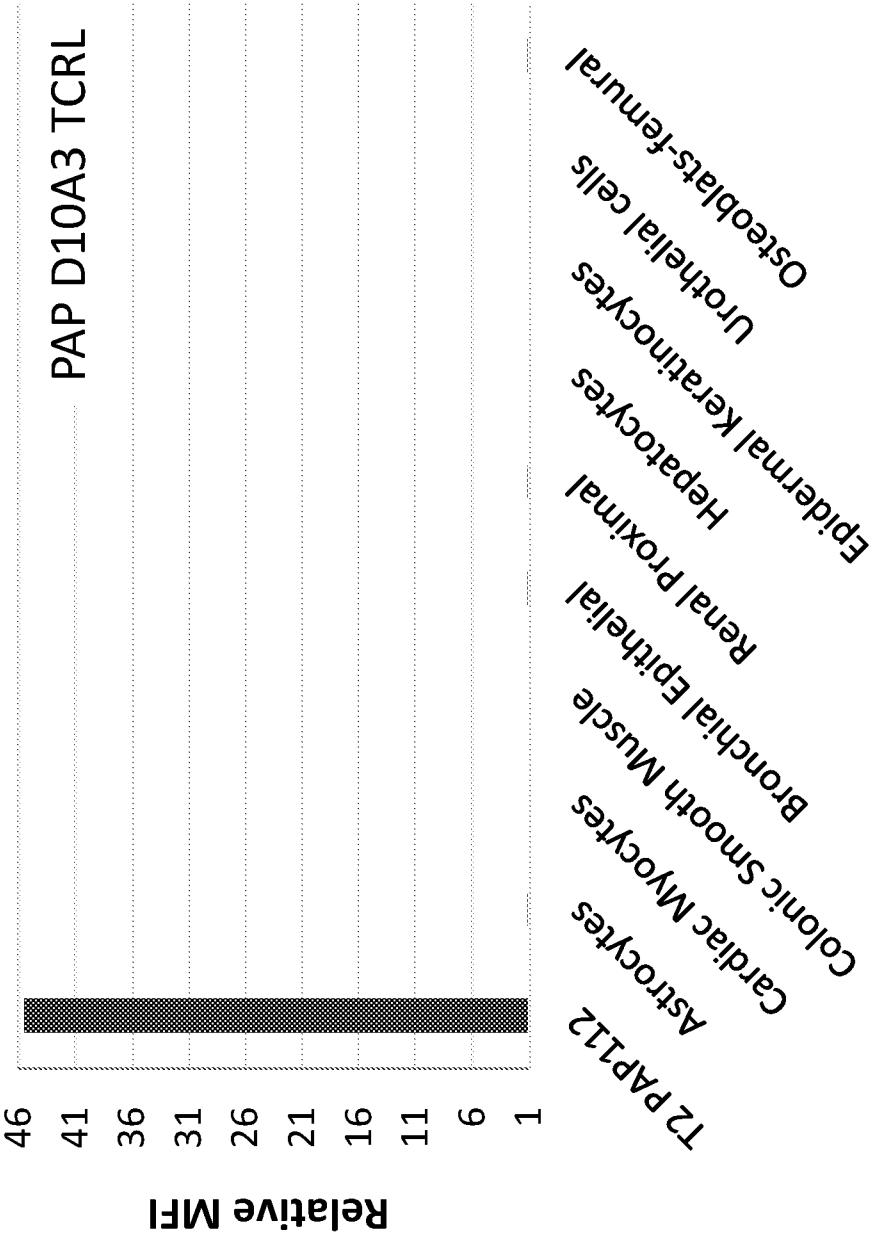


Figure 67

906-11-D11**Heavy chain: DNA sequence (1398 bp)**

Leader sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region-Stop codon

ATGGACAGGCTTACTTCCTCATTCCCTGCTGCTGATTGTCCCTGCATATGTCCTTTCCCAGGTAACCTC
 TGAAAGAGTCTGGCCCTGGGATATTGGCAGCCCTCCCAGACCCTCAGTCTGACTTGTTCCTTCTCTGG
 GTTTTCACTGACCCTTCTGGTATGGGTGTGAGCTGGATTTCCTCAGCCCTCAGGAAAGGGTCTGGAG
 TGGCTGGCACACATTTACTGGGATGATGACAAGCGCTATAACCCATCCCTGAAGAGCCGACTCACAA
 TCTCCAAGGATACCTCCAGAAACCAGGTATTCTCAAGATCACCAGTGTGGACGCTGCAGATACTGC
 CACATACTACTGTGCTCGAAAGGACTACGGTAGTAGCTTCTATGCTATCCACTACTGGGCTCAAGGA
 ACCTCAGTCACCGTCTCTCTCAGCCAAAACGACACCCCATCTGTCTATCCACTGCCCCCTGGATCTG
 CTGCCCCAACTAACTCCATGCTGACCTGGGATGGCTGGTCAAGGGCTATTTCCCTGAGCCAGTGCAC
 AGTGACCTCGAACTCTGCATCCCTGTCCAGCGGTGTGCACACCTTCCAGCTGTCTCTGCACTCTGAC
 CTCTACACTCTGAGCAGCTCAGTGACTGTCTCTCCAGCACCTGGCCAGCGAGACCCCTCACCTGCA
 ACCTTGGCCACCCGGGTCAGCAGCAACCAAGGTGGACAAGAAAATTGTGCCAGGGATTGTGGTTGTAA
 GCCTTGCATATGTACAGTCCCAAGATATCATCTGTCTTTCATCTTCCCCCAAAGCCCAAGGATCTG
 CTCACCATTAATCTGACTCTTAAGGTACGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 TCCACTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACCCCAACCCCGGAGAGCA
 GTTCAACAGCACTTTCCGCTCAGTCACTGAACTTCCCATCATGCCACAGCACTGCTCAATGGCAAG
 GAGTTCAAAATGCAGGGGTCAACAGTTCAGCTTTCCCTGCCGCCATCGAGAAAACCATCTCCAAAACCA
 AAGGCAGACCGAAGGCTCCACAGGTGTACACCATTCCACTTCCCAAGGAGCAGATGCCCAAGGATAA
 AGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGCCAGTGGAAAT
 GGGCAGCCAGCGGAGAACTACAAGAACTCAGCCCATCATGACACAGATGGCTCTTACTTCCCTCT
 ACAGCAAGCTCAATGTCCAGAAAGAGCAACTGGCAGCGCAGCAATACTTTCACCTGCTCTGTGTACA
 TCAGCGCCTGCACAACCACTATTGAGAAGAGCCTCTCCACTCTCTCTGTAAATGA

Heavy chain: Amino acids sequence (465 AA)

Leader sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region-Stop codon

MDRLTSSFLLLIVPAYVLSQVTLKESGPGILQPSQTLSTLCSFSGFSLTTSGMGVSWIRQPSGKLE
 WLAHIYWDDBKRYNPSLKSLFTISKDTSFNQVFLKITSVDAADTATYYCAR KDYGSSFYAMHYWGQG
 TSVTVSSAKTTPPSVYFLAPGSAAGTNSMVTLGCLVGYFPPEPVTVTWNSGSLSSGVHTFPVAVLQSD
 LYTLSSSVTVFSSSTWNPSETVTGNVAHPASSIKVLDKKIVPRDGGCKPCICTVFEVSVFIFPPKPKLV
 LTITLTPKVTCTVVDISKLDPEVQFQFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGK
 EFKCRVNSAAPPAPIEKTIKTKERPKAFQVYTIPEPKQMAKDQVSLTCTMITDFFPHDITVEWQWN
 GQPAENYKNTQPIMDTGGSYFVYGLNVDKSNWEAGNTFTCSVLHEGLNNHHTKSLSHSPGK

Light chain: DNA sequence (702 bp)

Leader sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region-Stop codon

ATGAGACCGTCTATTTCAGTTCCTGGGGCTCTTGTGTCTGGCTTCATGGTGCTCAGTGTGACATCC
 AGATGACACAGTCTCCATCCTCACTGTCTGCATCTCTGGGAGGCAAAGTCACCATCACATGCAAGGC
 AAGCCAAGACATTACAACTATATAGCTTGGTACCAACACAAGCCTGTAAAAGGTCCTAGGCTGCTC
 ATACATTACACATCTACATTACAGCCAGGCACCCCATCAAGGTTCAAGTGGAAAGTGGGTCTGGGAGAG
 ATTATTCCTTCAGCATCAGCAACCTGGAGCCTGAAGATATTGCAACTATTATTGTCTACAGTATGA
 TAATCTGTGGACGTTTGGTGGAGGCACCAAGCTGGAAATCAAACGGGCTGATGCTGCCACCACTGTA
 TCCATCTTCCCACCATCCAGTGAGCAGTTAACTCTGGAGGTGCTCAGTCTGTGTCTCTTGAACA
 ACTTCTACCCCAAAGACATCAATGTCAAGTGGAAAGATTGATGGCAGTGAACGACAAAATGGGCTCCT
 GAACAGTTGGACTGATCAGGACAGCAAGACAGCAGCTACAGCATGAGCAGCACCCCTCACGTTGACC
 AAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAAGACATCAACTTCACCCA
 TTGTCAAGAGCTTCAACAGCAATGAGTGTAG

Light chain: Amino acids sequence (233 AA)

Leader sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region-Stop codon

MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGKVTITCKASQDIHNYIAWYQHKPVKGPPELL
 IHYTSTLQPGTPSRFSGSGSGRDPYSFISINLEPEDIAITYCLQYDNLWTFGGGKLEIKRADAAPT
 VSIFFPSSSEQLTSGGASVVCFLNWFYKDIIVKWKIDGSEKQNGVLNWDQDSKDYSMSSSTLT
 KDEYERHNSYTCETHKSTSTSPIVKSFNRNEC

Figure 68

Heavy chain: DNA sequence (1380 bp)**Leader sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region-Stop codon**

ATGGCTGTCTGGTGTCTTCTCTGCCTGGTTGCATTTCCAAGCTGTGTCTGTCCCAGGTGCAAC
TGAAGGAATCAGGACCTGGTCTGGTGGCGGCTTCACAGAGCTGTCCATCACTTGCCTGTCTCTGG
GTTTTTCATTAAACCAGCTATGGTGTACACTGGSTTCGCCAGCTCCAGGAAAAGGGTCTGGAGTGGCTG
GGAGTAATATGGGCTGGTGGAAACCACAAATTATAATTGGGCTCTCATGTCCAGACTGAGCATCAGCA
GAGACAACCTCCAAGAGCCAACTTTTTCTTAGAAATGAACAGTCTGCAAACTGATGACACAGCCATTTA
CTACTGTGCCAGAGATGGTCACTTCCACTTTGACTTCTGGGGCCAAGCCACCCTCTCACAGTCTCC
TCAGCCAAAACGACACCCCATCTGTCTATCCACTGGCCCCCTGGATCTGCTGCCAAACTAACTCCA
TGGTGAACCTGGGATGCTCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAACCTCTGG
ATCCCTGTCCAGCGGTGTGCACACCTTCCAGCTGTCTCTGAGTCTGACCTCTACACTCTGAGCAGC
TCAGTGACTGTCCCTTCAGCACTTGGCCCCAGCGAGACCTGACCTGCAACCTTGGCCACCTGGCCCA
CCAGCACCAAGCTGGACAAGAAAATTGTGCCAGGATTTCTGTTGTAAGCCTTGCATATGTACACT
CCAGAAATATCATCTGTCTTCTCTCTTCCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTCACT
CCTAAGSTCACCTGTCTTCTGTGTAGACATCAGCAAGCATGATCCCGAGCTCCAGTTCAGCTGCTTTG
TAGATGATCTCCAGGTGCACACAGCTCAGACCCAAACCCCGGAGGAGCACTTCAACAGCACTTTCCG
CTCACTCACTGAACCTTCCCATCATGCAACAGGACTTGGCTCAATGGCAAGSAGTTCAAATCCAGGCTC
AACASTGCAGCTTTCCCTGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGCAGACCCSAAGGCTC
CACAGGTGTACACCATTCCACCTCCCAAGGAGCAGATGGCCAAAGGATAAAGTCAGTCTGACCTGCAT
GATAACAGACTTCTTCCCTGAAGACATTACTCTGAGTGGCACTGGAATGGGACCCAGCCGGACAAC
TACAAGAACTCAGCCCATCATGACACAGATGGCTCTTACTTGGTCTACAGCAAGCTCAATGTCC
AGAAGAGCAACTGGGAGCCAGGAAATACTTCACTGCTCTGTGTTACATGAGGCCCCGACACAACCA
CCATACTGAGAAGAGCTCTCTCCACTCTCTCTGCTAAATGA

Heavy chain: Amino acids sequence (459 AA)**Leader sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region-Stop codon**

MAVLVFLCLVAFPSVCLSVQVQLKESGPGLVAPSSLSITCTVSGFSLTSYGVHWVRQPPGKGLEWL
GVIWAGGTTNYSALMSRLSISPDNSKSKVFLMNSLQTDITAIYYCARDGHFHFDWGGQTLLTVS
SAKTEFPSSVYFLAPGSAQAQNSMVTLCCLVKGYPPEPVTVWNSSGLSCGVHTFFAVLQSDLYTLSS
SVTVFSSSTNPFSEVTYCNVAFASSTKVDKKIVPRLCCKPCICTVFEVSSVFIFPPKPKDVLITITLT
PKVTCVVDLISKDDPEVQFSWFVDDVEVHTAQTQPPFEEQFNSTFRVSELPIMHQDWLNGKEFKCRV
NSAAFPAPLEKTI SKTGRPKAPQVYTIPEPKQMAKDKVSLTOMITDFFPEDITVEWQWNGQPAEN
YKNTQFIMDTLGSYFVYSKLVNQKSNWEAGNFTCSVLBEGLEHNNHTEKSLSESPGK

Light chain: DNA sequence (705 bp)**Leader sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region-Stop codon**

ATGAGTGTGCCCCACTCAGGTCTCTGGGGTTGCTGCTGCTGTGGCTTACAGATGCCAGATGTGACATCC
AGATGACTCAGTCTCCAGCCTCCCTATCTGTATCTGTGGGAGAACTGTCAACATCACATGTGAGC
AAGTGATATTATTTACAGTAATTTAGCATGGTATCAGCAGAAACAGGGAAAAATCTCCTCAGCTCCTG
GTCTATGCTGCAACAAACTTAGCAGCTGGTGTGCCATCAAGGTTCACTGGCAGTGGATCAGGCACAC
AGTATTCCTCAAGATCAATAGCTTGCAGTCTGAAGATTTGGGACTTATTACTGTCAACATTTTTTG
GGGTAGTTCAATCTCGTTCCGCTCGGGGACAAAGTTGGAATAAAAACGGGCTGATGCTGCACCAACT
GTATCCATCTTCCCAACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCCTCAGTCTGTCTCTTCTGA
ACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAAGATTGATGGCAGTGAACGACAAAATGGCGT
CCTGAACAGTTGGACTGATCAGGACAGCAAAAGACAGCACTACAGCATGAGCAGCACCTCAGCTTG
ACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCAC
CCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAG

Light chain: Amino acids sequence (234 AA)**Leader sequence-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region-Stop codon**

MSVPTQVLGLLLLWLTDARCDIQMTQSPASLSVSVGETVTITCRASDIIYSNLAWYQQKQKSPQLL
VYAATNLAAGVPSRFGSGSGGTQYSLKINSLSQSEDFCTYYCQHFHWGSSISFGSGTKLEIKRADAAPT
VSIFFPSSSEQLTSGGASVVCFLNFFPKDINVEWKIDGSEKQNGVLNSWTDQDSKLSYSSSTLTLL
TKDEYERHNSYTCETHKISTSPIVKSFNNNEC

Figure 69

DIVLTQSPATLSVSPGDSVSLSCRASQSIENSLHWYQKSHESPRLLIKYASQSI SGIPSRFSGSGSGTDFTLSINSVETEDFGMYFCQQ
SYSWPLTFGAGSKLELKRADAAPT VSIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSE RQNGVLSWT
LQDSKDSITYGMSCTLTETKDEYERBN SYTCBATEKTSTSPILVKSENPNEC

Figure 70 continued

C106B9 MAGE-A4 TCRL**Heavy chain: DNA sequence**

FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region

Nuc-seq:

CAGGTTCAACTGCAGCAGTCTGGAGGTGAGGTGATGAAGCCTGGGGCCTCAGTGAAGCTTTCCTGCAAGGCTACT
 GGCTACACATTCAGTGGCTACTGGATAGAGTGGATAAAACAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGA
 GATTTTACCTGGAAGTGGTGGTACTAACTACAATGAGAAATTCAAGGGCAAGGCCACATTCAGTGCACATACATCC
 TCCAACACAGCCTACATGCAACTCAGCAGCCTGACAACTGAGGACTCTGCCATCTATTACTGTGCAAGGGATAGTA
 ACTCCTTTACTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTTCAGCCAAAAACGACACCCCATCTGTCTATC
 CACTGGCCCTGGATCTGTCTGCCAACTAACTCCATGGTGAACCTGGGATGGCTGGTCAAGGGCTATTT
 CCCTGAGGCGAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGTCACACCTTCCAGCTGTCT
 CTGCACTCTGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCTCCAGCACCTGGCCGAGCGAGACCG
 TCACCTGCAACGTTGGCCACCCGGCAGCAGCACTAAGGTGCACAAGAAAATTGTGCCAGGGATTGTGG
 TTGTAAGCCTTGCATATGTACAGTCCCGAAGTATCATCTGTCTTCATCTTCCCTCCAAAGCCCAAGGAT
 GTGCTCACCATTACTCTGACTCTAAGGTGACGTGTGTGTGTGGTAGACATCAGCAAGGATGATCCCGAGG
 TCCAGTTTCACTGGTGTGTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCTCCGGGAGGAGCAGTT
 CAACAGCACTTTCCGCTCAGTCAGTGAACCTTCCCATCATGCACAGGACTGGCTCAATGCCAAGGAGTTC
 AAATGCAGGCTCAACAGTGCAGCTTTCCCTGCCCCCATCGAGAAZACCATCTCCAAZACCAAGGCAGAC
 CGAAGGCTCCACAGGTGTACACCATCCACCTCCCAAGGAGCAGATGCCAAGGATAAAGTCAGTCTGAC
 CTGCATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGAAATGGGCAGCCAGCGGAG
 AACTACAAGAACACTCAGCCCATCATGGACACAGATGGCTCTTACTTCTGTCTACAGCAAGCTCAATGTGC
 AGAAGAGCAACTGGGAGGCAGGAAATACTTTCACCTGCTCTGTGTTACATGAGGGCCTGCACAACCA
 TACTGAGAAGAGCCTCTCCCACTCTCTCTGGTAAA

AA-seq:

QVQLQQSGGEVMPKPGASVKLSCKATGYTFTGYWIEWIKRPGHGLEWIGEILPGSGGTNYNEKFKGKATFTAHTSSN
 TAYMQLSSLTIEDSAIYYCARDSNSFTYWGQGLTVYSSAKTTTPSVYPLAPGSAAGTNSMVTLGCLVKGYFPEP
 VYVWNSSGSLSSGVHTFPAVLQCDLYTLSSSVTPSSWPSSTVTCNVASAPASSTKVDKKIVPRDCCGCKP
 CICTVPEVSSVFIFPPPKKDYLTITLTPKVTICVVDISKDPEVQPSWFEVDDEVEVHTAQTQPREEQFNST
 FRSVSELPIMHQDWLNKEFKCRVNSAAFPAPISKTKGRPKAPQV/TIFPPKEQMAKDKVSLTQMI
 TDFPEFEDITVEWQWNGQPAEWYKNTQPIMDTDGSYFVYSKLNQKSNWEAGNTFTCSVLHEGLNHHTEK
 SLRSPEK

Light Chain

Light chain: DNA sequence (705 bp)

FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region

CAAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATAACCTGCAGTGTCA
 GCTCAAGTGTAGATTACATTCAGTGGTCCAGCAGAAGCCAGGCACTTCTCCCAAATTCTGGATTTATAGCACATCC
 ATCCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGATCTGGGACCTCTTACTCTCTACAATCAGCCGAAT
 GGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAAAGGAGIAGTTACCCACCCACgTTCGGCTCGGGGACAAAGT

Figure 71

TGGAAATAAAACGGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCATCCAGTGAGCAGTTAACATCTG
GAGGTGCTTCAGTCGTGTGCTTCTTGAACAACCTTCTACCCCAAAGACATCAATGTCAAGTGGAAAGATTGA
TGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGC
ATGAGCAGCACCTTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACTGTGAGGCACTC
ACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGT

AA-seq:

QIVLTQSPAIMSASPGEKVTITCSVSSSVDIYHWFQOKPGTSPKFWIYSTSILASGVPARFSGSGSGTSYSLTISRMEAEDA
ATYYCQQRSSYPPTFGSGTKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVRWKIDGSEKQI
GVLNSWTDQDSKDSITYSMSSLTFLTKDEYERHNSYTCETHKTGTSEIVFSEFNRNEC

Figure 71 continued

F184C7 MAGE A9**Heavy chain: DNA sequence**

FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region

Nuc-seq:

CAGGTTGAGCTGCAGCAGTCTGGACCTGAGATGGTGAAGCCTGGGGCCTCAGTGAAGATTCCCTGCAAGGCTTCT
 GGCTACGCATTGAGTAGCTCCTGGATGAACTGGGTGAAGCAGAGGCCTGGAAAGGGTCTTGAGTGGATTGGACG
 GATTTATCCTGGAGATGGAGATACTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATC
 CTCCAGCACAGTCTACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTACTTCTGTGCAAGAGAGGCT
 ACTACGGTAGTGGCCCCGTAATACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAAAAAGA
 CACCCCATCTCTGTCTATCCACTGGGCCCTGGATCTGCTGCCCAAACTAACTCCATGGTGAACCTGGGATG
 CCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTG
 CACACCTTCCAGCTGTCTCTGCACTCTGACCTCTACACTCTGAGCAGCTCAGTGAAGTGTCCCTCCAGCA
 CCTGGGCCAGGAGACCGTCACTGCAACGTTGCCACCCGGCCAGCAGCAGCAAGGTGGACAAGAAAAAT
 TGTGCCAGGGATTGTGGTTGTAAAGCCTTGCATATGTACAGTCCCAGAAAGTATCATCTGTCTTCATCTTC
 CCCCCAAAGGCCAAGGATGTGCTCACCATTACTCTGACTCCCTAAGGTCAAGTGTGGTTGTGGTAGACATCA
 GCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCA
 ACCCCGGGAGGAGCAGTTCAACAGCAGCTTTCCGCTCAGTCACTGAAGTTCCTCATCATGCACCAGGACTGG
 CTCAATGGCAAGGAGTTCAAAATGCAGGGTCAACAGTGCAGCTTTCCCTGGCCCATCGAGAAAACCATCT
 CCAAAACCAAGGAGAGCCGAAGGCTCCACAGGTGTACACCATTTCCACCTCCCAAGGAGCAGATGGCCAA
 GGATAAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTAAGTGTGGAGTGGCAGTGG
 AATGGGCAGCTAGCGGAGAACTACAAGAACTCAGGCCATCATGGACACAGATGGCTCTTACTTCGTCT
 ACAGCAAGCTCAATGTGAGAGAGCAACTGGGAGGCAGGAAATACTTTACCTGCTCTGTGTTACATGA
 GGGCCTGCACAAACCACATACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA

AA-seq:

QVQLQSGPEMVKPGASVKIPCKASGYAFSSSWMNWVKQRPKGLEWIGRIYPGDGDTNYNEKFKGKATLTVDKSS
 STVYMQLSSLTSEDSAVYFCAREATTVVAPYYFDYWGOGTTLTVSSAKTTPPSVYPLAPGSAAGTNSMVTLGCLV
 KGIFYEPVTVWNISGLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCHVAHPASSTKVOKKIVP
 RDGCKPCICTVPEVSSVFIPFPKPDVLTITLTPKVTCTVVDISKDDPEVQFSWFVDDEVHTAQTQPK
 EQFNSTFPVSELPIMHODWLNGKEFRCKVNSAAPPAPIEKTLOKTKGPPKAPQVYTIIPFPKQMAKDK
 VSLTCHMITDFPPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAGNTFTCSVLHEGL
 HNHTEKSLSHSPGK

Light chain: DNA sequence

FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region

Nuc-seq:

GACATCAGATGACTCAGTCTCCAGCCTCCCTATCTGTATCTGTGGGAGAACTGTCACCATCACATGTCGAGCAA
 GTGAGAATATTTACAGAAATTTAGCATGGTATCAGCAGAAACAGGGAAAAATCTCCTCAACTCCTGGTCCATGCTGC
 AACAACTTAGCAGATGGTGTGCCATCAAGGTTCAAGTGGCAGTGGATCAGACACACAGTATCCCTCAAGATCAA
 CAGCCTGCAGTCTGAAGATTTTGGGAATTACTGTCAACATTTTGGGGGACTCCGCTCACGTTCCGTGCTGGG

Figure 72

ACCAAGCTGGAGCTGAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTT
AACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACCTTCTACCCCAGAGACATCAATGTCAAGTGG
AAGATTGATGSCAGTGAACGACAAAATGGCGTCTTGAACAGTTGGACTGATCAGGACAGCAAGACAGCA
CCTACAGCATGAGCAGTACCTTCACTTGAACAAAGGACGAGTATGAACGACATAACAGCTATACCTGTGA
GGCCACTCACAAGACATCAACTTCACTCATTGTCAAGAGCTTCAACAGGAATGAGTGT

AA-seq:

DIQMTQSPASLSVSVGETVTITCRASENIYRNLAWYQQKQKGKSPQLLVHAATNLADGVPSRFSGSGSDTQYSLKINSIQ
SEDFGNYYCQHFWGTPITFGAGTKLELKPADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDIWVKWIDG
SERQNGVILNQTDDQDEKDSITYCMSSITLITKDEYERKNSYTCRATKSTSPETVKSFNNEC

Figure 72 continued

D10A3 PAP TCRL**Heavy chain: DNA sequence**

FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region

Nuc seq

GAGGTCCAGCTGCAACAGTTTGGAACTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAA
 GGCTTCTGGCTACACATTCACTGACTACAACATGGACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGA
 GTGGATTGGAGATATTAATCCTAACTATGATACTACTACCTACAACCAGAAGTTCAAGGGAAAGGCCAC
 ATTGACTGTAGACAAGTCCCTCCAGCACAGCCTACATGGAGCTCCGCAGCCTGACTTCTGAGGACACTGC
 AGTCTTTTACTGTGCAAGAAGGAAGTATGGTAACTACGTGGGGTTTGACTTCTGGGGCCAAGGCACCAC
 TCTCACAGTCTCCTCAGGCAAAAACGACACCCCACTCTGTCTATCCACTGGGCCCCTGGCATCTGCTGCCCCAA
 CTAACCTCCATGGGTGACCCCTGGGATGCTTGGTCAAGGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAA
 CTCTGGATCCCTGTCCAGCGGTGTGACACACCTTCCCAAGCTGTCTCTGCAGTCTGACCTCTACACTCTGAGC
 AGCTCAGTGACTGTCCCTCCAGCACCTGGGCCCAGCGAGACCGTCACCTGCAACGTTGCCCCACCCGGCCA
 GCAGCACCAAGGTGGACAAGAAAAATTGTGCCAGGGATTGTGGTTGTAAAGCCTTGCATATGTACAGTCCC
 AGAAGTATCATCTGTCTTCTTCTTCCCCCAAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAG
 GTCACGTGTGTGTGTGGTAGACATCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATG
 TGGAGGTGCACACAGCTCAGACGCAACCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCACTGA
 ACTTCCCATCATGCAACAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTCAACAGTGCAGCTTTC
 CCTGCCCCCATCGAGAAAACCATCTCCAAAACCAAGGCAGACCGAAGGCTCCACAGGTGTACACCATTC
 CACCTCCCAAGGAGCAGATGGCCAAGGATAAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGA
 AGACATTACTGTGGAGTGGCAGTGGGAATGGGCAGCCAGCGGAGAACTACAAGAACACTCAGGCCATCATG
 GACACAGATGGCTCTTACTTCGTCTACAGCAAGCTCAATGTGCAGAAAGAGCAACTGGGAGGCAGGAAATA
 CTTTCACCTGCTCTGTGTTACATGAGGGCCTGCACAACCACCATACTGAGAAGAGCCTCTCCCACTCTCC
 TGGTAAA

AA-seq:

EVQLQQFGTELVKPGA5VKISCKASGYFTDYNMDWVKQSHGKSLEWIGDINPNYDTTYYNQKFKGKATLT
 VDKSSSTAYMELRSLTSEDVAVFYCARRNYGNYVGFDWVGQGTTLTVSSAKTTEPSVYPLAPGSAQAQNSM
 VTLCCLVKGYPEPEFVTVTNSSGLSSGVHTFEAVLQSDLYTLSSSVTVPSSTWPSSETVTONVAHPASSTK
 VDKKIIVPRDCGCRPCICTVPEVSSVFIFPEKPKOVLTITLTPKVTGVVVDISKDDPEVQPSWFDVDDVEVH
 TAQTQPPPEEQFNSTFRVSESLPIMHQDWLNGKEFKRVNSAAFPAPIEKTISKTKGEPKAPQVYTIPEPK
 EQMAKDKVSLTCHITDFPEOITVEWQWNGQFAENYKNTQPIIMDTDGSYFVYSKLVNQKSNWEAGNTFTC
 SVLEGLHNQHTKSLSHSPGK

Light chain: DNA sequence

FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-Constant region

Nucseq:

AATATTGTGCTGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTTCCATAACCTGCA
 AGGCCAGTCAGCGTGTGAATAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGC
 TGATATACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGG

Figure 73

ATTTCACTTTTACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAG
CTCTCCATTTCACGTTTCGGCTCGGGGACAAAAGTTGGAAATAAAAACGGGCTGATGCTGCACCAACTGTATCO
ATCTTCCOACCAECCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACCTTCT
ACCCCAAAGACATCAATGTCAAGTGGAGATTGATGGCAGTGAACGACAAAATGGOGTCTTGAACAGTTG
GACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCTCAGCTTGACTAAGGACGAGTAT
GAACGACATAACAGCTATACTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCA
ACAGGAATGAGTGT

AA-seq

NIVLTQTPKFLVVSAGDRVSITCKASQVRVNDVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGYGTD
FTFTISTVQAEDLAVYFCQQDYSSPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI
NVKWKIDGSERQNGVLNSWTDQDSKDYSSMSSTLTLTKEDEYERHNSYTCEATHKTSTSPIVKSFNRNEC

Figure 73 continued