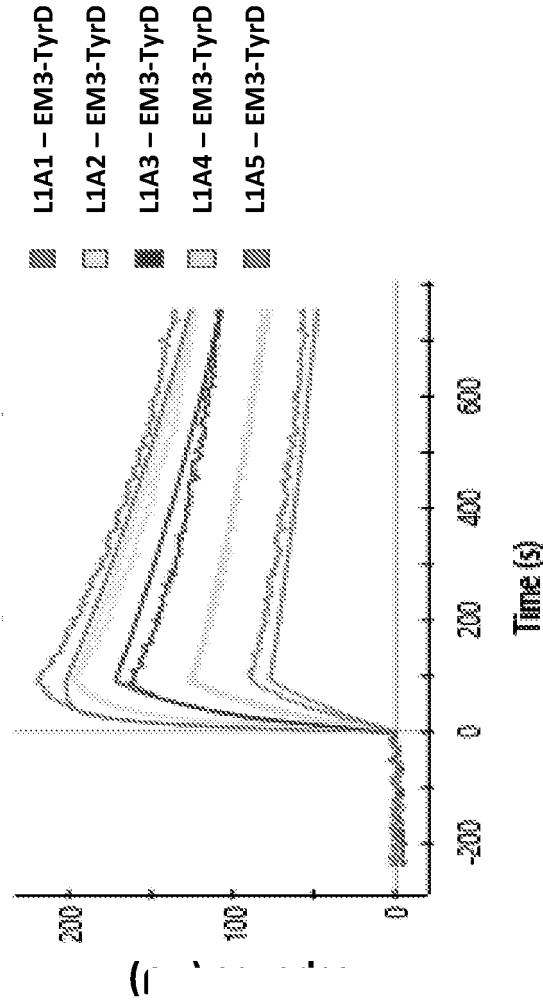


D11 - 4.1nM

L1 - 11_EM3-TyrD Cycle1

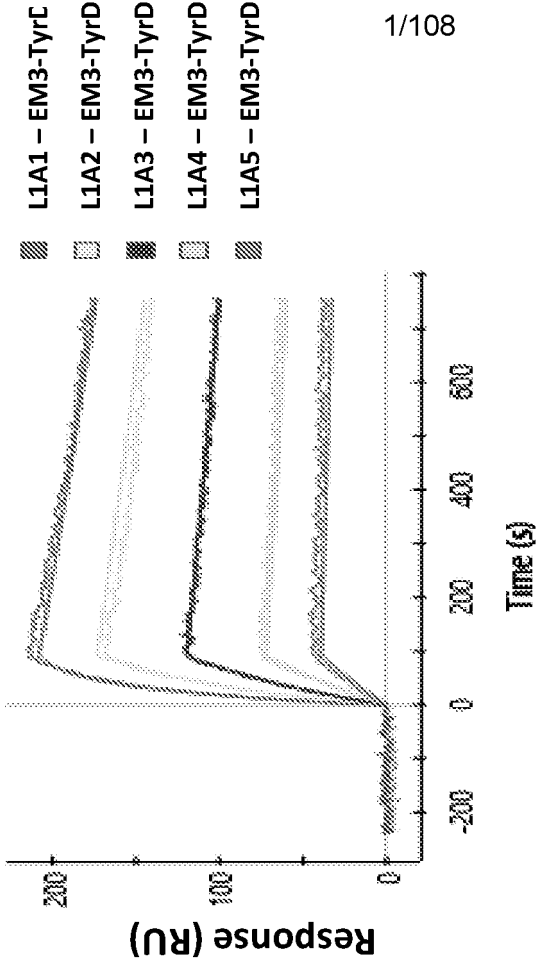
ka:1.72E+05 1/Ms kd:7.14E-04 1/s KD:4.14E-09 M



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



1/108

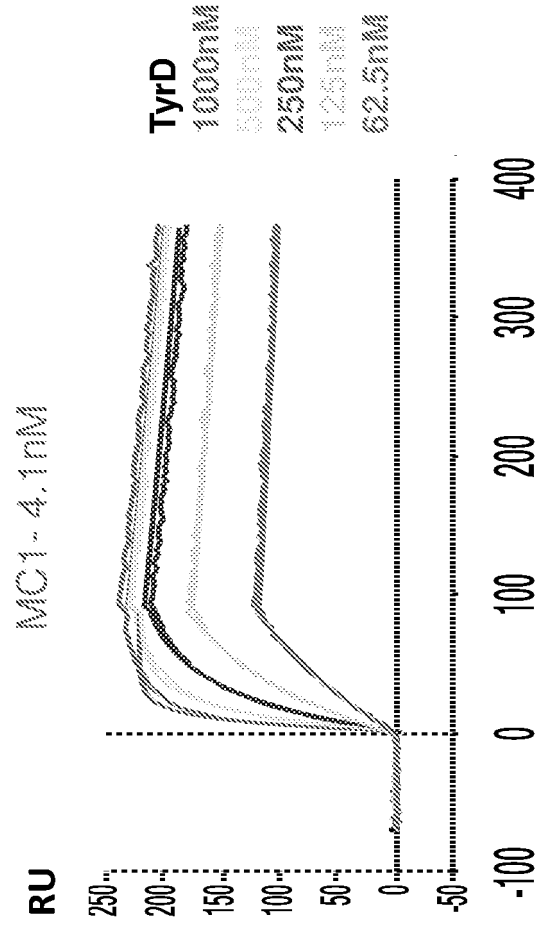
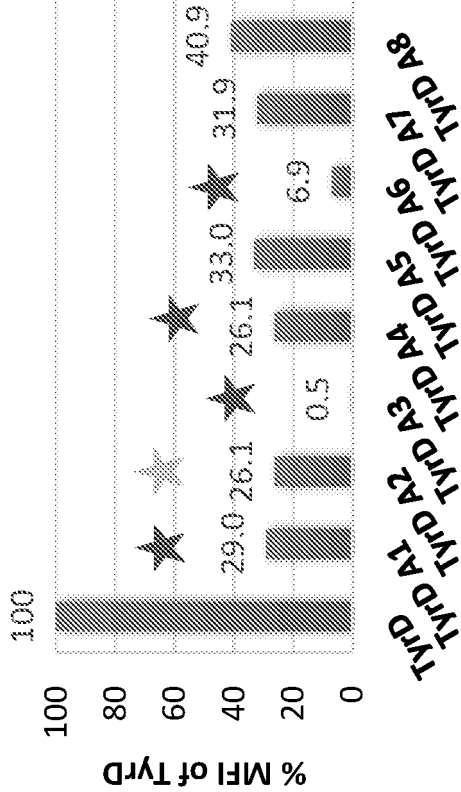


Figure 1

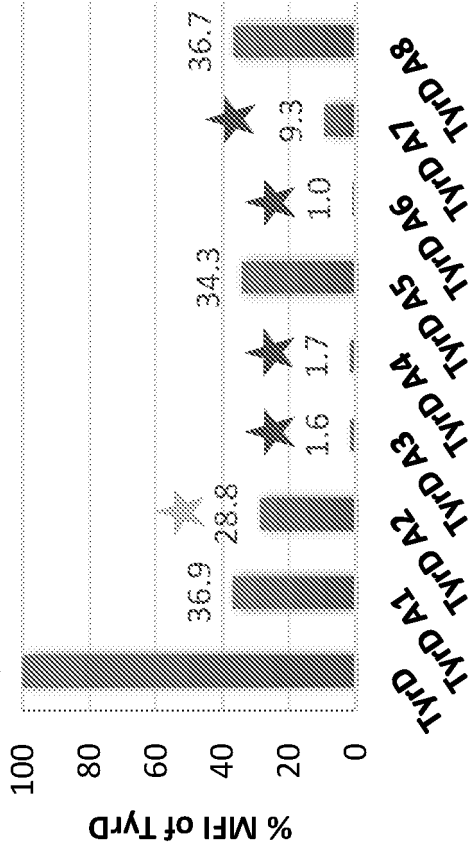
TyrD	YMDGTMSQV
TyrD A1	AMDGTMSQV
TyrD A2 anchor position	YADGTMSQV
TyrD A3	YMAGTMSQV
TyrD A4	YMDATMSQV
TyrD A5	YMDGAMSQV
TyrD A6	YMDGTASQV
TyrD A7	YMDGTMASQV
TyrD A8	YMDGTMSAV

Alanine scanning D11B10 10µg/ml



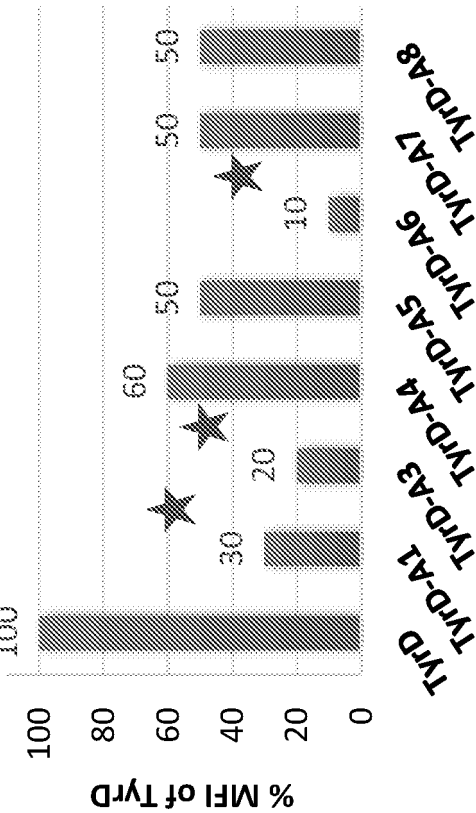
- Decrease of >90% at two positions # 3, 6
- Decrease of > 70% in five positions # 1, 2, 3, 4, 6

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 2

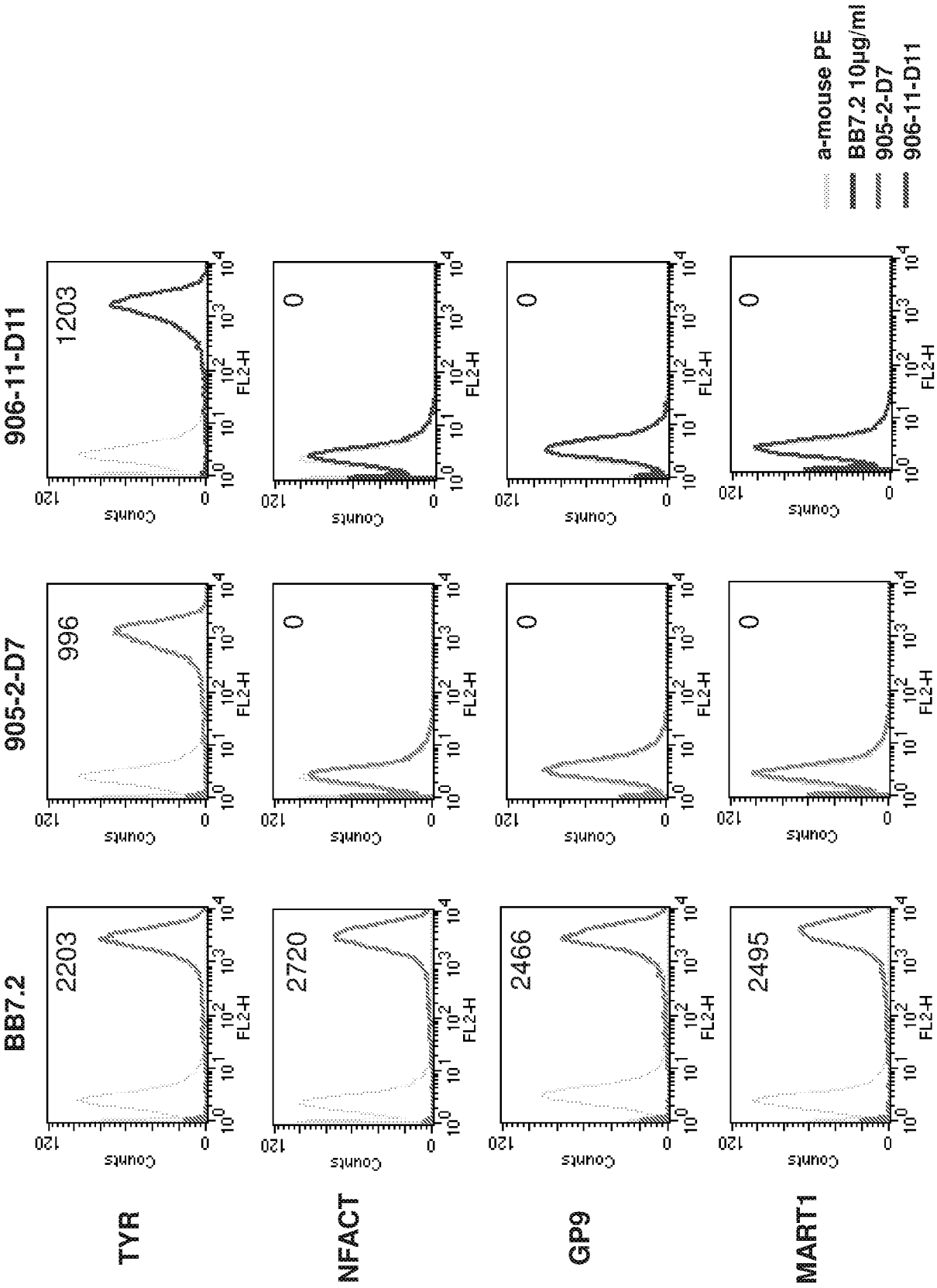


Figure 3

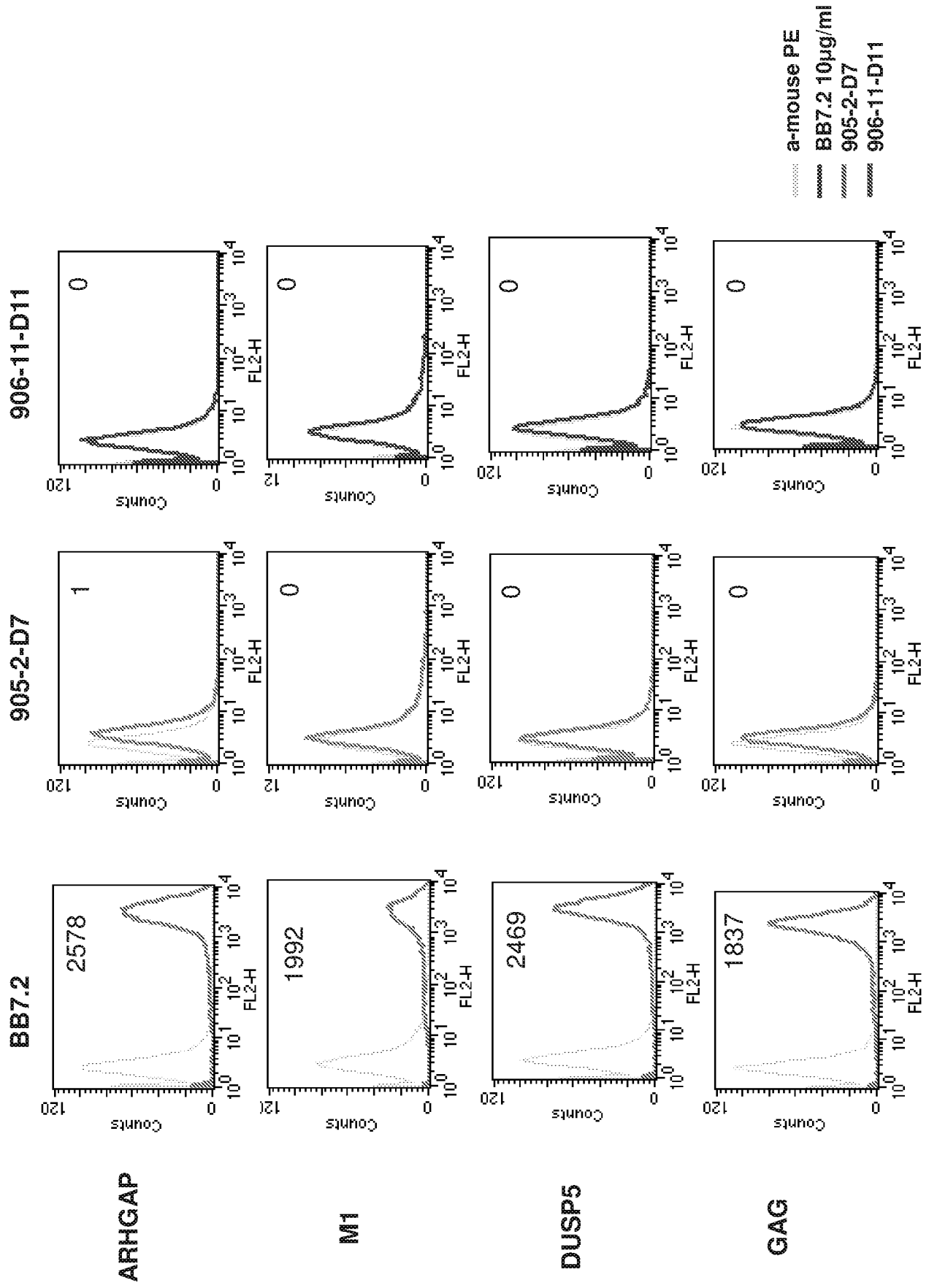


Figure 3 - continued

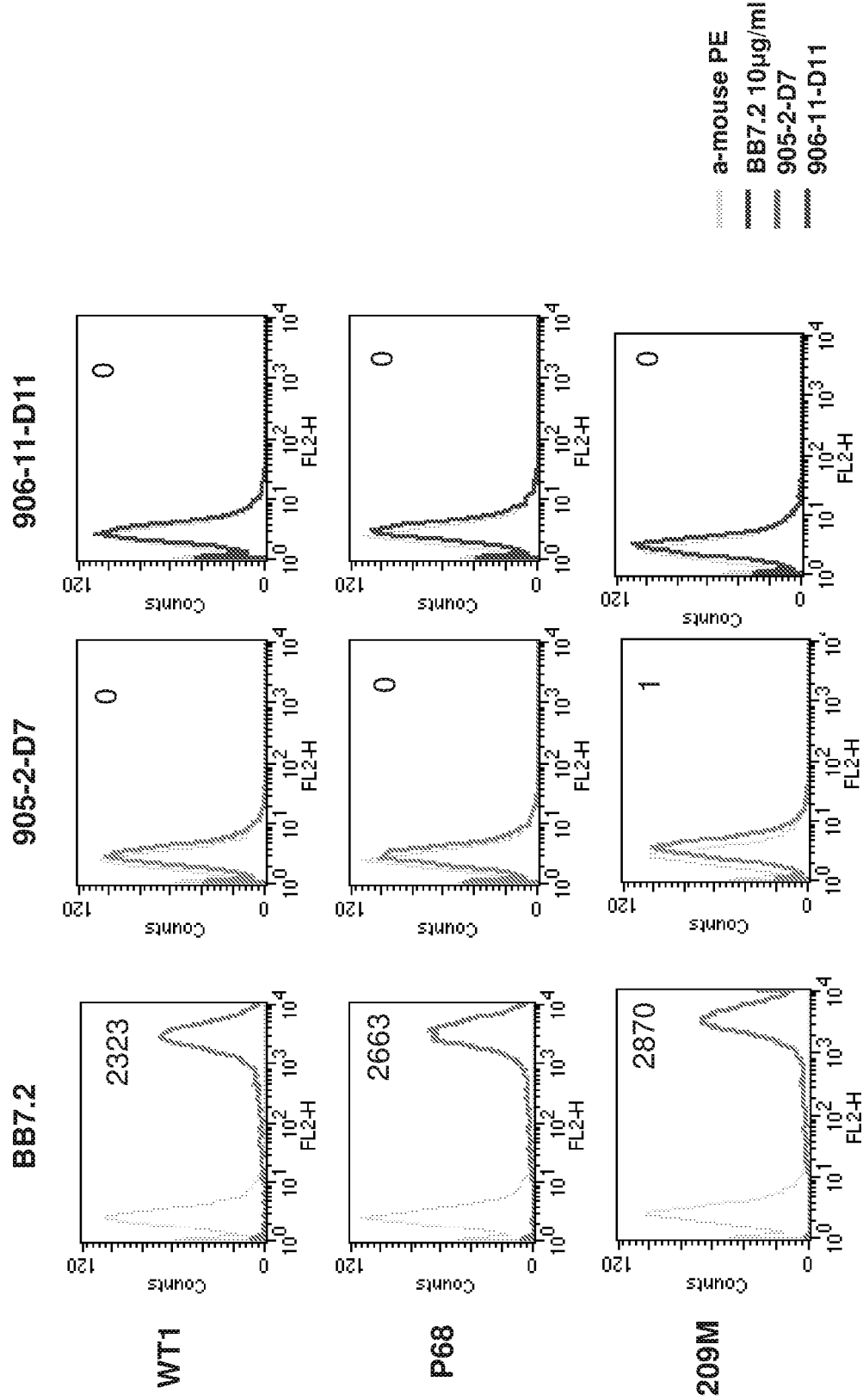


Figure 4

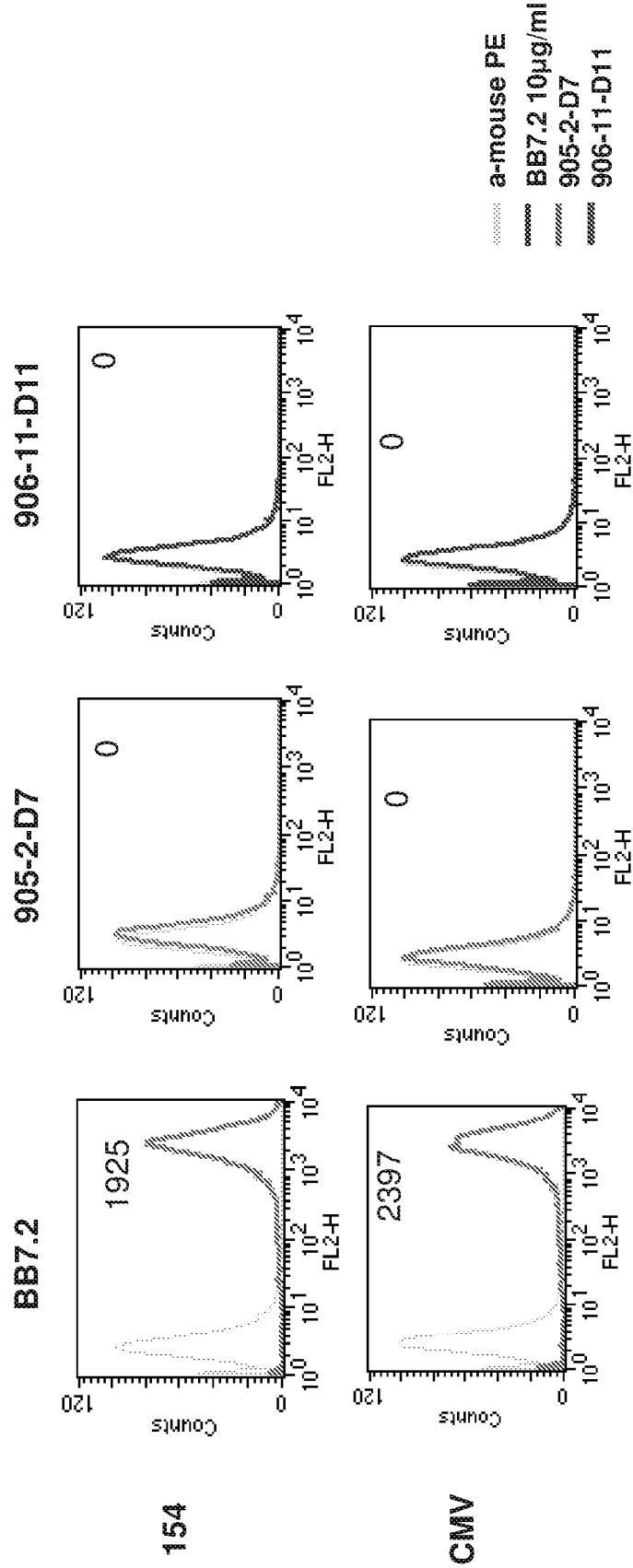
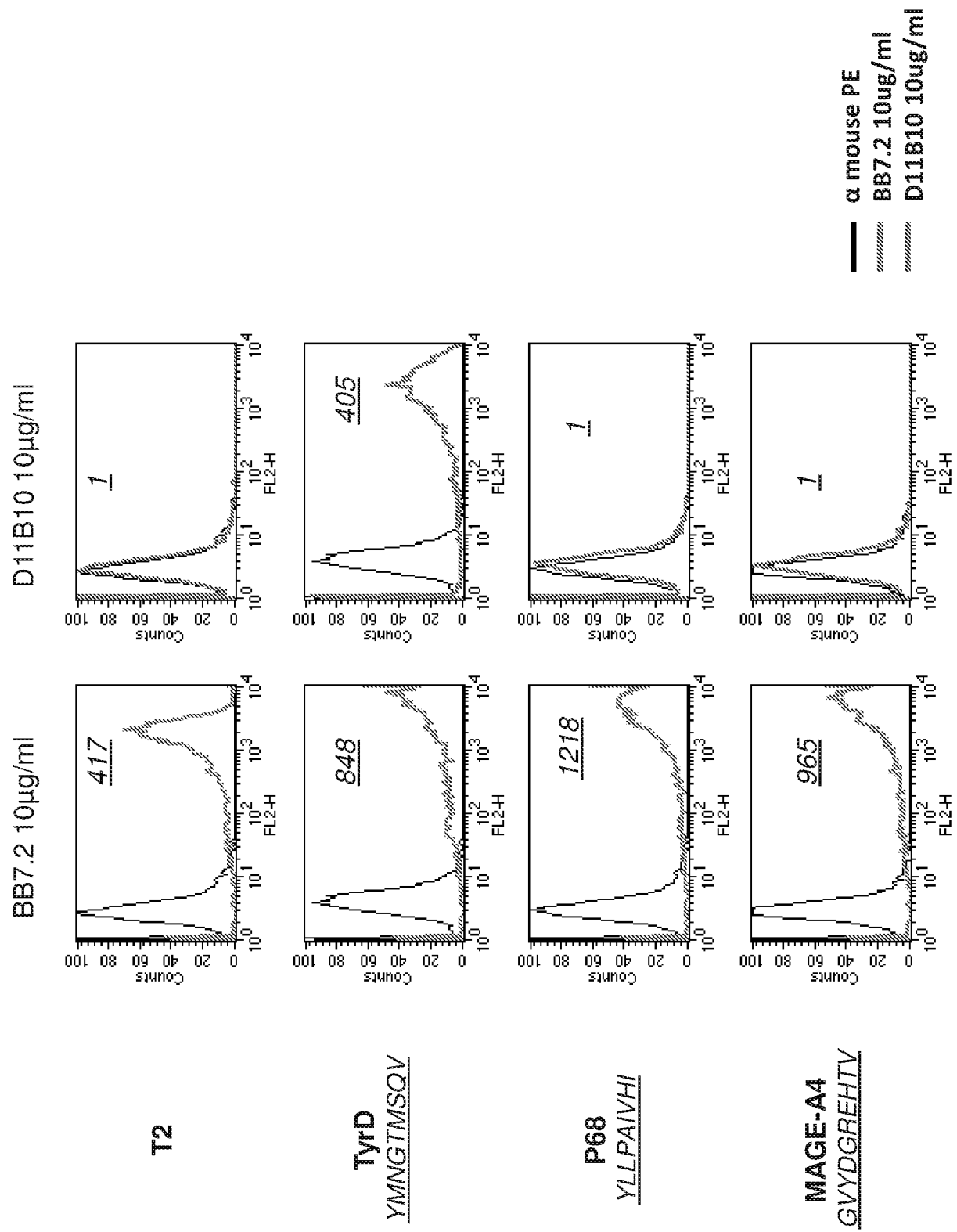
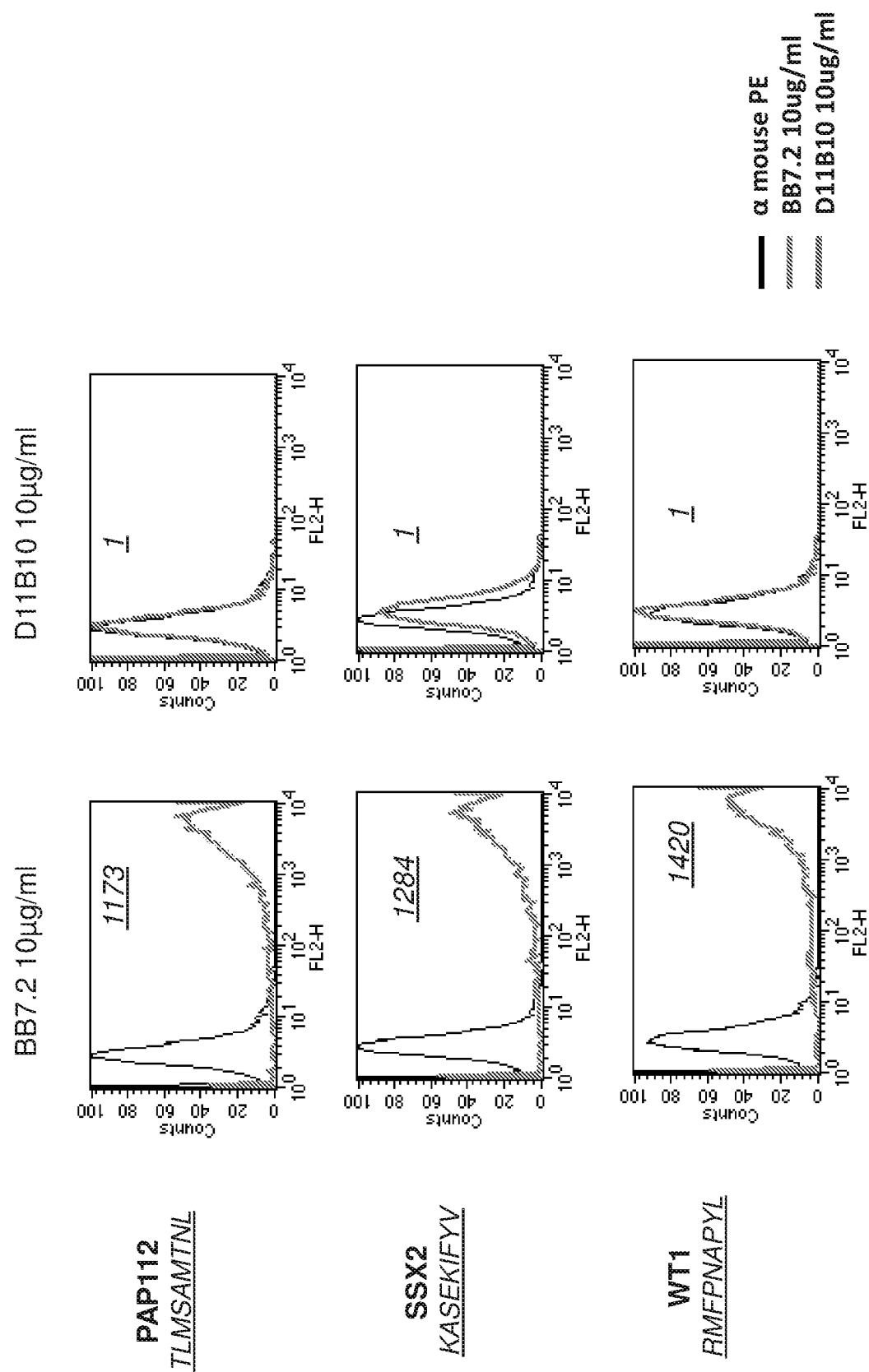


Figure 4 - continued



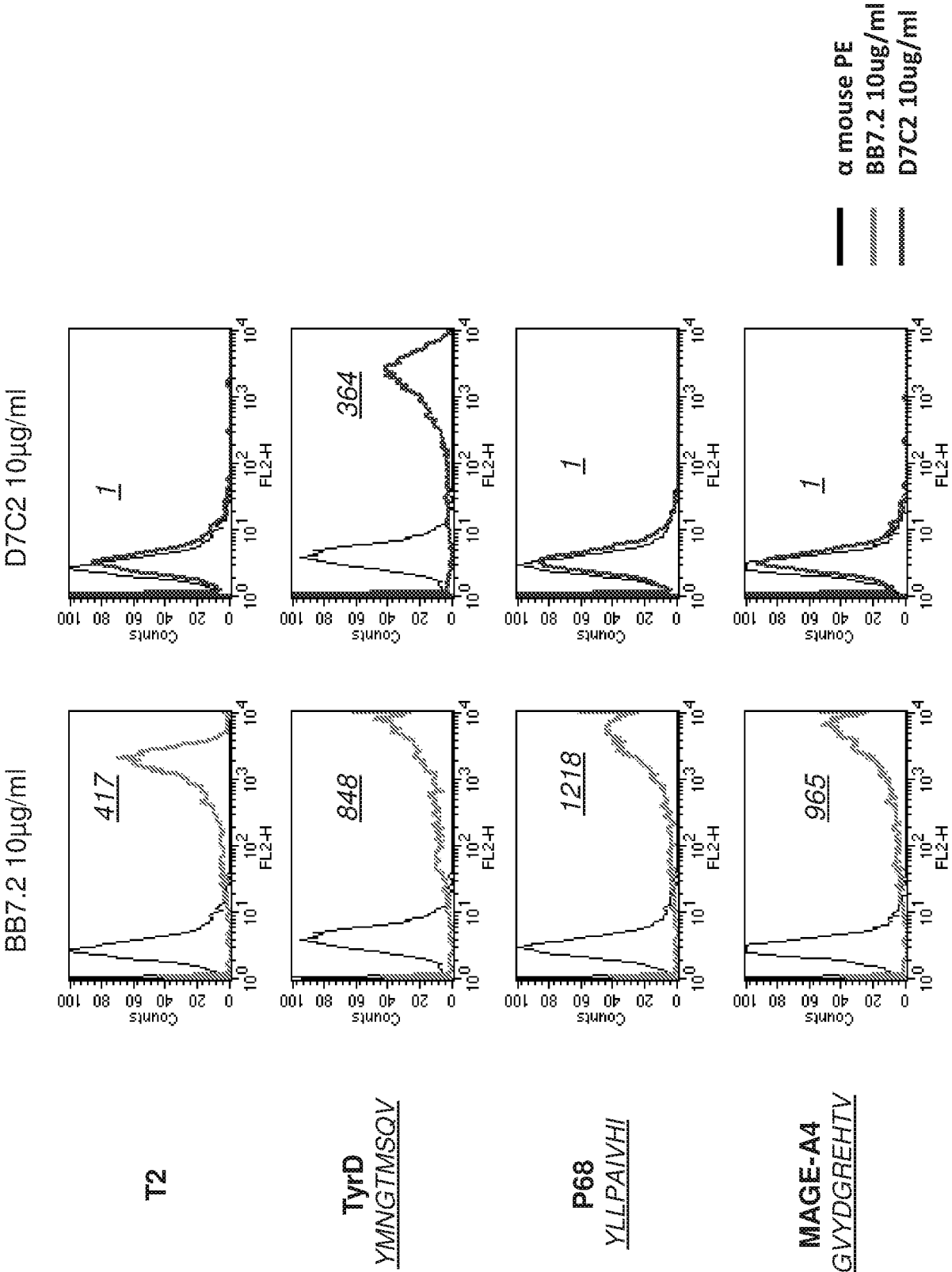
MFI values are relative to background. Value of `1` means no binding

Figure 5



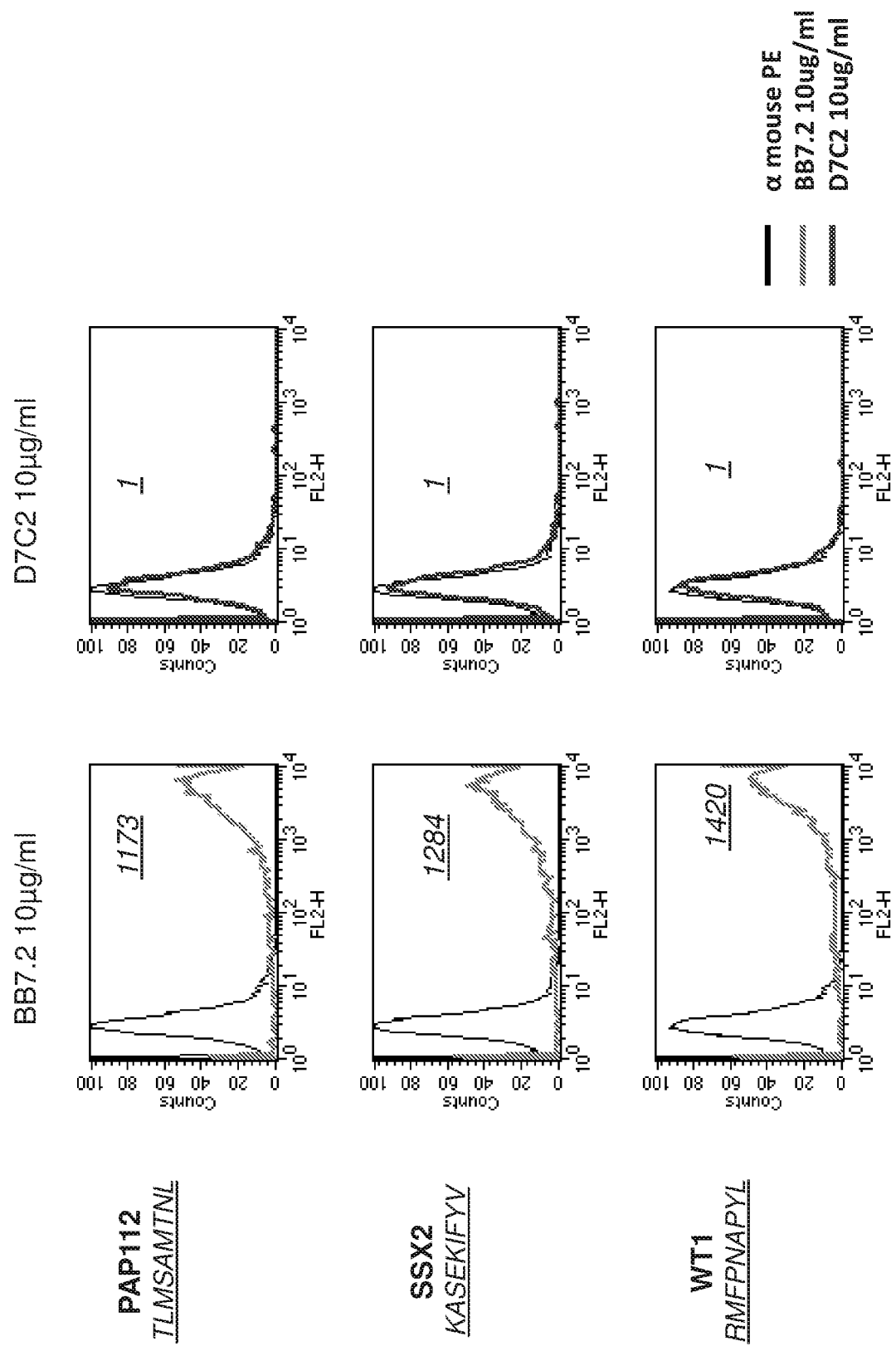
MFI values are relative to background. Value of `1` means no binding

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

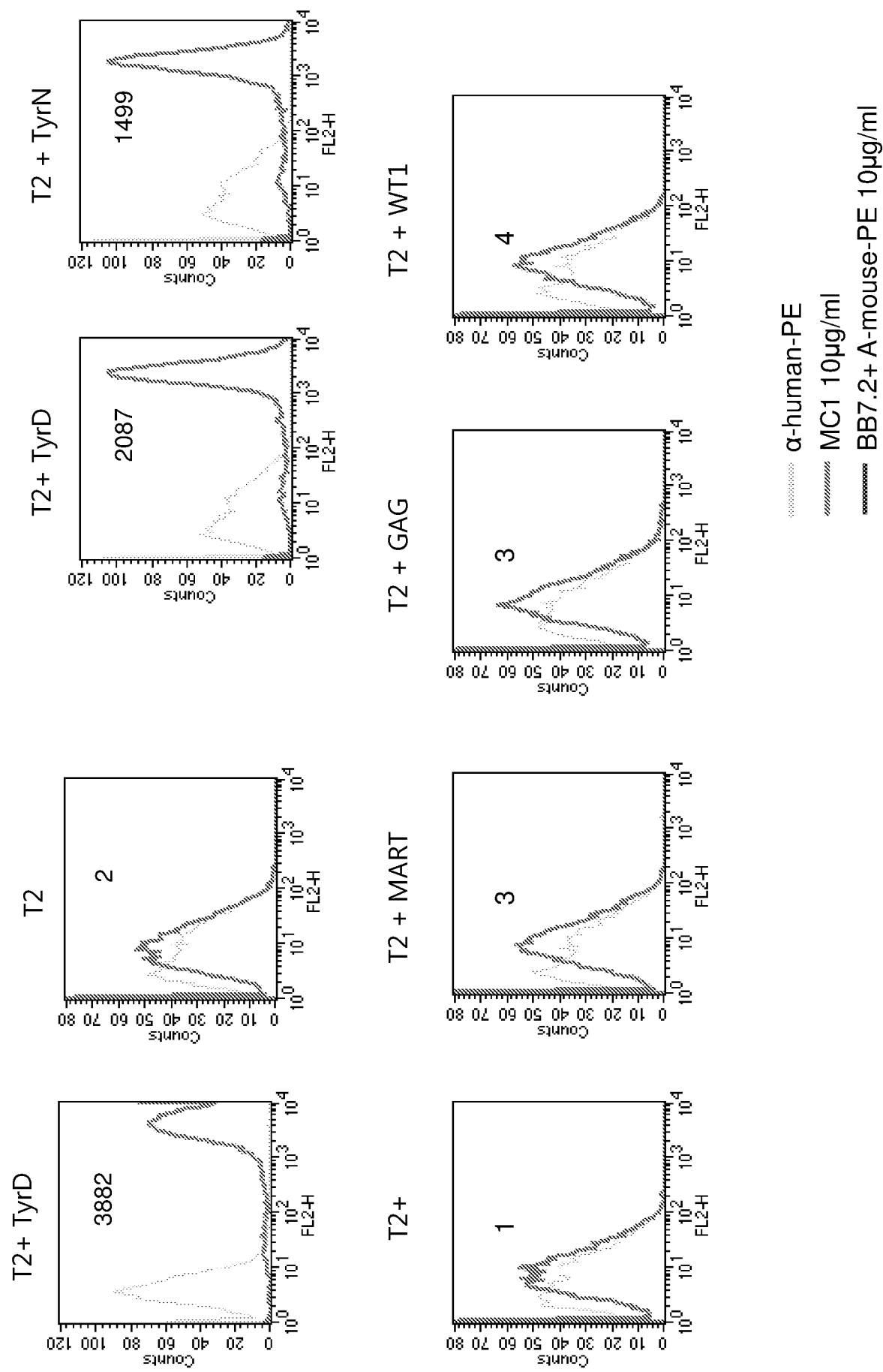


Figure 7

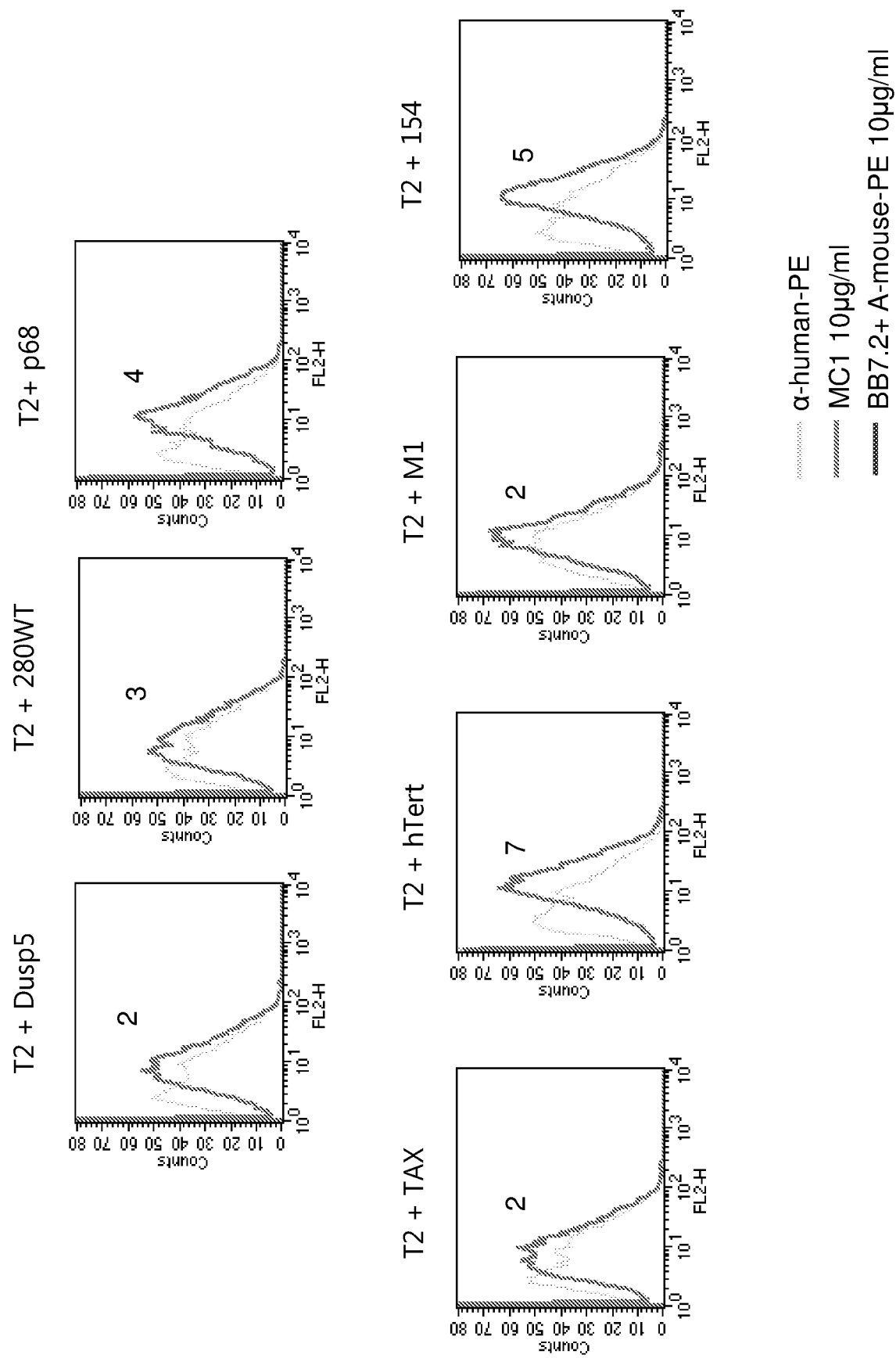


Figure 7 - continued

BB7.2 on A2+ Melanoma cells

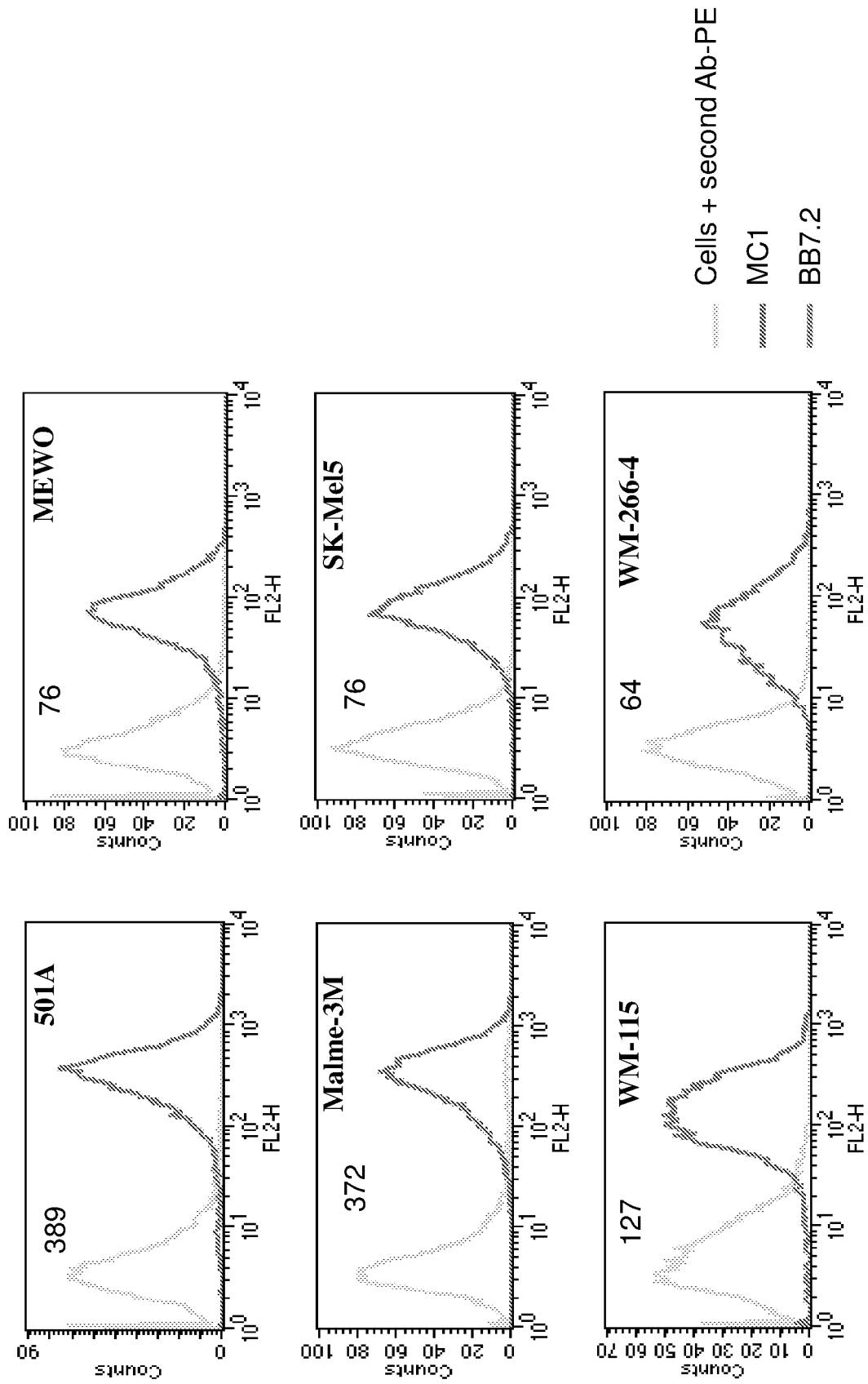


Figure 8

MC1 on A2+ Melanoma cells

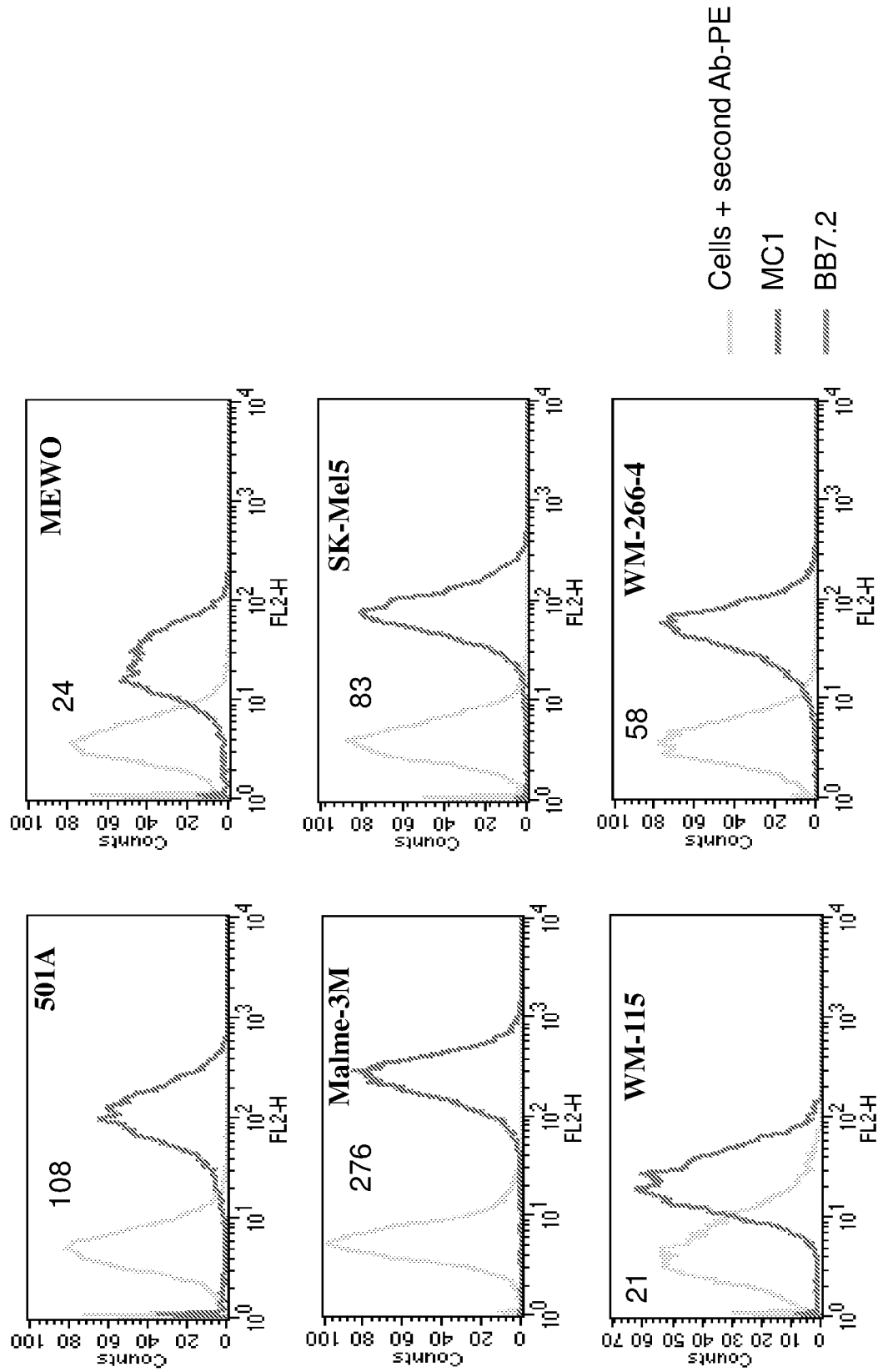
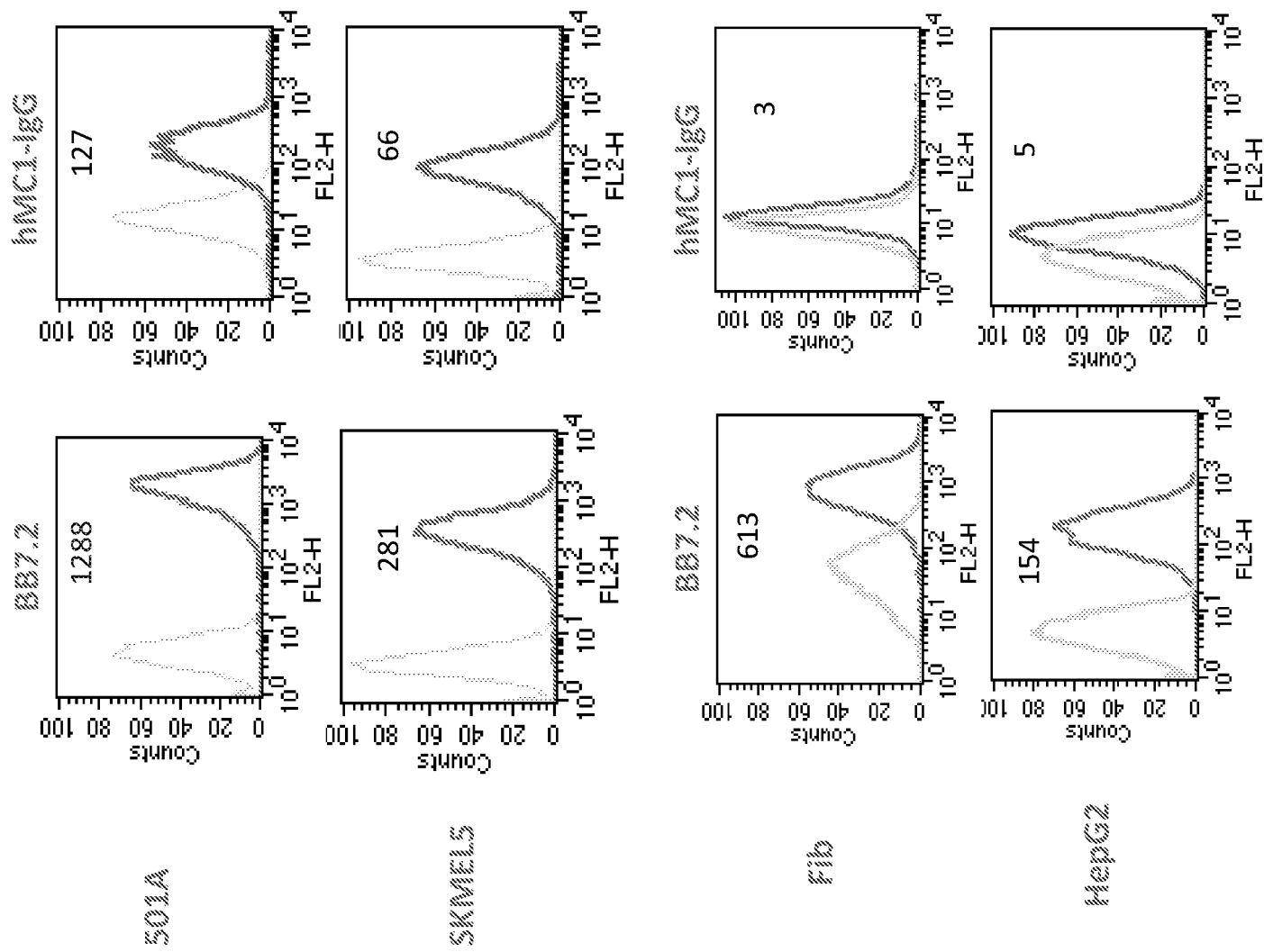
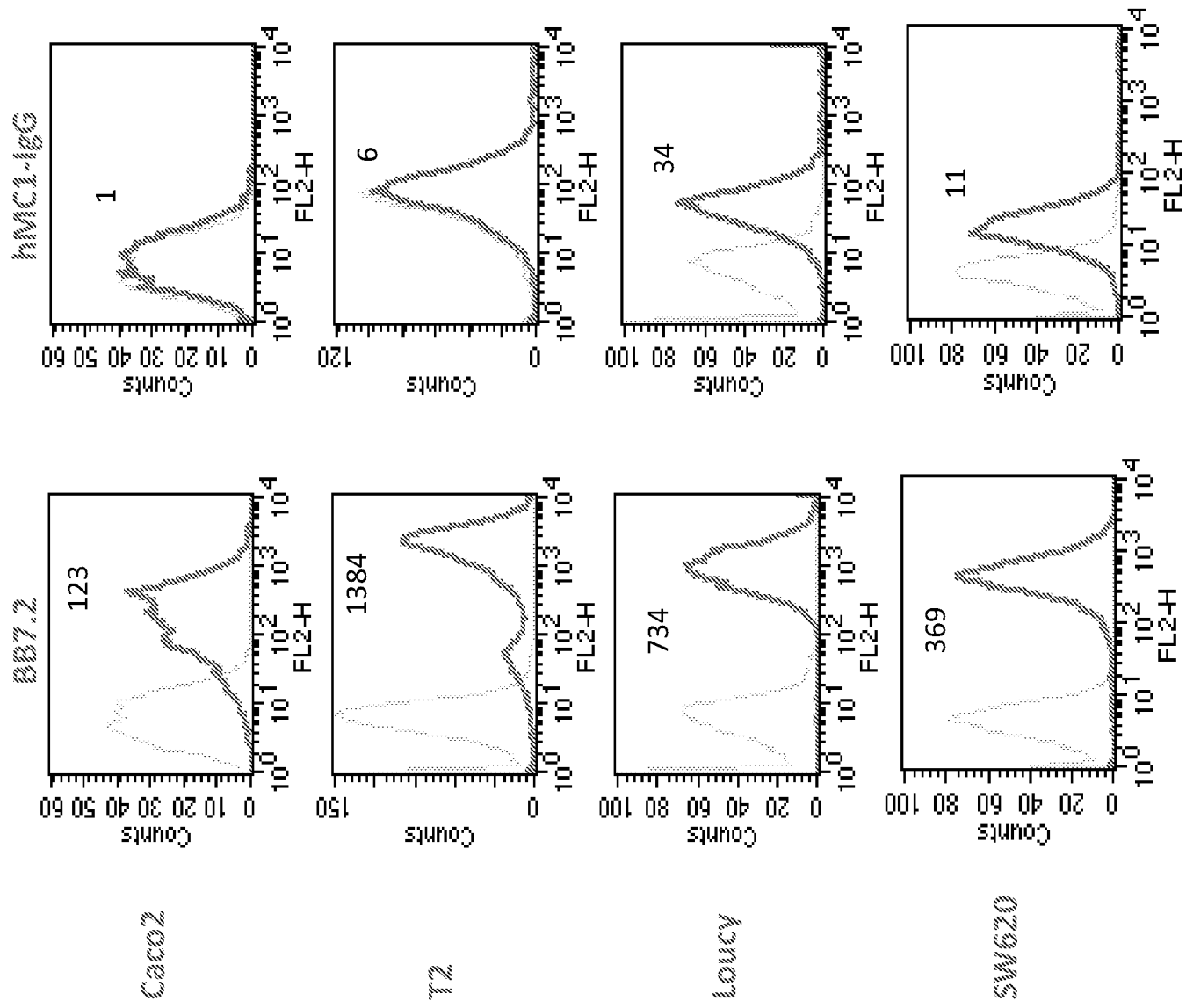


Figure 8 - continued



GeoMean number indicated

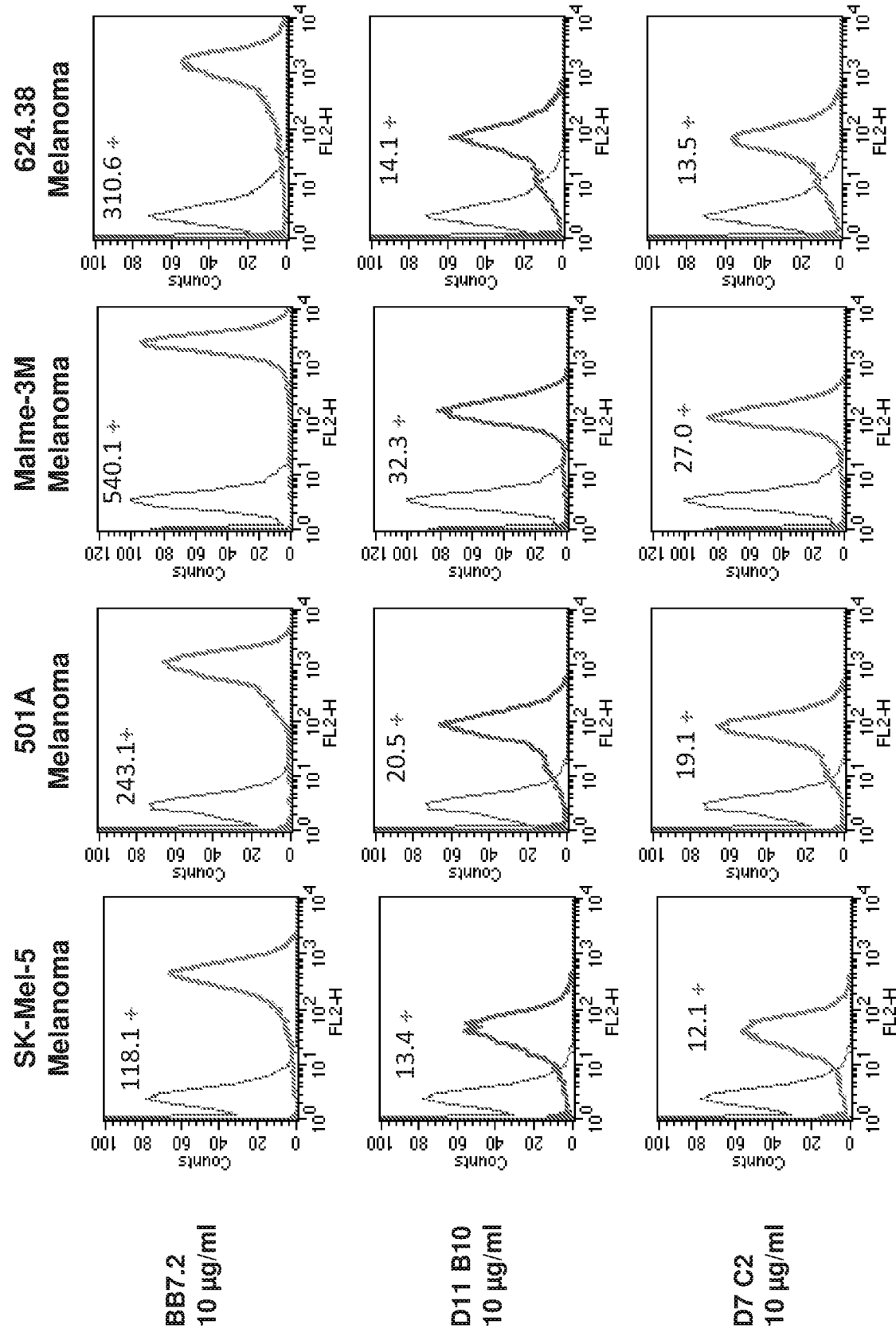
Figure 9



GeoMean number indicated

Figure 9 - continued

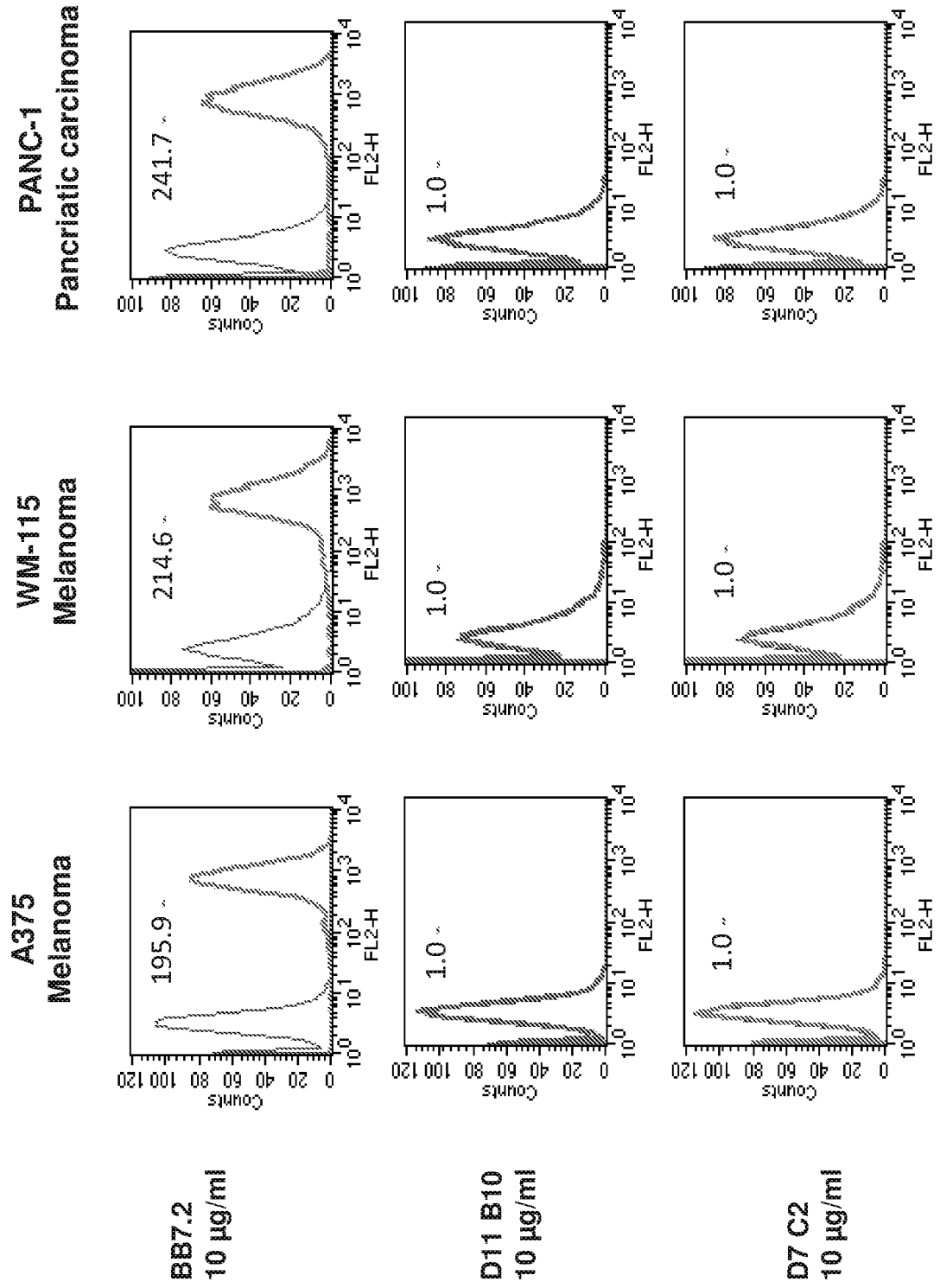
Antigen positive Melanoma cells



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

Figure 10

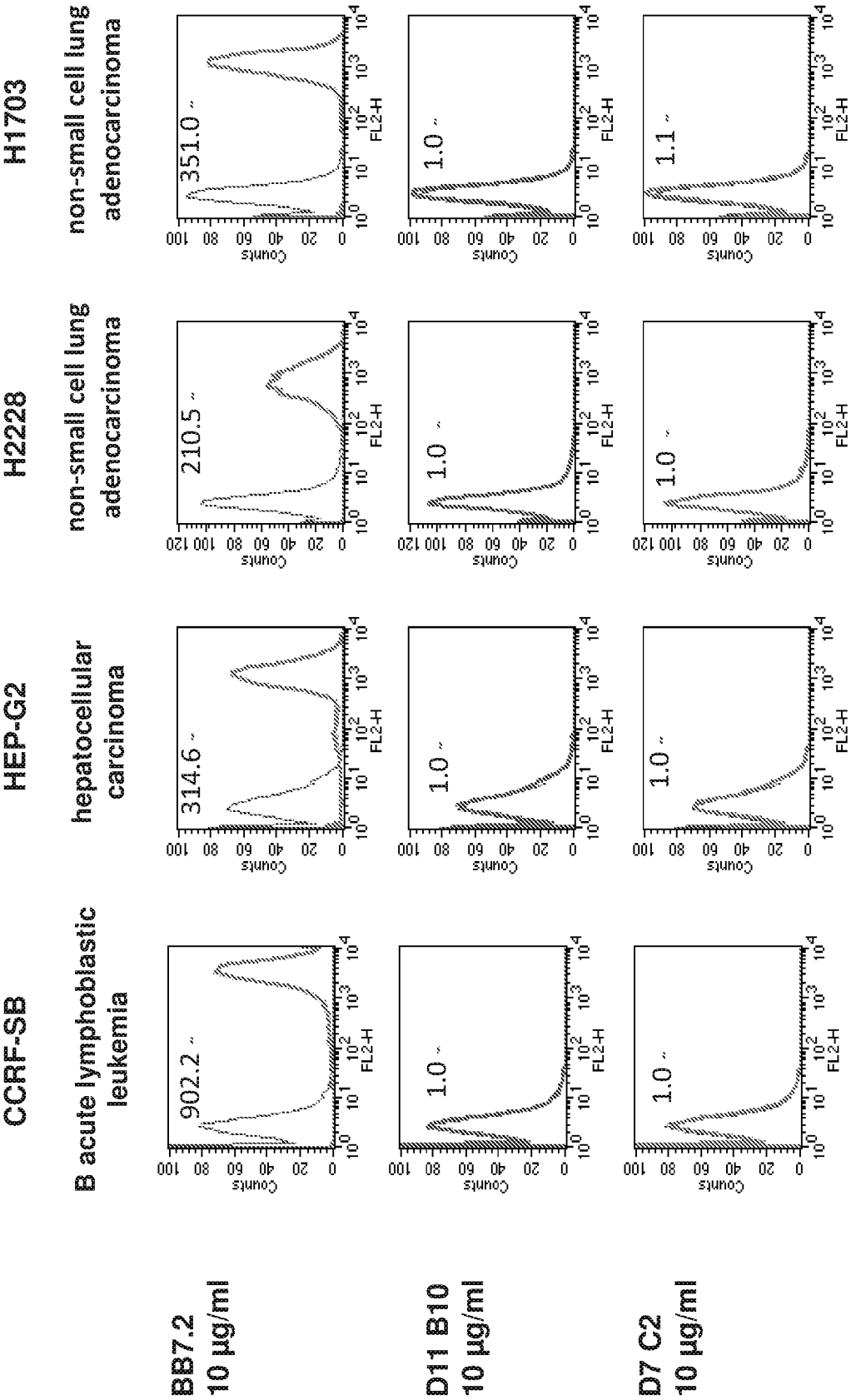
Antigen negative cell lines



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

Figure 10 - continued

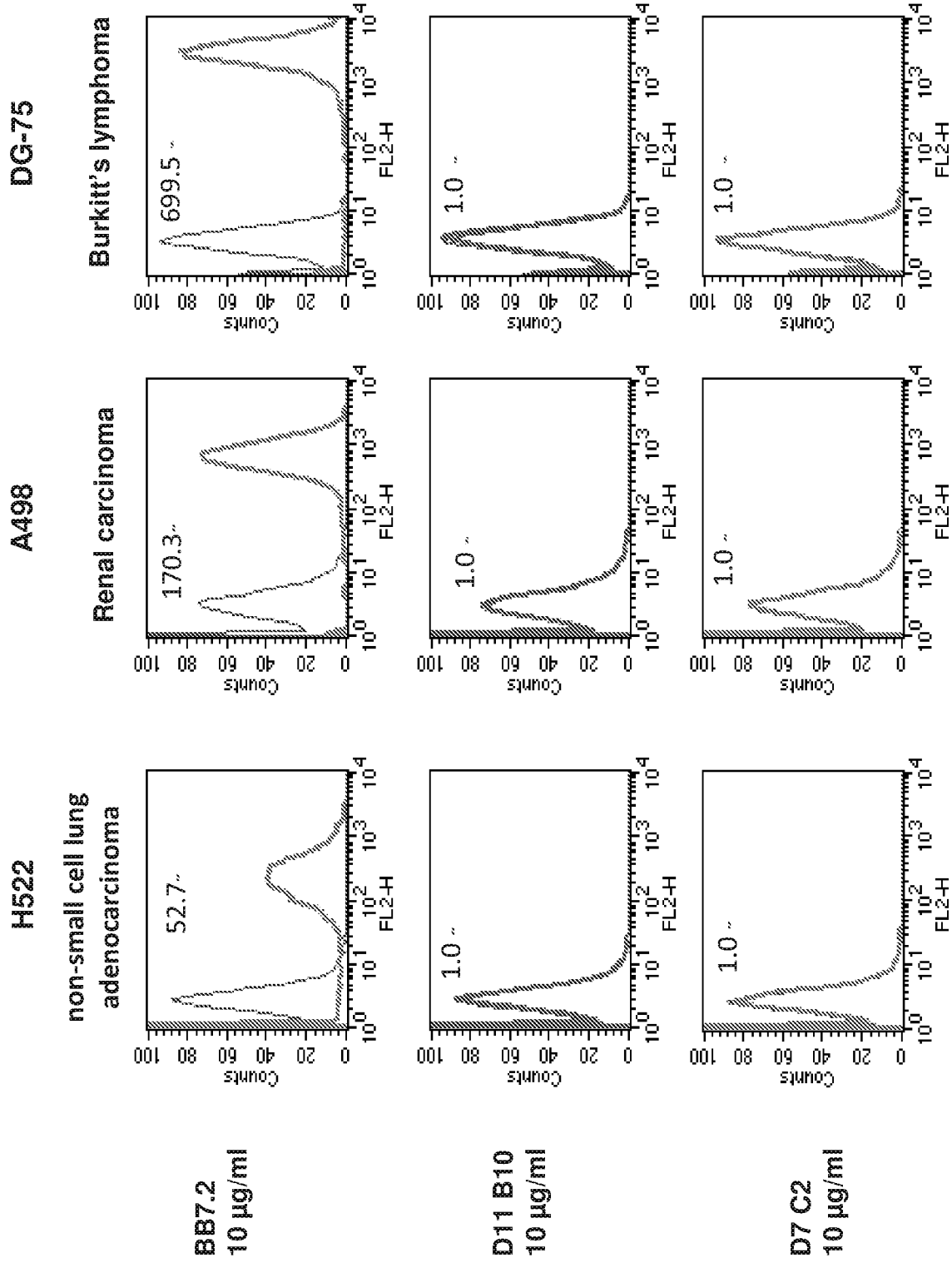
Antigen negative cell lines



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

Figure 10 - continued

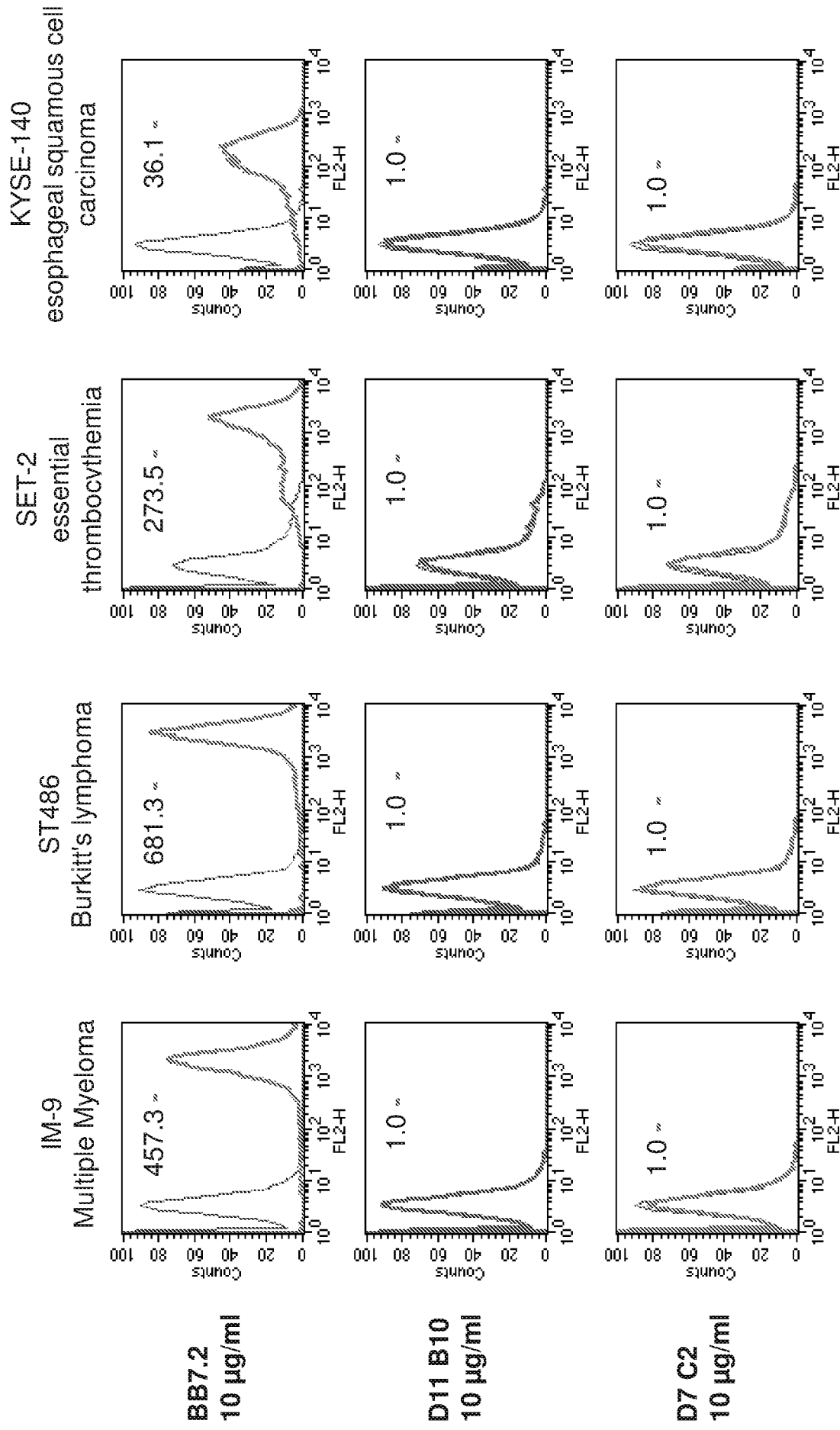
Antigen negative cell lines



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

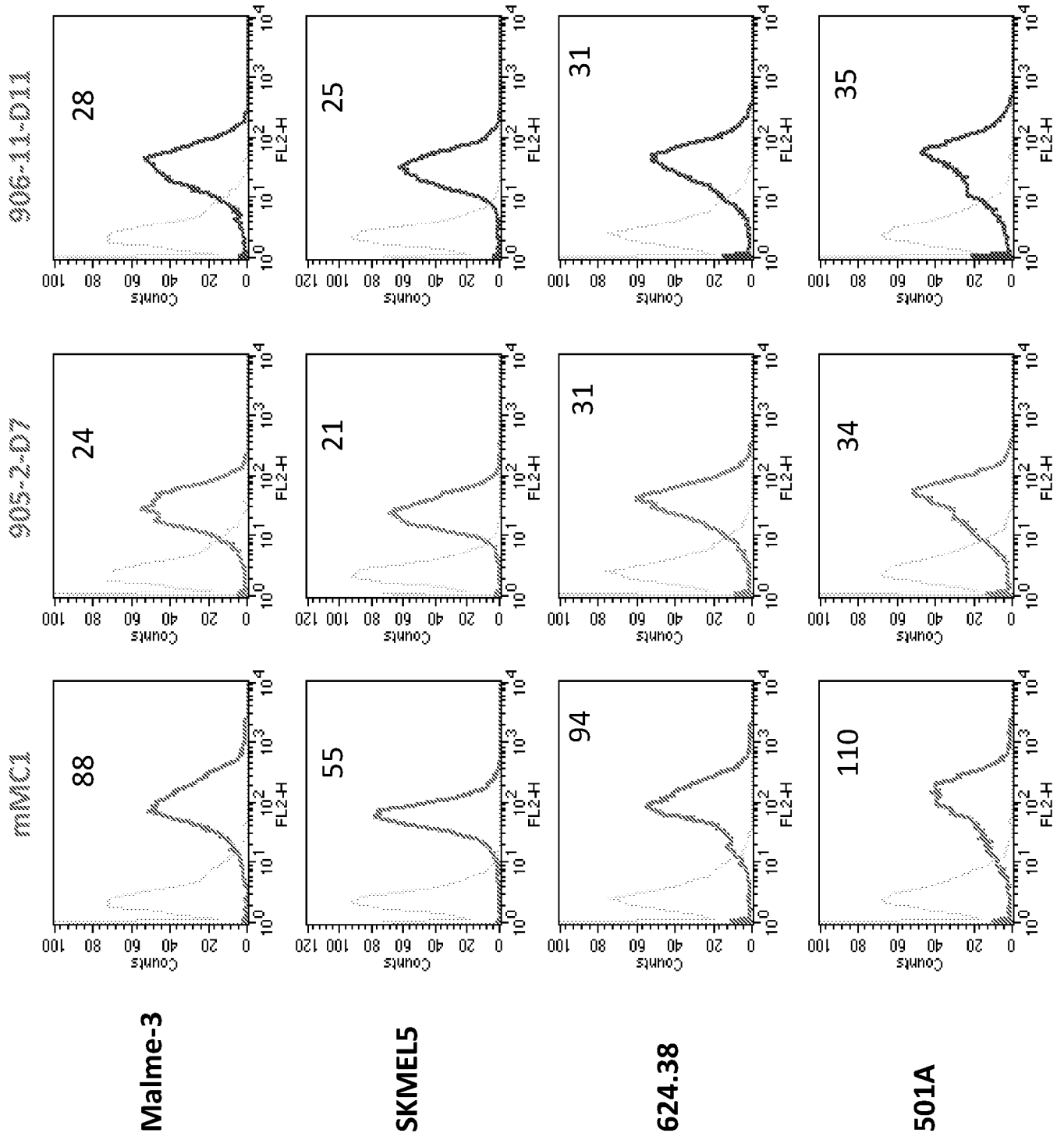


Figure 12

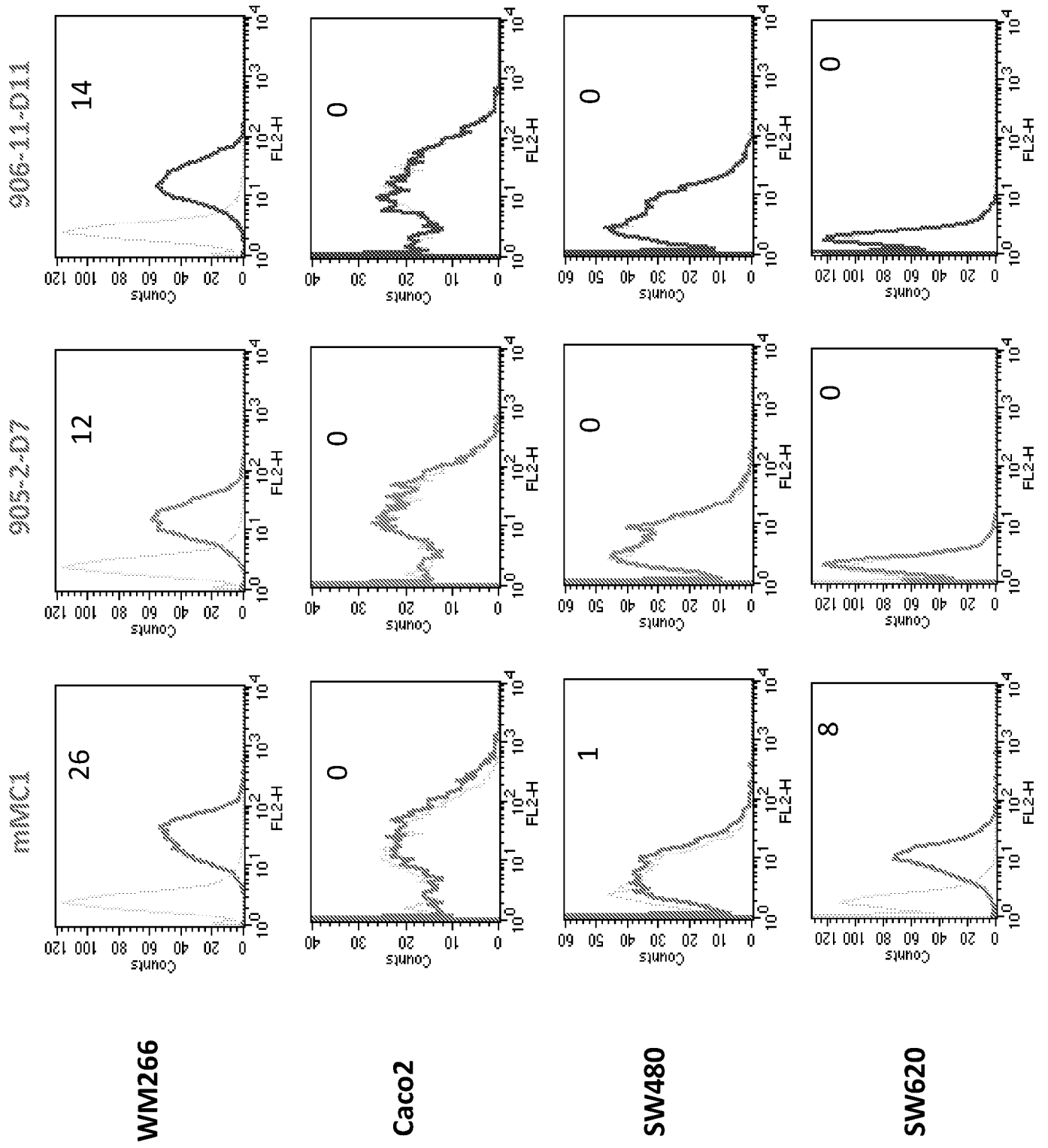


Figure 12 - continued

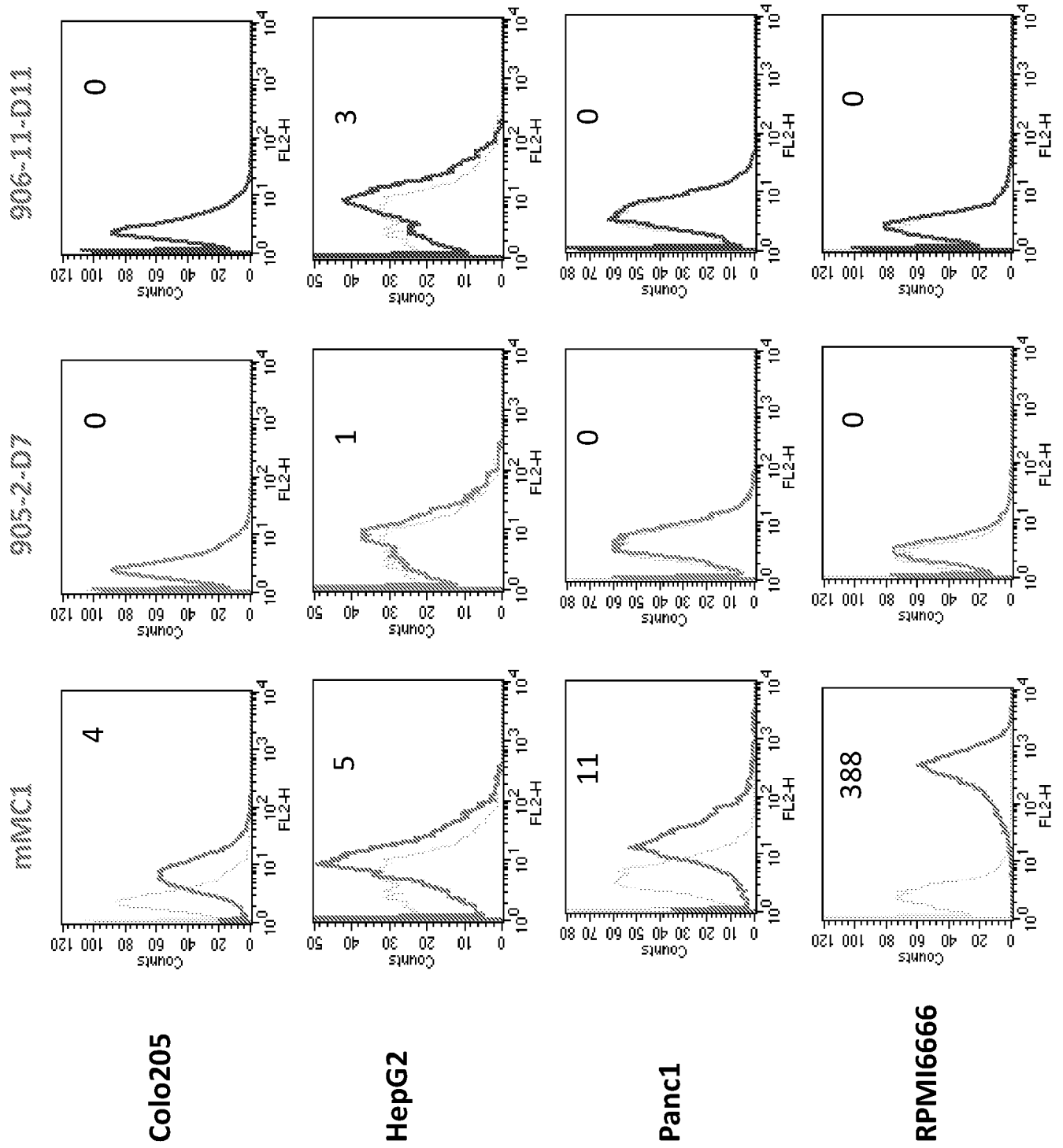


Figure 12 - continued

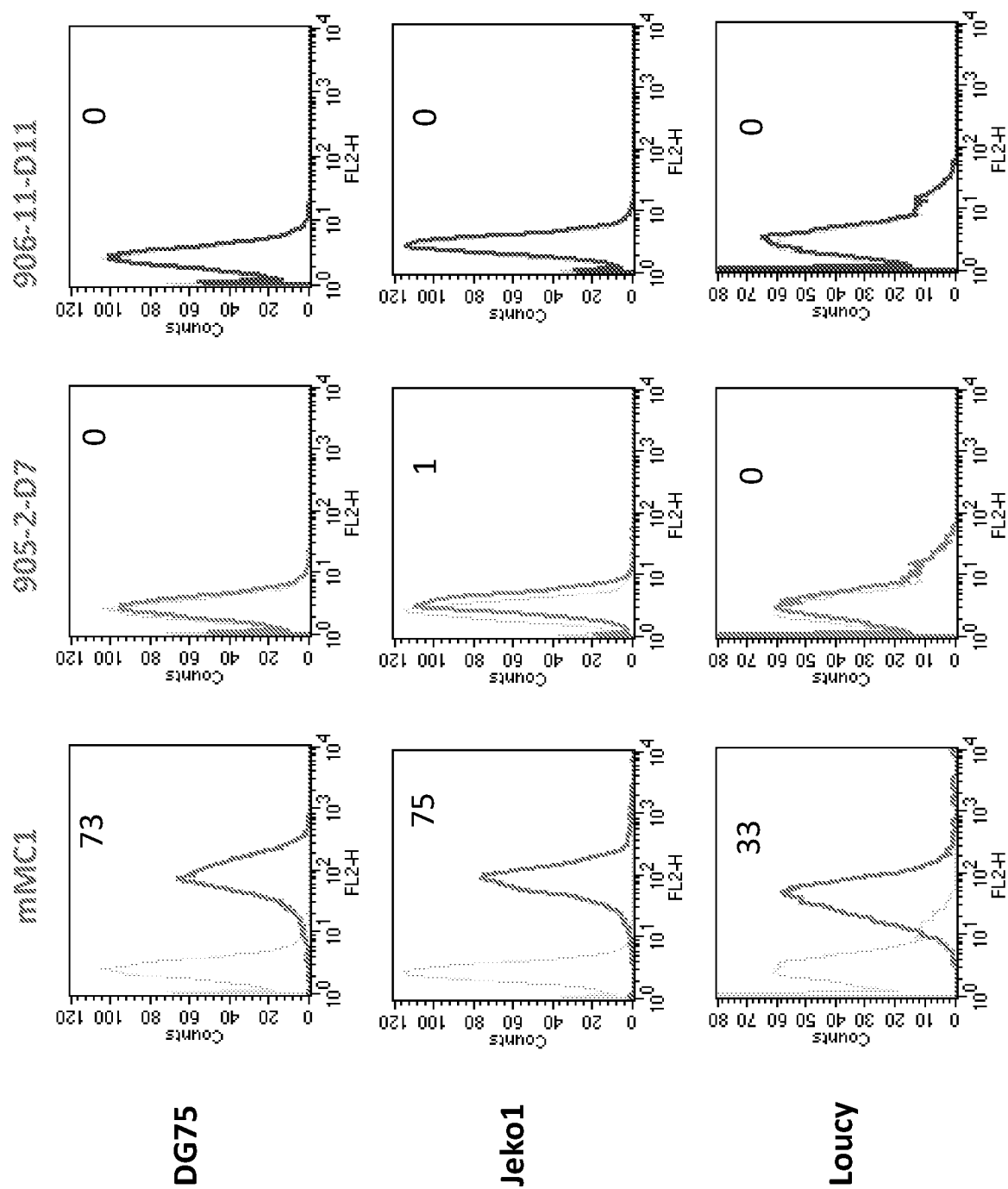


Figure 12 - continued

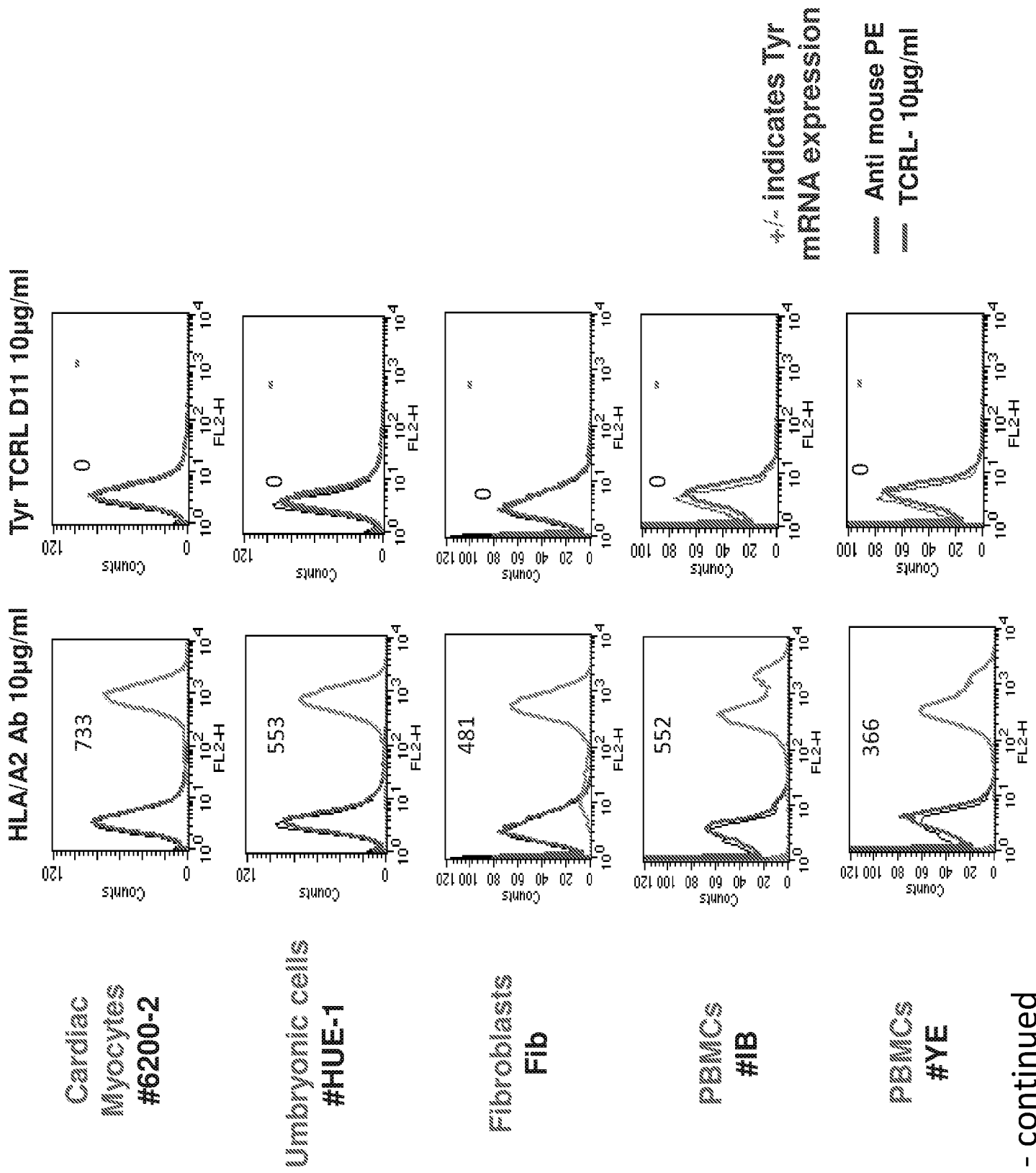


Figure 13 - continued

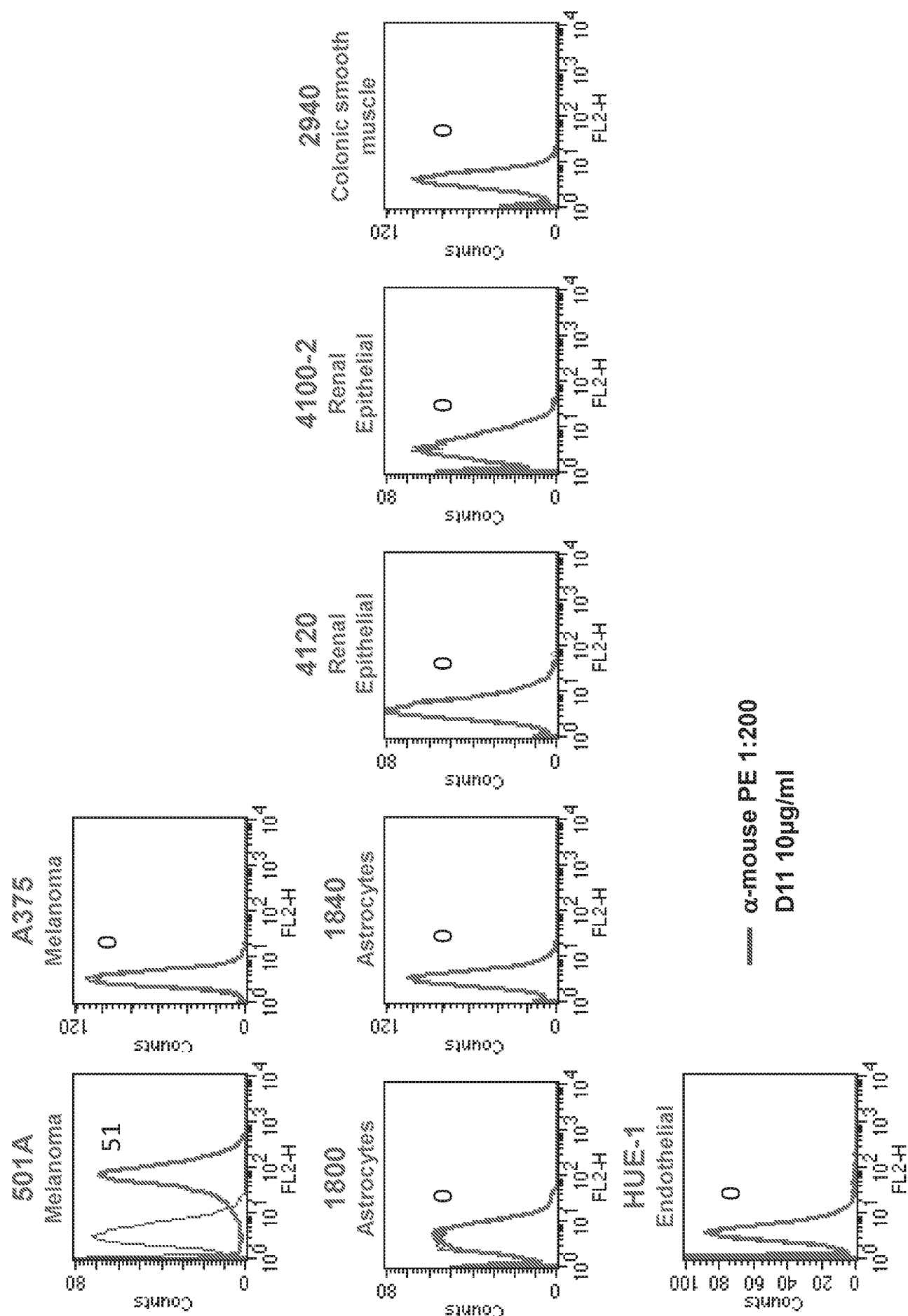


Figure 14

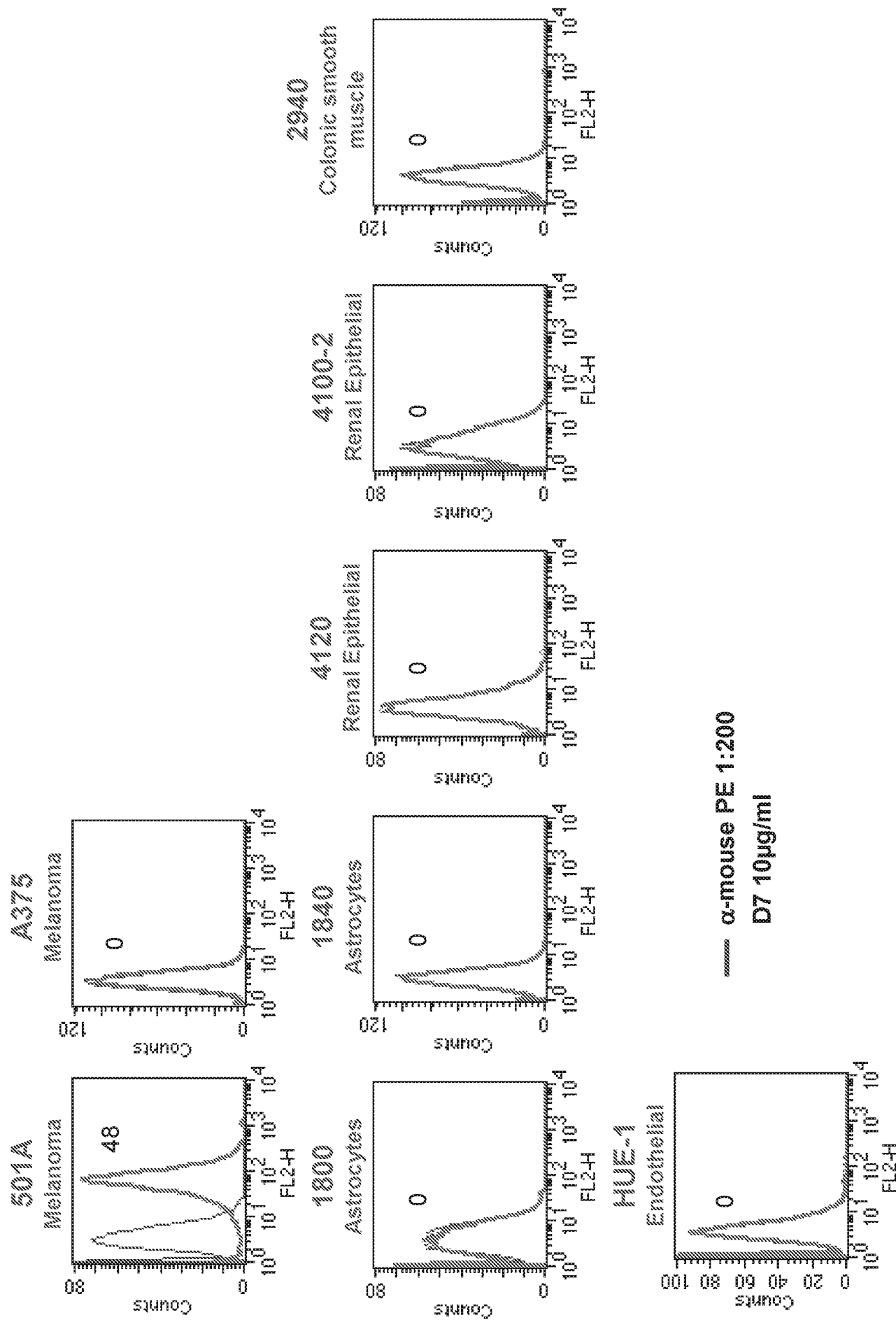


Figure 15

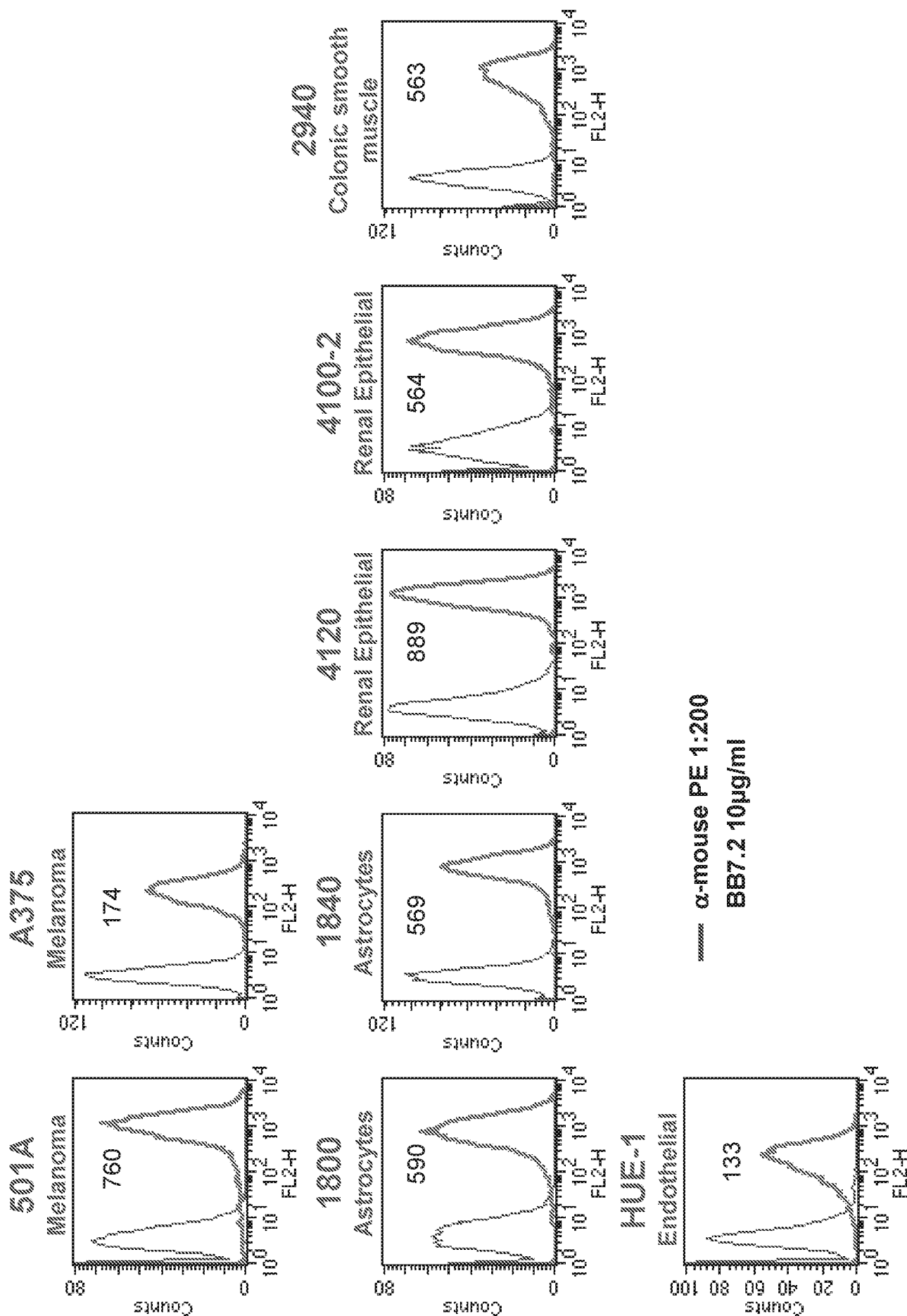


Figure 16

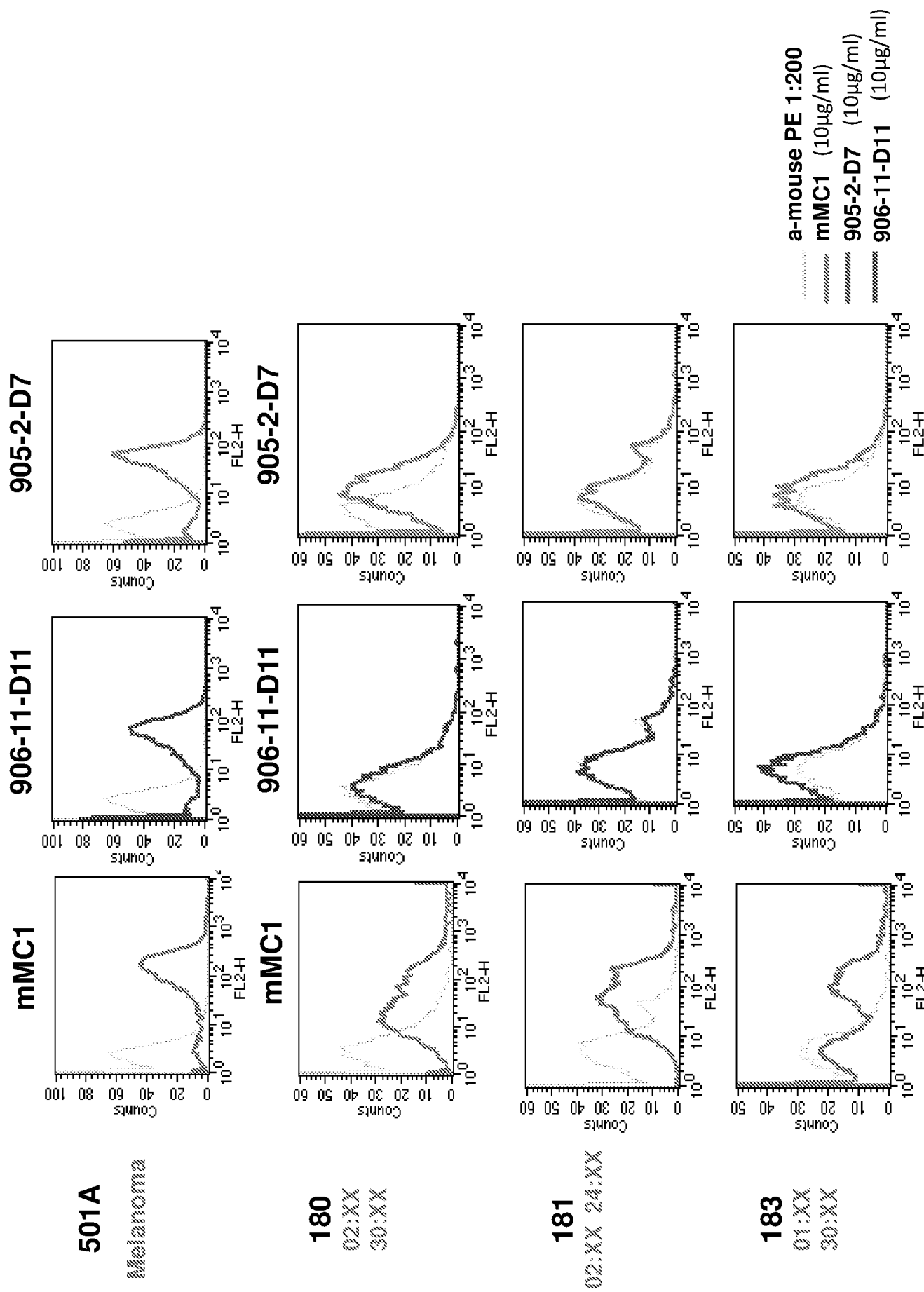


Figure 17

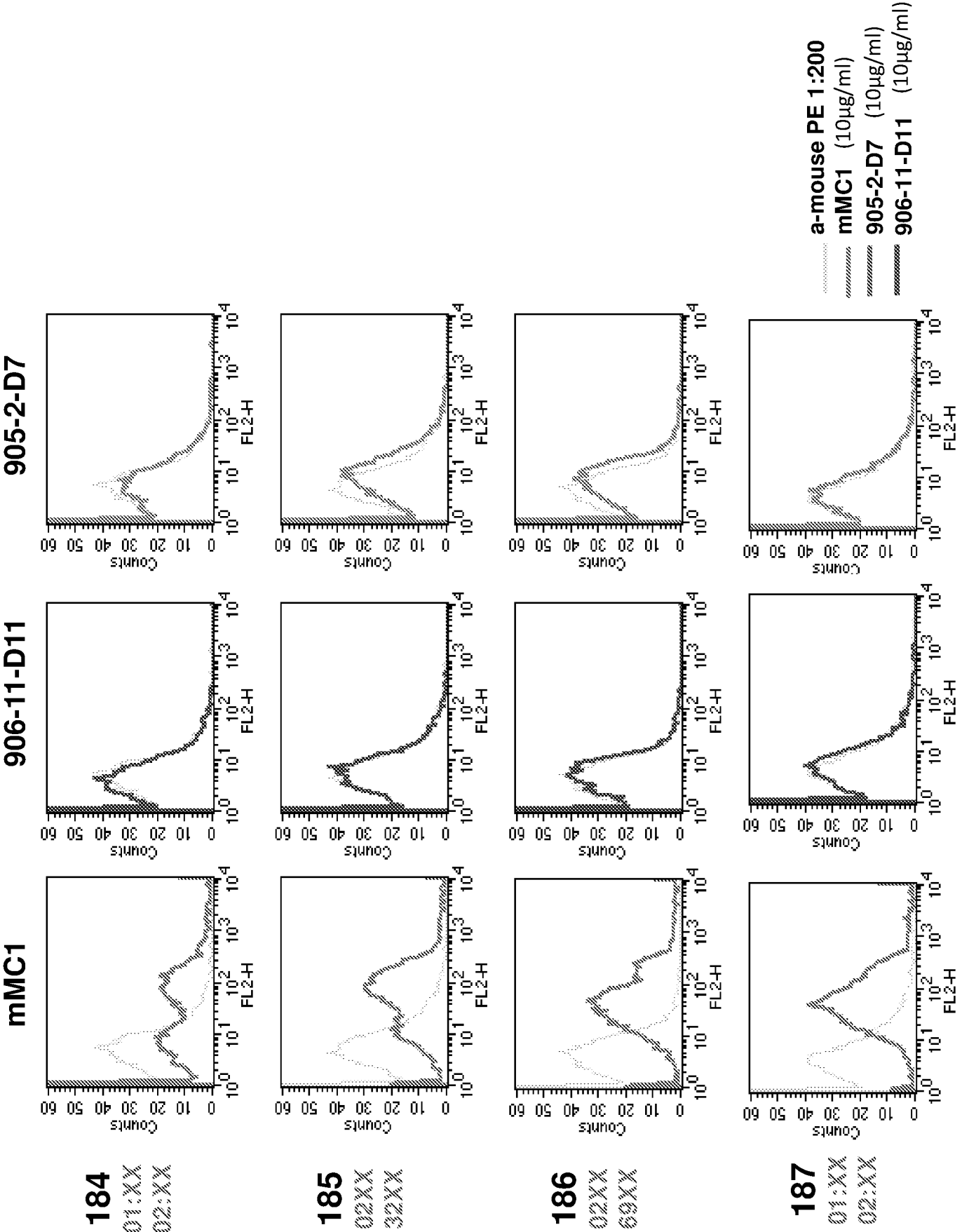
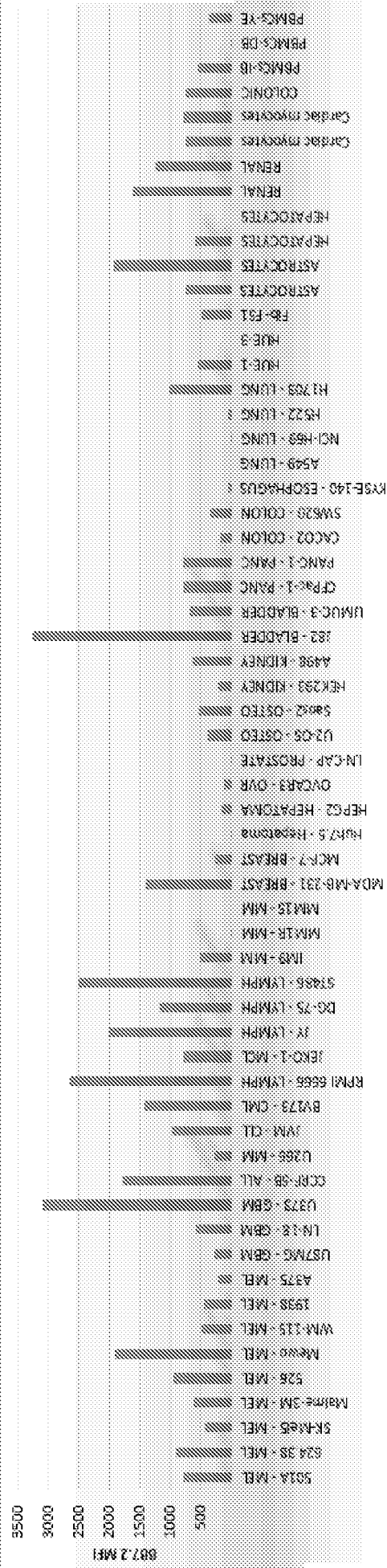


Figure 17 - continued

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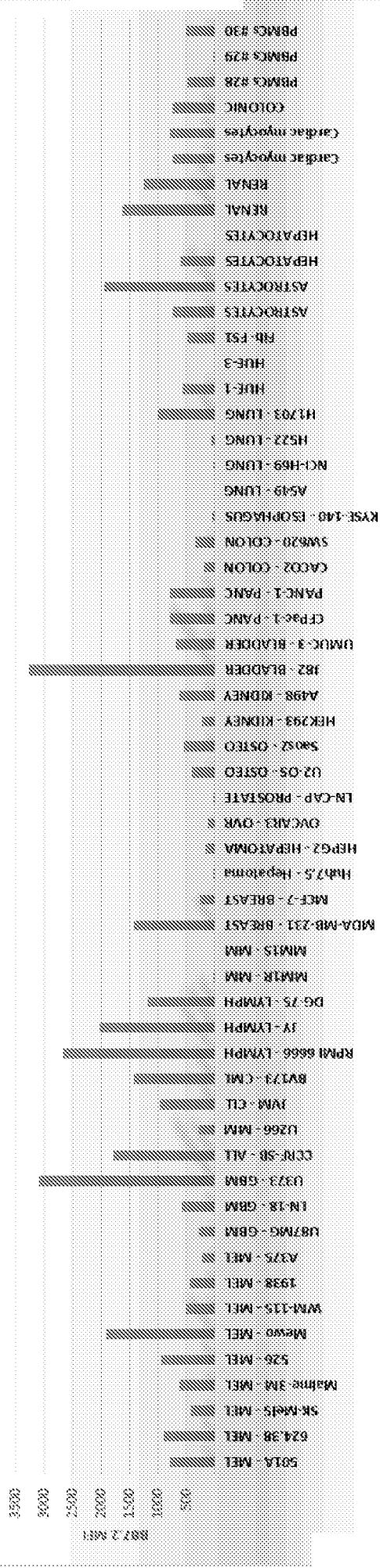


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[illegible]

Figure 18

HLA-A2 (BB7.2 binding)

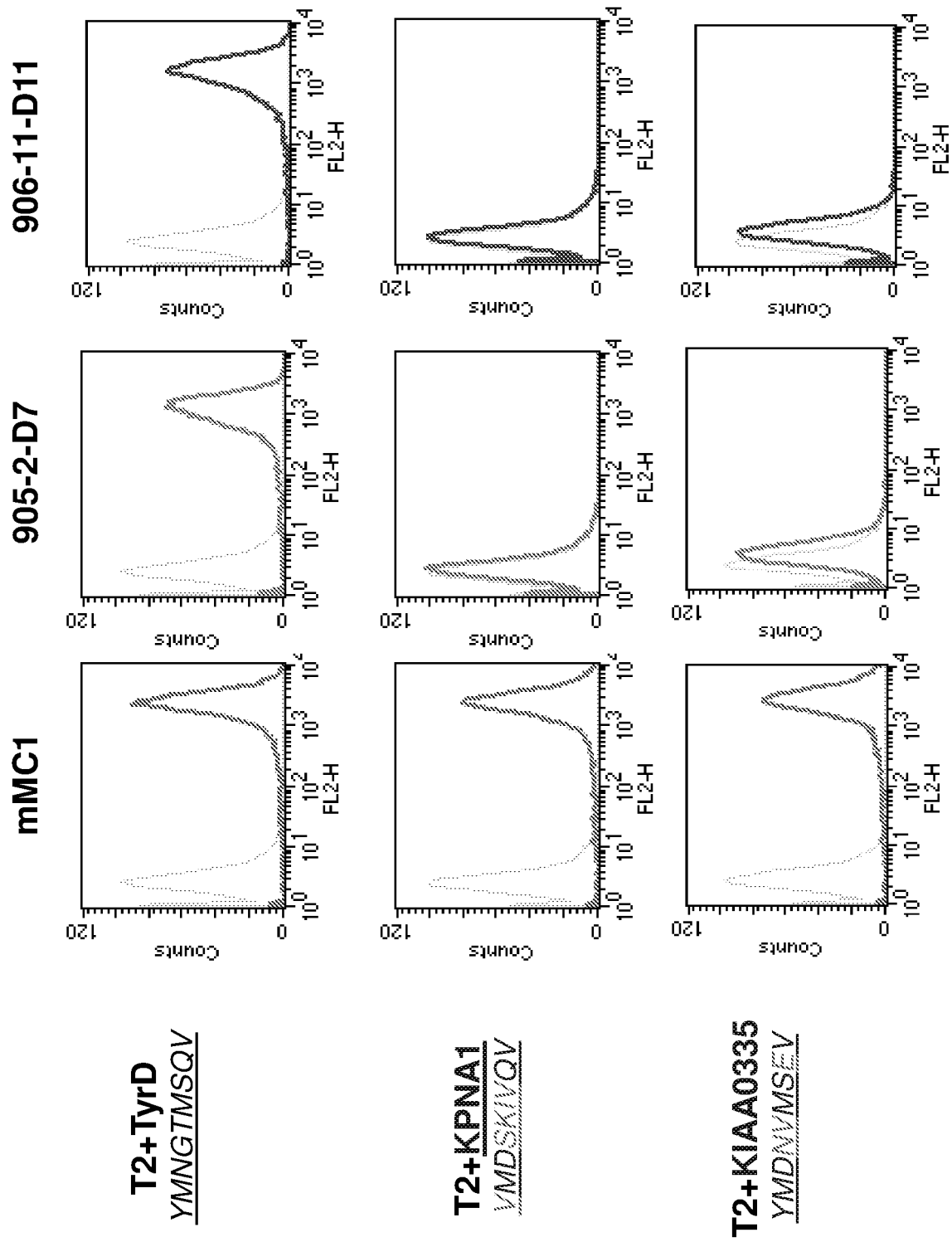


D7 Tyr TCPL binding to cells



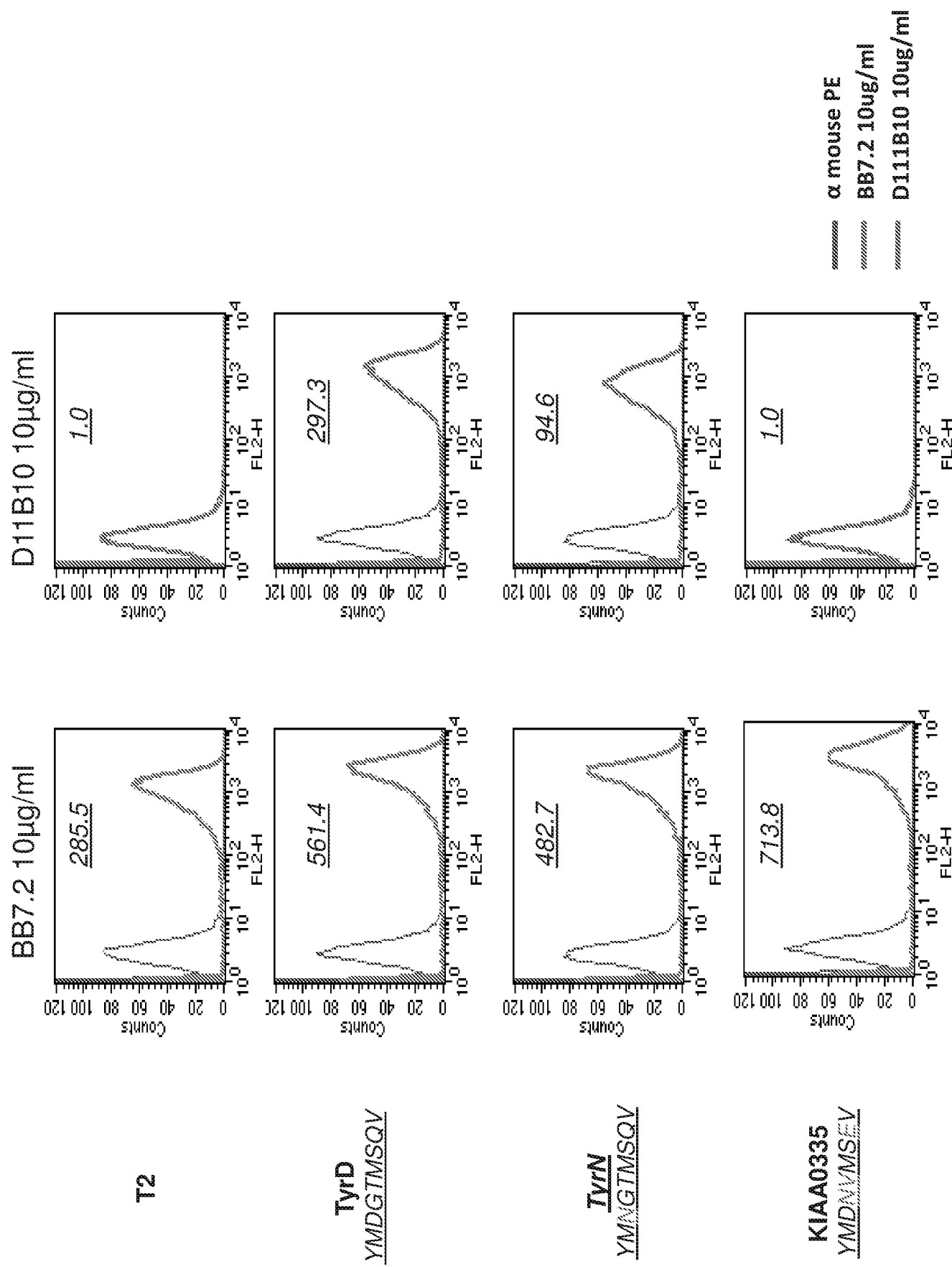
mRNA	protein	Melanoma										GBM					Hematological					Breast					Lung					PBMCs																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
		501A-MEL	624.38-MEL	SK-Mel5-MEL	Maligne-3M-MEL	526-MEL	U373-GBM	LN-18-GBM	U87MG-GBM	CCRF-58-ALL	U266-MIM	JYM-CIL	BV173-CML	RPMI 6666-LYMPH	JY-LYMPH	DG-75-LYMPH	MIM1R-MIM	MIM15-MIM	MDA-MB-231-BREAST	MCF-7-BREAST	Huh7.5-Hepatoma	HEPG2-HEPATOMA	OVCAR3-OVR	LN-CAP-PROSTATE	U2-OS-OSTEO	Saos2-OSTEO	HEK293-KIDNEY	A498-KIDNEY	J82-BLADDER	UMUC-3-BLADDER	CFPAC-1-PANC	PANC-1-PANC	CAC02-COLON	SW620-COLON	KYSE-140-ESOPHAGUS	A549-LUNG	NCI-H69-LUNG	H522-LUNG	H1703-LUNG	HUE-1	HUE-3	RB-F51	ASTROCYTES	HEPATOCYTES	HEPATOCYTES	RENAL	RENAL	Cardiac myocytes	COLONIC	PBMCs #28	PBMCs #29	PBMCs #30																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
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Figure 19



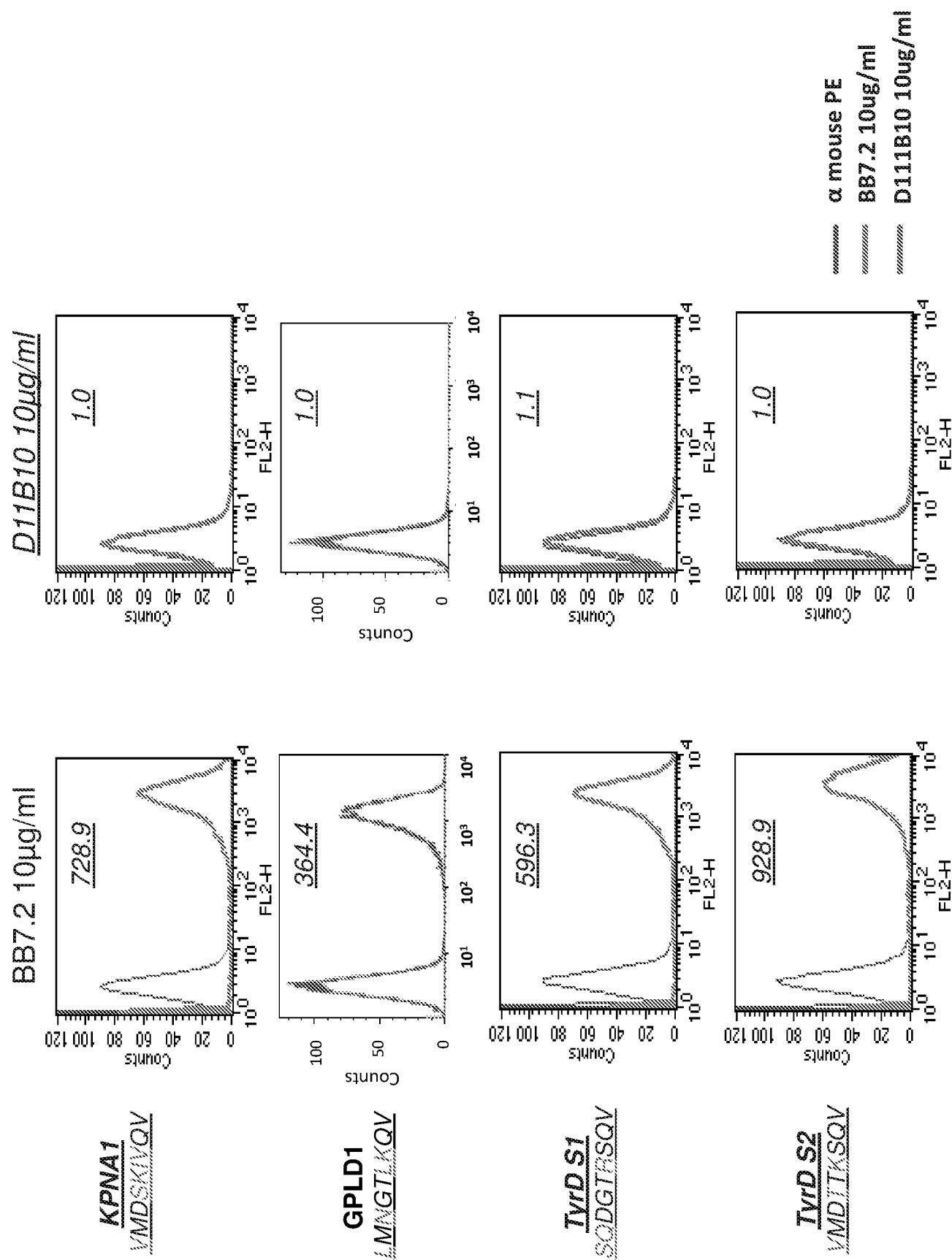
Similar Peptides

Figure 20



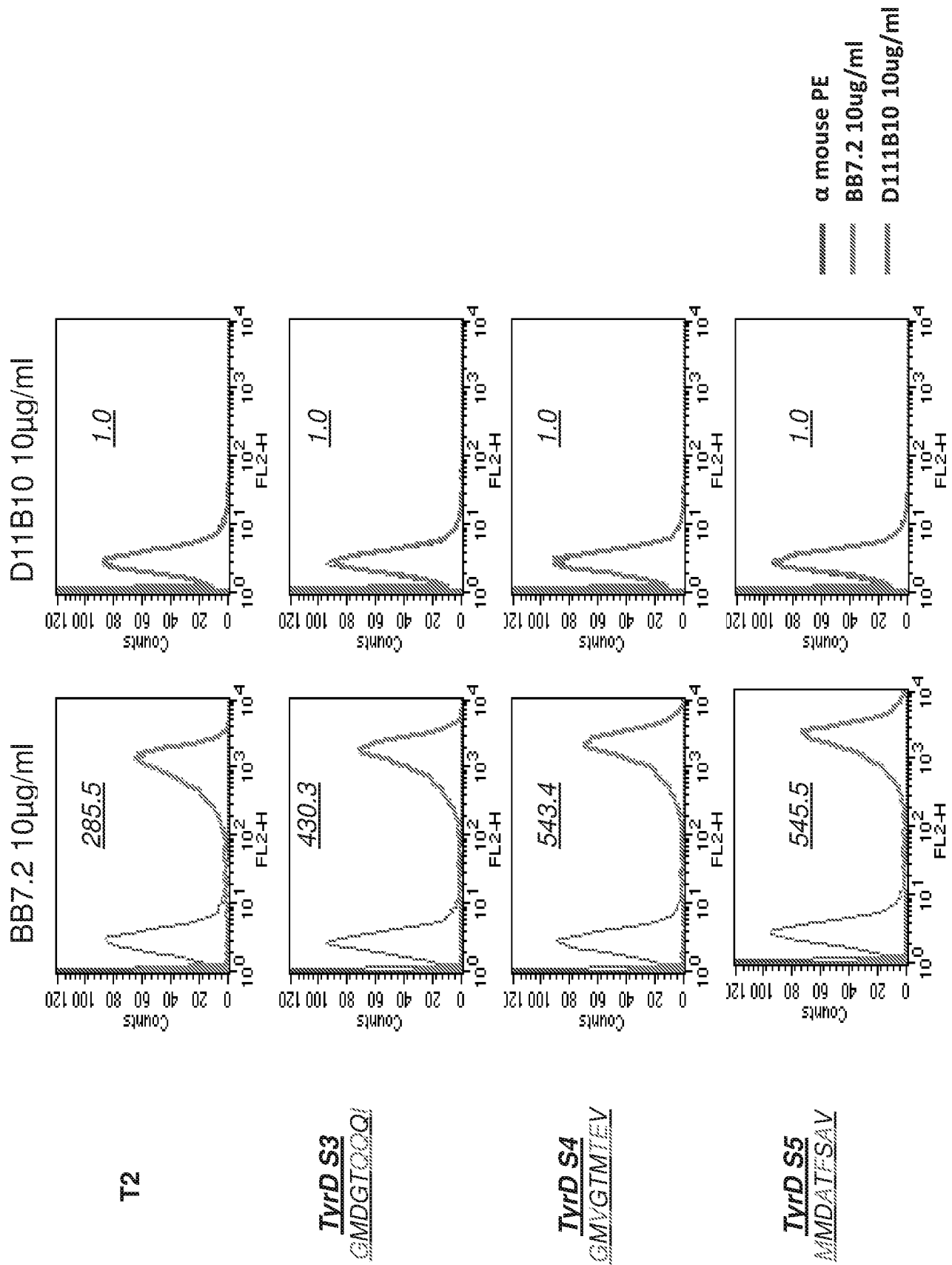
MFI values are relative to background. Value of `1` means no binding

Figure 21



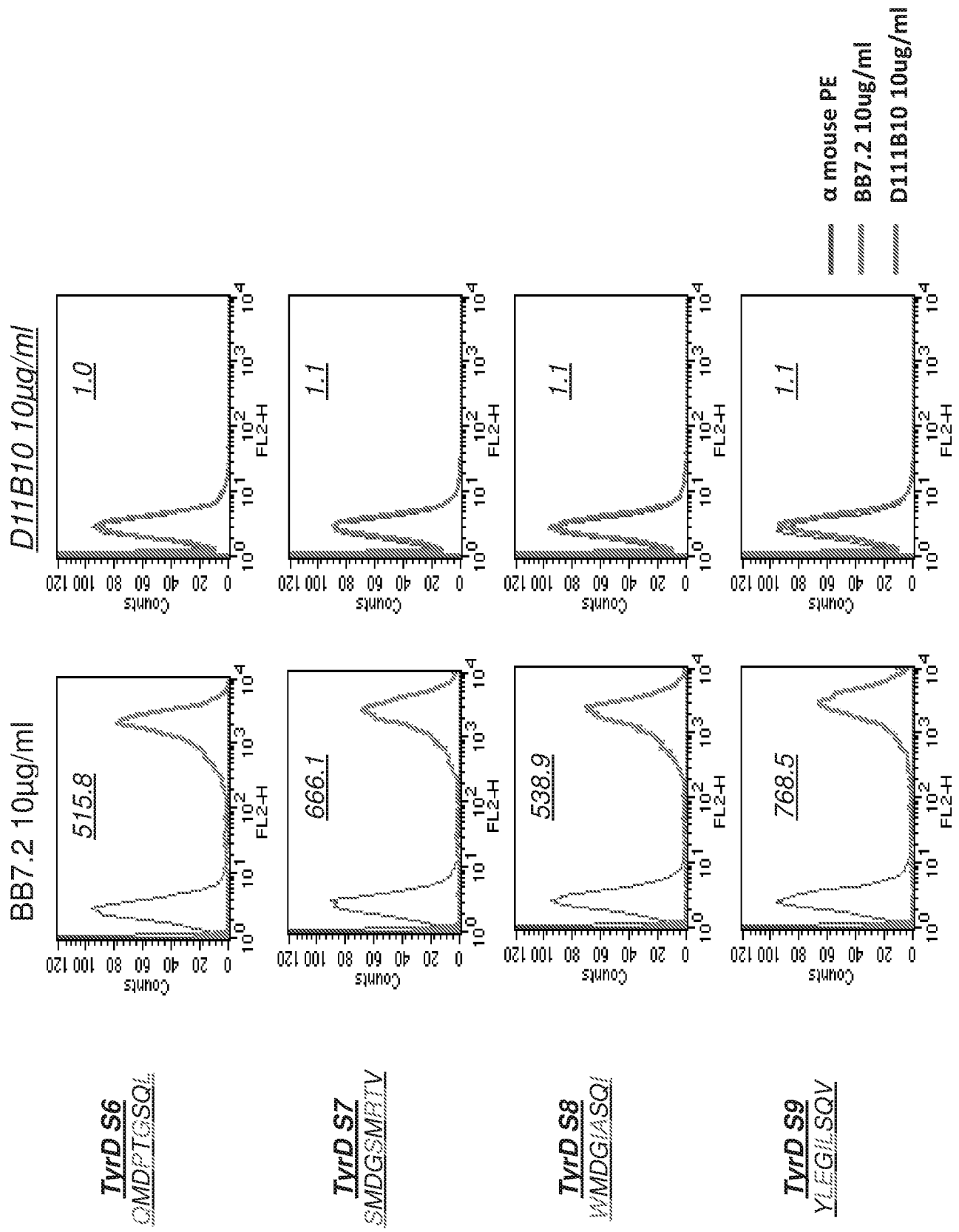
MFI values are relative to background. Value of `1` means no binding

Figure 21 - continued



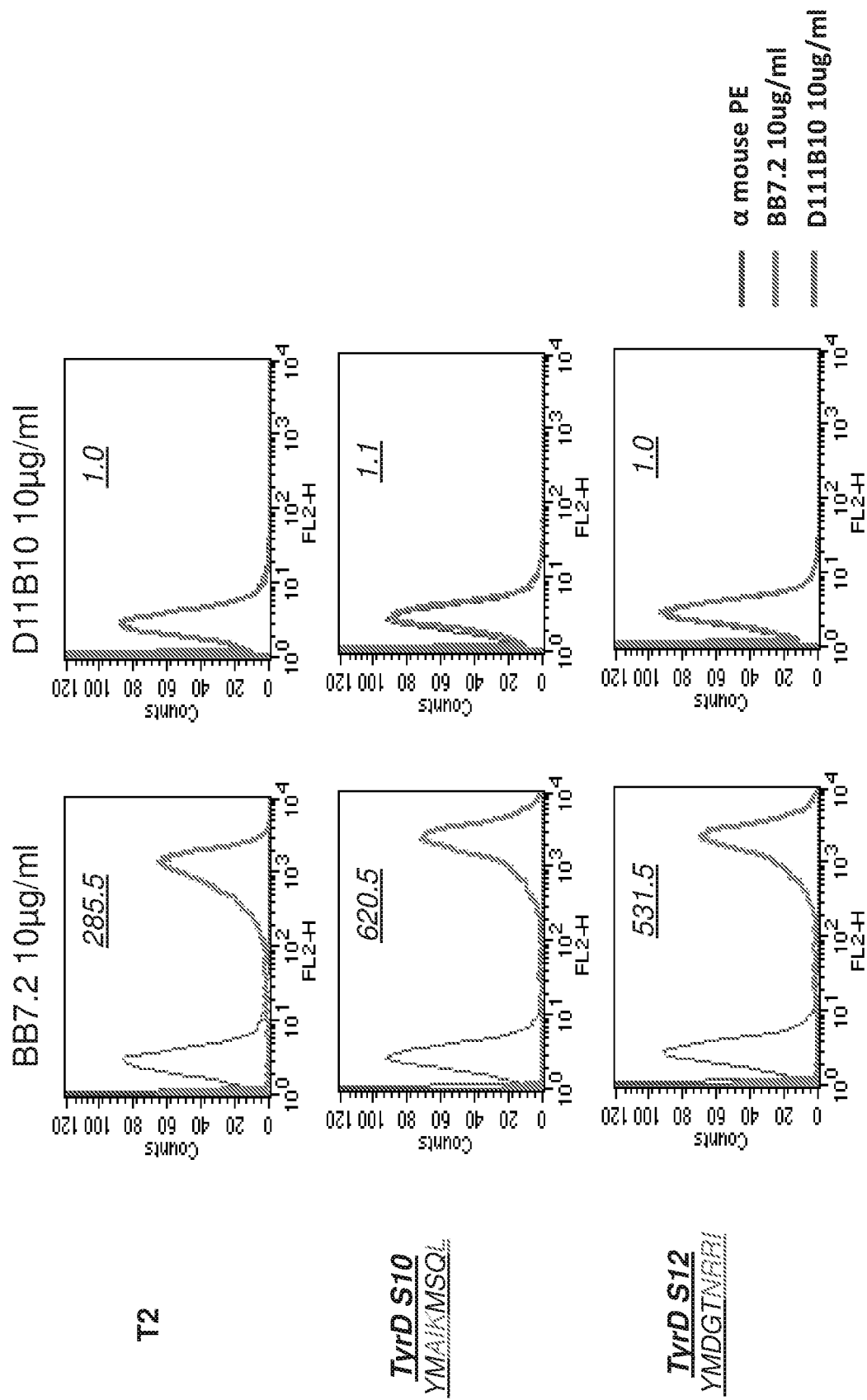
MFI values are relative to background. Value of `1` means no binding

Figure 22



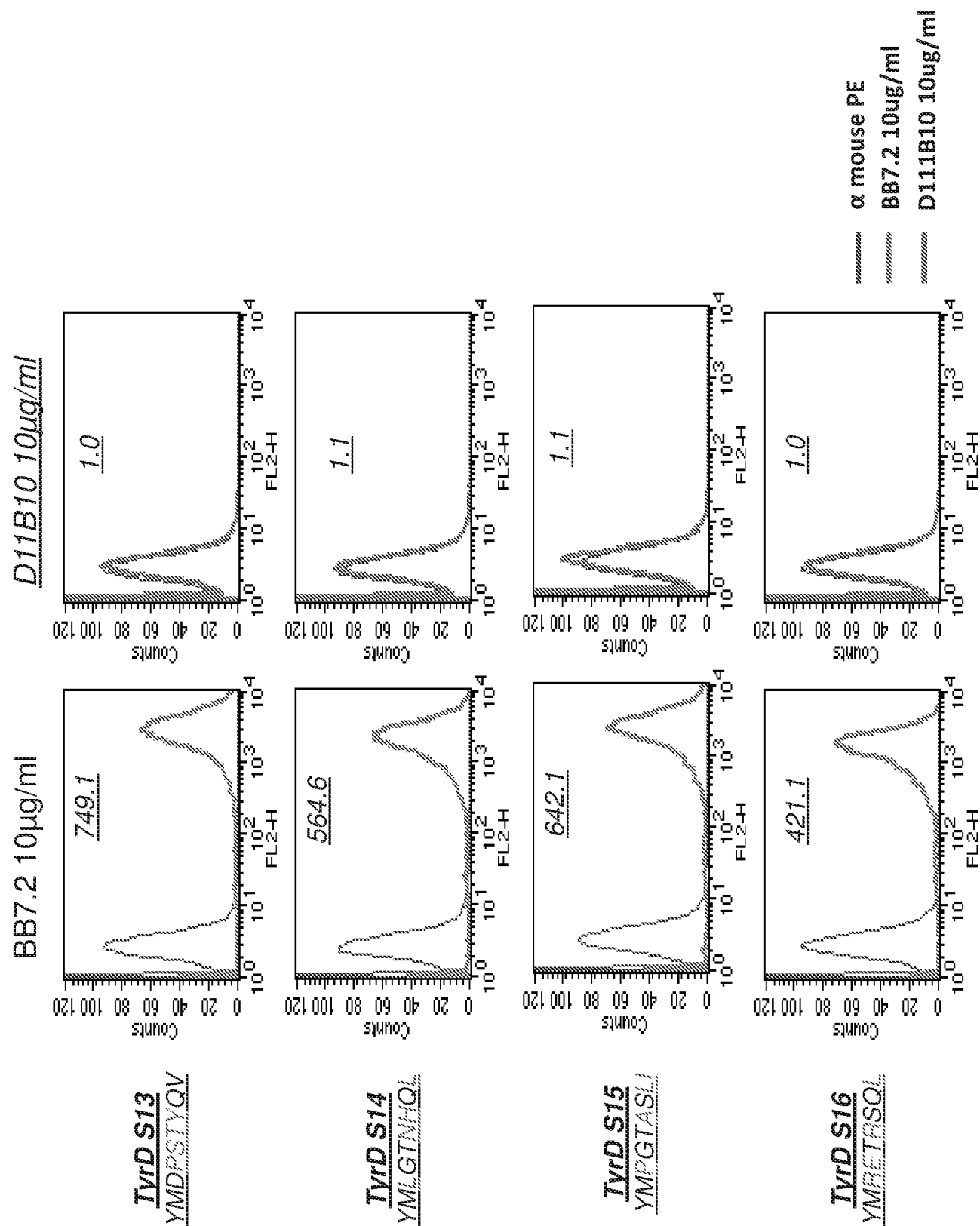
MFI values are relative to background. Value of `1` means no binding

Figure 22 - continued



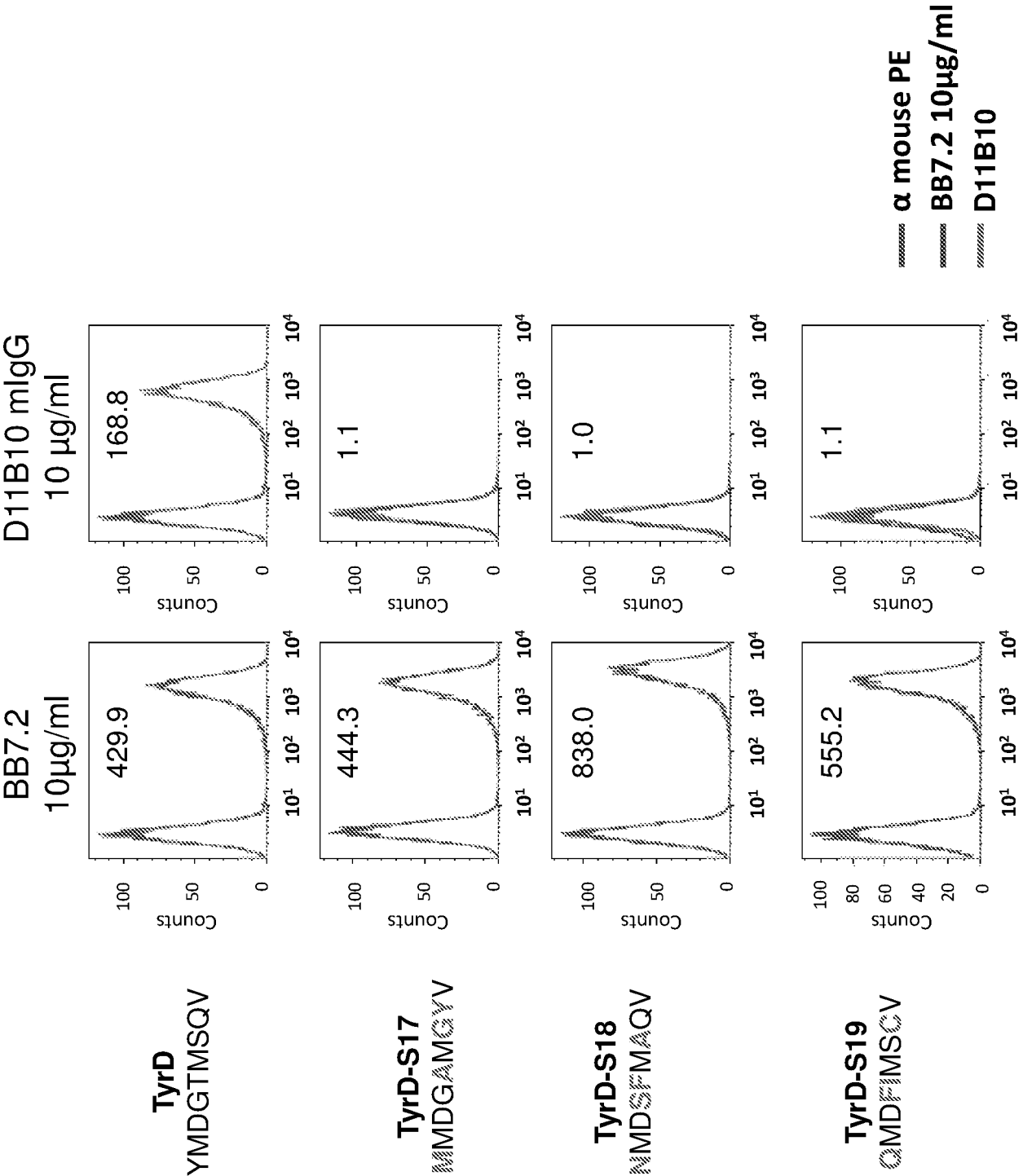
MFI values are relative to background. Value of `1` means no binding

Figure 23



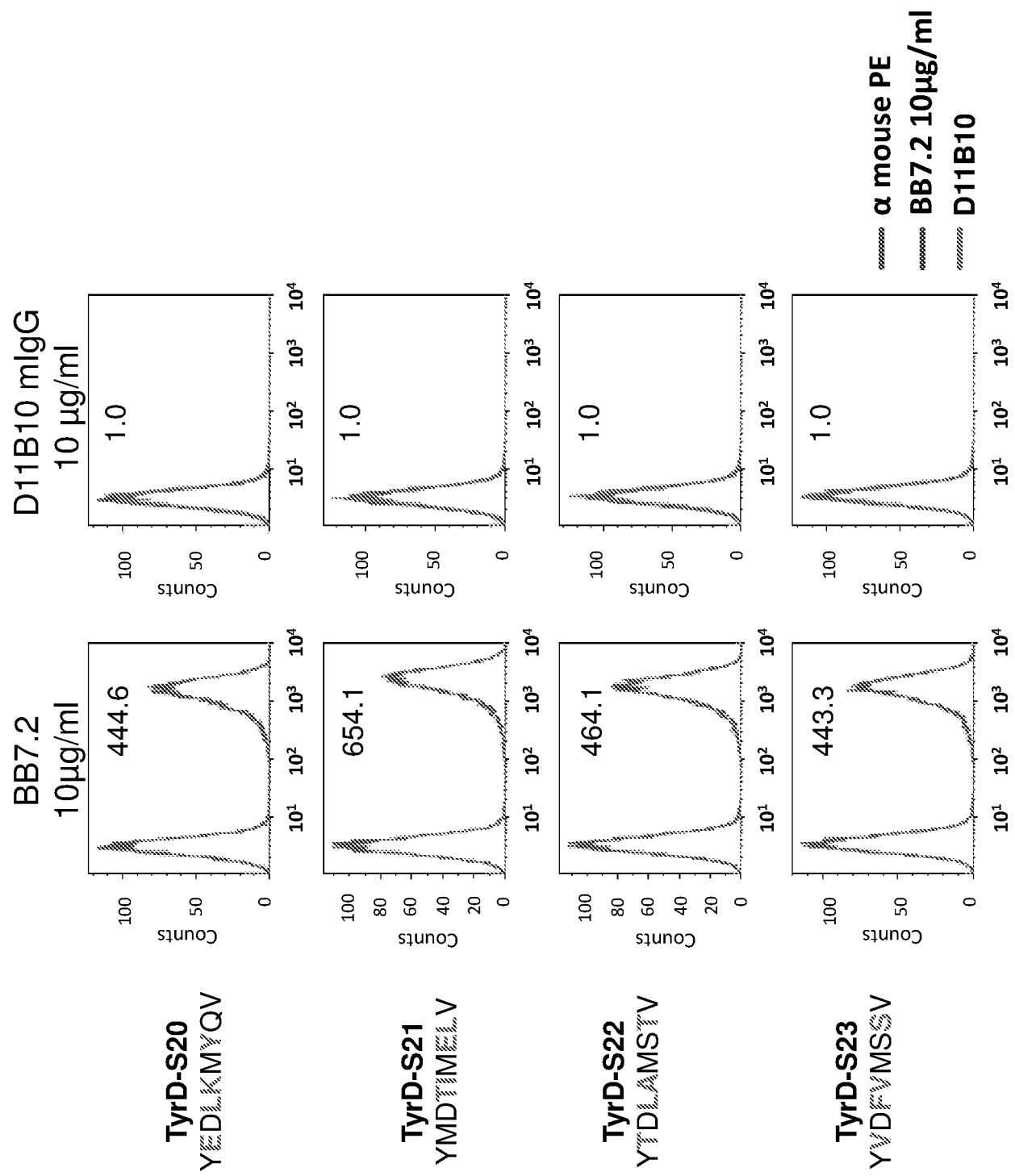
MFI values are relative to background. Value of `1` means no binding

Figure 23 - continued



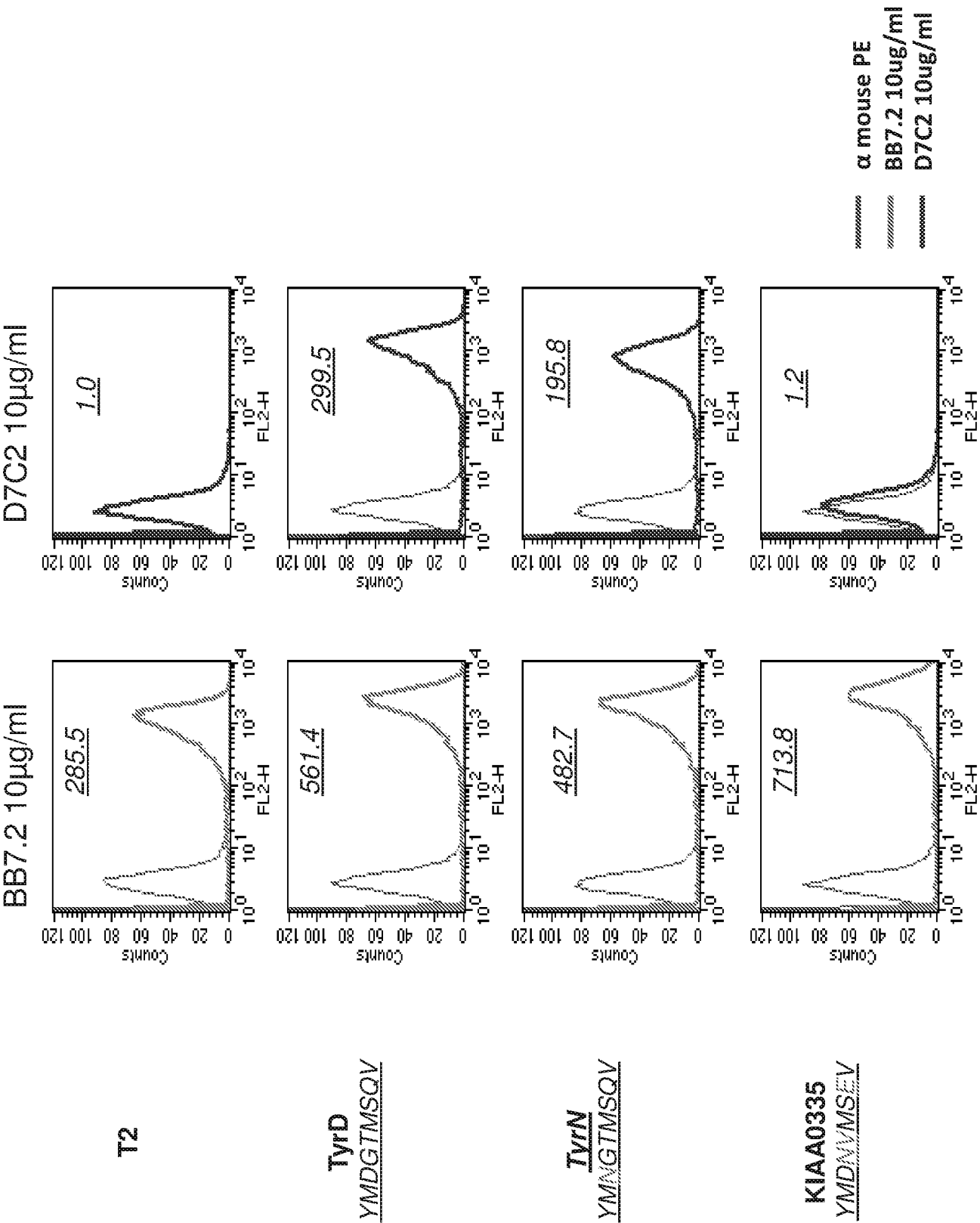
MFI values are relative to background. Value of `1` means no binding

Figure 24



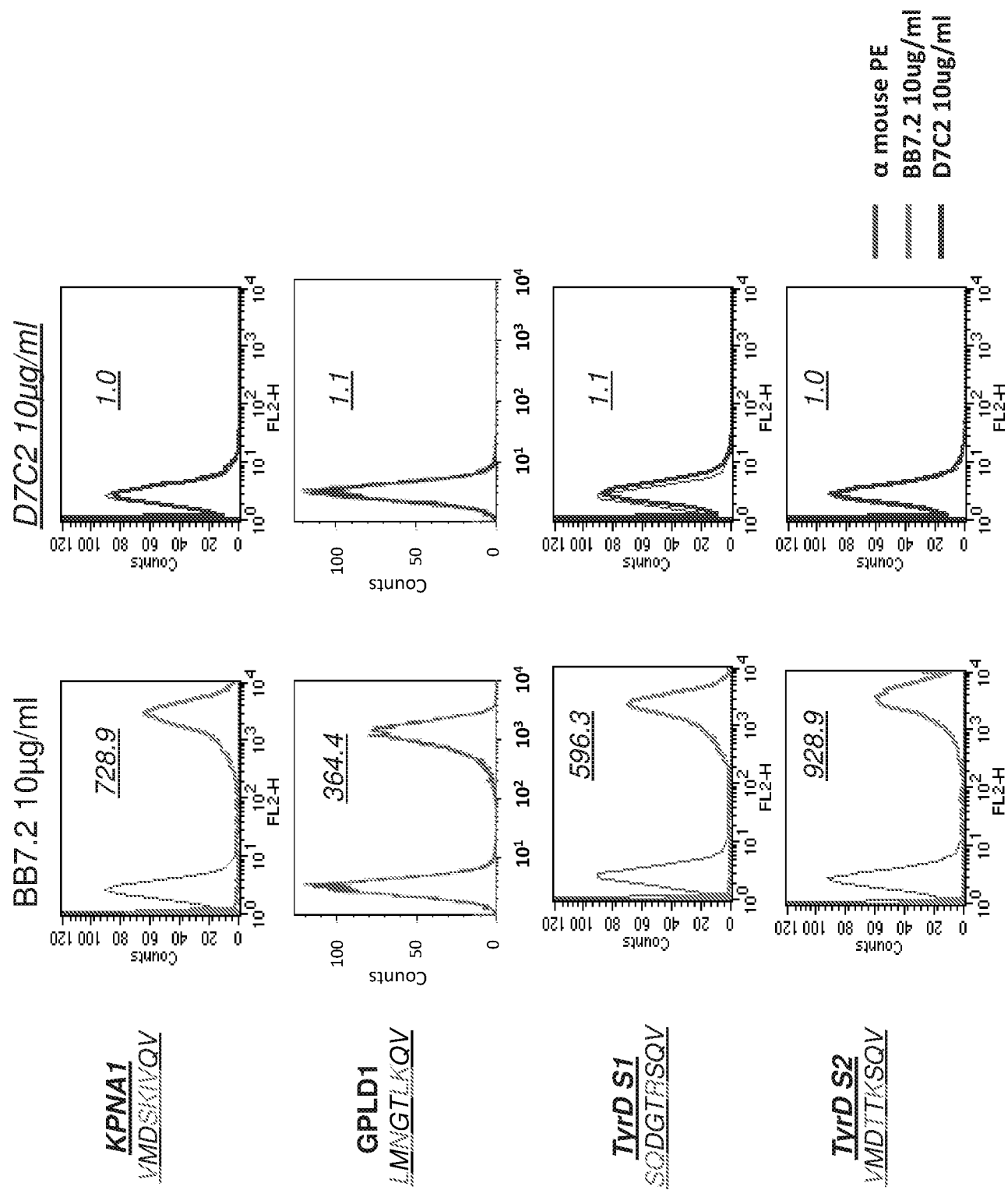
MFI values are relative to background. Value of `1` means no binding

Figure 24 - continued



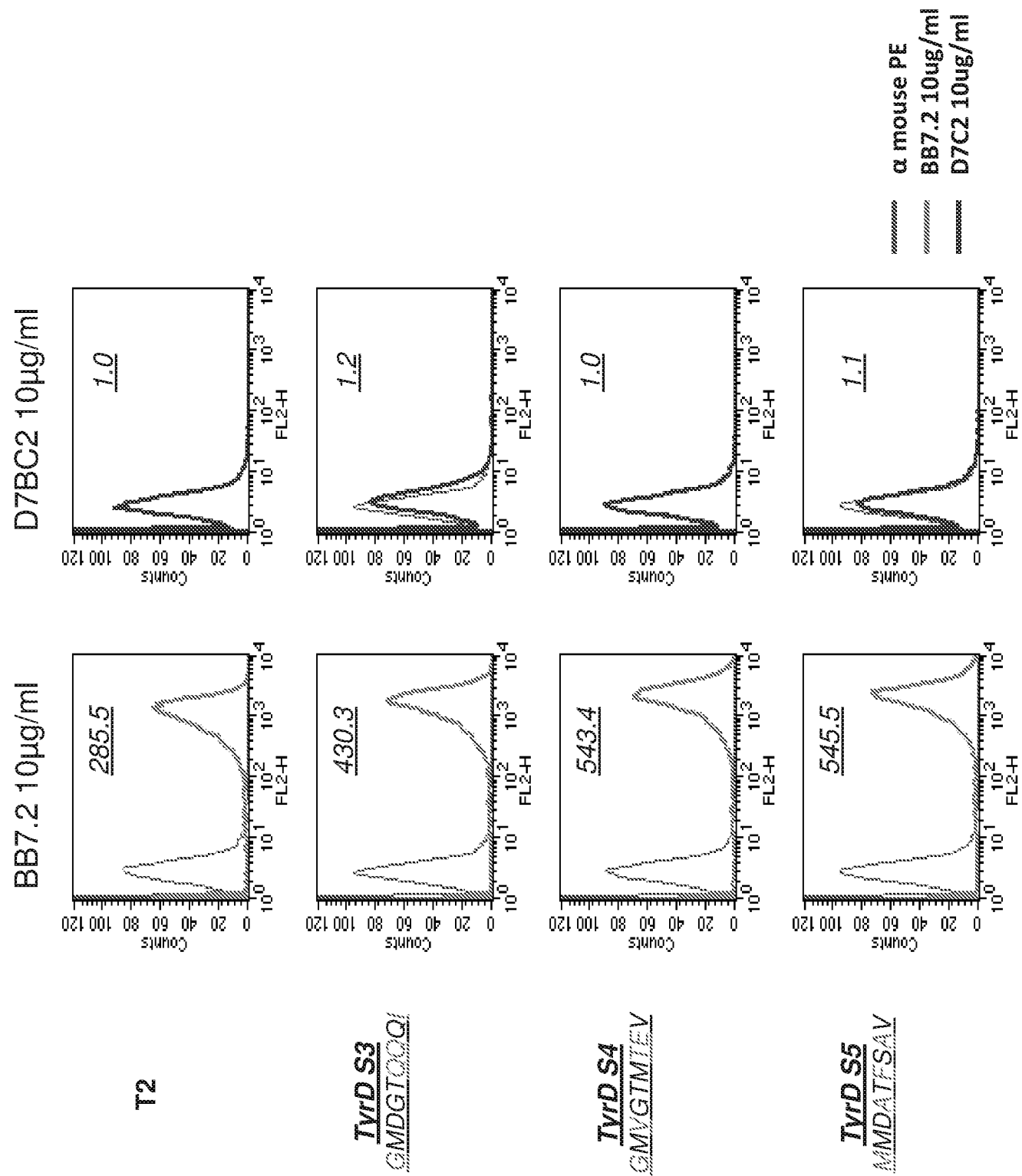
MFI values are relative to background. Value of `1` means no binding

Figure 25



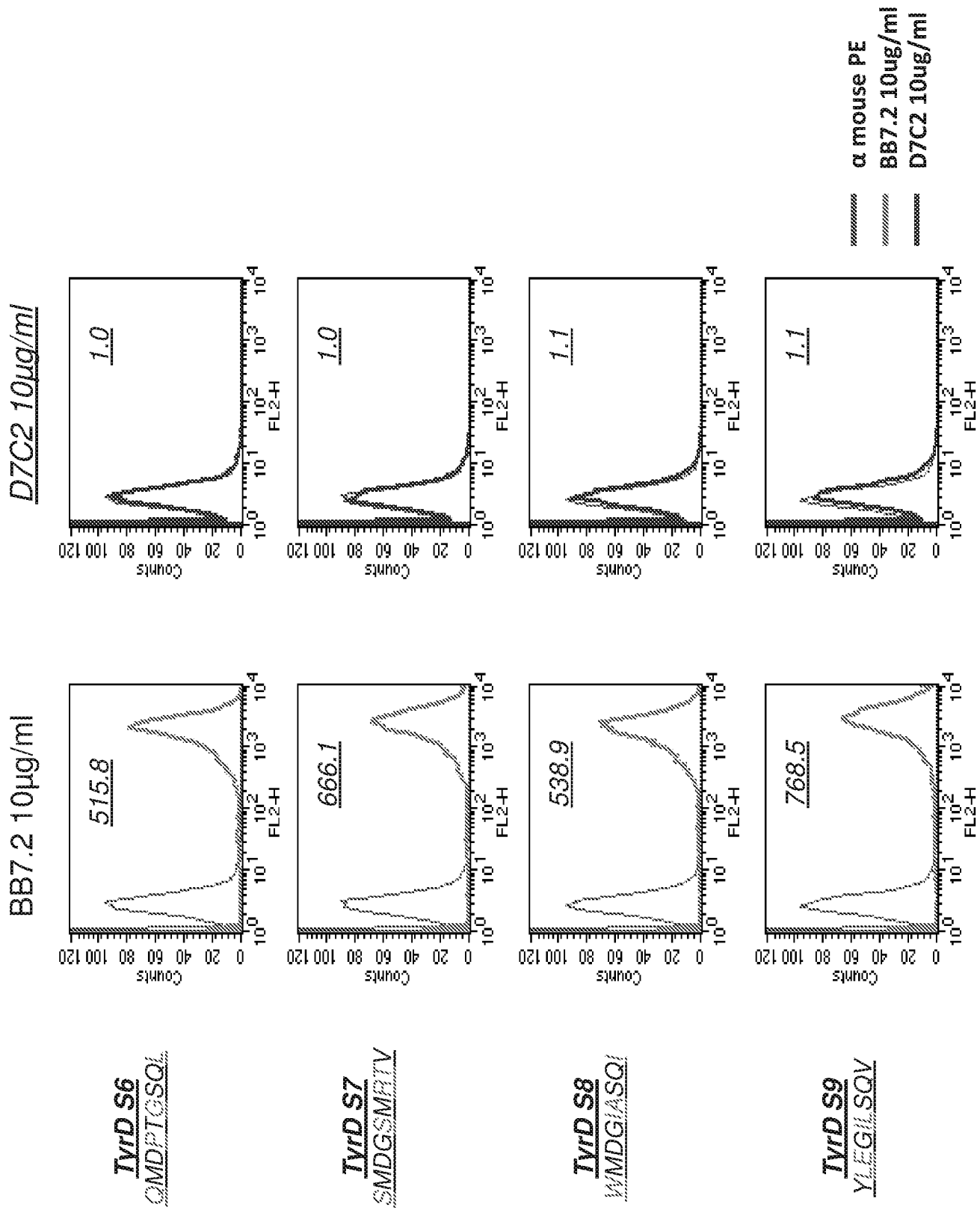
MFI values are relative to background. Value of `1` means no binding

Figure 25 - continued



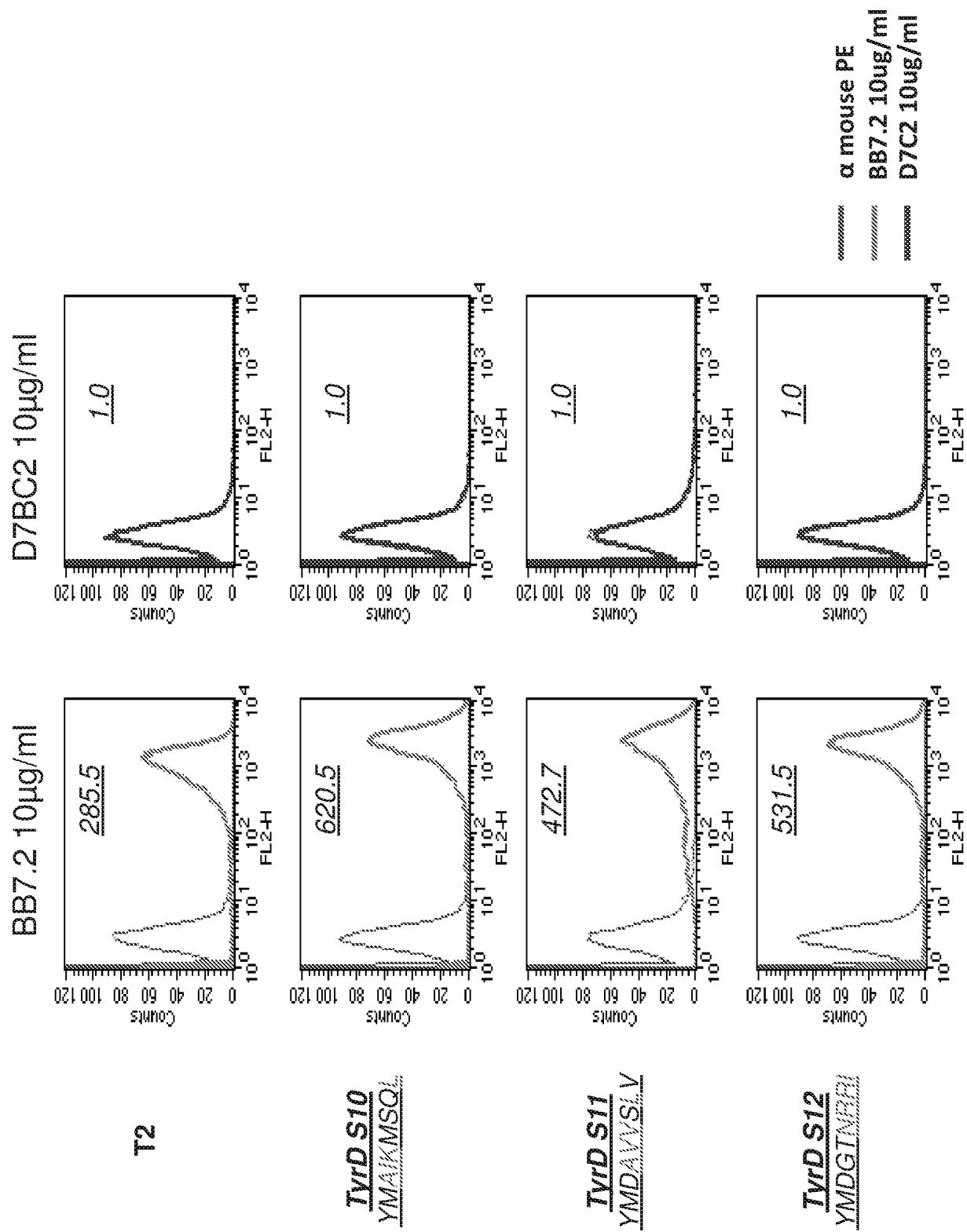
MFI values are relative to background. Value of 1 means no binding

Figure 26



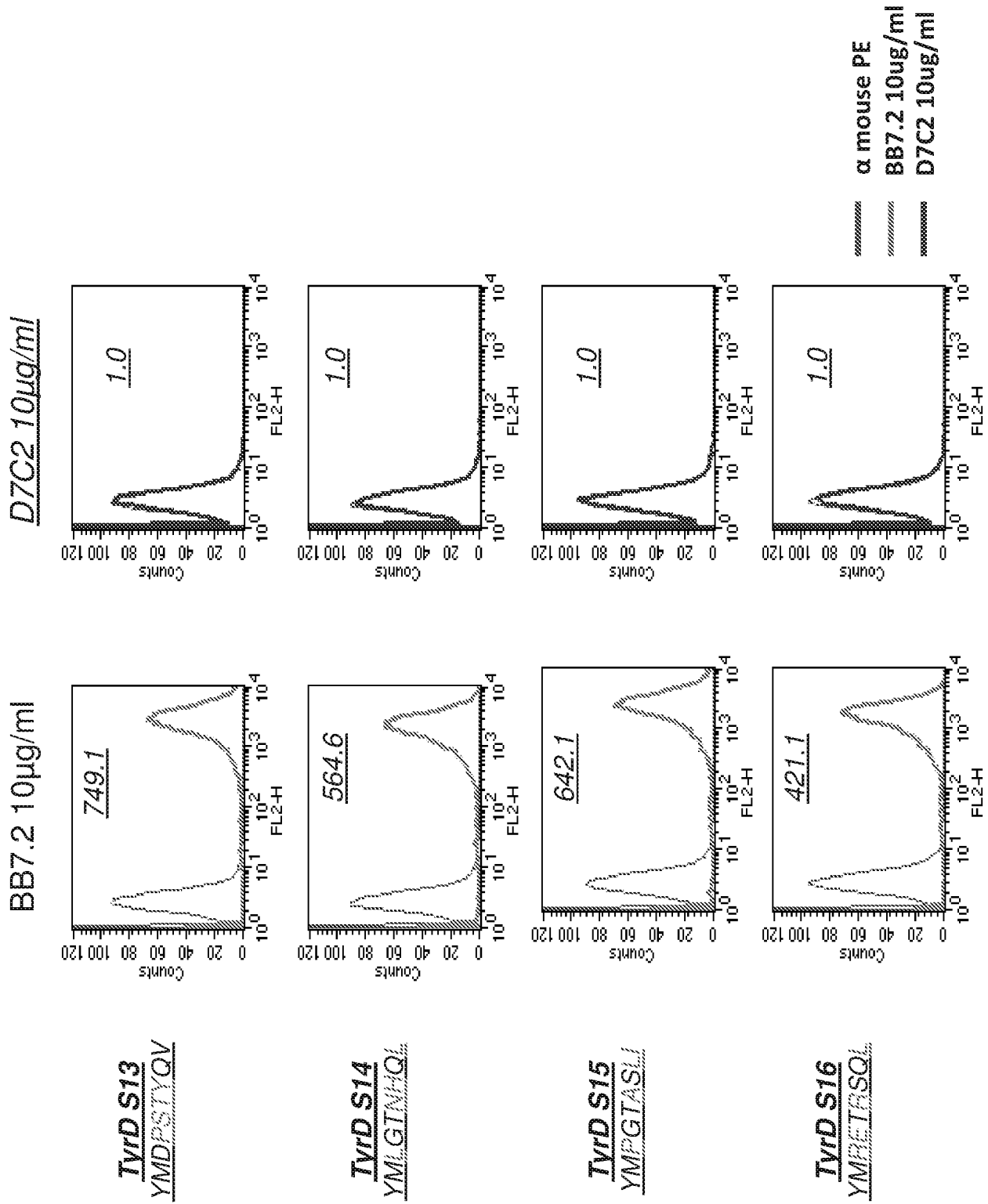
MFI values are relative to background. Value of 1` means no binding

Figure 26 - continued



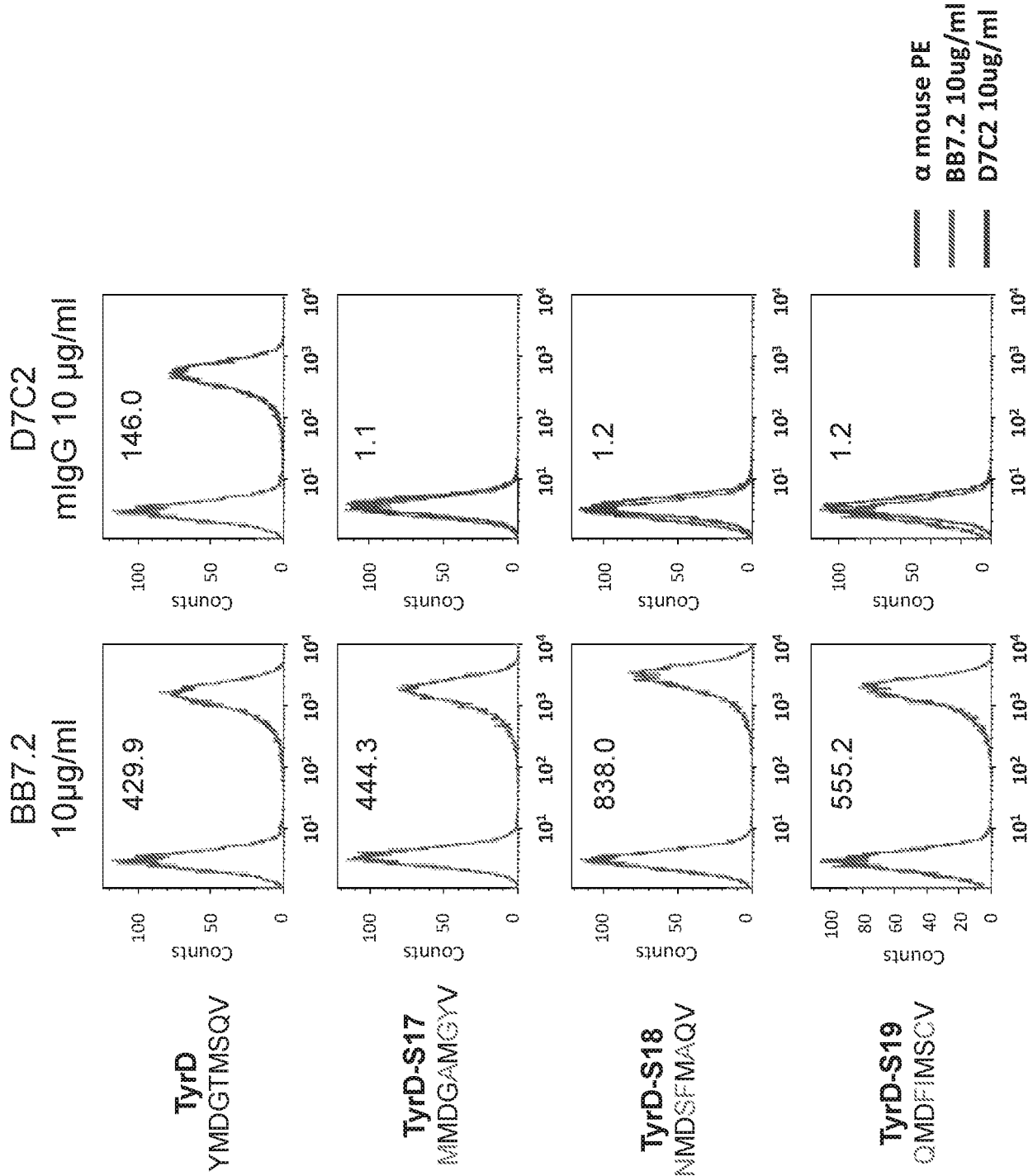
MFI values are relative to background. Value of `1` means no binding

Figure 27



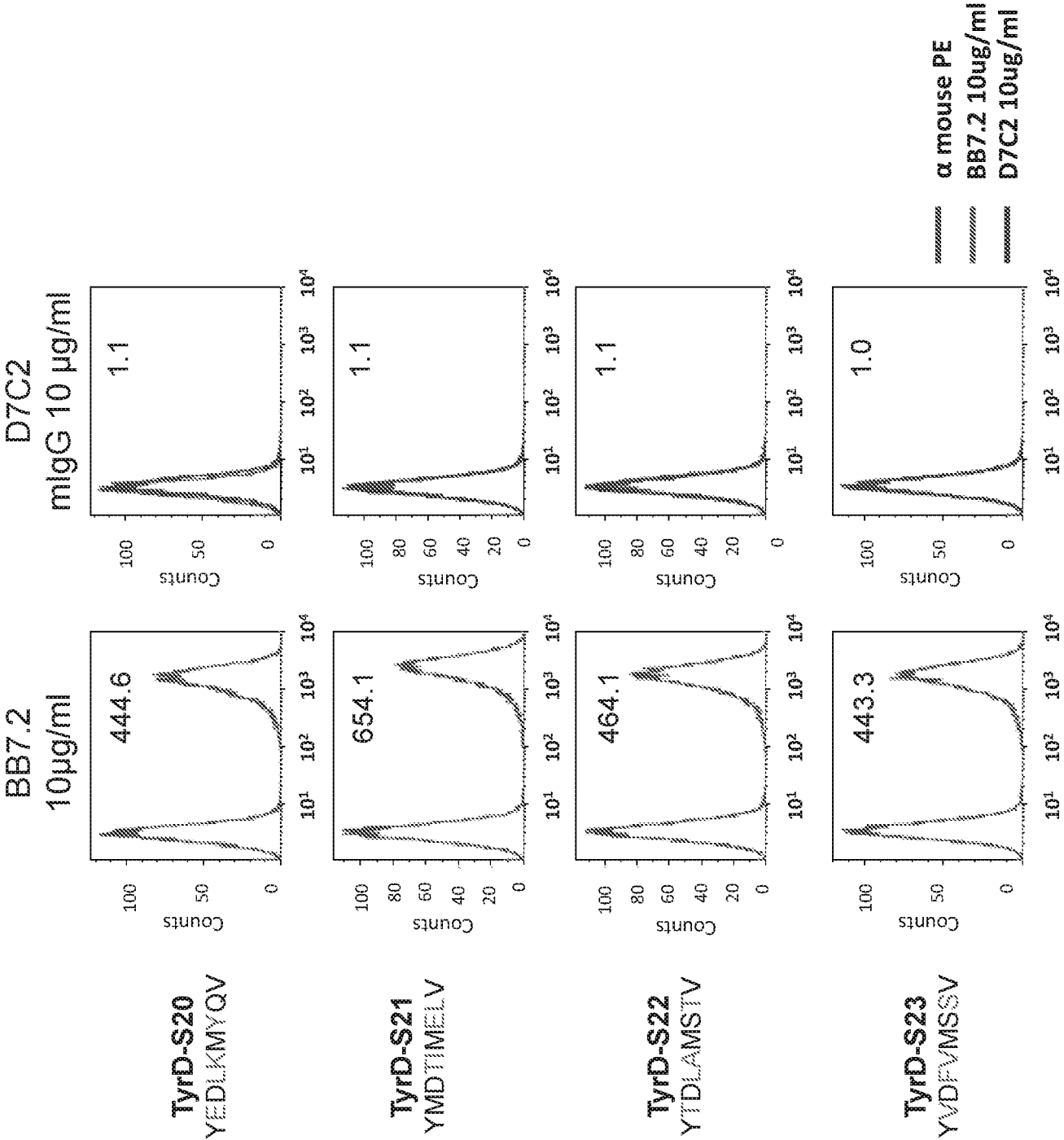
MFI values are relative to background. Value of `1` means no binding

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

Ligand --- WT1 TCRL B47B6 via anti-mouse

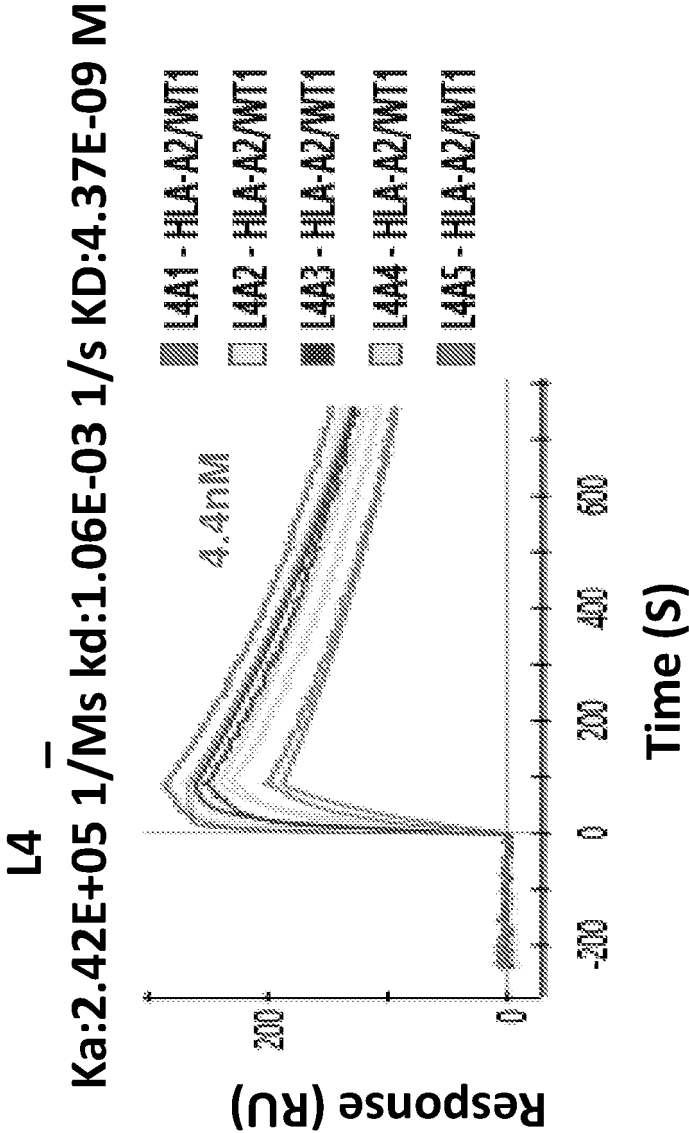
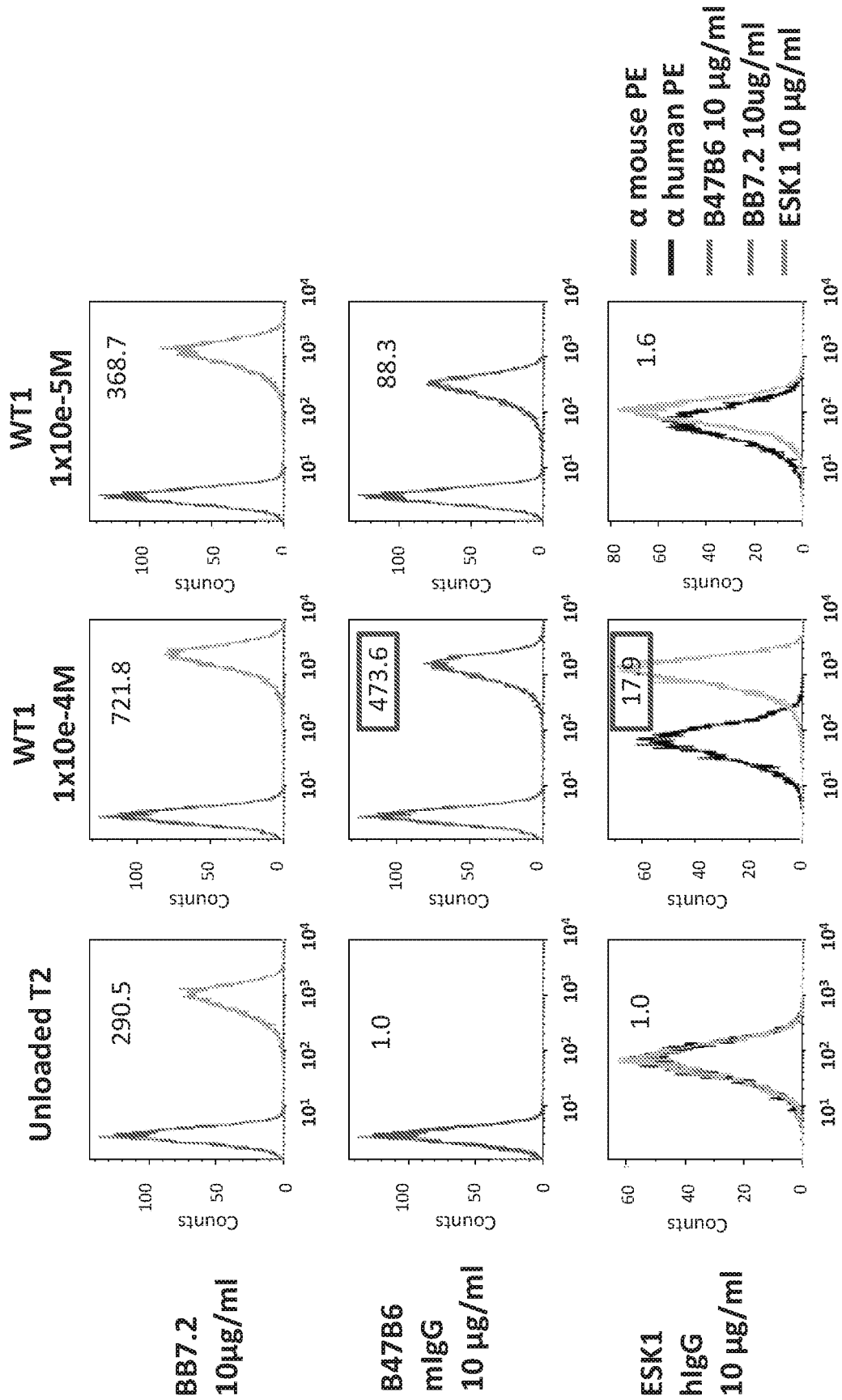


Figure 29



Low intensity stain with ESK1 compared to B47

Sharp decrease in binding of ESK1 compared to B47 with 10x decrease in [peptide]

Figure 30

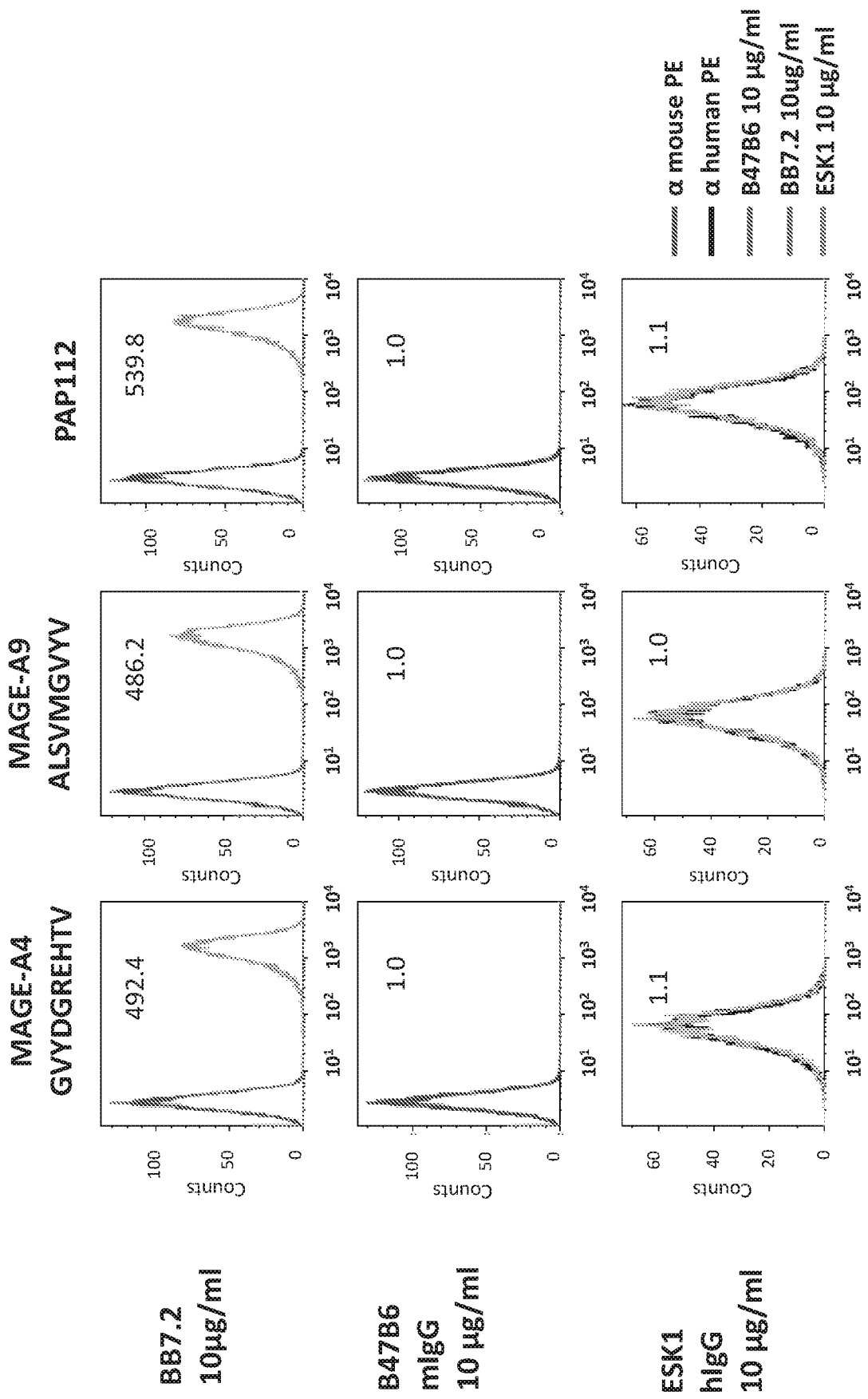


Figure 31 - continued

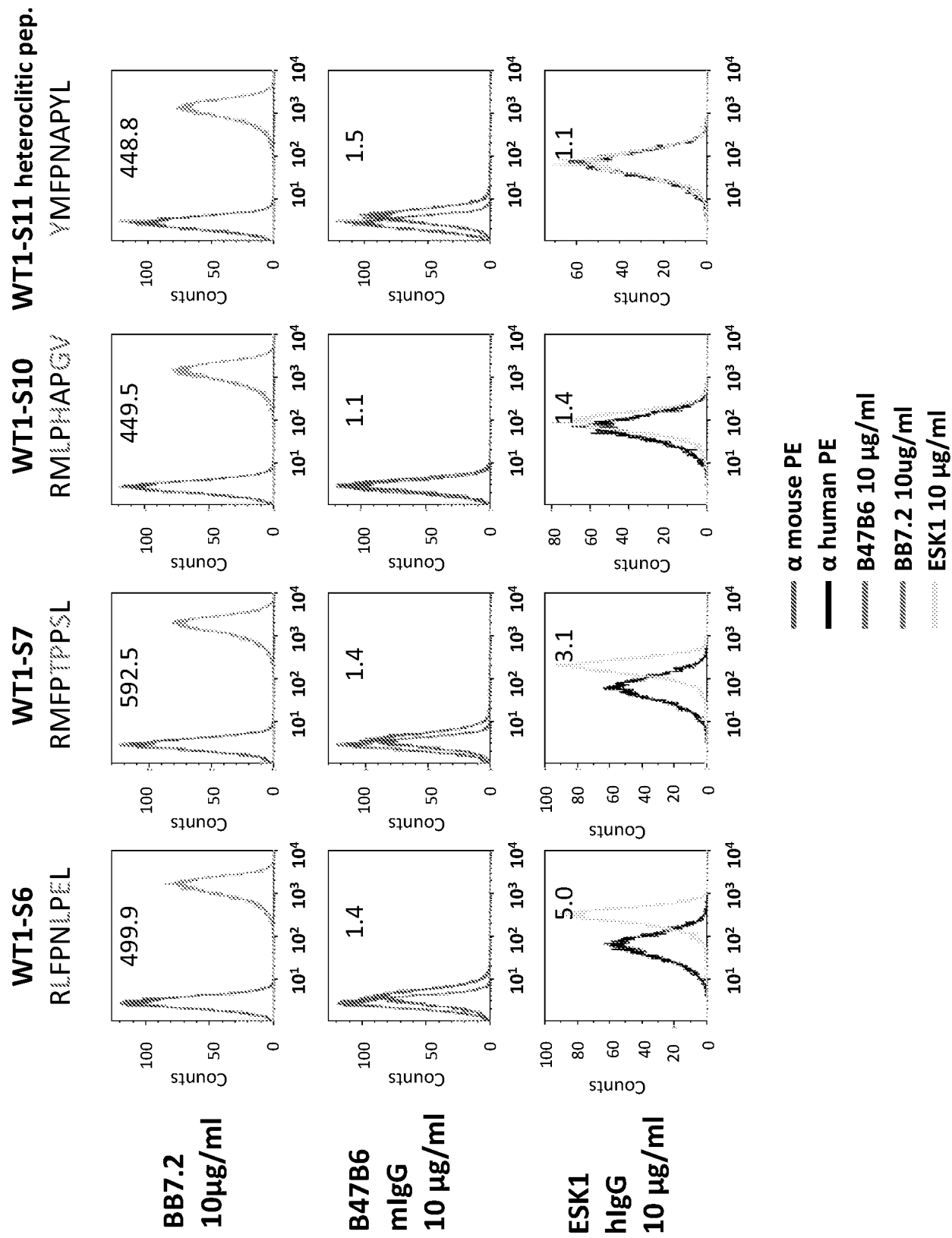


Figure 32

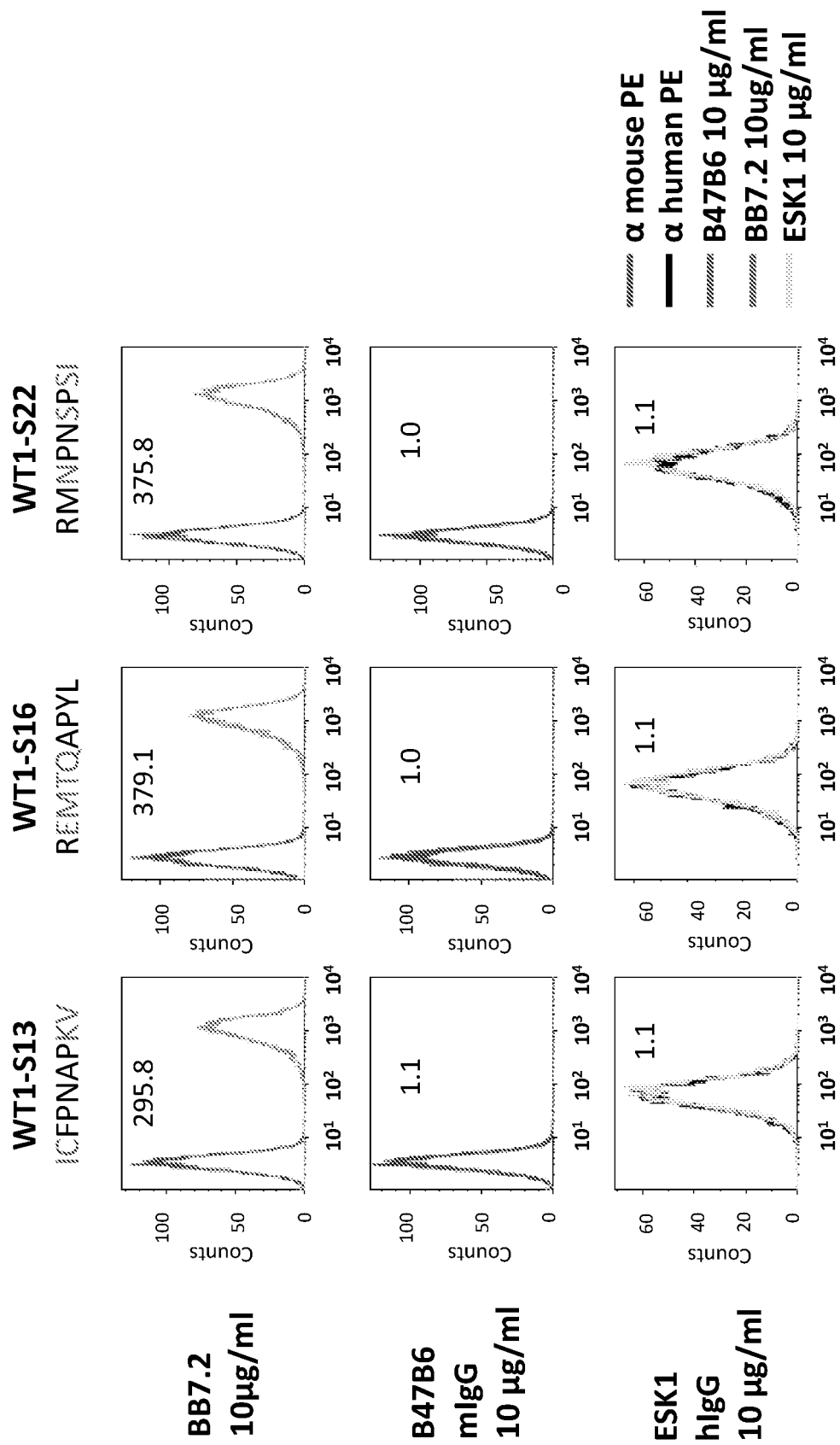


Figure 32 - continued

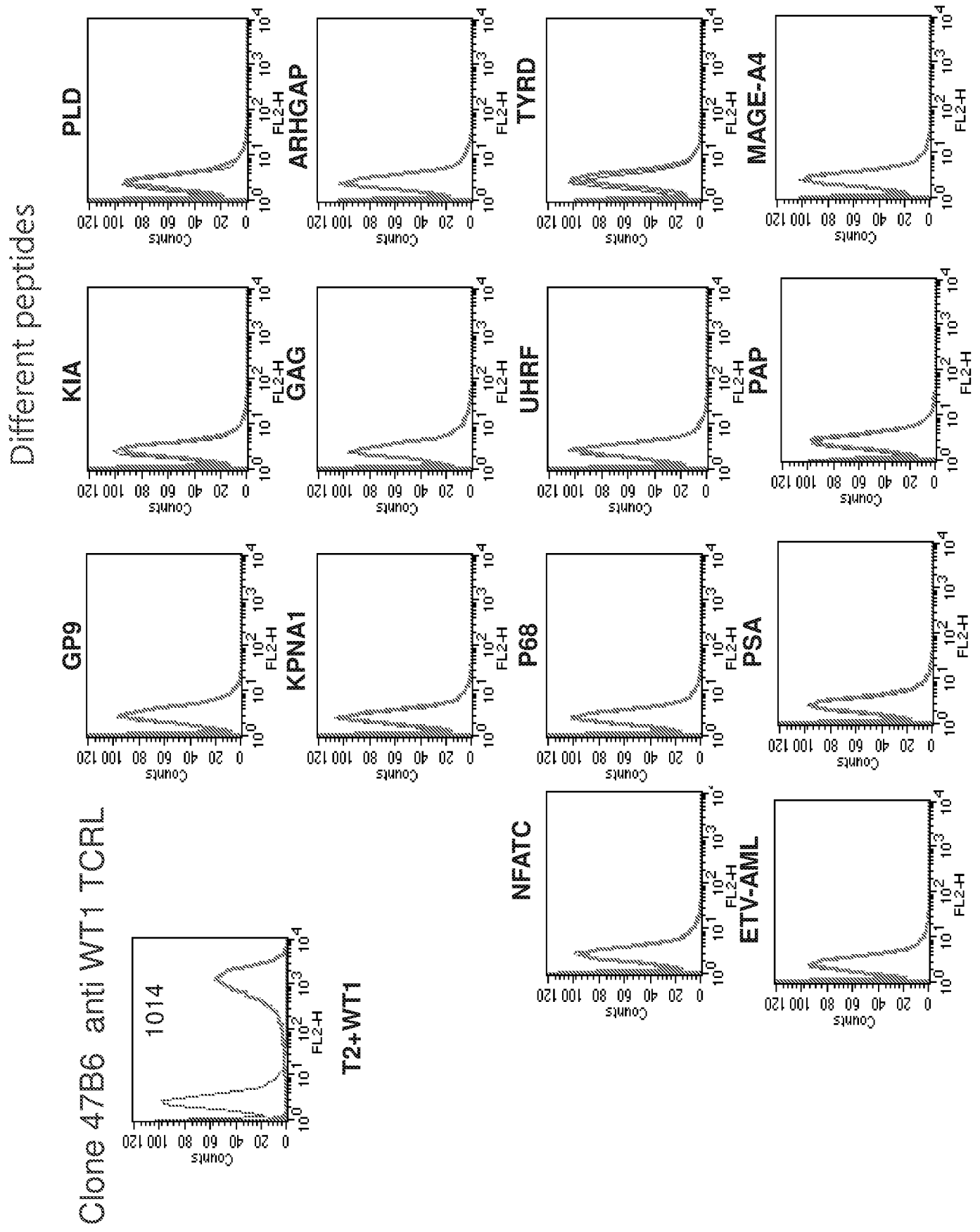
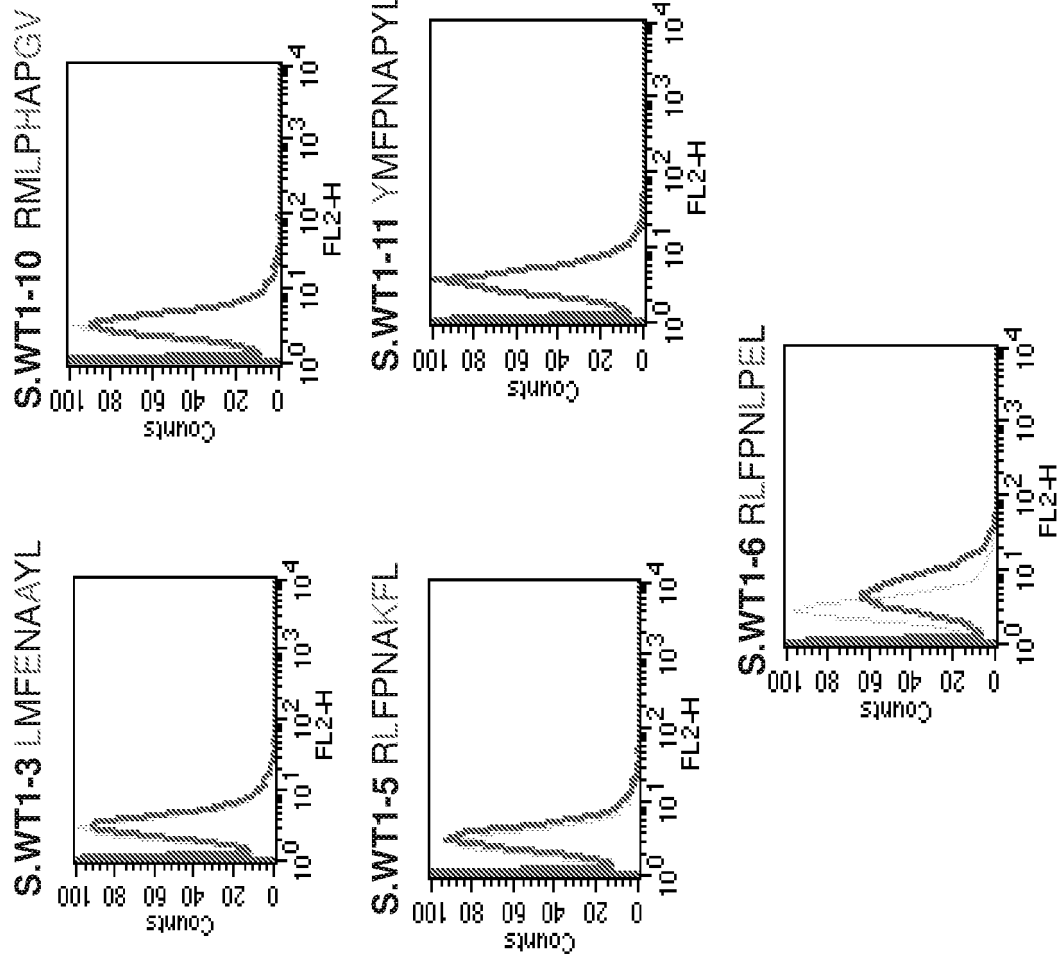


Figure 33

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)

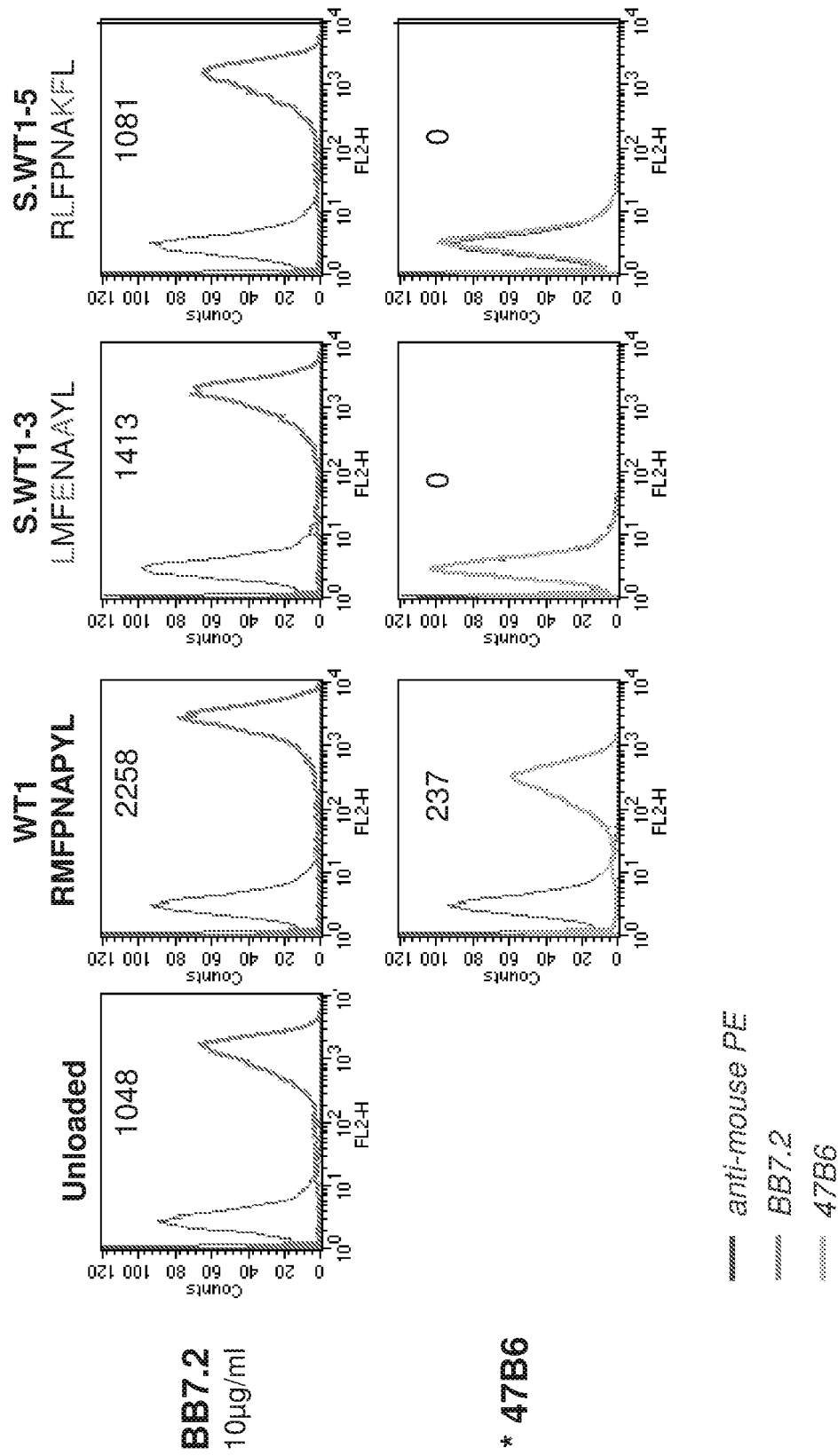


Figure 34

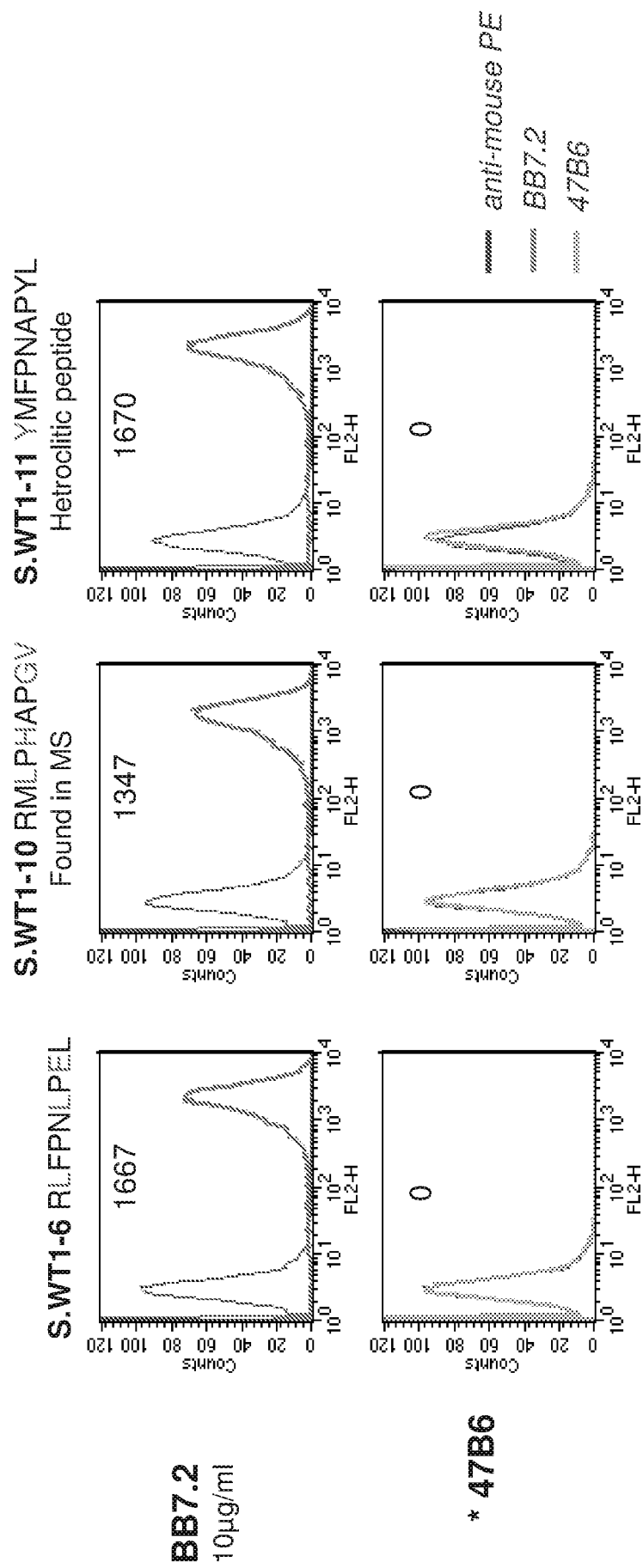


Figure 34 - continued

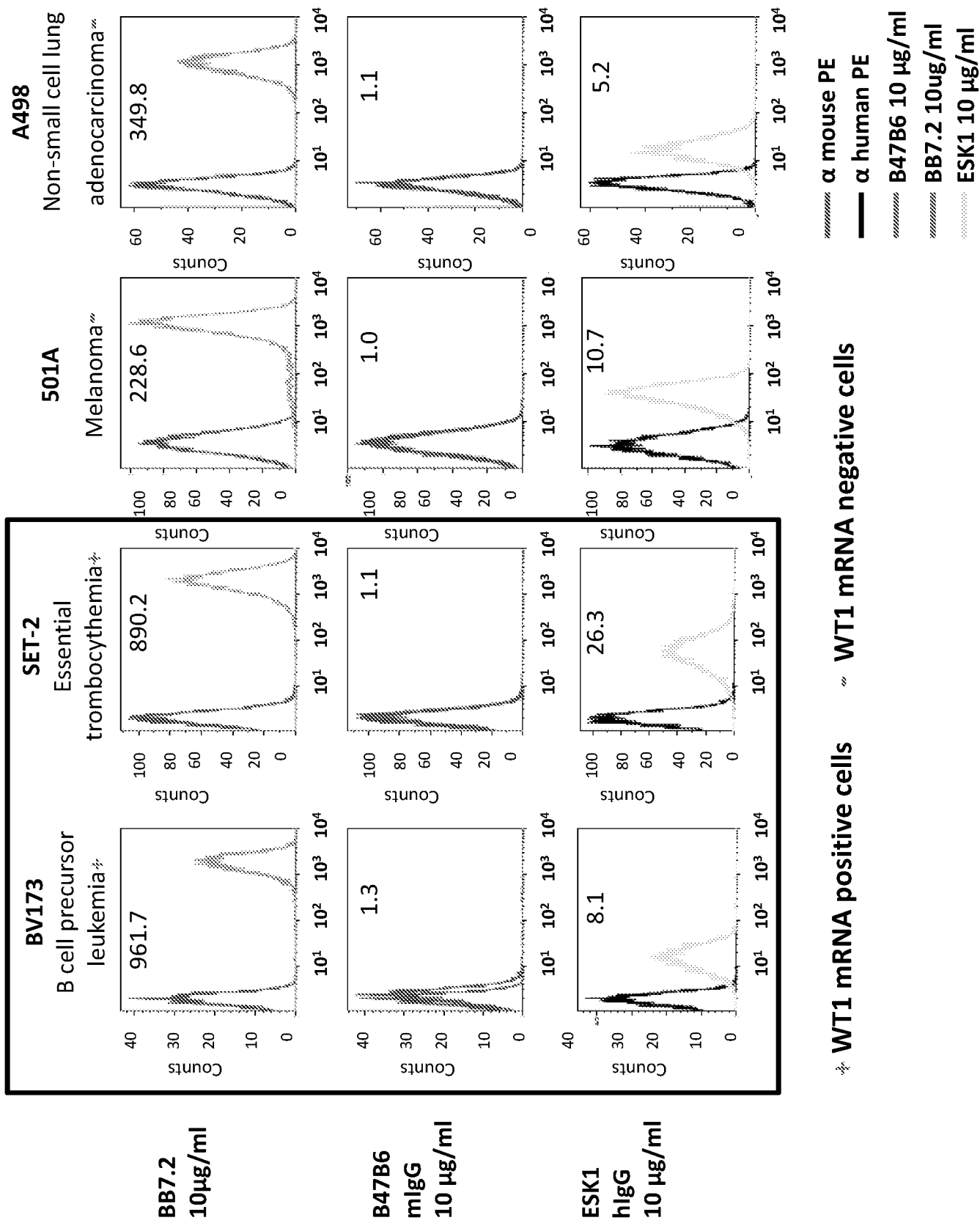


Figure 35

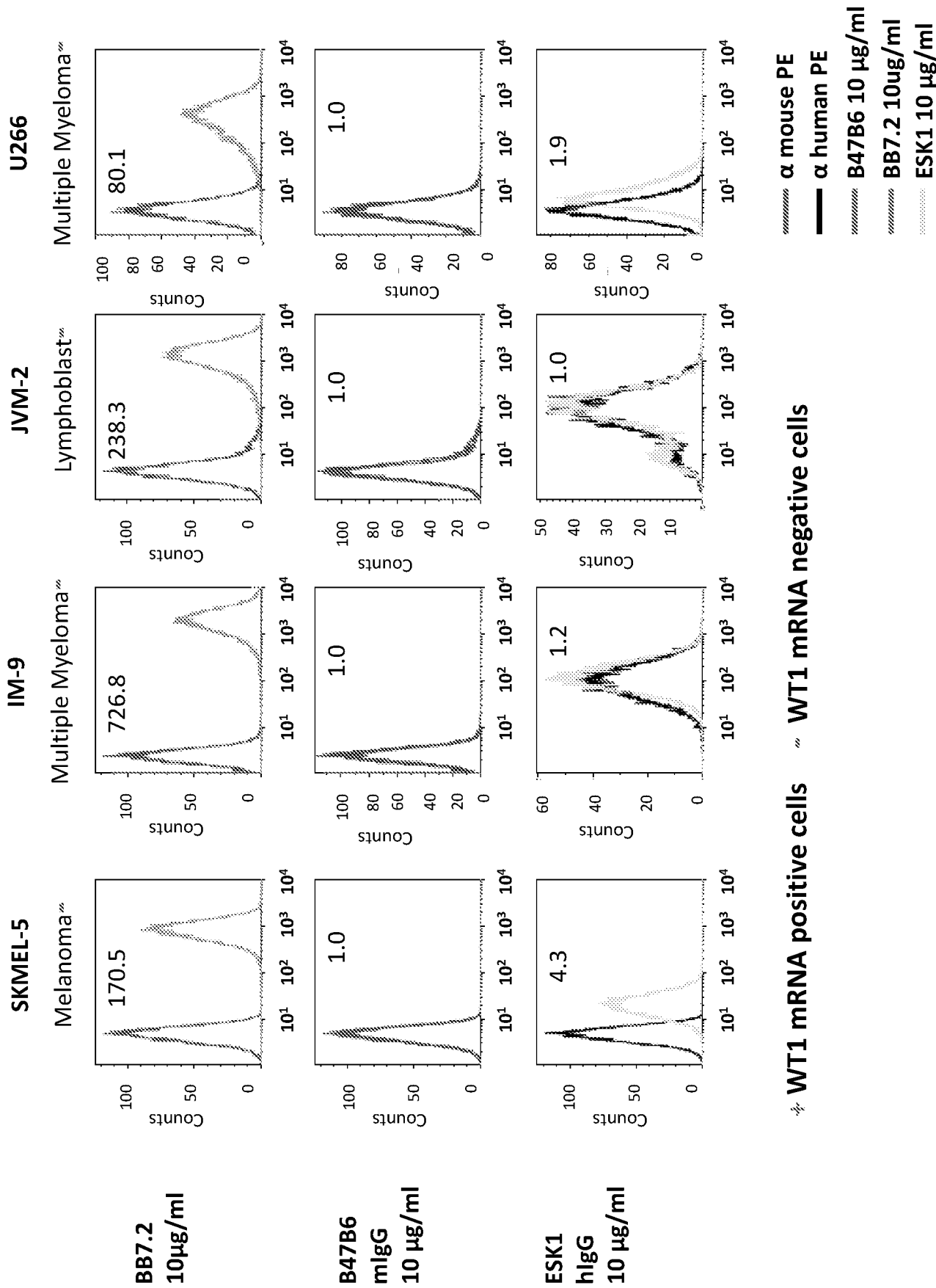
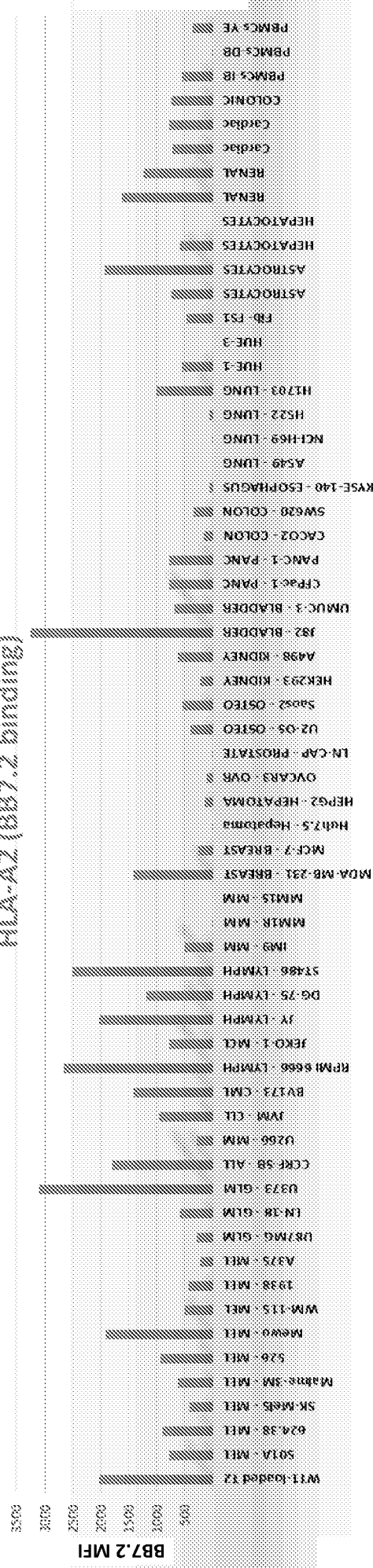


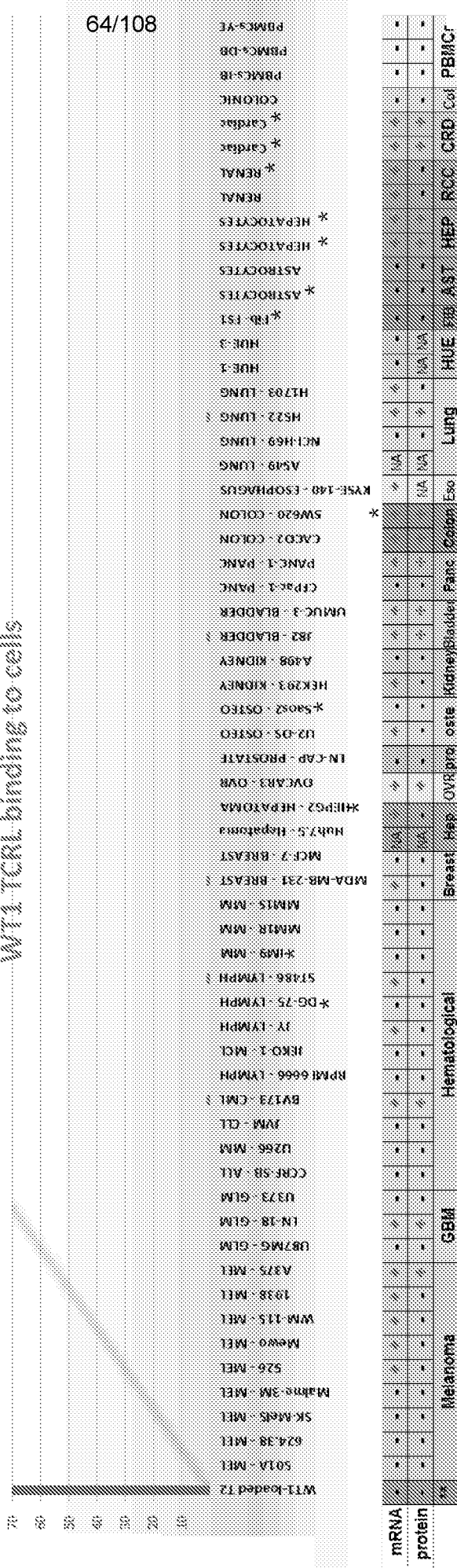
Figure 35- continued

HLA-A2 (B27.2 binding)



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WT1-TCR binding to cells



Primary normal cells

Cancer cell lines

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

Figure 36

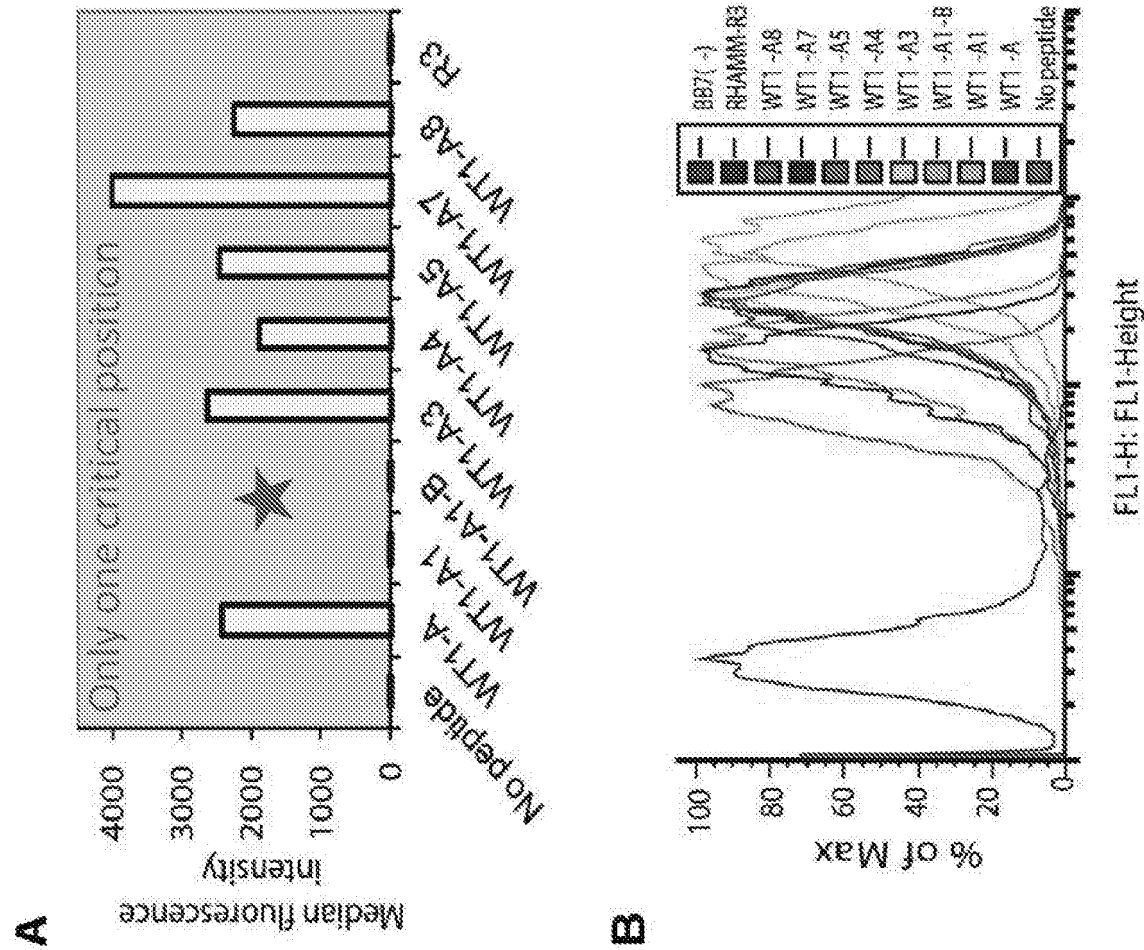


Figure S1. Epitope specificity. The RMF peptide sequence was substituted with alanine at positions 1, 3, 4, 5, 7, or 8, or with tyrosine (WT1-A1B) at position 1 (sequences in table S1). (A) T2 cells were pulsed with indicated peptides at 50 μ g/ml and the binding of ESK1 was measured by flow cytometry. (B) In order to show that the analog peptides still bound to HLA-A0201, cells were simultaneously stained with anti-HLA-A2 mAb, clone BB7.2 to measure the relative binding of the peptides to HLA-A2 molecule.

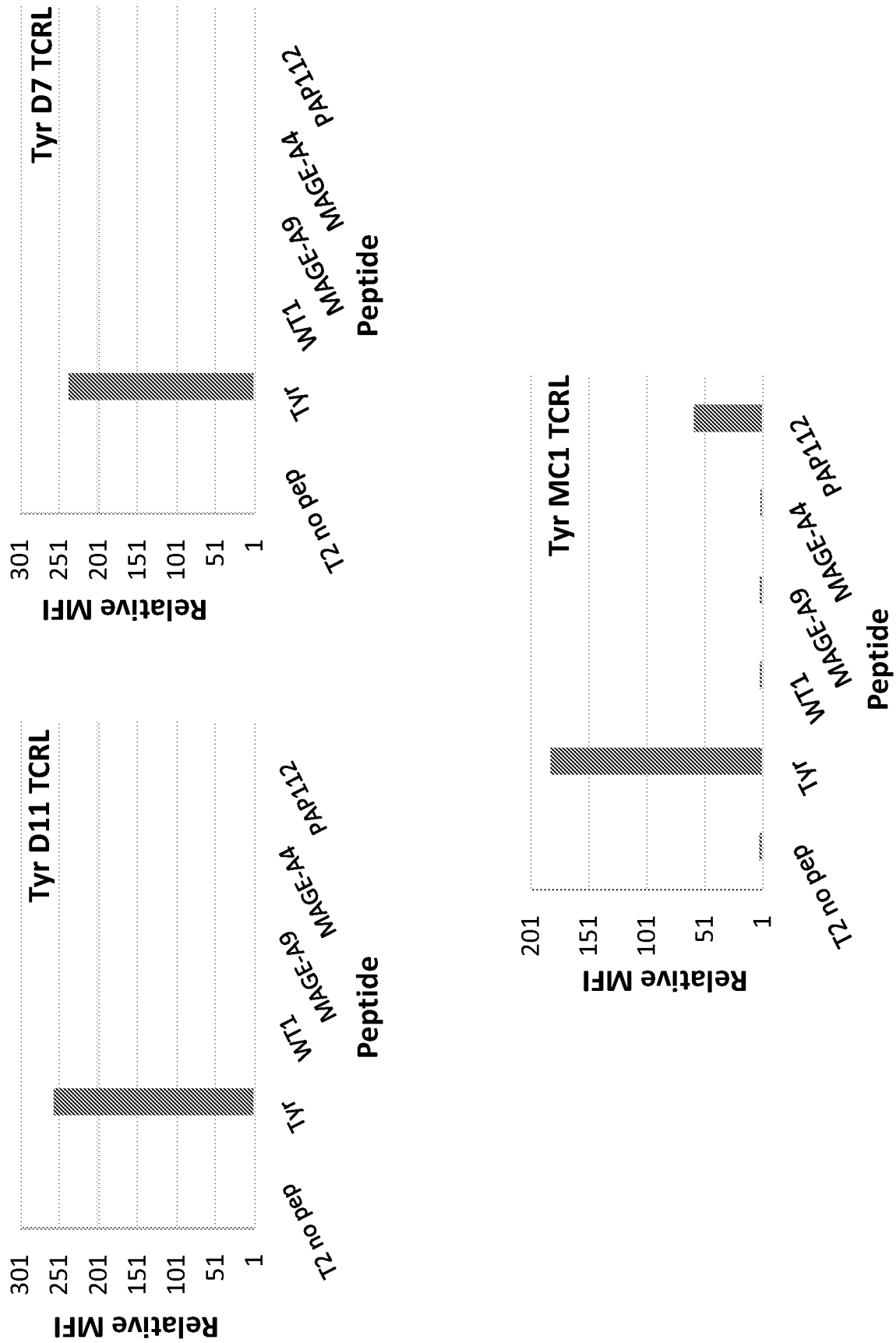
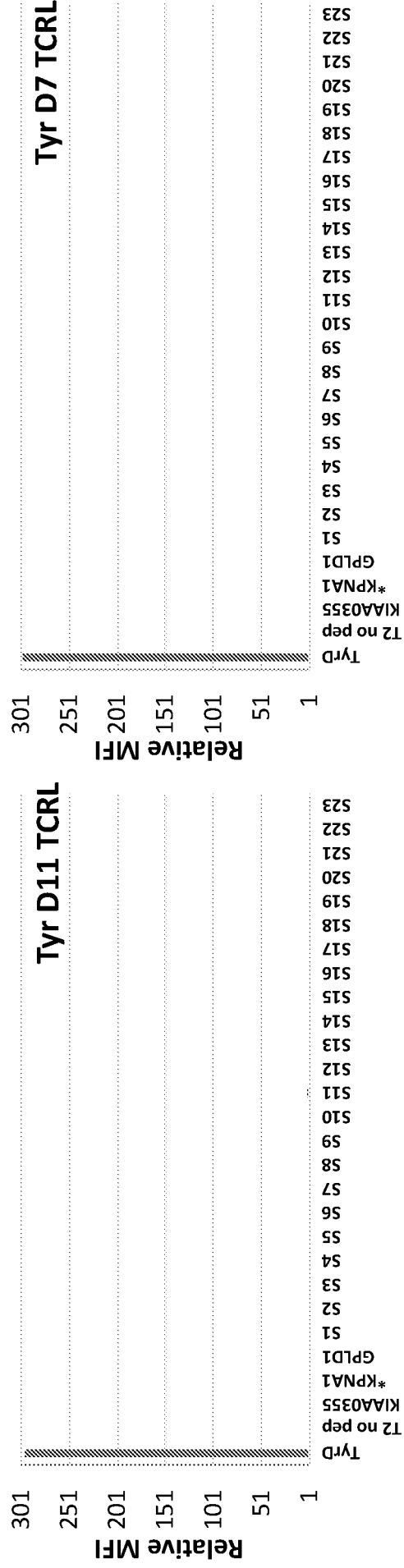
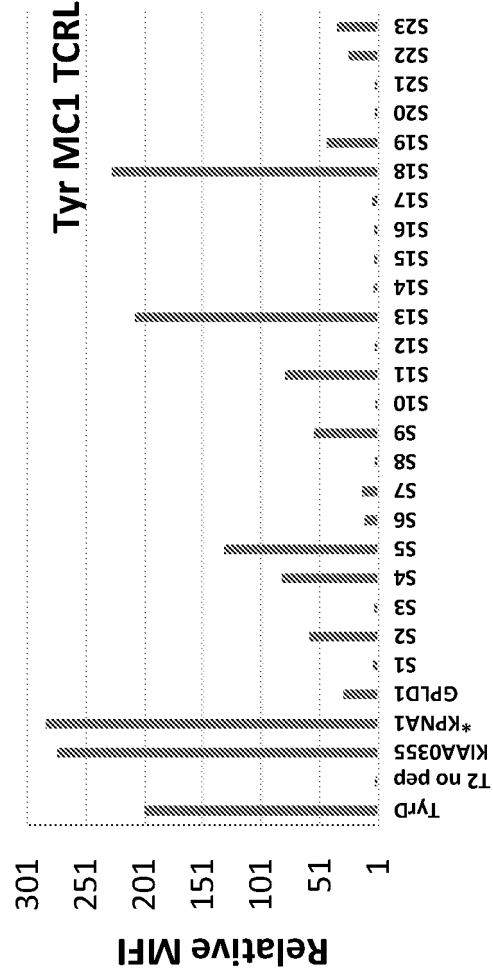


Figure 38



Peptide

Peptide



* Found by MS in normal tissues

Figure 39

A) Tyr D111 TCRL



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

Figure 40A

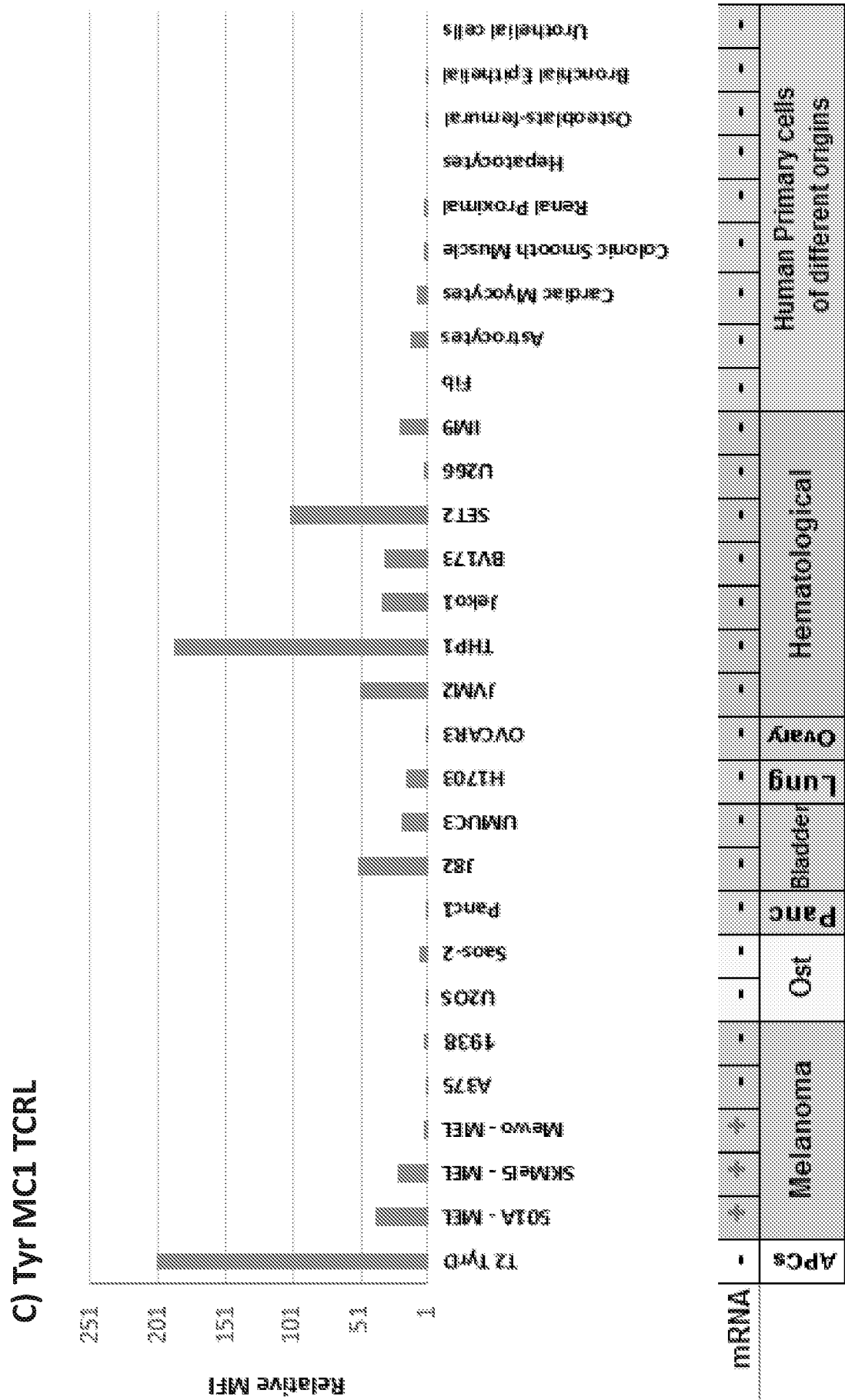


Figure 40C

Tyr D11 BS TCRL - killing assay on cell lines

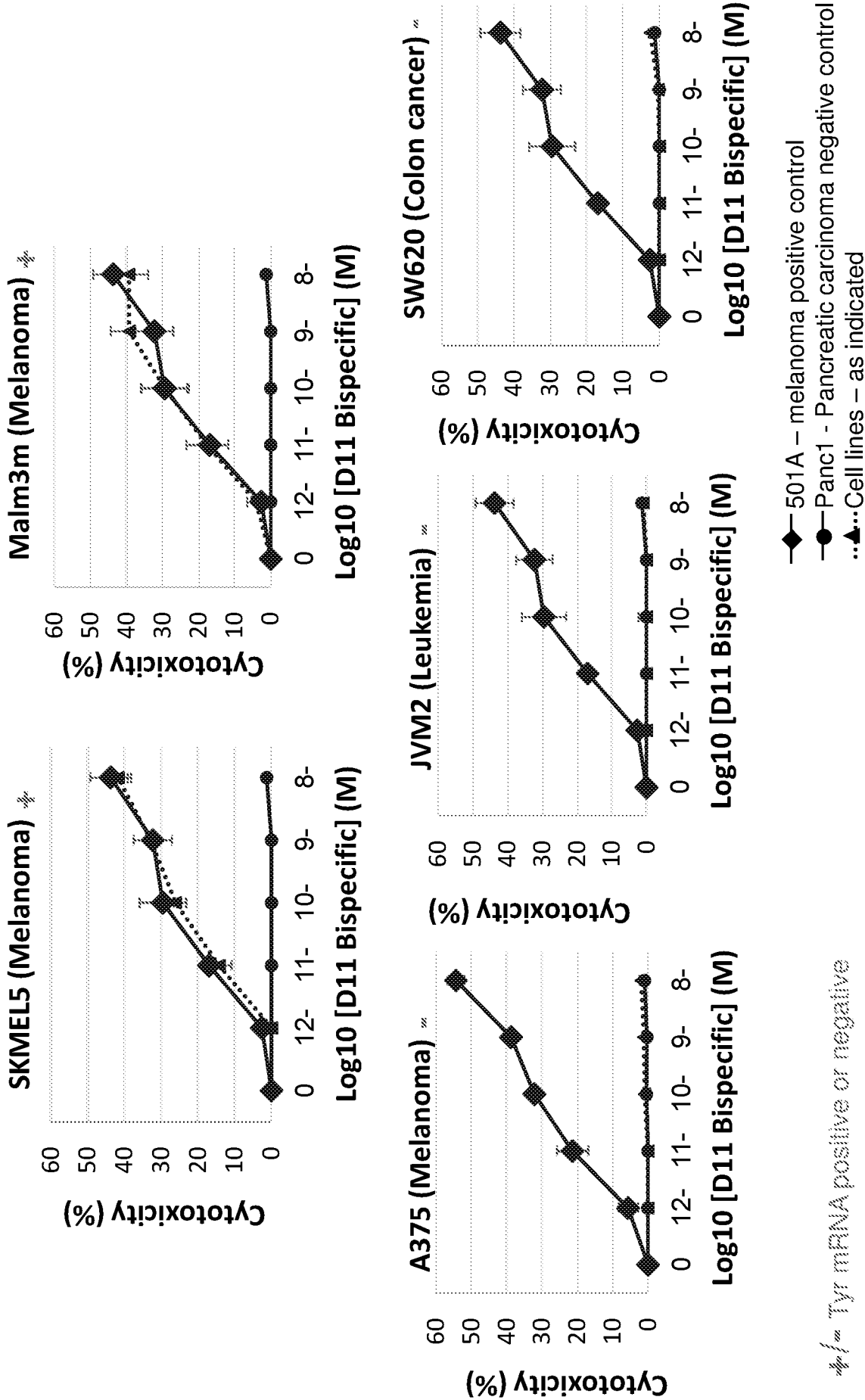


Figure 41

Tyr D11 BS TCRL - killing assay on normal primary cells

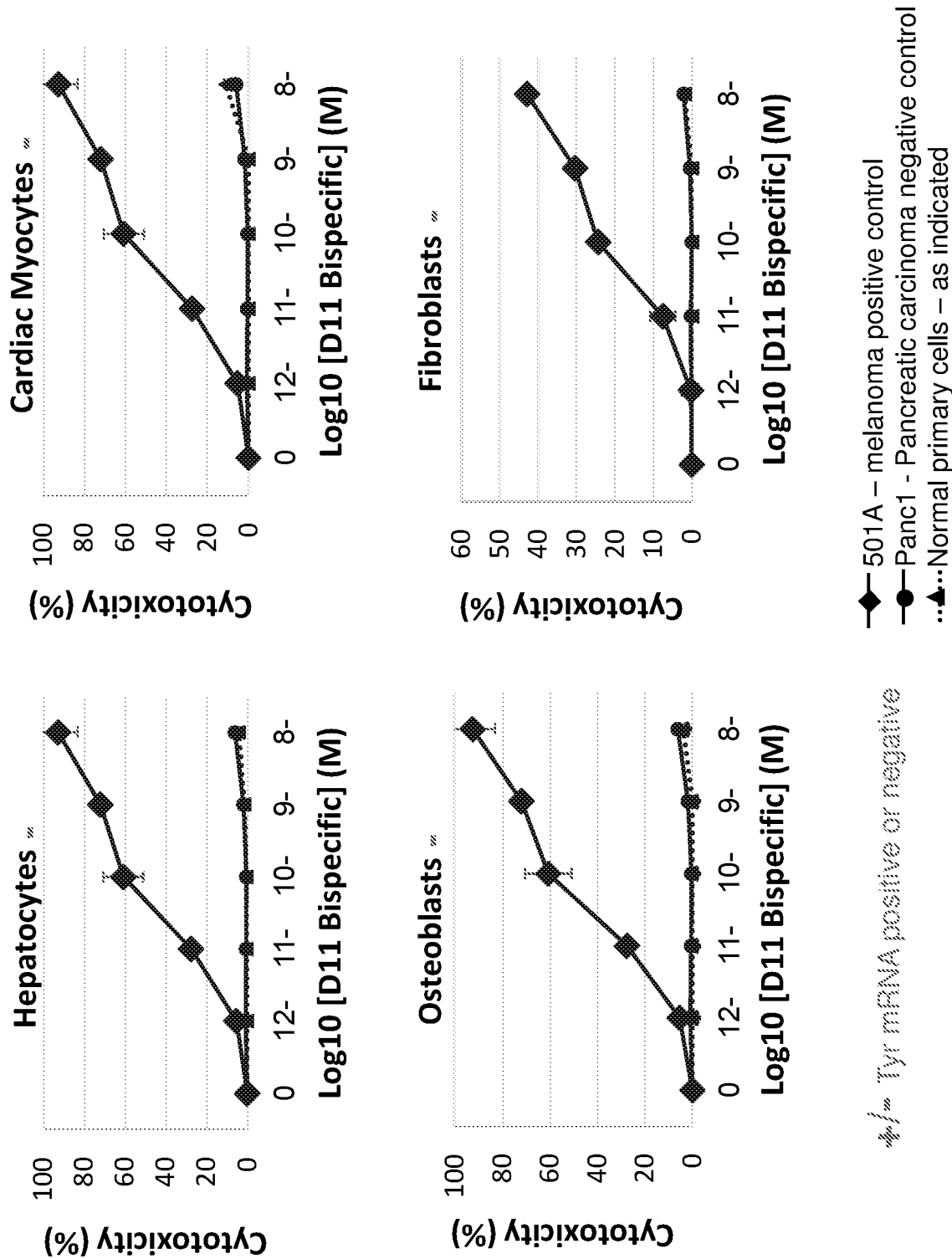


Figure 42

Tyr D7 BS TCRL - killing assay on cell lines

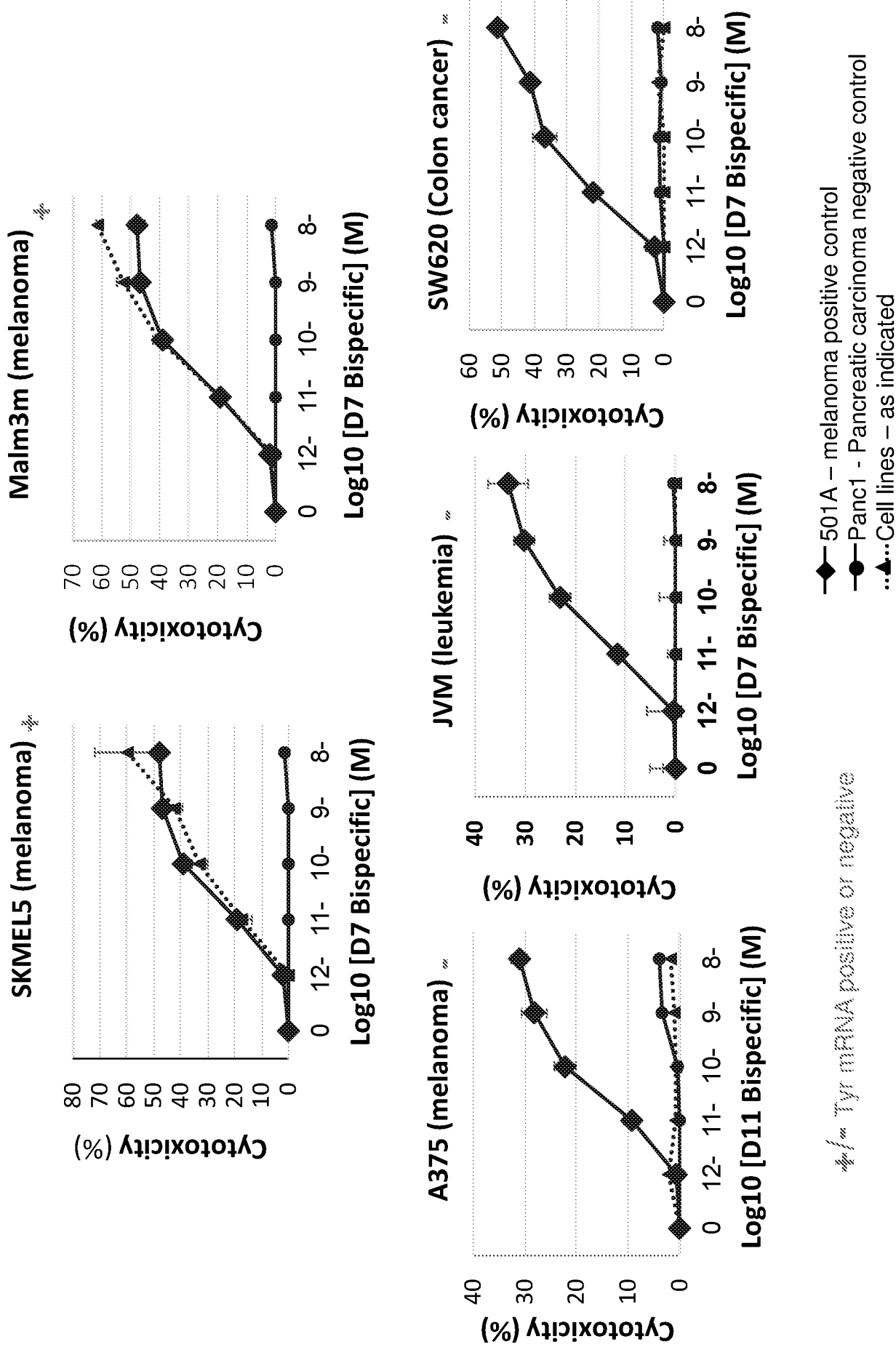


Figure 43

Tyr D7 BS TCRL - killing assay on normal primary cells

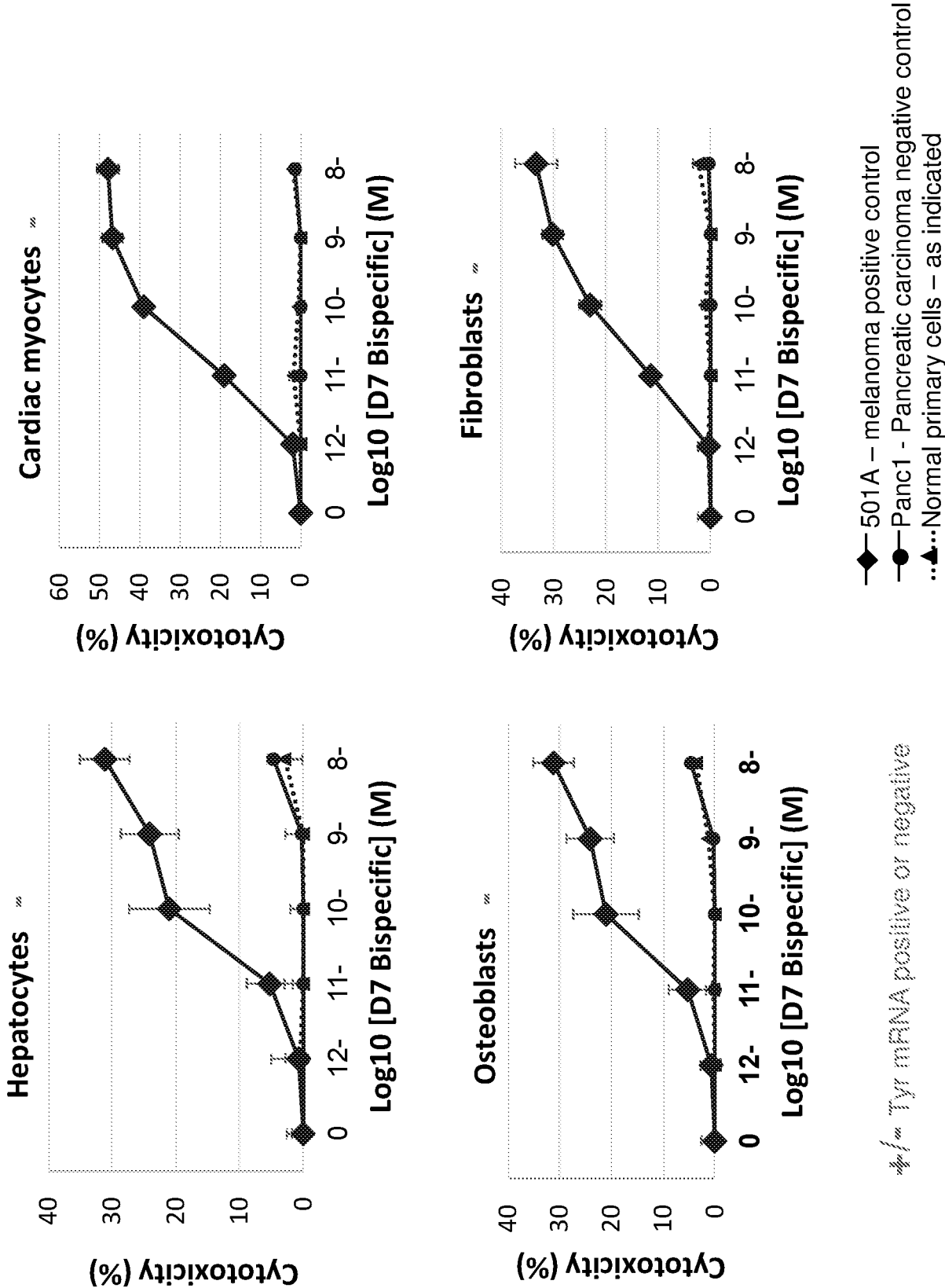


Figure 44

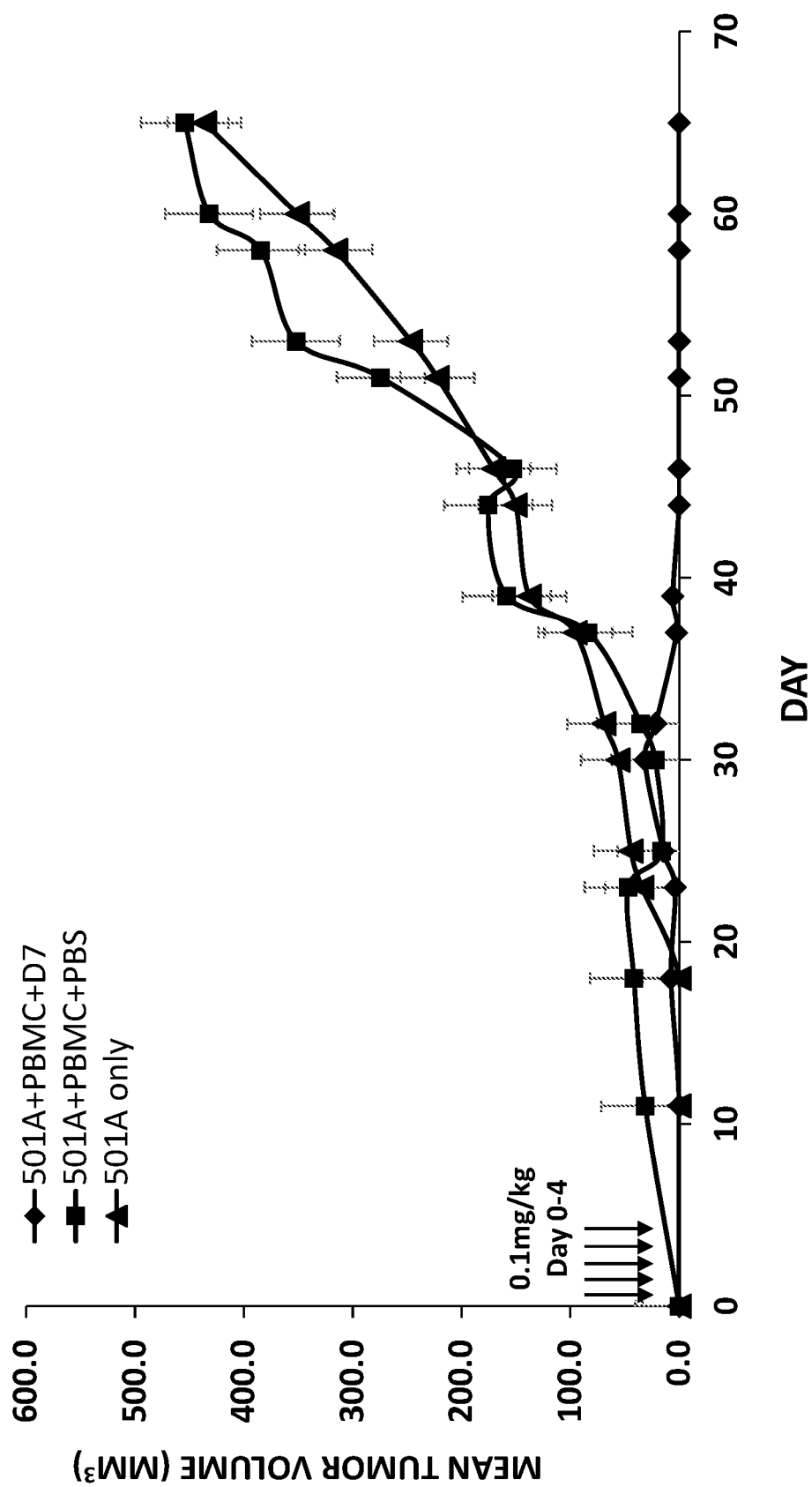


Figure 45

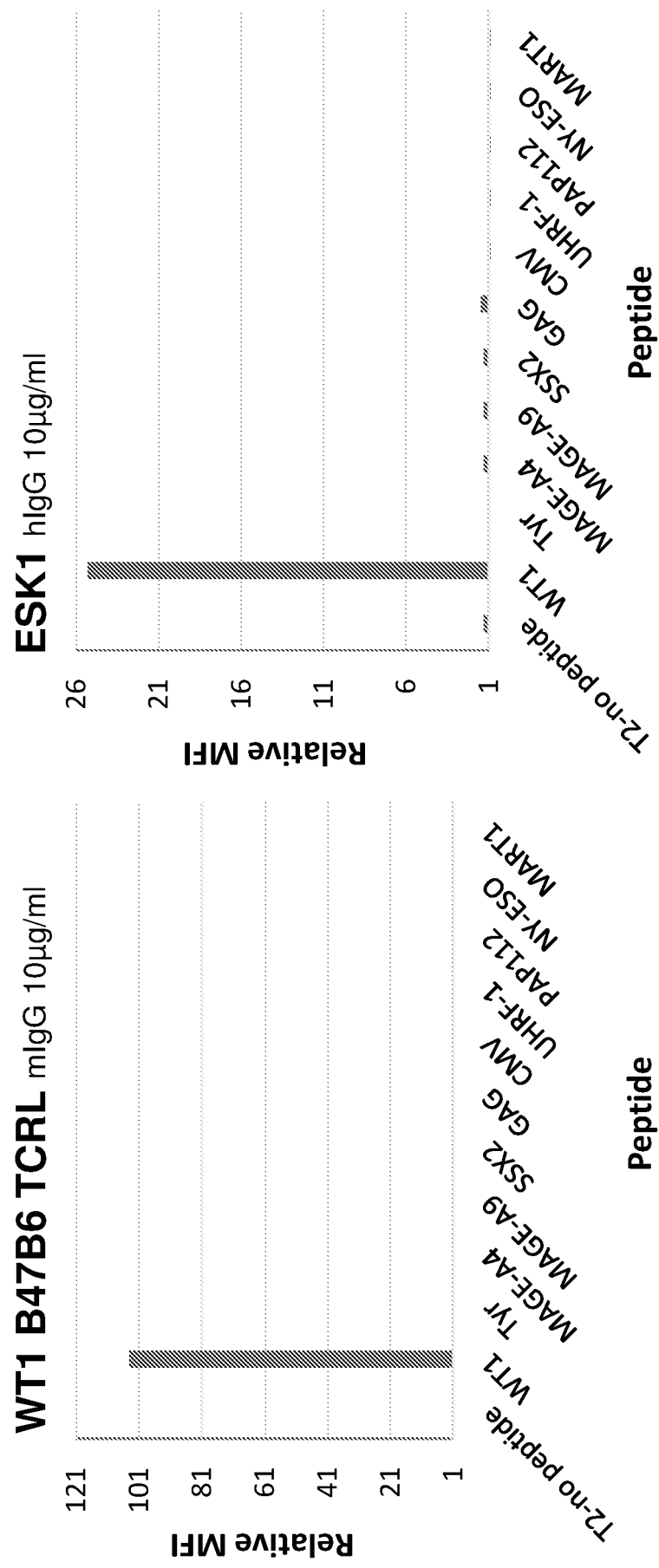
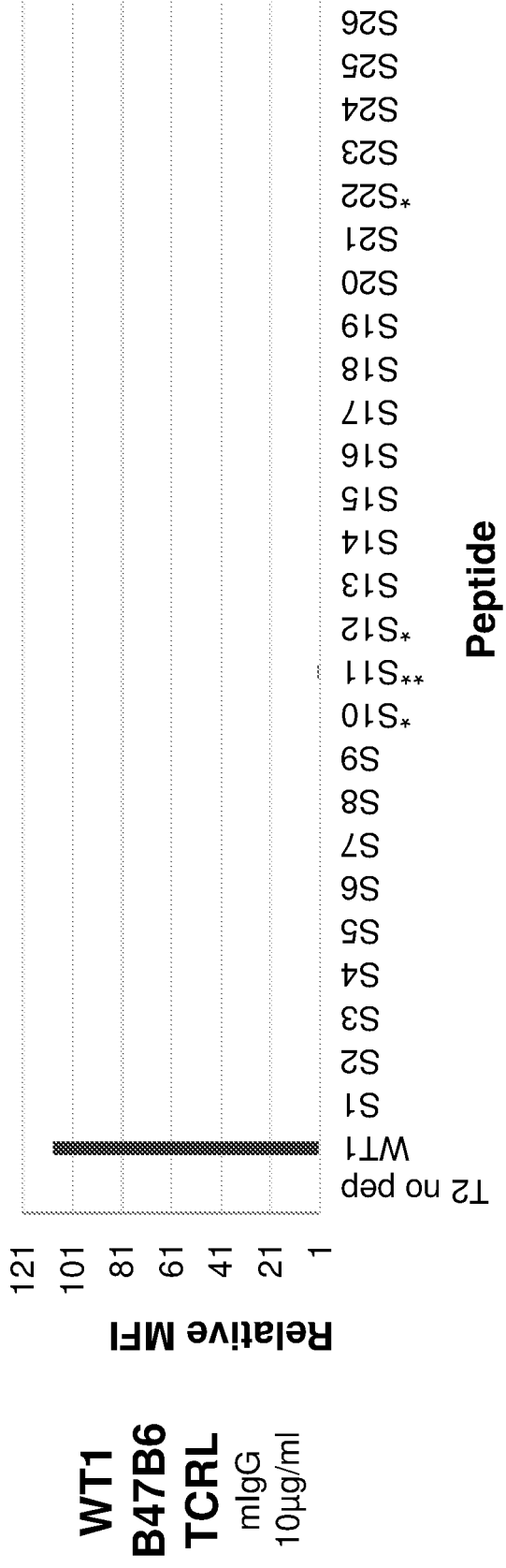
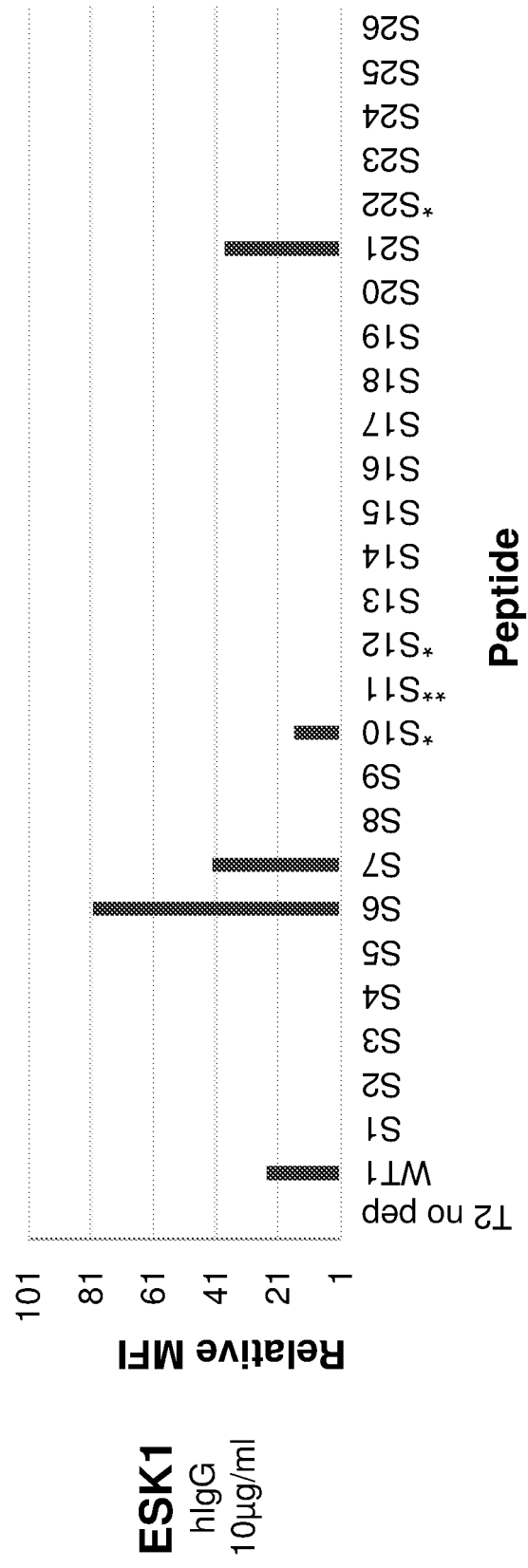


Figure 46



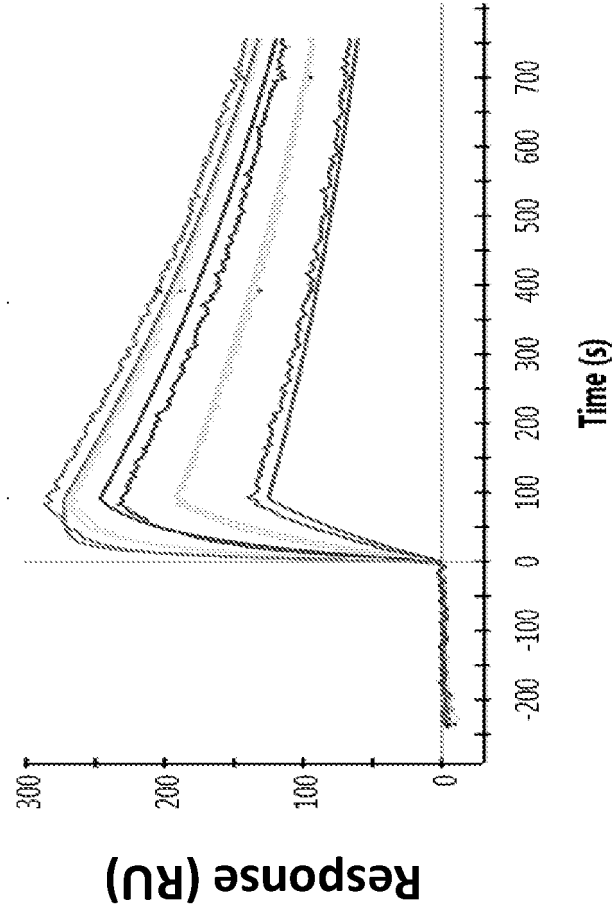
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•Found by MS in normal tissues

Figure 47

B47B6— 5nM



ESK1— 200nM

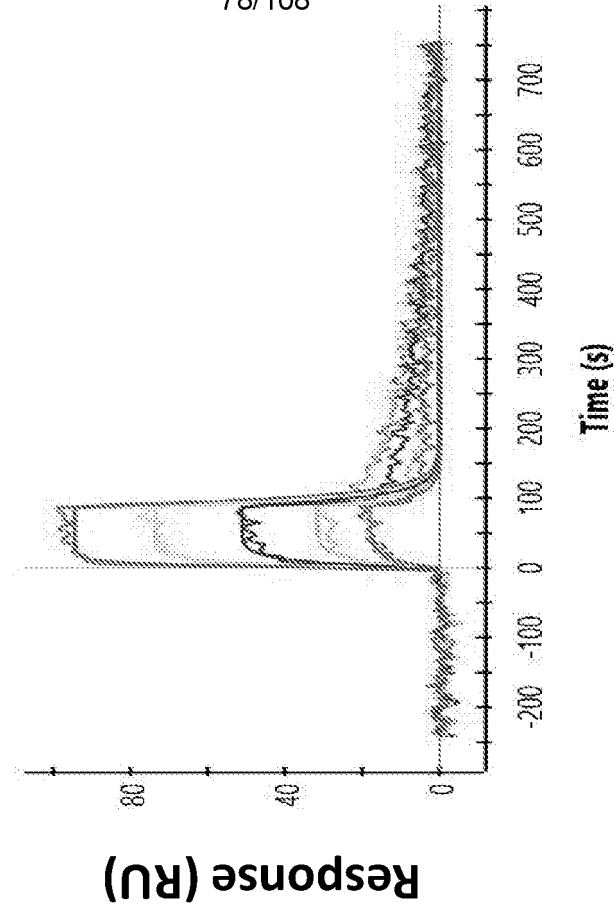


Figure 48

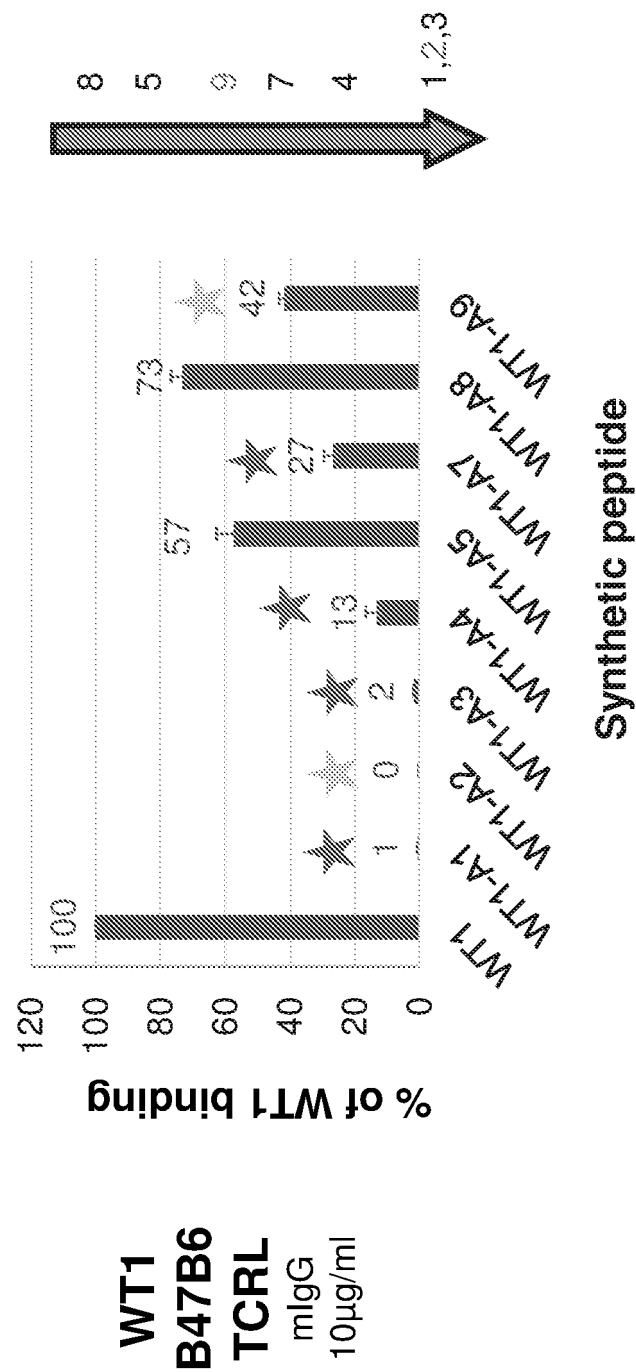
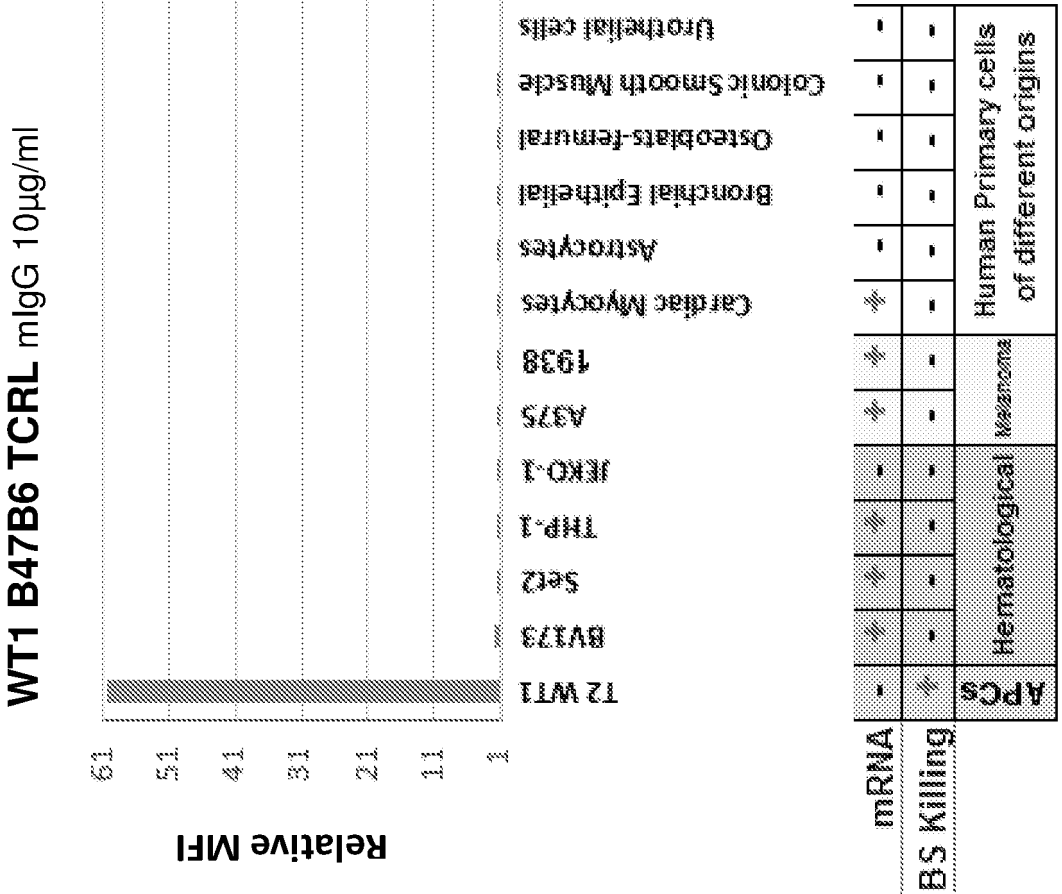
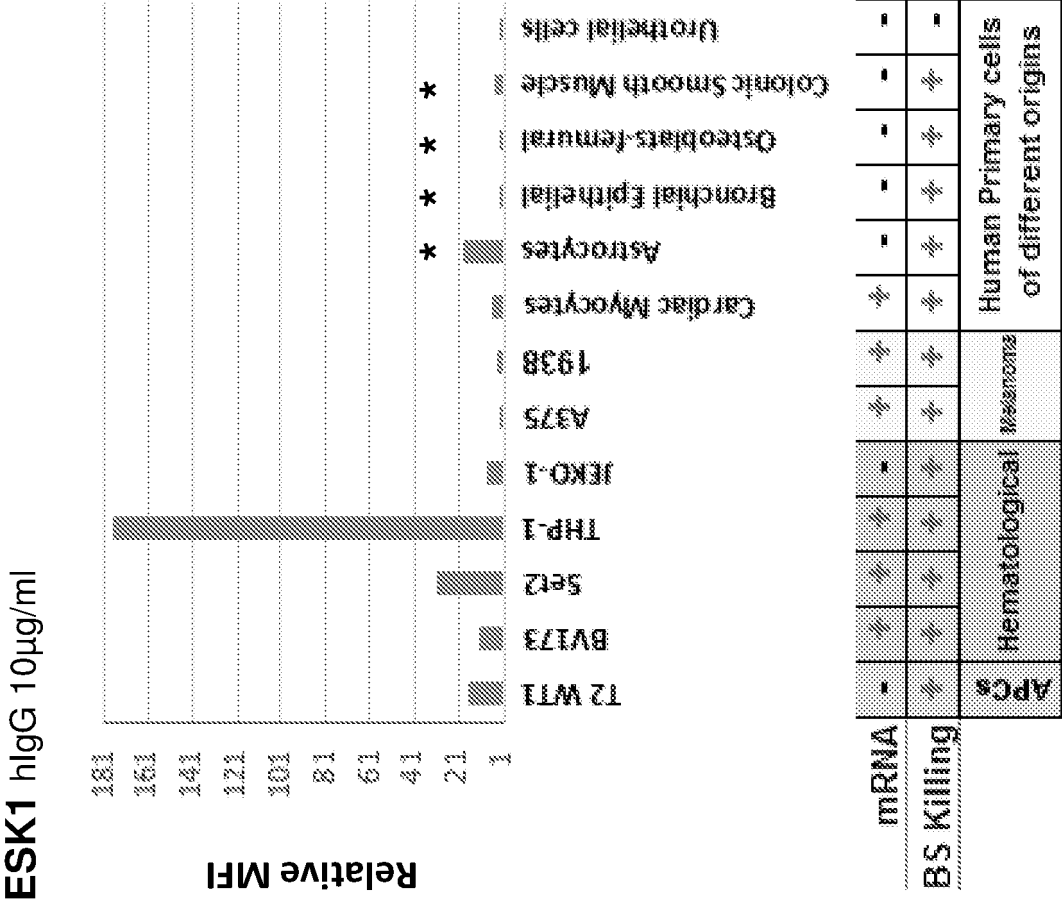


Figure 49



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

Figure 50

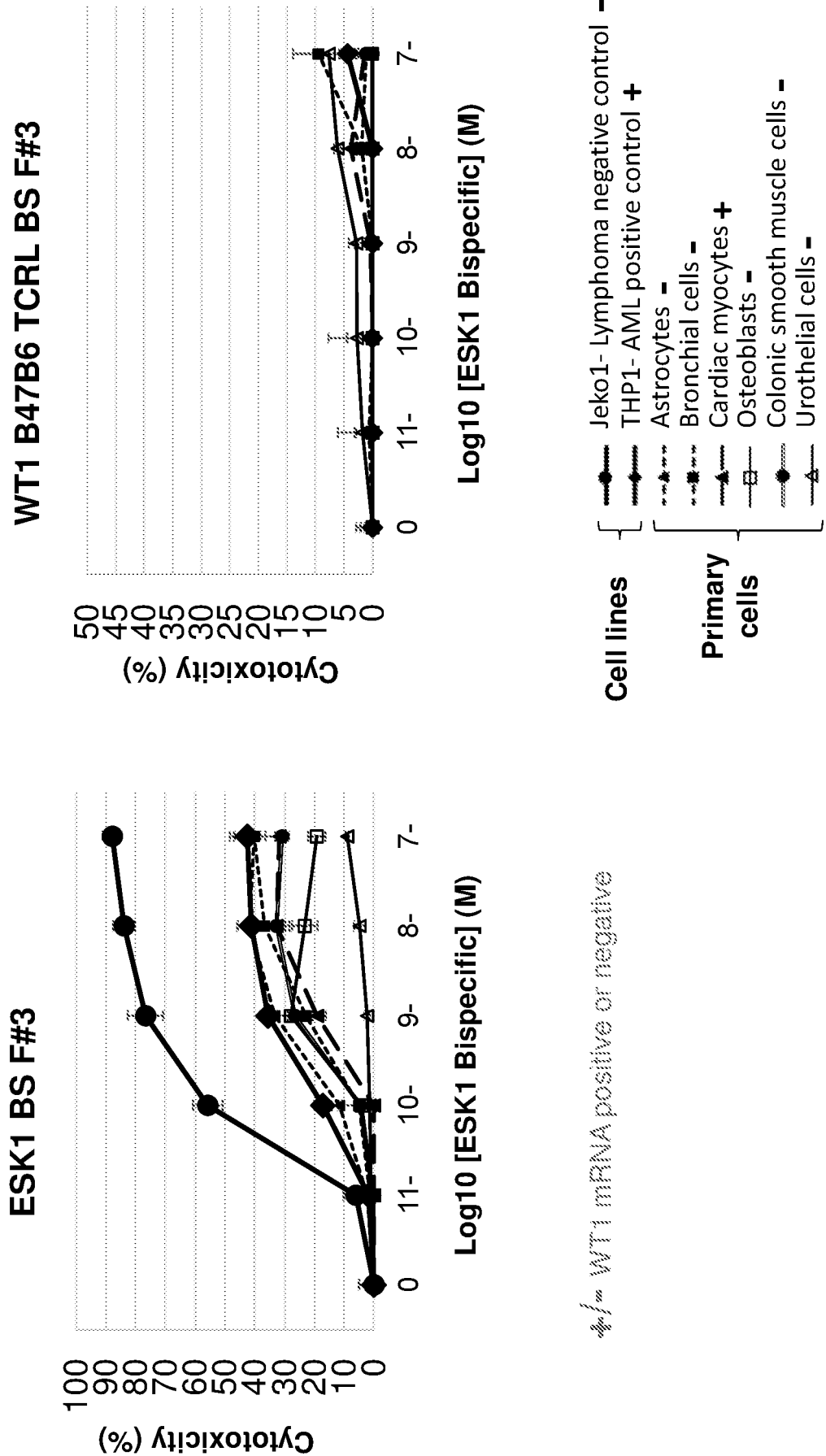
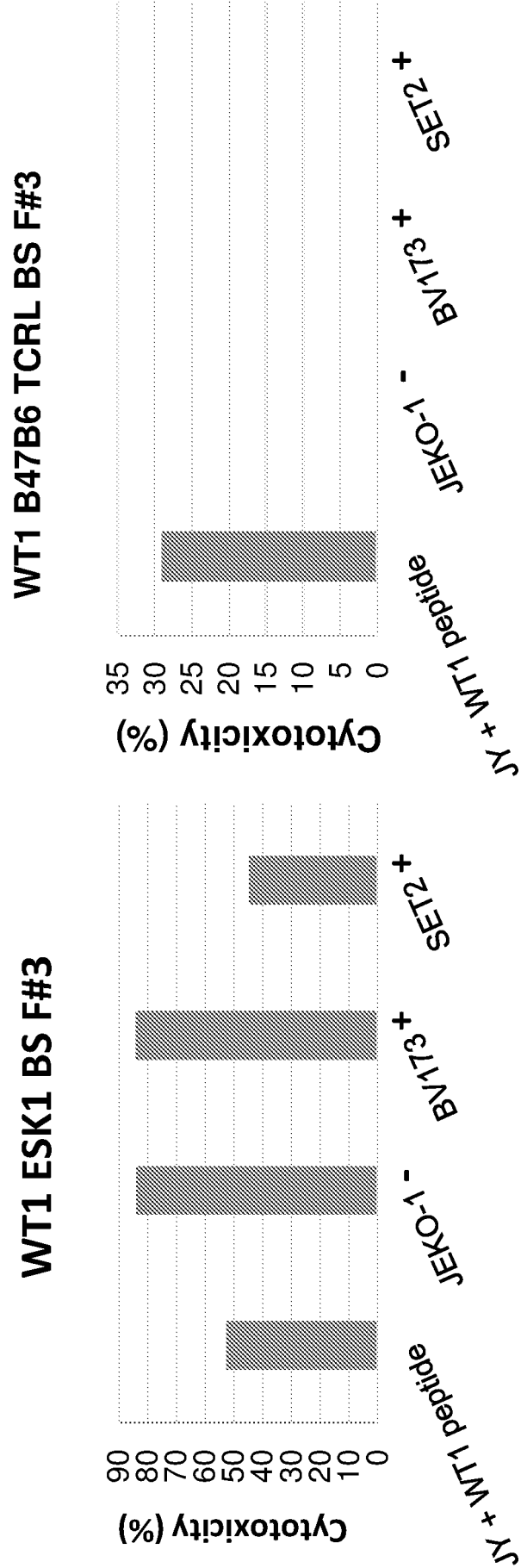


Figure 51A



+/- WT1 mRNA positive or negative

Figure 51B

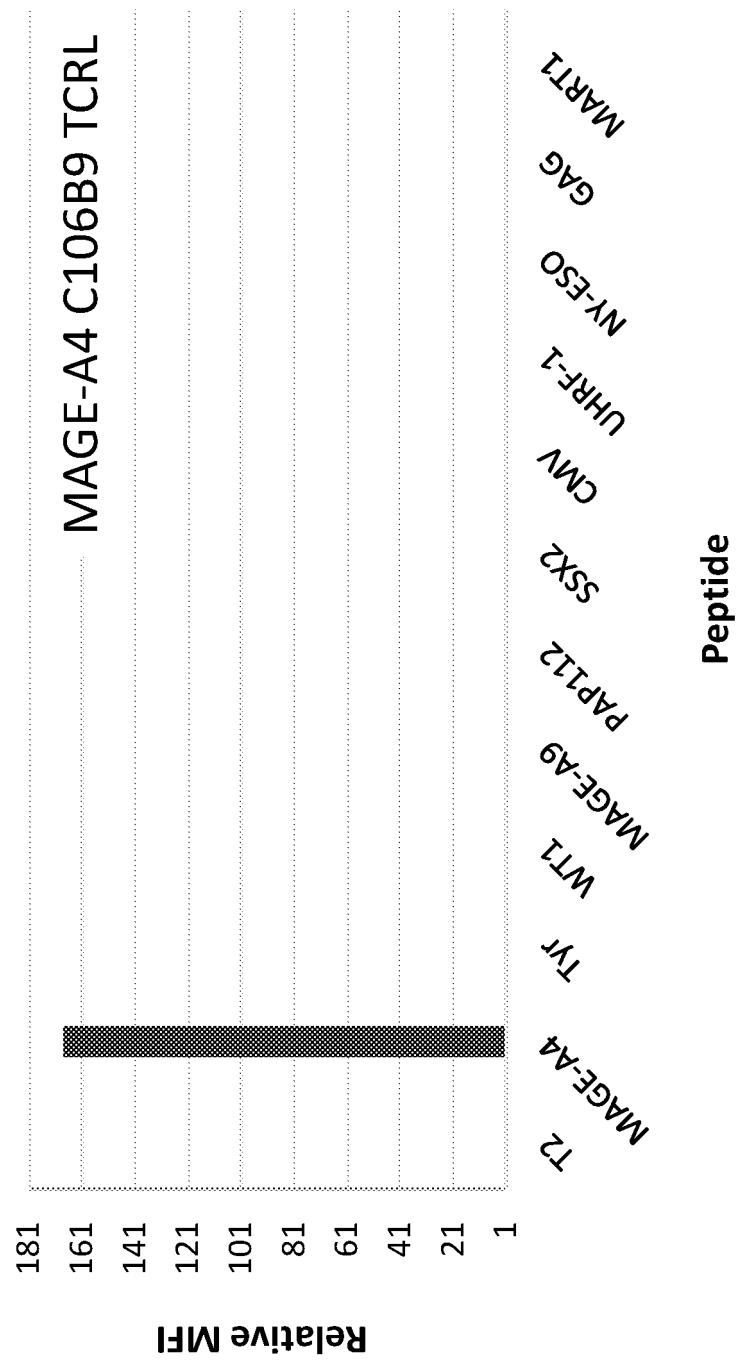
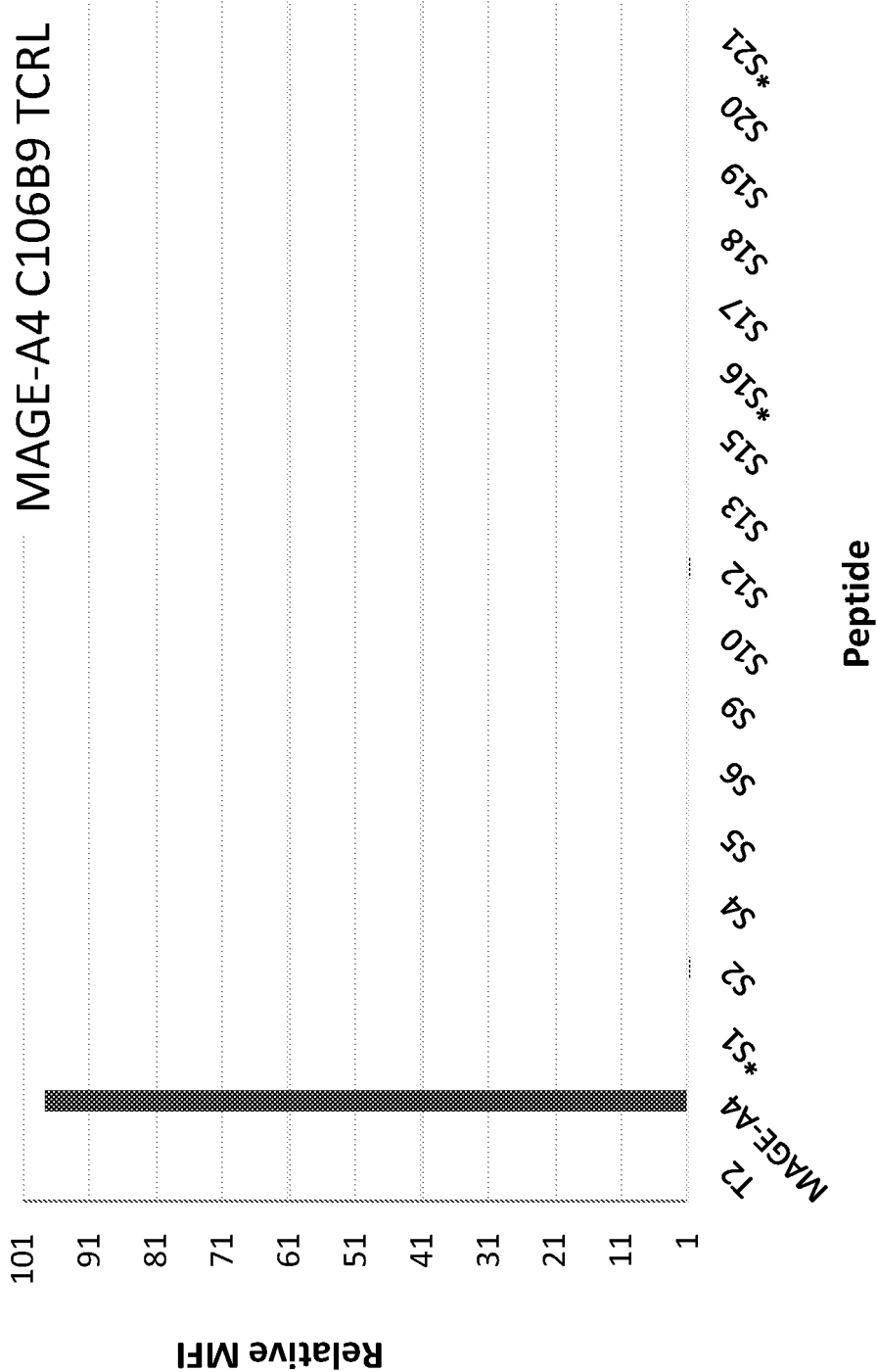


Figure 52



* Found by MS in normal tissues

Figure 53

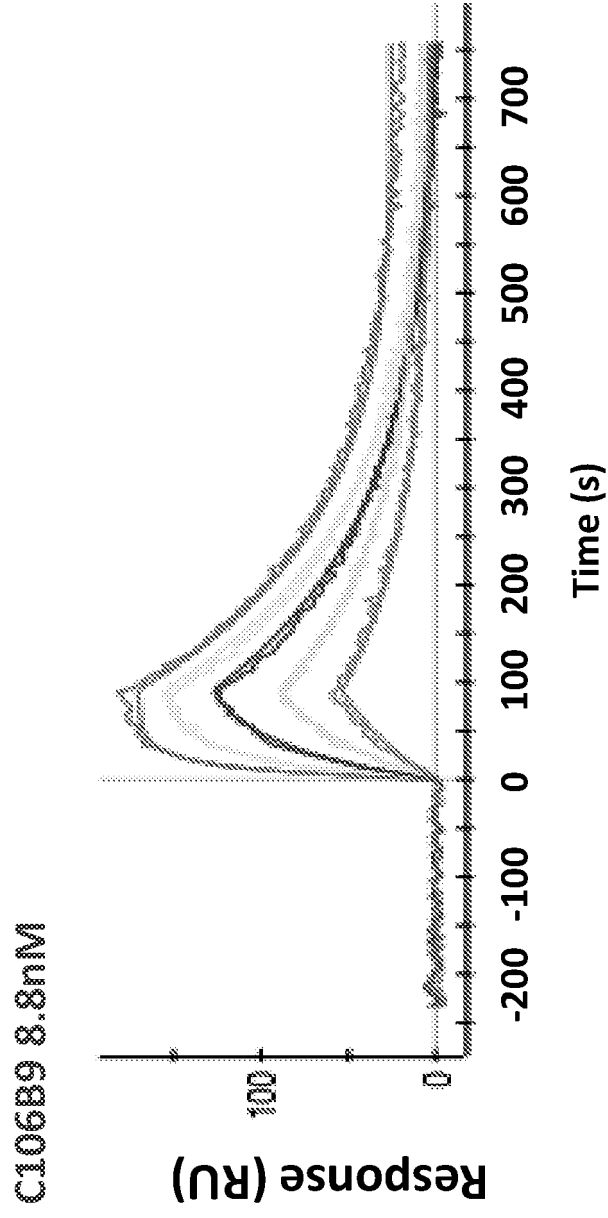


Figure 54

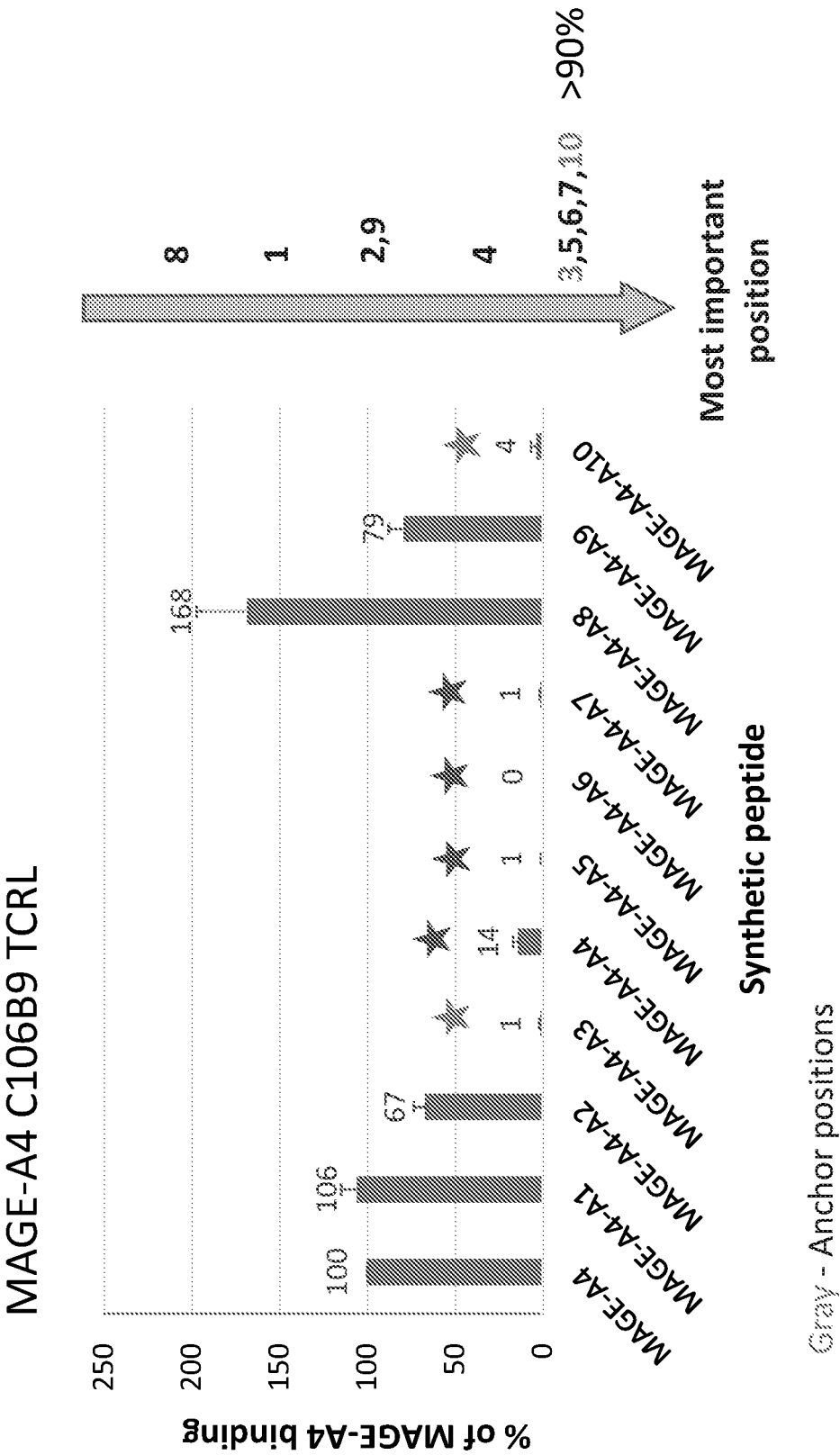


Figure 55

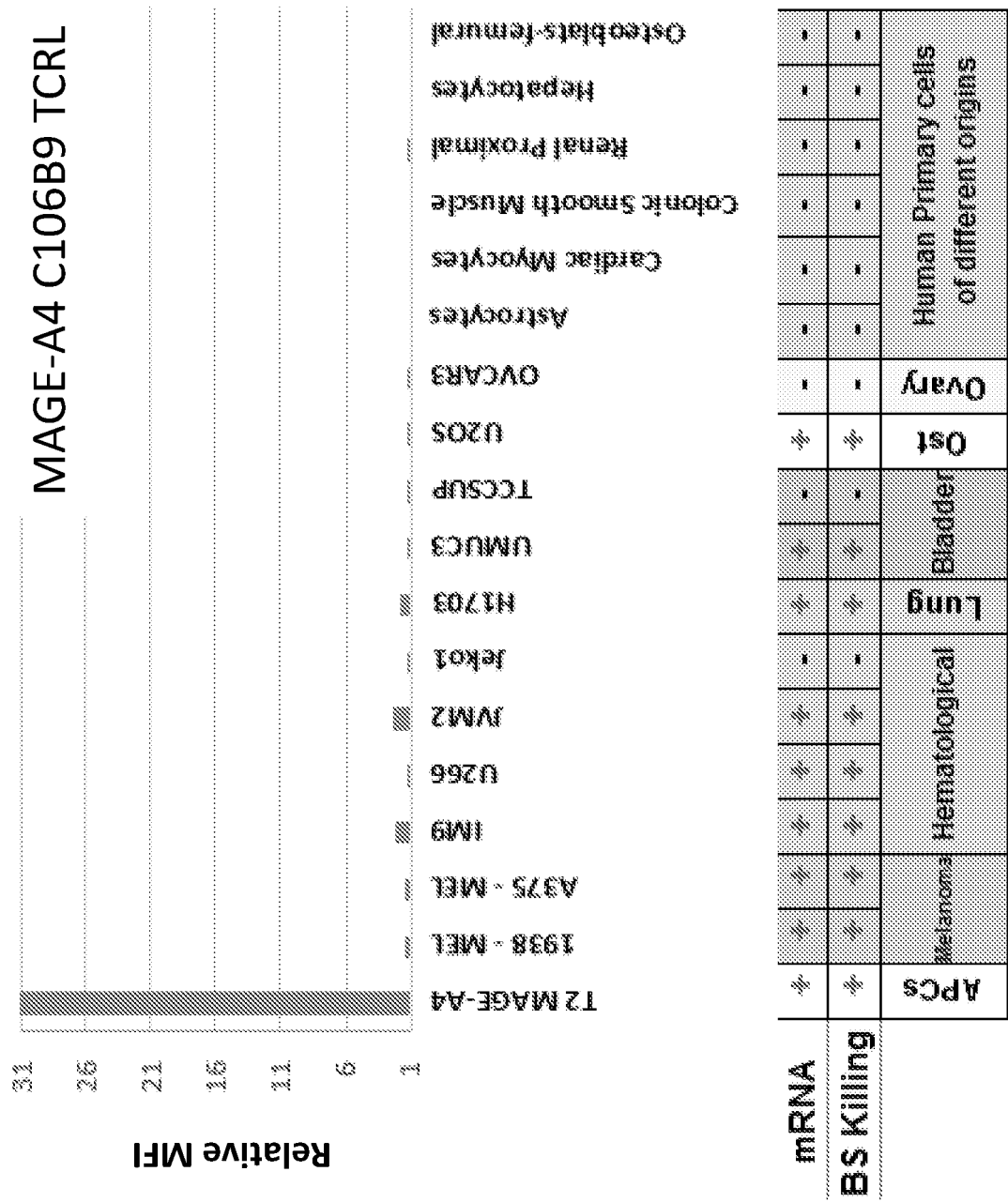
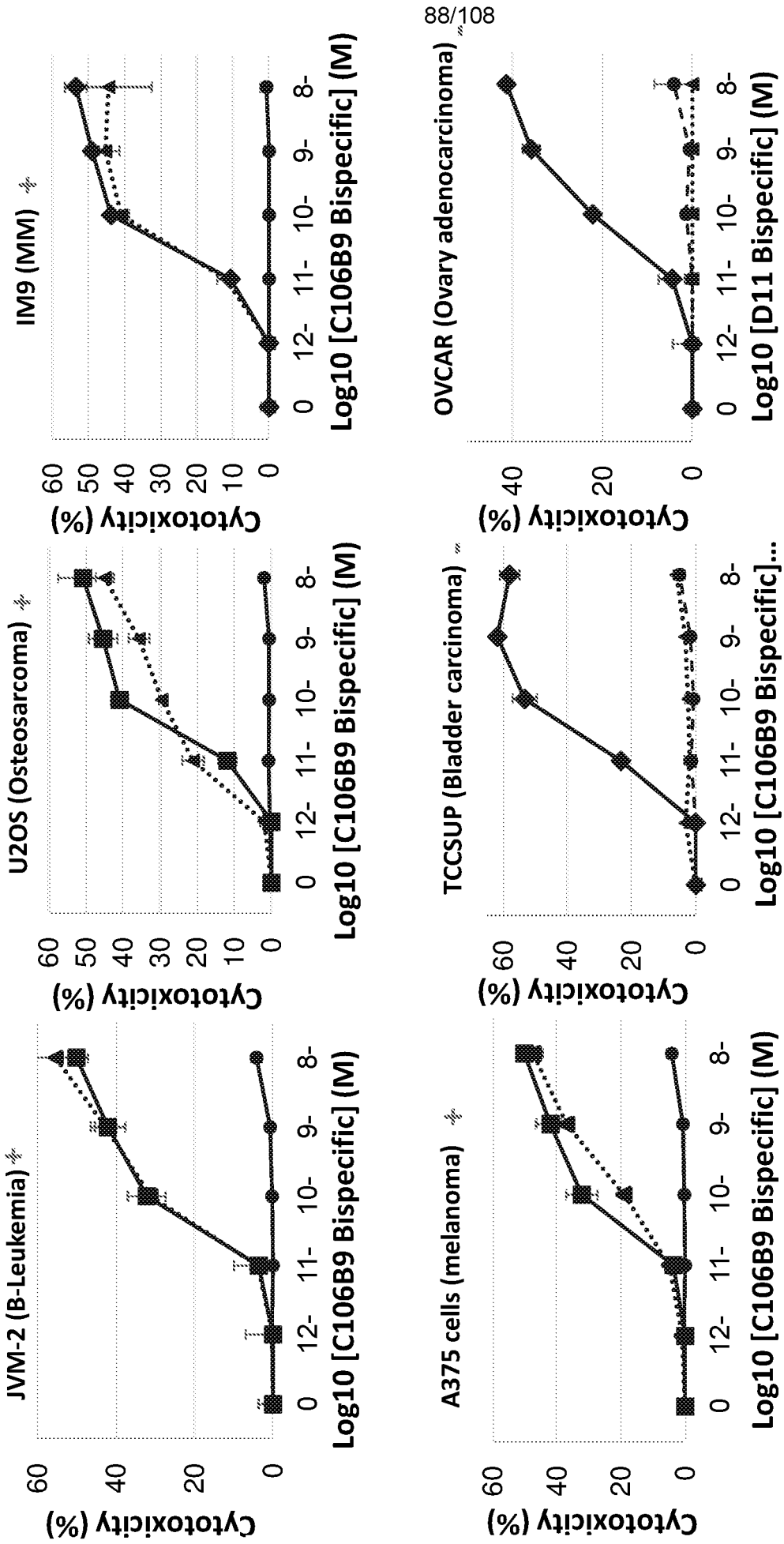


Figure 56

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



1938 – melanoma positive control
IM9 – MM positive control
Panc1 – negative control
JEKO1 – negative control
Cell lines – as indicated

Figure 57

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

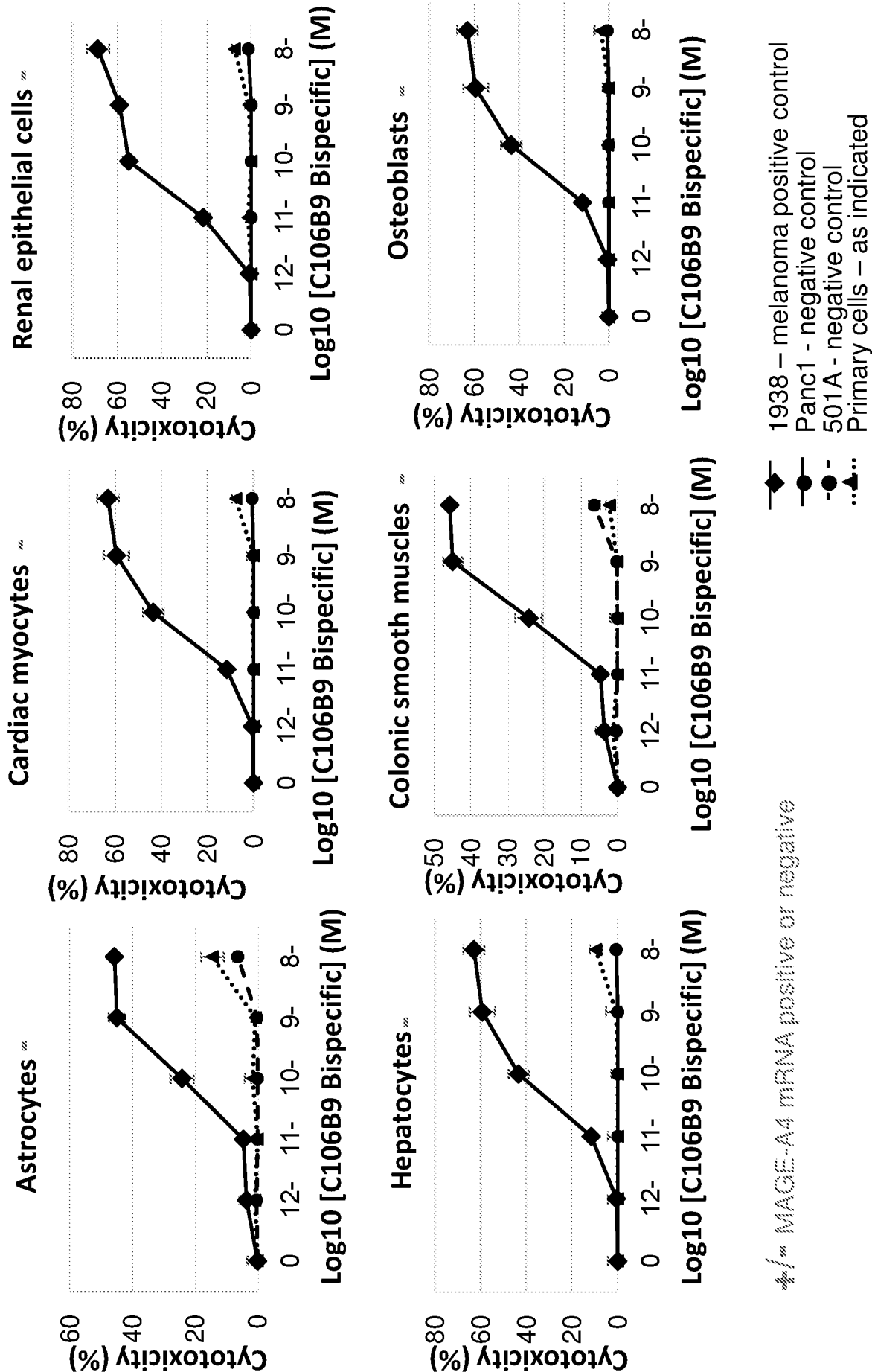


Figure 58

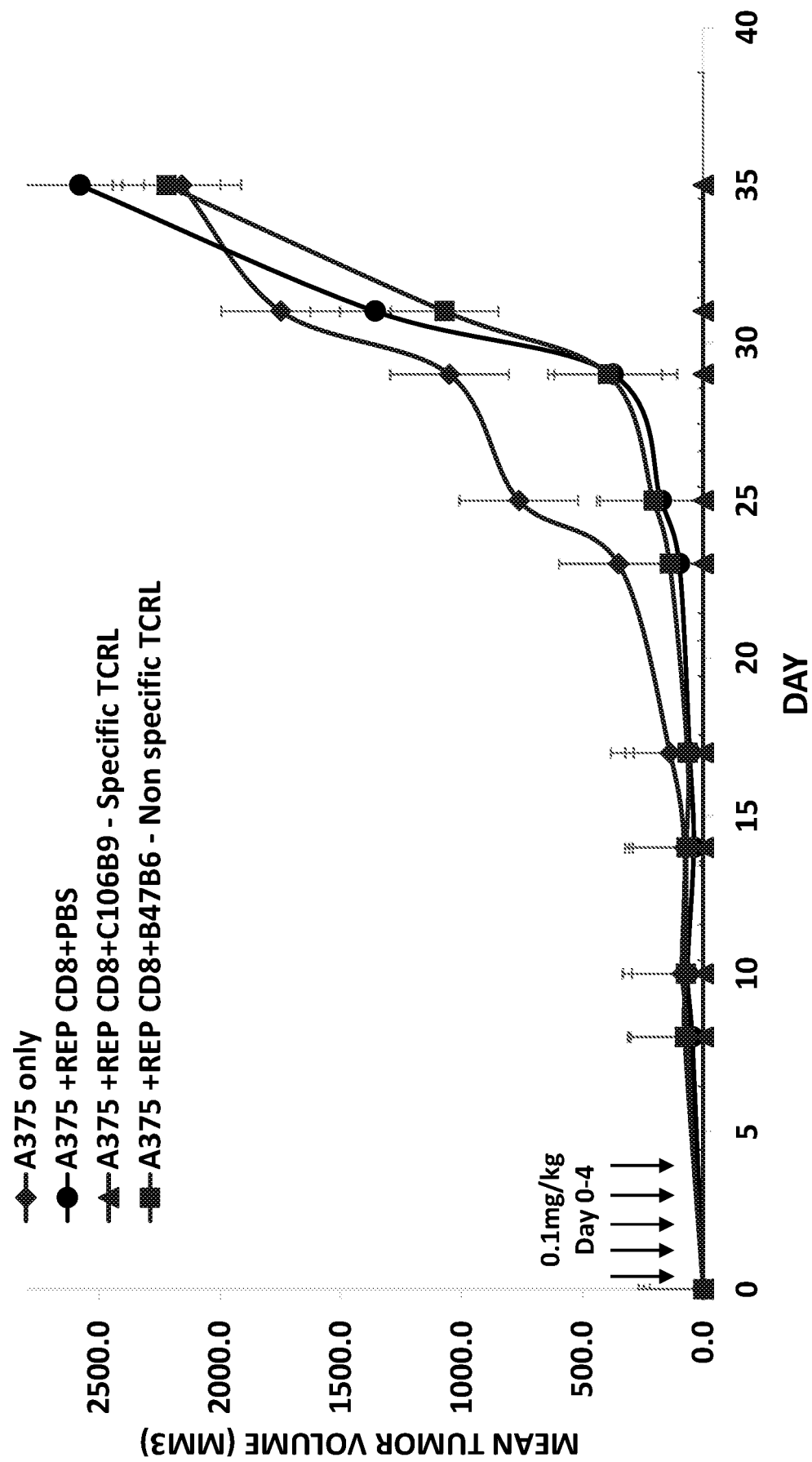


Figure 59

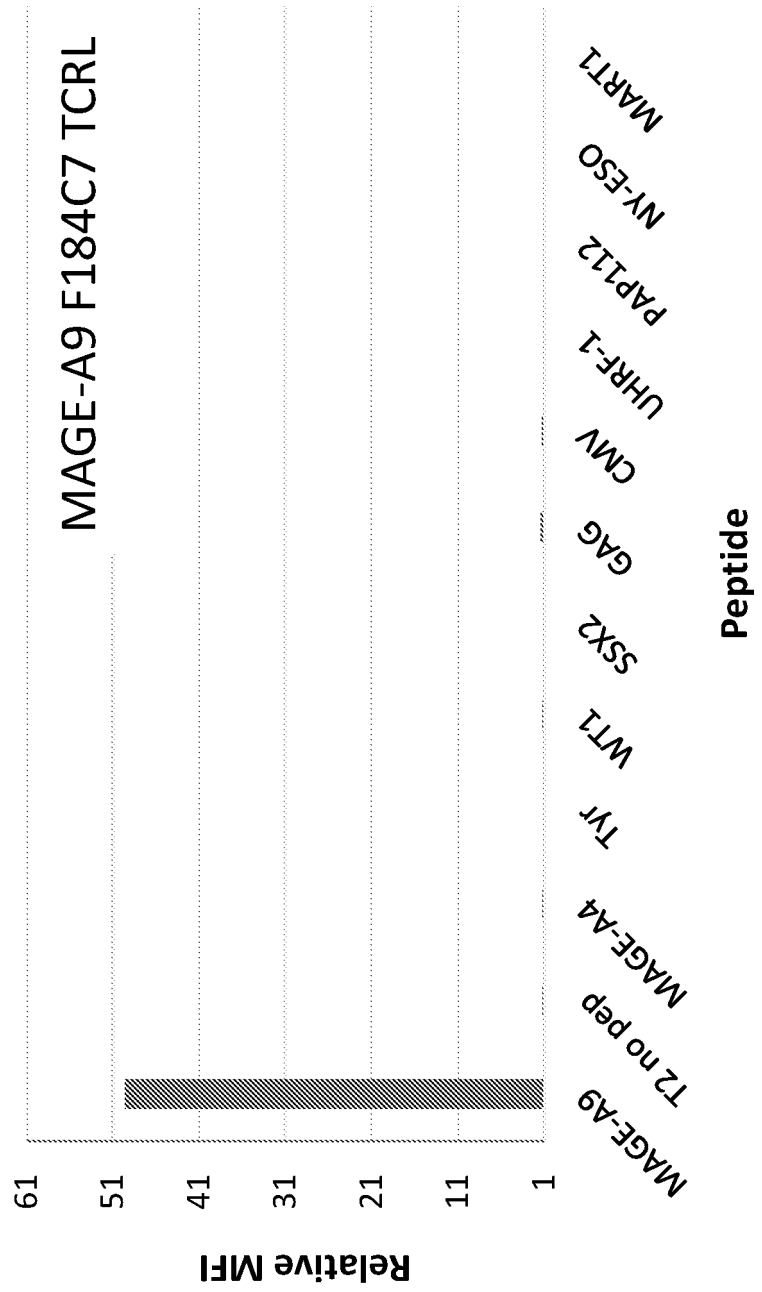
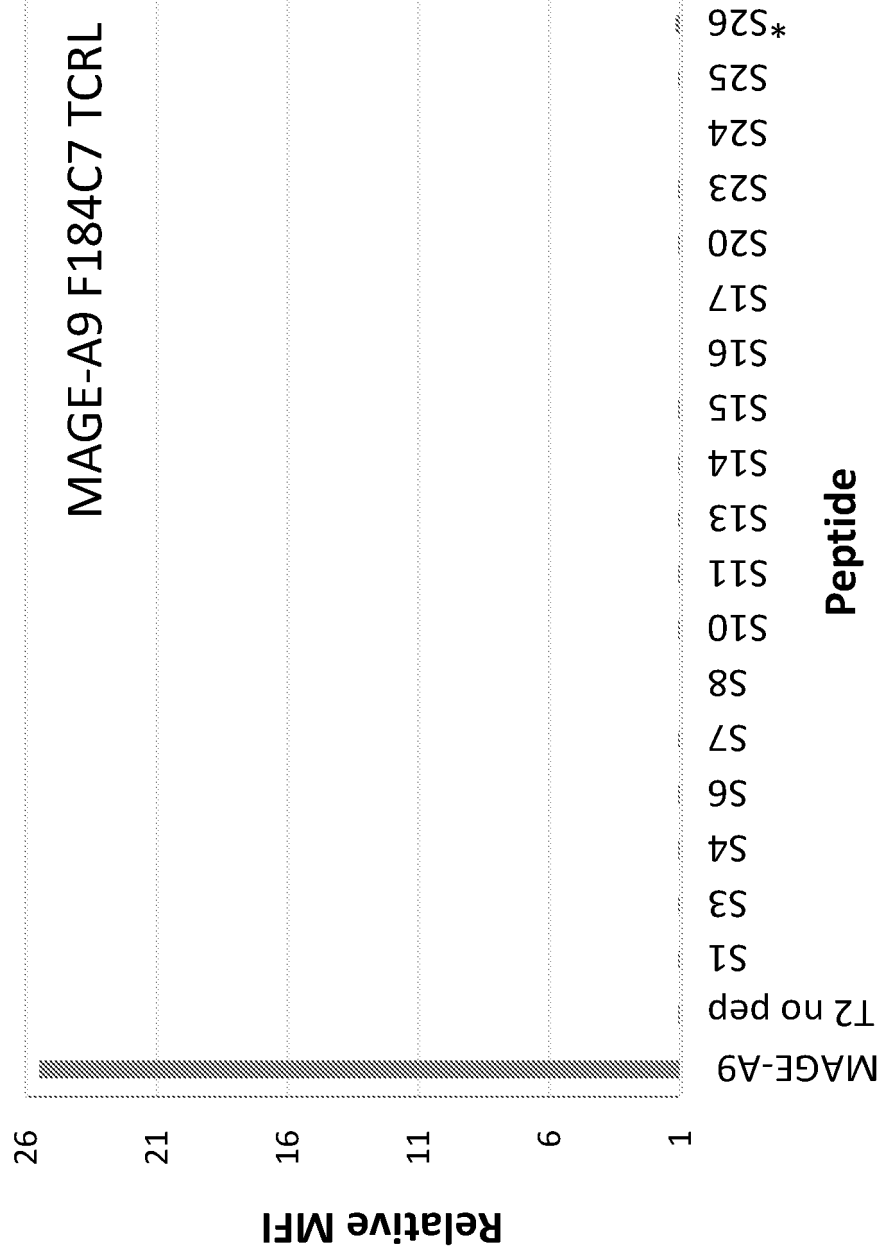


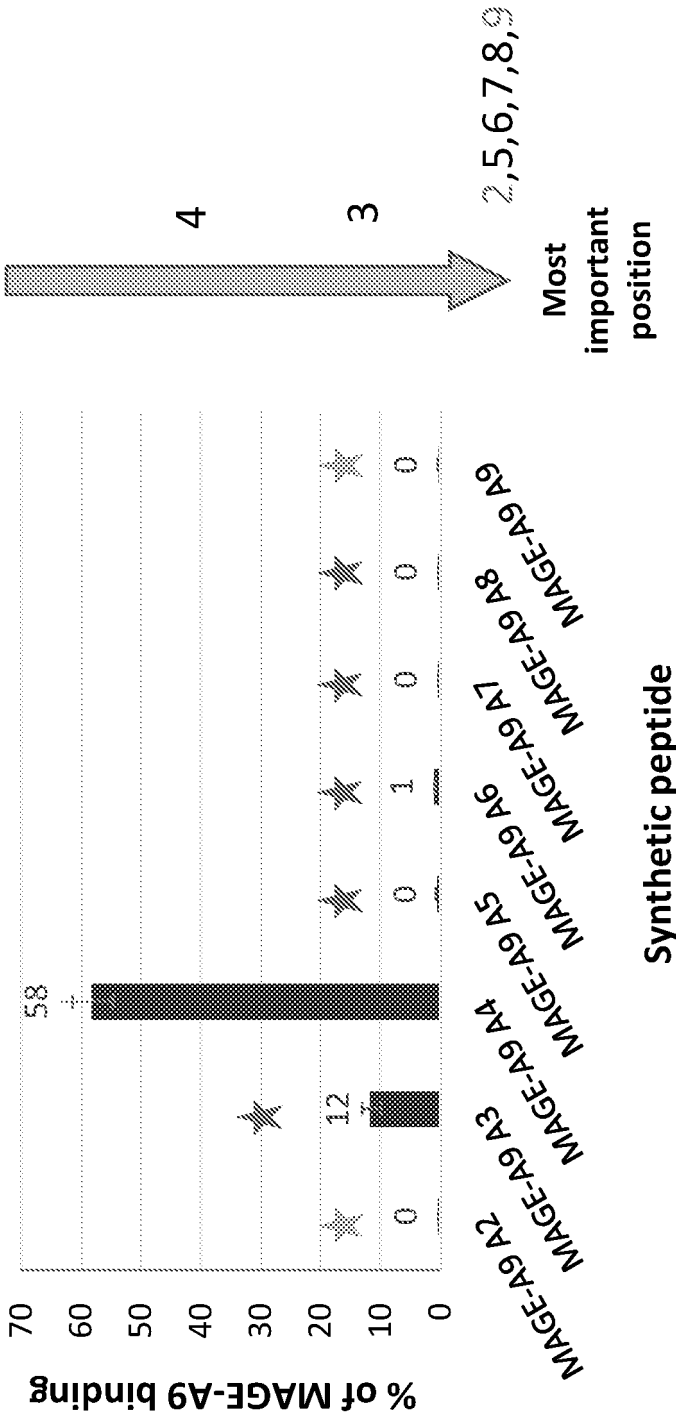
Figure 60



* Found by MS in normal tissues

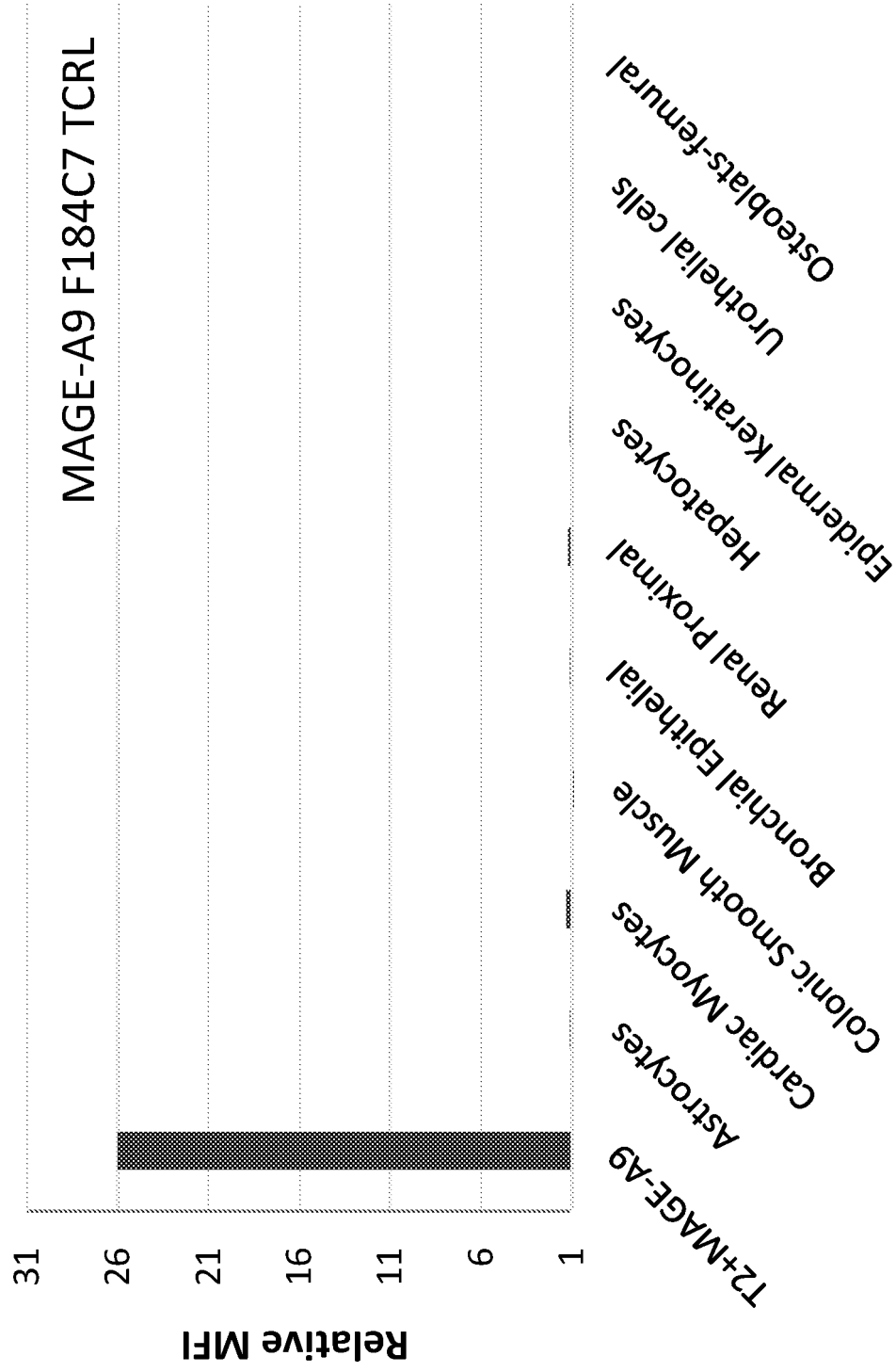
Figure 61

MAGE-A9 F184C7 TCRL



Gray - Anchor positions

Figure 62

**Figure 63**

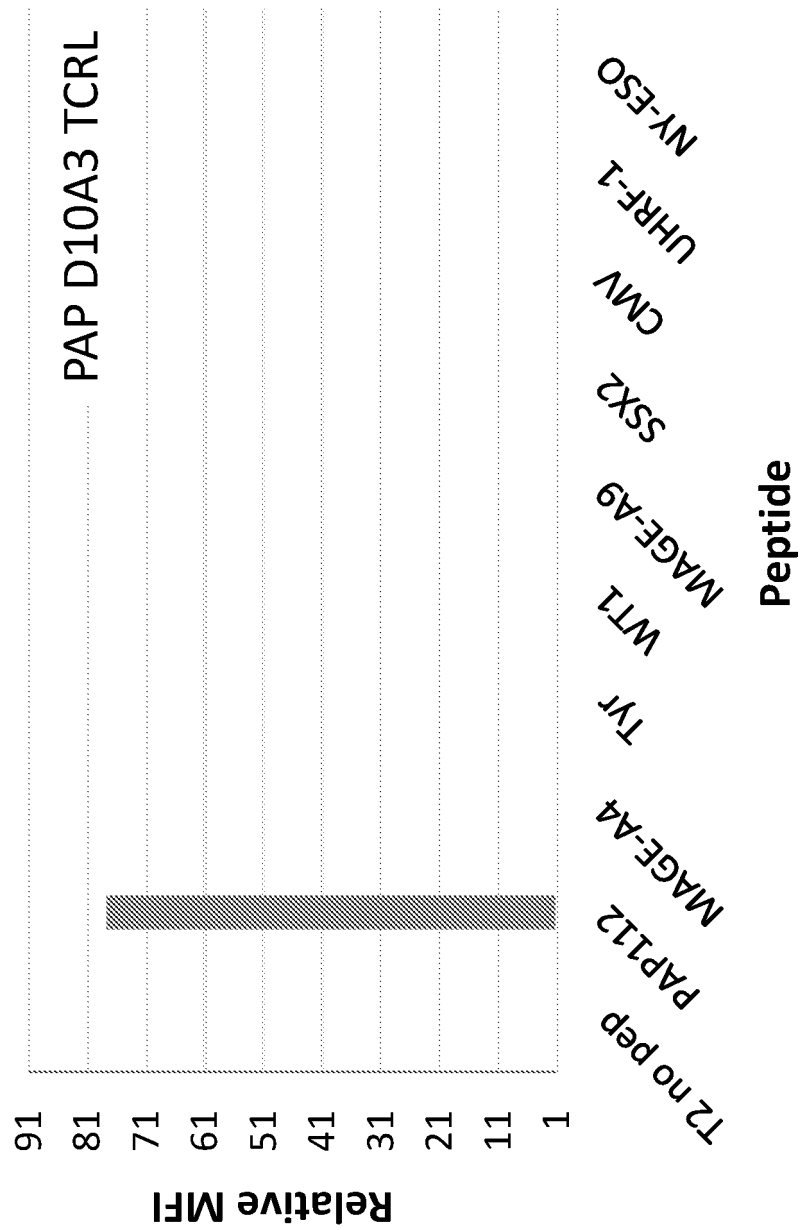
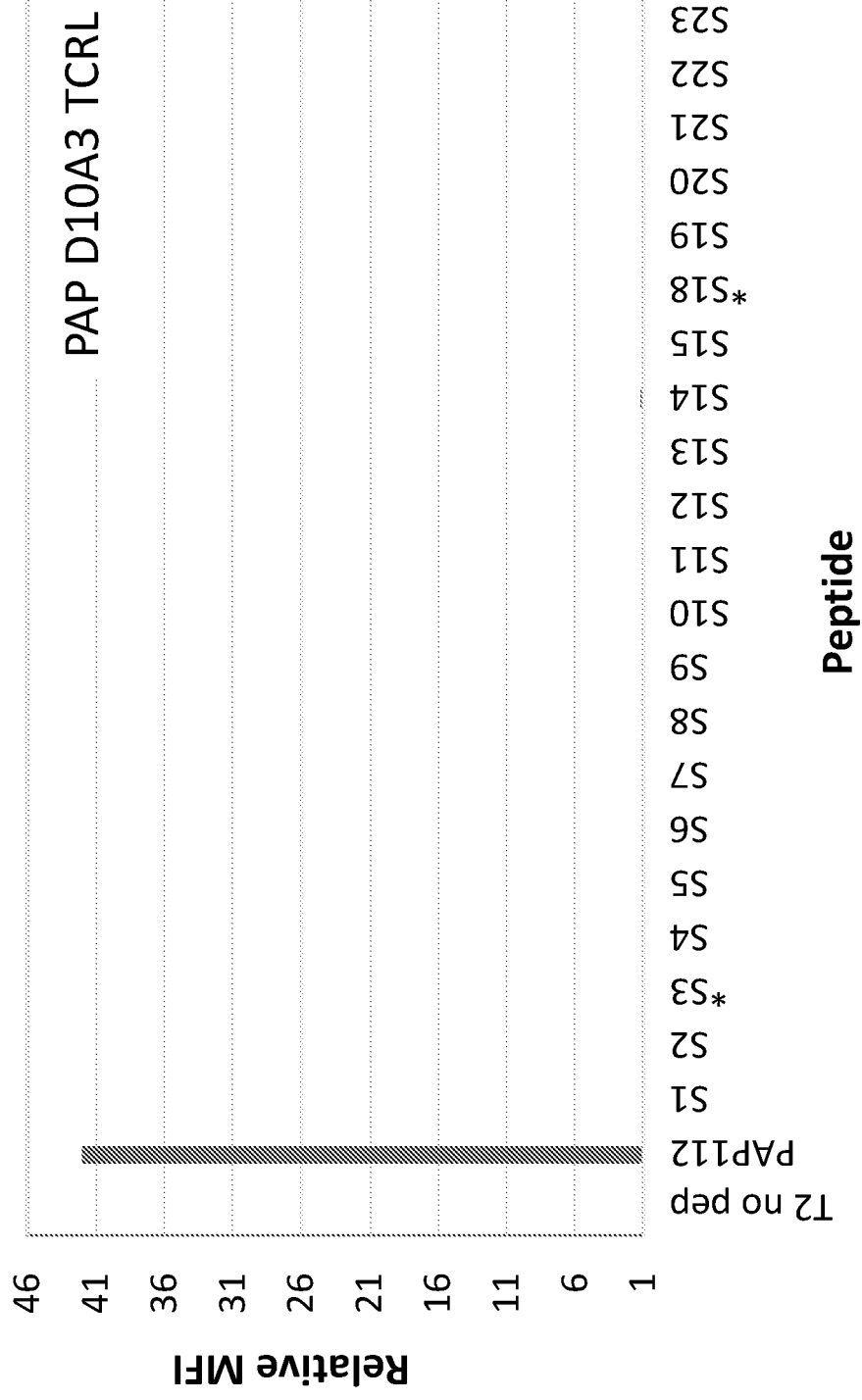


Figure 64



* Found by MS in normal tissues

Figure 65

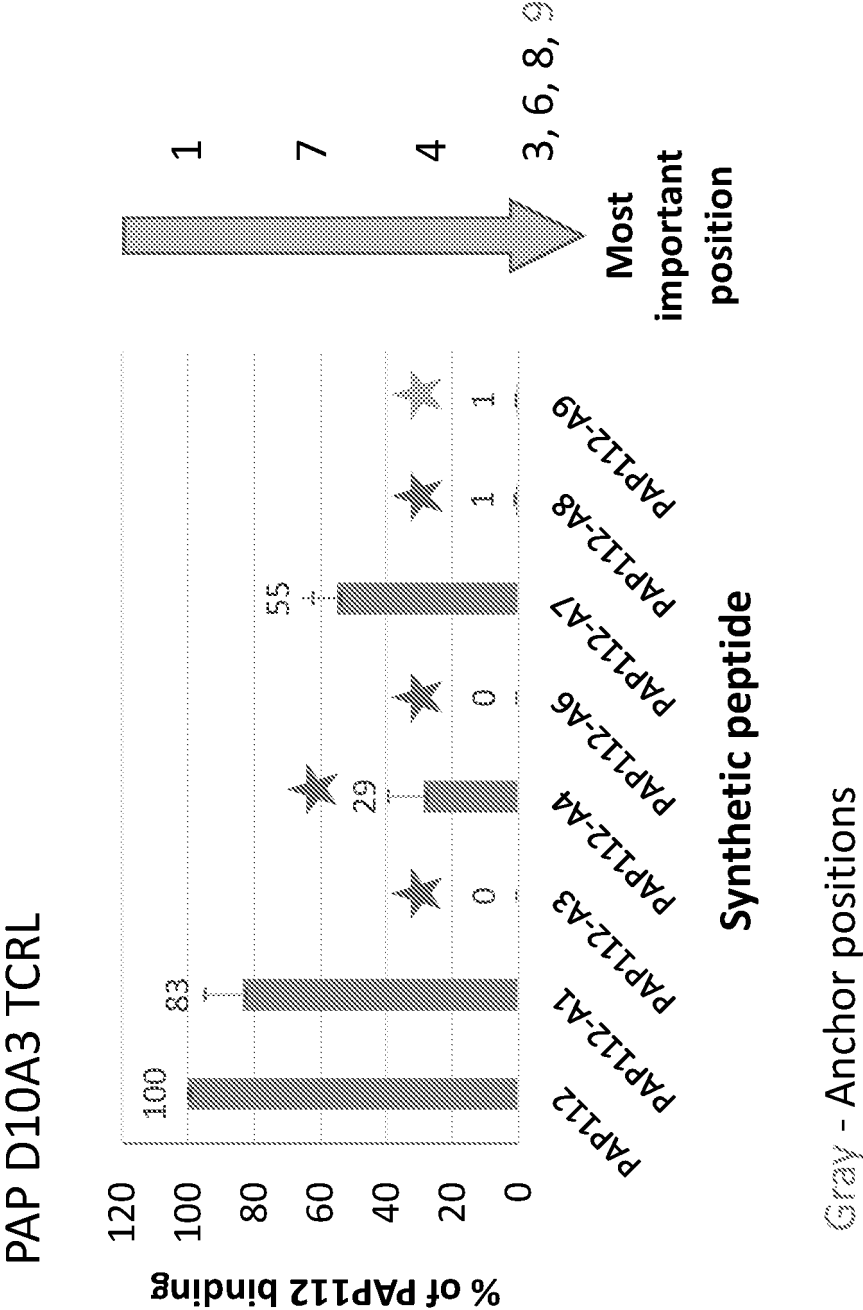
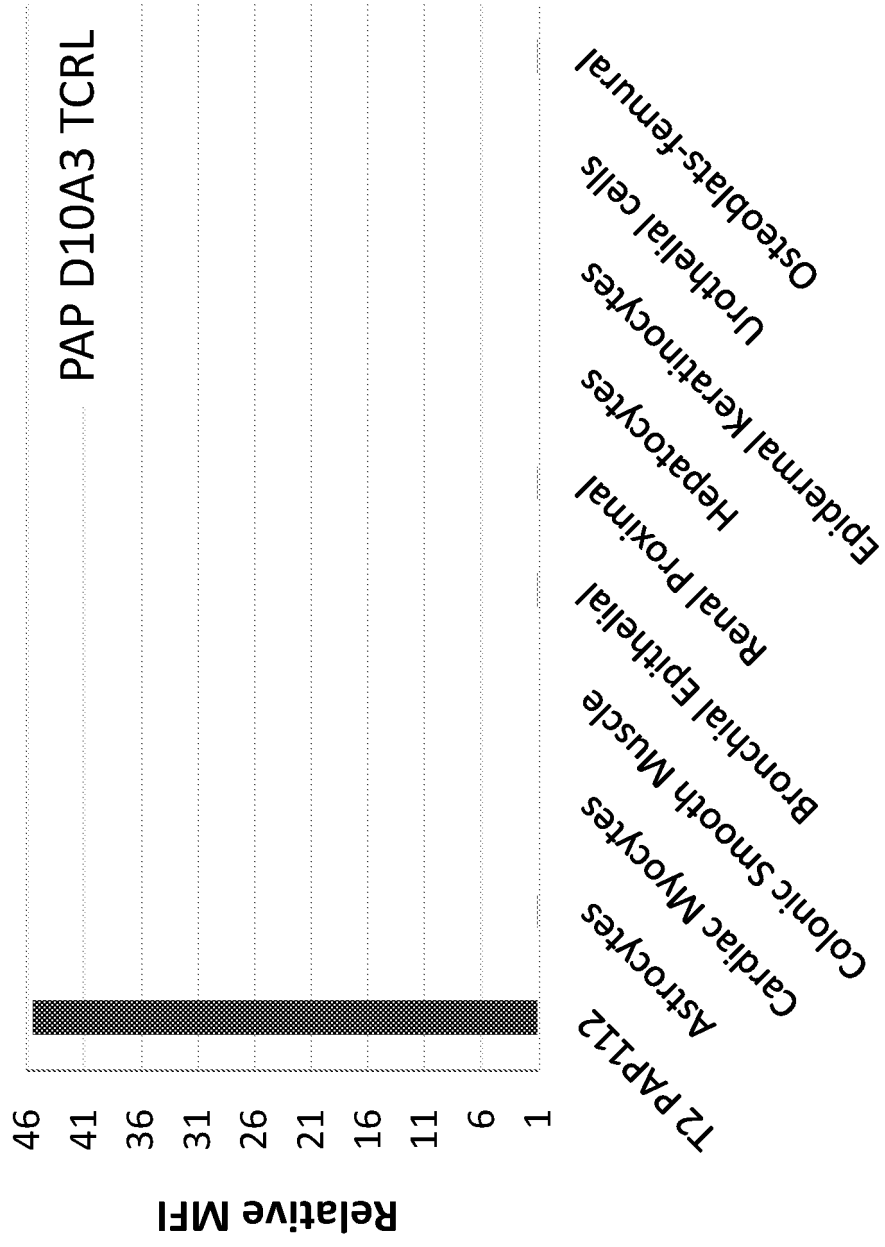


Figure 66

**Figure 67**

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

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

ATGGACAGGCTTACTTCTCATTCTGCTGCTGATTGTCCCTGCATATGTCCTTTCCAGGTAACCTC
 TGAAAGAGTCTGGCCCTGGGATATTGCAGGCCTCCCAGACCTCAGTCTGACTTGTTCCTTCTCTGG
 GTTTTCACCTGACCACTTCTGGTATGGGTGTGAGCTGGATTGCTCAGCCTTCAGGAAAAGGGTCTGGAG
 TGGCTGGCACACATTTACTGGGATGATGACAAGCGCTATAACCCATCCCTGAAGAGCCGACTCACAA
 TCTCCAAGGATACCTCCAGAAACCAGGTATTTCCTCAAGATCACCAGTGTGGACGCTGCAGATACTGC
 CACATACTACTGTGCTCGAAAGGACTACGGTAGTAGCTTCTATGCTATGCACTACTGGGGTCAAGGA
 ACCTCAGTCACCGTCTCTCTCAGCCAAAACGACACCCCATCTGTCTATCCACTGGCCCCCTGGATCTG
 CTGCCCCAACTAACTCCATGCTGACCTGGGATGGCTGGTCAAGGGCTATTTCCCTGAGCCAGTGC
 AGTGACCTGGAACCTTGGATCCCTGTCCAGCGGTGTGCACACCTTCCAGCTGTCTCTGAGTCTGAC
 CTCTACACTCTGAGCAGCTCAGTGACTGTCTCTCCAGCACTCTGGCCAGCGAGACCGTCACTGCA
 ACCTTGGCCACCCGGGACAGCAGCAACCAAGGTGGACAAGAAAATTGTGCCAGGGATTGTGGTTGTAA
 GCCTTGCATATGTACAGTCCCAAGATATCATCTGTCTTTCATCTTCCCCCAAAGCCCAAGGATGTG
 CTCACCACTTACTCTGACTCTTAAGGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 TCCAGTTTCAGCTGGTTTGTAGATGATGTGGAGGTCCACACAGCTCAGACGCAACCCCGGAGGAGCA
 GTTCAACAGCACTTTCGGCTCAGTCACTGAACTTCCCATCATGCACCAAGCACTGGCTCAATGGCAAG
 GAGTTCAAATGACAGGGTCAACAATGTCAGCTTTCCTTGGCCCATCGAGAAAACCATCTCCAAAACCA
 AAGGCAGACCGAAGGCTCCACAGGTGTACACCAATTCCACCTCCCAAGGAGCAGATGCCCAAGGATAA
 AGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGAAAT
 GGGCAGCCAGCGGAGAACTACAAGAACTCAGCCCATCATGACACAGATGGCTCTTACTTCTCTCT
 ACAGCAAGCTCAATGTCCAGAAAGAGCAACTGGCAGCGCAGGAAATACTTTCACCTGCTCTGTGTACA
 TCAAGCCCTGCACAACCACTACTCAGAAGAGCTCTCTCCACTCTCTCTGTAATGA

Heavy chain: Amino acids sequence (465 AA)

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

MDRLTSSFLLLIVPAYVLSQVTLKESGPGILQPSQTLSTLCSFSGFSLTSGMGVSWIRQPSGKGL
 WLAHIYWDDBKRYNPSLKSLFTISKDTSFNQVFLKITSVDAADTATYYCARNDYGSSEFYAMHYWGQG
 TSVTVSSAKTTPPSVYFLAPSSAAQTNMVLGCLVYGYFPEPVTVTWNSGSLSSGVHTFFAVLQSD
 LYTLSSSVTVFSSSTWPSSETVTGNVAHPASSIKVLKKIVPRDGGCKPCICTVPEVSVVFIFPKPKLV
 LTITLTPKVTCTVVDLISKLDPEVQF3WFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGK
 EFKCRVNSAAPPAPIEKTI SKTERPKEAFQVYTIPEPKDOMANDKVS LTMITDFPFEDITVEWQWN
 GQPAENYKNTQFIMDTDGSYFVYGLNVQKSNWEAGNTFTCSVLHEGLNHNHTEK3LSHSPGK

Light chain: DNA sequence (702 bp)

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

ATGAGACCGTCTATTTCAGTTCTTGGGGCTCTTGTGTGTTCTGGCTTCATGGTGCTCAGTGTGACATCC
 AGATGACACAGTCTCCATCCTCACTGTCTGCATCTCTGGGAGGCAAAGTCACCATCACATGCAAGGC
 AAGCCAAGACATTACAACTATATAGCTTGGTACCAACACAAGCCTGTAAAAGGTCTAGGCTGCTC
 ATACATTACACATCTACATTACAGCCAGGCACCCCATCAAGGTTTCAAGTGGAGTGGGTCTGGGAGAG
 ATTATTCCTTCAGCATCAGCAACCTGGAGCTTGAAGATATTCGAACTTATTTATTTCTACAGTATGA
 TAATCTGTGACGTTTGGTGGAGGCACCAAGCTGGAAATCAAACGGGCTGATGCTGCACCAACTGTA
 TCCATCTTCCCAACCATCCAGTGAGCAGTTAACATCTGGAGGTGCTCAGTCTGTGCTTCTTGAACA
 ACTTCTACCCCAAAGACATCAATGTCAAGTGGAAAGATTGATGGCAGTGAACGACAAAATGGCGTCTT
 GAACAGTTGGACTGATCAGGACAGCAAGACAGCACCTACAGCATGAGCAGCACCTCACGTTGACC
 AAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCA
 TTGTCAAGAGCTTCAACAGGAATGAGTGTAG

Light chain: Amino acids sequence (233 AA)

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

MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGKVTITCKASQDIHNYIAWYQHKPVKGPRL
 IHYTSTLQPGTPSRFSGSGSGRDYSFISINLEPEDIATYYCLQYDNLWTFGGGKLEIKRADAAPT
 VSIFFPSSEQLTSGGASVVCFLNNFYKDIHVYKWKIDGGERQNGVLN3WTDQDSKSTYSMSSTLT
 KDEYERHNSYTCETHKTSTSPIVKSEFNREC

Figure 68

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

ATGGCTGTCTCTGGTGTCTTCTCTGCCTGGTTGCATTTCCAAGCTGTGTCTCTGTCCCAGGTGCAAC
TGAAGGAATCAGSAGCTGGTCTGGTGGCGCCCTCACAGAGCCTGTCCATCACTTGCCTGTCTCTGG
GTTTTTCATTAACCAGCTATGGTGTACACTGGSTTCGCCAGCTCCAGGAAAGGGTCTGAGTGGCTG
GGAGTAATATGGCTGGTGGAAACCACAAATTATAATTGGCTCTCATGTCCAGACTGAGCATCAGCA
GAGACAACCTCCAAGAGCCAAAGTTTTCTTAGAAATGAACAGTCTGCAAACTGATGACACAGCCATTTA
CTACTGTGCCAGAGATGGTCACTTCCACTTTGACTTCTGGGGCCAAGGCACCCTCTCACAGTCTCC
TCAGCCAAAACGACACCCCATCTGTCTATCTACTGGCCCTTGATCTGCTGCCAAAACCTAACTCCA
TGGTGACCTCTGGATGGCTGGTCAAGGGCTATTTCCCTGAGCCAGTGCAGTGCACCTGGAACCTCTGG
ATCCCTGTCCAGCGGTGTGCACACCTTCCCACTGTCTCTGAGTCTGACCTCTACACTCTGAGCAGC
TCAGTGACTGTCCCTTCCAGCACTTGGCCCAAGGAGACCTGACCTGCAACGTTGGCCCAACCGGCCA
GCAGCACCAAGCTGCACAAGAAAATTGTGCCAGCGATTGTGCTTGTAAAGCCTTGCATATGTACACT
CCAGAAATATCATCTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
CCTAAGGTCACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
TACATCATCTCTGAGGTGCACACAGCTCAGACGCAACCCCGGAGGAGCACTTCAACAGCACTTTCCG
CTCAGTCACTGAACCTTCCCATCATGCAACAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGCTC
AAGAGTGCAGCTTTCCCTCCCTCCCTCATCGAGAAAACCATCTCTCAAAACCAAGGCAGACCGAAGGCTC
CACAGGTGTACACCATTTCCACCTCCCAAGGAGCAGATGGCCAAAGGATAAAGTCACTCTGACCTGCAT
GATAACAGACTTCTTCCCTGAAGACATTACTGTGAGTGGCACTGGAATGCGCAGCCAGCGGAGAAC
TACAGAACACTCAGCCCATCATGGACACAGATGGCTCTTACTTGGTCTACAGCAAGCTCAATGTGC
ACAAGAGCAACTGGGAGCCAGGAAATACTTTCACTGCTCTGTGTTACATGAGGCGCTCCACAACCA
CCATACTGAGAAGAGCTCTCTCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT

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

MAVLVFLCLVAFPSCVLSQVQLKESGPGLVAPSSLSITCTVSGFSLTSYGVHWVRQPPGKGLEWL
GVIWAGGTTNYSALMSRLSISPDNKSQVFLMNSLQTDDBAIYYCARDGHFHFDWGGQTTTLTVS
SAKTIFFPSVYFLAPSSAAQTNSMVTLCCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSS
SVTVFSSITNPSETVTCNVAPASSTKVDKKIVPRLCCKPCICTVVEVSSVFIFFPKPKDVLTTITLE
PKVTCVVDLISKDDFEVQFSWFVDDVEVHTAQTQPPFEEQFNSTFFSVSELPIMHQDWLNGKEFRCRV
NSAAFPAPLEKTI SKTNGRPKAPQVYTIFFPKPEQMAKDKVSLTCTMTDFFEDITVEWQWNGQPAEN
YKNTQPIMDTLGSIYFVYSKLVNQKENWEAGNTFTCSVLSEGLHNHGTESLSLSPPGK

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

ATGAGTGTGCCCCTCAGGTCCTGGGGTTGCTGCTGCTGTGGCTTACAGATGCCAGATGTGACATCC
AGATGACTCAGTCTCCAGCCTCCCTATCTGTATCTGTGGGAGAAACTGTCAACCATCACATGTGAGC
AAGTGATATTATTTACAGTAATTTAGCATGGTATCAGCAGAAACAGGGGAAAATCTCCTCAGCTCCTG
GTCTATGCTGCAACAAACTTAGCAGCTGGTGTGCCATCAAGGTTCAAGTGGCAGTGGATCAGGCACAC
AGTATTCCTCAAGATCAATAGCTTGCAGTCTGAAGATTTTGGGACTTATTACTGTCAACATTTTTTG
GGGTAGTTCAATCTCGTTCCGCTCGGGGACAAAGTTGGAAATAAAAACGGCTGATGCTGCACCAACT
GTATCCATCTTCCCAACCATCCAGTGAGCAGTTAACATCTGGAGGTGGCTCACTCGTGTCTCTCTTGA
ACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAAGATTGATGGCAGTGAACGACAAAATGGCGT
CCTGAACAGTTGGAGTGTATCAGGACAGCAAGACAGCACTTACAGCATGAGCAGCACCCCTCAGGTTG
ACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAAGACATCAACTTCAC
CCATTGTCAAGAGCTTCAACAGGAATGAGTGTAG

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

MSVPTQVLGLLLLWLTDARCDIQMTQSPASLSVSVGETVTITCRASDIIYSNLAWYQQRQCKSPQLL
VYAATNLAAGVPSRFSGSGSCTQYSLKINSIQSEDFGTYYCQHFHWGSSISFGSGTKLEIKRADAAPT
VSIFPPSSEQLTSGGASVVCFLNFFPKDINVEWKIDGSEKQNGVLNSWTDQDSKLSSTYSMSSTLT
TKDEYERHNSYTCETHTKSTSPIVKSFNNEC

Figure 69

DIVLTQSPATLSVSPGDSVSLSCRASQSI5NLHWYQKSHESPRILUKYASQ5ISGIP5RFSG5SGSGTDFTLSINSVETEDFGMYFCQQ
SYSWPLTFGAGSKLELKRADAAPT5SIEPP55SEQLTSGGASVVCF5LNWFYP5DIN5KWKIDG5ERQ5NGVLNSWT
LQDSKDS5TVGMS5TL5TLTKDEYER5NSYTCEAT5K5T5T5PIVK55NP5NEC

Figure 70 continued

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

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

Nuc-seq:

CAGGTTCAACTGCAGCAGTCTGGAGGTGAGGTGATGAAGCCTGGGGCCTCAGTGAAGCTTTCCTGCAAGGCTACT
 GGCTACACATTCACTGGCTACTGGATAGAGTGGATAAAACAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGA
 GATTTTACCTGGAAGTGGTGGTACTAACTACAATGAGAAATTCAAGGGCAAGGCCACATTCAGTGCACATACATCC
 TCCAACACAGCCTACATGCAACTCAGCAGCCTGACAACCTGAGGACTCTGCCATCTATTACTGTGCAAGGGATAGTA
 ACTCCTTTACTTACTGGGGCCAAGGGACTCTGGTCACCTGTCTTTCAGCCAAAAACGACACCCCTCATCTGTCTATC
 CACTGGCCCTTGGATCTGCTGCCCAACTAACTCCATGGTGAACCTGGGATGGCTGGTCAAGGGCTATTT
 CCCTGAGCCAGTGCAGTGAACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGTCACACCTTCCAGCTGTCT
 CTGCAGTCTGAACCTCTACACTCTGAGCAGCTCAGTGAACCTGTCCCTTCCAGCACTTGGCCAGCGAGACCG
 TCACCTGCAACGTTGGCCACCCGGCCAGCAGCACTAAGGTGGACAAAGAAATTGTGCCAGGGATTGTGG
 TTGTAAGCCTTGTCATATGTACAGTCCCAAGATATCATCTGTCTTCATCTTCCCCCAAGGCCAAGGAT
 GTGCTCACCATTACTCTGACTCTTAAGGTACGCTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAGG
 TCCAGTTTCACTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCCCGGAGGAGCAGTT
 CAACAGCACTTTCCGCTCAGTCAGTGAACCTTCCCTCATGACACAGGACTGGCTCAATGGCAAGGAGTTC
 AATGCAGGCTCAACAGTGCAGCTTTCCCTGCCCCATCGAGAAACCATCTCCAAACCAAGGCAGAC
 CGAAGGCTCCACAGGTGTACAACCTCCACCTCCCAAGGAGCAGATGGCCAAGGATAAAGTCAGTCTGAC
 CTGCATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGGAATGGCCAGCCAGCGGAG
 AACTACAAGAACACTCAGCCCATCATGGACACAGATGGCTCTTACTTCTGTCTACAGCAAGCTCAATGTGC
 AGAAGAGCAACTGGGAGGCAGGAATACTTTCACCTGCTCTGTGTACATGAGGGCCTGCACAACCAACA
 TACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA

AA-seq:

QVQLQQSGGEVMPKPGASVKLSCKATGYTFTGYWIEWIKRPPGHGLEWIGEILPGSGGTNYNEKFKGKATFYAHTSSN
 TAYMQLSSLTIEDSAIYYCARDSNSFTYWGQGLTVYSSAKTTPFSVYPLAPGSAAGTNGMVTLGCLVKGYFPEP
 VYVTVNWSGSLSSGVETFPAYLQGLYTLSSSVTPSSSTWFSRTVTCNVASAPASSTKVDKKIVPROCGCKP
 CICTVPEVSSVFIFPPKPKDVLITITLTPKVTCTVVDISKDDPEVQPSWFEVDDVEVHTAQTQPREEQFNST
 FRSVSELPIMBQDWLNGKEFKCRVNSAAFPAPISKTIKTKGRPKAPQV/TIIPPKEQMAKDKVSLTOMI
 TDFEEDITVEWQWNGQPAEWYKWTQPMOTDGSYFVYSKLNQKSNWEAGNTFTCSVLHEGLHNHHTK
 SLRSPGK

Light Chain

Light chain: DNA sequence (705 bp)

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

CAAATTGTTCTACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATAACCTGCAGTGTCA
 GCTCAAGTGTAGATTACATTCAGTGGTTCCAGCAGAAGCCAGGCACCTTCTCCCAAATTCTGGATTATAGCACATCC
 ATCCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGATCTGGGACCTCTTACTCTCTCACAATCAGCCGAAT
 GGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAAAGGAGIAGTTACCCACCCACgTTCGGCTCGGGGACAAAGT

Figure 71

TGGAAATAAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTG
GAGGTGCTTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAGATTGA
TGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGC
ATGAGCAGCACCTTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACTGTGAGGCCACTC
ACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGT

AA-seq:

QIVLTQSPAIMSASPGEKVTITCSVSSSVDYIHWFQOKPGTSPKFWIYSTSILASGVPARFSGSGSGTSYSLTISRMEAEDA
ATYYCQQRSSYPPTFGSGTKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVRWKIDGSEKQNI
GVLNSWTDQDSKDSITYSMSSLTFLTKDEYERHNSYICEATHKTTSTSPIVFSENRNEC

Figure 71 continued

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

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

Nuc-seq:

CAGGTTTCAGCTGCAGCAGTCTGGACCTGAGATGGTGAAGCCTGGGGCCTCAGTGAAGATTCCCTGCAAGGCTTCT
 GGCTACGCATTTCAGTAGCTCCTGGATGAACTGGGTGAAGCAGAGGCCTGGAAAGGGTCTTGAGTGGATTGGACG
 GATTTATCCTGGAGATGGAGATACTAACTACAATGAGAAGTTCAAGGGCAAGGCCCACTGACTGTAGACAAATC
 CTCCAGCACAGTCTACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTACTTCTGTGCAAGAGAGGCT
 ACTACGGTAGTGGCCCCGTAATACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAAAAACGA
 CACCCCATCTGTCTATCCACTGGGCCCTGGATCTGCTGCCCCAACTAACTCCATGGTGGACCTGGGATG
 CCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTG
 CACACCTTCCAGCTGTCTCTGCACTCTGACCTCTACACTCTGAGCAGCTCAGTGAAGTGTCCCTCCAGCA
 CCTGGGCCAGCGAGACCGTCACTGCAACGTTGCCACCCGCGCCAGCAGCACCAGGTGGACAAGAAAAAT
 TGTGCCCAAGGATTGTGGTTGTAAAGCCTTGCATATGTACAGTCCCAGAAAGTATCATCTGTCTTTCATCTTC
 CCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCTCAAGGTCAAGTGTGTGTGGTGGTAGACATCA
 GCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCA
 ACCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAAGTGAAGTCTCCCATCATGCACCAGGACTGG
 CTCAATGGCAAGGAGTTCAAAATGCAGGGTCAACAGTGCAGCTTTCCCTGCCCCCATCGAGAAAAACCATCT
 CCAAAACCAAAAGGCAGACCGAAGGCTCCACAGGTGTACACCATTTCCACCTCCCAAGGAGCAGATGGCCAA
 GGATAAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTAAGTGTGGAGTGGCAGTGG
 AATGGGCGAGCTAGCGGAGAACTACAAGAACTCAGGCCATCATGGACACAGATGGCTCTTACTTCGTCT
 ACAGCAAGCTCAATGTGCAGAAAGAGCAACTGGGAGGCAGGAAATACTTTCACCTGCTCTGTGTTACATGA
 GGGCCTGCACAACCAACATACTGAGAAGAGCCTCTCCCACTCTCTGGTAAA

AA-seq:

QVQLQSGPEMVKPGASVKIPCKASGYAFSSSWMNWVKQRPGKLEWIGRIYPGQGDNTNYNEKFKGKATLTVDKSS
 STVYMQLSSLTSEDSAVYFCAREATTVPVYFDYWGQGTTLTVSSAKTTPPPSVYFLAPGSAAGTNSMVTLGCLV
 KGYYEPVPVTVWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHFASSTKVDDKIVP
 RDGCKPCICTVPEVSSVFIPPPKPDVLTITLTYPKVTCVVVDISKDDPEVQFSWFVDDEVVHTAQTQPK
 EQGFNSTFFCVSELPIMHQDWLNGKEFKCKVNSAAFPAPIEKTITKTKGPPKAPQVYTIPTPPSEQMAKDK
 VELTCMITDFFPEDLTVWQWNGQPAENYKNTQPIMDTDGSYFVYKLNQKSNWEAGHTFTCCVLEGL
 HNHETBKSLSHSPGK

Light chain: DNA sequence

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

Nuc-seq:

GACATCAGATGACTCAGTCTCCAGCCTCCCTATCTGTATCTGTGGGAGAACTGTCACCATCACATGTCGAGCAA
 GTGAGAATATTTACAGAAATTTAGCATGGTATCAGCAGAAACAGGGGAAAATCTCCTCAACTCCTGGTCCATGCTGC
 AACAACTTAGCAGATGGTGTGCCATCAAGGTTCAAGTGGCAGTGGATCAGACACACAGTATTCCTCAAGATCAA
 CAGCCTGCAGTCTGAAGATTTTGGGAATTATTACTGTCAACATTTTGGGGGACTCCGCTCACGTTCCGTTGCTGGG

Figure 72

ACCAAGCTGGAGCTGAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTT
AACATCTGGAGGTGGCTCAGTCGTGTGCTTCTTGAACAACCTCTACCCCAAAGACATCAATGTCAAGTGG
AAGATTGATGSCAGTGAACGACAAAATGGGCTCTCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCA
CCTACAGCATGAGCAGCACTCTCAGCTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGA
GGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGT

AA-seq:

DIQMTQSPASLSVSVGETVTITCRASENIYRNLAWYQQKQKGKSPQLLVHAATNLADGVPSRFSGSGSDTQYSLKINSIQ
SEDFGNYYCQHFWGTPITFGAGTKLELKEADAAPTYSIFPPESSEQLTSGGASVVCFLINFEYFKDINVKWKIDG
GEFQNGVLENGWTDQDSKDDSTYSMSSTLTILTKDEYERBNSYTCBATAKTSTGPIVKSFNPNRC

Figure 72 continued

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

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

Nuc seq

GAGGTCCAGCTGCAACAGTTTGGAACTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAA
 GGCTTCTGGCTACACATTCAGTACTACAACATGGACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGA
 GTGGATTGGAGATATTAATCCTAACTATGATACTACTACCTACAACCAGAAGTTCAAGGGAAAGGCCAC
 ATTGACTGTAGACAAGTCCCTCCAGCACAGCCTACATGGAGCTCCGCAGCCTGACTTCTGAGGACACTGC
 AGTCTTTTACTGTGCAAGAAGGAAGTATGGTAACTACGTGGGGTTTGACTTCTGGGGCCAAGGCACCAC
 TCTCACAGTCTCCTCAGCCAAAACGACACCCCTCTGTCTATCCACTGGGCCCTGGGATCTGTTGCCAAA
 CTAACCTCCATGGGTGACCTGGGATGCTTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAA
 CTCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCAGCTGTCTCTGCAGTCTGACCTCTACACTCTGAGC
 AGCTCAGTGACTGTCCCTCCAGCACCTGGGCCAGCGAGACCGTCACCTGCAACGTTGGCCACCCGCGCA
 GCAGCACCAAGGTGGACAAAGAAAATTGTGCCAGGGATTGTGGTTGTAAGCCTTGCCATATGTACAGTCCC
 AGAAGTATCATCTGTCTTCTATCTTCCCCCAAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAG
 GTCACGTGTCTTGTGGTAGACATCAGCAAGGATGATCCCGAAGTCCAGTTCAGCTGGTCTGTAGATGATG
 TGGAGGTGCACACAGCTCAGACGCAACCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGA
 ACTTCCCATCATGCAACAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTCAACAGTGACAGCTTTC
 CCTGCCCTCATCGAGAAAACCATCTCCAAAACCAAAGGCAGACCGAAGGCTCCACAGGTGTACACCATTC
 CACCTCCCAAGGAGCAGATGGCCAAAGGATAAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGA
 AGACATTACTGTGGAGTGGCASTGGAATGGGCAGCCAGCGGAGAACTACAAGAACACTCAGCCCATCATG
 GACACAGATGGCTCTTACTTCGTCTACAGCAAGCTCAATGTGCAGAAAGAGCAACTGGGAGGCAGGAAATA
 CTTTCACCTGCTCTGTGTTACATGAGGGCTGCACAACCACCATACTGAGAAGAGCCTCTCCCACTCTCC
 TGGTAAA

AA-seq:

EVQLQQFGTELVKPGASVKISCKASGYFTDYNMDWVKQSHGKSLEWIGDINPNYDTTYYNQKFKGKATLT
 VDKSSSTAYMELRSLTSEDYAVFYCARRNYGNYVGFDFWGQGTTLTVSSAKTTEPSVYPLAPGSAQTNSM
 VTLCGLVKGYFPEFVTVTNCGSLSSGVHTEFAVLQSDLYTLSSSVTVFSSSTWPSSETVTGNVAHPASSTK
 VDKKIVPRDCGCKPCICTVPEVSSVFIFPEKPKXOVLTITLTTPKVTCTVVDISKDDPEVQPSWFDVDDVEVH
 TAQTQPPPEEQFNSTFRSVSBLIFMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGEPKAPQVYITPPPK
 EQMAKDKVSLTCMIIDFFPEDLTVEWQWNGQPAENYKNTQPIIMDTDGSYFVYKLVNQKSNWEAGNTFTC
 SVLEGLHNHSTKSLSHSPGK

Light chain: DNA sequence

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

Nucseq:

AATATTGTGCTGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTTCCATAACCTGCA
 AGGCCAGTCAGCGTGTGAATAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGC
 TGATATACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGG

Figure 73

ATTTCACTTTTACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAG
 CTCTCCATTTCACGTTTCGGCTCGGGGACAAAAGTTGGAAATAAAAACGGGTGATGCTGCACCAACTGTATCC
 ATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT
 ACCCCAAAGACATCAATGTCAAGTSGAAGATTGATGGCAGTGAACGACAAAATGGGGTCTCTGAACAGTTG
 GACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCAACCTTCAGTTTGAACAAAGACGAGTAT
 GAACGACATAACAGCTATACTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCA
 ACAGGAATGAGTGT

AA-seq

NIVLTQTPKFLLVSAGDRVSITCKASQVRVNDVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGYGTD
 FTFTISTVQAEDLAVYFCQQDYSSPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI
 NVKWKIDGSERQNGVLNSWTDQDSKDYSTMSTLTLTKEYERHNSYTCEATHKTSTSPIVKSFNRNEC

Figure 73 continued