

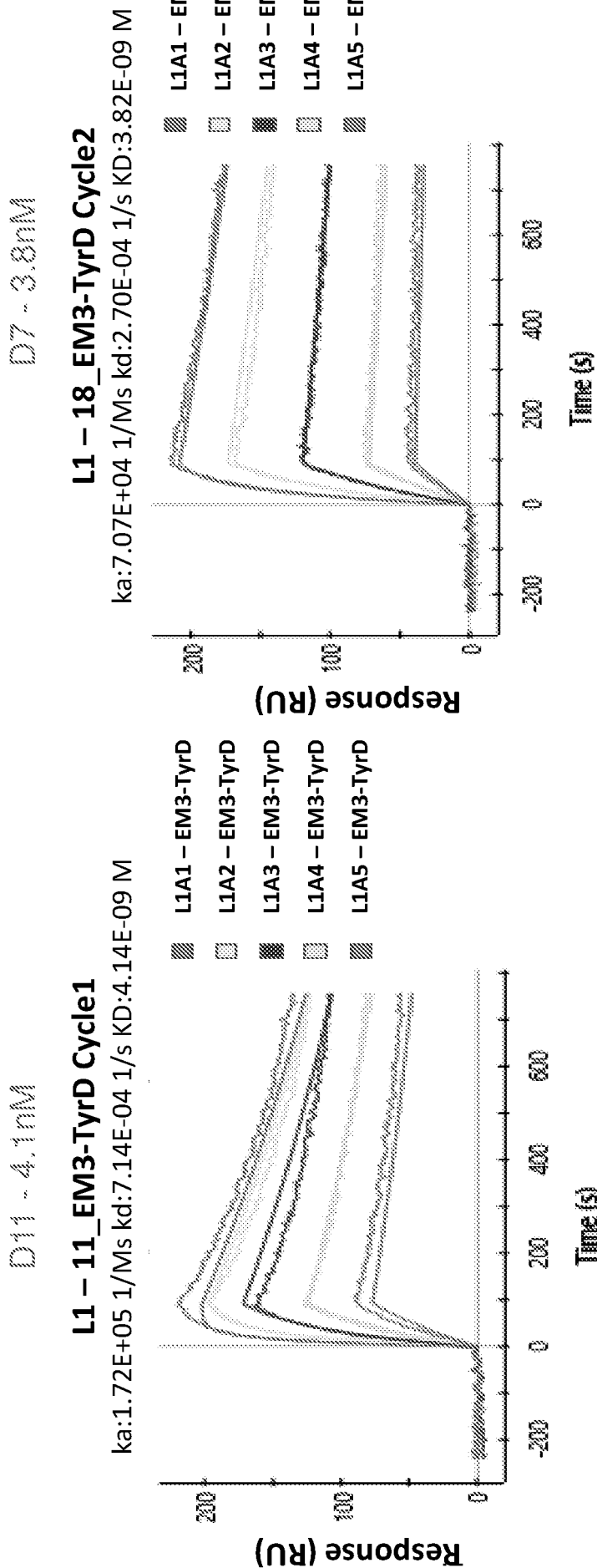
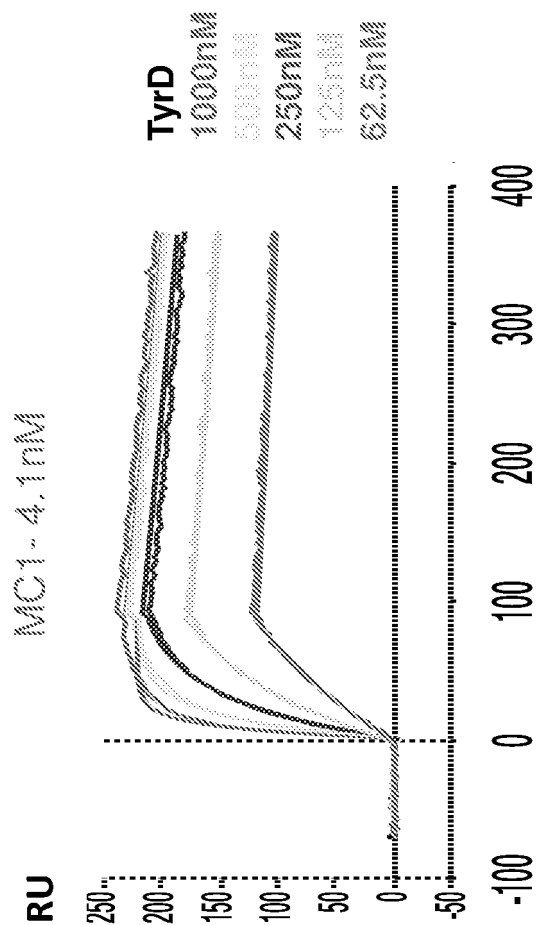


Figure 1

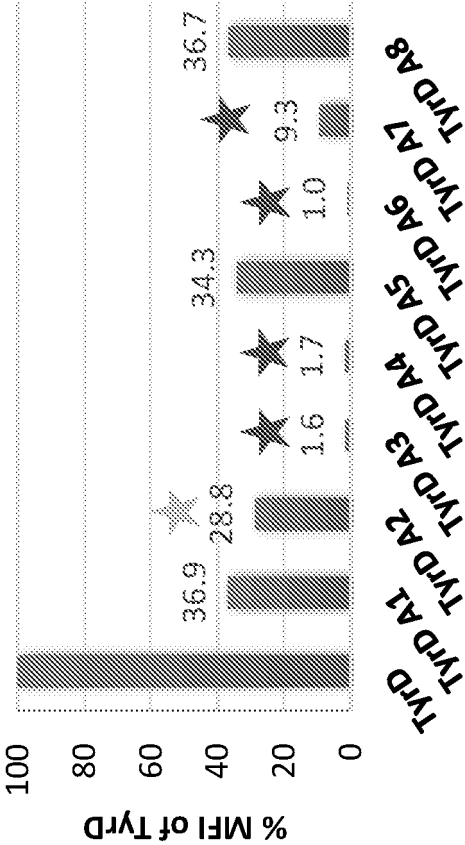
TyrD	YMDGTMSQV
TyrD A1	A MDGTMSQV
TyrD A2 anchor position	Y A DGTMSQV
TyrD A3	YM A GTMSQV
TyrD A4	YMD A TMSQV
TyrD A5	YMDG A MSQV
TyrD A6	YMDGT A SQV
TyrD A7	YMDGTM A QV
TyrD A8	YMDGTMS A V

Alanine scanning D11B10 10µg/ml



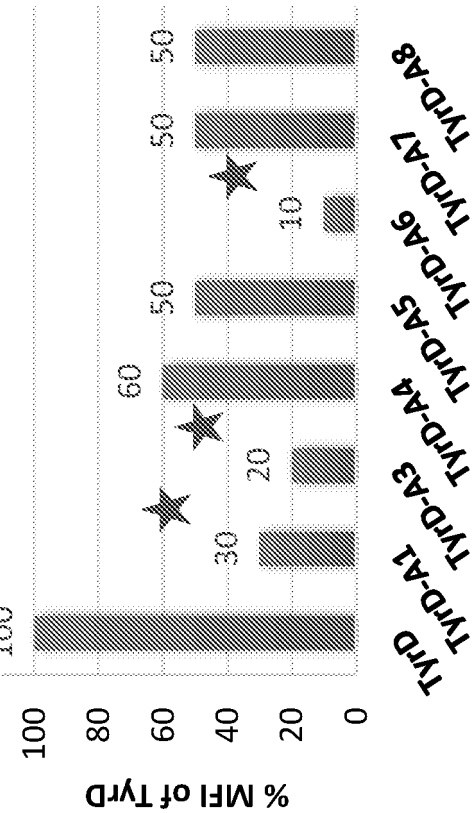
- Decrease of >90% at two positions # 3, 6
- Decrease of > 70% in five positions # 1, 2, 3, 4, 6

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



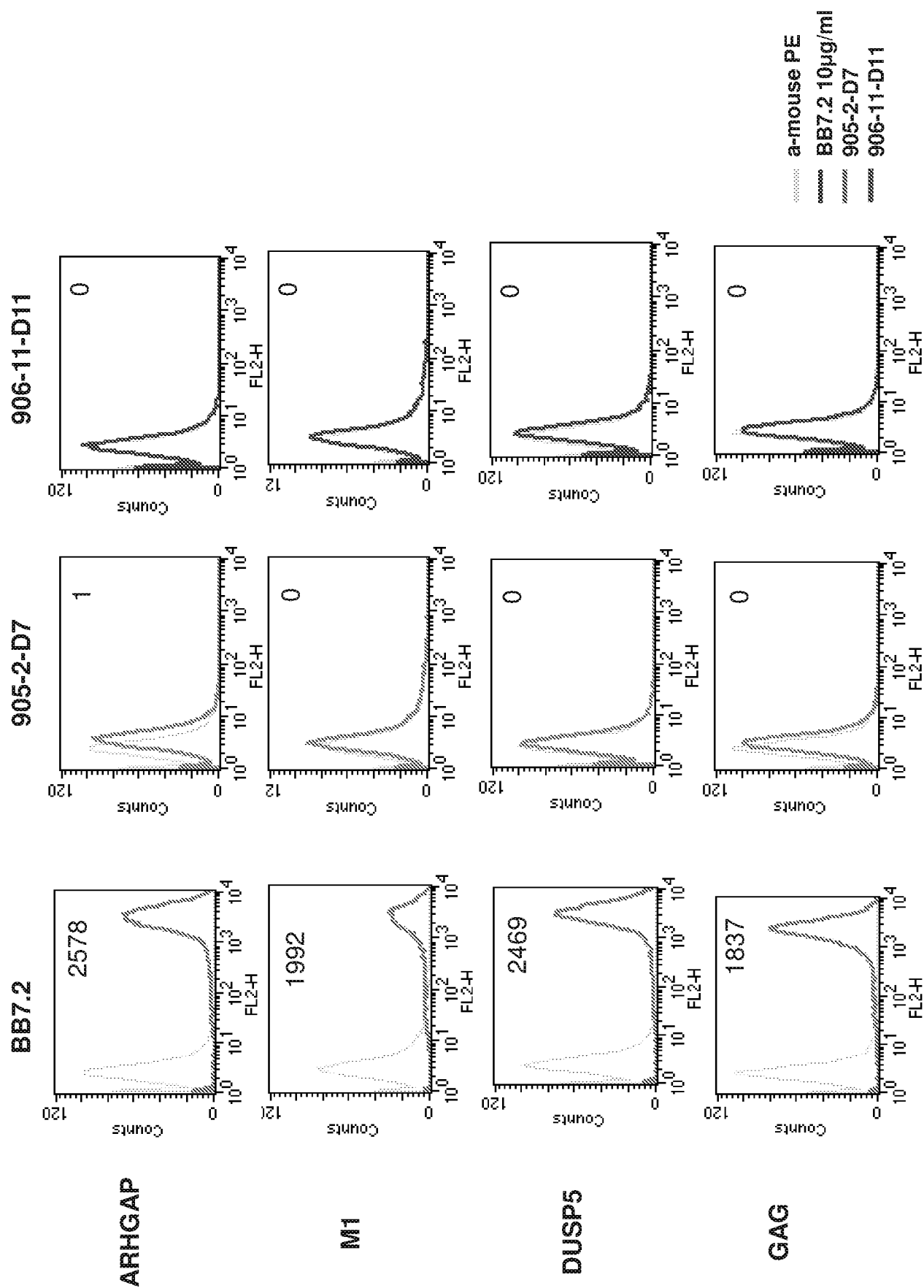


Figure 3 - continued

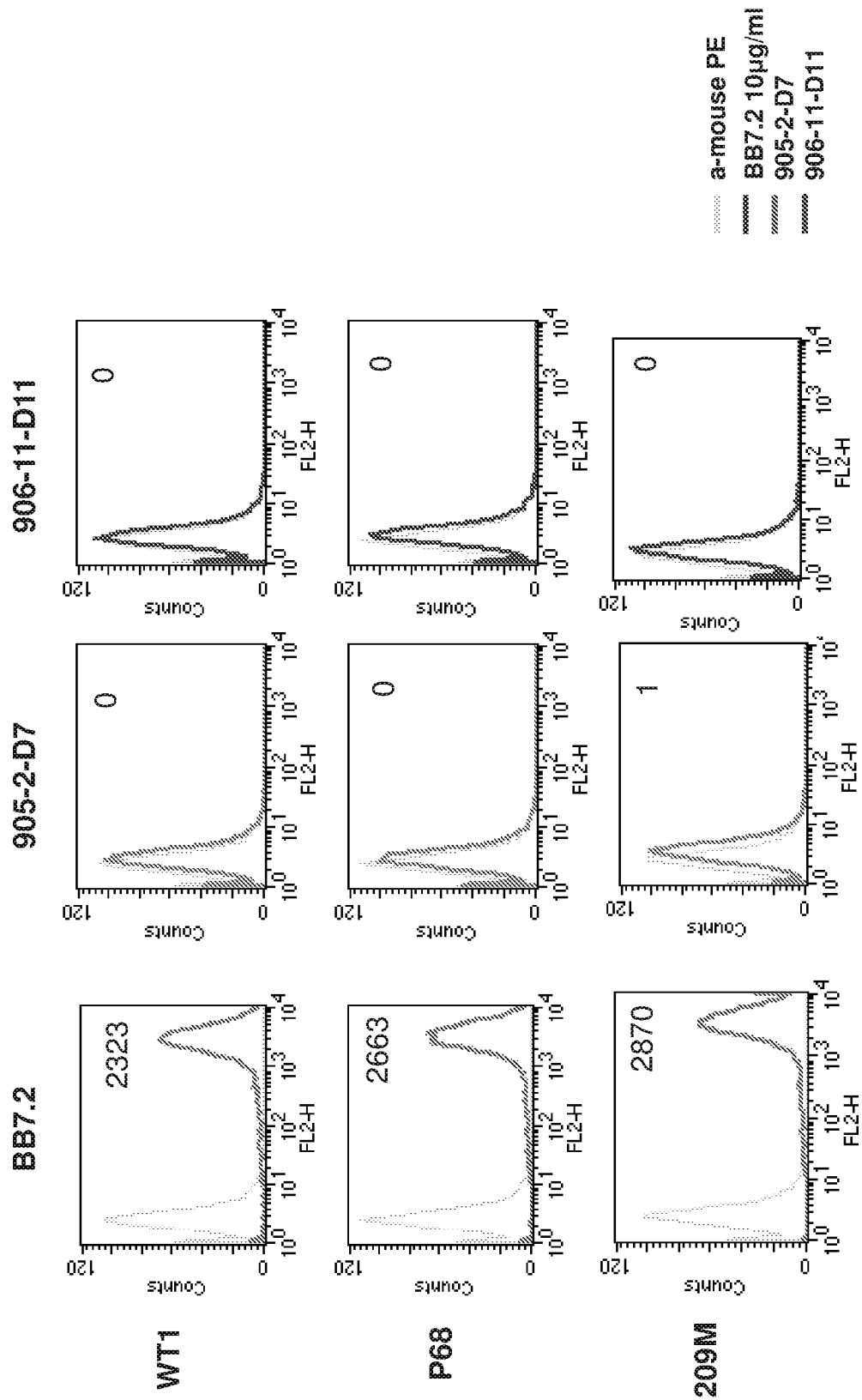


Figure 4

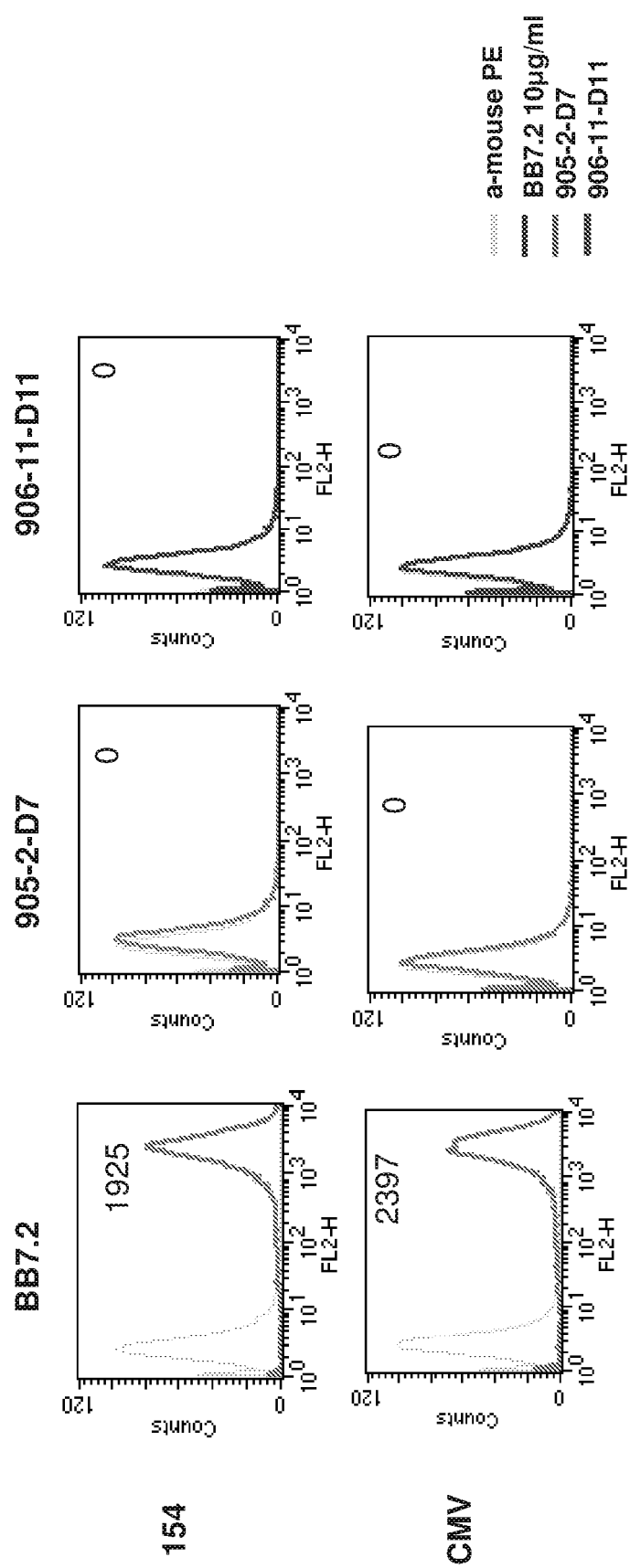
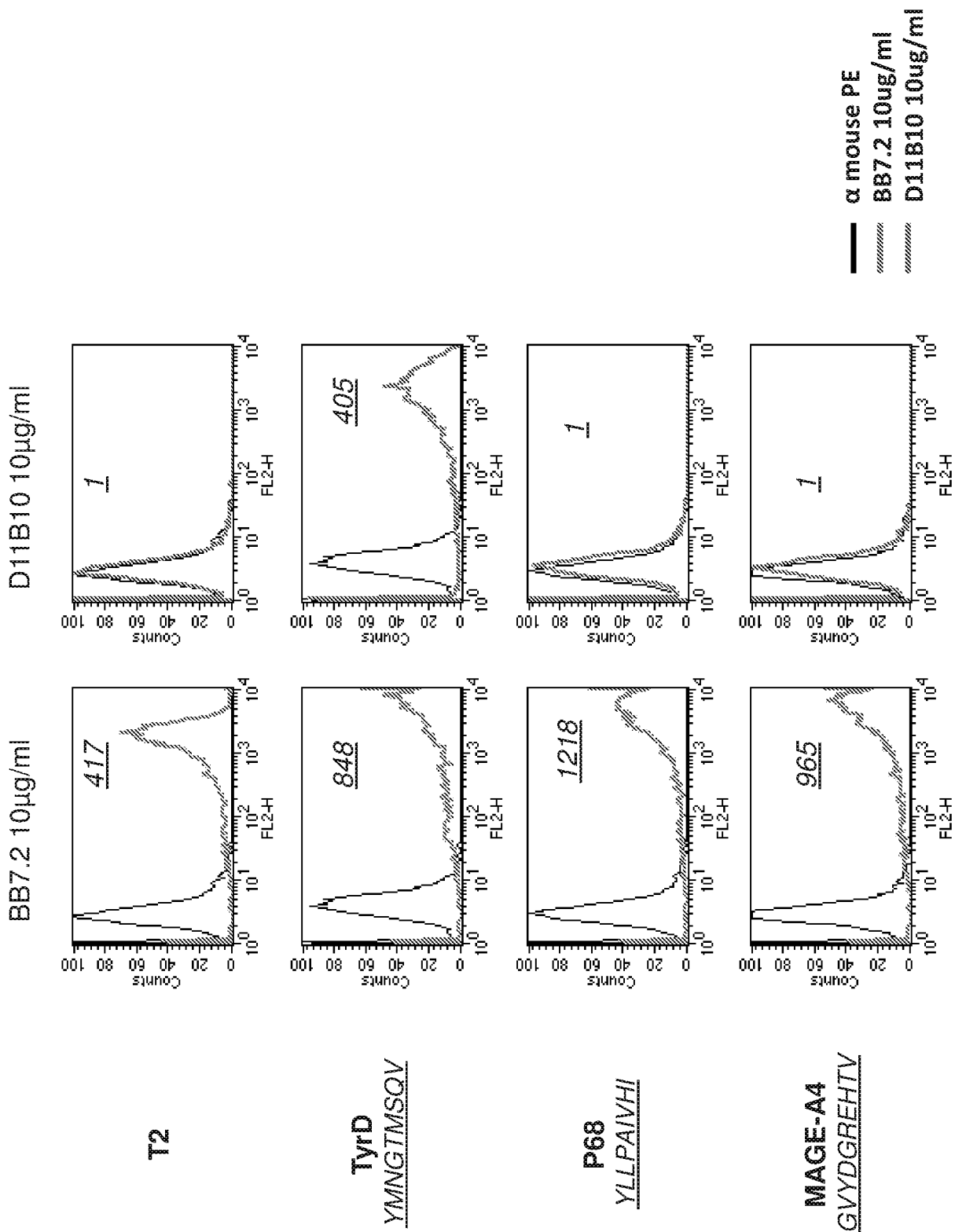
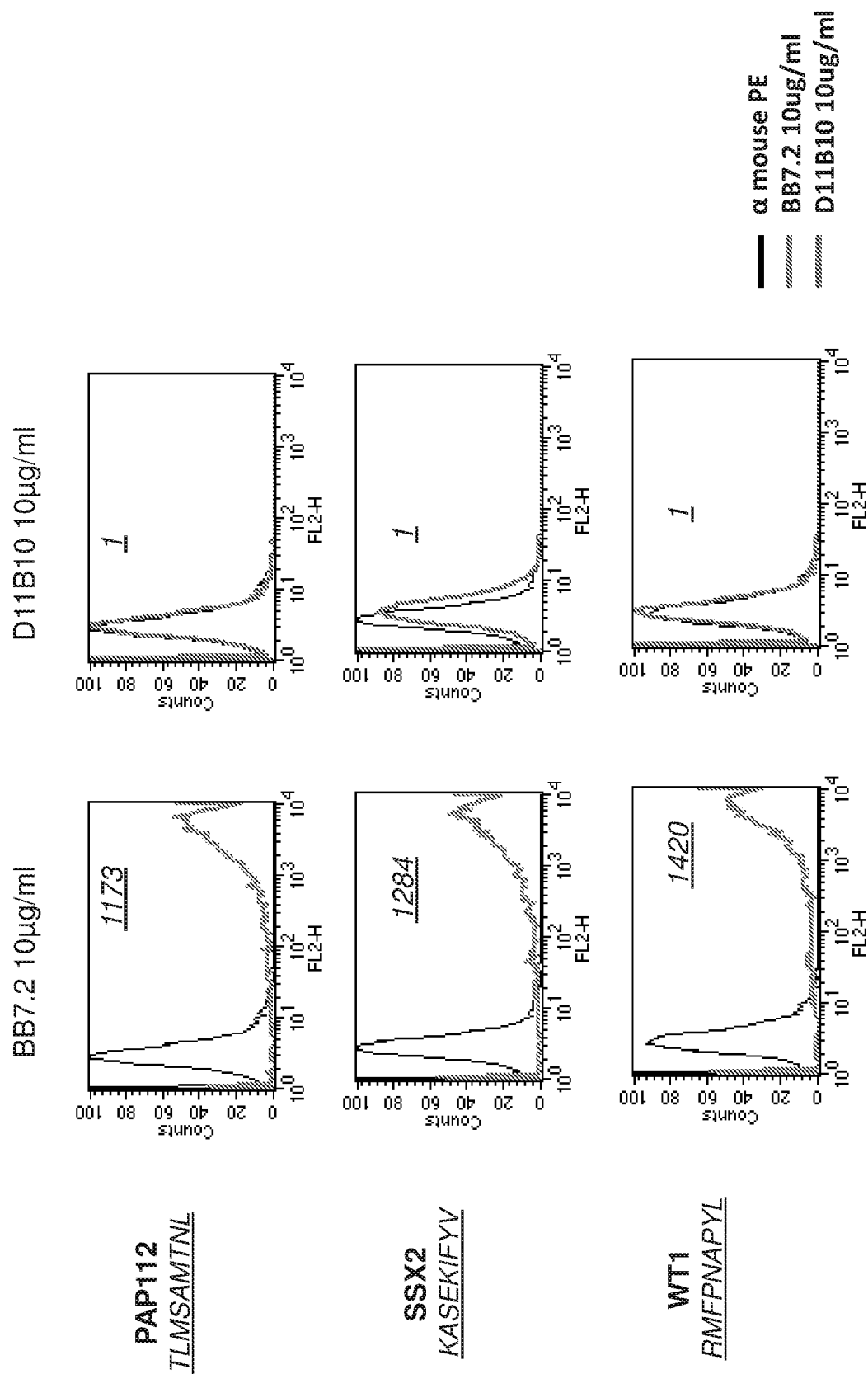


Figure 4 - continued



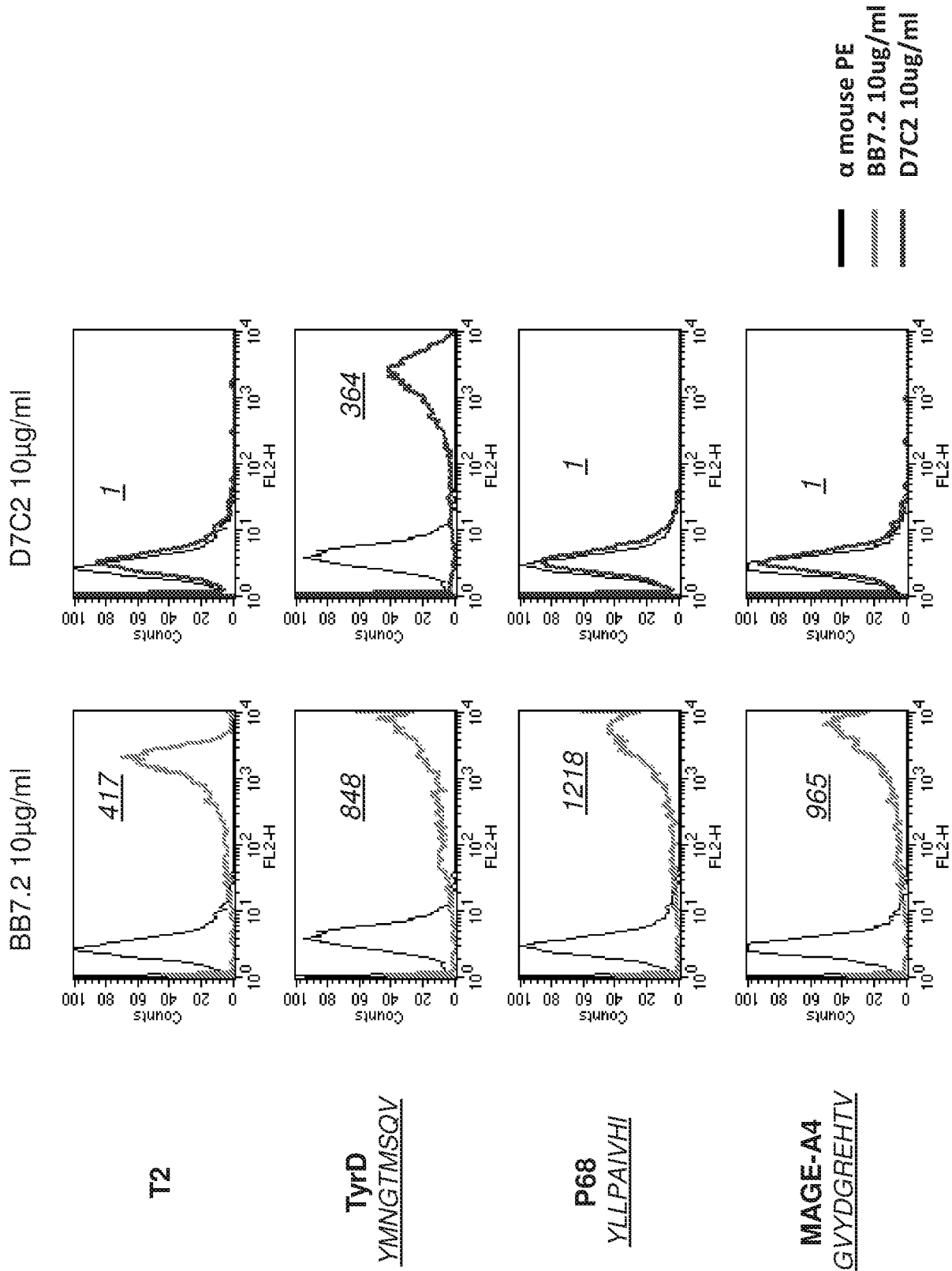
MFI values are relative to background. Value of `1` means no binding

Figure 5



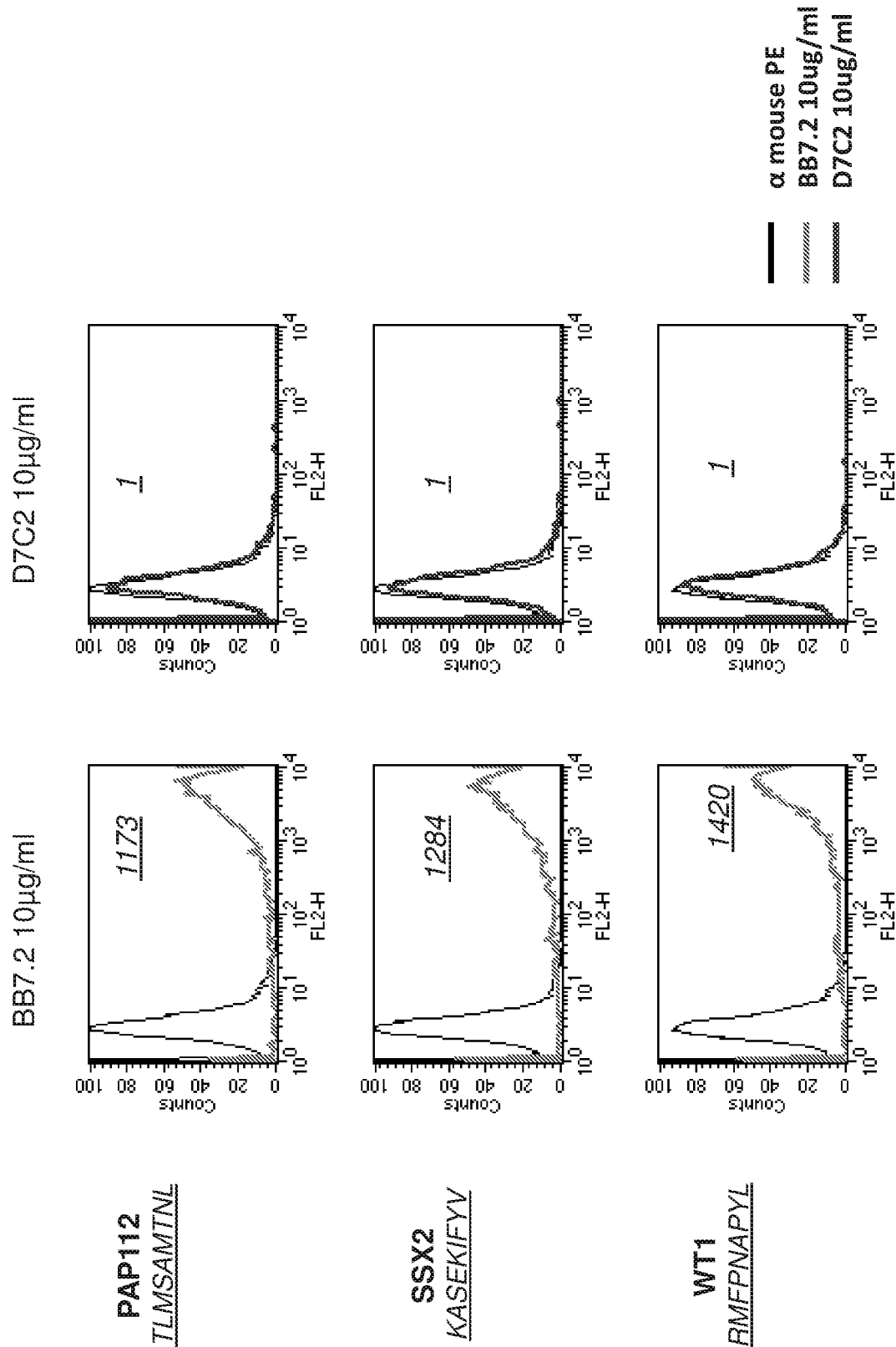
MFI values are relative to background. Value of `1` means no binding

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

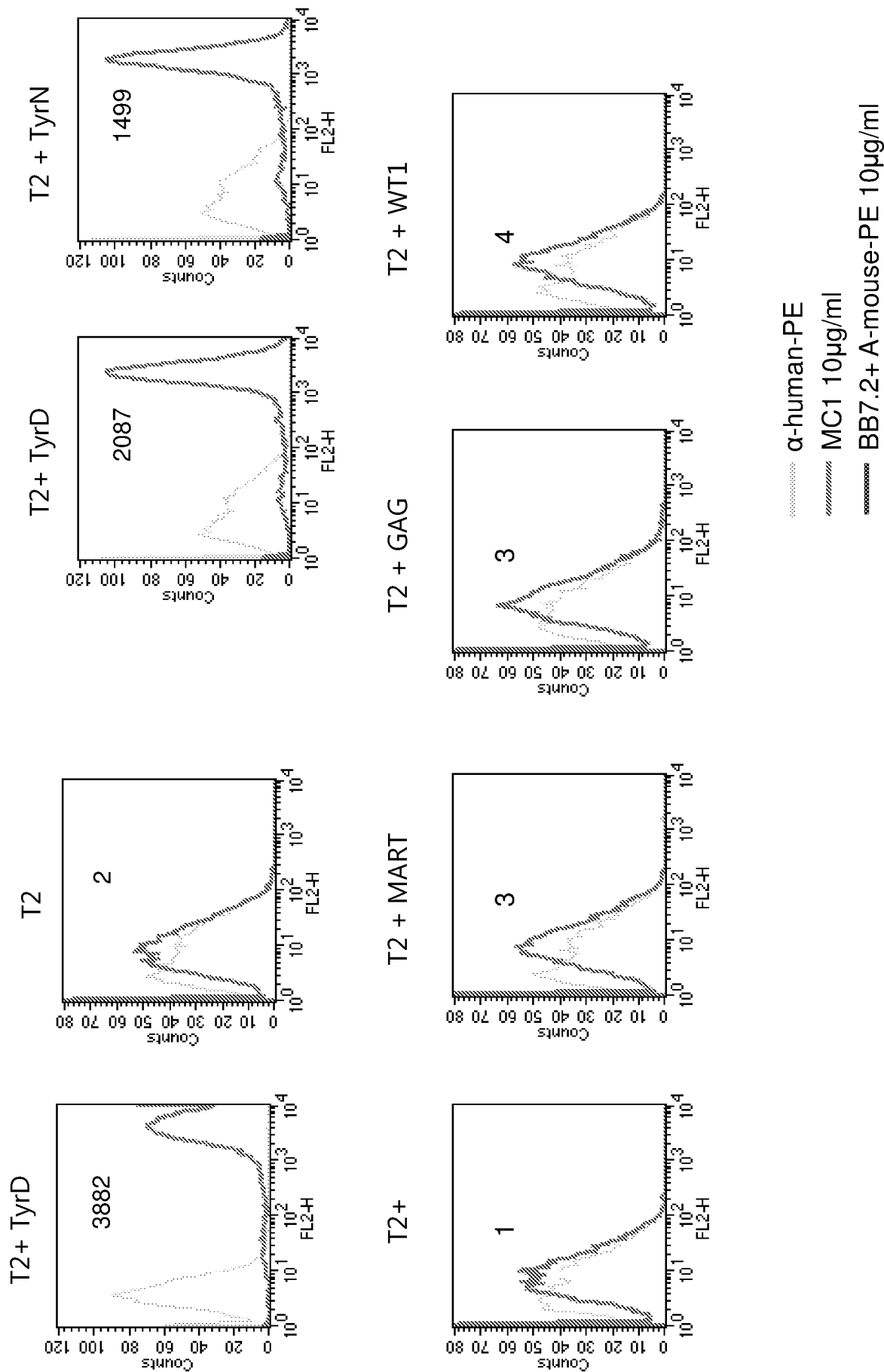
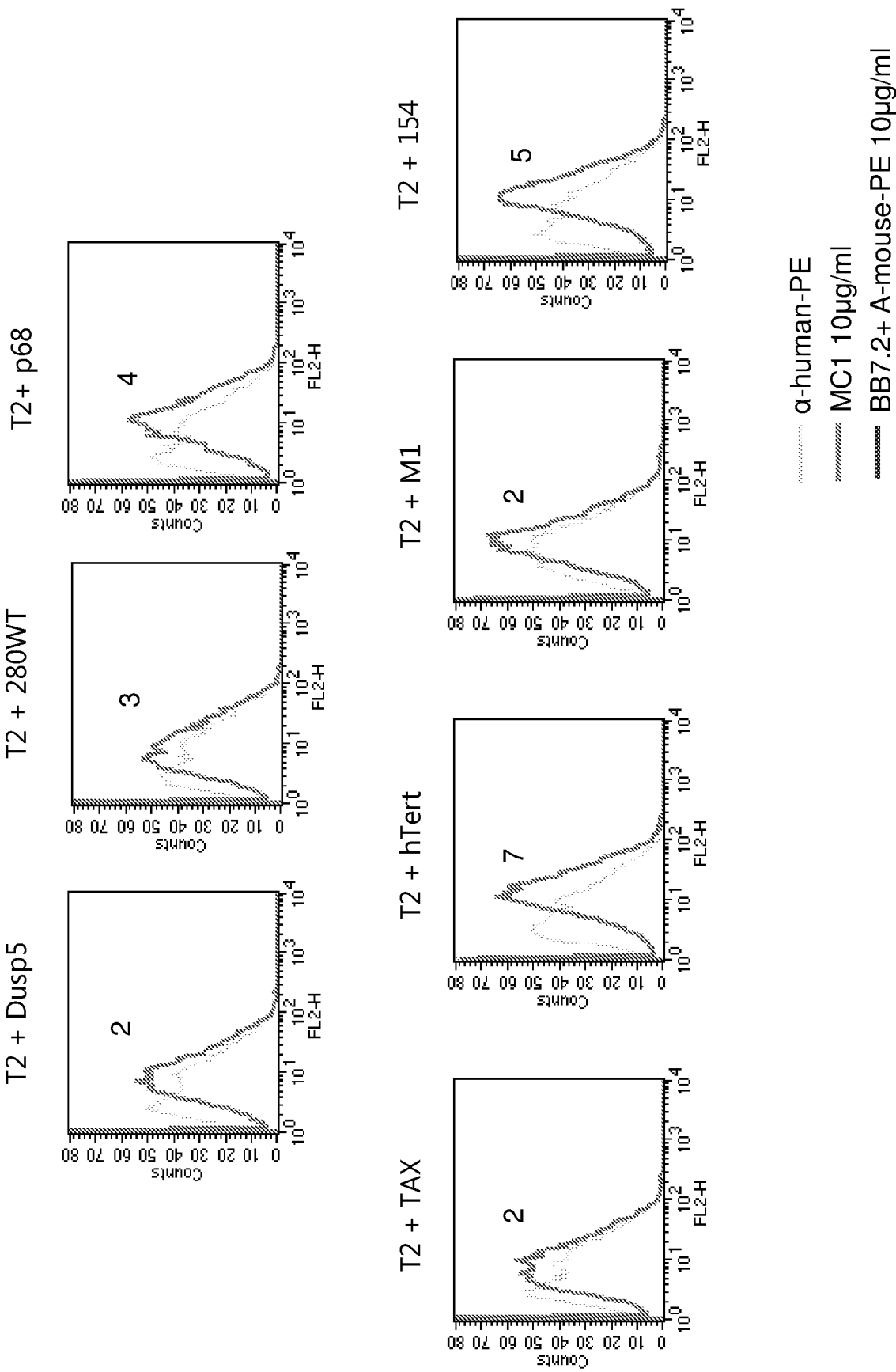


Figure 7



BB7.2 on A2+ Melanoma cells

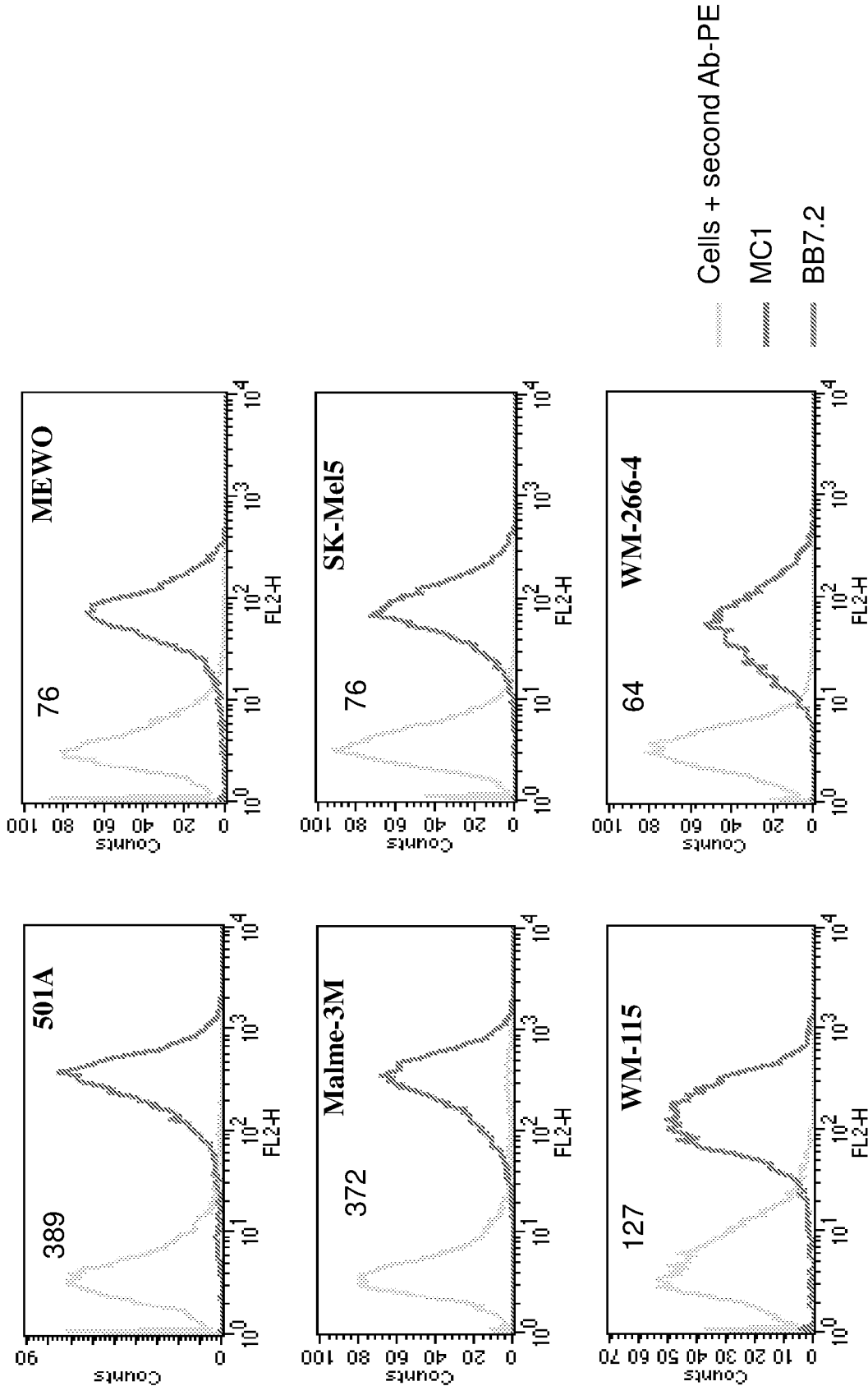


Figure 8

MC1 on A2+ Melanoma cells

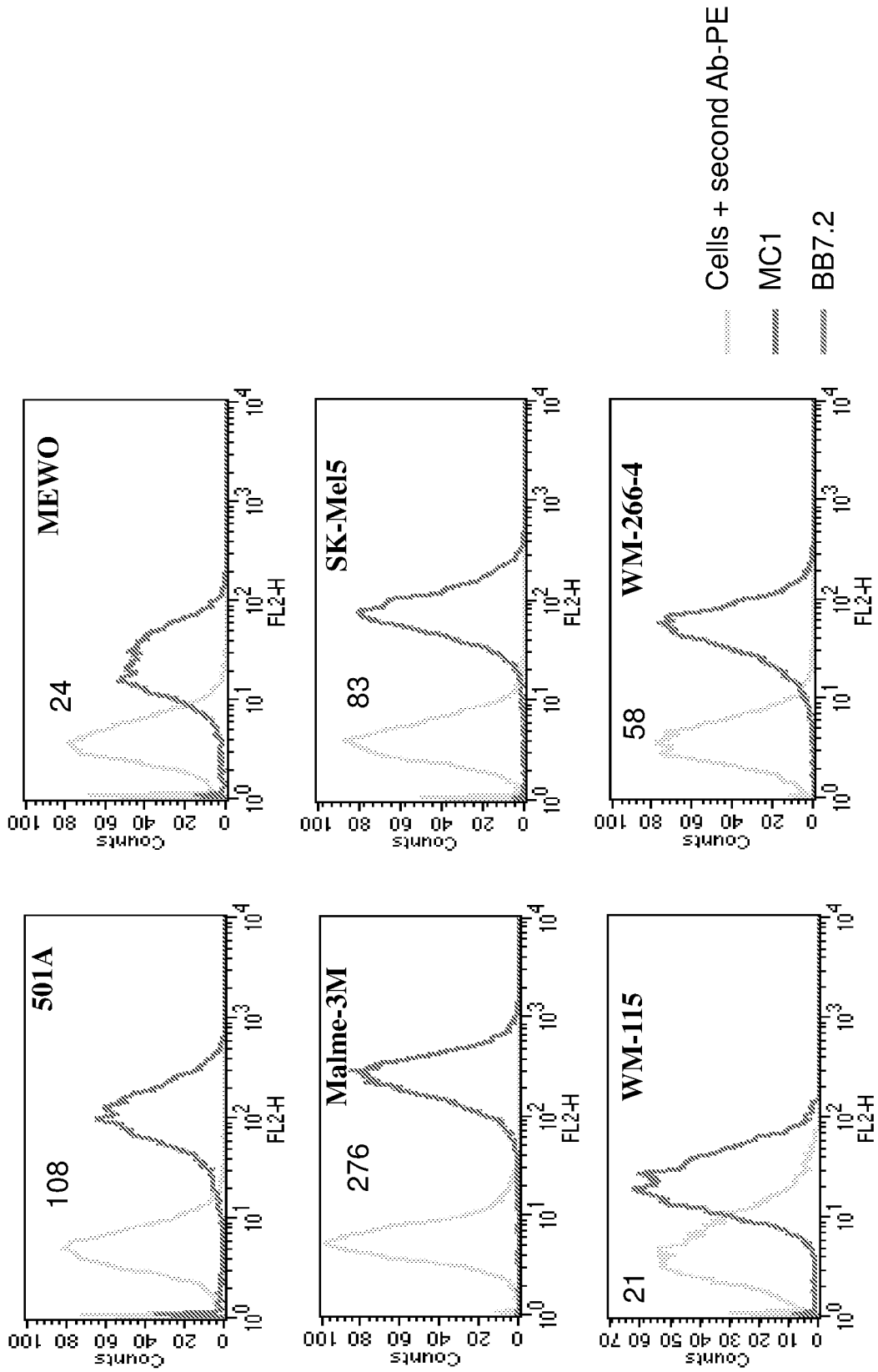
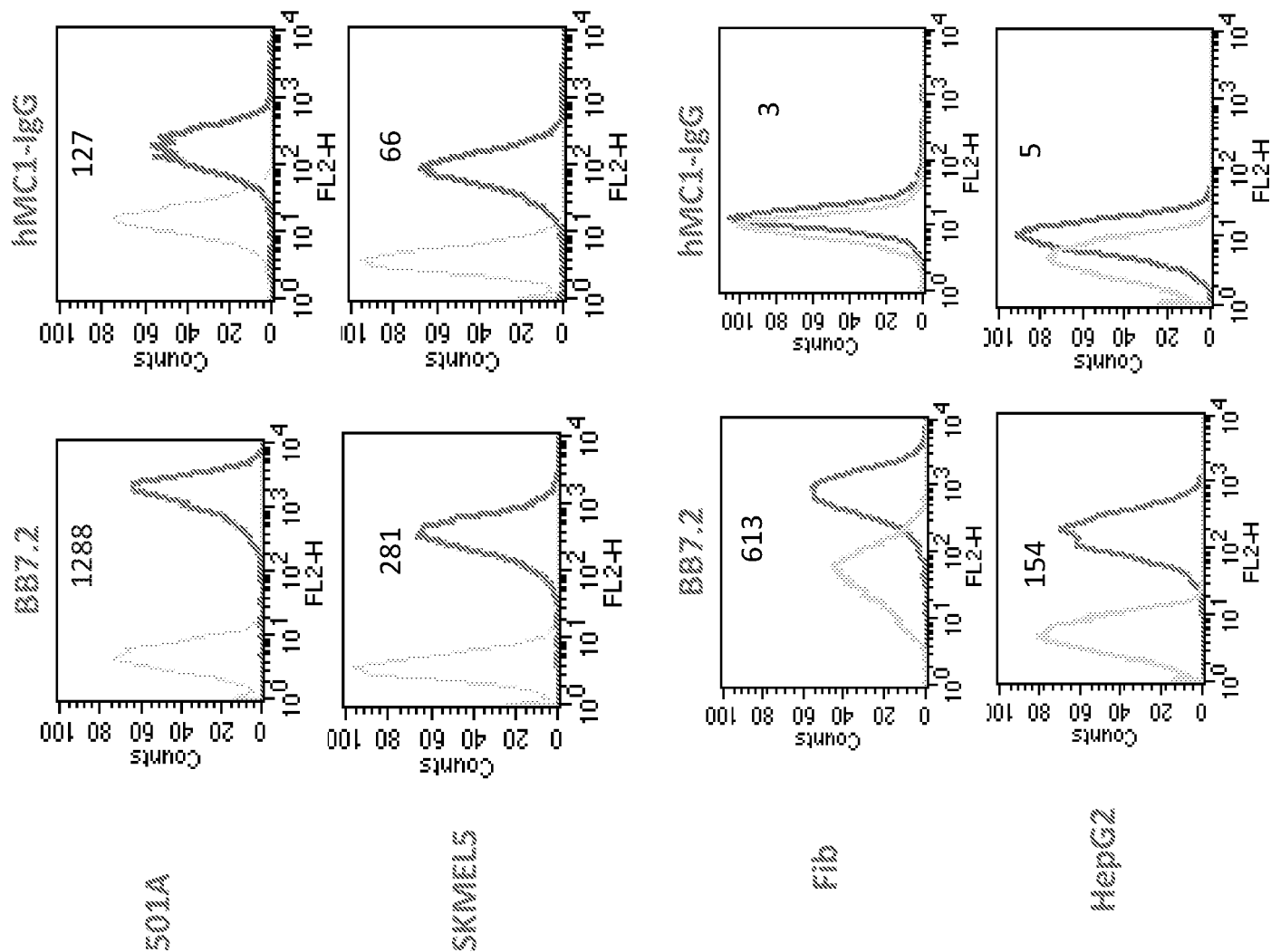
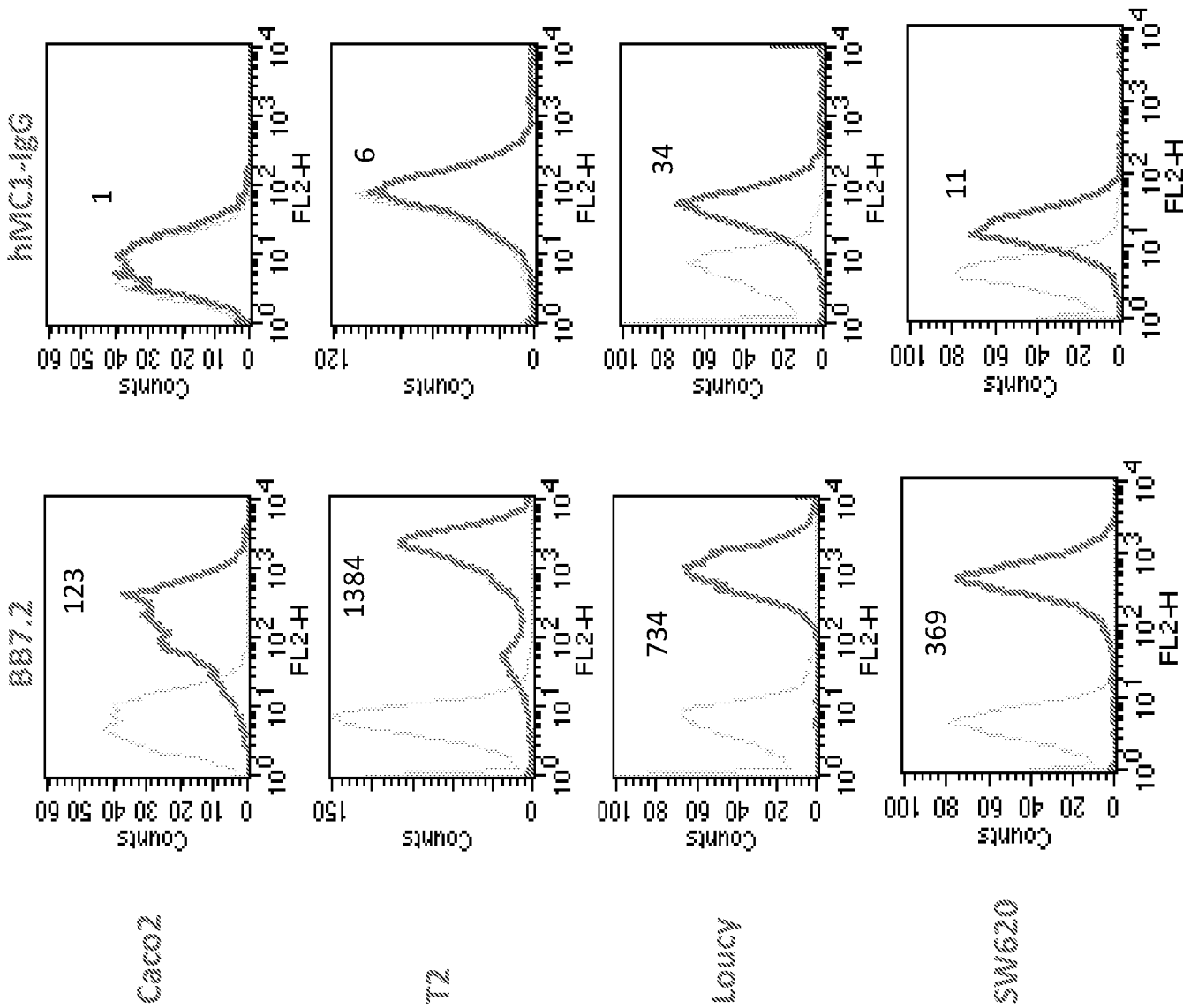


Figure 8 - continued



GeoMean number indicated

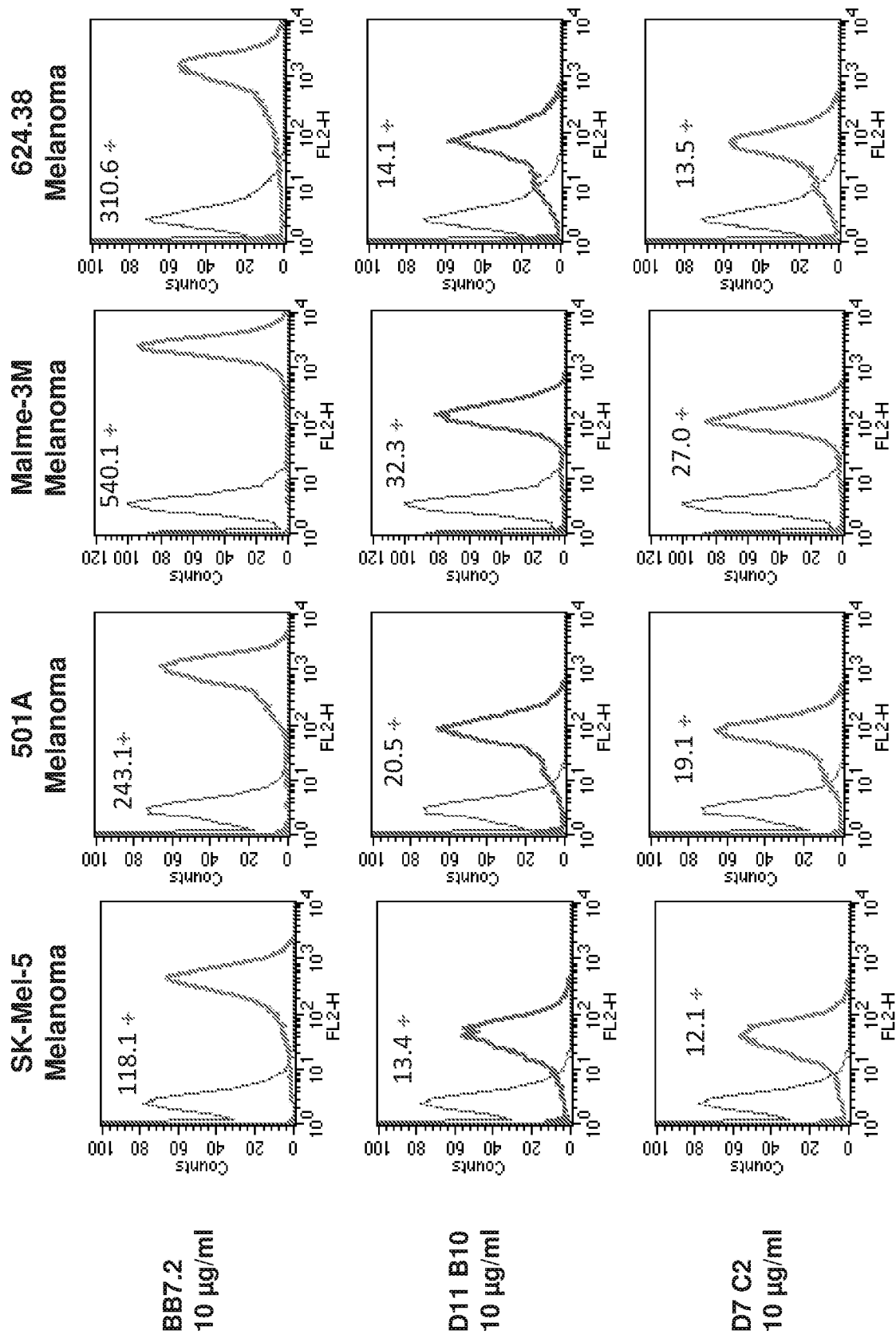
Figure 9



GeoMean number indicated

Figure 9 - continued

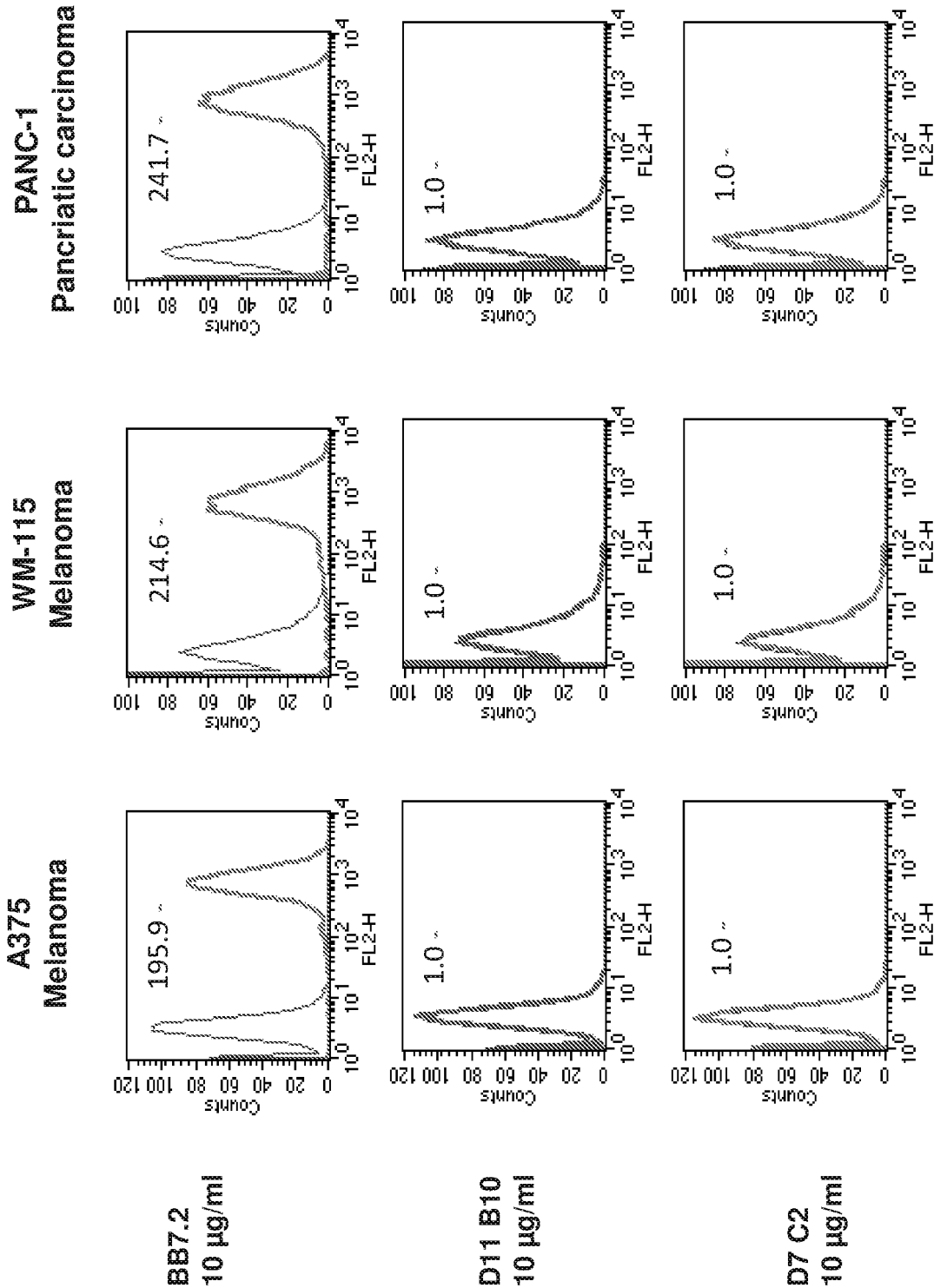
Antigen positive Melanoma cells



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

Figure 10

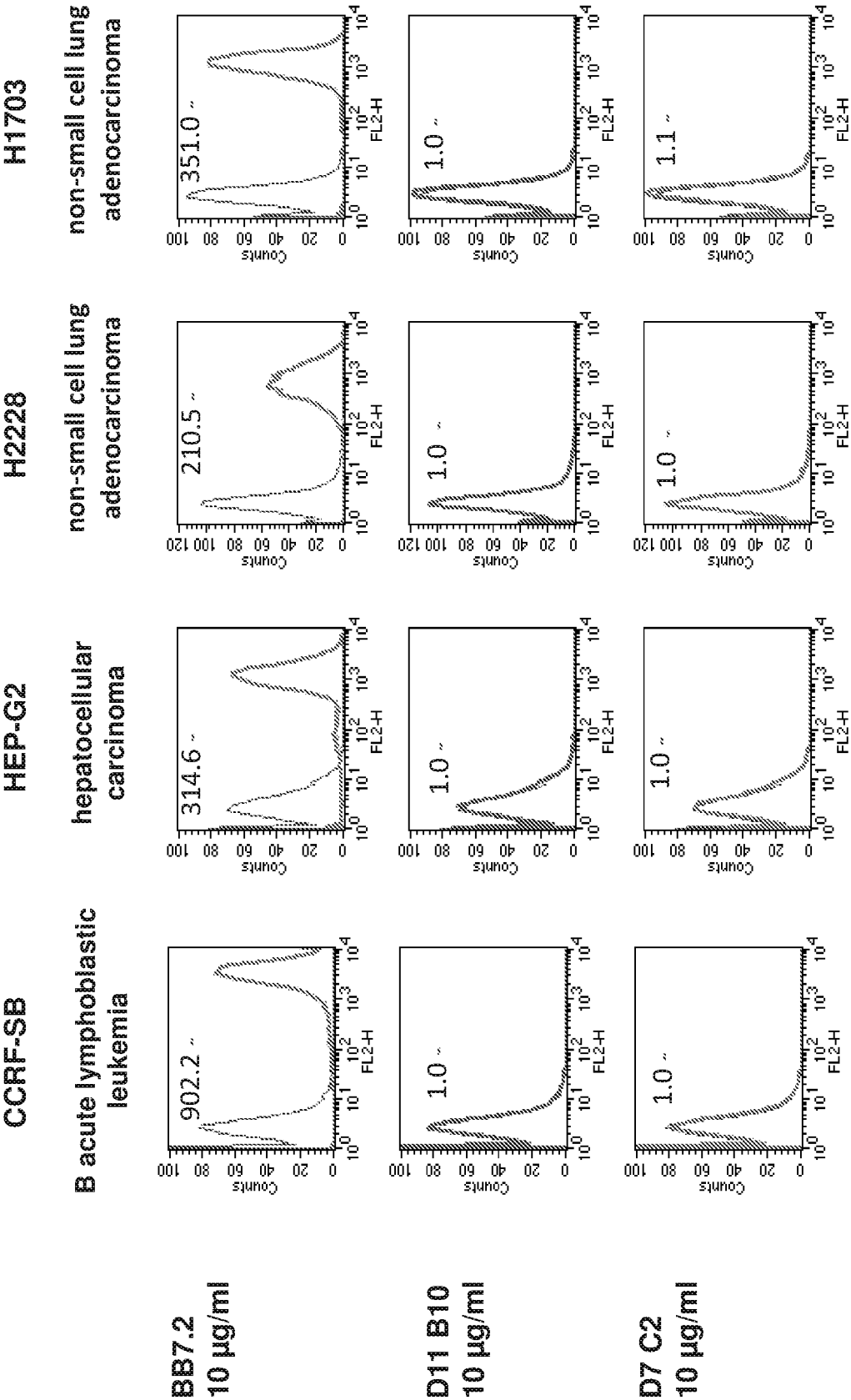
Antigen negative cell lines



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

Figure 10 - continued

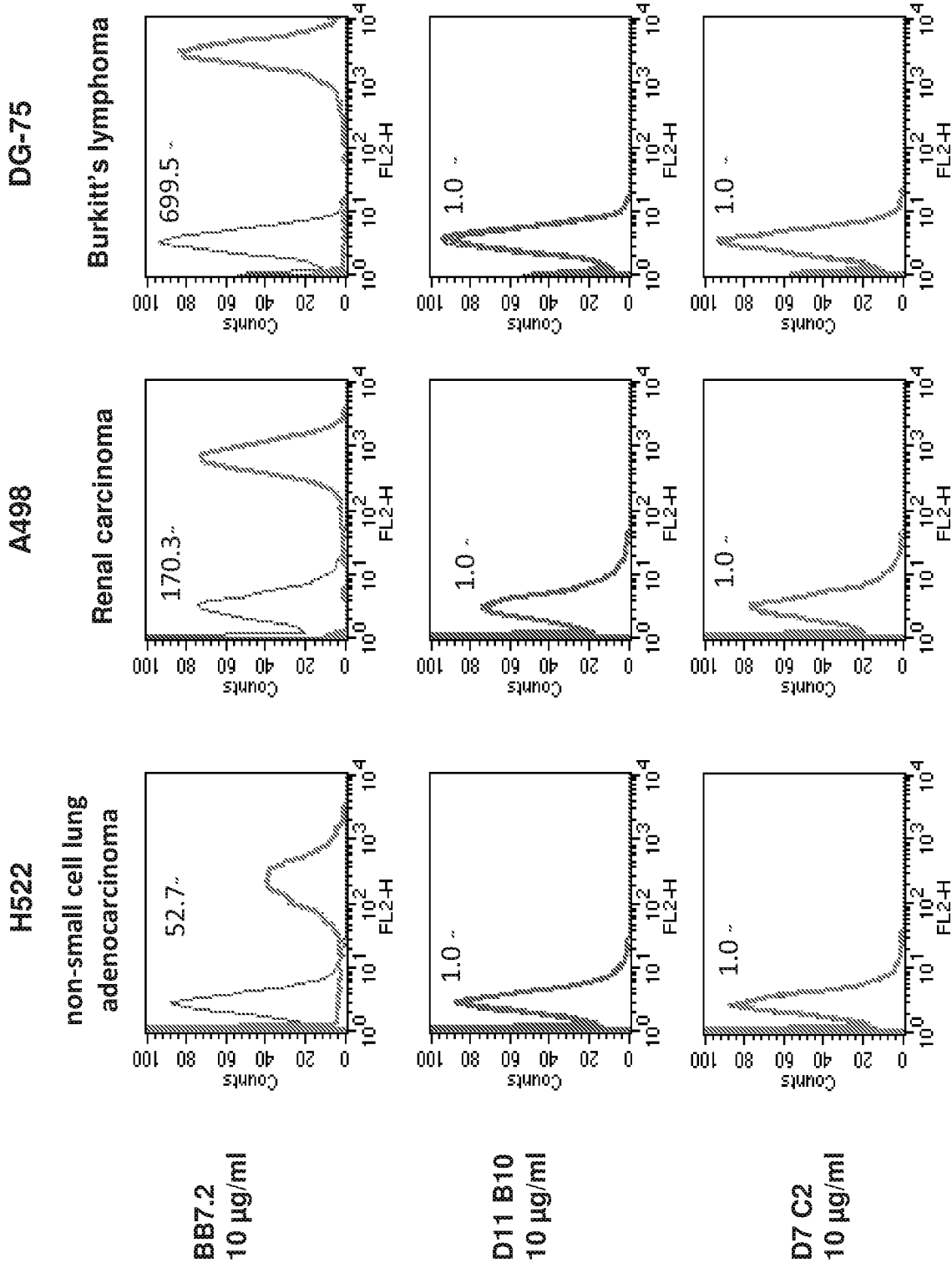
Antigen negative cell lines



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

Figure 10 - continued

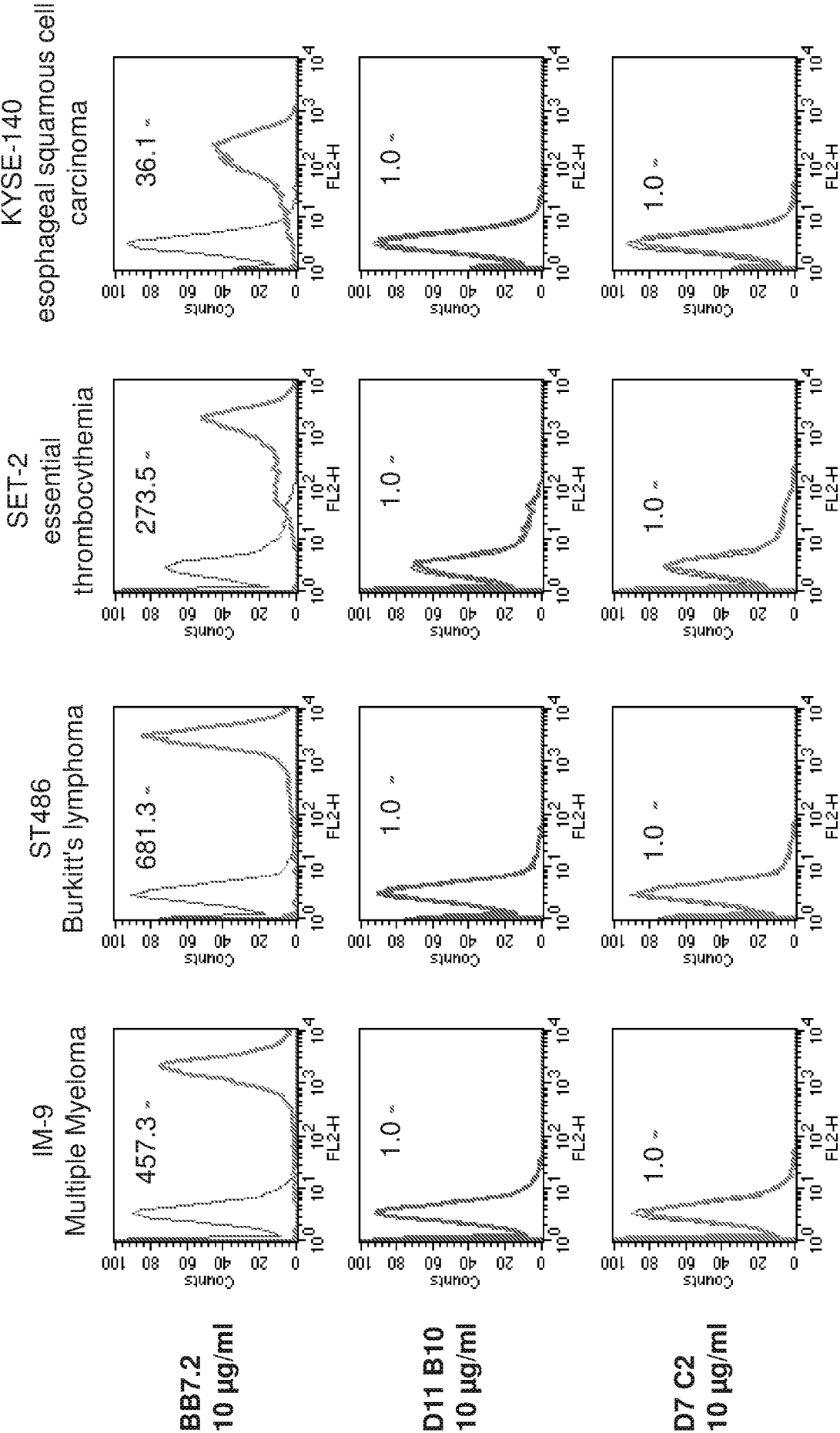
Antigen negative cell lines



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

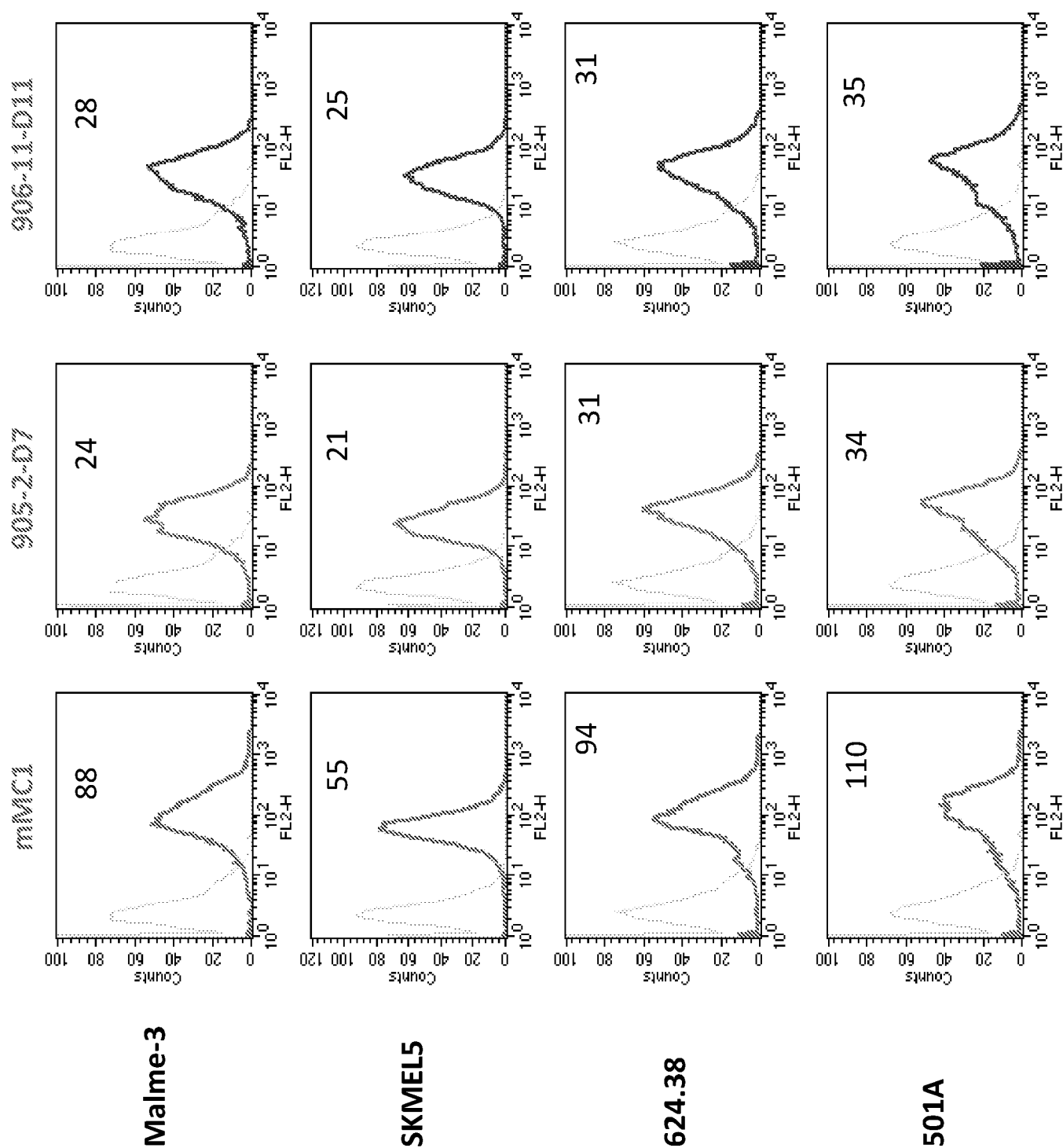
Figure 10 - continued

Antigen negative cell lines



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

Figure 11



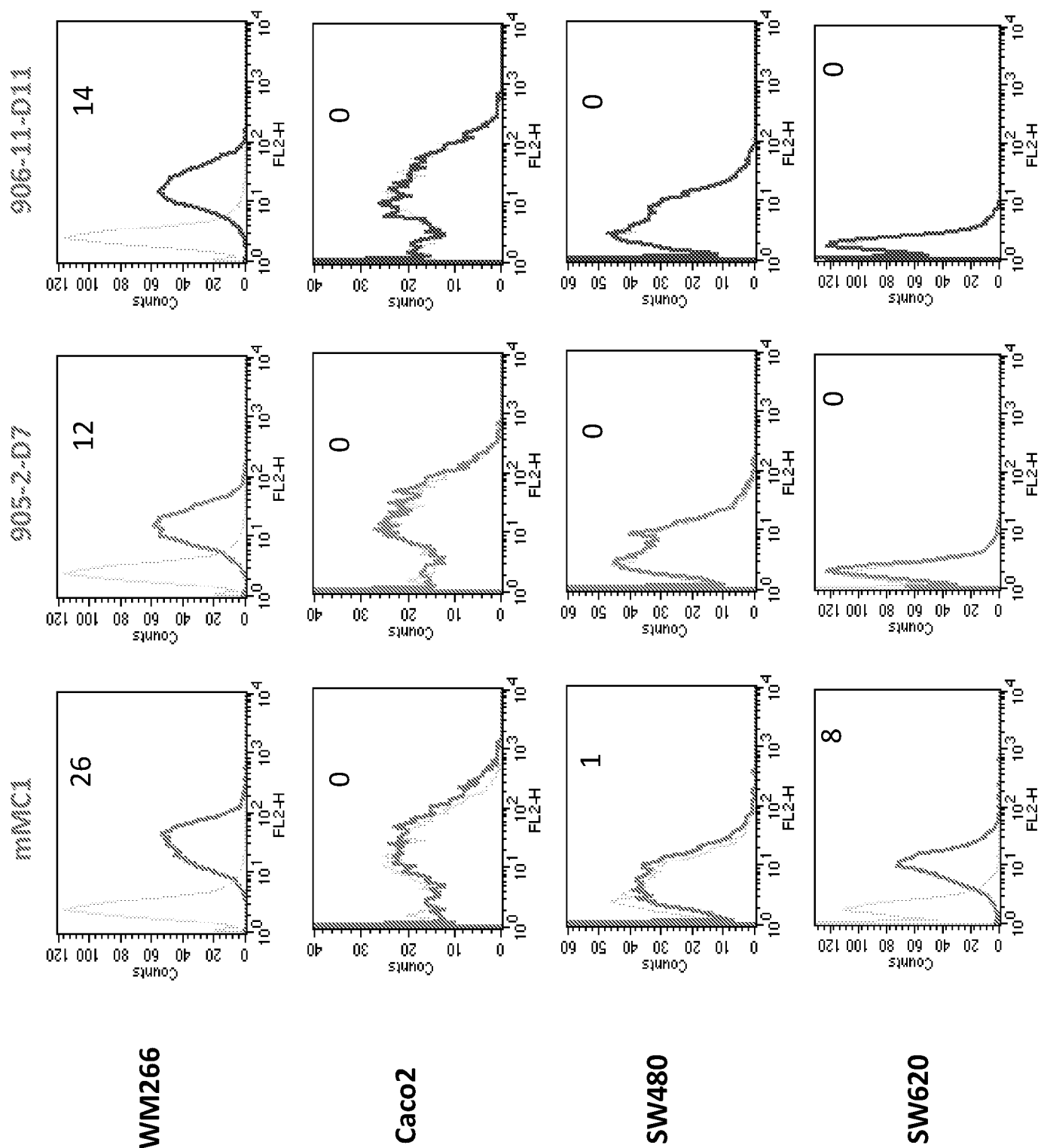


Figure 12 - continued

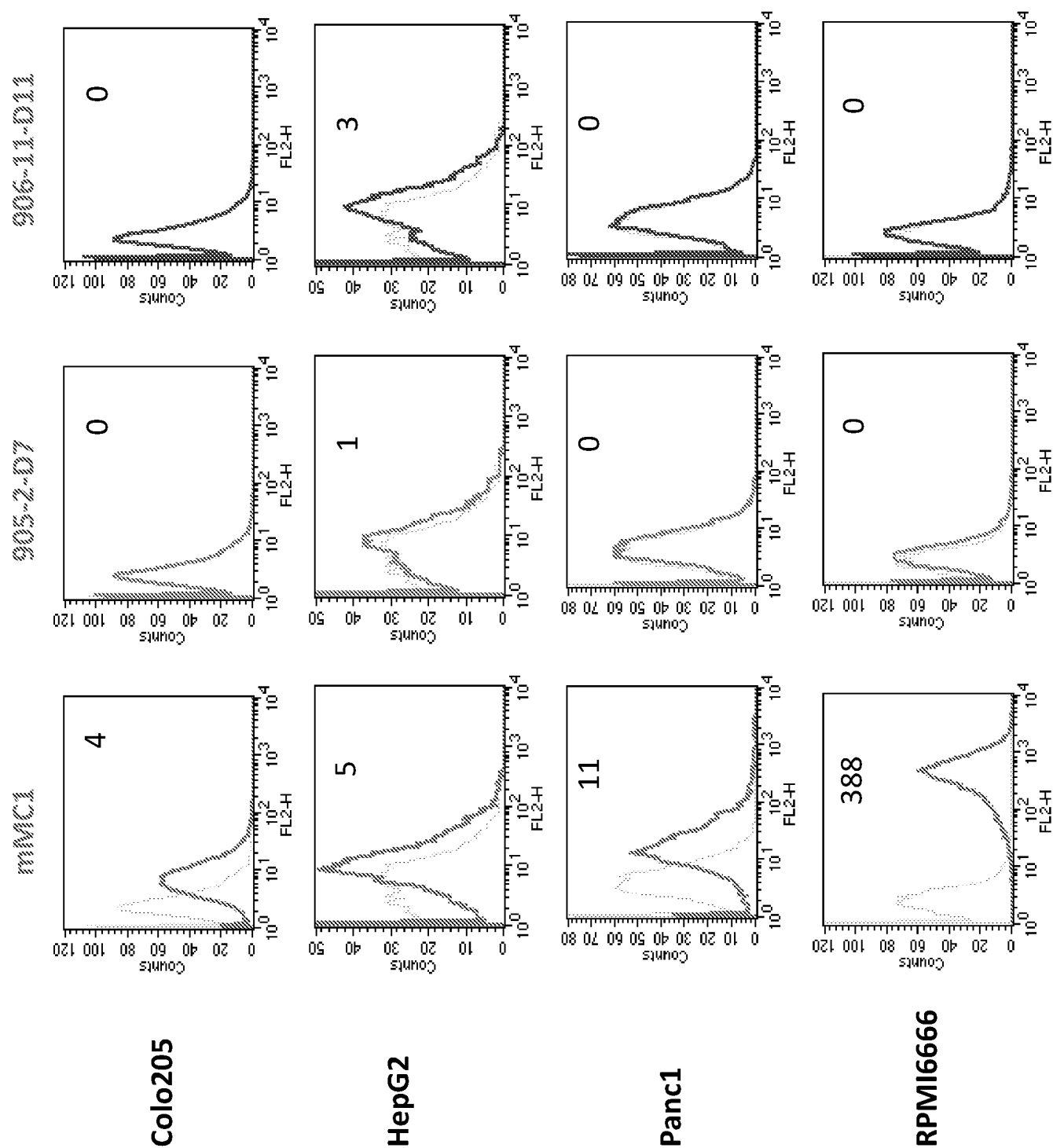


Figure 12 - continued

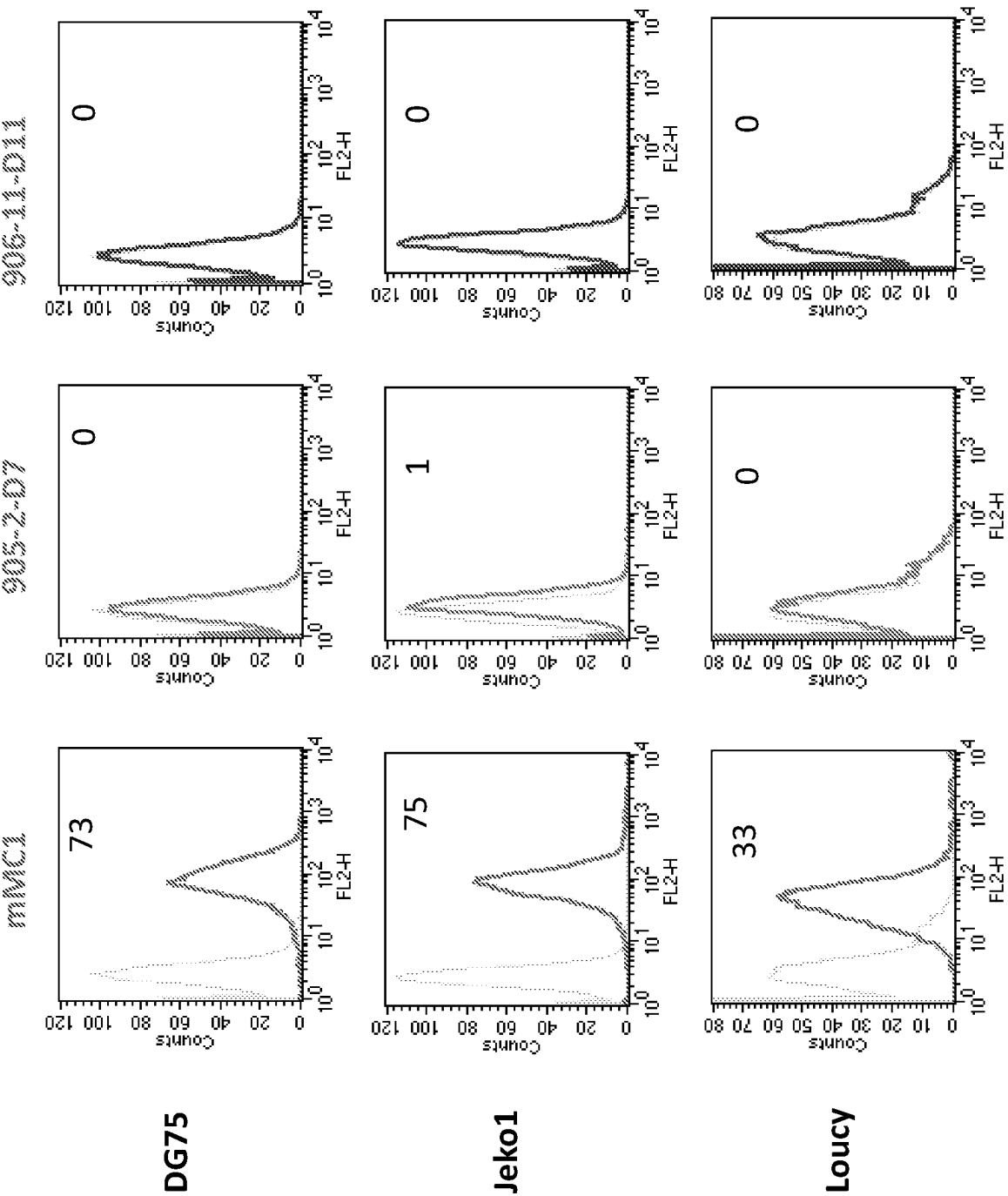


Figure 12 - continued

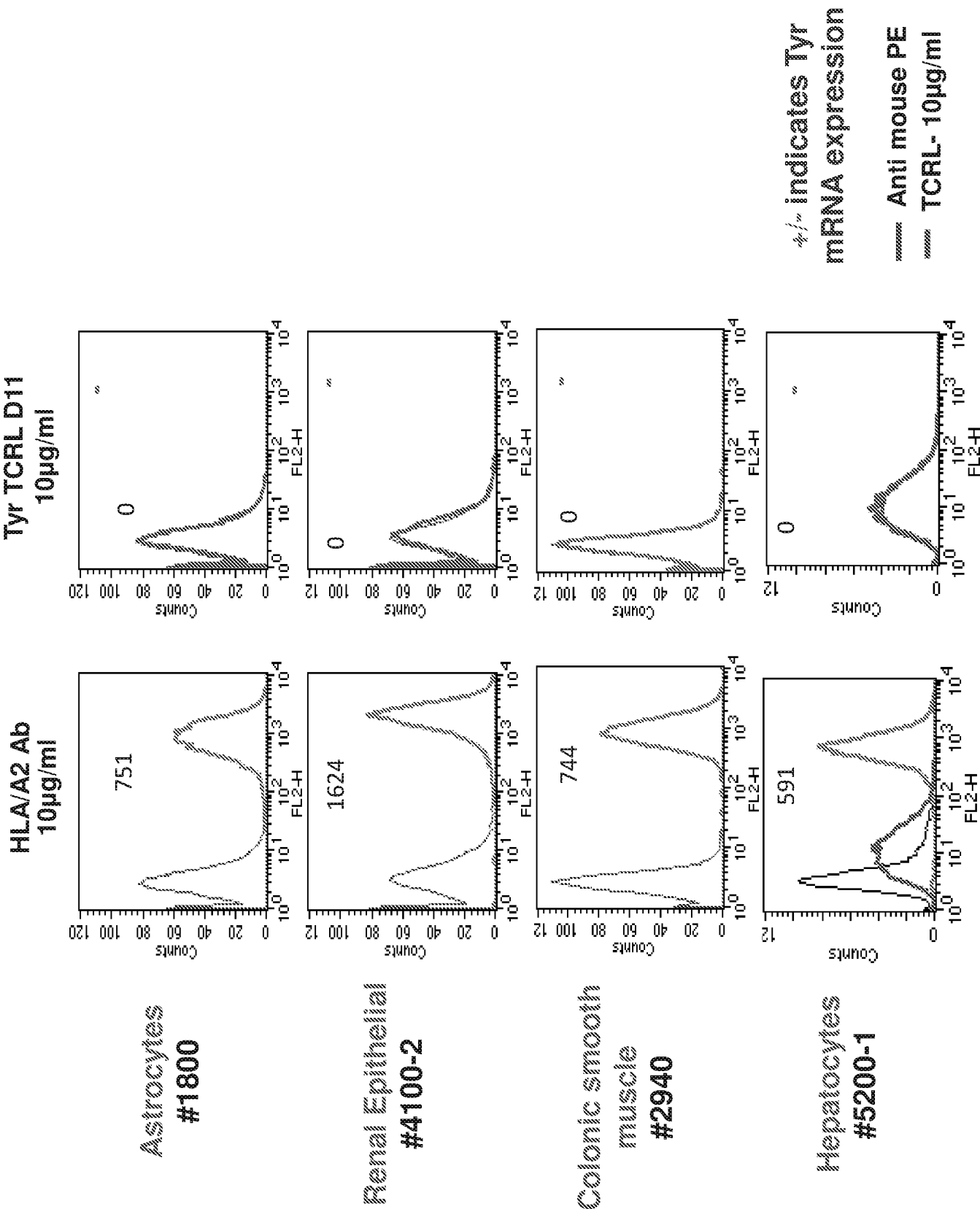


Figure 13

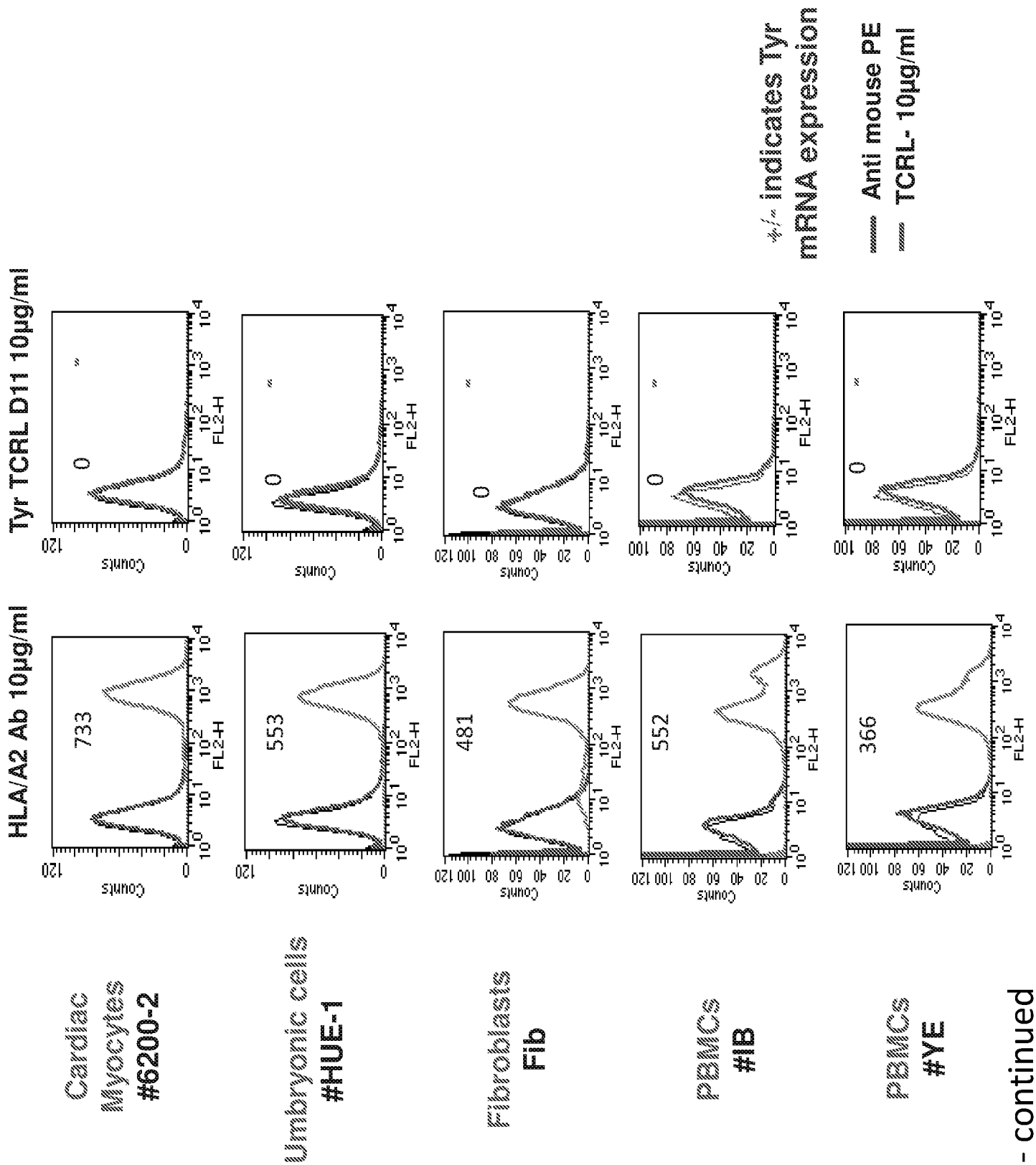


Figure 13 - continued

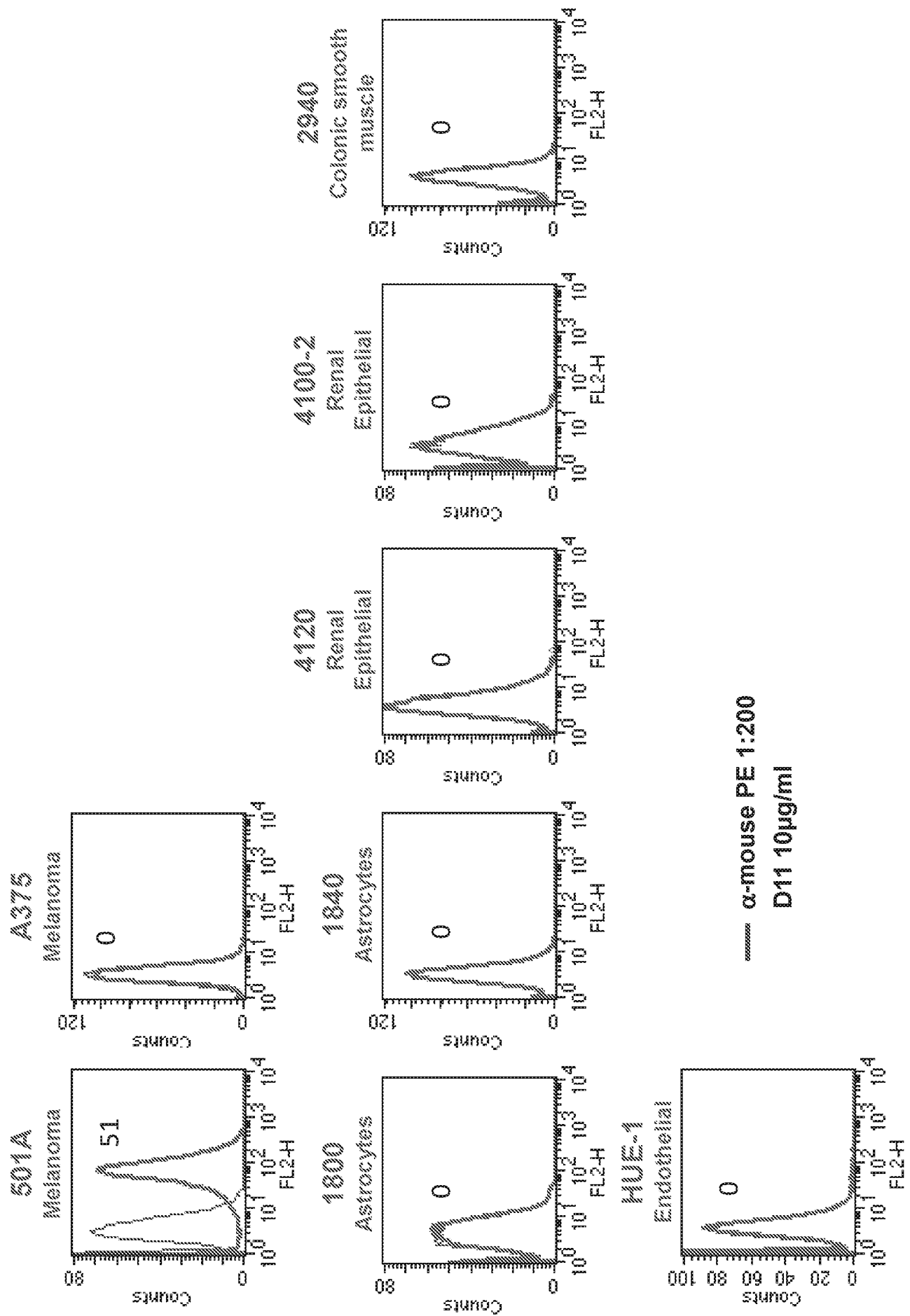


Figure 14

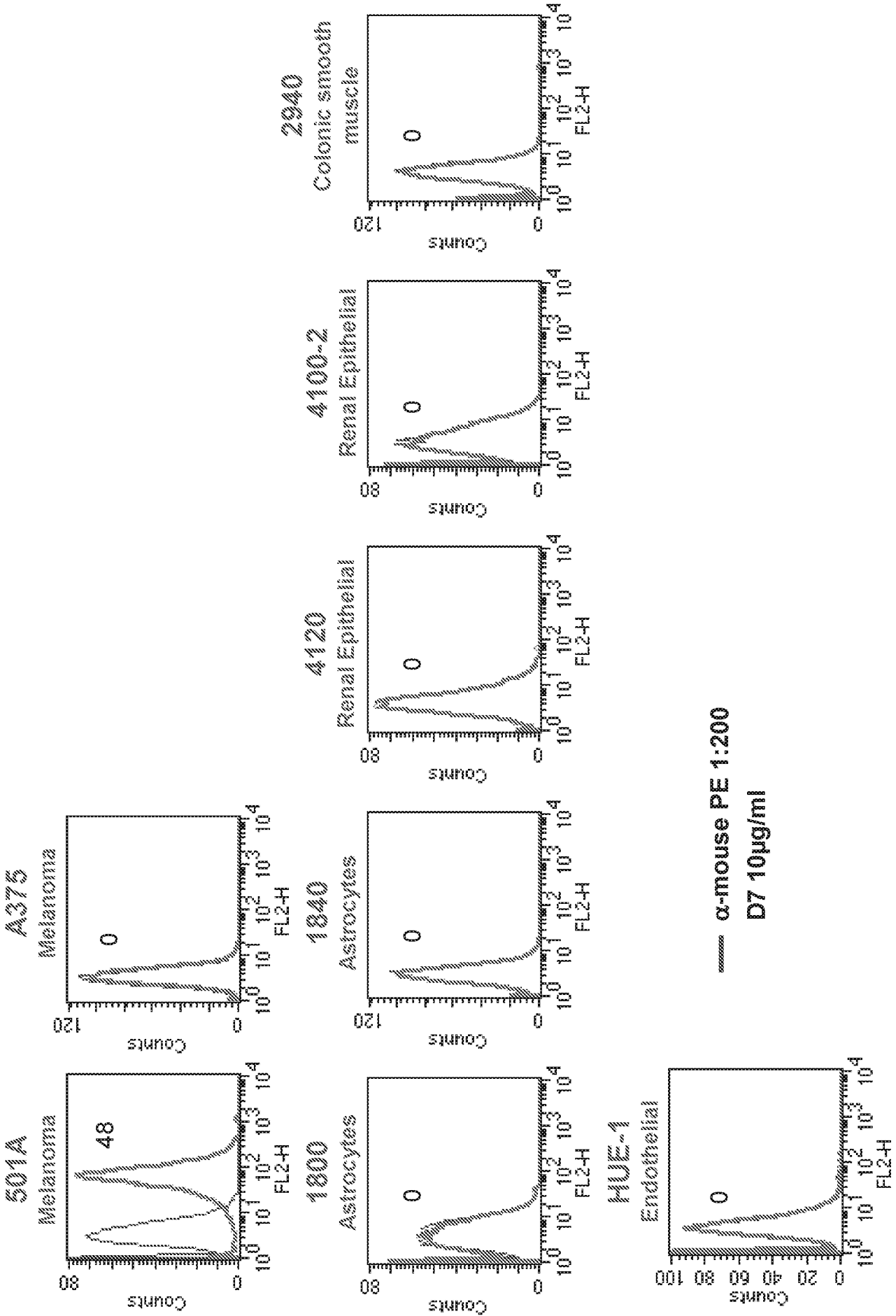


Figure 15

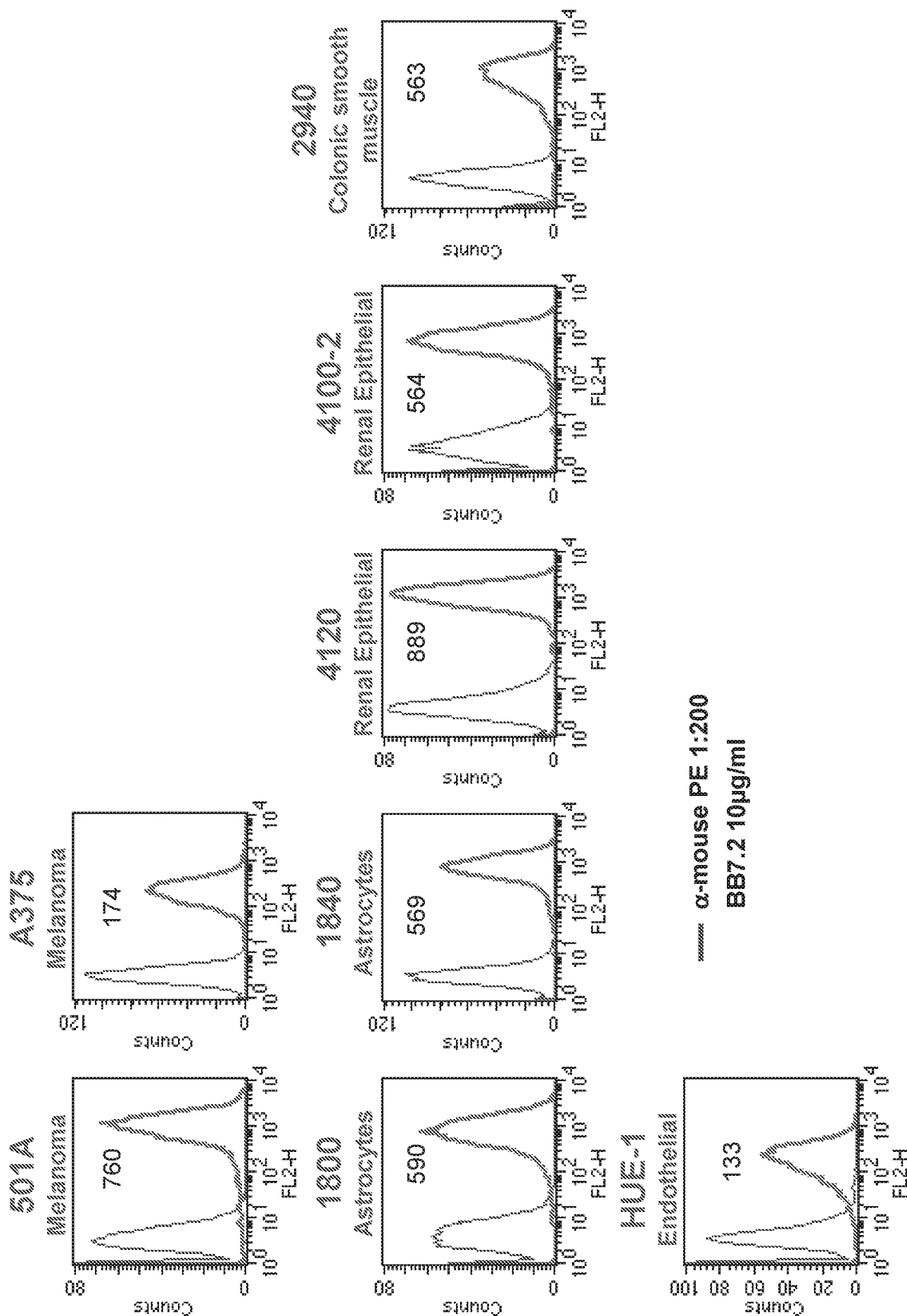


Figure 16

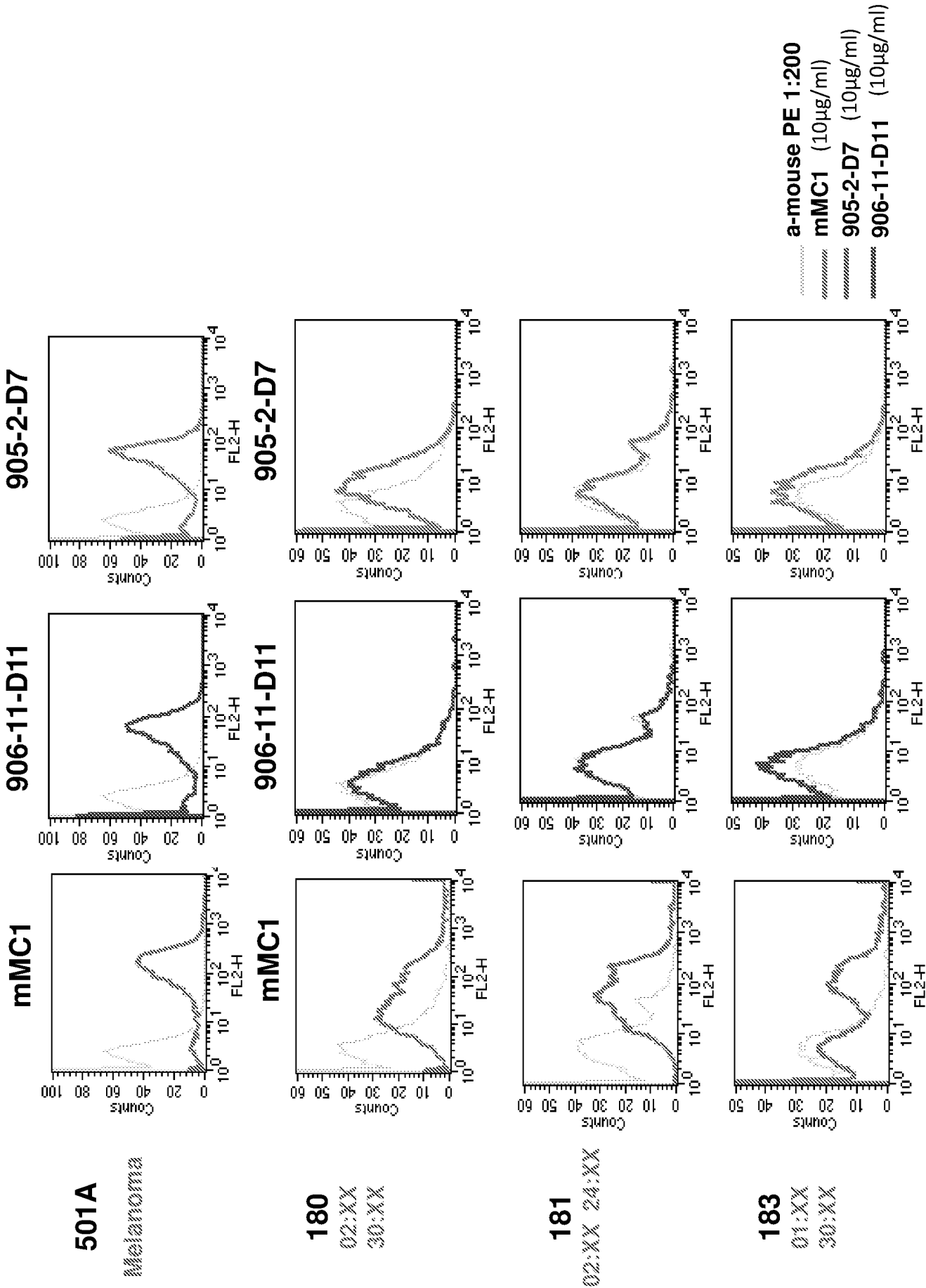


Figure 17

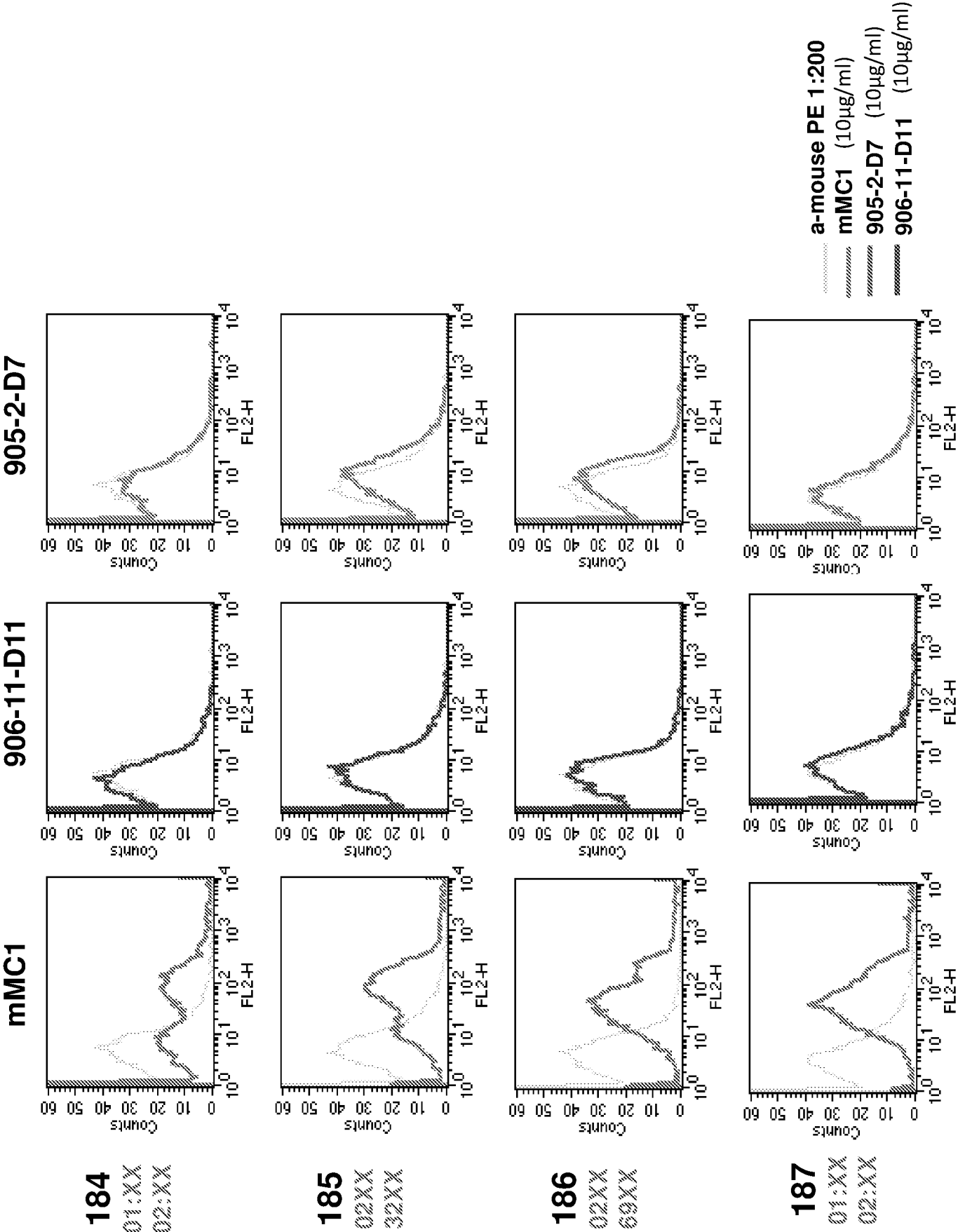
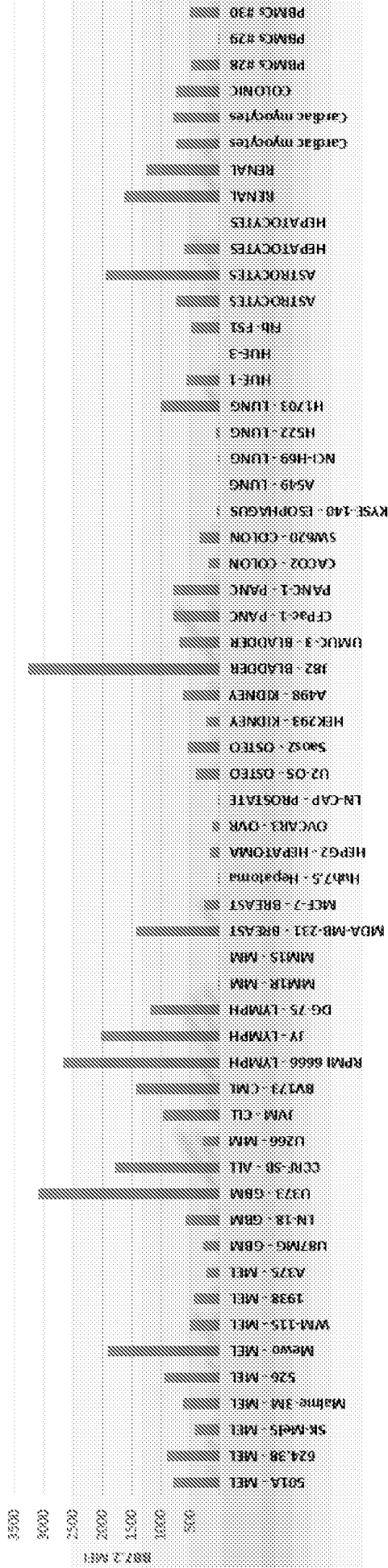


Figure 17 - continued

62-2020-20



SUBSTITUTE SHEET (RULE 26)

34/108

Section 101.10



Primary normal cells

Cancer cell lines

	miRNA	protein	Melanoma	GBM	Hematological	Breast	Hep	Ov	pro	oste	Kidney	Bladder	Panc	Colon	Eso	Lung	HUE	TH	AST	HBP	RCC	Crd	Col	PBMCs
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	NA	NA	-	-	-	-	-	-

Figure 19

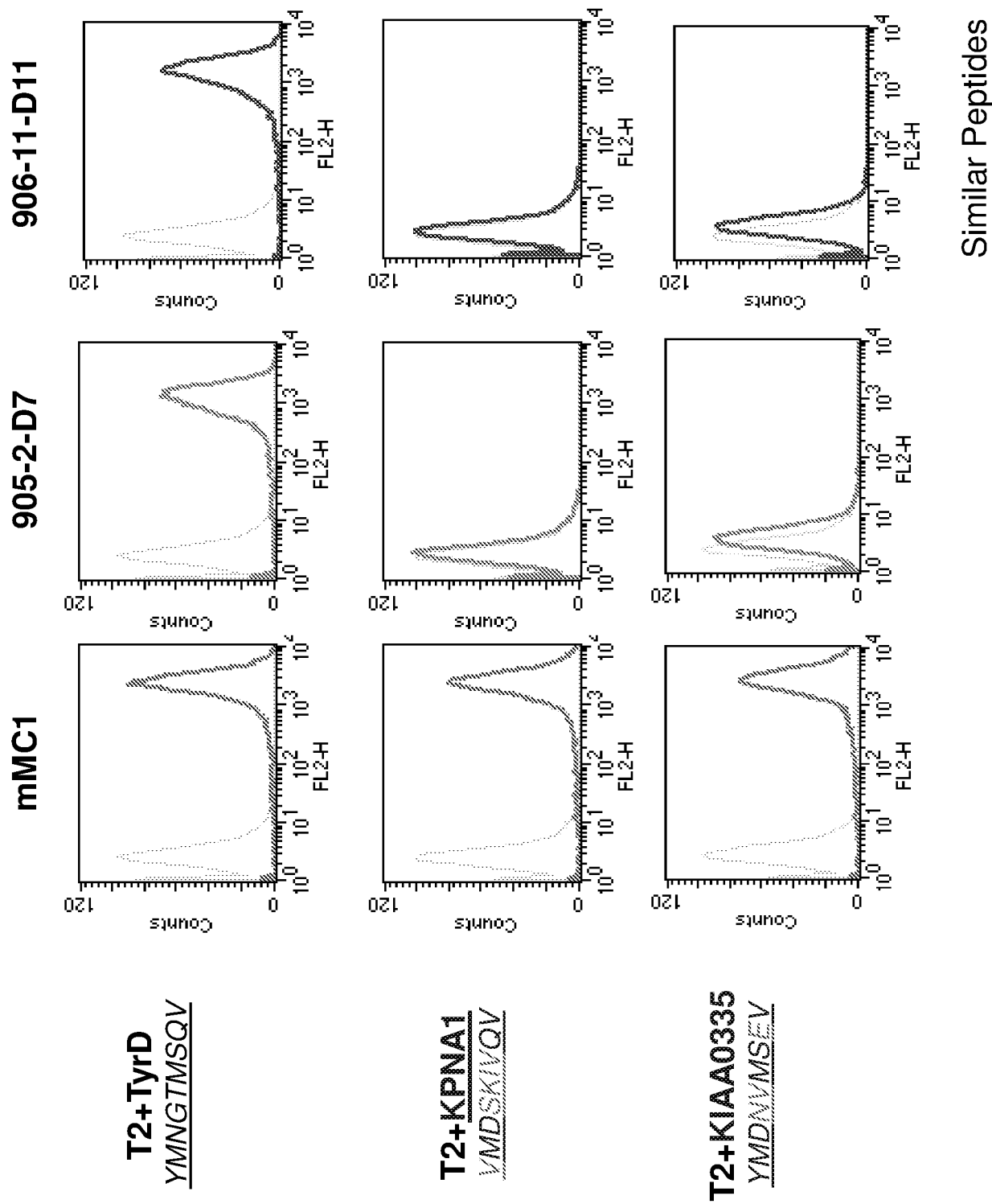
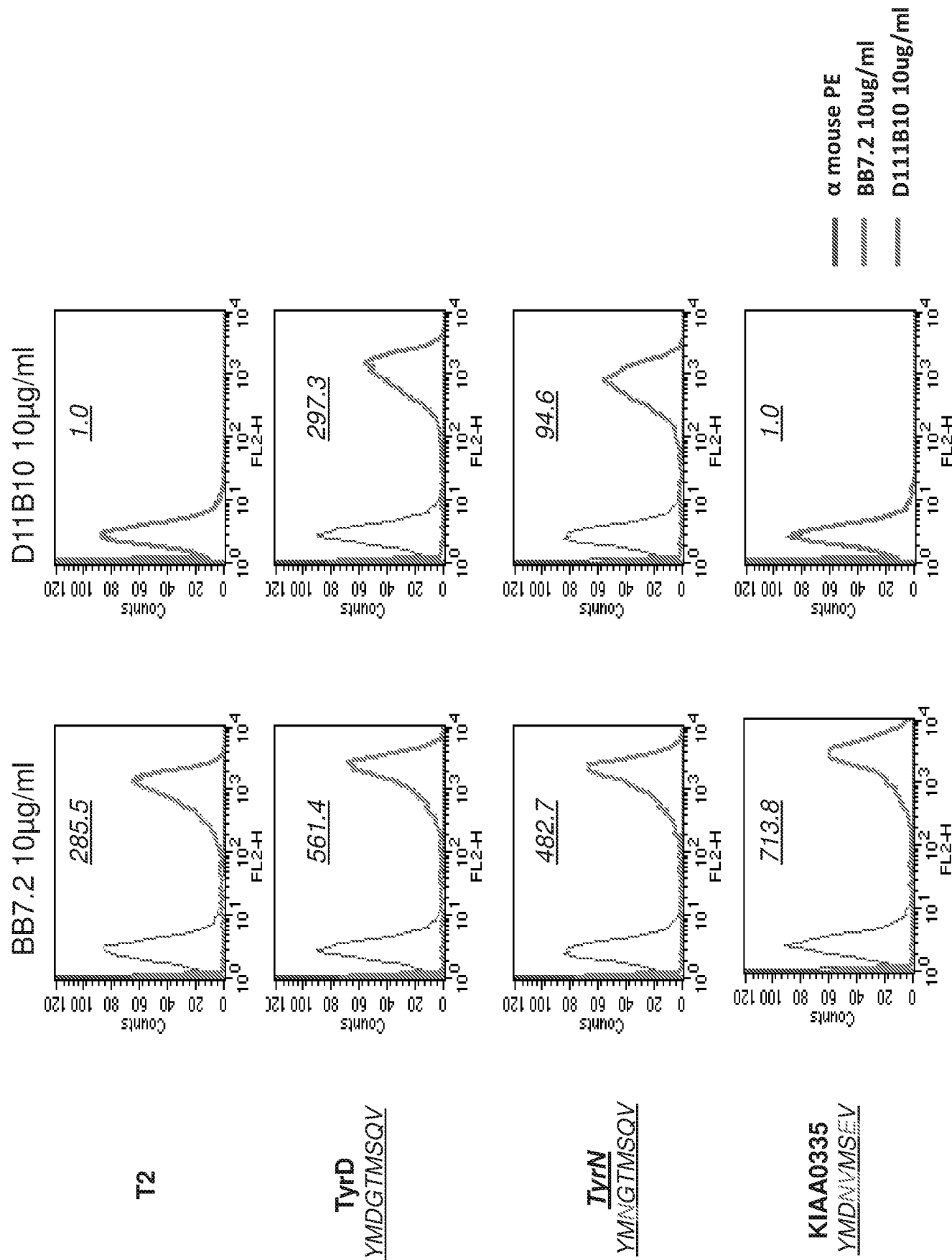
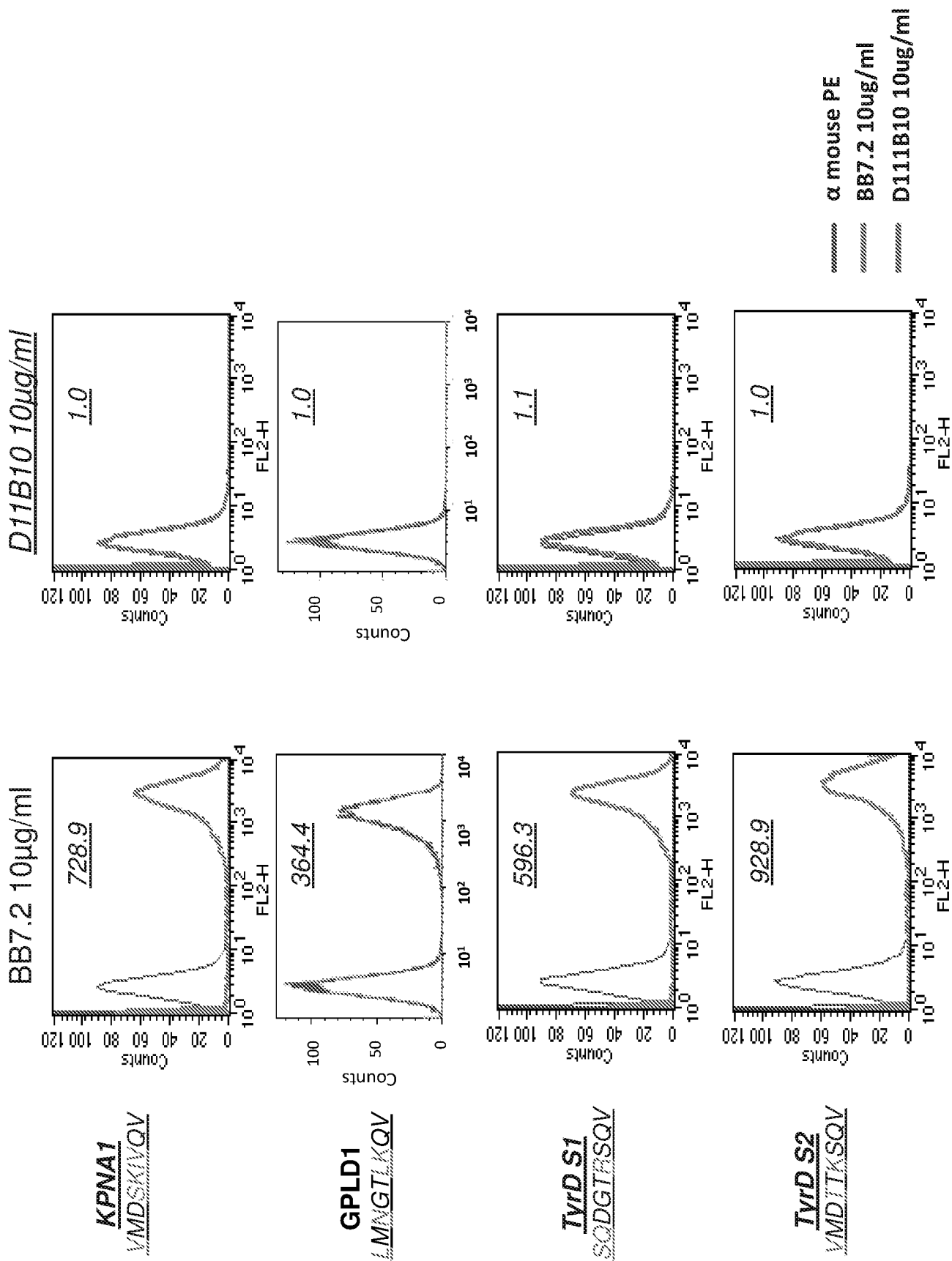


Figure 20



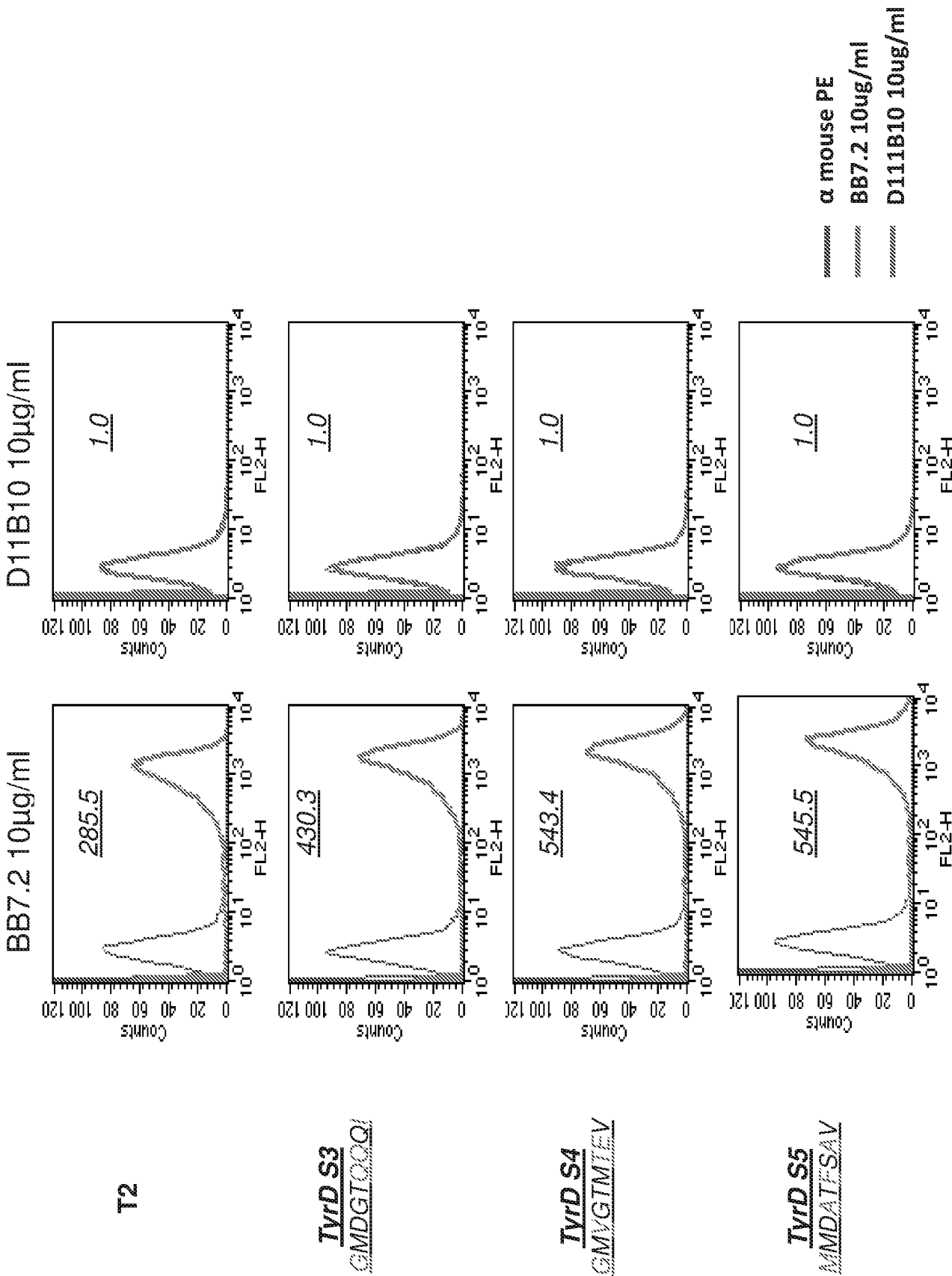
MFI values are relative to background. Value of `1` means no binding

Figure 21



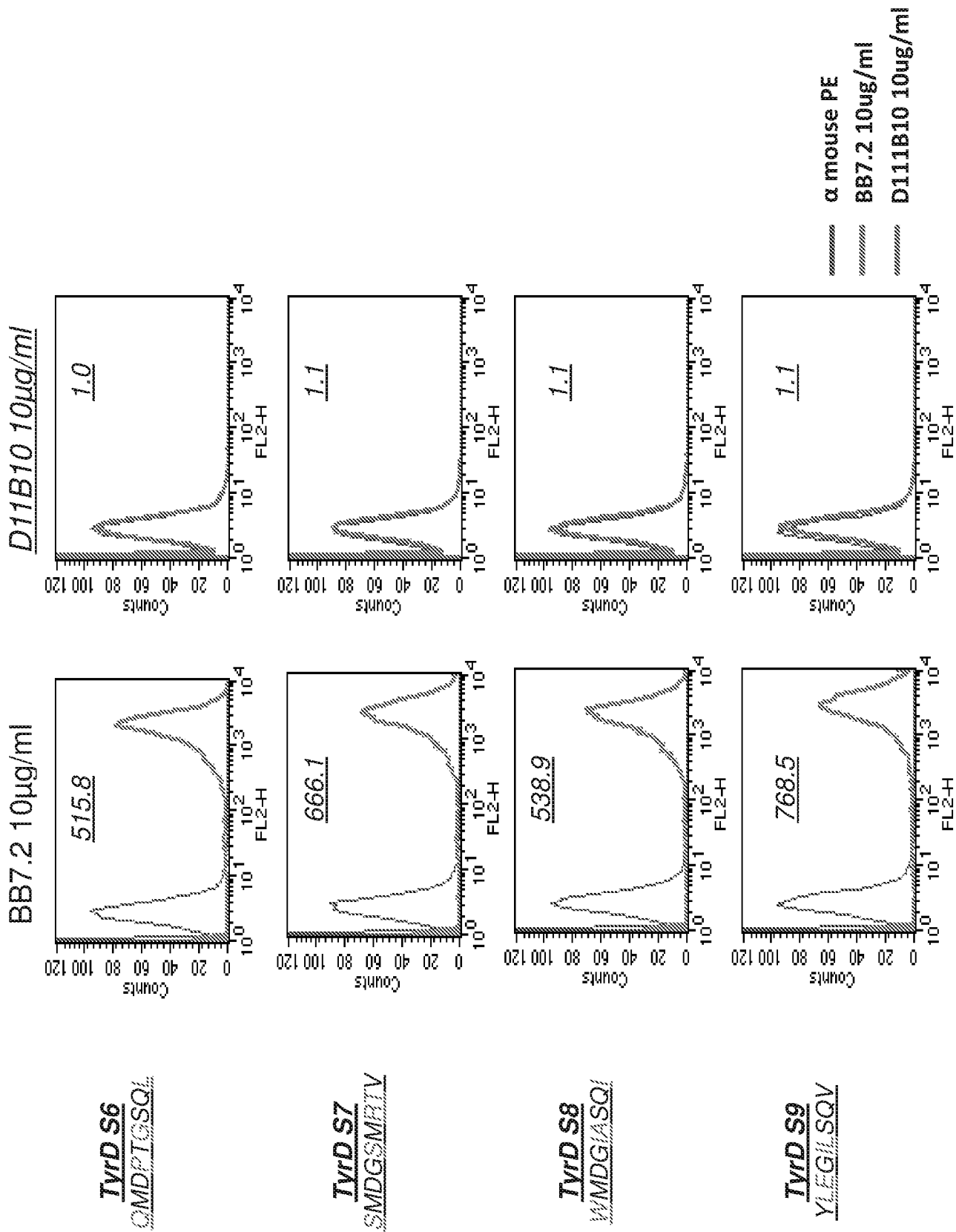
MFI values are relative to background. Value of `1` means no binding

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

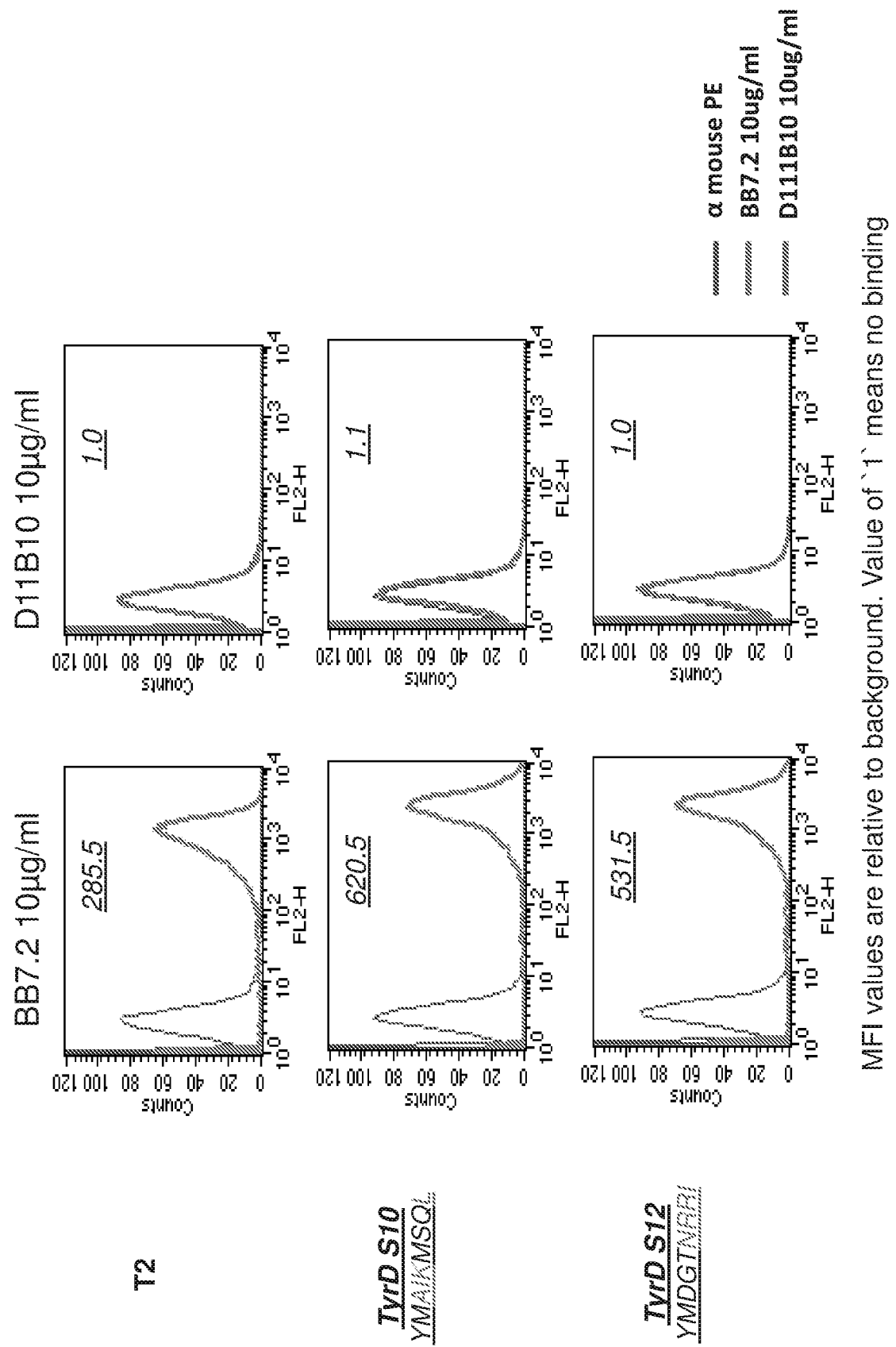
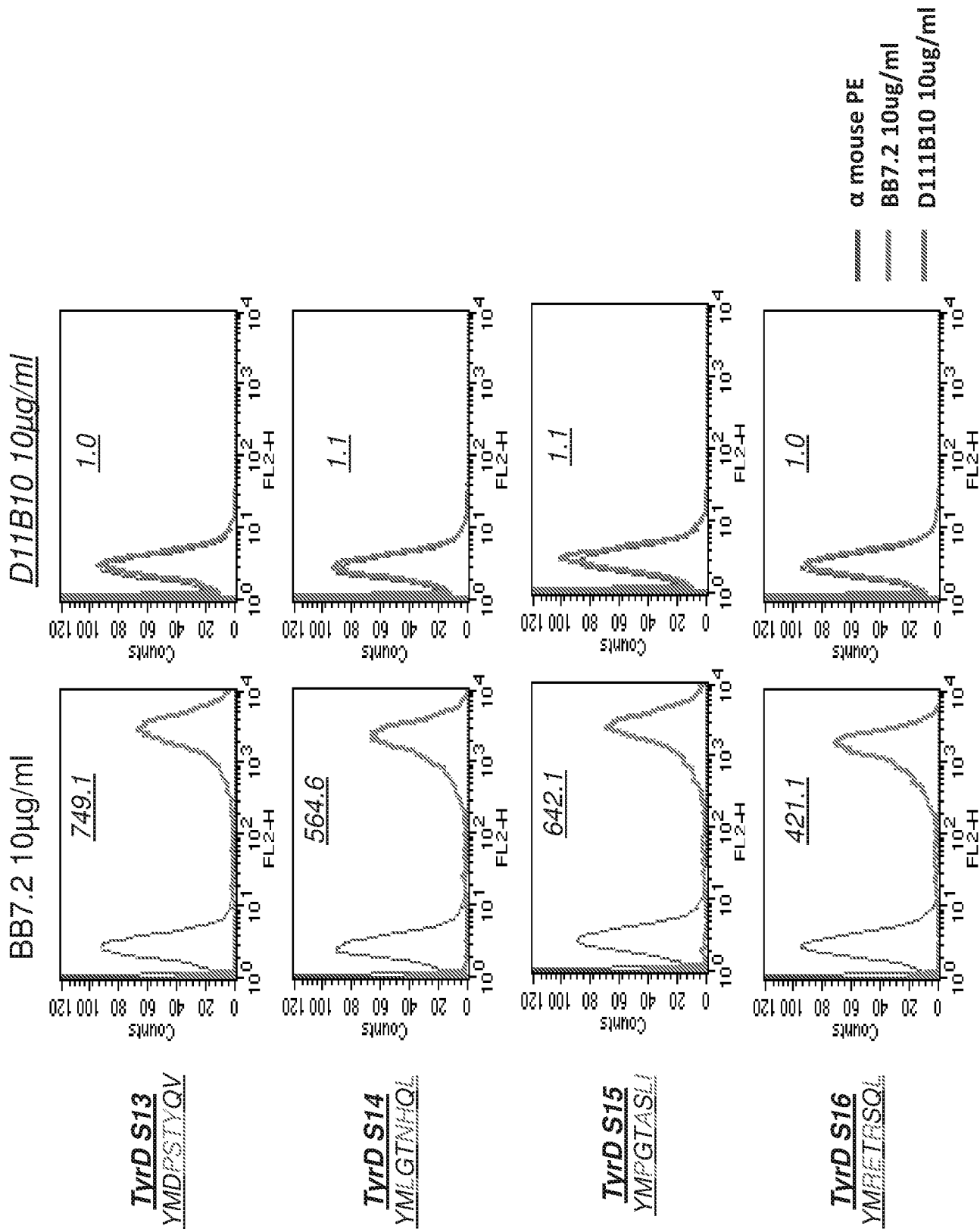
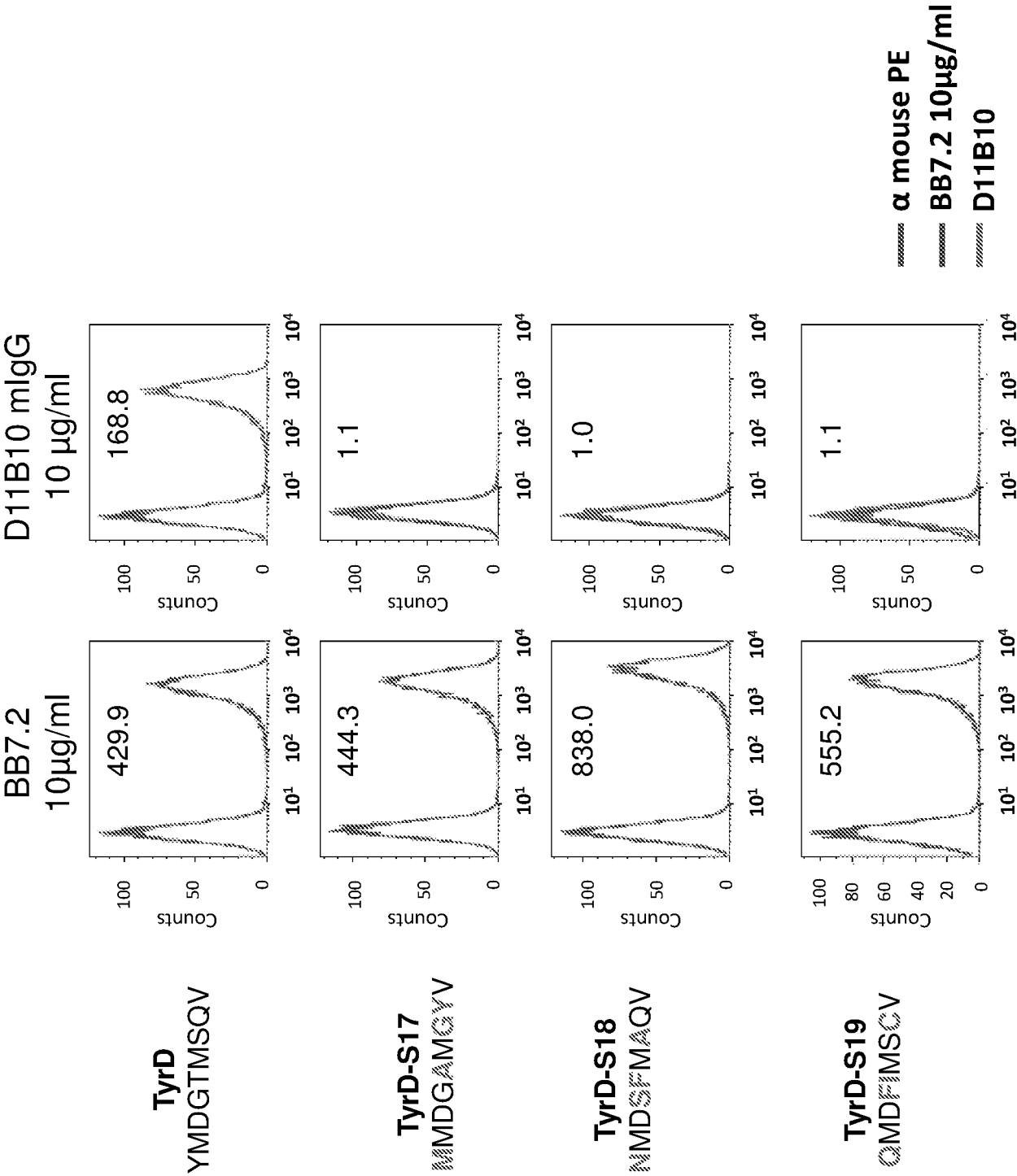


Figure 23



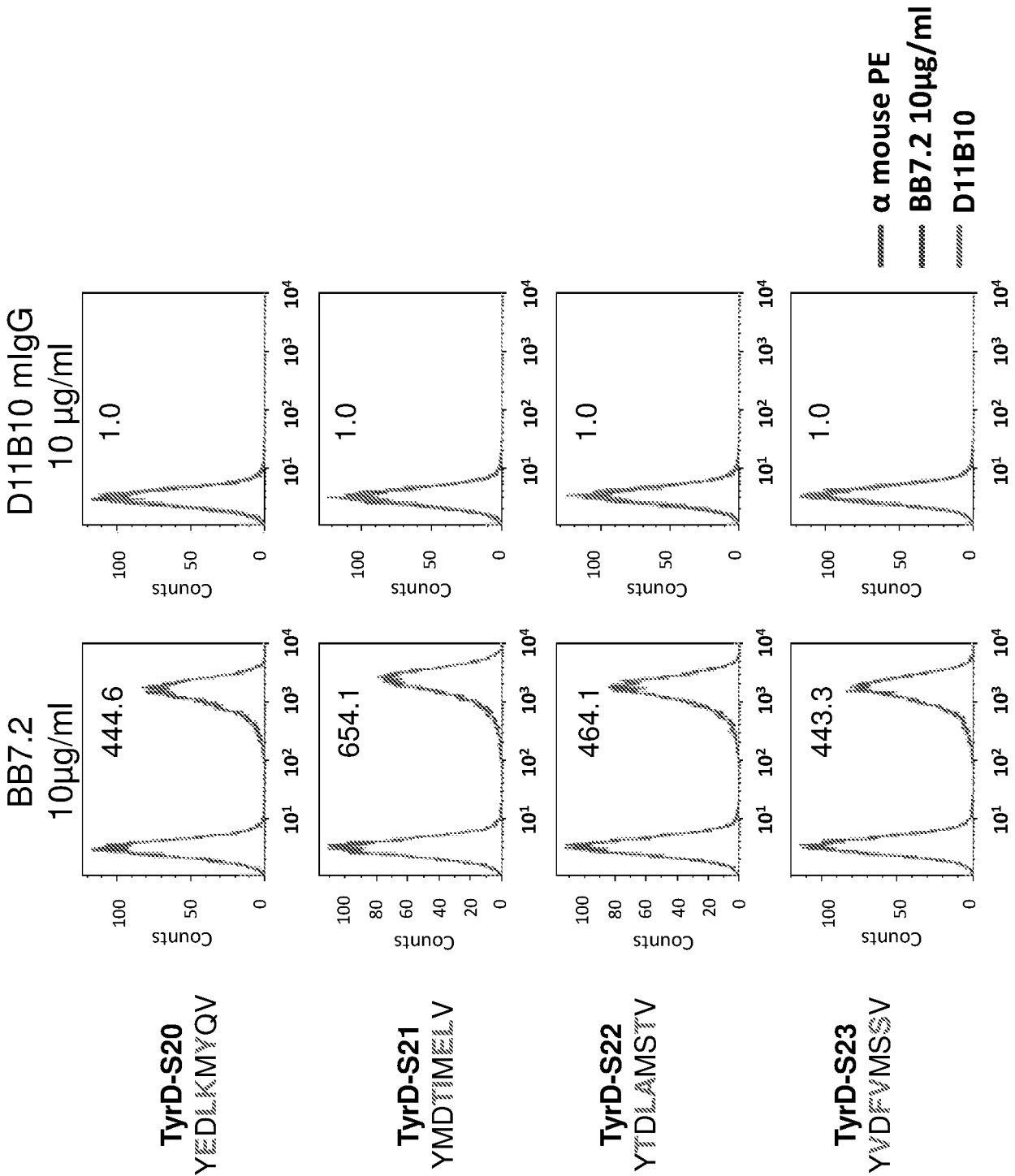
MFI values are relative to background. Value of `1` means no binding

Figure 23 - continued



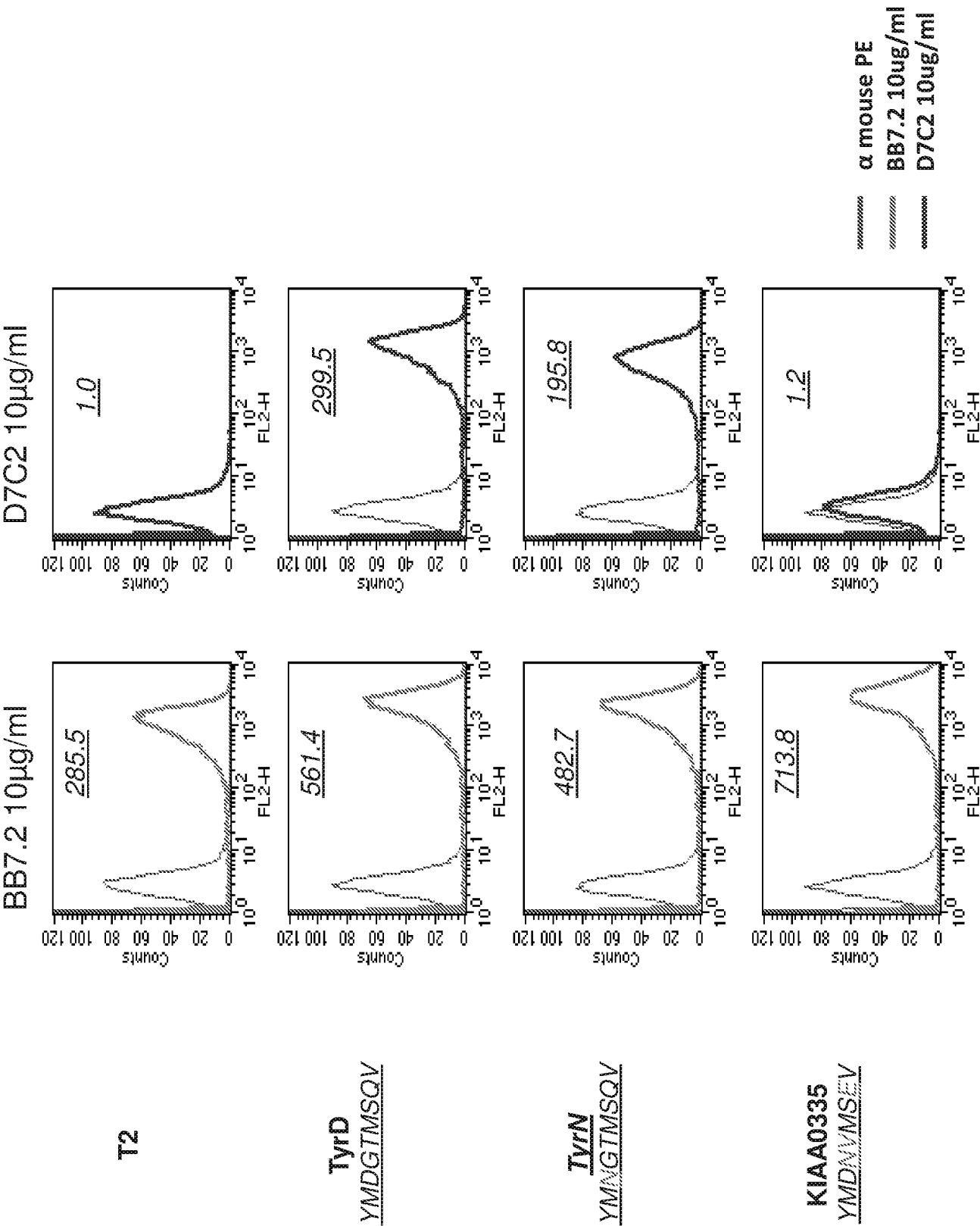
MFI values are relative to background. Value of `1` means no binding

Figure 24



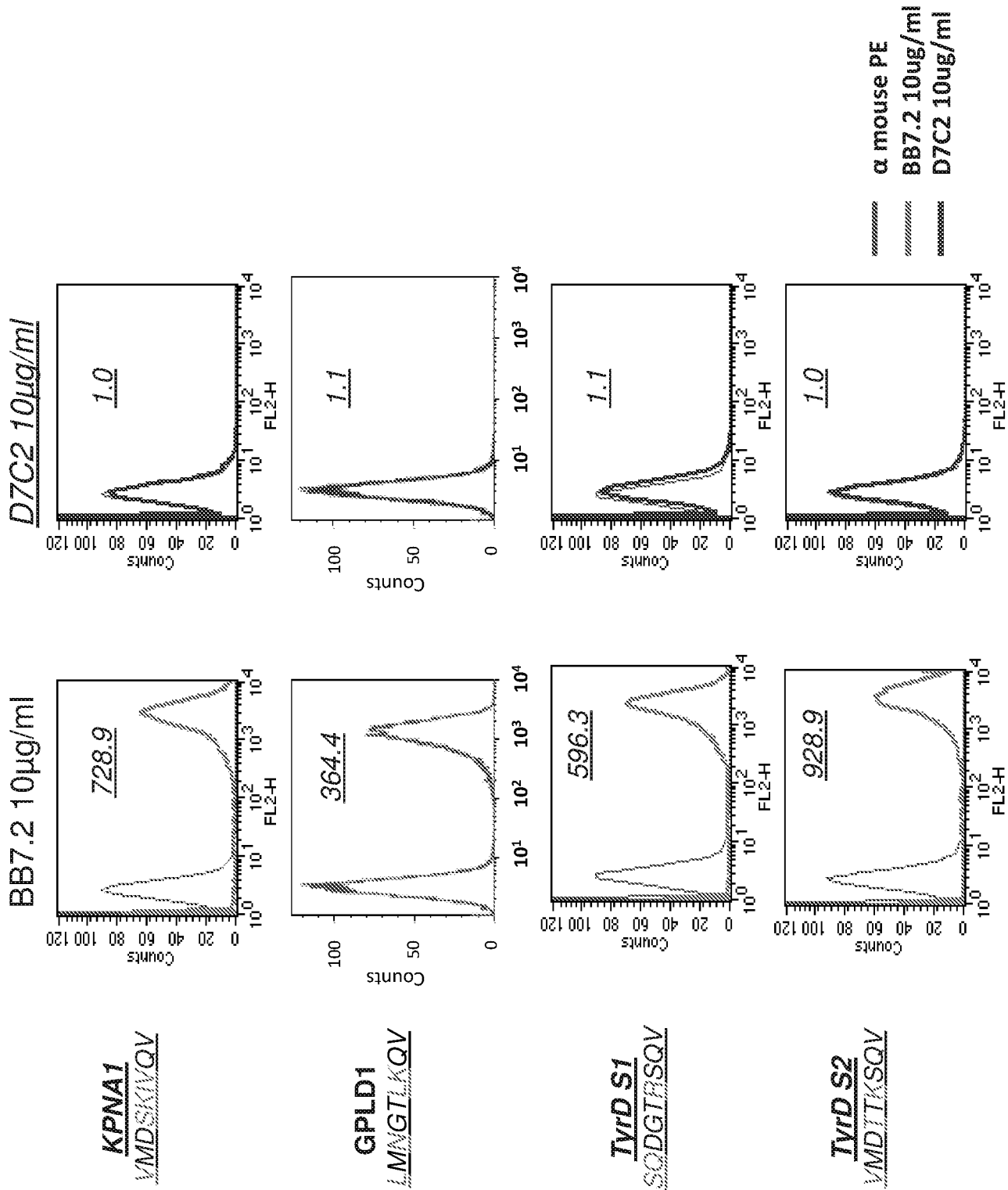
MFI values are relative to background. Value of '1' means no binding

Figure 24 - continued



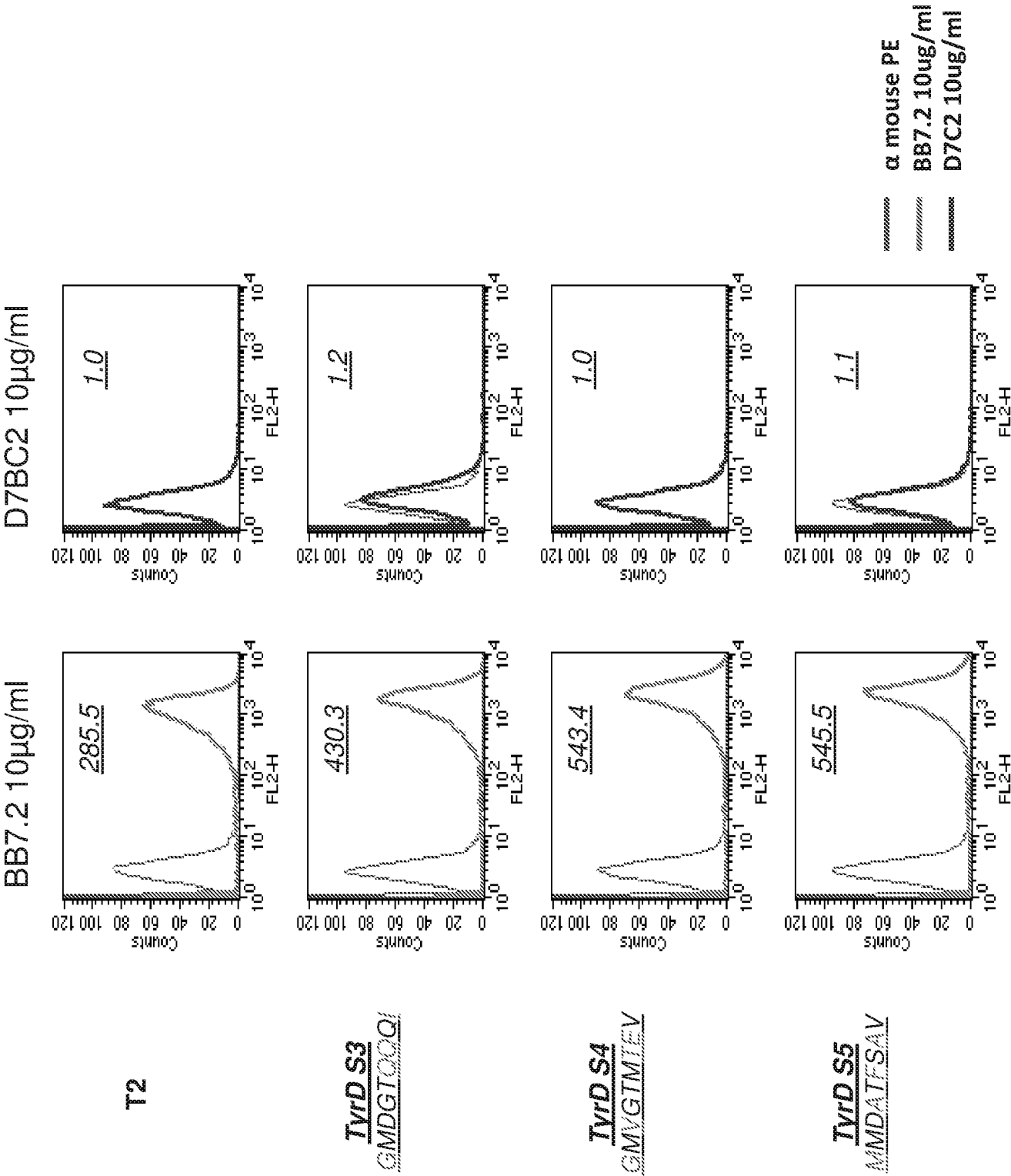
MFI values are relative to background. Value of `1` means no binding

Figure 25



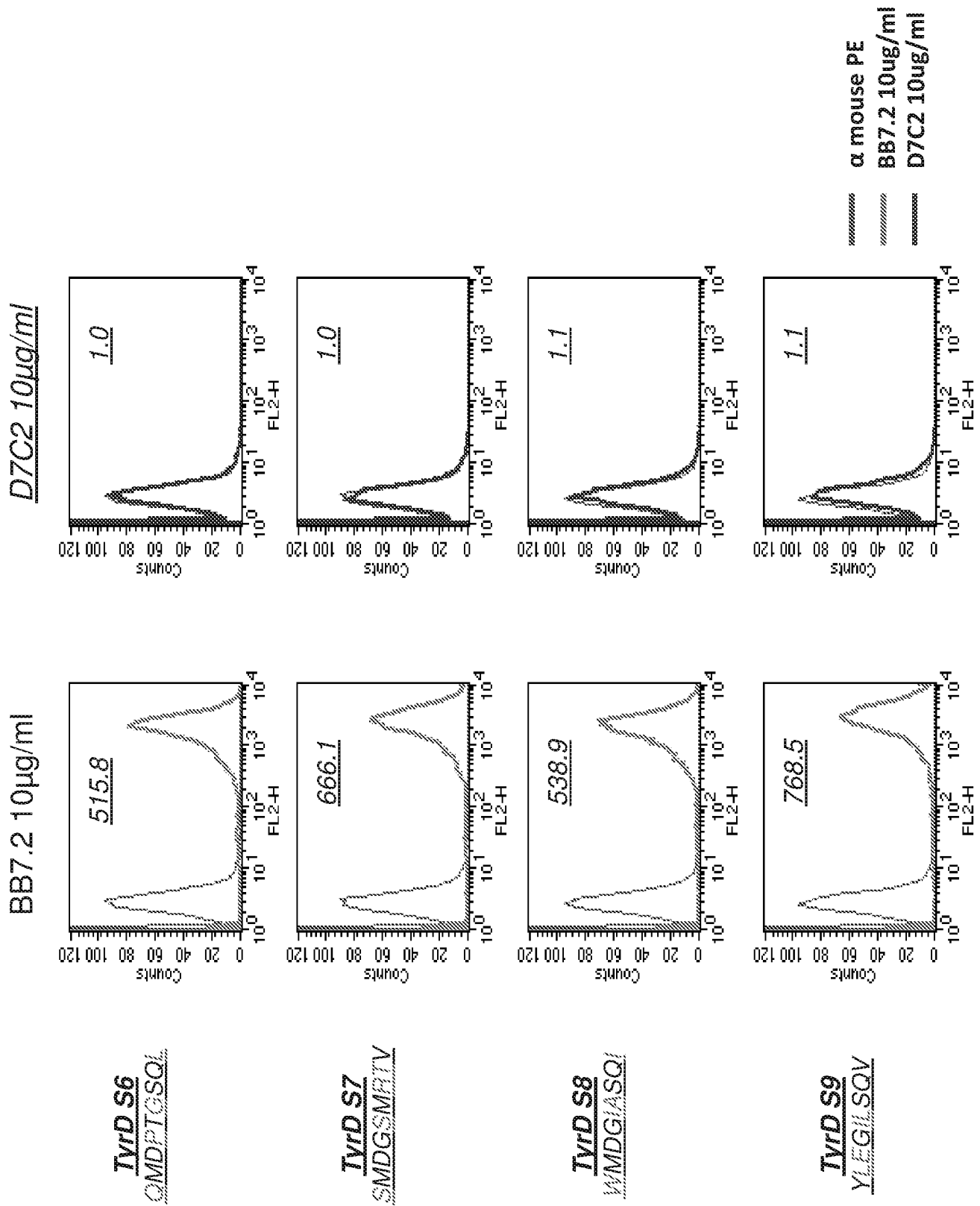
MFI values are relative to background. Value of `1` means no binding

Figure 25 - continued



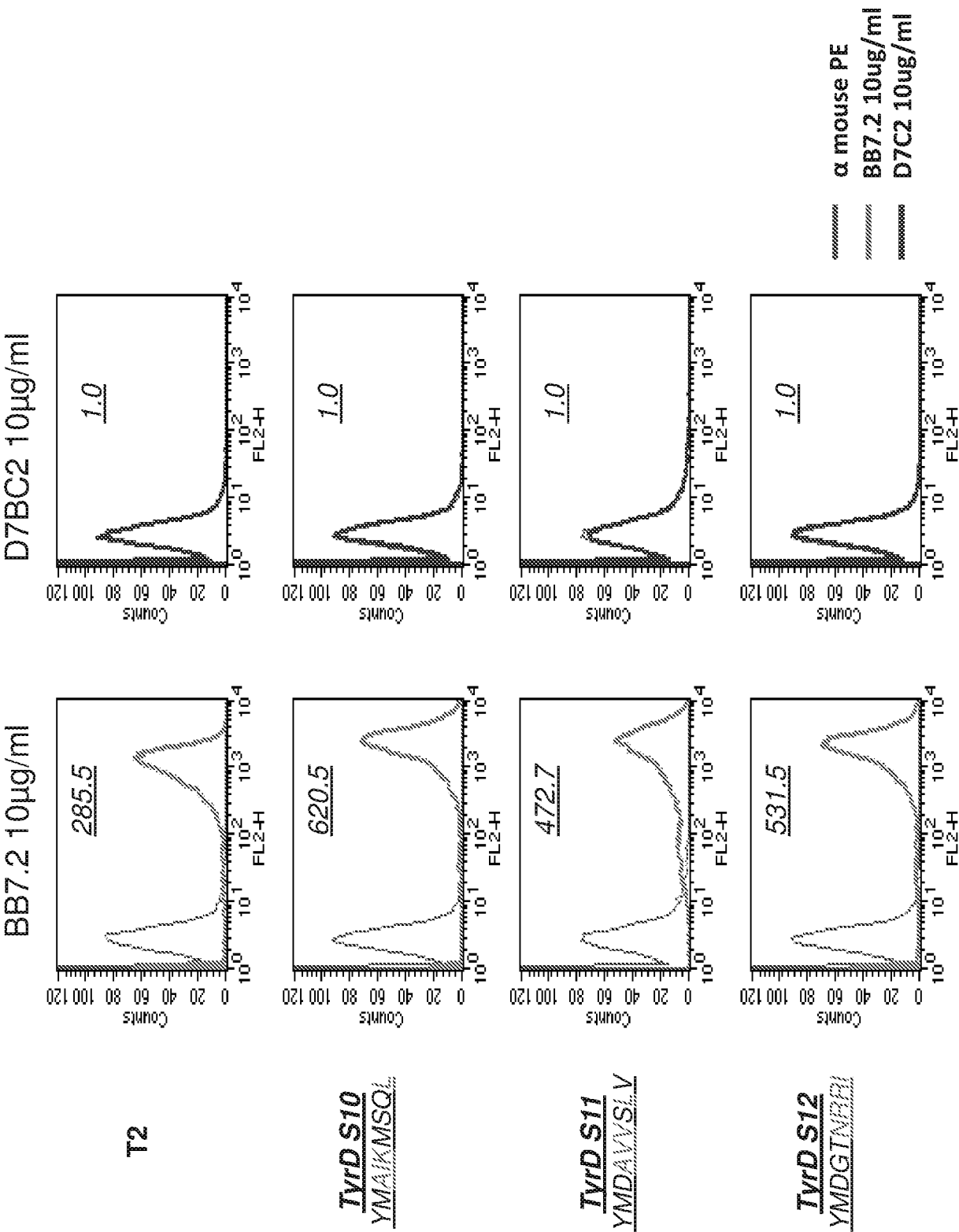
MFI values are relative to background. Value of 1 means no binding

Figure 26



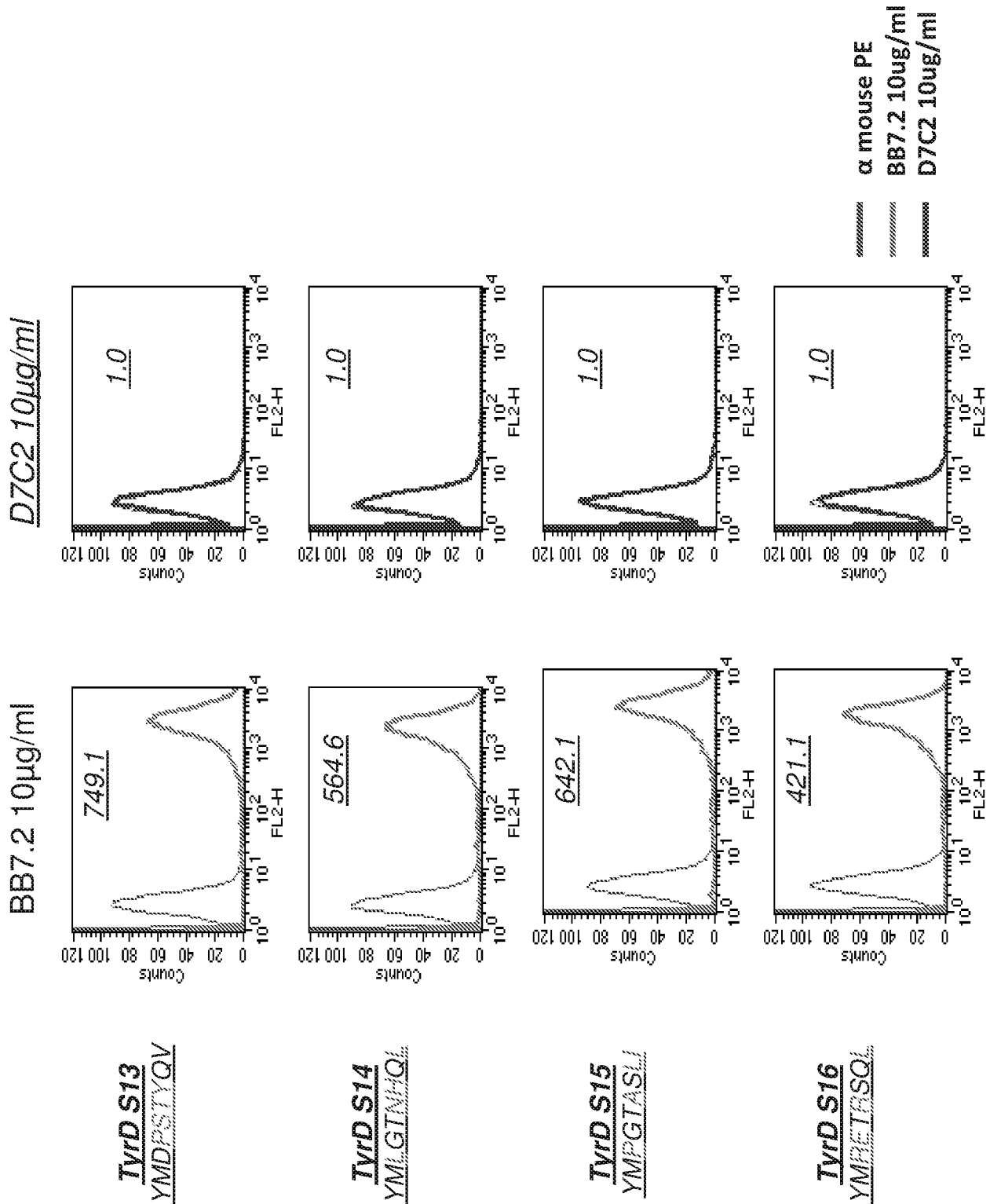
MFI values are relative to background. Value of 1 means no binding

Figure 26 - continued



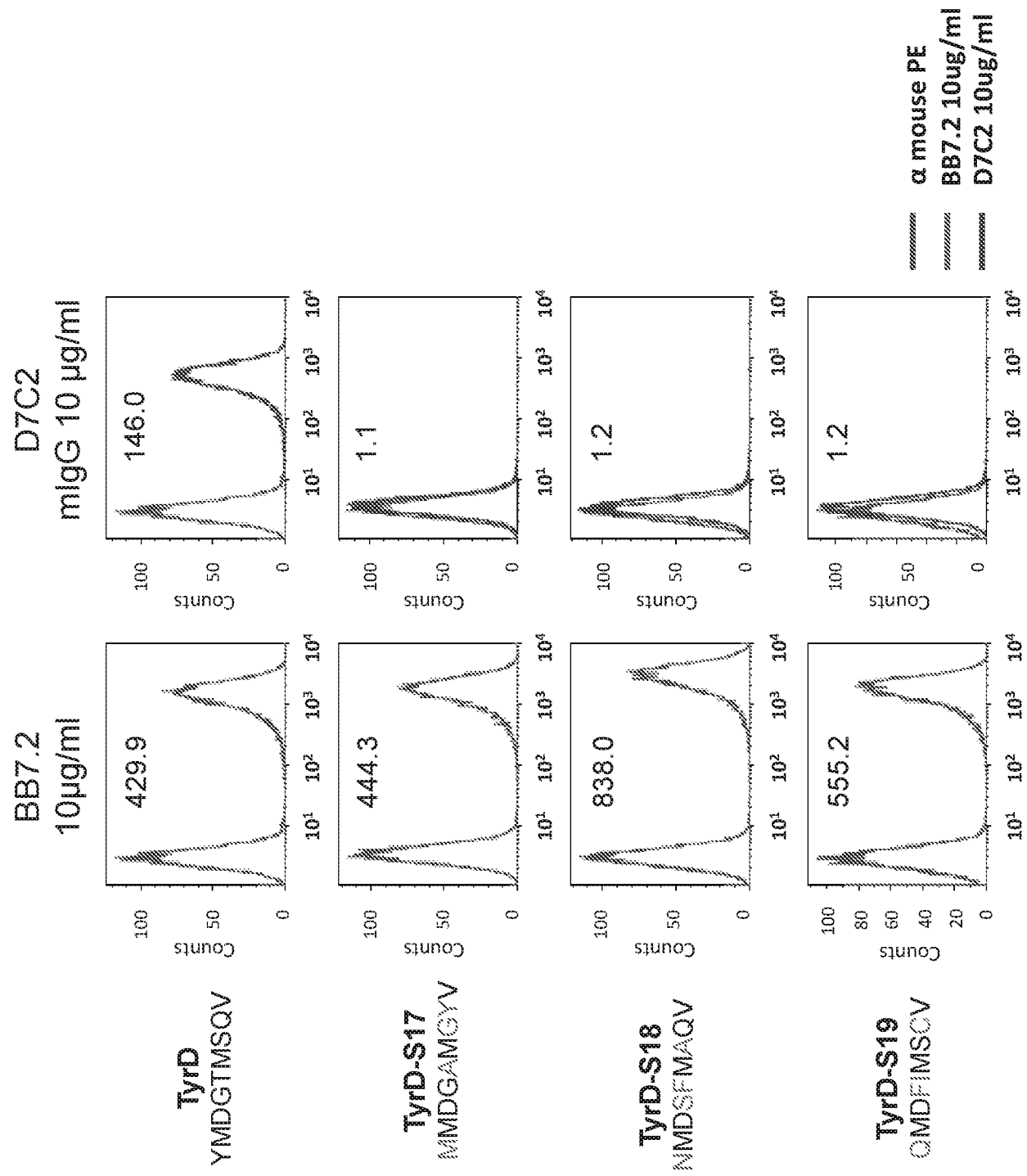
MFI values are relative to background. Value of `1` means no binding

Figure 27



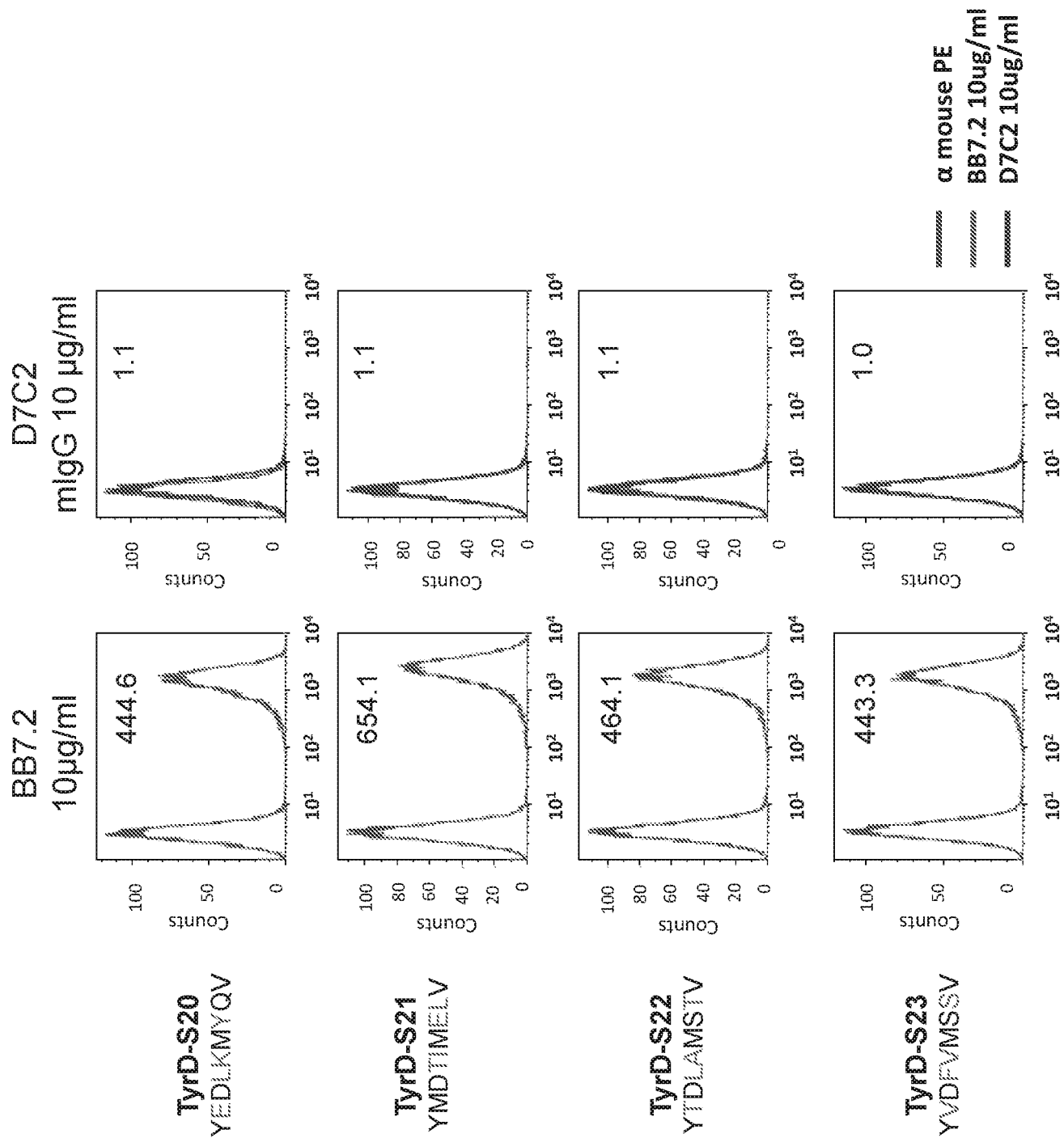
MFI values are relative to background. Value of `1` means no binding

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

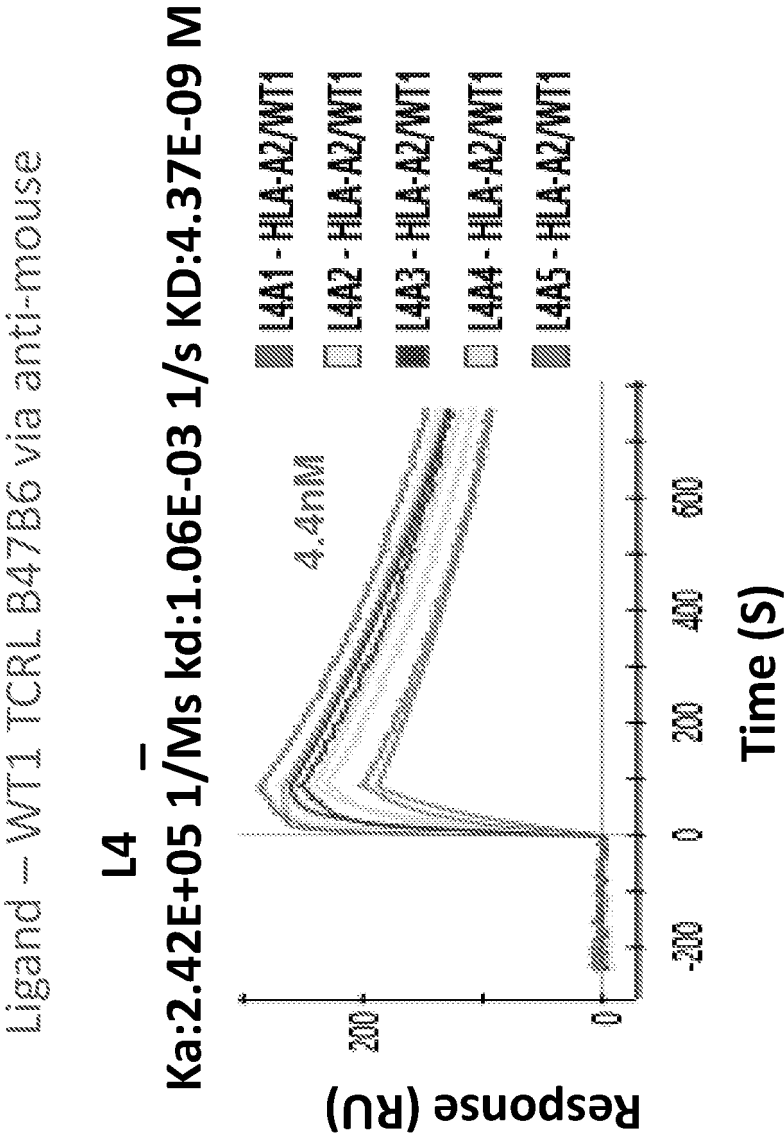
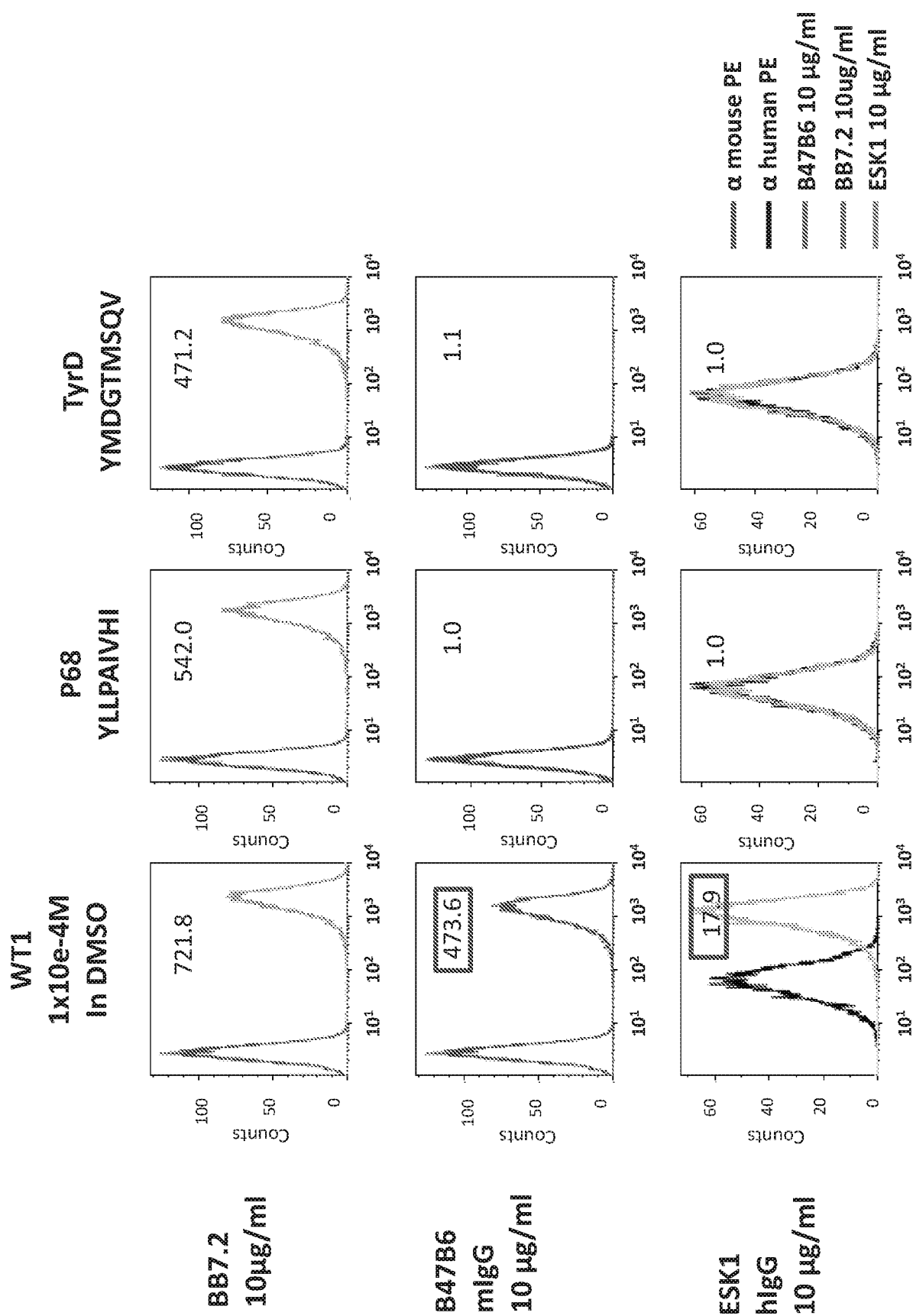


Figure 29



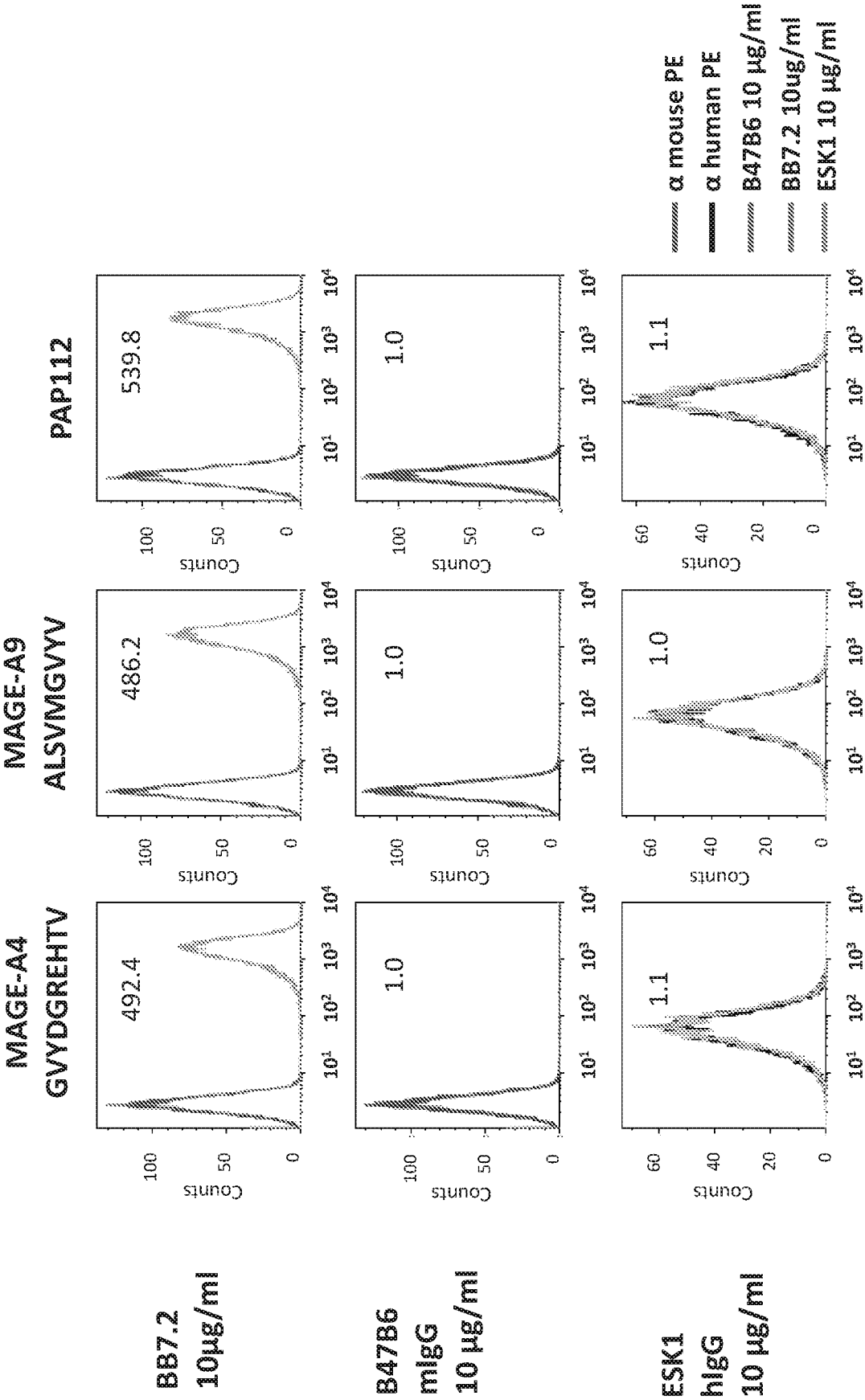


Figure 31 - continued

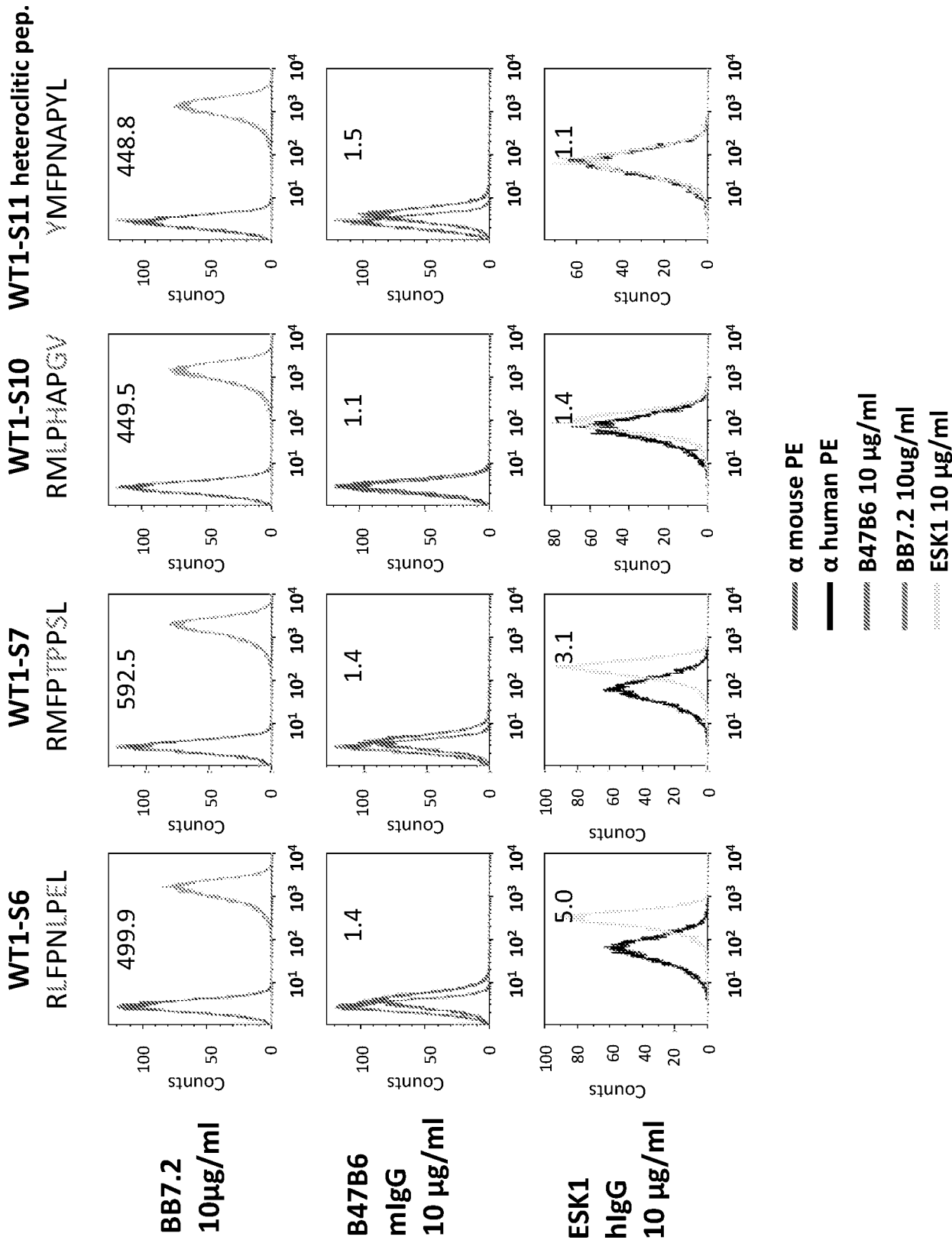


Figure 32

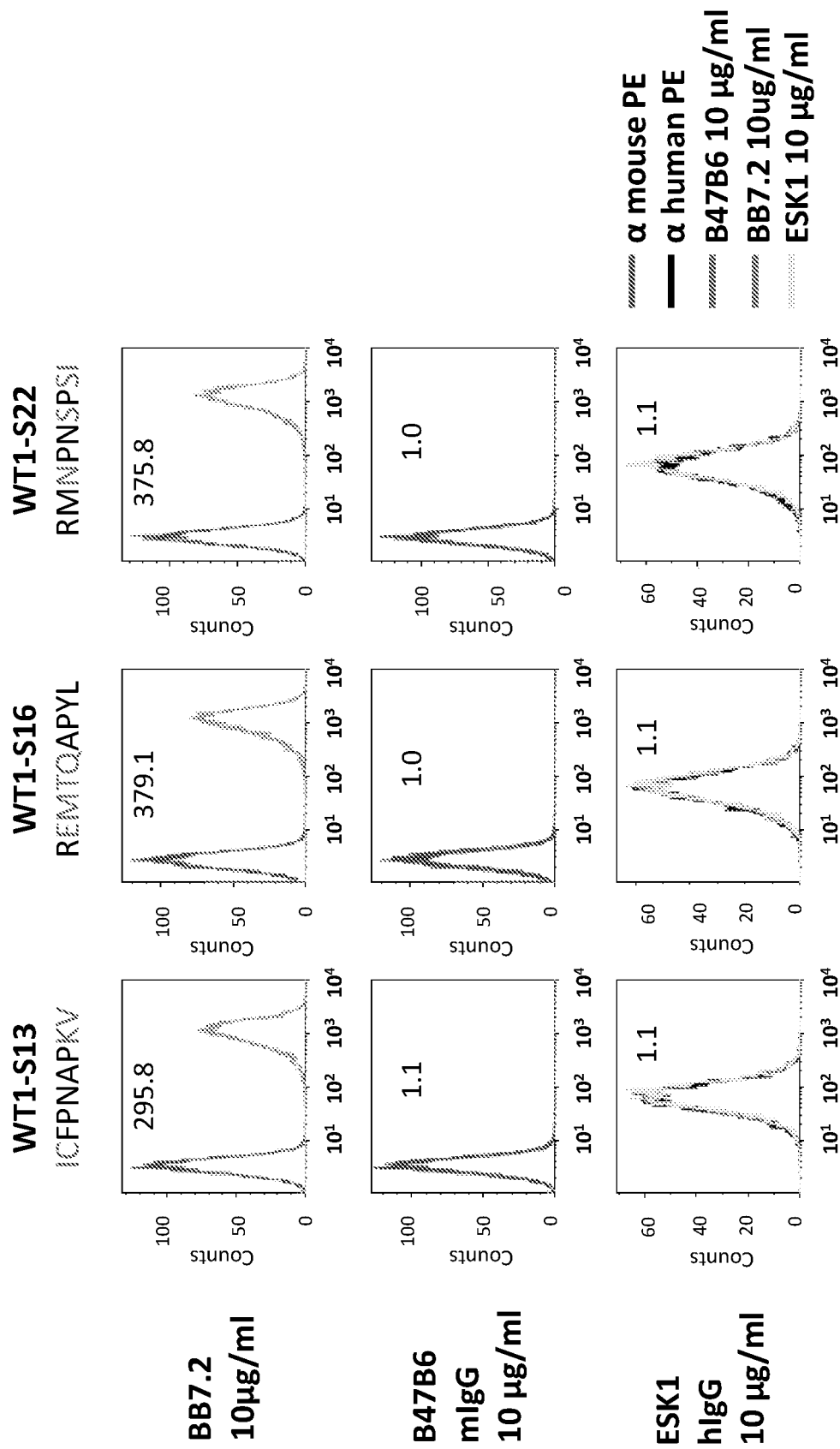
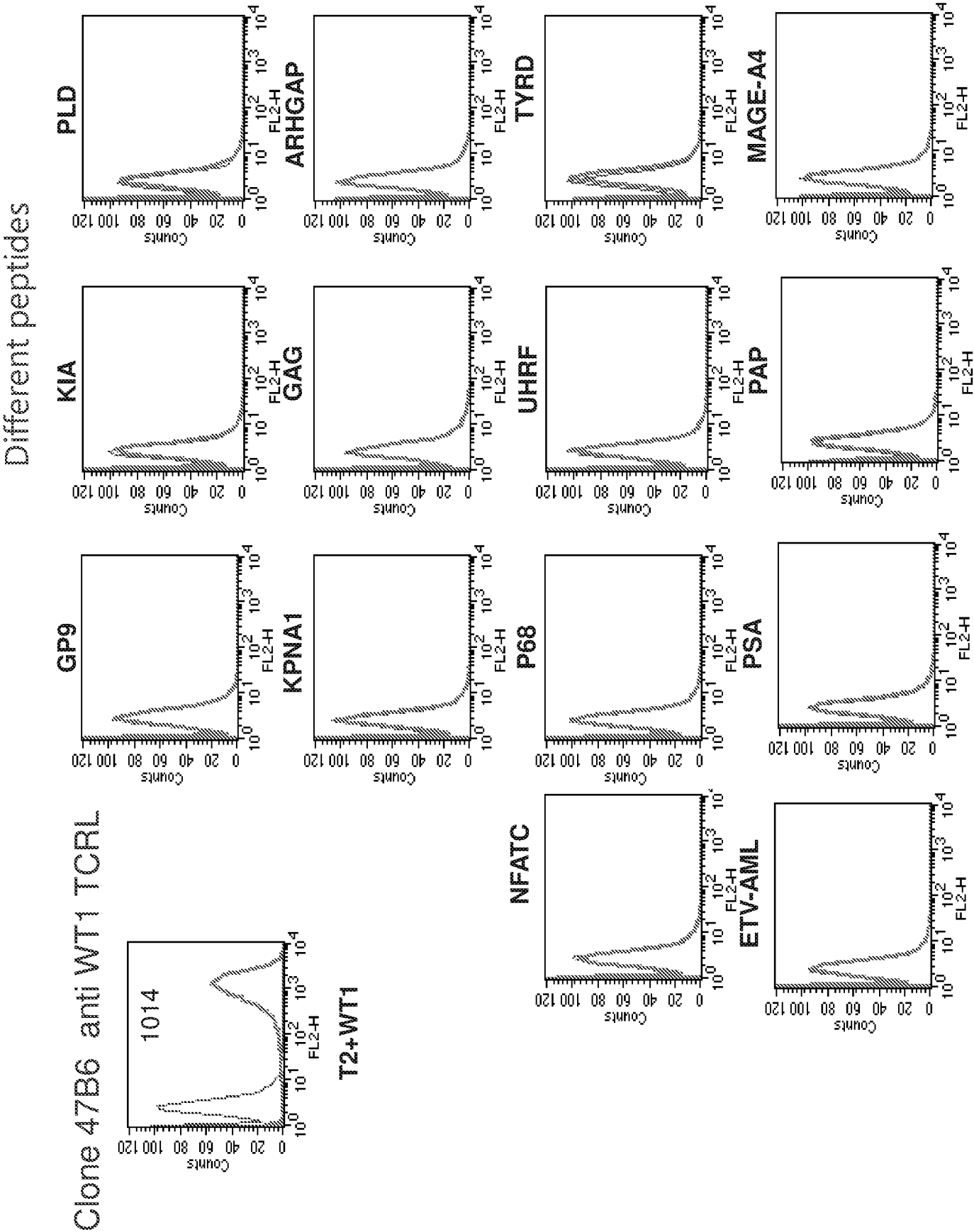
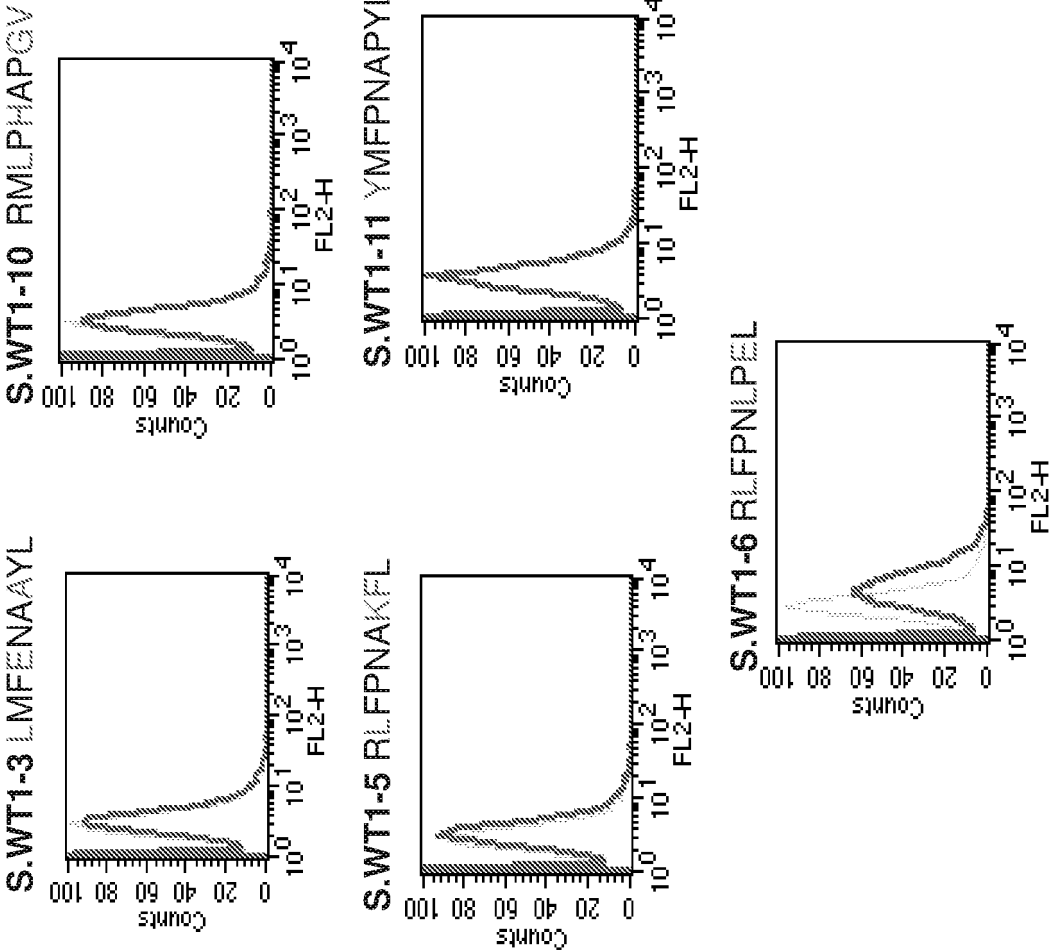


Figure 32 - continued



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 33 - continued

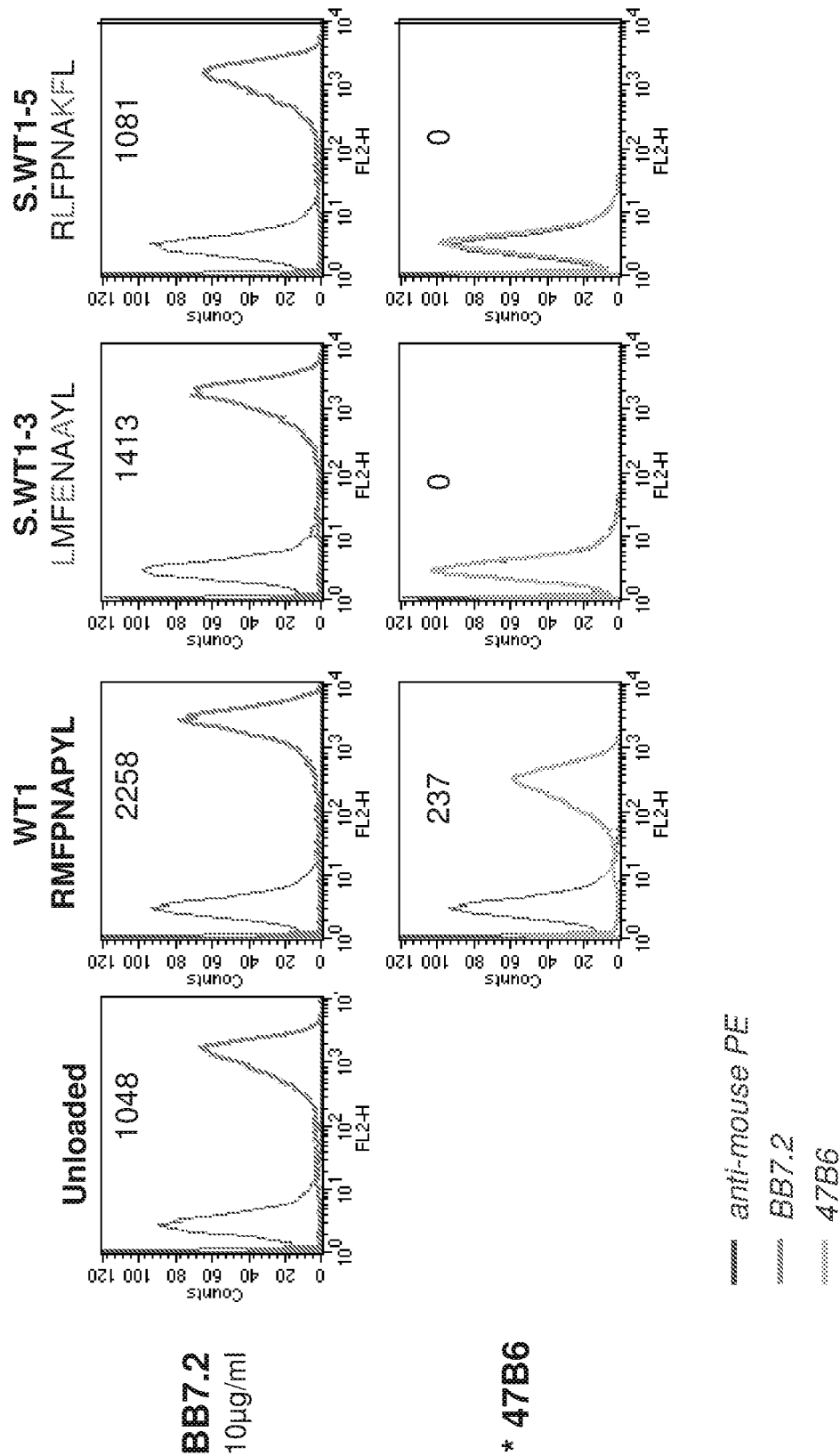


Figure 34

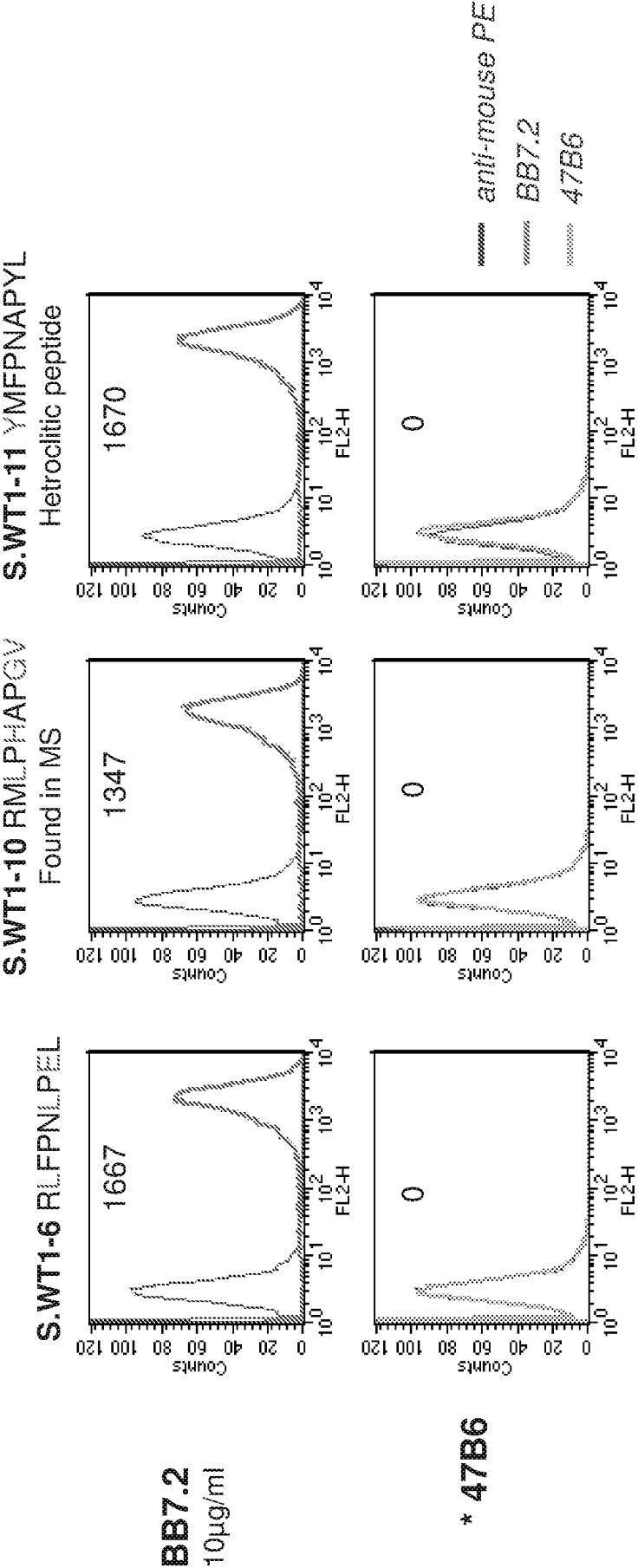
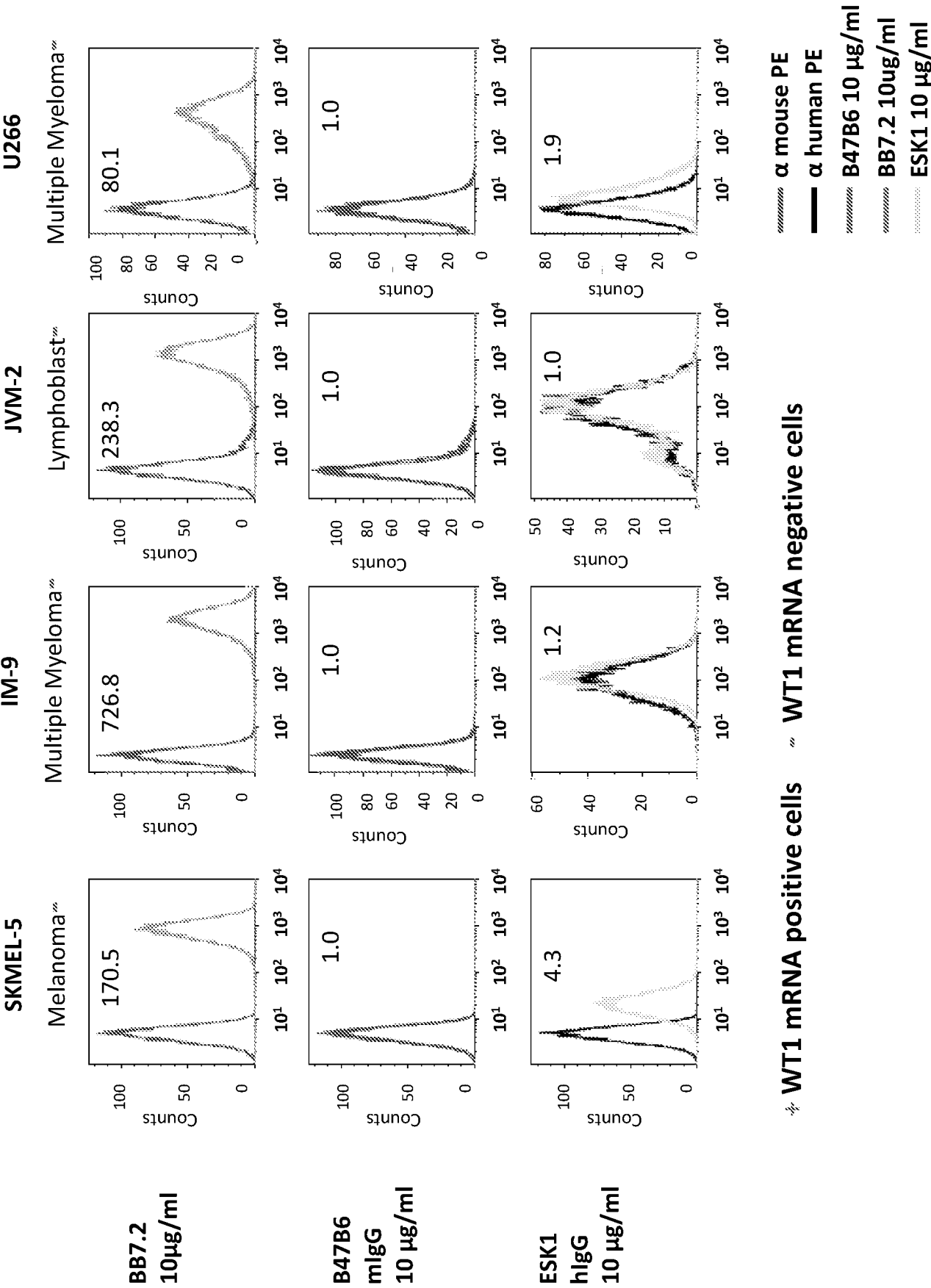


Figure 34 - continued

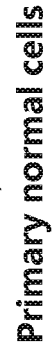


Figure 35





... ..



Cancer cell lines

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

Figure 36

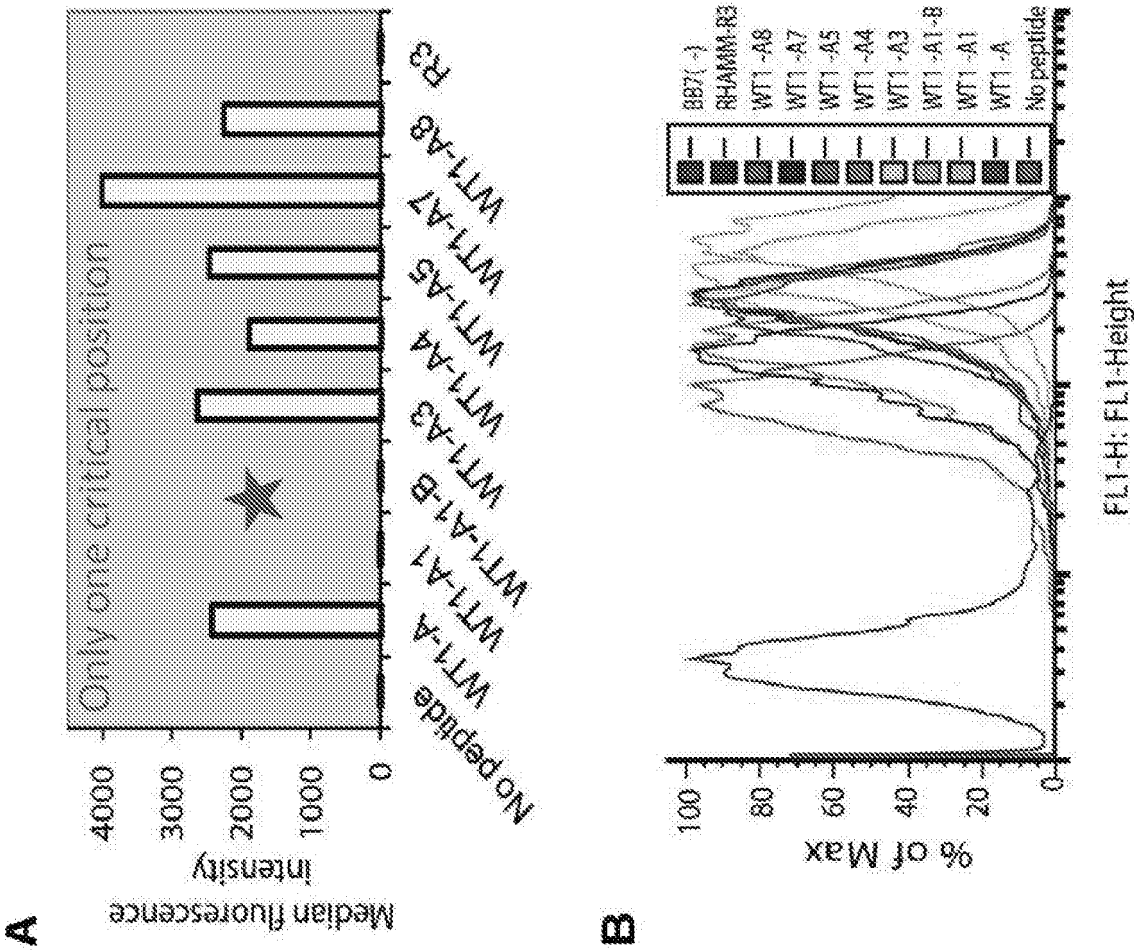


Figure S1. Epitope specificity. The RMF peptide sequence was substituted with alanine at positions 1, 3, 4, 5, 7, or 8, or with tyrosine (WT1-A1B) at position 1 (sequences in table S1). (A) T2 cells were pulsed with indicated peptides at 50 µg/ml and the binding of ESK1 was measured by flow cytometry. (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.

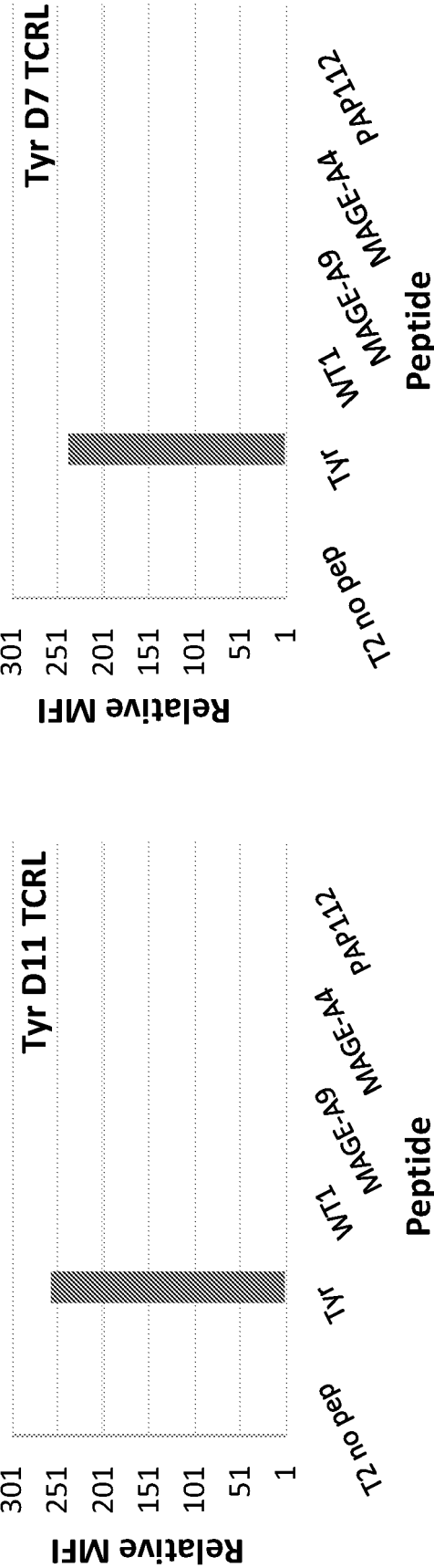
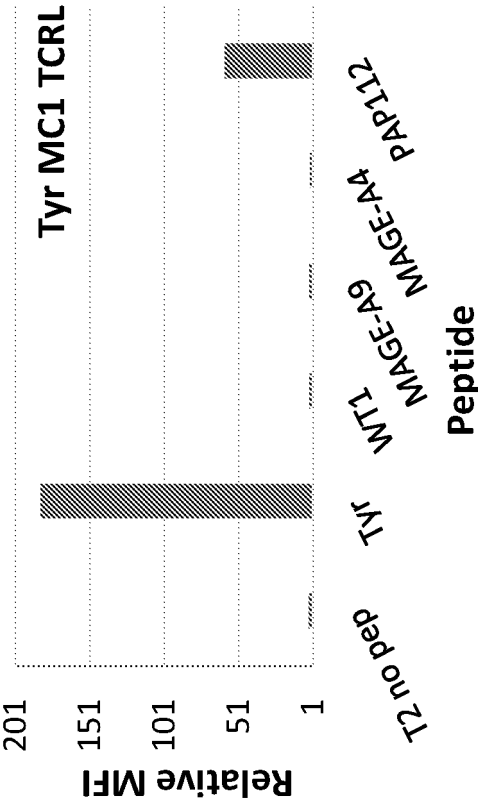
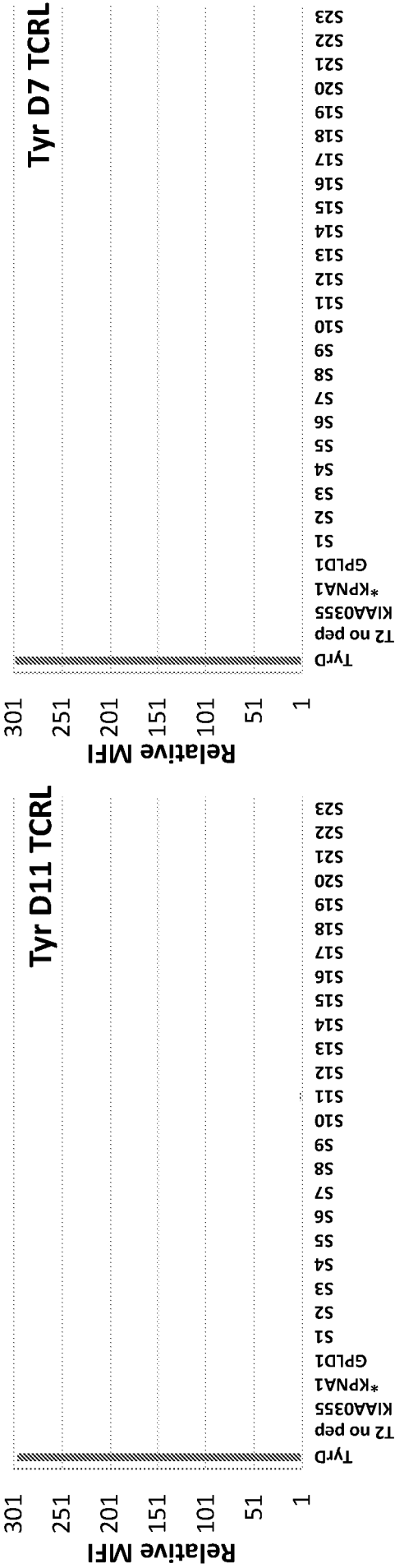
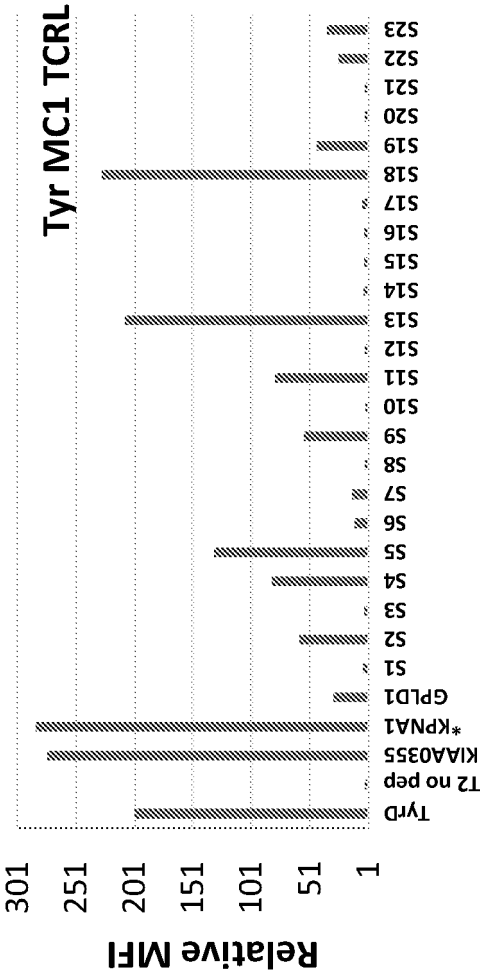


Figure 38



* Found by MS in normal tissues

Figure 39

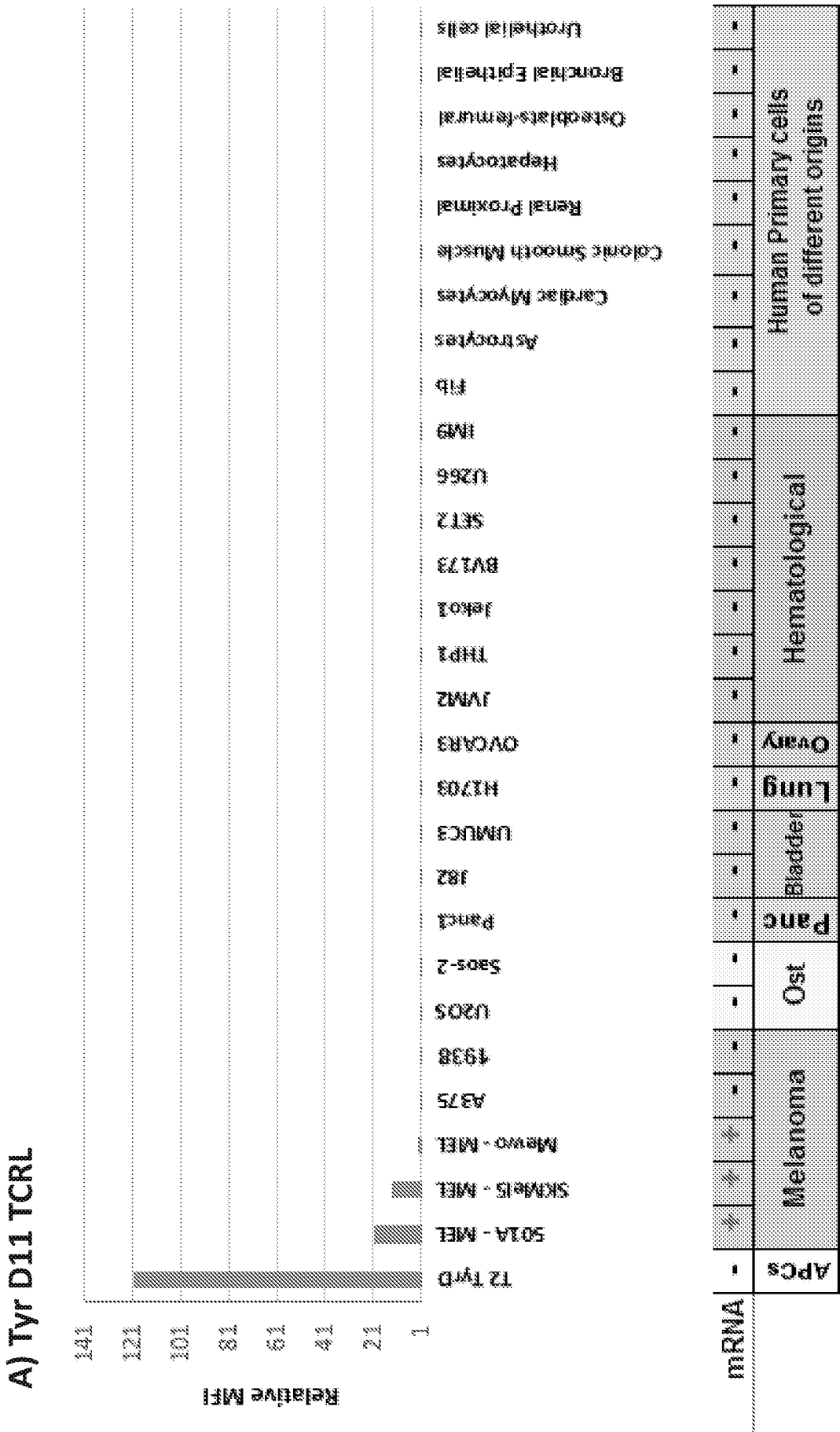


Figure 40A

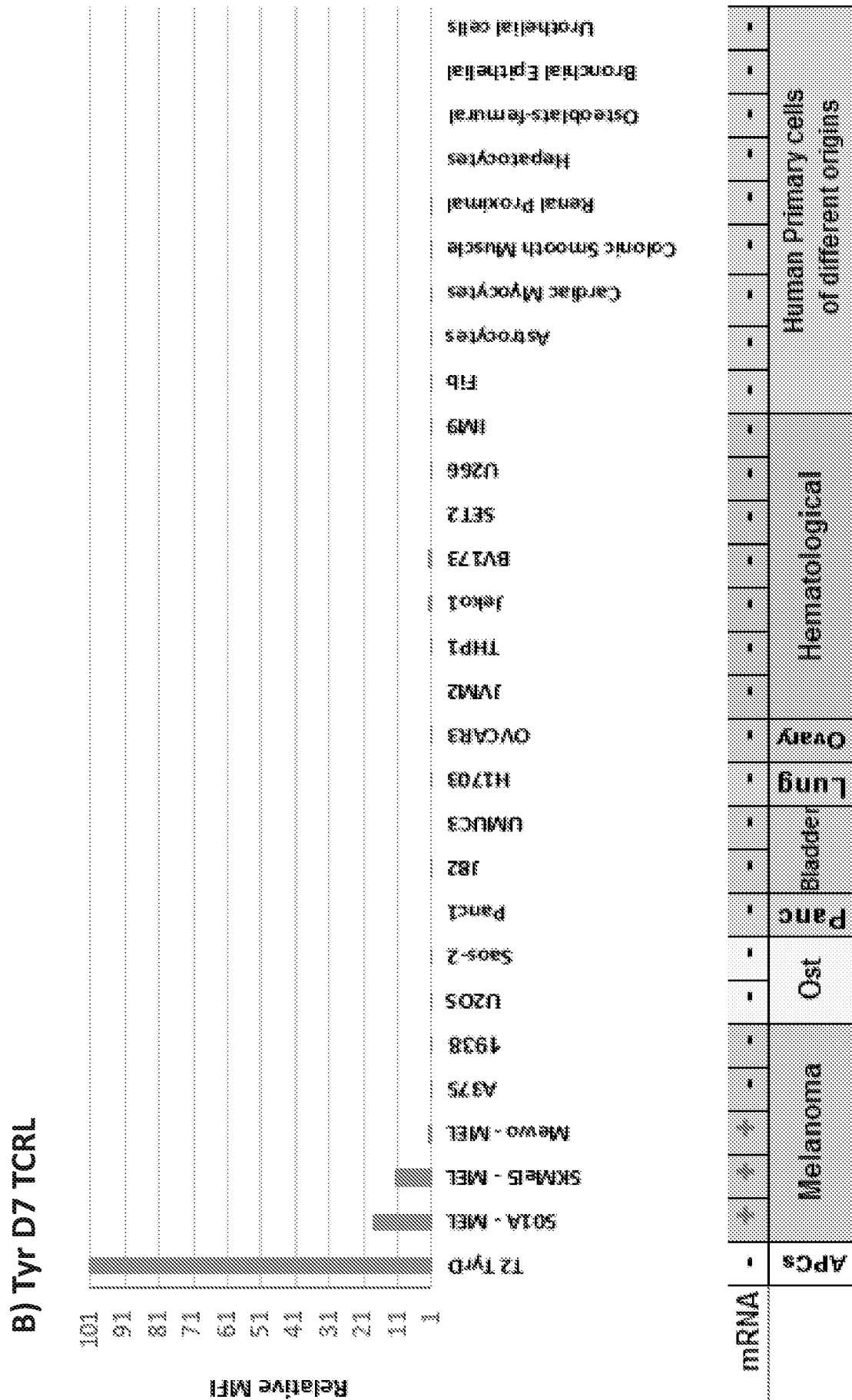


Figure 40B

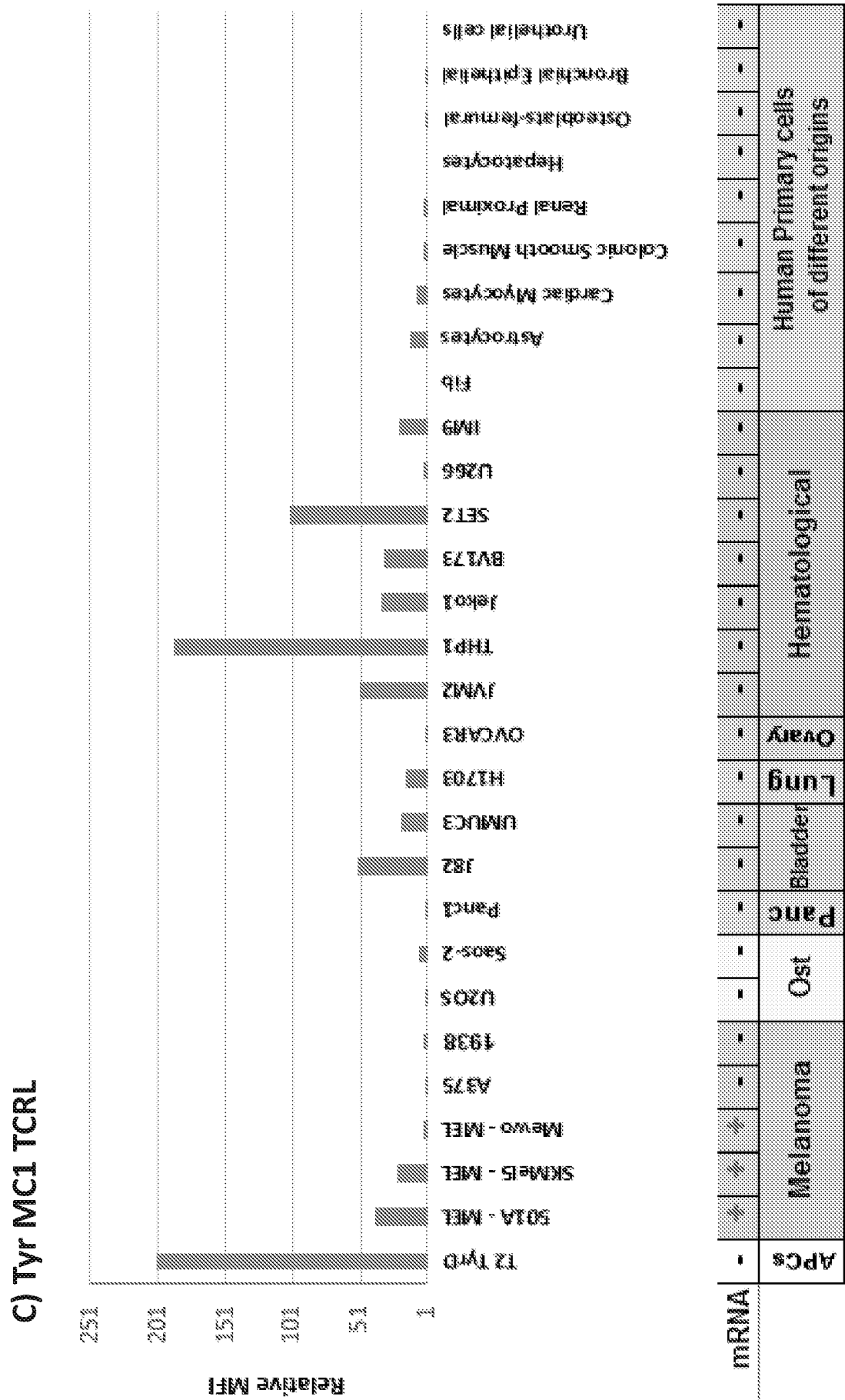
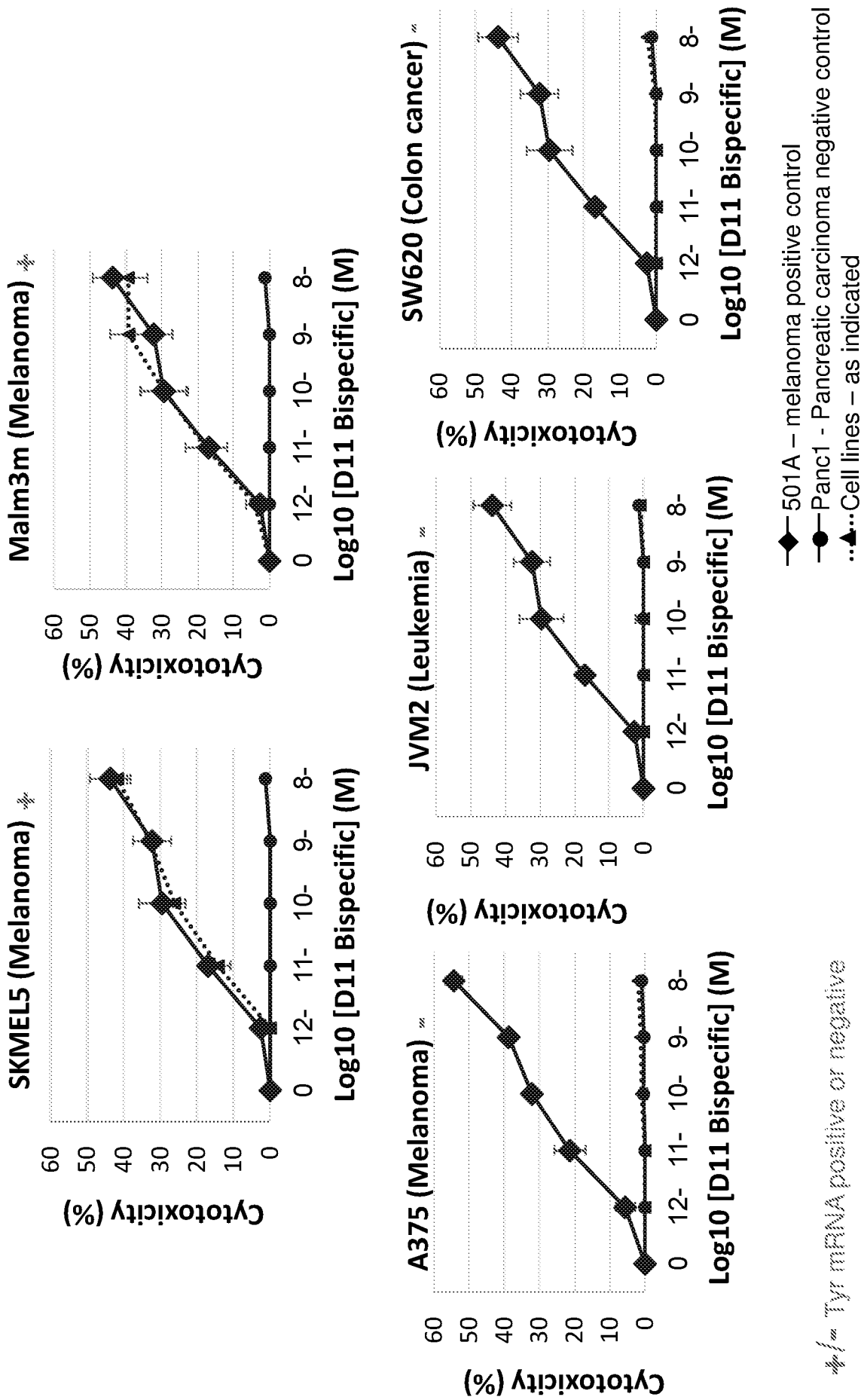


Figure 40C

Tyr D11 BS TCRL - killing assay on cell lines



◆ 501A - melanoma positive control
● Panc1 - Pancreatic carcinoma negative control
▲ Cell lines - as indicated

Figure 41

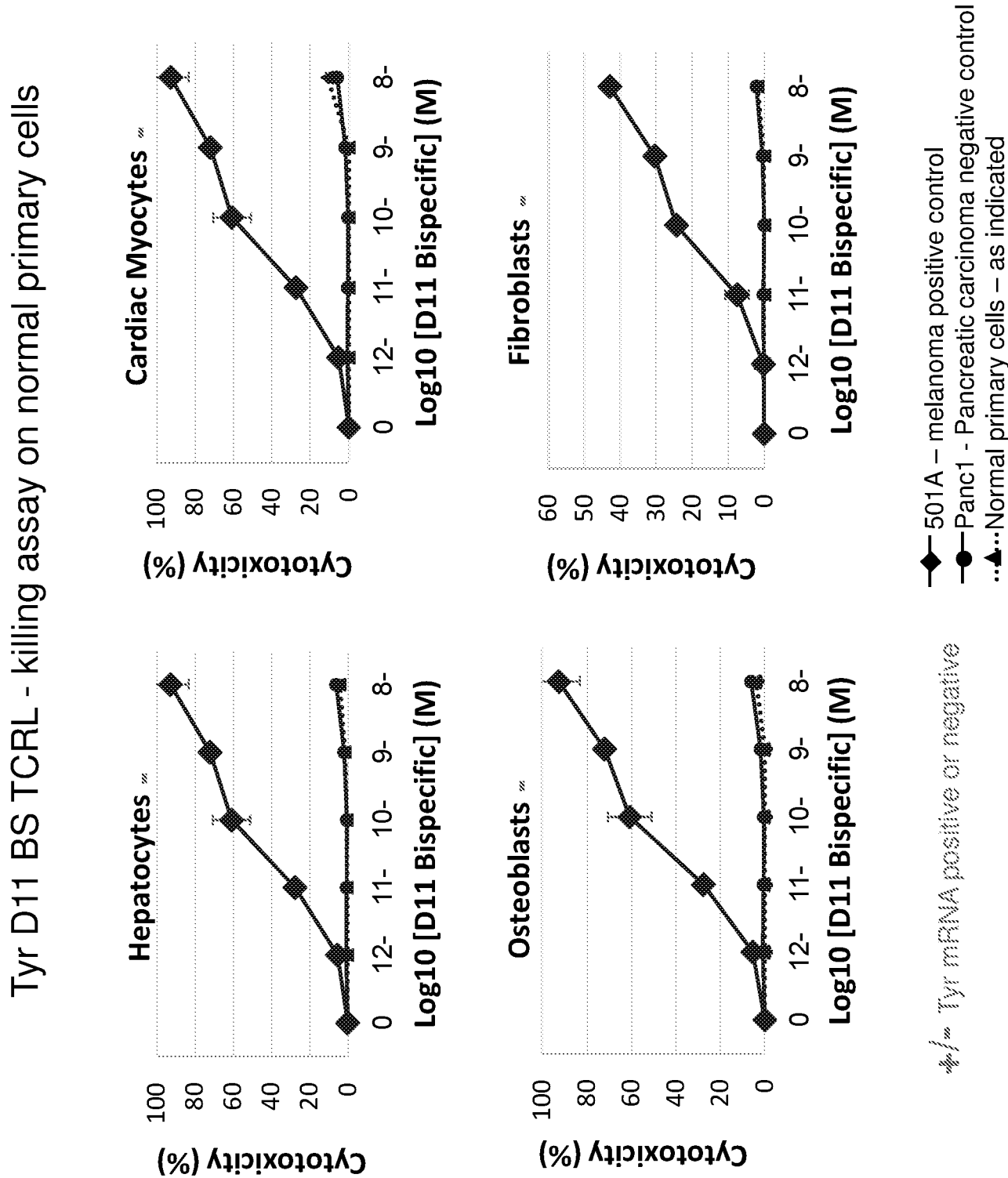


Figure 42

Tyr D7 BS TCRL - killing assay on cell lines

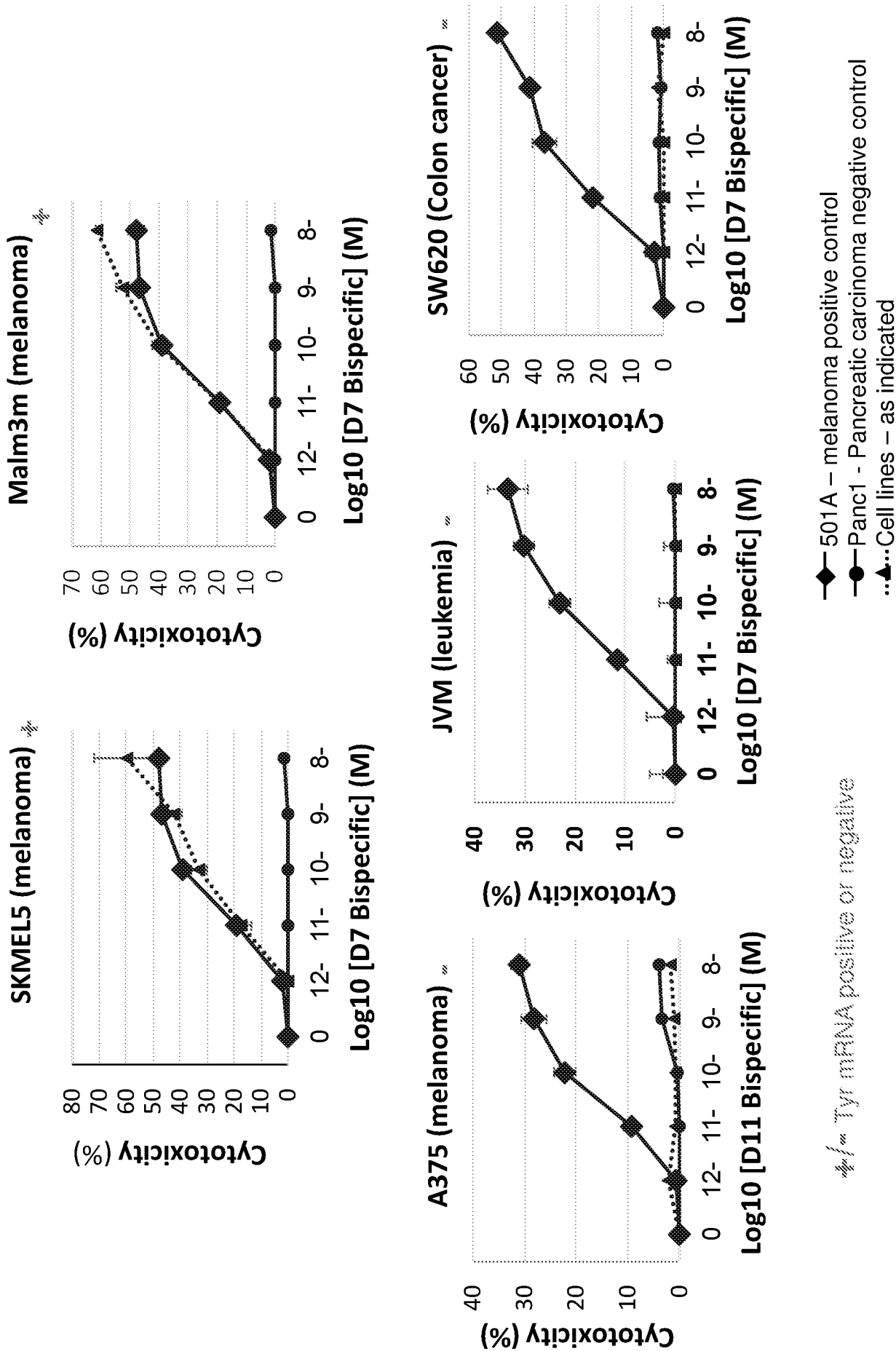


Figure 43

Tyr D7 BS TCRL - killing assay on normal primary cells

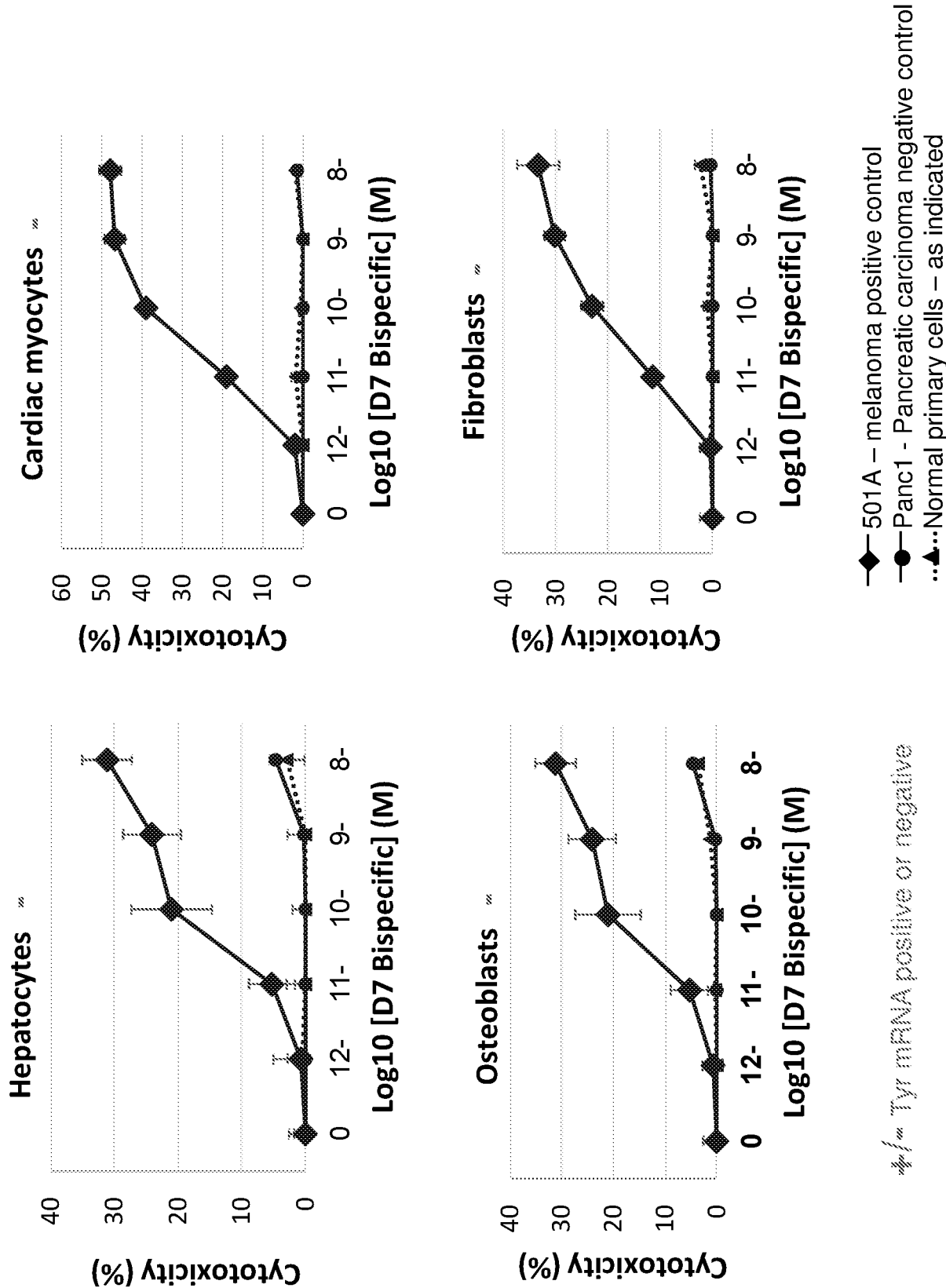


Figure 44

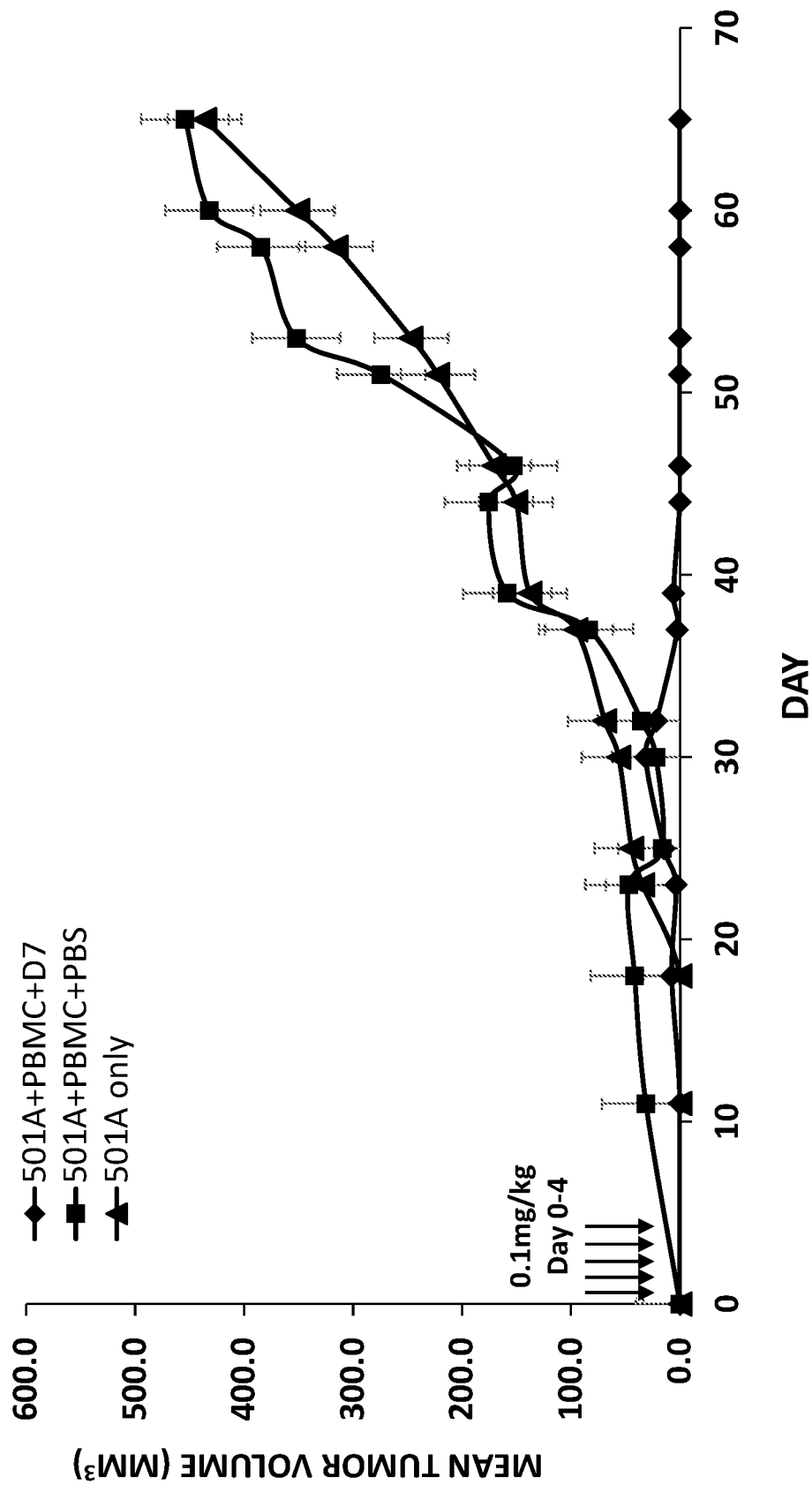


Figure 45

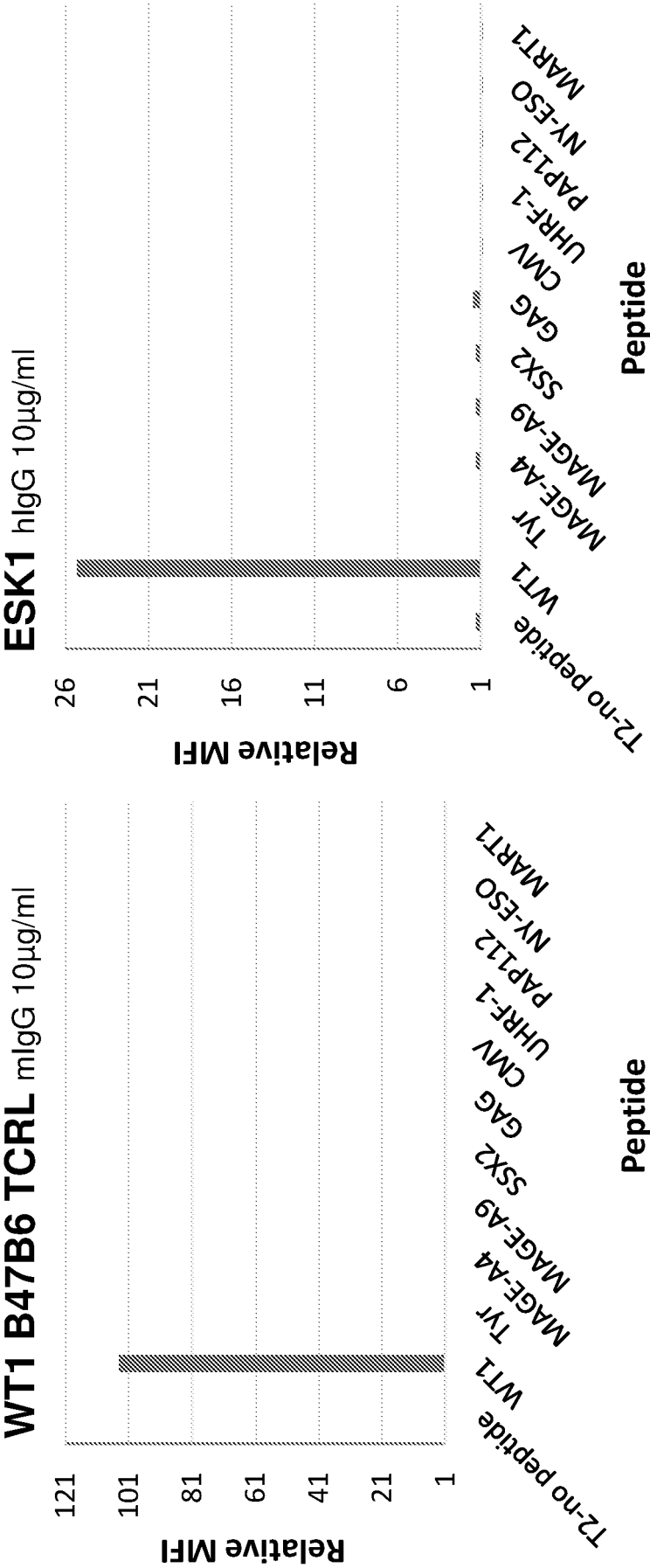
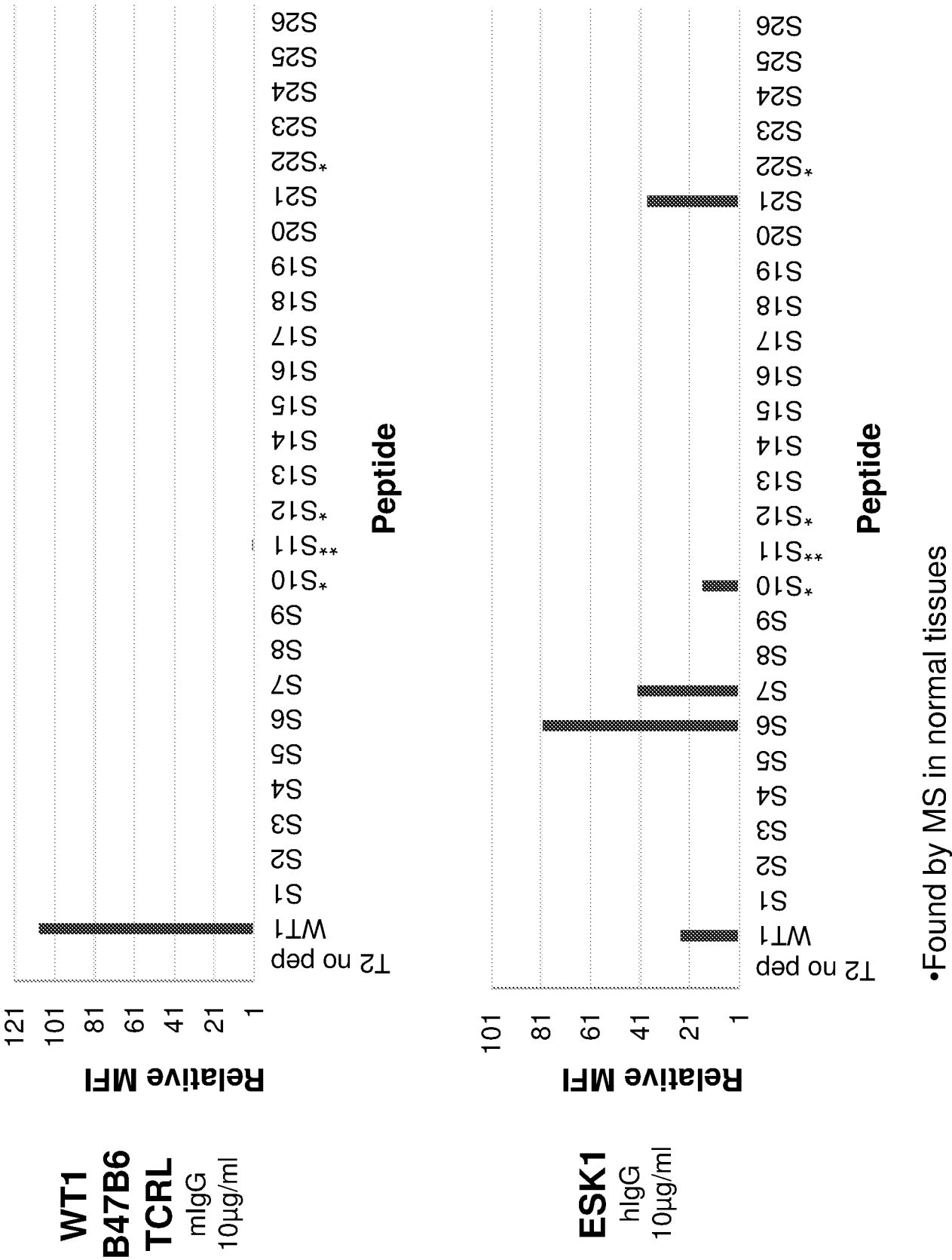
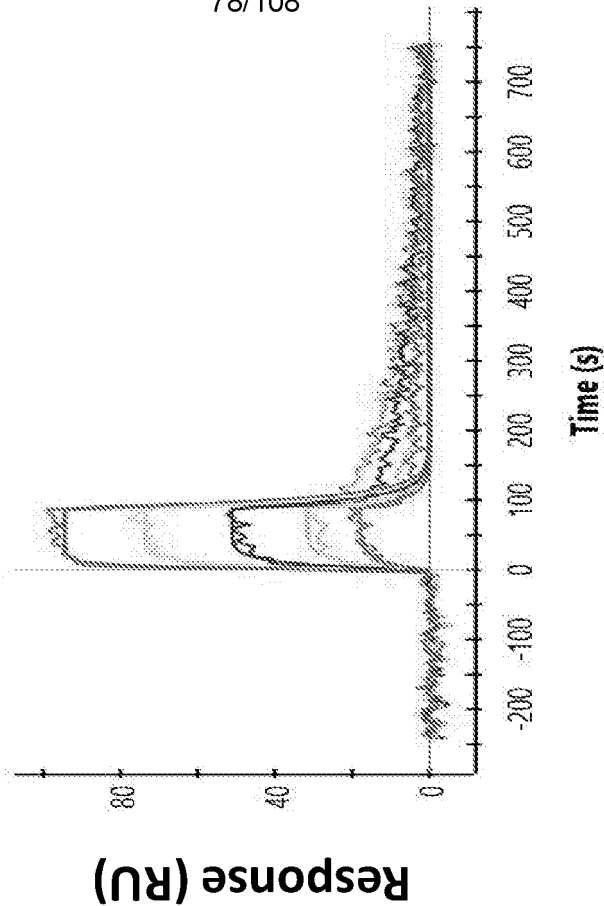


Figure 46



ESK1 – 200nM



B47B6 – 5nM

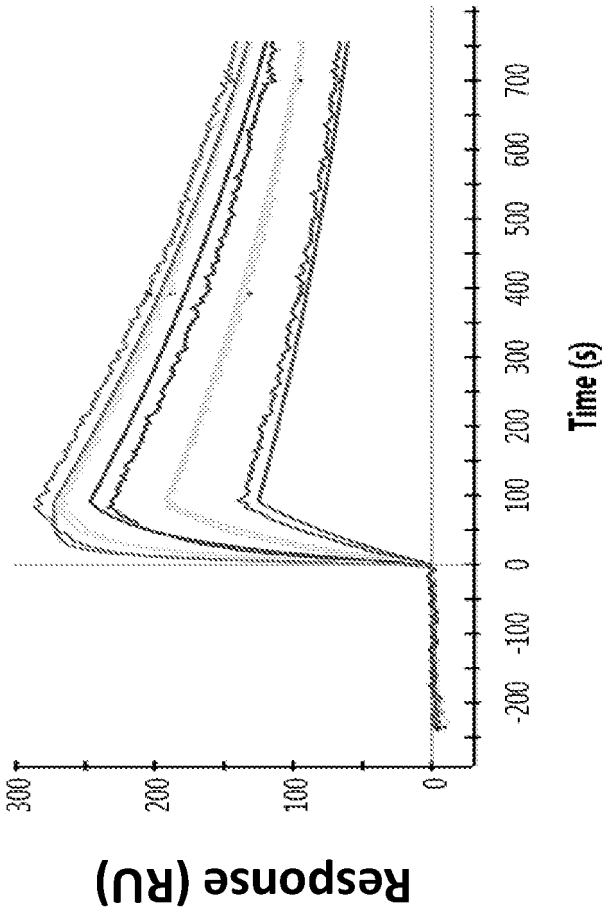


Figure 48

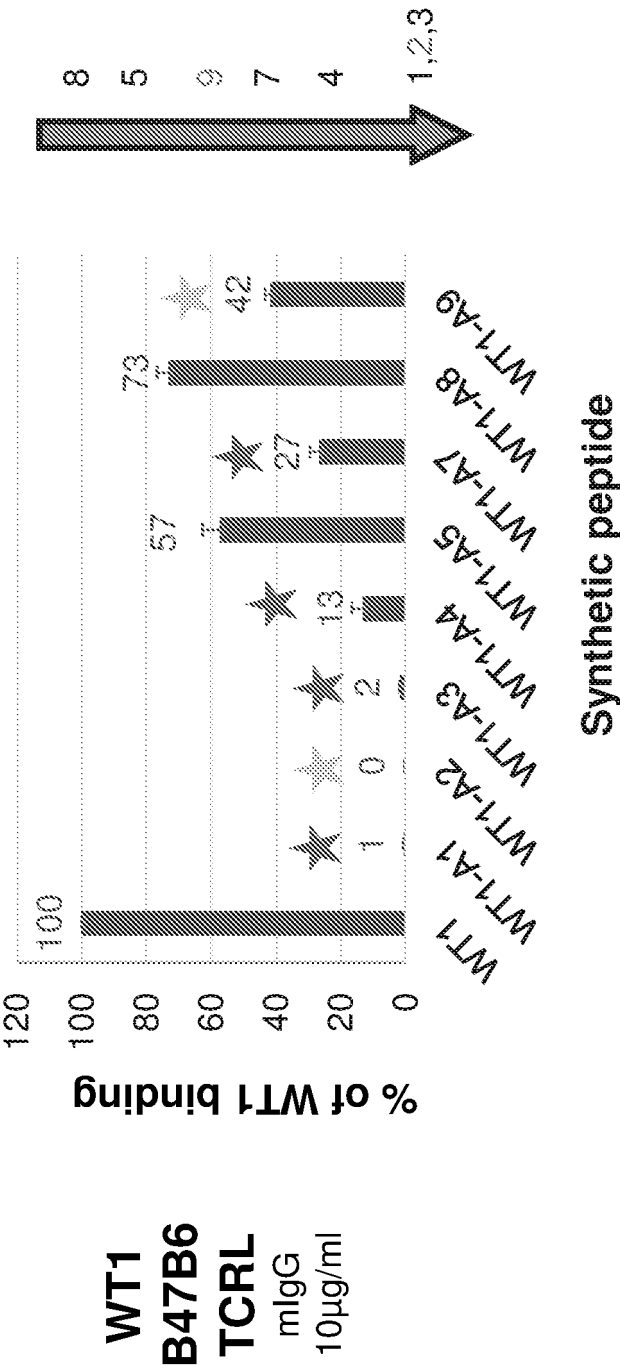
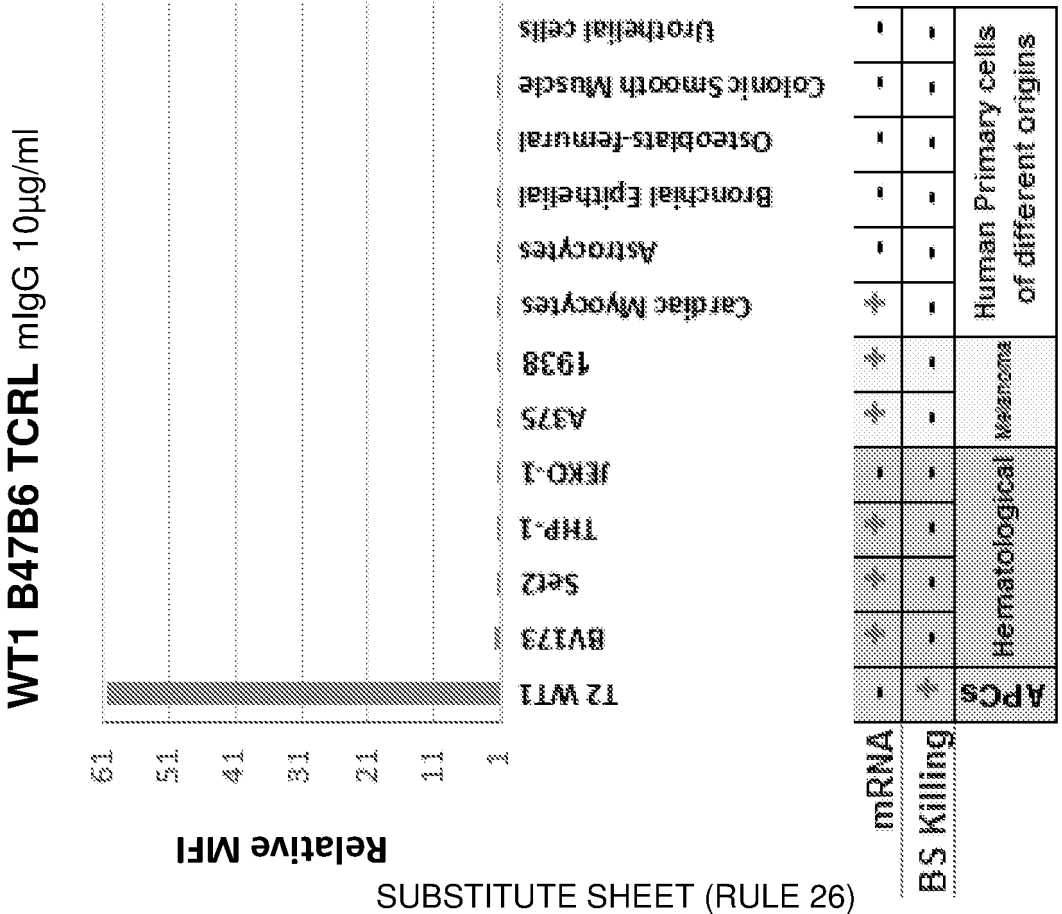
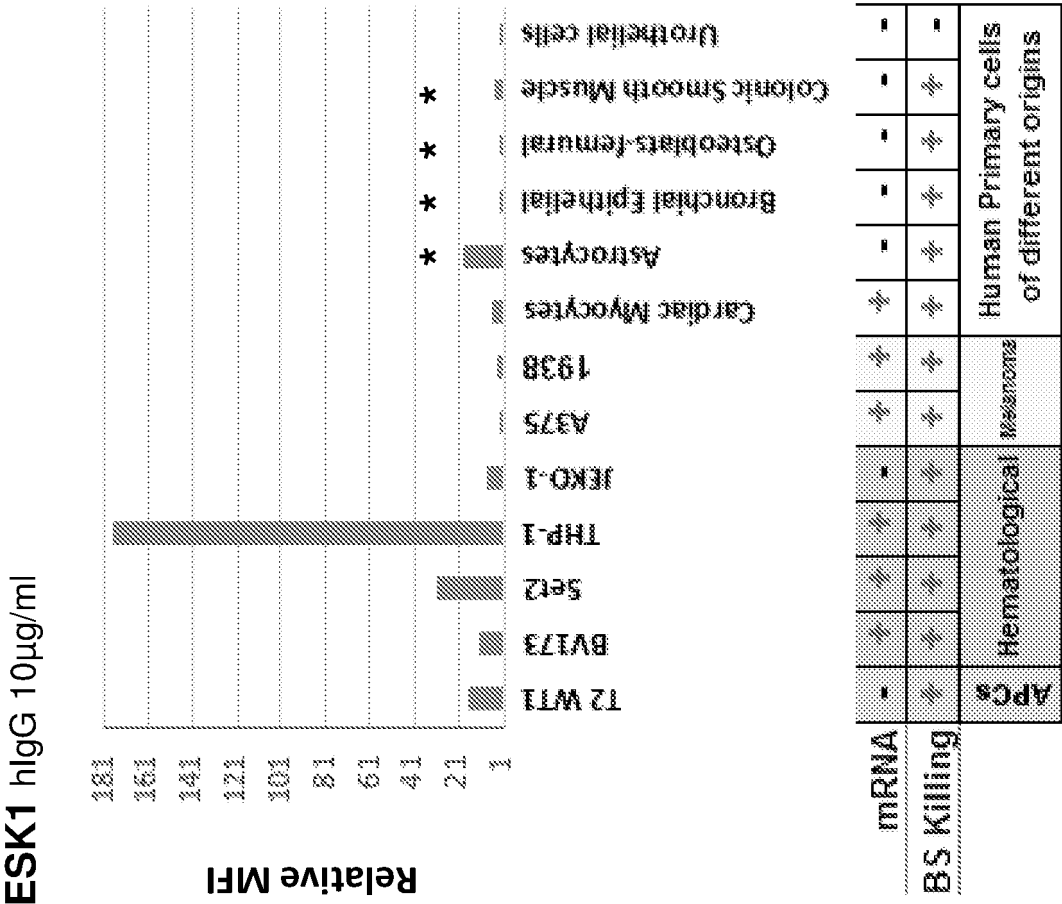


Figure 49



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

Figure 50

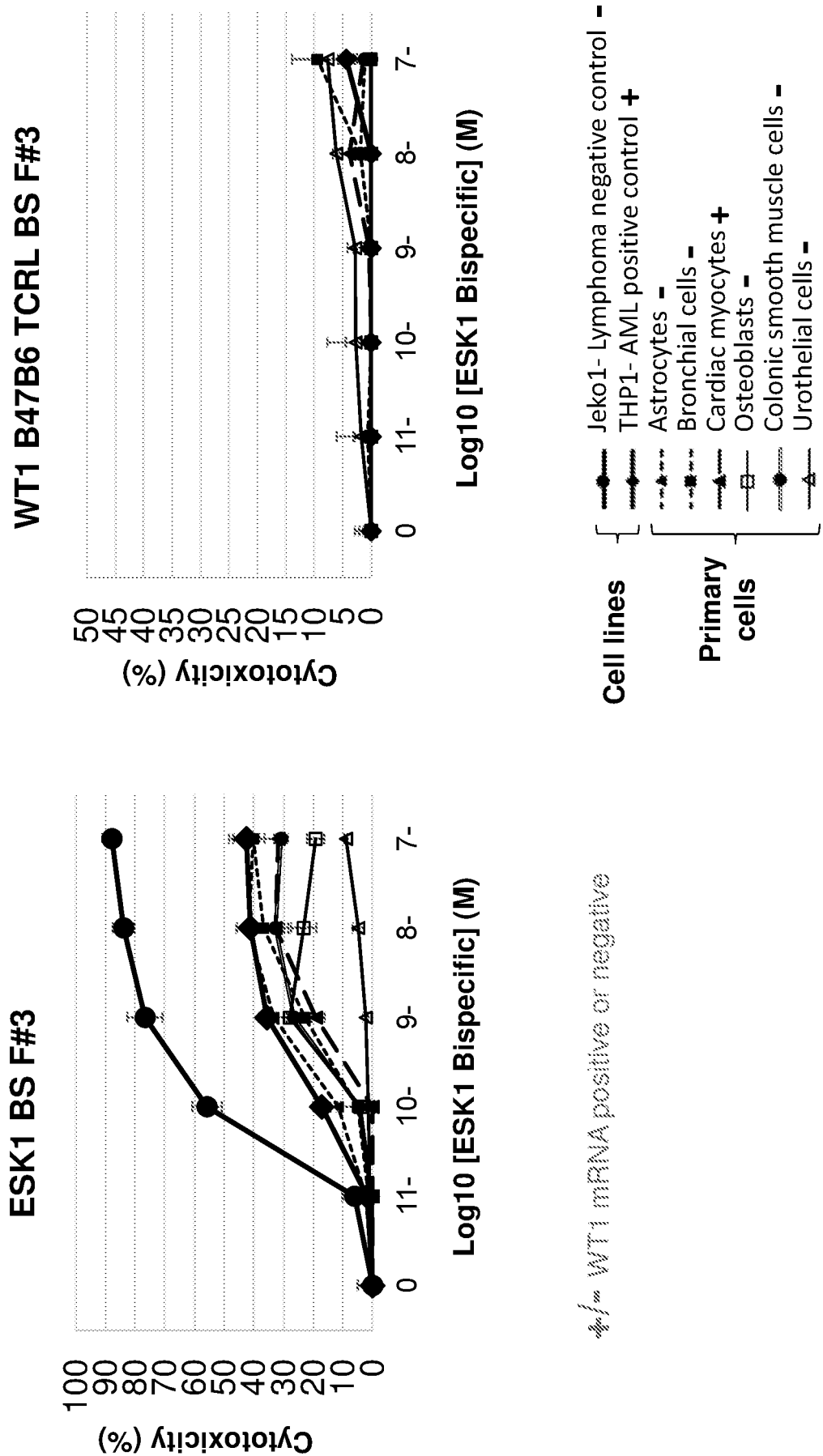
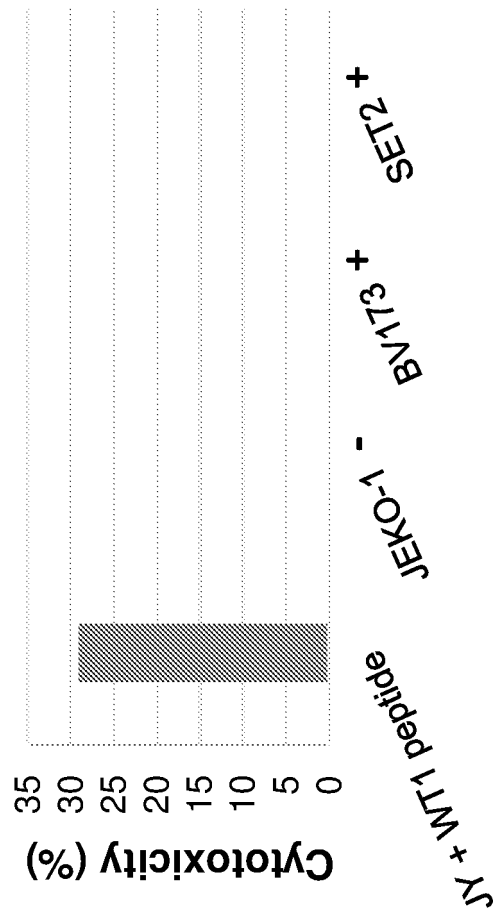
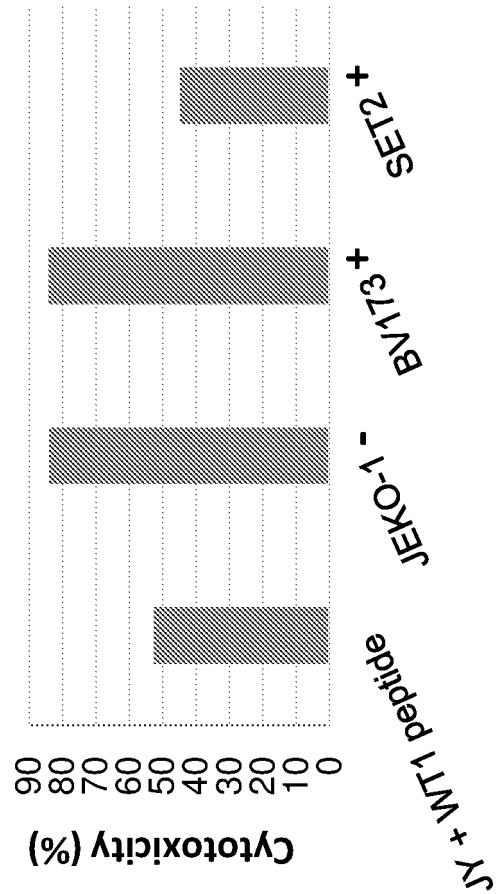


Figure 51A

WT1 B47B6 TCRL BS F#3



WT1 ESK1 BS F#3



+/- WT1 mRNA positive or negative

Figure 51B

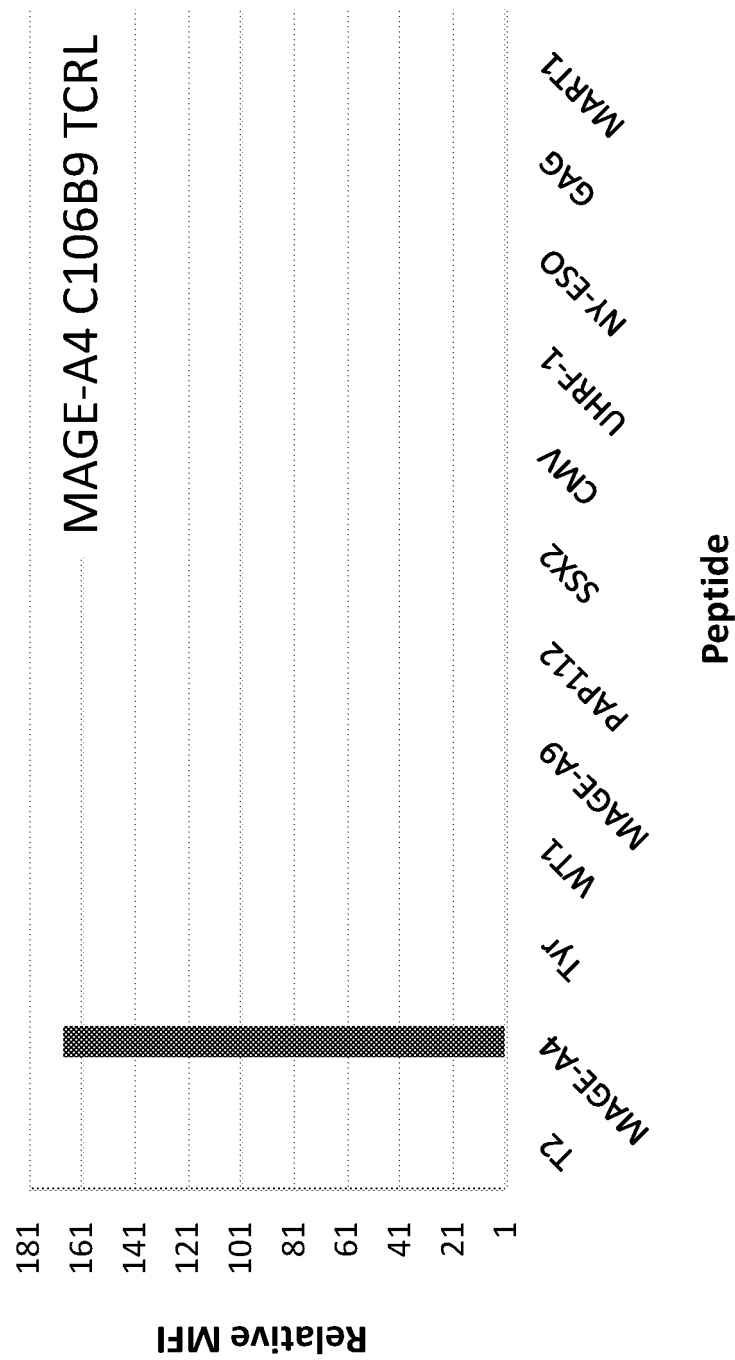
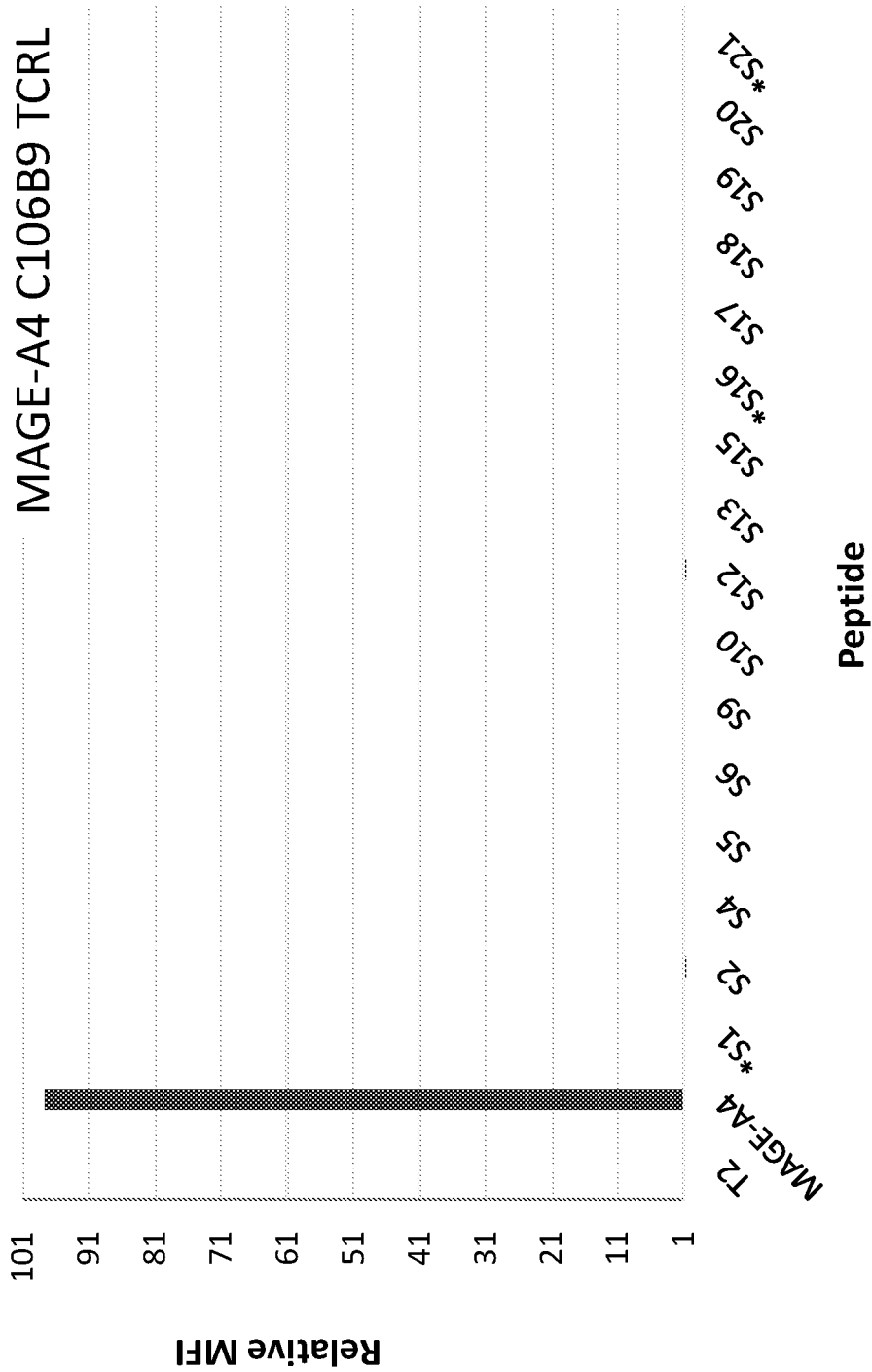


Figure 52



* Found by MS in normal tissues

Figure 53

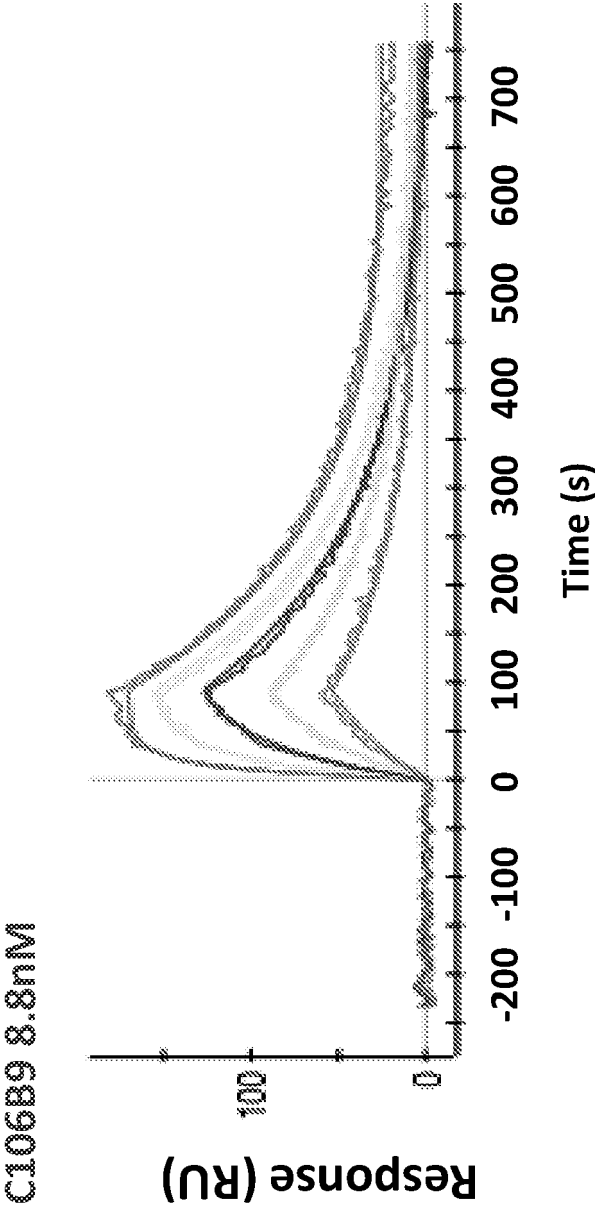


Figure 54

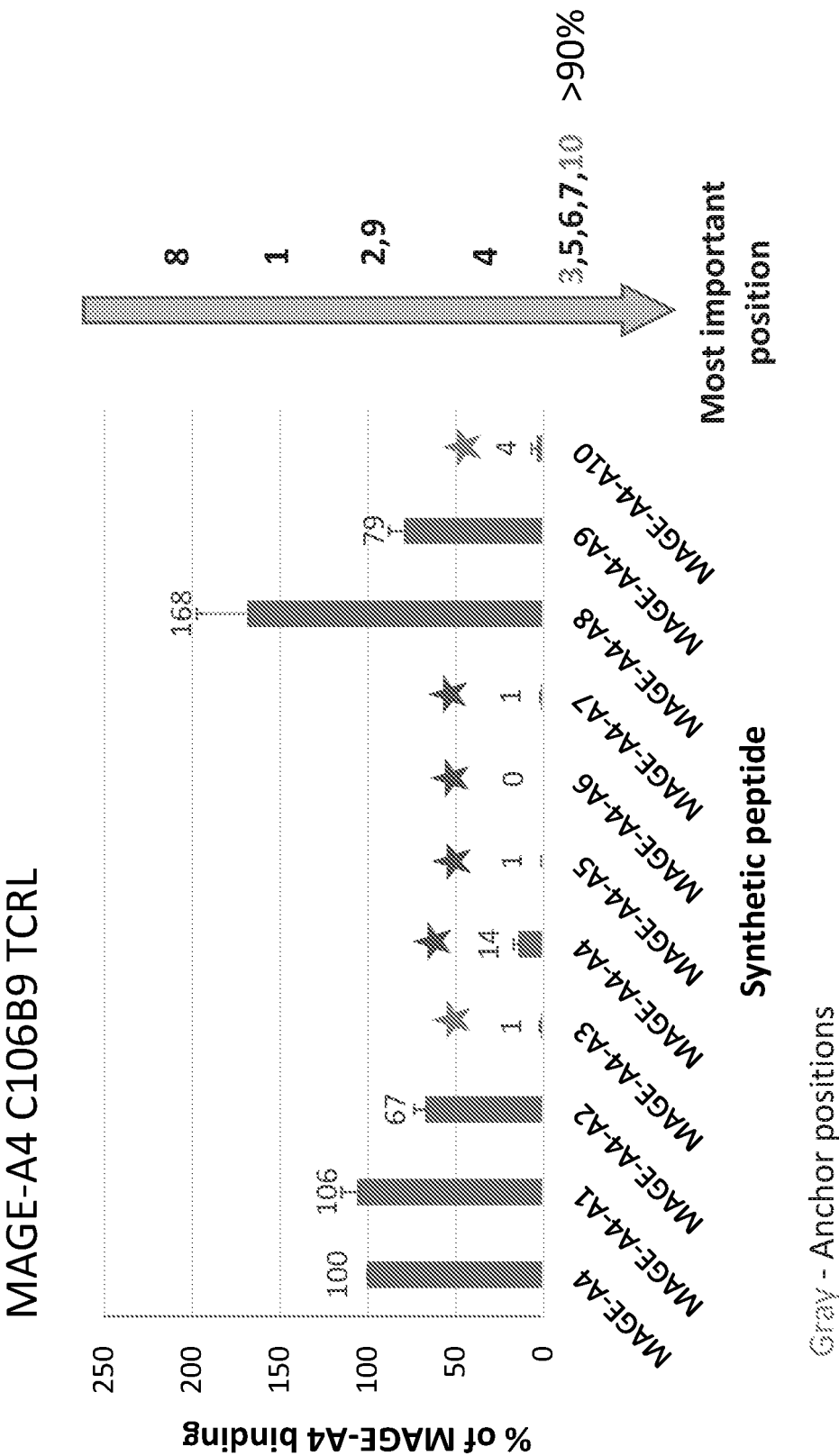


Figure 55

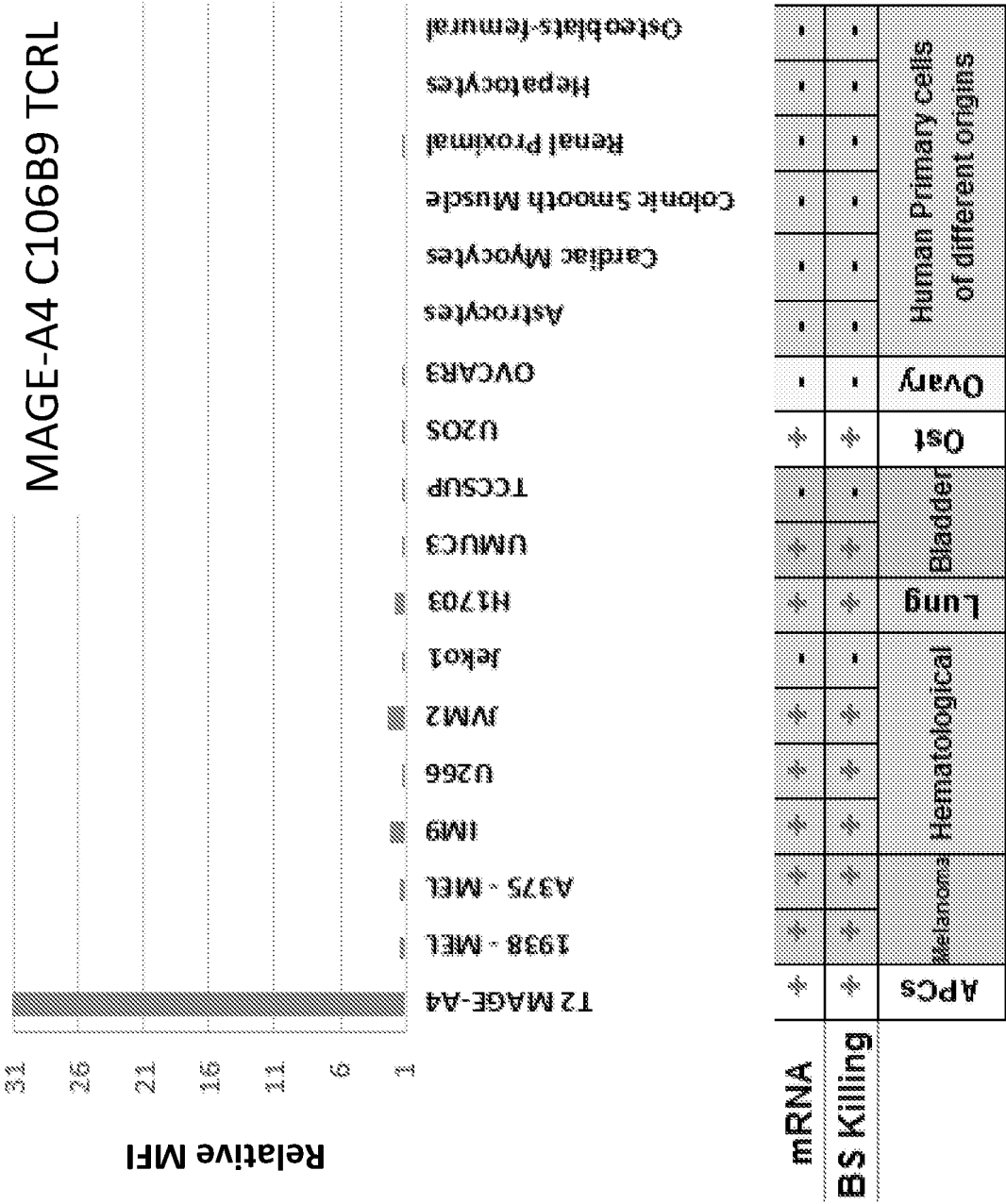
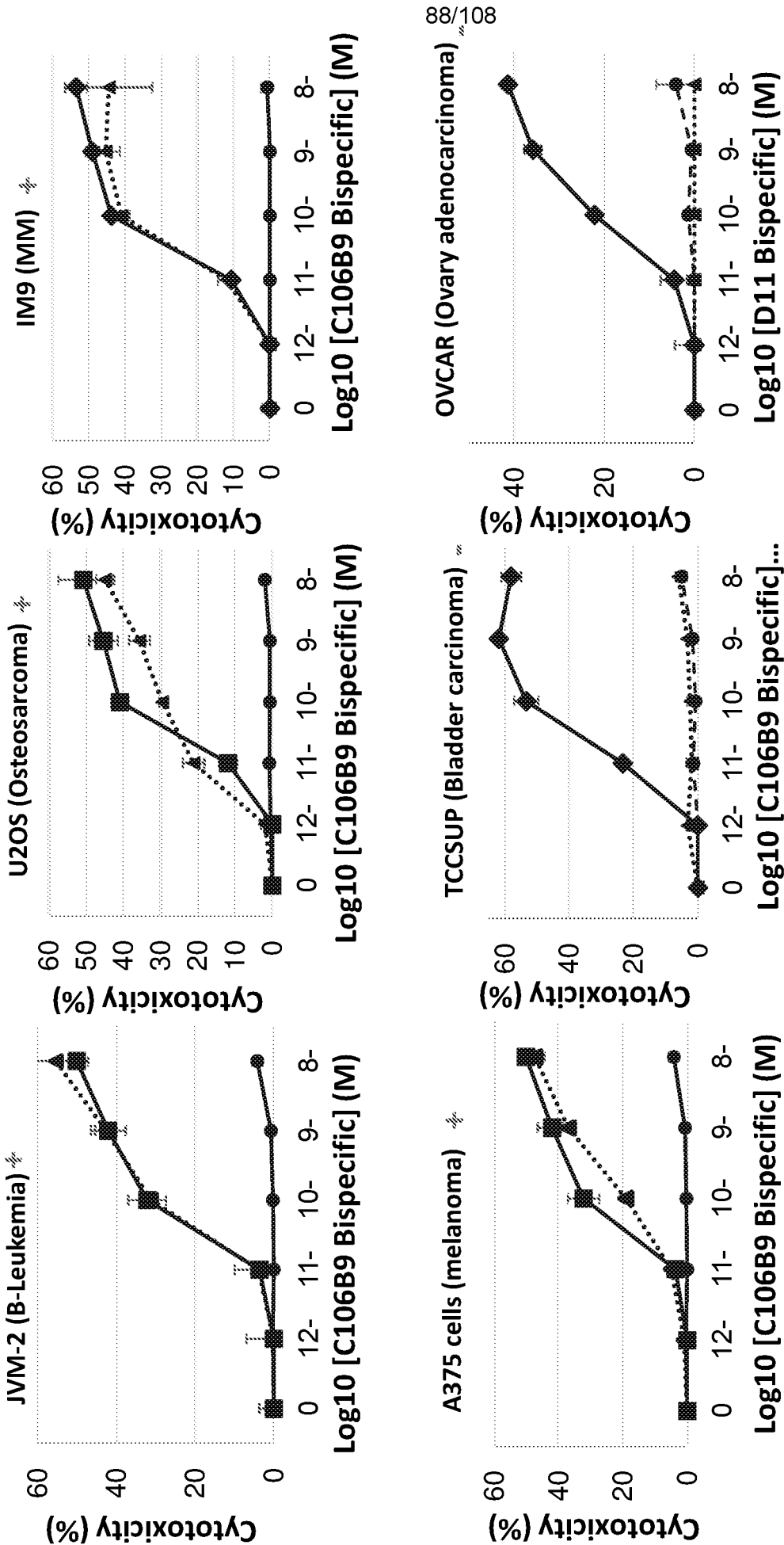


Figure 56

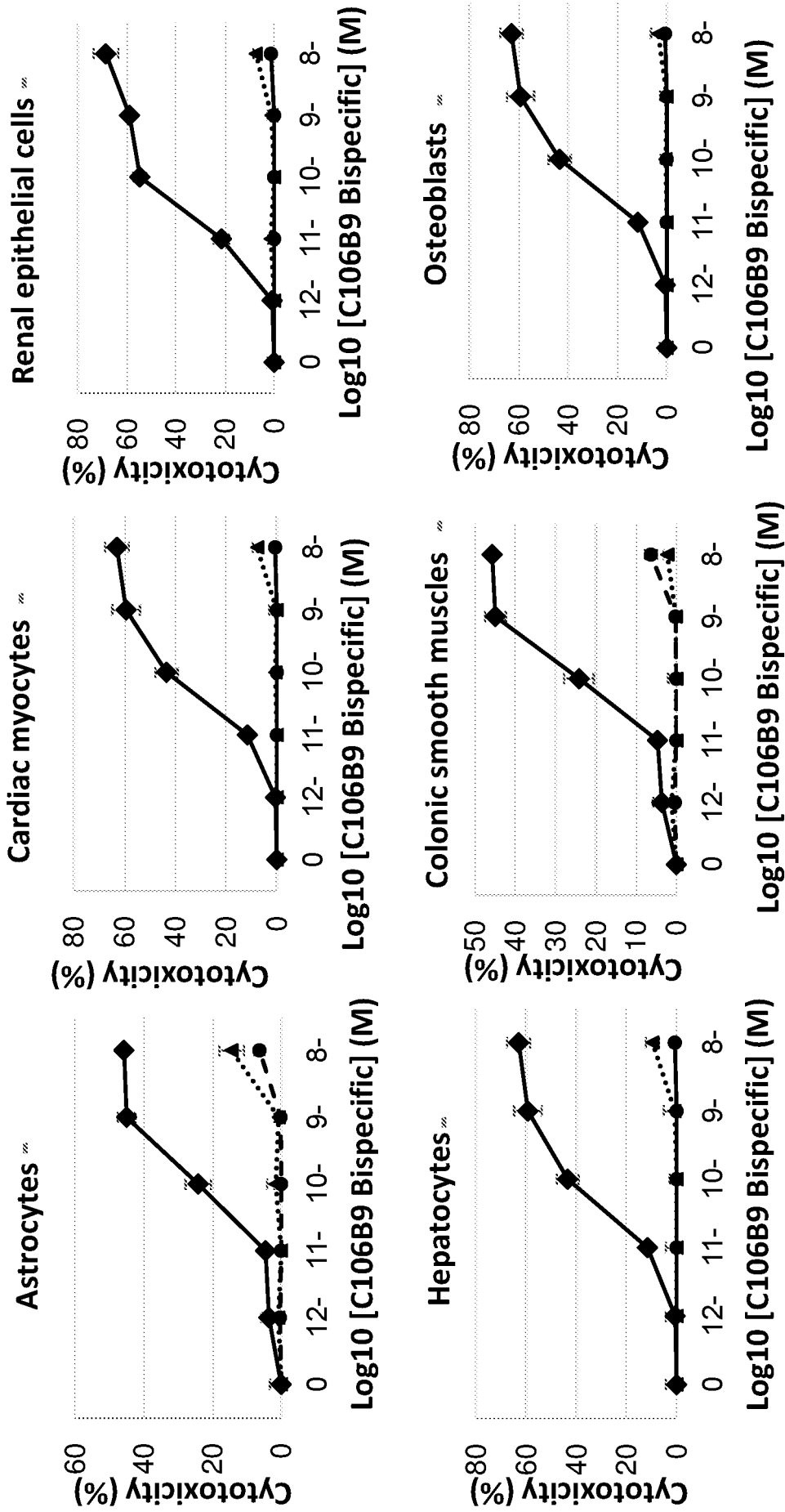
MAGE-A4 C106B9 BS TCRL - killing assay on cell lines



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

Figure 57

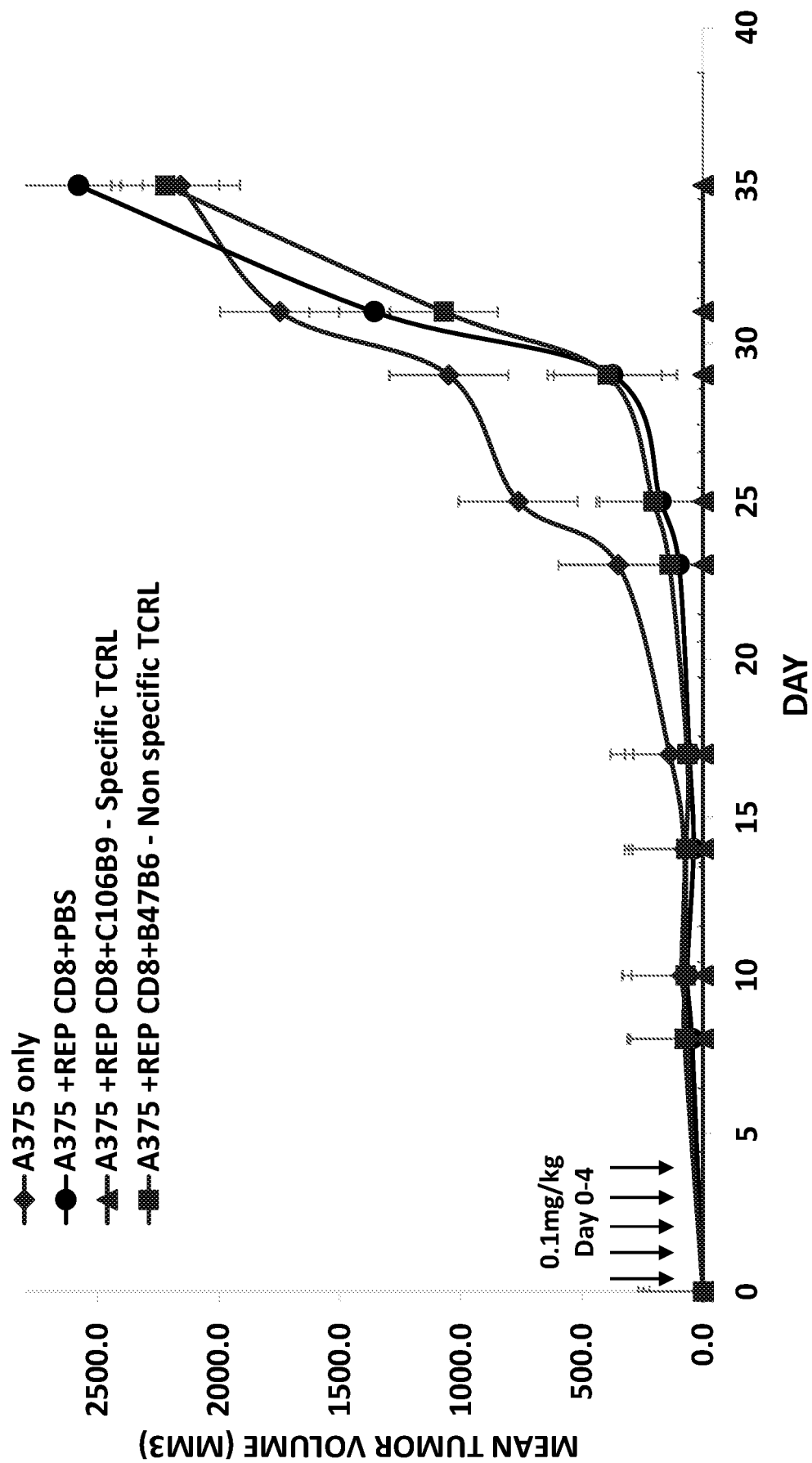
MAGE-A4 C106B9 BS TCRL - killing assay on normal primary cells



◆/●/○/▲ MAGE-A4 mRNA positive or negative

◆ 1938 – melanoma positive control
● Panc1 - negative control
○ 501A - negative control
▲ Primary cells – as indicated

Figure 58



SUBSTITUTE SHEET (RULE 26)

Figure 59

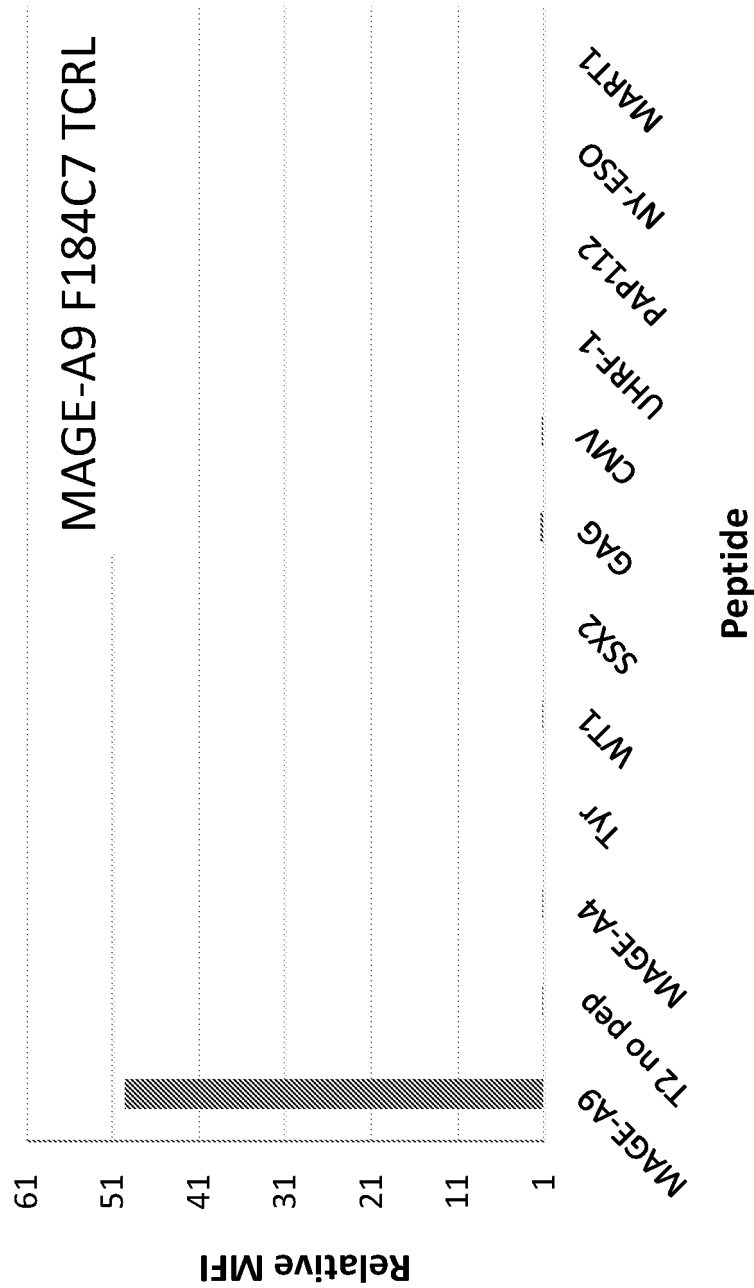
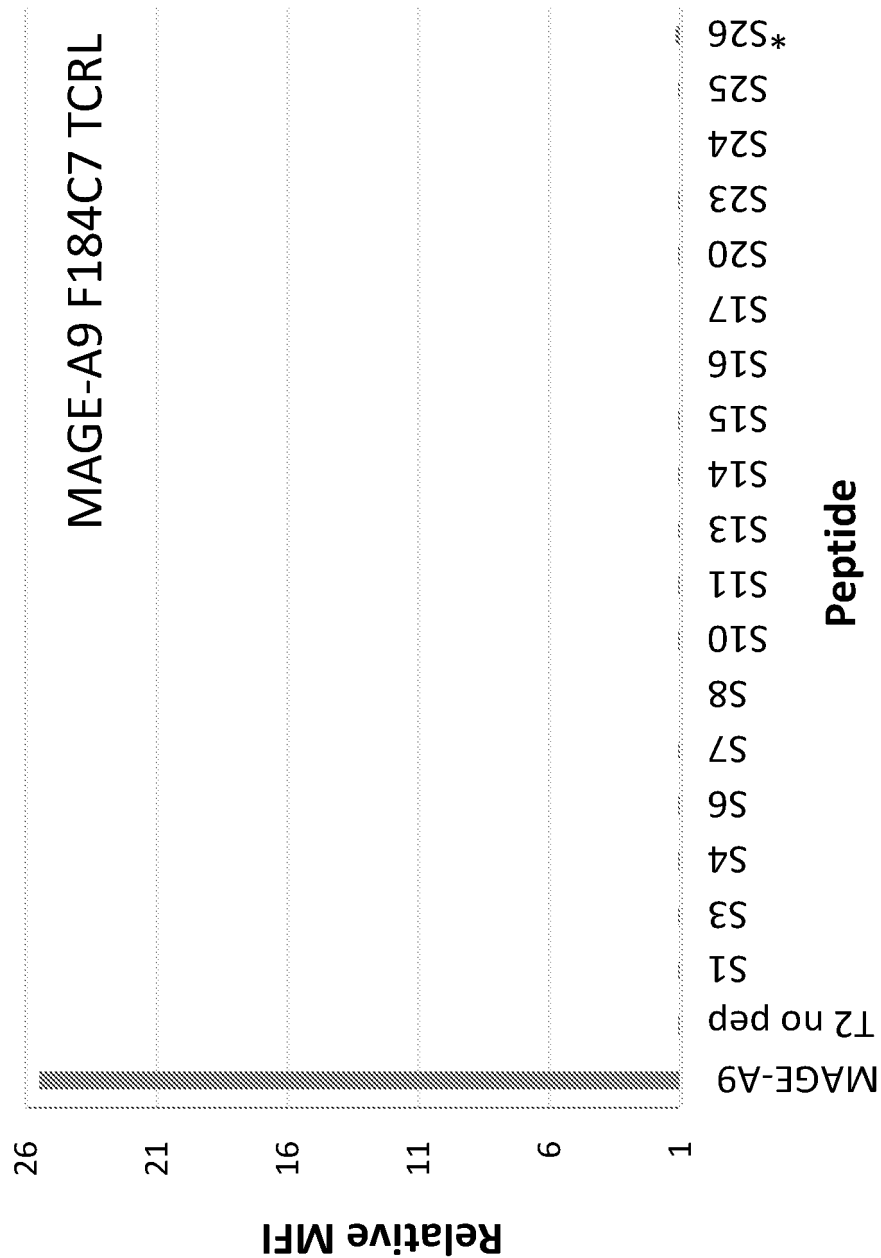


Figure 60



* Found by MS in normal tissues

Figure 61

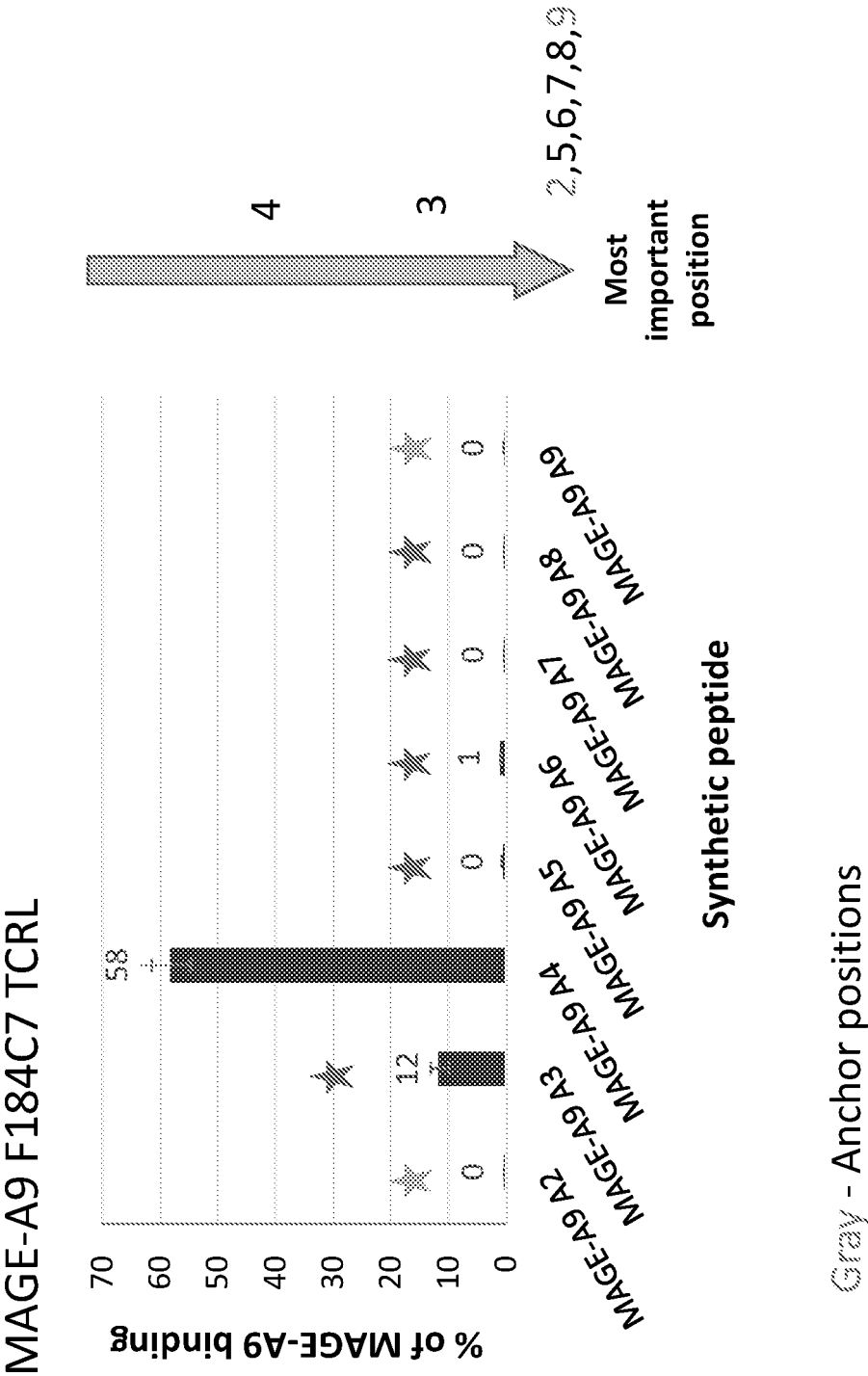


Figure 62

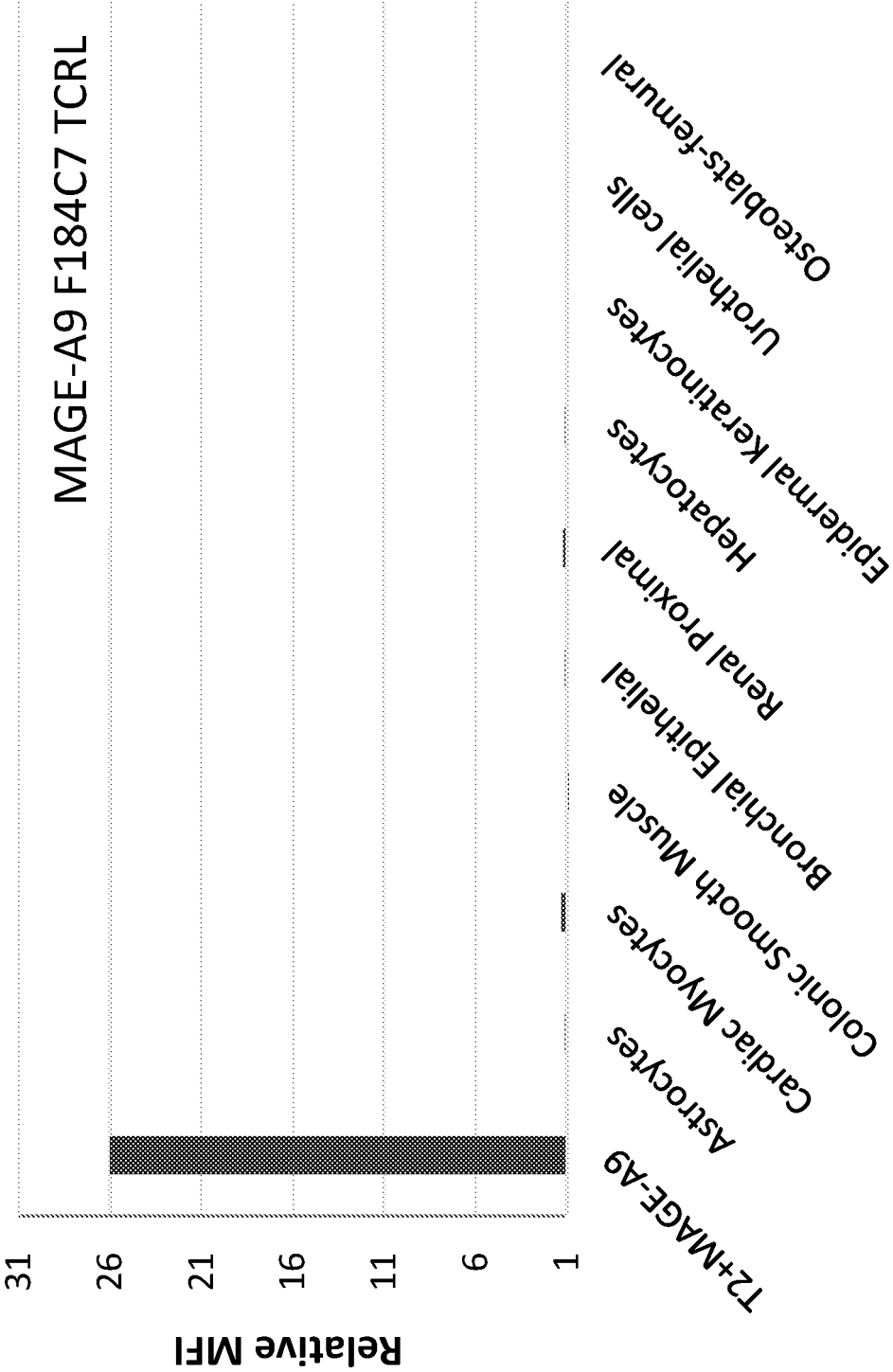


Figure 63

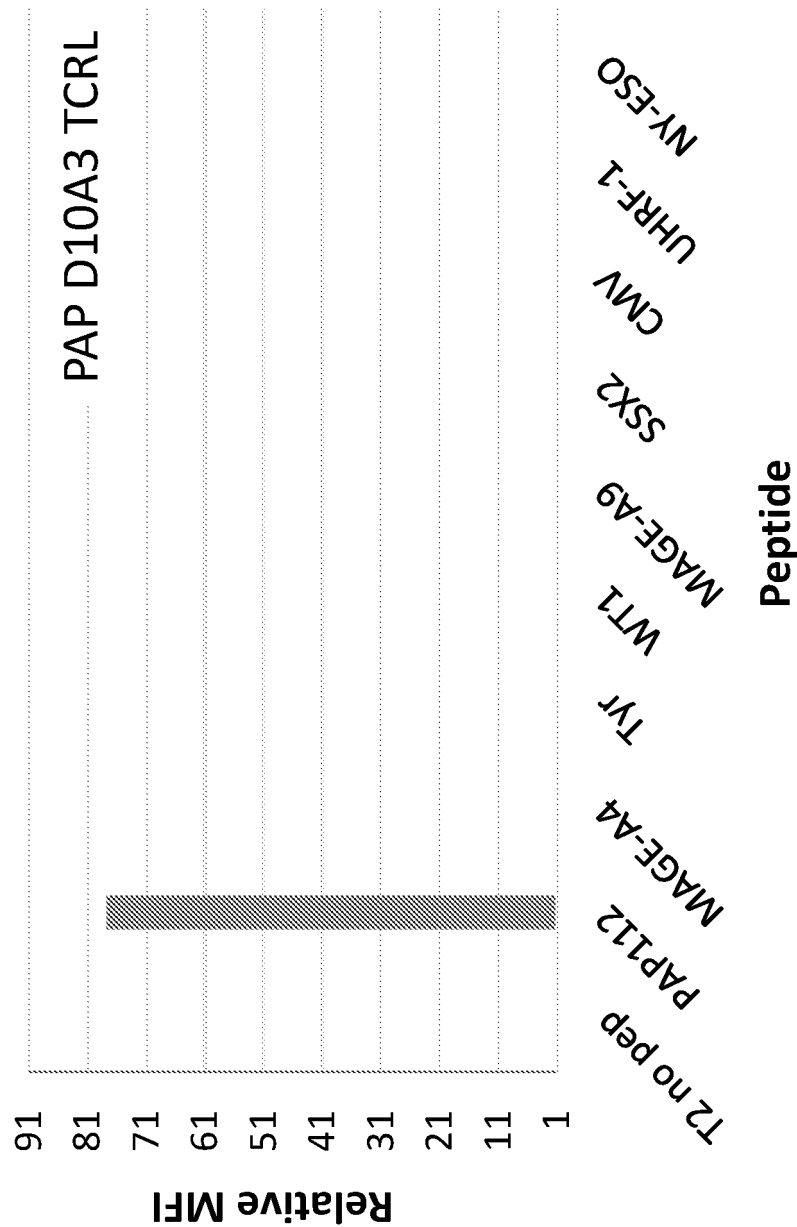
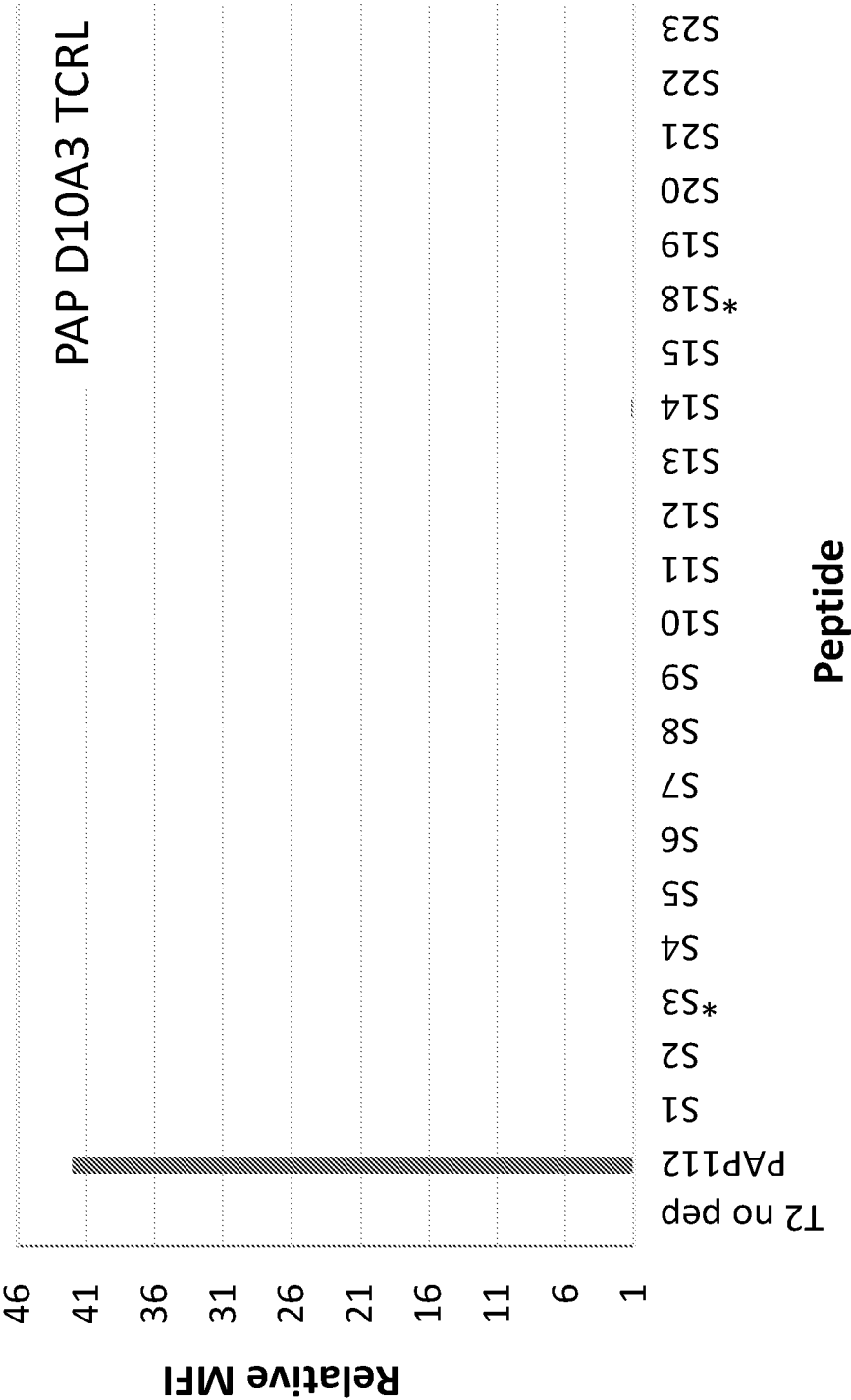


Figure 64



* Found by MS in normal tissues

Figure 65

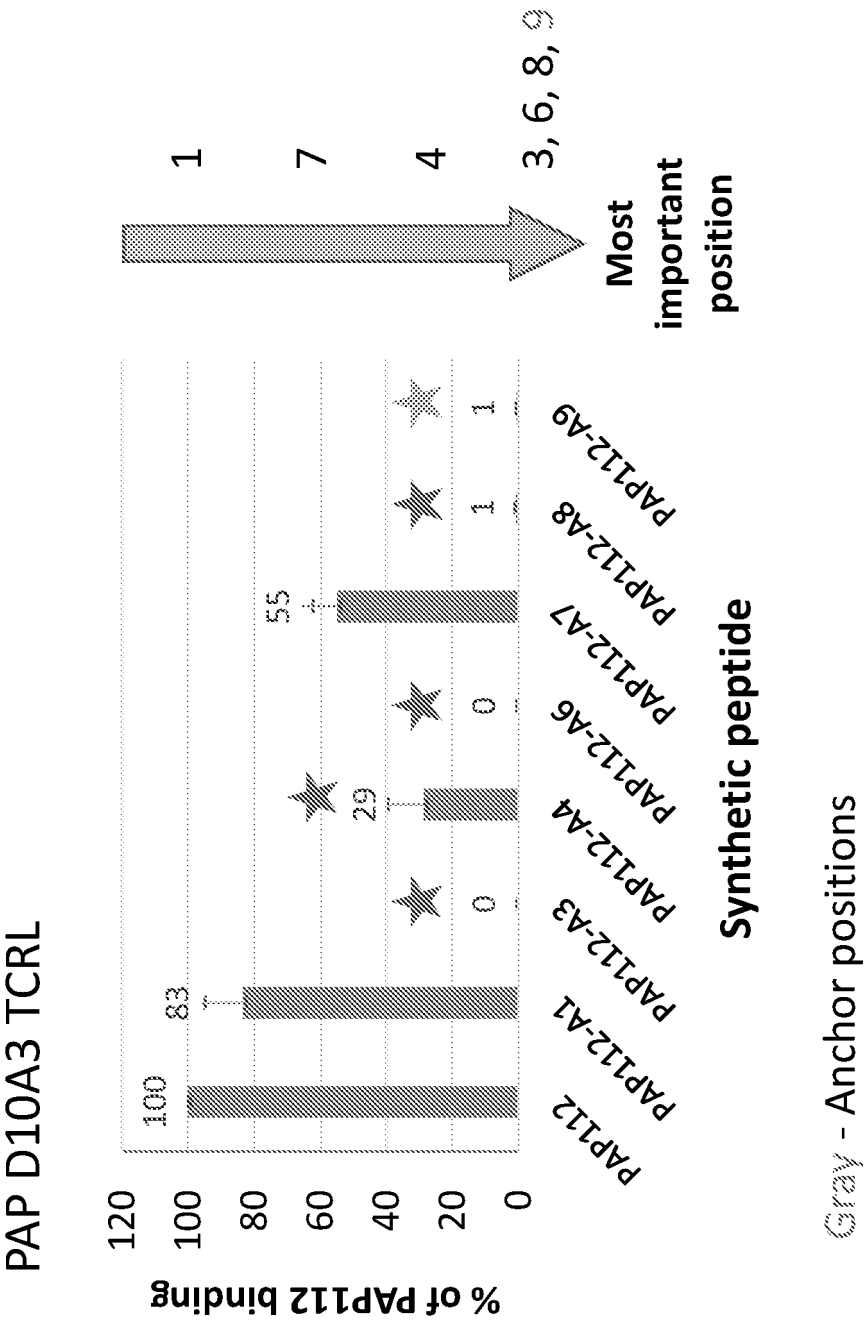


Figure 66

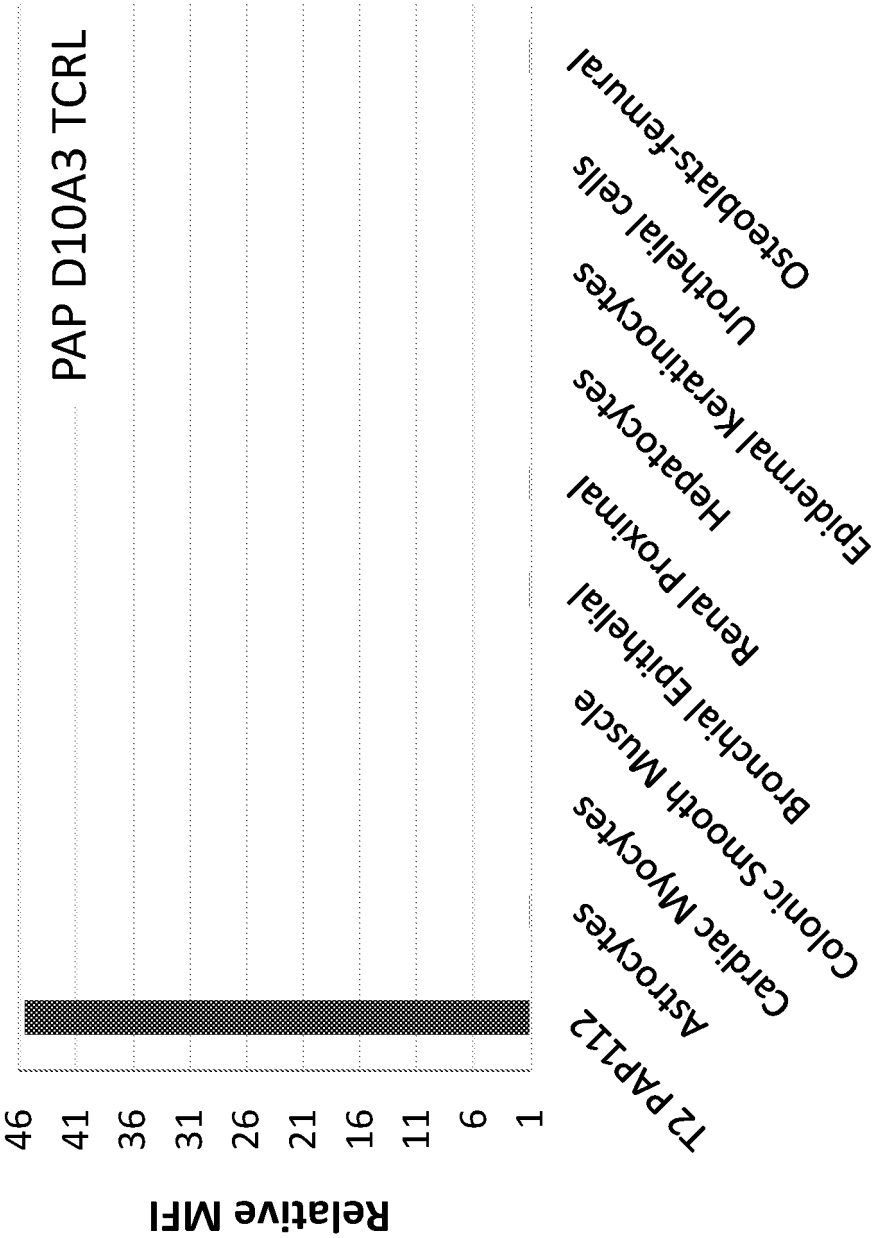


Figure 67

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

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

ATGGACAGGCTTACTTCTCATTCTGCTGCTGATTGTCCCTGCATATGTCCTTTCCAGGTAACCTC
 TGAAAGAGTCTGGCCCTGGGATATTGCAGGCTTCCCAGACCTCAGTCTGACTTGTTCCTTCTCTGG
 GTTTTCACTGACCACTTCTGGTATGGGTGTGAGCTGGATTGCTCAGGCTTCAGGAAAAGGGTCTGGAG
 TGGCTGGCAGACATTTACTGGGATGATGACAAGCGCTATAACCCATCCCTGAAGAGCCGACTCACAA
 TCTCCAAGGATACCTCCAGAAACCAGGTATTTCCTCAAGATCACCAGTGTGGACGCTGCAGATACTGC
 CACATACTACTGTGCTCGAAAGGACTACGGTAGTAGCTTCTATGCTATGCACTACTGGGGTCAAGGA
 ACCTCAGTCACCGTCTCTCTCAGCCAAAACGACACCCCATCTGTCTATCCACTGGCCCCCTGGATCTG
 CTGCCCCAACTAACTCCATGCTGACCTGGGATGGCTGGTCAAGGGCTATTTCCCTGAGCCAGTGCAC
 AGTGACCTGGAACCTTGGATCCCTGTCCAGCGGTGTGCACACCTTCCAGCTGTCTCTGAGTCTGAC
 CTCTACACTCTGAGCAGCTCAGTGACTGTCTCTCCAGCACTCTGGCCAGCGAGACCGTCACTCTGCA
 ACCTTGGCCACCCGGGAGCAGCAGCAAGGTTGAGCAAGAAAATTGTGCCAGGGATTGTGGTTGTAA
 GCCTTGCATATGTACAGTCCAGAAAGTATCATCTGTCTTTCATCTTCCCCCAAAGCCCAAGGATGTG
 CTCACCACTTACTCTGACTCTTAAGGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 TCCAGTTTCAAGCTGGTTTGTAGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 GTTCAACAGCACTTTCGGCTCAGTCACTGAACTTCCCATCATGCACCAAGCACTGGCTCAATGGCAAG
 GAGTTCAAATGACAGGGTCAACAATGTCAGCTTTCCTTGGCCCATCGAGAAAACCATCTCCAAAACCA
 AAGGCAGACCGAAGGCTCCACAGGTGTACACCAATTCCACCTTCCCAAGGAGCAGATGCCCAAGGATAA
 AGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGCAT
 GGGCAGCCAGCGGAGAACTACAAGAACTCAGCCCATCATGAGACACAGATGGCTCTTACTTCTCTCT
 ACAGCAAGCTCAATGTGACAGAGAGCAACTGGCAGCGCAGGAAATACTTTCACCTCTCTCTGTGTACA
 TCAAGGCTCTGACAAACCACTACTGAGAAGAGCTCTCTCCACTCTCTCTGTAATGA

Heavy chain: Amino acids sequence (465 AA)

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

MDRLTSSFLLLIVPAYVLSQVTLKESGPGILQPSQTLSTLCSFSGFSLTSGMGVSWIRQPSGKGL
 WLAHIYWDDBKRYNPSLKSFLTISKDTSFNQVFLKITSVDAADTATYYCARKDYGSSFYAMHYWGQG
 TSVTVSSAKTTPPSVYFLAPSSAAQTNMVLGCLVYGYFPEPVTVTWNSGSLSSGVHTFFPAVLQSD
 LYTLSSSVTVFSSSTWPSSETVTGNVAHPASSIKVLKKIVPRDGGCKPCICTVPEVSVVFIFFPKPLV
 LTITLTPKVTCTVVDLISKLDPEVQF3WFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGK
 EFKCRVNSAAPPAPIEKTI SKTERPKEAFQVYTIPEPKDOMANDKVS LTMITDFHFFEDITVEWQWN
 GQPAENYKNTQFIMDTDGSYFVYGLNVQKSNWEAGNTFTCSVLHEGLNHNHTEK3LSHSPGK

Light chain: DNA sequence (702 bp)

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

ATGAGACCGTCTATTTCAGTTCTTGGGGCTCTTGTGTGTTCTGGCTTCATGGTGCTCAGTGTGACATCC
 AGATGACACAGTCTCCATCCTCACTGTCTGCATCTCTGGGAGGCAAAGTCACCATCACATGCAAGGC
 AAGCCAAGACATTACAACTATATAGCTTGGTACCAACACAAGCCTGTAAAAGGTCCTAGGCTGCTC
 ATACATTACACATCTACATTACAGCCAGGCACCCCATCAAGGTTTCAAGTGAAGTGGGTCTGGGAGAG
 ATTATTCCTTCAGCATCAGCAACCTGGAGCTTGAAGATATTCGAACTTATTTATTTCTACAGTATGA
 TAATCTGTGACGTTTGGTGGAGGCACCAAGCTTGAAGATCAAACGGGCTGATGCTGCACCAACTGTA
 TCCATCTTCCCAACCATCCAGTGAGCAGTTAACATCTGGAGGCTGCTCAGTCTGTGCTTCTTGAACA
 ACTTCTACCCCAAAGACATCAATGTCAAGTGAAGATTGATGGCAGTGAACGACAAAATGGCGTCTT
 GAACAGTTGGACTGATCAGGACAGCAAGACAGCACCTACAGCATGAGCAGCACCTCACGTTGACC
 AAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCA
 TTGTCAAGAGCTTCAACAGGAATGAGTGTTAG

Light chain: Amino acids sequence (233 AA)

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

MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGKVTITCKASQDIHNYIAWYQHKPVKQPELL
 IHYTSTLQPGTPSRFSGSGSRDYSFISINLEPEDIATYYCLQYDNLWTFGGGKLEIKRADAAPTV
 SIFPPSSEQLTSGGASVVCFLNNFYFKDINVKWKIDGGSRQNGVLN3WTDQDSKSTYSMSSTLTLE
 KDEYERHNSYTCETHKTSTSPIVKSEFNRNEC

Figure 68

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

ATGGCTGTCTCTGGTGTCTTCTCTGCTGGTTGCATTTCCAAGCTGTGTCTCTGTCCCAGGTGCAAC
 TGAAGGAATCAGSAGCTGGTCTGGTGGCGCCCTCACAGAGCCTGTCCATCACTTGCCTGTCTCTGG
 GTTTTCATTAACCAGCTATGGTGTACACTGGSTTCGCCAGCTCCAGGAAAGGGTCTGAGTGGCTG
 GGAGTAATATGGCTGGTGGAAACCACAAATTATAATTGGCTCTCATGTCCAGACTGAGCATCAGCA
 GAGACAACCTCCAAGAGCCAAAGTTTTCTTAGAAATGAACAGTCTGCAAACTGATGACACAGCCATTTA
 CTACTGTGCCAGAGATGGTCACTTCCACTTTGACTTCTGGGGCCAAGCCACCCTCTCACAGTCTCC
 TCAGCCAAAACGACACCCCATCTGTCTATCTACTGGCCCTTGATCTGCTGCCAAACTAACTCCA
 TGGTGACCTCTGGATGGCTGGTCAAGGGCTATTTCCCTGAGCCAGTGCAGTGCACCTGGAAGTCTGG
 ATCCCTGTCCAGCGGTGTGCACACCTTCCCACTGTCTCTGAGTCTGACCTCTACACTCTGAGCAGC
 TCAGTGAATGTCTCTCTCCAGCACTTGGCCCAAGGAGACCTGACCTGCAAGCTTGGCCACCCGCGCA
 GCAGCACCAAGCTGCACAAGAAAATTGTGCCAGCGATTGTGCTTGTAAAGCTTGCATATGTACACT
 CCCAGAAGTATCATCTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 CCTAAGGTCACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 TACATCATCTCTGAGGTGCACACAGCTCAGACGCAACCCCGGAGGAGCACTTCAACAGCACTTTCCG
 CTCACTCACTGAACCTTCCCATCATGCAACAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGCTC
 AACAGTGCAGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 CACAGTGTACACCACTTCCACCTTCCCAAGGAGCAGATGGCCAAAGGATAAAGTCACTCTGACCTGCA
 GATAACAGACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 TACAAGAACTTCAAGCCATCATGGACACAGATGGCTCTTACTTGGTCTACAGCAAGCTCAATGTGC
 ACAAGAGCAACTGGGAGCCAGGAAATACTTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 CCATACTGAGAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT

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

MAVLVFLCLVAFPSCVLSQVQLKESGPGLVAPSSLSITCTVSGFSLTSYGVHWVRQPPGKGLEWL
 GVIWAGGTTNYSALMSRLSISPDNKSQVFLMNSLQTDDBTAIYYCARDGHFHFDWGGQTTTLTVS
 SAKTIFPSVYFLAPSSAAQTNSMVTLCCLVKGYPPEPVTVTNNSGSLSSGVHTFPAVLQSDLYTLSS
 SVTVFSSTNPFSETVTCNVAFPASSTKVDKIVFRLCGCKPCICTVVEVSSVFIFPPKPKDVLITITL
 PKVTCVVDLISKDDFEVQFSWFVDDVEVHTAQTQPPFEEQFNSTFPVSGELPDMHODWLNGKEFRCRV
 NSAAFPAPLEKTIKTKGRPKAPQVYTIIPPKPEQMAKDKVSLTCTMTDFFEDITVEWQWNGQPAEN
 YKNTQFIMDTLGSYFVYSKLVNQKENWEAGNTFTCSVLBEGLEHNHSTKSLSSSPGK

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

ATGAGTGTGCCCCTCAGGTCTCTGGGGTTGCTGCTGCTGTGGCTTACAGATGCCAGATGTGACATCC
 AGATGACTCAGTCTCCAGCCTCCCTATCTGTATCTGTGGGAGAAACTGTCAACATCACATGTGAGC
 AAGTGATATTATTTACAGTAATTTAGCATGGTATCAGCAGAAACAGGGGAAAATCTCCTCAGCTCCTG
 GTCTATGCTGCAACAAACTTAGCAGCTGGTGTGCCATCAAGGTTCAAGTGGCAGTGGATCAGGCACAC
 AGTATTCCTCAAGATCAATAGCTTGCAGTCTGAAGATTTTGGGACTTATTACTGTCAACATTTTTG
 GGGTAGTTCAATCTCGTTCTGGCTCGGGGACAAAGTTGGAAATAAAAAGGGCTGATGCTGCACCAACT
 GTATCCATCTTCCCAACATCCAGTGAGCAGTTAACATCTGGAGGTGGCTCACTCGTGTCTCTCTTGA
 ACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAAGATTGATGGCAGTGAACGACAAAATGGCGT
 CCTGAACAGTTGGAGTGTATCAGGACAGCAAGACAGCACTTACAGCATGAGCAGCACCCCTCAGGTTG
 ACCAAGGAGCAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAAGACATCAACTTCAC
 CCATTGTCAAGAGCTTCAACAGGAATGAGTGTAG

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

MSVPTQVLGLLLLWLTDARCDIQMTQSPASLSVSVGETVTITCRASDIIYSNLAWYQQKQCKSPQLL
 VYAATNLAAGVPSRFSGSGSQTQYSLKINSLSQSEDFGTYYCQHFHWGSSISFGSGTKLEIKRADAAPT
 VSIFPPSSEQLTSGGASVVCFLNFFPKDINVEWIKDGERQNGVLNSWTDQDSKLSSTYSMSSTLT
 TKDEYERHNSYTCETAKTSTSPIVKSFNNNEC

Figure 69

WT1 B47B6 TCRL SEQUENCE**Heavy chain: DNA sequence**

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

GAAGTGCAGTTGGTGGAGTCGGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCTGTGCAGCCTC
TGGATTTCGTTTTCAGTAGCTATGACATGTCTTGGGTTTCGCCAGGCTCAGGAGAAGAGGCTGGAGTGGGTGCGATA
CATGAGTAGTGGTGGCGGCCACTACTATCCAGACACTGTGAAGGGCCGATTACCATCTCCAGAGACAATGCCAA
GAACACCCTGCACCTGCAAATGAGCAGCCTGAAGTCTGAGGACACAGCCATGTATTACTGTGCAAGACATGATGA
GATTACTAACTTTGACTACTGGGGCCAAAGGCACCCTCTCACAGTCTCCTCAGCCAAAACGACACCCCCATCTGT
CTATCCACTGGCCCTCGGATCTGCTGCCCAAATAACTCCATGGTGACCTCGGGATGCTGTGCAAGGGC
TATTTCCCTGAGCCAGTGACAGTGACCTGGAACCTCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCAG
CTGTCTCTGCACTCTGACCTCTACACTCTGAGCAGCTCAGTGAAGTGTCCCTCCAGCACTTGGCCAGCGA
GACCGTCACTTGCACACCTTGGCCACCTGGCCAGCAGCAGCAAGGTGGACAAGAAAATTTGTGCCCAAGGGAT
TGTGGTTGTAAAGCCTTGCATATGTACAGTCCCAGAAAGTATCATCTGTCTTCTATCTTCCCCCAAGGCCA
AGGATGTGCTCACCATTACTCTGACTCCTAAGGTCAAGTGTGTGTGTGTGTAGACATCAGCAAGGATGATCC
CGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCCCGGGAGGAG
CAGTTCACACAGCACTTTCCGCTCAGTCAGTGAAGCTTCCCATCATGCACCAGGACTGGCTCAATGGCAAG
GAGTTCAAATGCAGGGTCAACAGTGCAGCTTTCCCTGCCCCCATCGAGAAAACCATCTCCAAAACCAAAG
GCAGACCGAAGGCTCCACAGGTGTACACCATTCCACCTCCCAAGGAGCAGATGGCCAAGGATAAAGTCAG
TCTGACCTGCATGATAACAGACTTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGATGGGCAGCCA
GCGGAGAACTACAAGAACAACCTCAGCCCATCATGGACACAGATGGCTCTTACTTCTGTCTACAGCAAGCTCA
ATGTGCAGAAAGAGCAACTGGGAGGCAGGAAATACTTTCACTGCTCTGTGTGTACATGAGGGCTGCACAA
CCACCATACTGAGAAGAGCCTCTCCCACTCTCTCTGTTAAA

EVQLVESGGGLVKPGGSLKLSAASGFVFSYDMSWVRQAQEKRLWVAYMSSGGGTYYPDITVKGRFTISRDNKNT
LHLQMSSSLKSEDTAMYYCARHDEITNFDYWGQGTTLTVSSAXITTPPSVYPLAEFGSAAQNTSMVTLGCLVKGYFP
EPVTVTVNWSGLSSGVHTEFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAPASSTKVDKKEIVPEDCGC
KPCICTVPEVSSVFIEPPKPKDVLITLTPEKVTGVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFN
STFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPLEKTIKTKGRPKAPQVYTIPEPPKEQMARDKVSILTC
MITDFFFPEDITVEWQWNGQPAENYKNTQPLMDTDGSYFVYSKLNVQKSNWEAGNITFTCSVLHEGLHNNHT
EXSLSSSPGK

Light chain: DNA sequence

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

GATATTGTGCTCACTCAGTCTCCAGCCACCCTGTCTGTGAGTCCAGGAGATAGCGTCAGTCTTCTCTGCAGGGCCAGCCAAAAGT
ATTAGCAACAGCCTACACTGGTATCAACAAAAATCACATGAGTCTCCAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTG
GAATCCCTCTAGGTTCAAGTGGCAGTGGATCAGGGACAGATTTACACTCAGTATCAACAGTGTGGAGACTGAAGATTTTGA
ATGATTTTCTGTCAACAGAGTTACAGCTGGCCTCTCACGTTCCGCTGCTGGGTCCAAGCTGGAGCTGAAAAGGGCTGATGCT
GCACCAACTGTATCCATCTTCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCTTCAGTCTGTGTGCT
TCTTGAACAACTTTTACCCCAAAGACATCAATGTCAAGTGGAAAGATTGATGGCAGTGAACGACAAAATGG
CGTCTGAACAGTTGGACTGATCAGGACAGCAAAAGACAGCACCTACAGCATGAGCAGCACCCTCAGCTTG
ACCAAGGACGAGTATGAACGACATAACAGCTATACTGTGAGGGCACTCACAAGACATCAACTTCACCCA
TTGTCAAGAGCTTCAACAGGAATGAGTGT

Figure 70

DIVLTQSPATLSVSPGDSVLSCLASQSSINSLHWYQKSHESPRILUKYASQSSIGIPSRFSGSGSGTDFTLSINSVETEDFGMYFCQQ
SYSWPLTFTGAGSKLELKRADAAPTIVSIEPPSSSEQLTSGGASVVCFINNFYPIEDINVKWKIDGSERQNGVLNSWT
LQDSKDSSTVGMSTLTTLTKDEYERPNSTCEATSKTSTSPILVKSENPNEC

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
 CACTGGCCCTTGGATCTGCTGCCCCAACTAACTCCATGSGTGAACCTGGGATGGCCTGGTCAAGGGCTATTT
 CCCTGAGCCAGTGCAGTGAACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGTCACACCTTCCAGCTGTCT
 CTGCAGTCTGAACCTCTACACTCTGAGCAGCTCAGTGAACCTGTCCCTTCCAGCACTTGGCCAGCGAGACCG
 TCACCTGCAACGTTGGCCACCCGGCCAGCAGCACTAAGGTGGACAAAGAAATTGTGCCAGGGATTGTGG
 TTGTAAGCCTTGTCATATGTACAGTCCCAAGATATCATCTGTCTTCATCTTCCCCCAAGGCCAAGGAT
 GTGCTCACCATTACTCTGACTCTTAAGGTGACGTGTGTGTGTGGTAGACATCAGCAAGGATGATCCCGAGG
 TCCAGTTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCCCGGGAGGAGCAGTT
 CAACAGCACTTTCCGCTCAGTCACTGAACCTTCCCTCATGTCACCAAGGACTGGCTCAATGGCAAGGAGTTC
 AATGCAGGCTCAACAGTGCAGCTTTCCCTGCCCCCATGAGAAAACTATCTCCAAAAACCAAGGCAGAC
 CGAAGGCTCCACAGGTGTACAACCTTCCACCTCCCAAGGAGCAGATGGCCAAGGATAAAGTCAGTCTGAC
 CTGCATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGGGAATGGCCAGCCAGCGGAG
 AACTACAAGAACACTCAGCCCATCATGGACACAGATGGCTCTTACTTCTGTCTACAGCAAGCTCAATGTGC
 AGAAGAGCAACTGGGAGGCAGGAAATACTTTCACCTGCTCTGTGTACATGAGGGCCTGCACAACCAACA
 TACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA

AA-seq:

QVQLQQSGGEVMPKPGASVKLSCKATGYTFTGYWIEWIKRPGHGLEWIGEILPGSGGTNYNEKFKGKATFYAHTSSN
 TAYMQLSSLTIEDSAIYYCARDSNSFTYWGQGLTVYSSAKTTPFSVYPLAPGSAQTNGMVTLGCLVKGYFPEP
 VYVTVNSGSLSSGVETFPAYLQCOLYTLSSSVTPSSWFSESTVTCNVASAPASSTKVDKKIVPROCGCKP
 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
 GGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAAAGGAGIAGTTACCCACCCACGTTCCGGCTCGGGGACAAAGT

Figure 71

TGGAAATAAAAAAGGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTG
GAGGTGCTTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAGATTGA
TGGCAGTGAACGACAAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGC
ATGAGCAGCACCTTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACTGTGAGGCCACTC
ACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGT

AA-seq:

QIVLTQSPAIMSASPGEKVTITCSVSSVDYIHWFQOKPGTSPKFWIYSTSILASGVPARFSGSGSGTSYSLTISRMEAEDA
ATYYCQQRSSYPPTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVRWKIDGSEKQNI
GVLNSWTDQDSKSTYSMSSTLTLTDEYERHNSYICEATHKTSTSPIVFSENRNEC

Figure 71 continued

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

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

Nuc-seq:

CAGGTTTCAGCTGCAGCAGTCTGGACCTGAGATGGTGAAGCCTGGGGCCTCAGTGAAGATTCCCTGCAAGGCTTCT
 GGCTACGCATTTCAGTAGCTCCTGGATGAACTGGGTGAAGCAGAGGCCTGGAAAGGGTCTTGAGTGGATTGGACG
 GATTTATCCTGGAGATGGAGATACTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATC
 CTCCAGCACAGTCTACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTACTTCTGTGCAAGAGAGGGCT
 ACTACGGTAGTGGCCCCGTAATACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAAAAACGA
 CACCCCATCTGTCTATCCACTGGGCCCTGGATCTGCTGCCCCAACTAACTCCATGGTGGACCTGGGGATG
 CCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTG
 CACACCTTCCAGCTGTCTCTGCACTCTGACCTCTACACTCTGAGCAGCTCAGTGAAGTGTCCCTCCAGCA
 CCTGGGCCAGCGAGACCGTCACTGCAACGTTGCCACCCGCGCCAGCAGCACCAGGTGGACAAAGAAAT
 TGTGCCCAAGGATTGTGGTTGTAAAGCCTTGCATATGTACAGTCCCAGAAAGTATCATCTGTCTTTCATCTTC
 CCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCTCTAAGGTCAAGTGTGTGTGGTGGTAGACATCA
 GCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCA
 ACCCCGCGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAAGTGAAGTCTCCCATCATGCACCAGGACTGG
 CTCAATGGCAAGGAGTTCAAAATGCAGGGTCAACAGTGCAGCTTTCCCTGCCCCCATCGAGAAAAACCATCT
 CCAAAACCAAGGCAGACCGAAGGCTCCACAGGTGTACACCATTTCCACCTCCCAAGGAGCAGATGGCCAA
 GGATAAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAAGACATTAAGTGTGGAGTGGCAGTGG
 AATGGGCGAGCTAGCGGAGAACTACAAGAACTCAGGCCATCATGGACACAGATGGCTCTTACTTCGTCT
 ACAGCAAGCTCAATGTGCAGAAAGAGCAACTGGGAGGCAGGAAATACTTTACCTGCTCTGTGTTACATGA
 GGGCCTGCACAACCACTACTGAGAAGAGCCTCTCCCACTCTCTGTTAAA

AA-seq:

QVQLQSGPEMVKPGASVKIPCKASGYAFSSSWMNWVKQRPGKLEWIGRIYPGQGDNTYNEKFKGKATLTVDKSS
 STVYMQLSSLTSEDSAVYFCAREATTVPVYFDYWGQGTTLTVSSAKTTPPVSYP LAFGSAAGTNSMVTLGCLV
 KGYPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTPSSSTWPSSETVTCHVAHPASSTKVDDKIVP
 RDGCKPCICTVPEVSSVFIPPPKPDVLTITLTPKVTCVVDISKDDPEVQFSWFVDDEVHTAQTQPK
 EQFNSTFFCVSELPIMHQDWLNGKEFKCKVNSAAFPAPIEXTLQKTKGPPKAPQVYTIPTPFSEQMAKDK
 VELTCMTIDFFPEDLTVWQWNGQPAENYKNTQPIMDTDGSYFVYKLVQKSNWEAGHTFTCCVLEGL
 HNHETBKSLSHSPGK

Light chain: DNA sequence

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

Nuc-seq:

GACATCAGATGACTCAGTCTCCAGCCTCCCTATCTGTATCTGTGGGAGAACTGTCACCATCACATGTCGAGCAA
 GTGAGAATATTTACAGAAATTTAGCATGGTATCAGCAGAAACAGGGAAATCTCCTCAACTCCTGGTCCATGCTGC
 AACAACTTAGCAGATGGTGTGCCATCAAGGTTCAAGTGGCAGTGGATCAGACACACAGTATTCCTCAAGATCAA
 CAGCCTGCAGTCTGAAGATTTTGGGAATTACTGTCAACATTTTGGGGGACTCCGCTCACGTTCCGTTGCTGGG

Figure 72

ACCAAGCTGGAGCTGAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTT
AACATCTGGAGGTGGCTCAGTCGTGTGCTTCTTGAACAACCTCTACCCCAAAGACATCAATGTCAAGTGG
AAGATTGATGSCAGTGAACGACAAAATGGGCTCTTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCA
CCTACAGCATGAGCAGCACTCTCAGCTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGA
GGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGT

AA-seq:

DIQMTQSPASLSVSVGETVTITCRASENIYRNLAWYQQKQKGKSPQLLVHAATNLADGVPSRFSGSGSDTQYSLKINSIQ
SEDFGNYYCQHFWGTPITFGAGTKLELKFADAAPTYSIFPPESSEQLTSGGASVVCFLINFEYFKDINVKWKIDG
GEFQNGVLEWNTDQDSKDDTYSMSSITLTITKDEYERBNSYTCBATEKTSTGPVKSFIWNEEC

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
 GCAGCACCAAGGTGGACAAGAAAATTGTGCCAGGGATTGTGGTTGTAAGCCTTGCCATATGTACAGTCCC
 AGAAGTATCATCTGTCTTCTCTCCCTCCAAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAG
 GTCACGTGTCTTGTGGTAGACATCAGCAAGGATGATCCCGAAGTCCAGTTCAGCTGGTCTGTAGATGATG
 TGGAGGTGCACACAGCTCAGACGCAACCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGA
 ACTTCCCATCATGCAACAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTCAACAGTGACAGCTTTC
 CCTGCCCTCATCGAGAAAACCATCTCCAAAACCAAGGCAGACCGAAGGCTCCACAGGTGTACACCATTC
 CACCTCCCAAGGAGCAGATGGCCAAAGGATAAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGA
 AGACATTACTGTGGAGTGGCASTGGAATGGGCAGCCAGCGGAGAACTACAAGAACACTCAGCCCATCATG
 GACACAGATGGCTCTTACTTCTGTCTACAGCAAGCTCAATGTGCAGAGAGCAACTGGGAGGCAGGAATA
 CTTTCACCTGCTCTGTGTTACATGAGGGCTGCACAACCACCATACTGAGAAGAGCCTCTCCCACTCTCC
 TGGTAAA

AA-seq:

EVQLQQFGTELVKPGASVKISCKASGYFTDYNMDWVKQSHGKSLEWIGDINPNYDTTYYNQKFKGKATLT
 VDKSSSTAYMELRSLTSEDYAVFYCARRNYGNYVGFDFWGQGTTLTVSSAKTTEPSVYPLAPGSAQTNSM
 VTLCCLVKGYPFVTVTWNGSLSSGVHTEFAVLQSDLYTLSSSVTVFSSSTWPSSETVTCNVVHPASSTK
 VDKKIIVPRDCGCKPCICTVPEVSSVFIFPPKPKOVLTITLTTPKVTCTVVDISKDDPEVQPSWFDVDDVEVH
 TAQTQPPPEQFNSTFRSVSBLIFIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGEPKAPQVYITPPPK
 EQMAKDKVSLTCLITDFPPEOLTVEWQWNGQPAENYKNTQPIIMDTDGSYFVYKLVNQKSNWEAGNTFTC
 SVLEGLHNHSTKSLSHSPGK

Light chain: DNA sequence

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

Nucseq:

AATATTGTGCTGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTTCCATAACCTGCA
 AGGCCAGTCAGCGTGTGAATAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGC
 TGATATACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGG

Figure 73

ATTTCACTTTTACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAG
CTCTCCATTTCACGTTTCGGCTCGGGGACAAAAGTTGGAAATAAAAACGGGTGATGCTGCACCAACTGTATCC
ATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCT
ACCCCAAAGACATCAATGTCAAGTSGAAGATTGATGGCAGTGAACGACAAAATGGGCTCTTGAACAGTTG
GACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCAACCTTCAGTTTGAACAAAGACGAGTAT
GAACGACATAACAGCTATACTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCA
ACAGGAATGAGTGT

AA-seq

NIVLTQTPKFLVLSAGDRVSITCKASQVRVNDVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGYGTD
FTFTISTVQAEDLAVYFCQQDYSSPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI
NVKWKIDGSERQNGVLNSWTDQDSKDYSTMSTLTLTKEVERHNSYTCEATHKSTSPIVKSFNRNEC

Figure 73 continued