

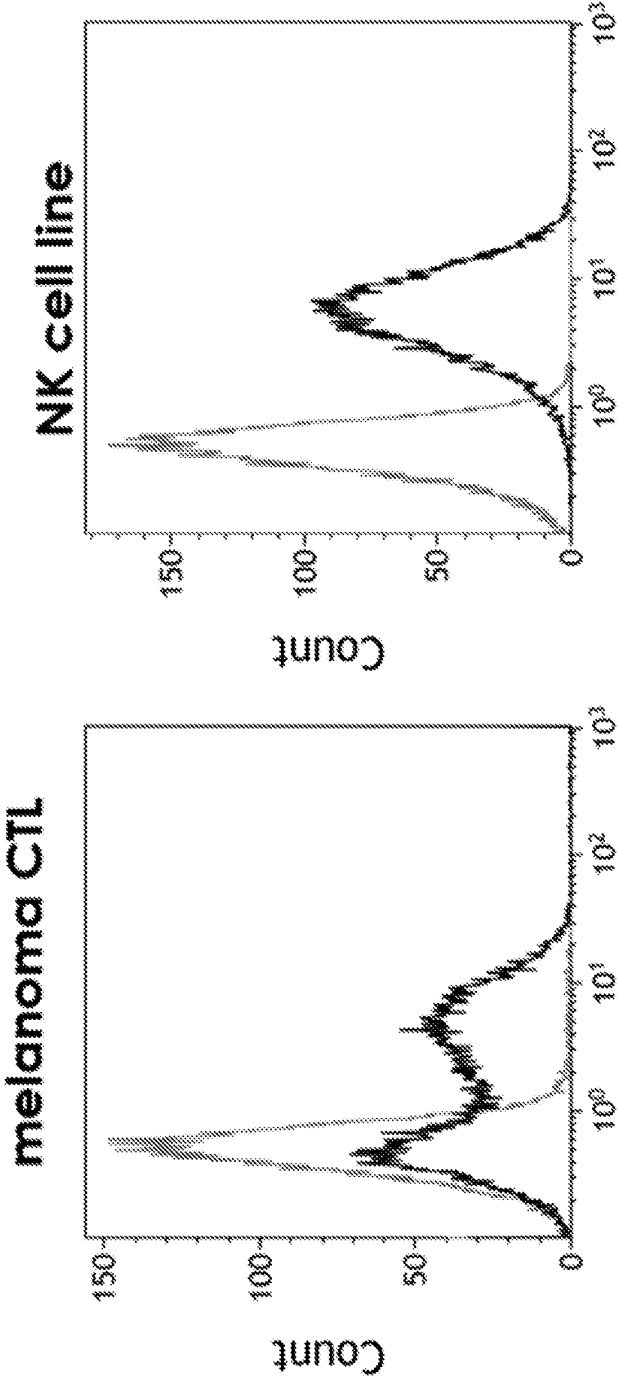


Fig. 1

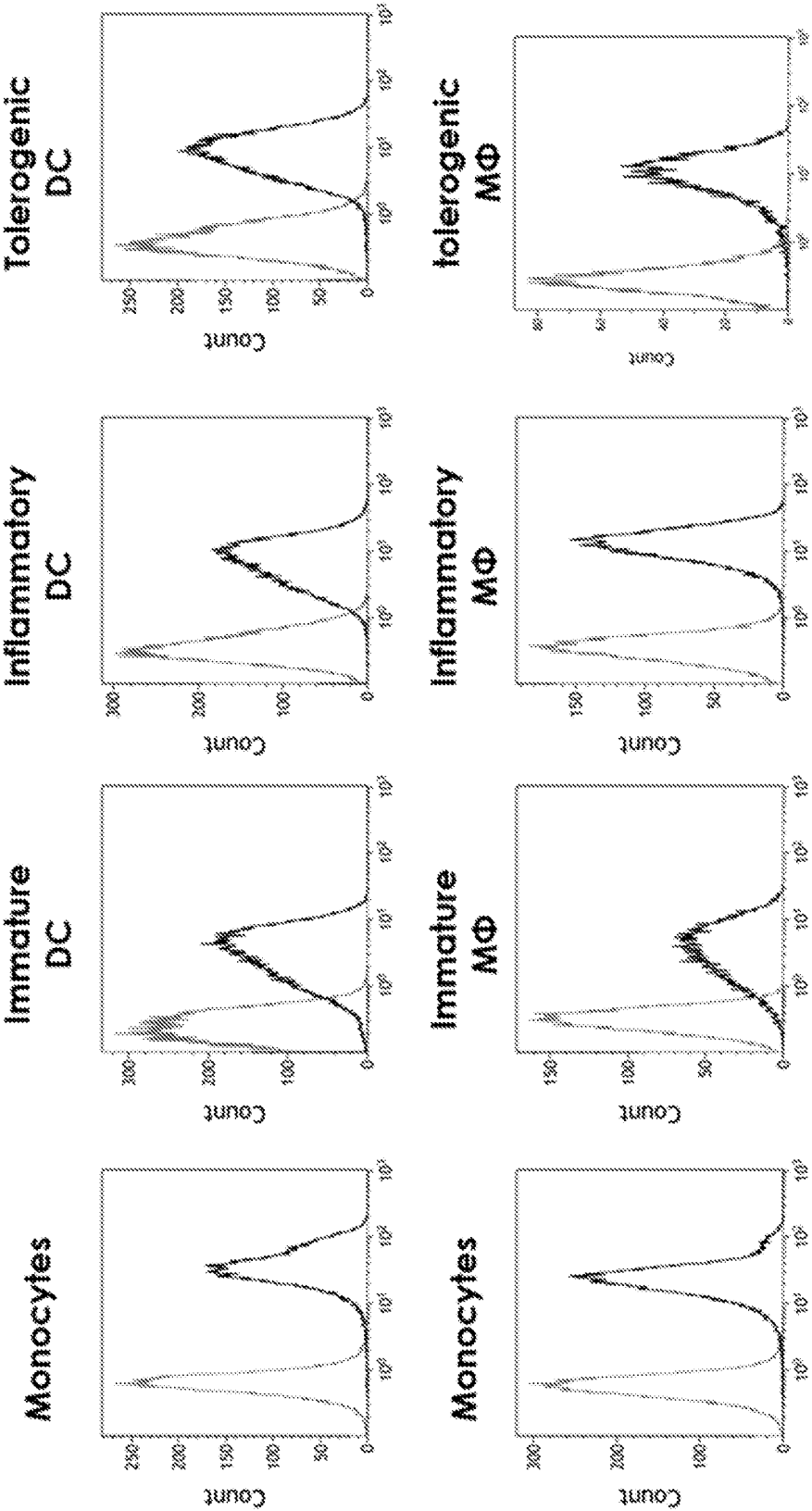


Fig. 2

TCGA Cancer Type	Cancer name	Fold Over Expression (vs Normal)	N samples
KIRC	Kidney renal clear cell carcinoma	10.4	534
KIPAN	Pan kidney cohort (KIRC, KIRP, KICH)	7.74	891
SARC	Sarcoma	3.03	263
GBM	Glioblastoma multiform	2.67	166
UCEC	Uterine Corpus Endometrial Carcinoma	2.33	546
HNSC	Head and Neck squamous cell carcinoma	2.2	522

Fig. 3A

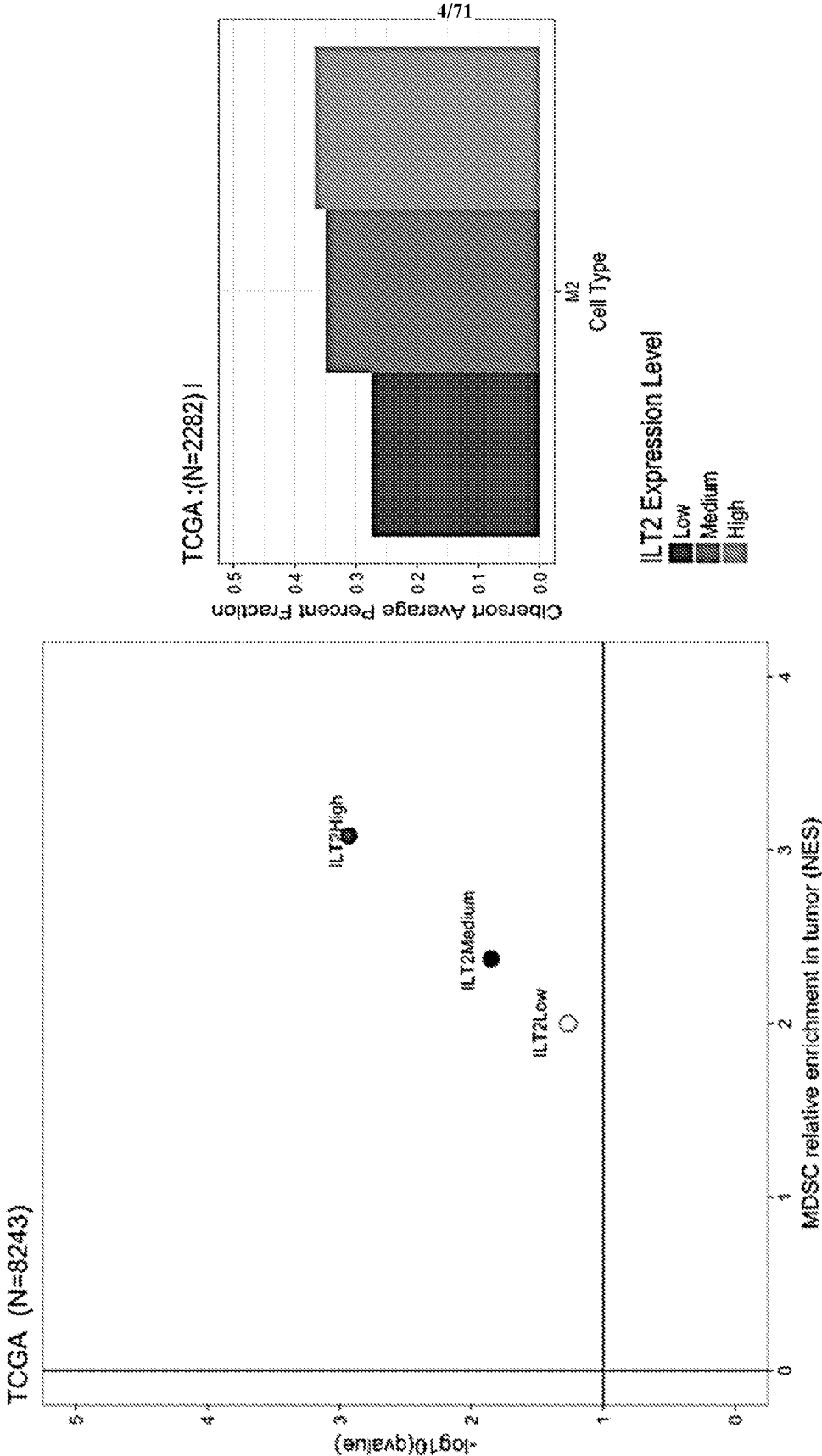


Fig. 3B

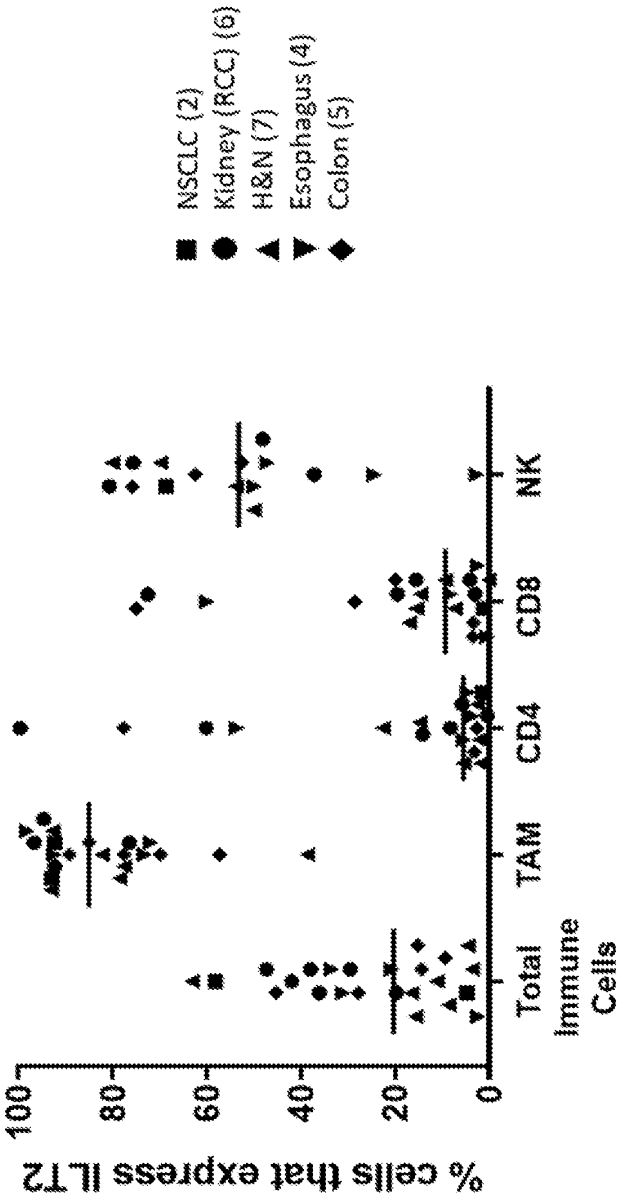


Fig. 3C

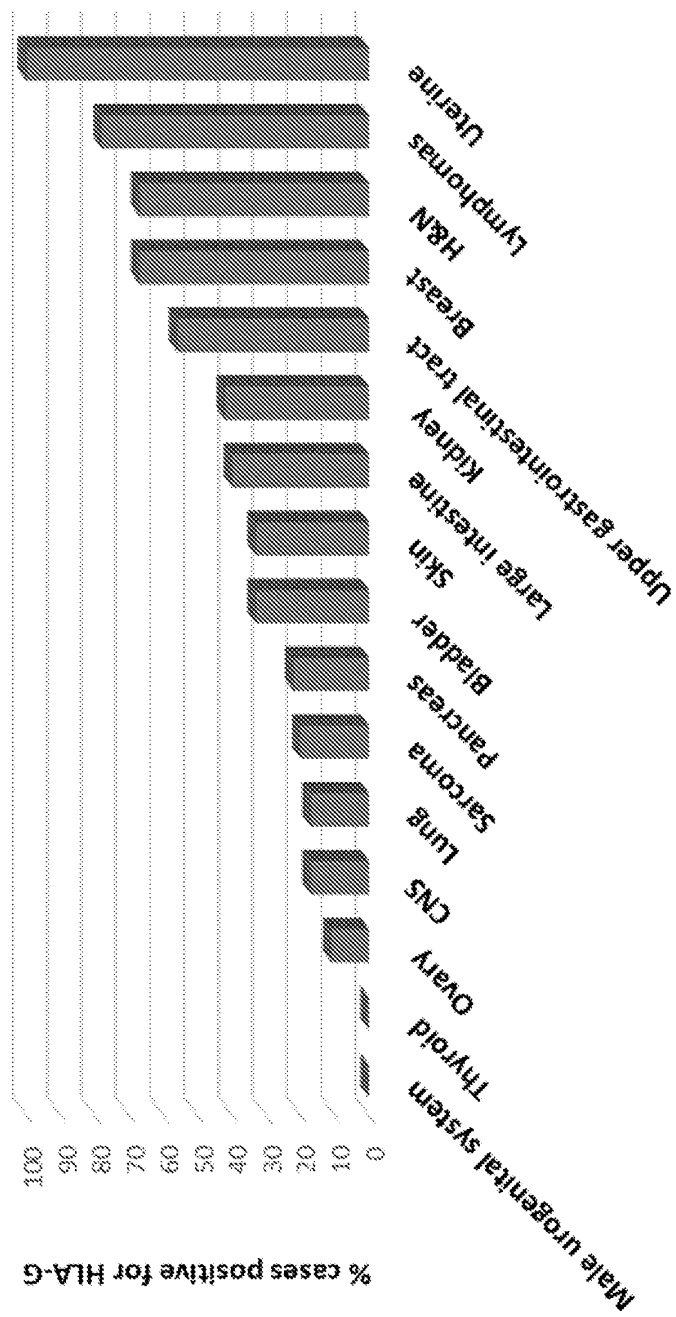


Fig. 4A

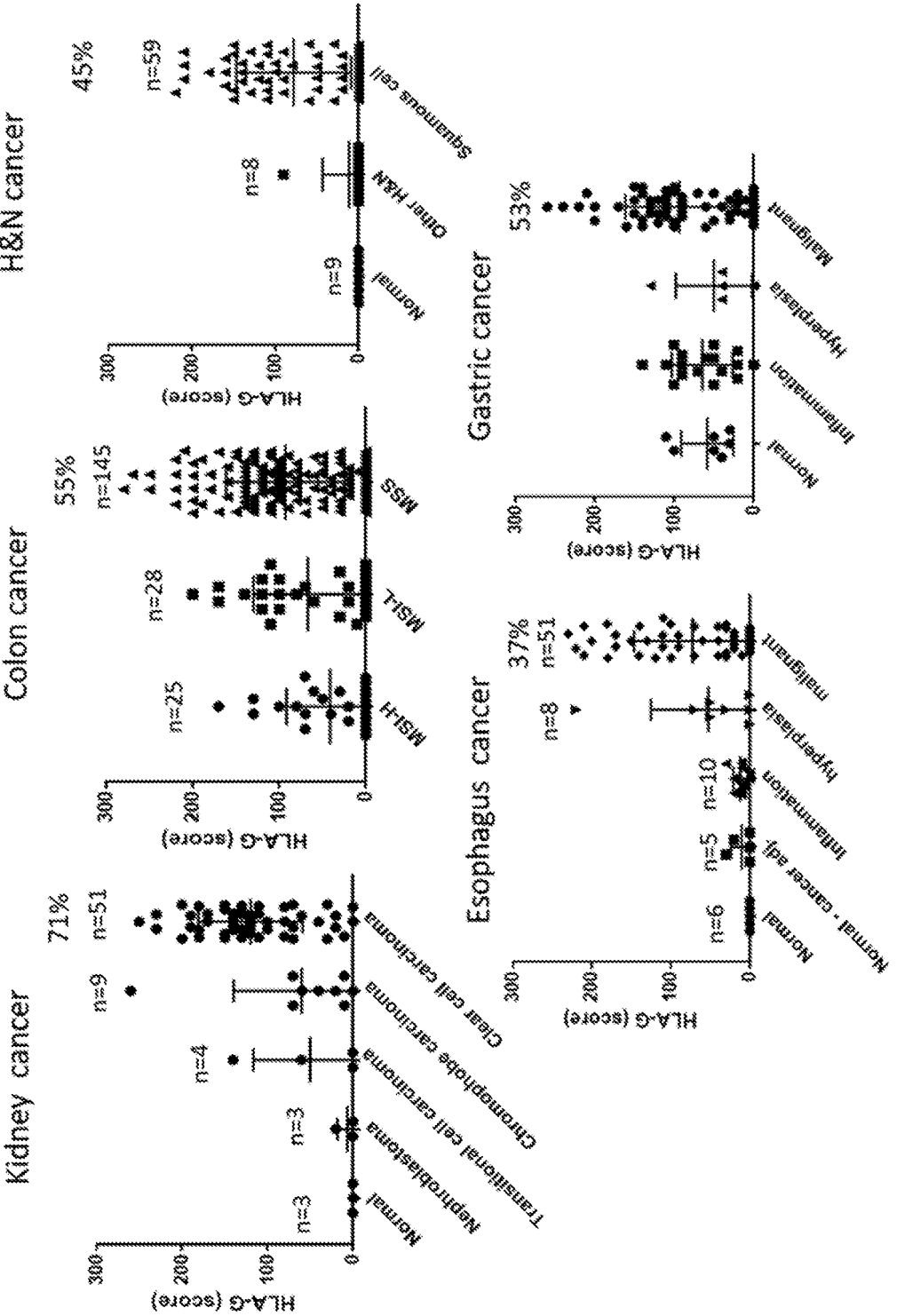


Fig. 4B

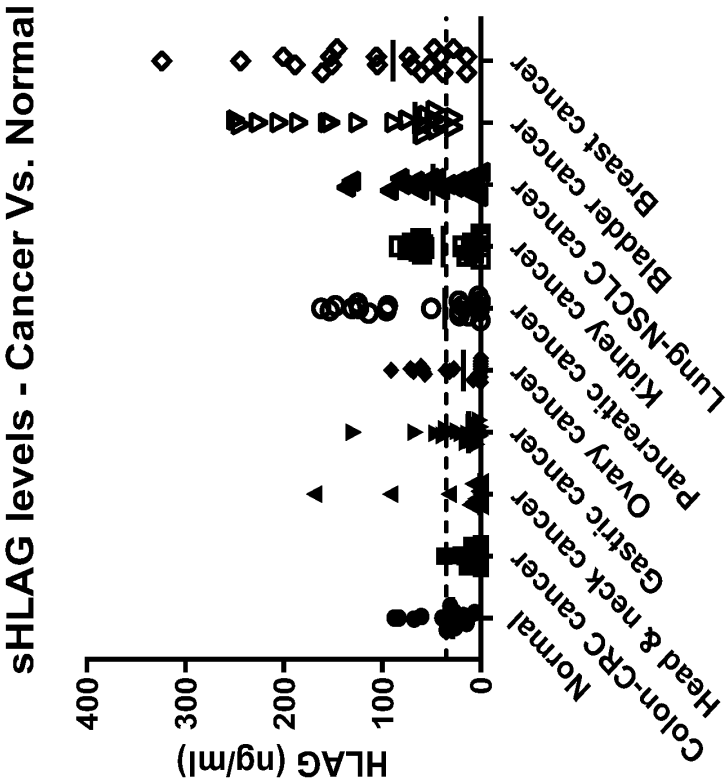


Fig. 5

19E3 heavy chain variable region (Murine)

10 20 30 40 50 60 70 80 90
CAGGTTCAAGTGCAGTCTGGAGCTGAGCTGGCGAGGCTTGGGCTTCAGTGAAGCTGCTGCAAGGCTTCTGACCTTACACCTTCAAGCTAIGGTA 100
Q V Q L Q Q S G A E L A R P G A S V K L S C K A S G Y T F T S Y G I 34
YAGCTGGGTGAAGCAGAGAACTGGACAGGGCCCTTGAGTGGGTTGGAGAGATTTATCTTGGAGTGGTAATTTCTTACTACAAATGAGAAATTCAGAGGCAA 200
S W V K Q Q R T G Q Q G L E W V G E I V P G S G N S Y Y N E K F K G K 67
GGCCACACTGACTGCAGACAAATCCTCCAGCACAGCGTACATGGAGCTCCGAGGCTGACATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGATCGAAT 300
A T L T A D K S S S T A Y M E L R S L T S E D S A V Y F C A R S N 100
GATGGTTACCTGACTACTGGGSCCAAGGSCACCACTCTCACAGTCTCTCA 351 SEQ ID NO: 32
D G Y P D Y W G Q G T T L T V S S 117 SEQ ID NO: 21

19E3 light chain variable region (Murine)

10 20 30 40 50 60 70 80 90
GACATCCAGATGACACAACTCTTCATCTCTACTTGTCTGTATCTCTAGGAGGACAGATCACCATTACTTGGCAAGGCAAGTGACCACTTAATAATTGGTTAG 100
D I Q M T Q S S S Y L S V S L G G R V T I T C K A S D H I N W N L A 34
CCTGGTATCAGCAGAAACCCAGGAAATGCTCTTAGGCTCTTAATAATCTGGTGCACCACTGGTGGAACTGGGGTTCCTTTCAGAGATTCAGTGGCAGTGGATC 200
W Y Q Q K P G N A P R L L I S G A T S L E T G V P S R F S G S 67
TGGAAAGGATTACACTCTCAGCATTACCAAGCTTCAGACTGAAGAATGTTGCTACTTATTACTGTCAACAGTATTGGAGTACTCCGTGGACGTTCCGGTGGGA 300
G K D Y T L S I T S L Q T E D V A T Y Y C Q Q Y W S T P W T F G G 100
GGCACCAGGCTGGAAATCAAA 321 SEQ ID NO: 39
G T K L E I K 107 SEQ ID NO: 22

Fig. 6A

15G8 light chain variable region (Murine)

[illegible]

Fig. 6A (cont.)

15G8 heavy chain variable region (Human)

10	20	30	40	50	60	70	80	90	
GATGTCCAGCTGCAAGGCTCTGGCCCTGGACTGGTTAAGCCCTCCGAGACACTGTGCTGACCTGCTGTGTGACCGGCTACTCTATCACCCTCCGGCTACT									100
D V Q L Q G S G P G L V K P S E T L S L T C S V T G Y S I T S G Y Y									34
ACTGGAACTGGATCAGACAGTTCCCCCGSCAAGAAACTGGAAATGGATGGGCTACATCTCTTACGACGGCTCCAACTACAACTCCAGCCCTGAGAGAACCG									200
W N W I R Q F P G K K L E W M G Y T S Y D G S N W Y N P S L K N R									67
GATCACCATCTCTCGGGACACCTCCCAAGAACCACTGTTCTCCCTGAAGCTGAACCTCGTGACCGCTGCGATACCGCTACCTACTACTGTGCTCAGCGGTAC									300
I T I S R D T S K N Q F S L K L N S V T A A D T A T Y Y C A H G Y									100
TCCTACTACTAGGCCATGGATGCTTGGGGCCAGGGCACATCTGTGACAGTGTCTCT	357	SEQ ID NO: 34							
S Y Y Y A M D A W G Q G T S V T V S S	119	SEQ ID NO: 28							

15G8 light chain variable region (Human)

10	20	30	40	50	60	70	80	90	
GACATCCAGATGACCCAGTCTCCATCTCTGTGCTGCTCTGTGGGGGACAGAGTGACCAATCACCCTGTGGACCTCTCAGGACATCTCCCACTACCTGGA									100
D I Q H T Q S P S S L S A S V G D R V T I T C R T S Q D I S N Y L N									34
ACTGGTATCAGCAGAAACCCGGCAAGGCCGTGAAGCTGCTGATCTCTTACACCTCCAGACTGCACTCTGCGCTGCTCCAGATTTTCTGGCTCTGGATC									200
W Y Q Q K P G K A V K L L I S Y T S R L H S G V P S R F S G S									67
TGGCACCAGCTACACCTGACCATCAGTCTCTGACGCTGAGGACTTCGCCACTACTACTGTGTCAGCAGGGCAACACCTTGGCTACCTTTGGCCAGGGAC									300
G T D Y T L T I S S L Q P E D F A T Y Y C Q Q G N T L P T F G Q G									100
ACCAAGCTGGAATCAAG	318	SEQ ID NO: 38							
T K L E I K	106	SEQ ID NO: 24							

Fig. 6A (cont.)

17F2 heavy chain variable region (Murine)

```

10      20      30      40      50      60      70      80      90     100
CAGGTTCAAGCTGCAACAACTCTGAGGCTGAGTTGGTGAACCTGGAGCTTCAGTGAAGATATCCYGCAGGGTTTCYGGCTACAGCCTTCACCTGACCAATACCTA
Q V Q L Q Q S Q A E L V K P Q A S V K I S C K V S G Y T F T Q H T
10      20      30      40      50      60      70      80      90     100
YTCACYGGATGAAGCAGAGGCTGCAACAGGCTGGAATGGATTGGATATATTTATCTAGAGATGGTAGTACTAAGTCAATCAATGAGAAAGTTCAGAGGGCAA
I H W M R Q R P E Q Q L E W I Q Y I Y P R D Q S T K Y N E K F K G R
10      20      30      40      50      60      70      80      90     100
GGCCACATTGACTGCAGACAAATCTCCAGCAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACCTCTGCAGTCTATTTCTGTGCAAGAAAGCTTGG
A T L T A D K S S S T A Y M Q L N S L T S E Q S A V Y F C A R T W
10      20      30      40      50      60      70      80      90     100
GACTACTTTGACTACTGGGCGAAGGCCACCACTCTCACAGTCTGCTGA
Q Y F Q Y W G Q G T T L T Y S S
99101
110
```

SEQ ID NO: 35
SEQ ID NO: 19

17F2 light chain variable region (Murine)

```

10      20      30      40      50      60      70      80      90     100
GACATTGTGCTGACCCCAATCTCCAGCTTTCTTTGGCTGTCTCTTAGCGGCAGAGGGCCACCATATCTGCACAGCCCAAGTGAAGTGTGATAGTATAGCCAA
D I V L T Q S P A S L A V S L Q R A T I S C R A S E S V Q S Y G
10      20      30      40      50      60      70      80      90     100
ATAGTTTATGCACTGCTGACCAAGAAACCAAGACACGCAACCACTCTCTCATCTATCTGTCATCTGCACTGCAACCACTGAGAAATCTGGGATCTCTGCAAGTTCCAG
N G F M H W Y Q Q K P Q Q P K L L I Y R A S N L E S G I P A R F S
10      20      30      40      50      60      70      80      90     100
TGGCAGTGGTCTAGGACAGACTTCAGCCCTCACCATTAACTCTCTGAGGCTGATGATGTTCAGACCTATTACTGTCTCAGGAAAAGTAAATGAGGATCCGATAC
Q G S R T D F T L T I N P V E A D Q V A Y Y C Q Q S N E Q P Y
10      20      30      40      50      60      70      80      90     100
ACGTTCCGAGAGGCGGACCAAGCTGGAATATAA
T F G G G T K L E I K
100
```

SEQ ID NO: 36
SEQ ID NO: 20

Fig. 6A (cont.)

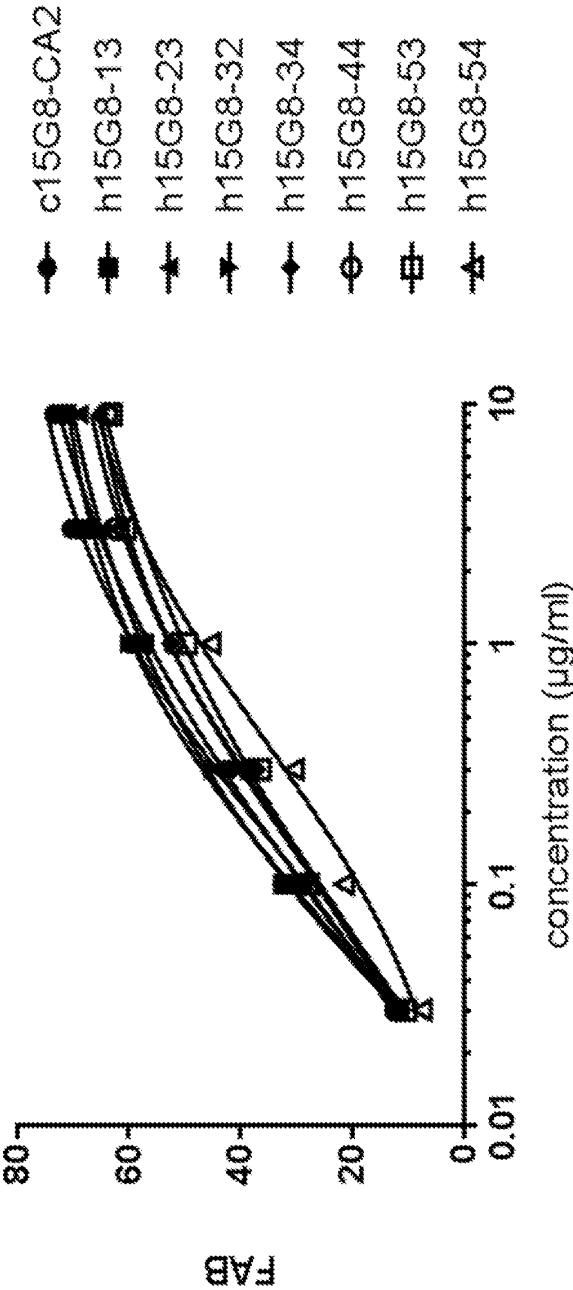


Fig. 6B

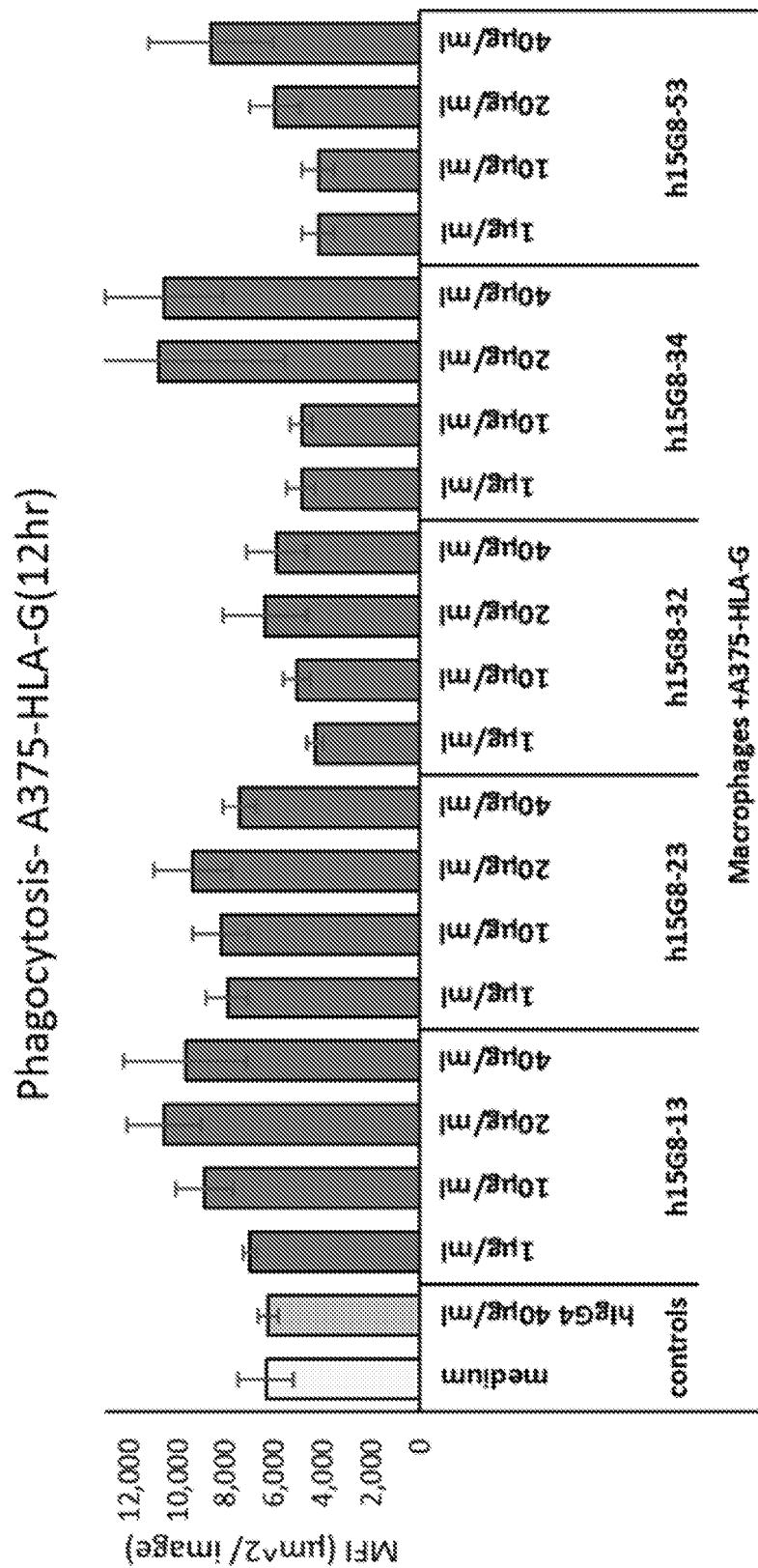


Fig. 6C

Phagocytosis- Normal donor Macrophages (7hr)

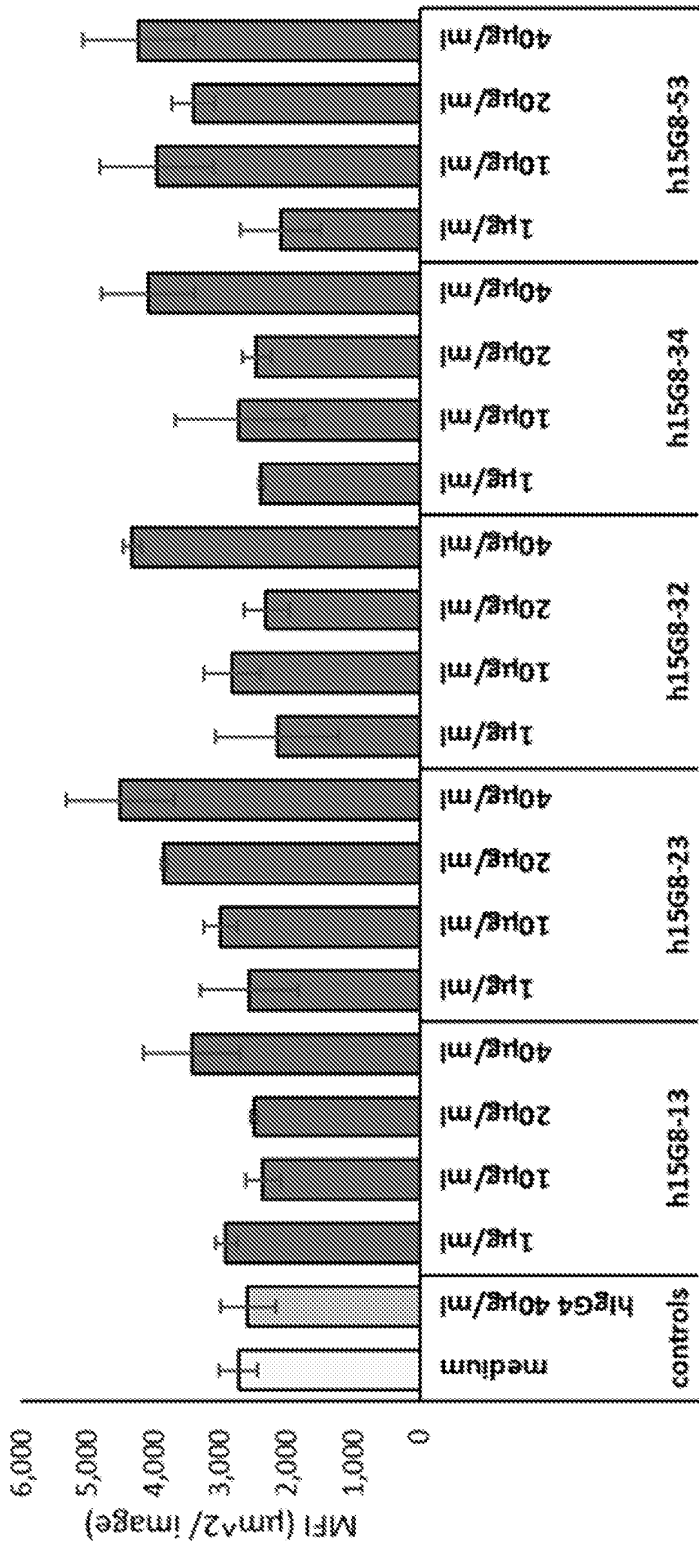


Fig. 6D

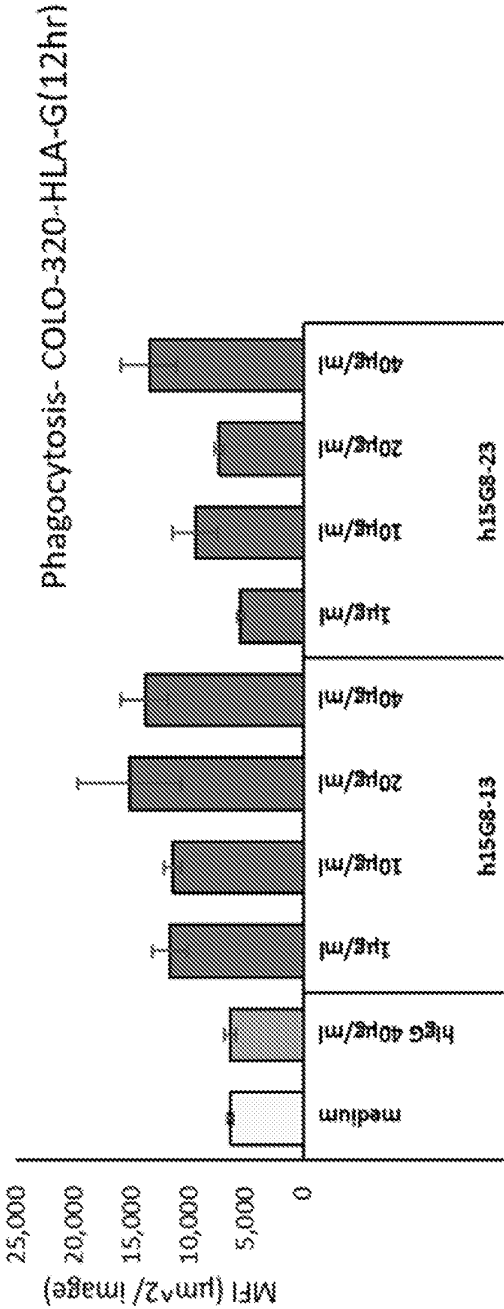


Fig. 6E

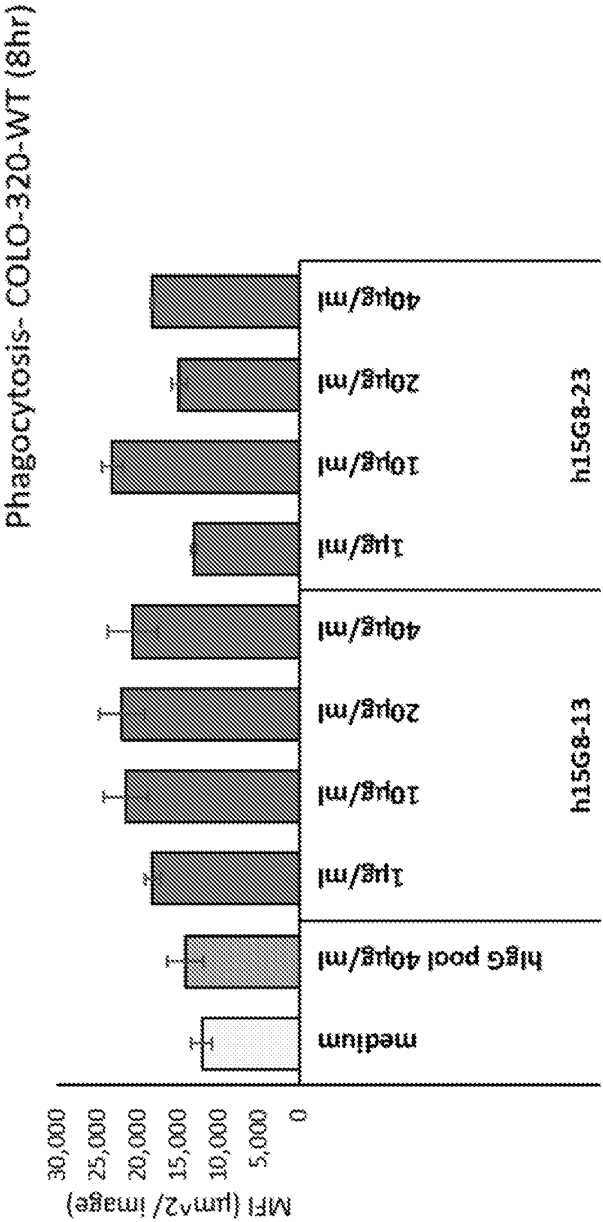
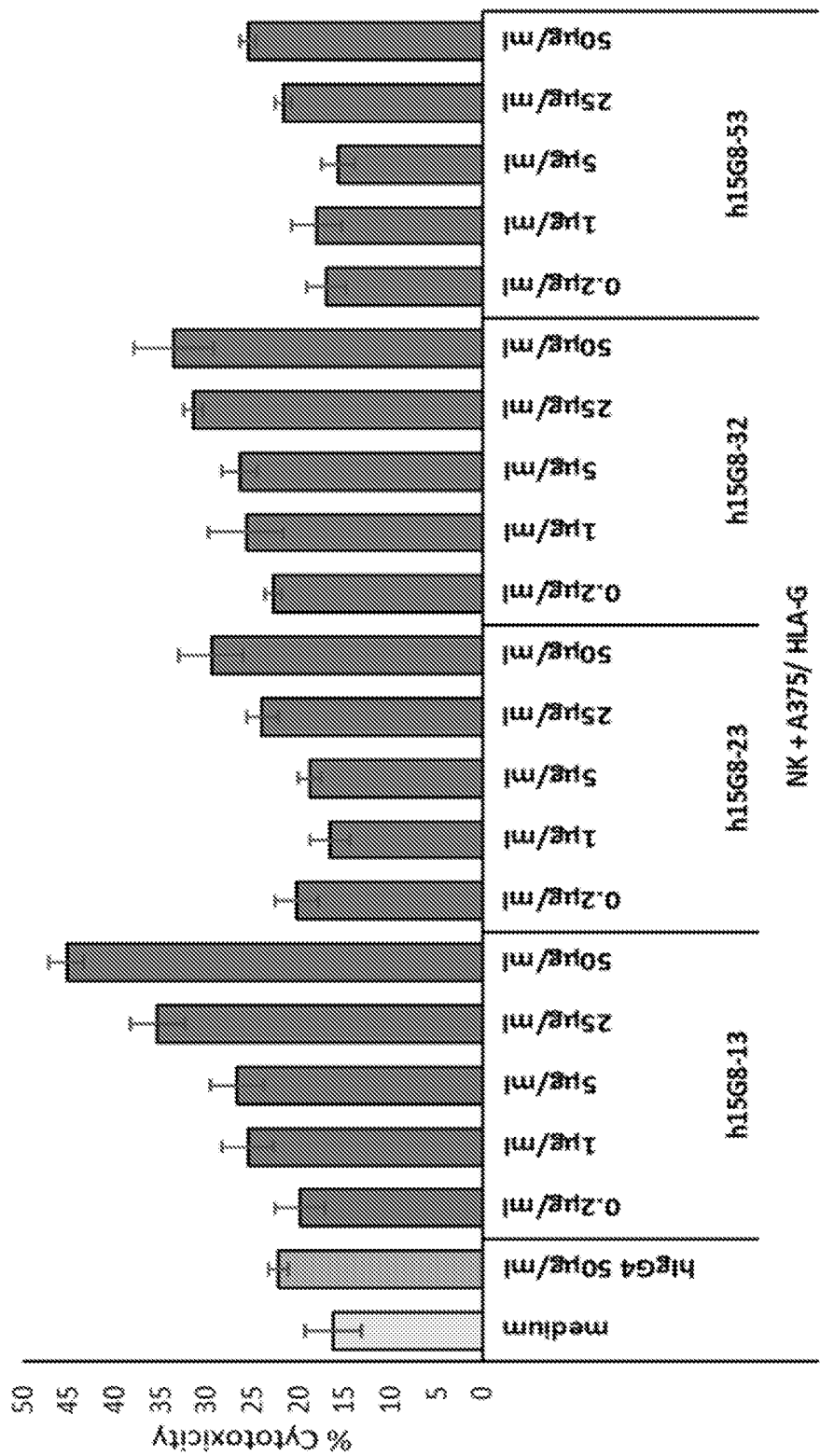


Fig. 6F



NK + A375/ HLA-G

Fig. 6G

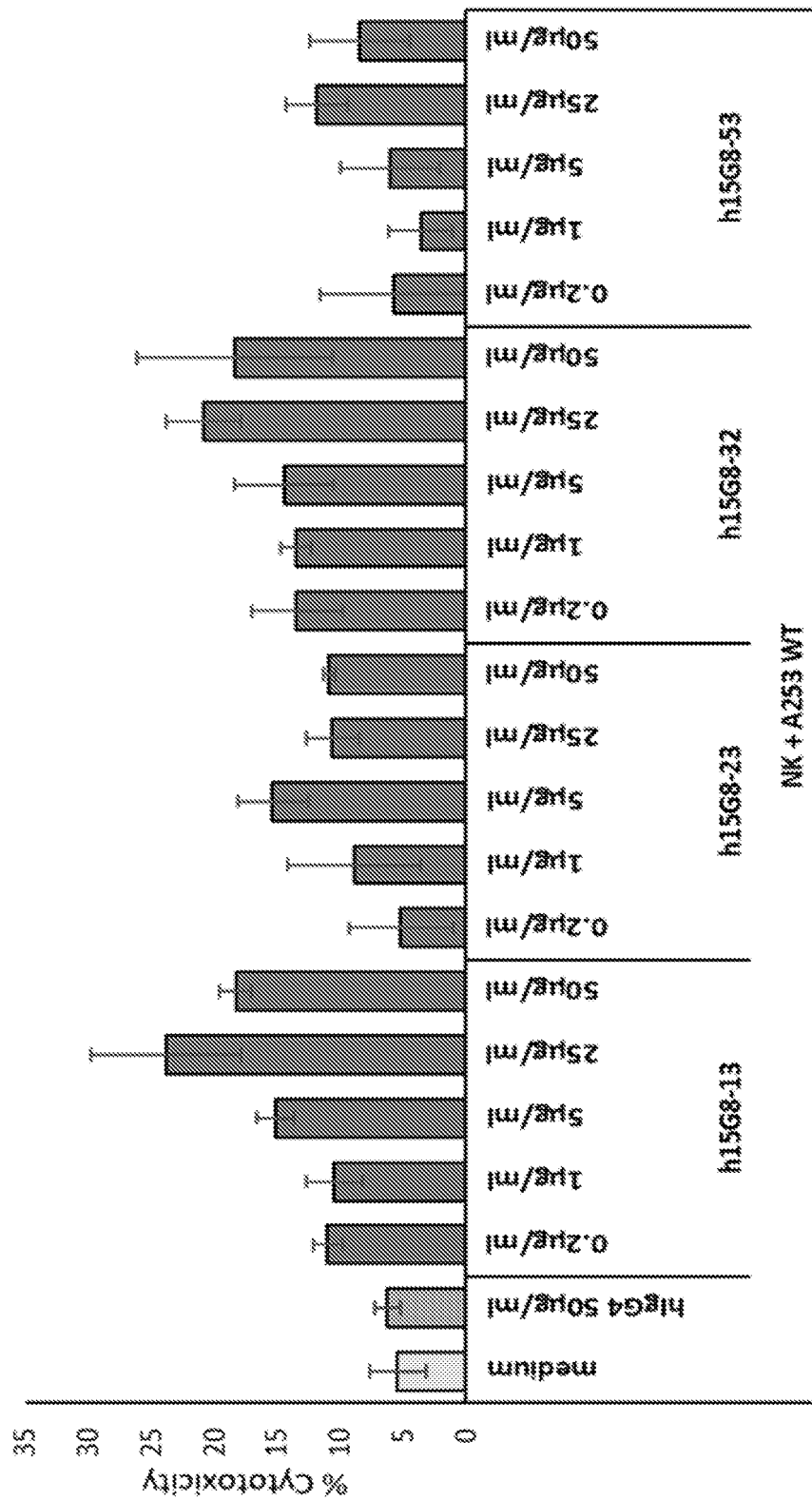


Fig. 6H

Clone#	ELISA (OD)			
	hILT2-Fc	PIRB	hILT6-His	hLILRA1-His
17F2	1.89	0.06	0.06	0.08
19E3	2.61	0.14	0.13	0.11
15G8	1.11	0.08	0.07	0.14
Positive	2.45	4.73	4.86	4.39
Negative	0.05	0.0575	0.071	0.13

Fig. 7A

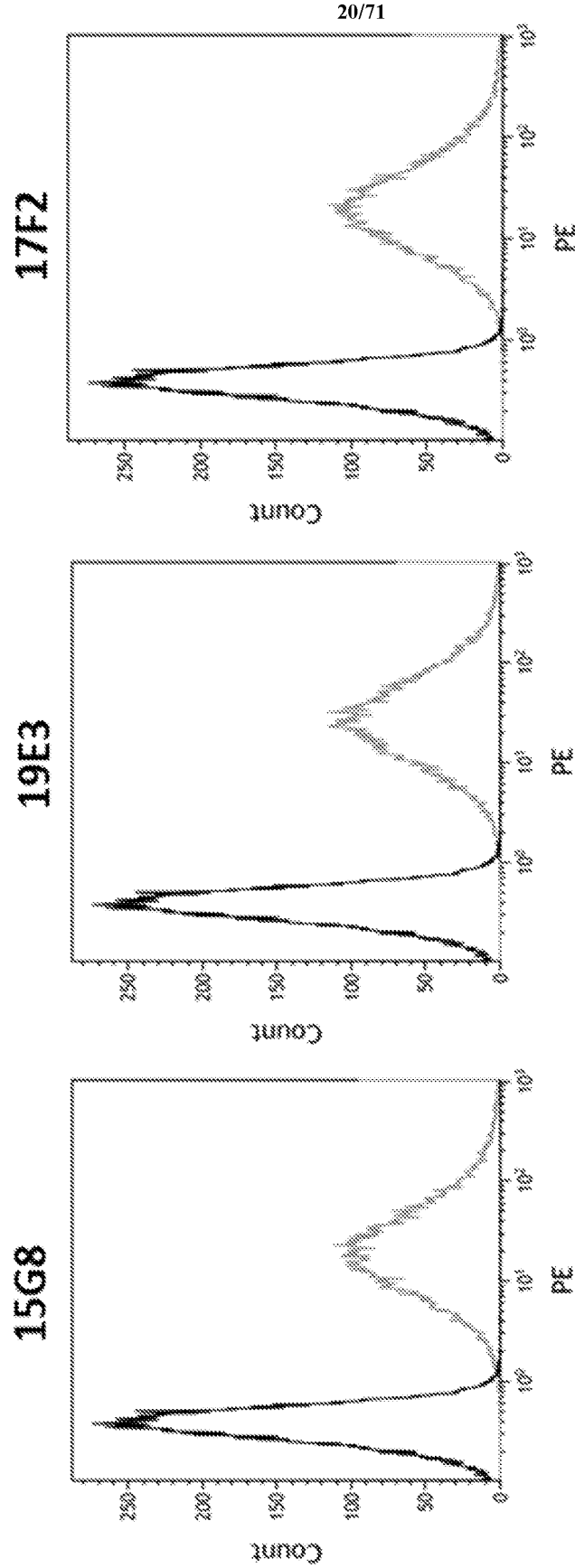


Fig. 7B

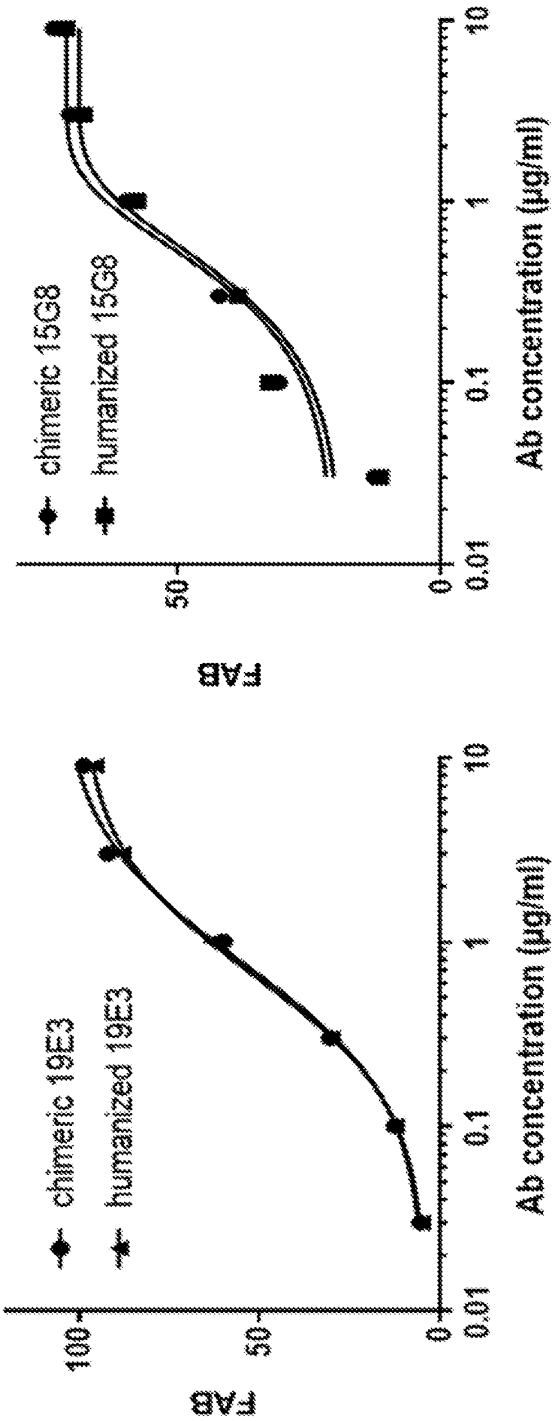


Fig. 7C

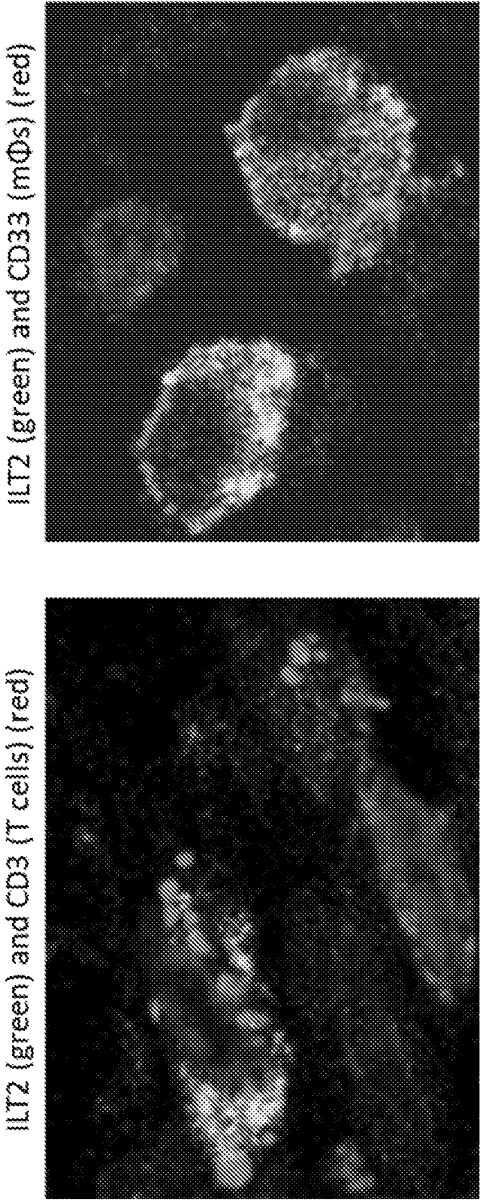


Fig. 7D

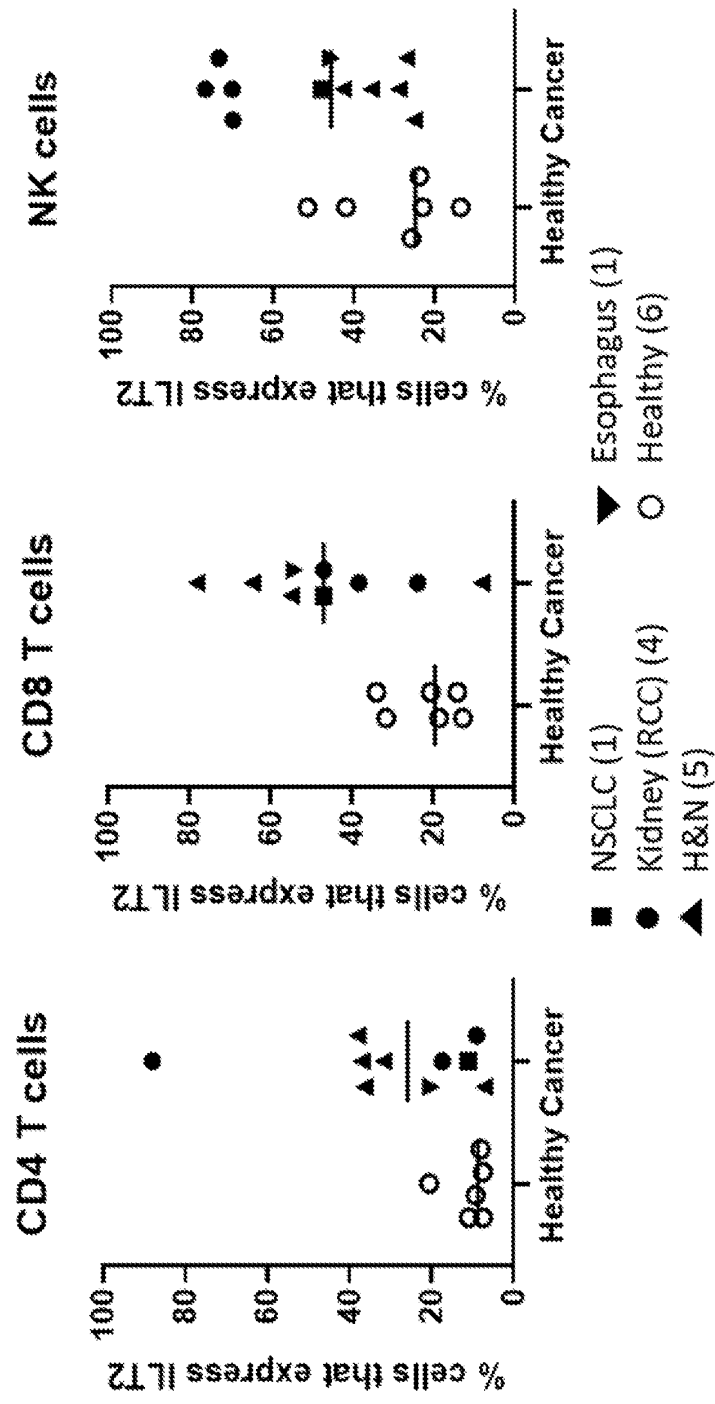
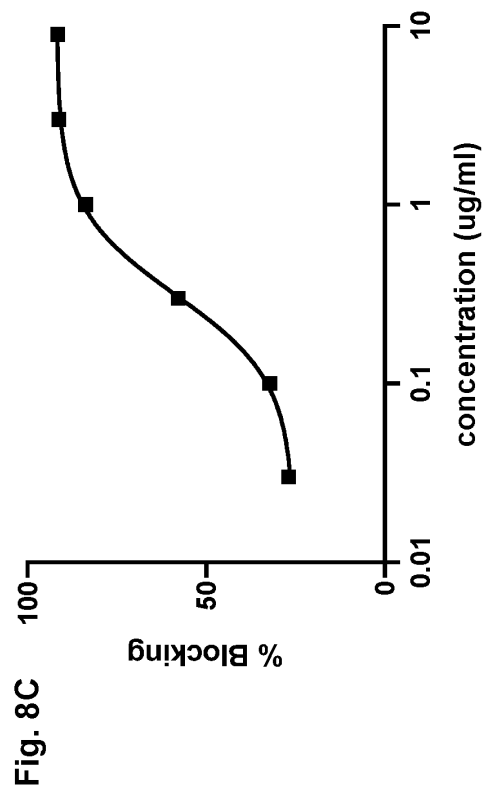
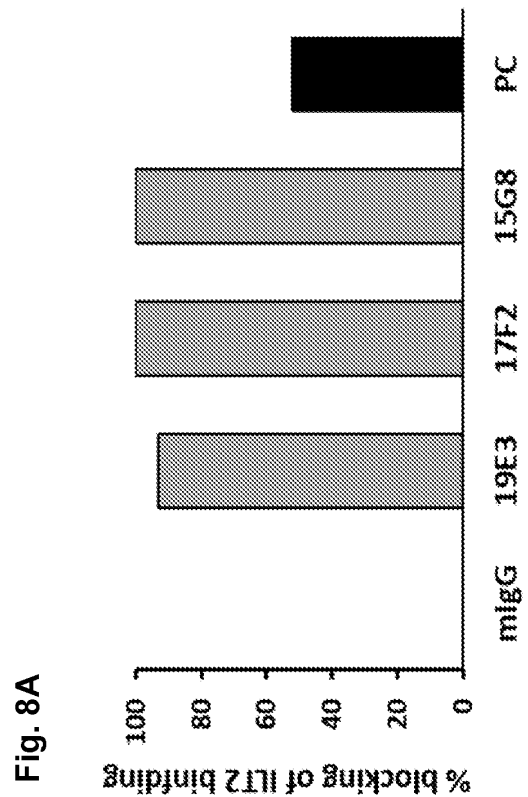
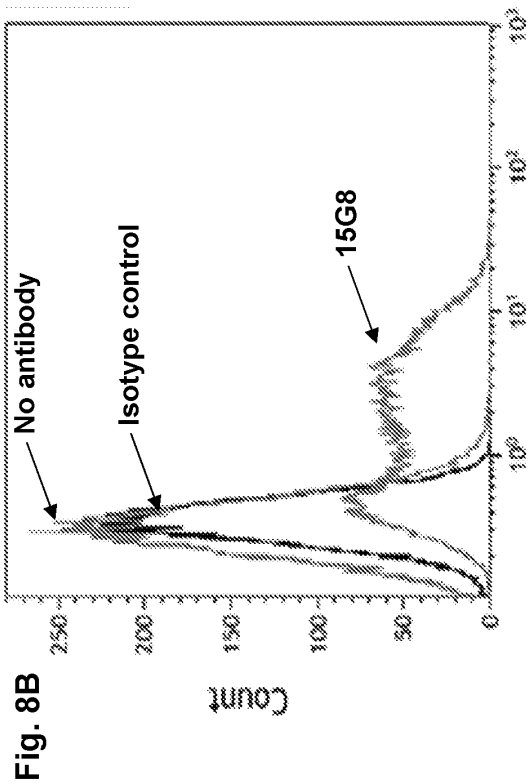


Fig. 7E



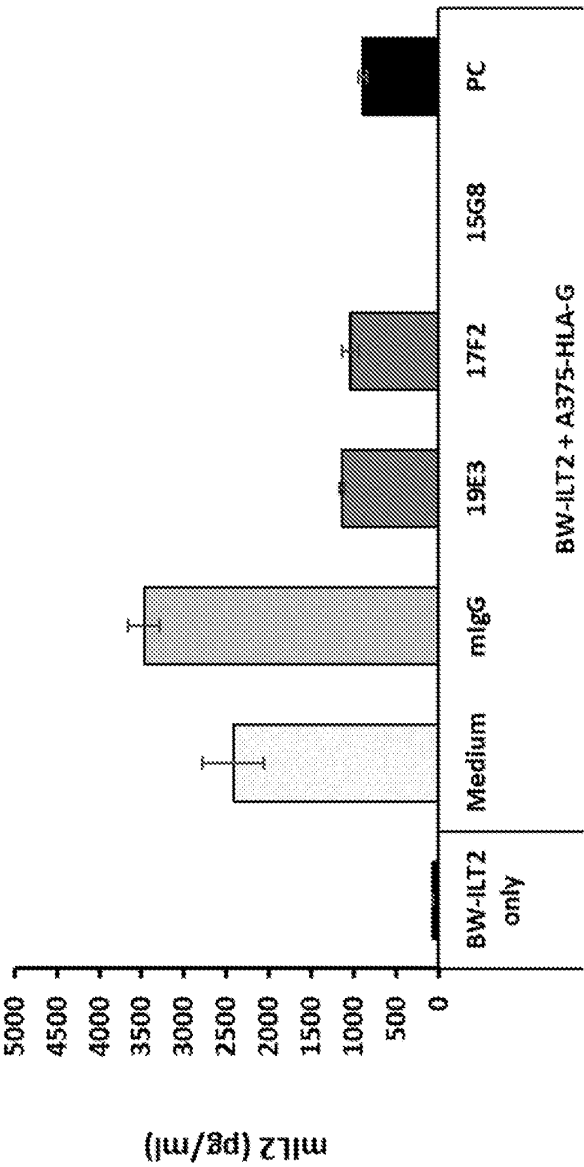
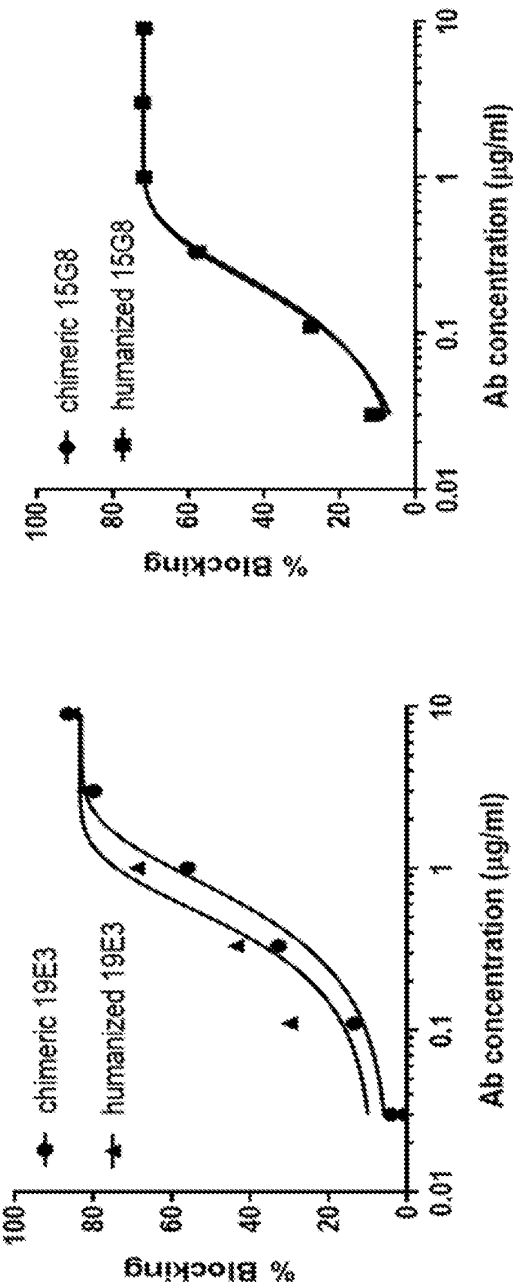


Fig. 8F

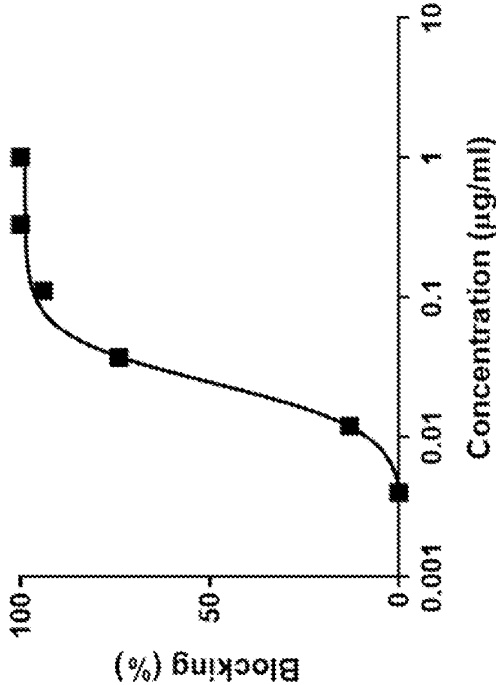
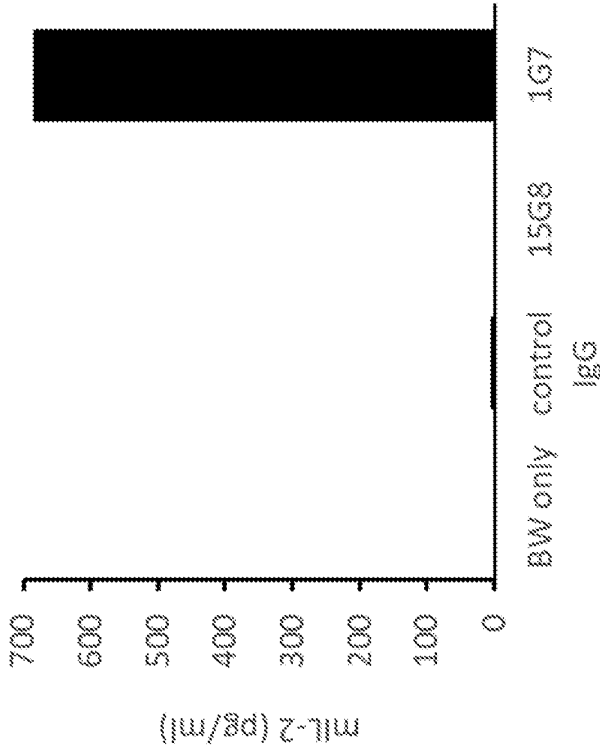
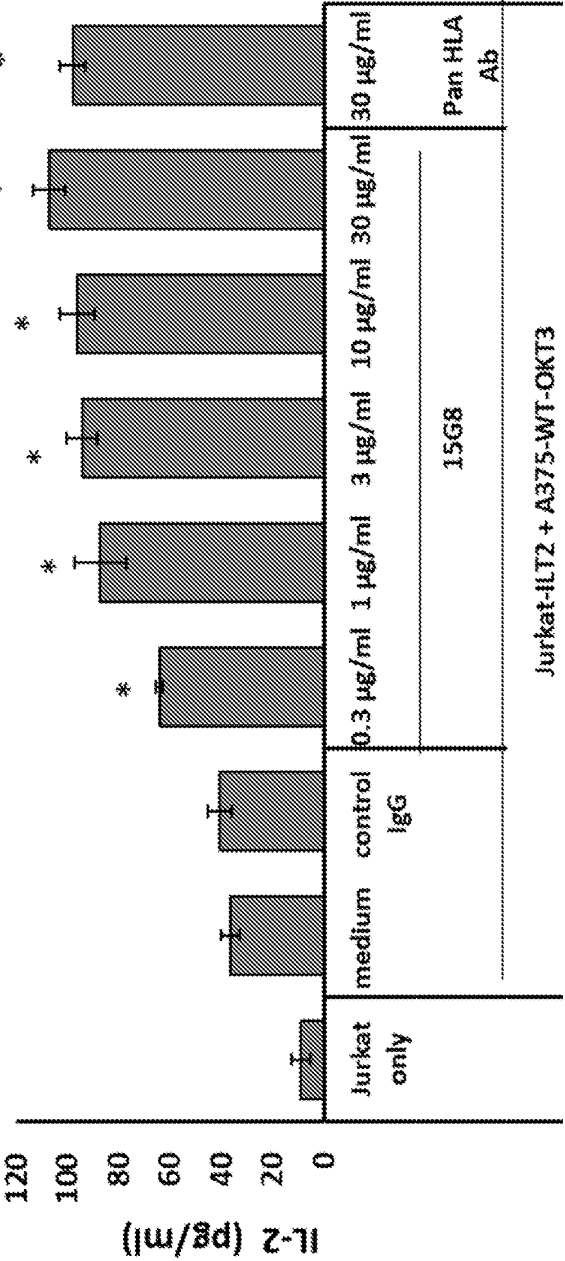
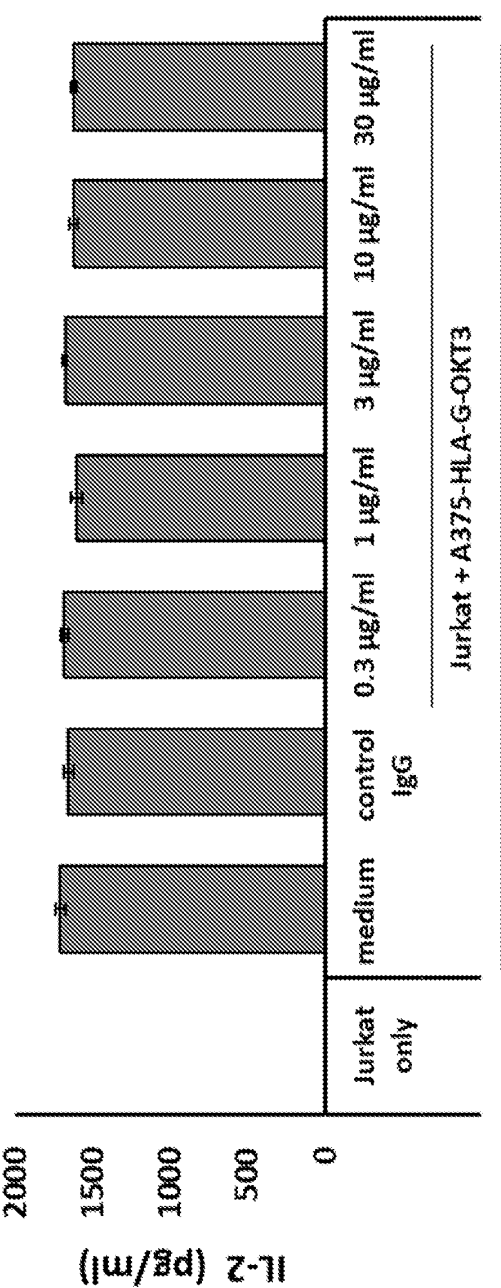
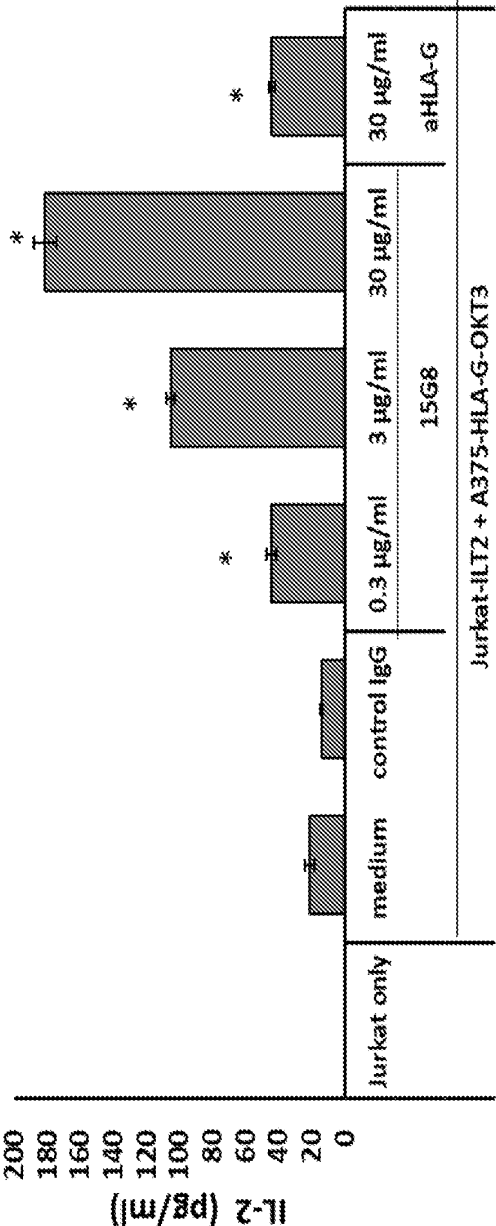
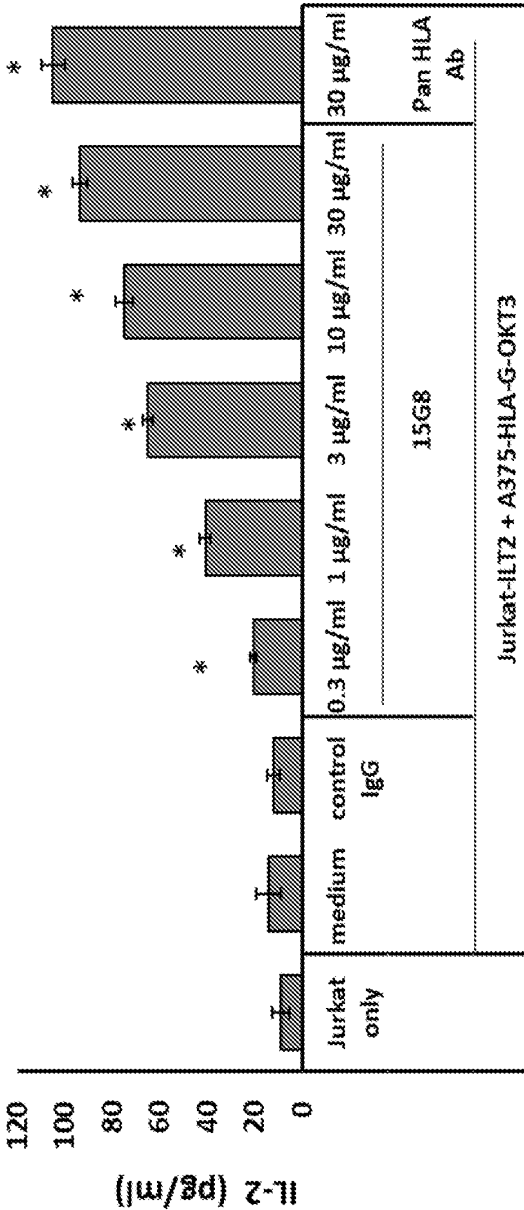


Fig. 8G







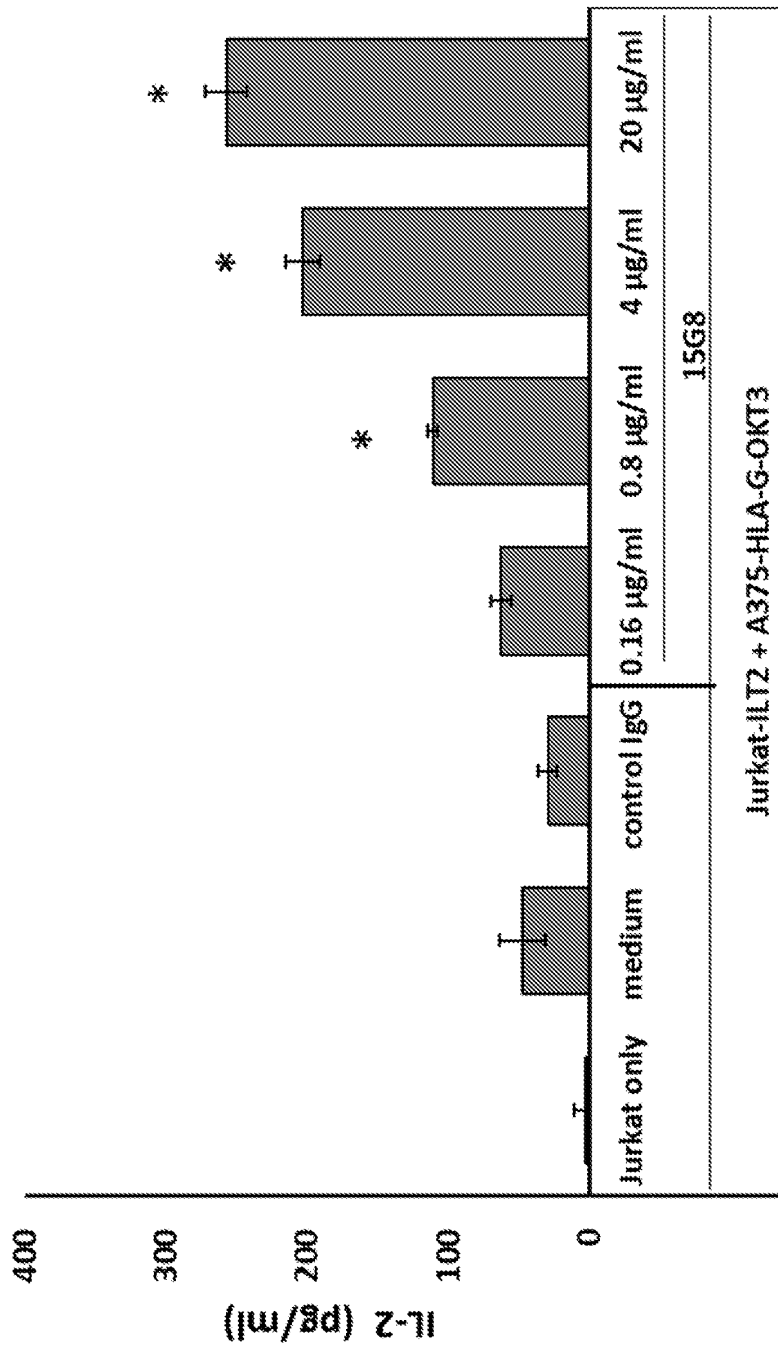


Fig. 8L

Fig. 8M

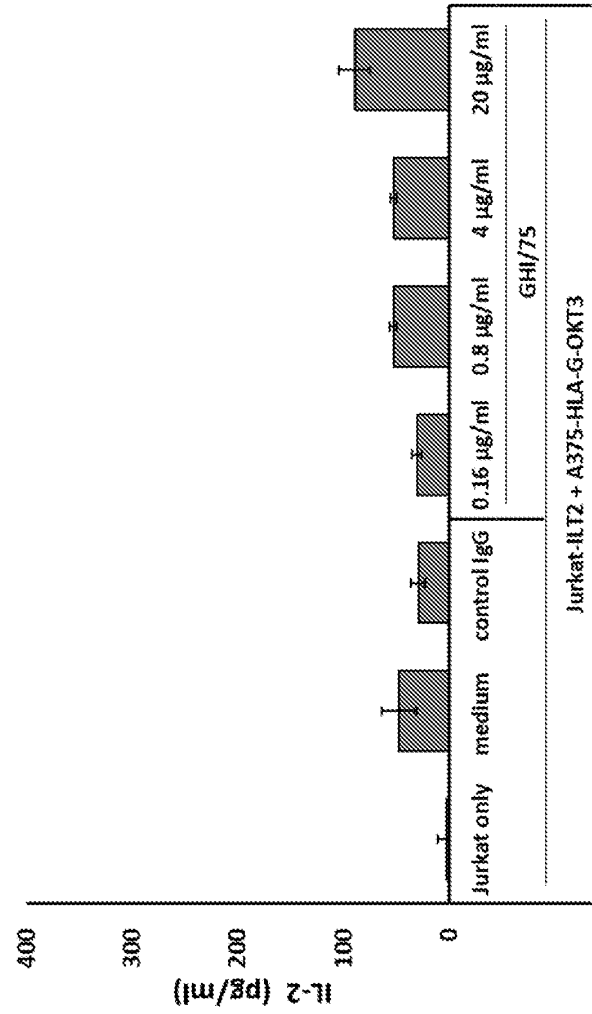


Fig. 8N

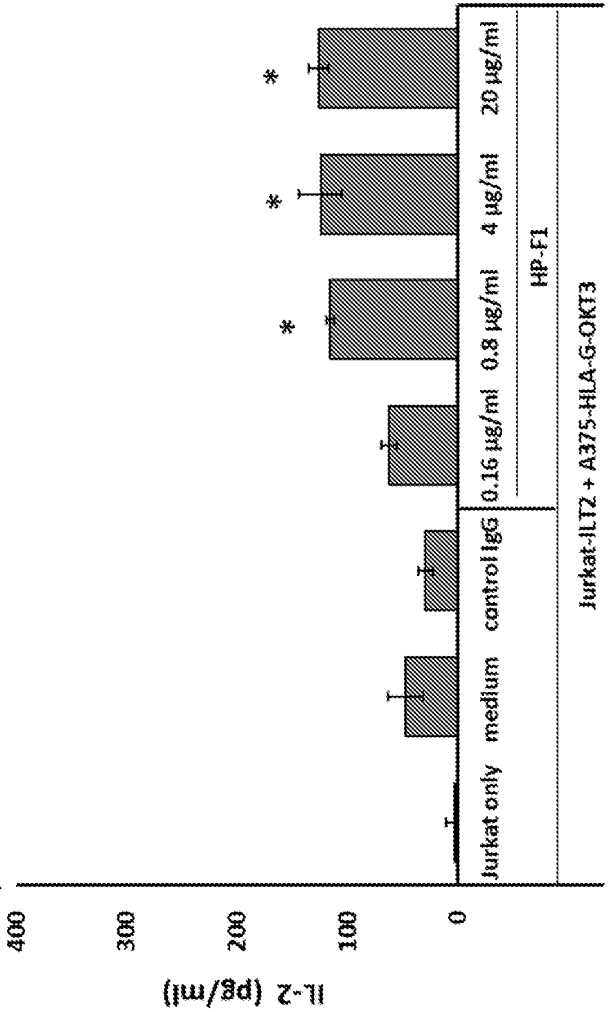


Fig. 8O

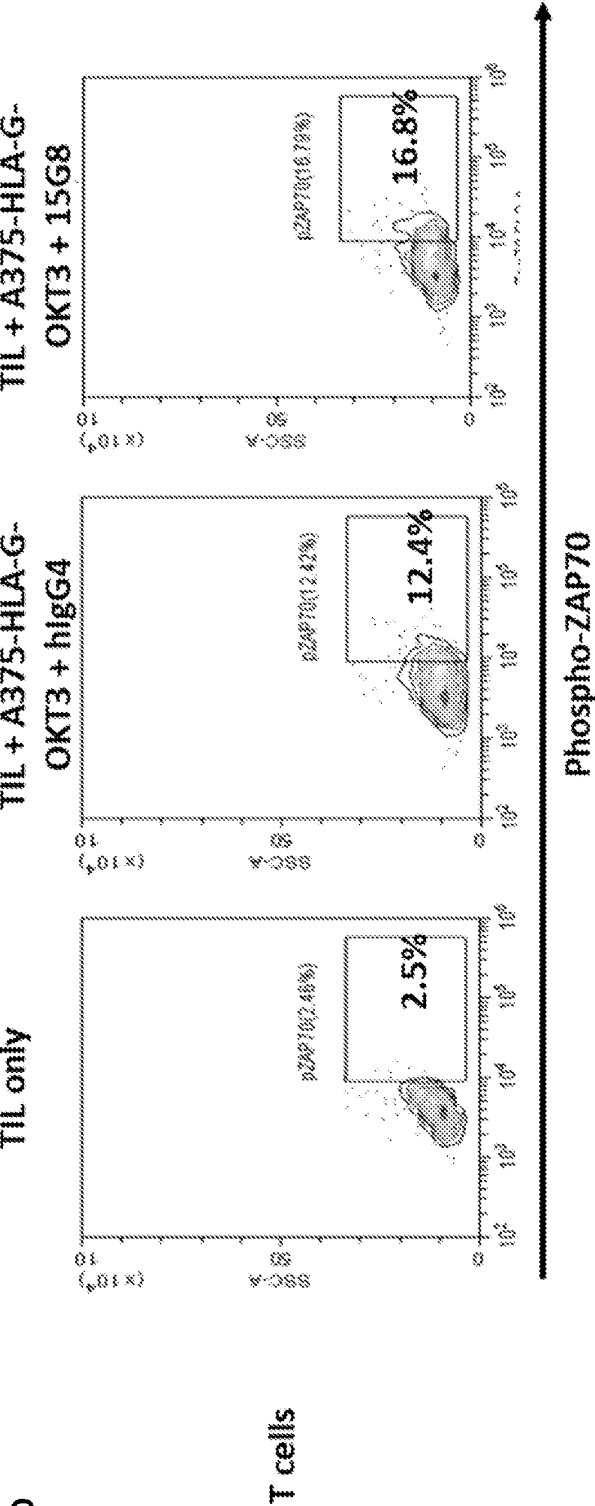
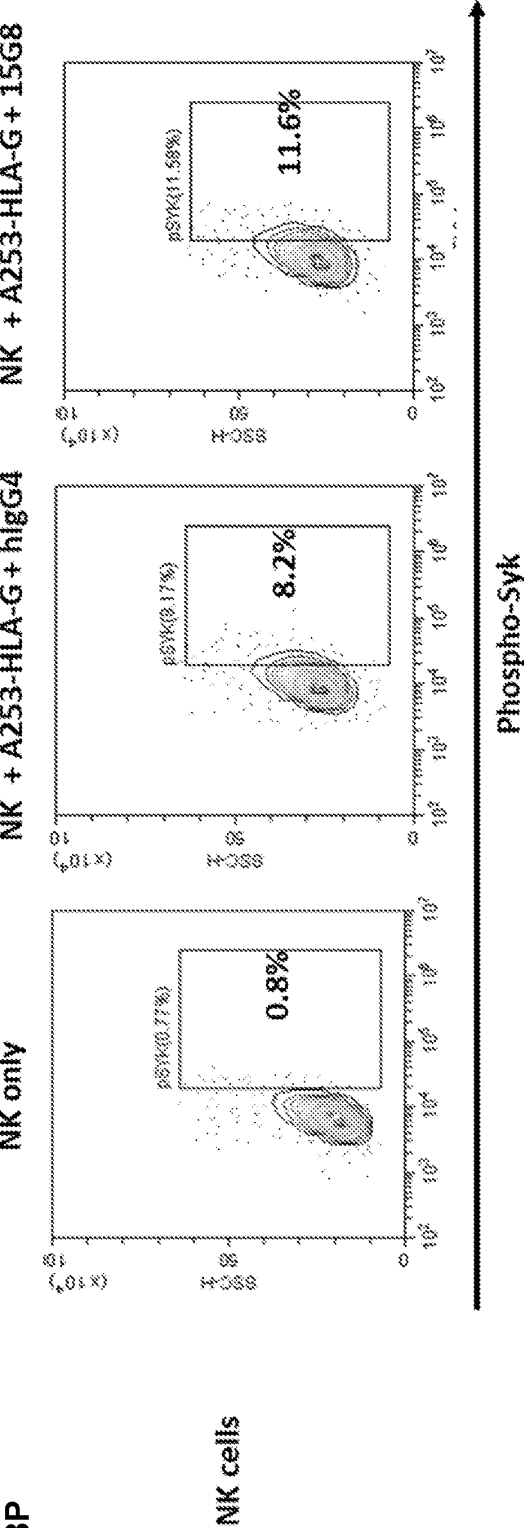


Fig. 8P



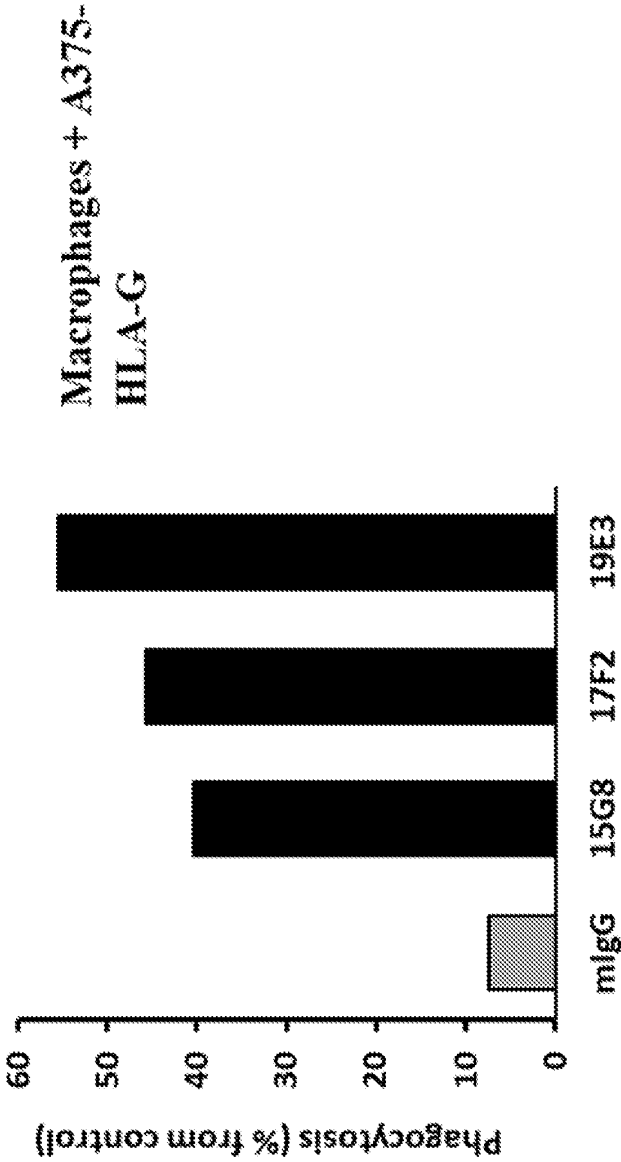


Fig. 9A

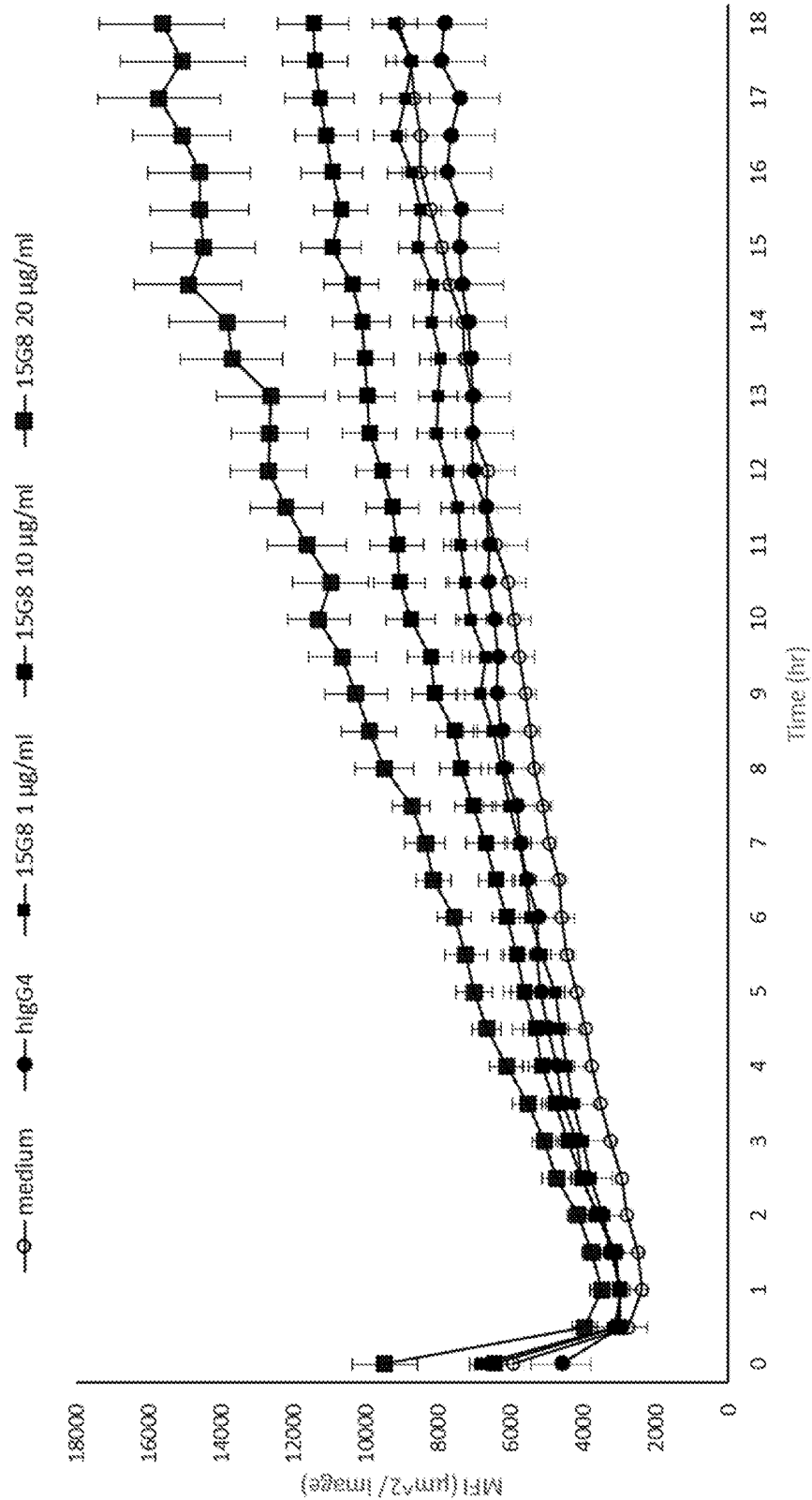
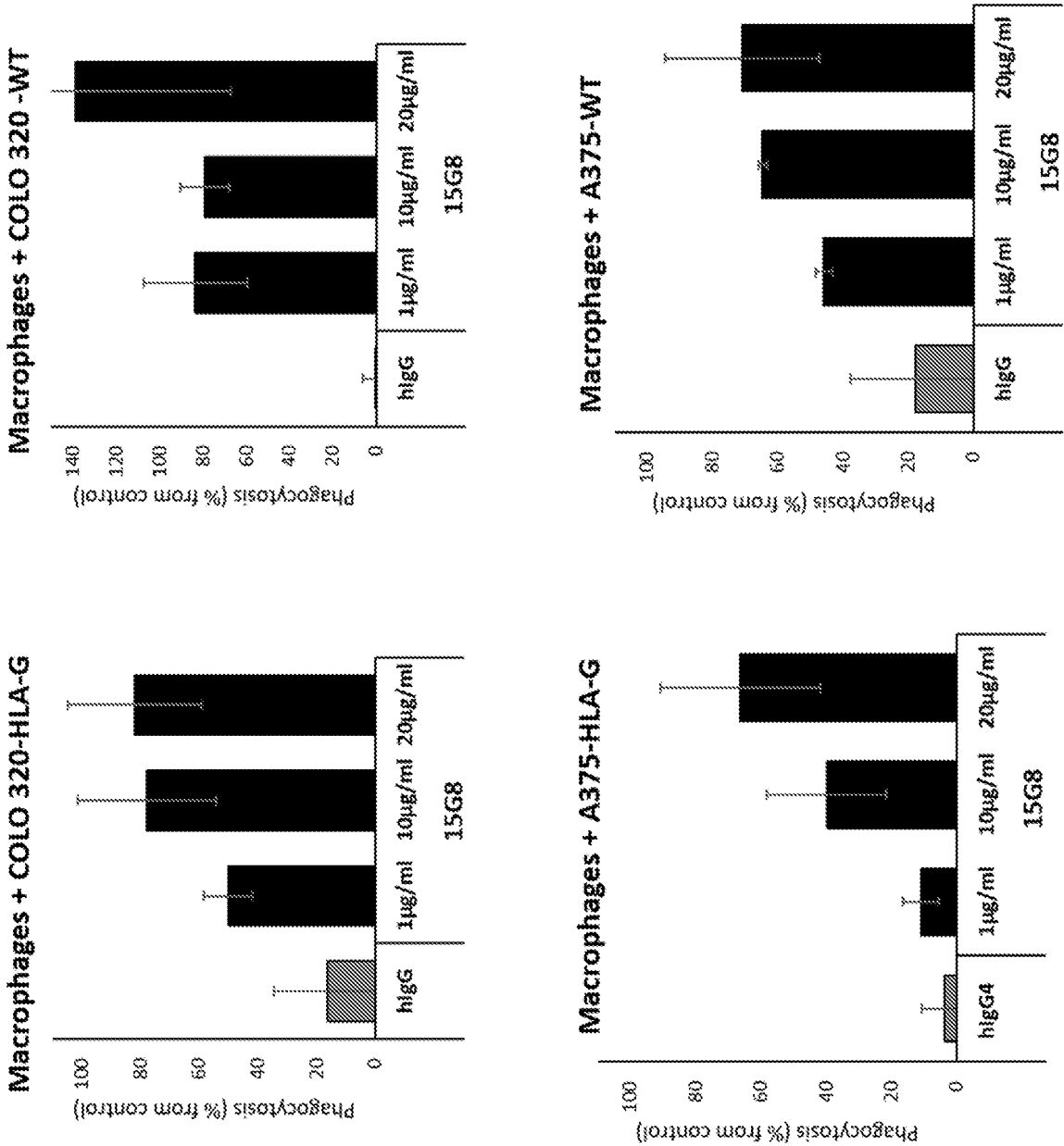


Fig. 9B

Fig. 9C



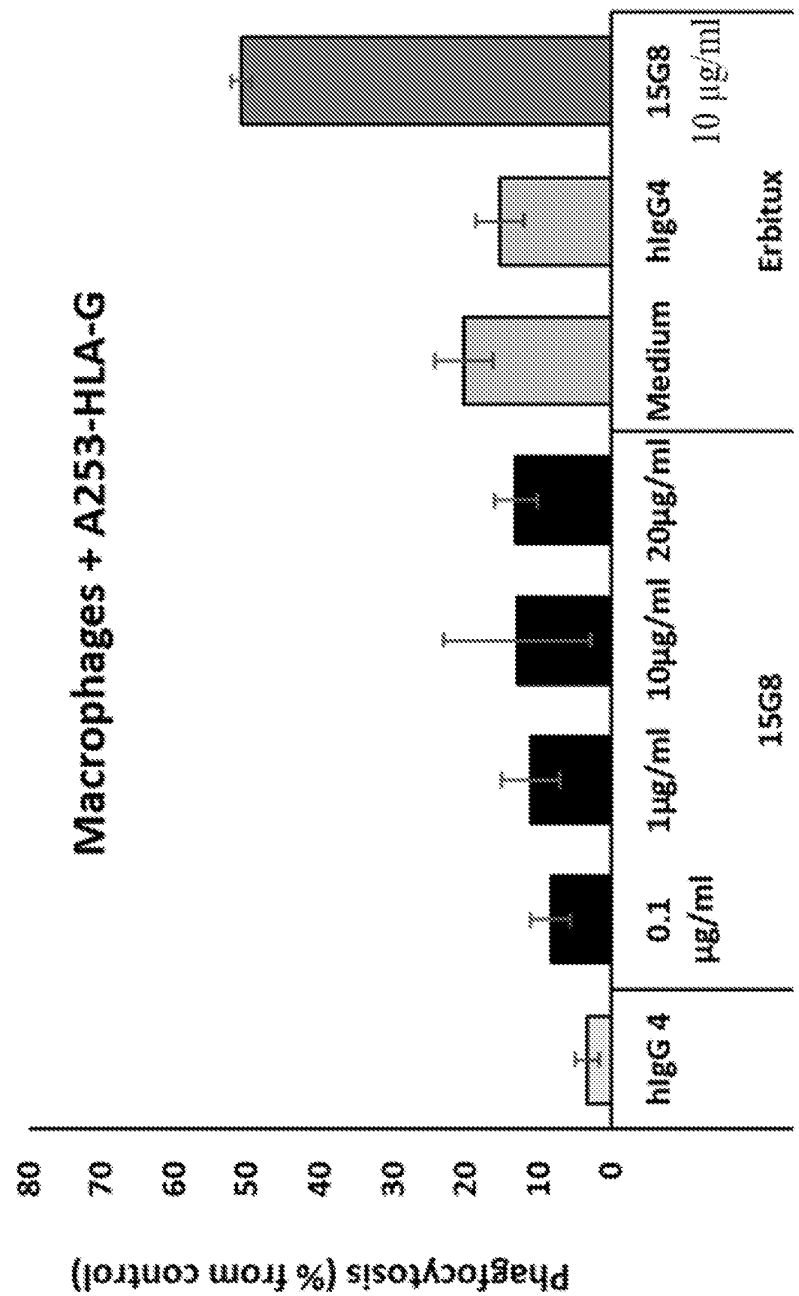
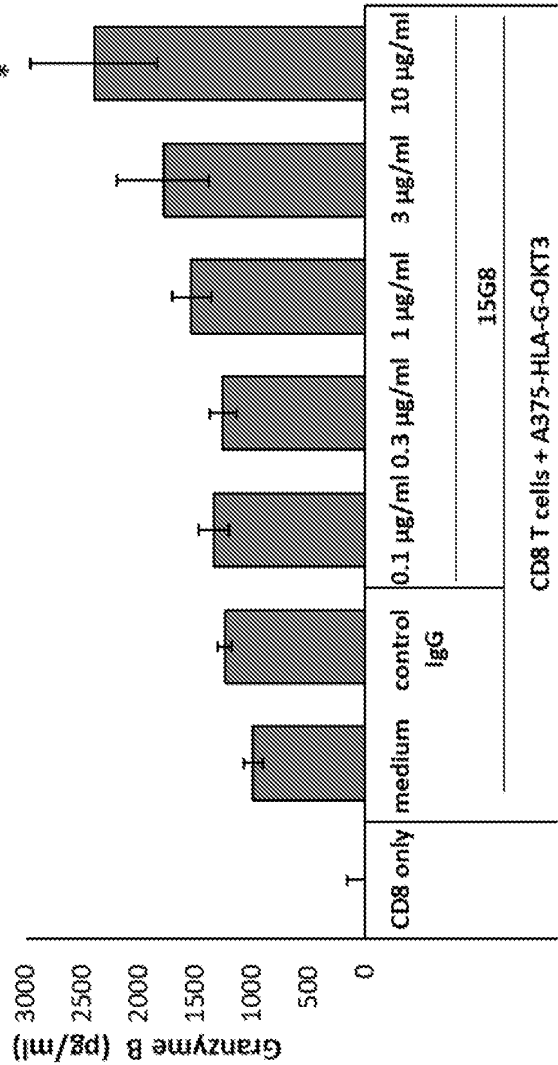
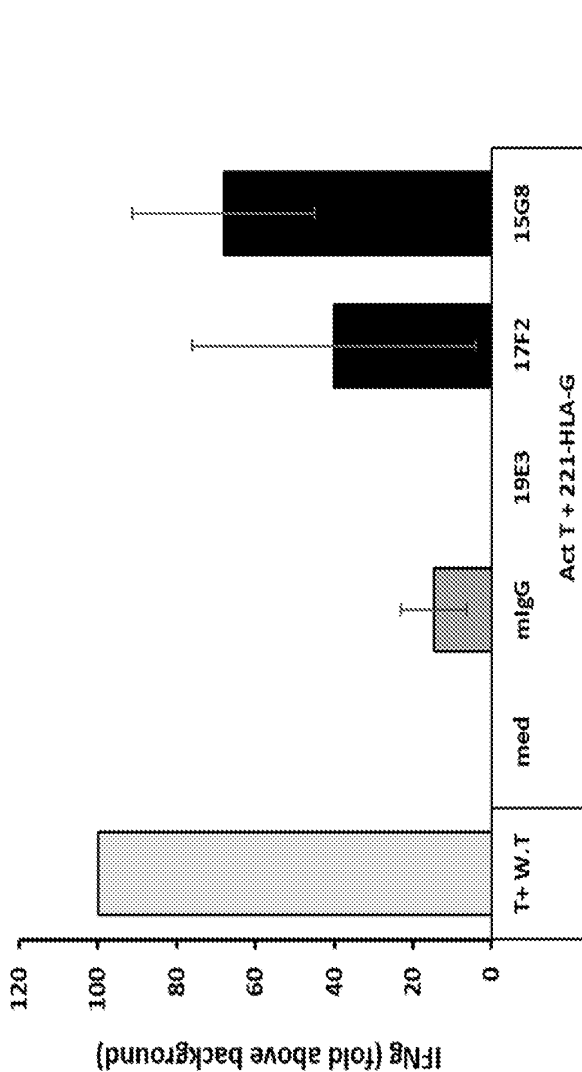


Fig. 9D



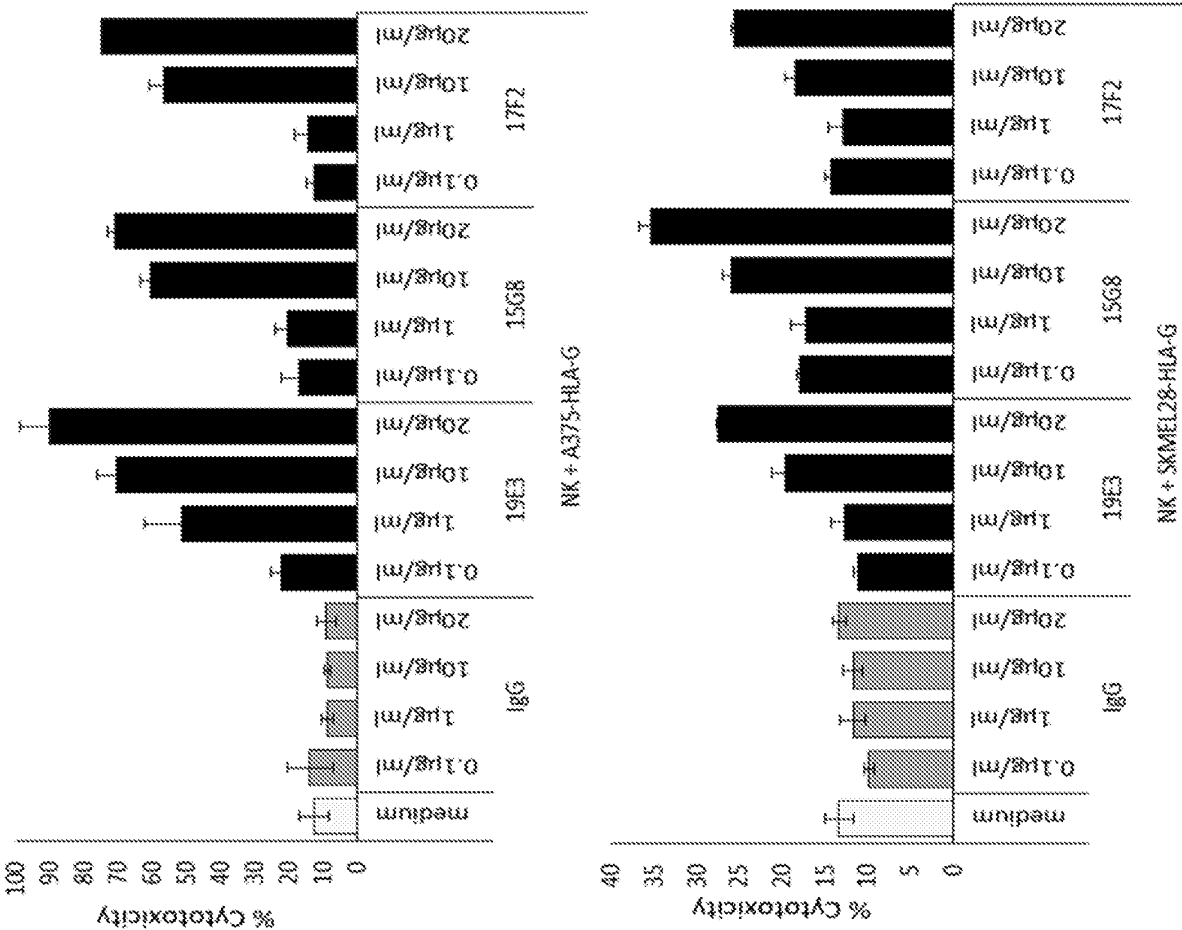


Fig. 11A

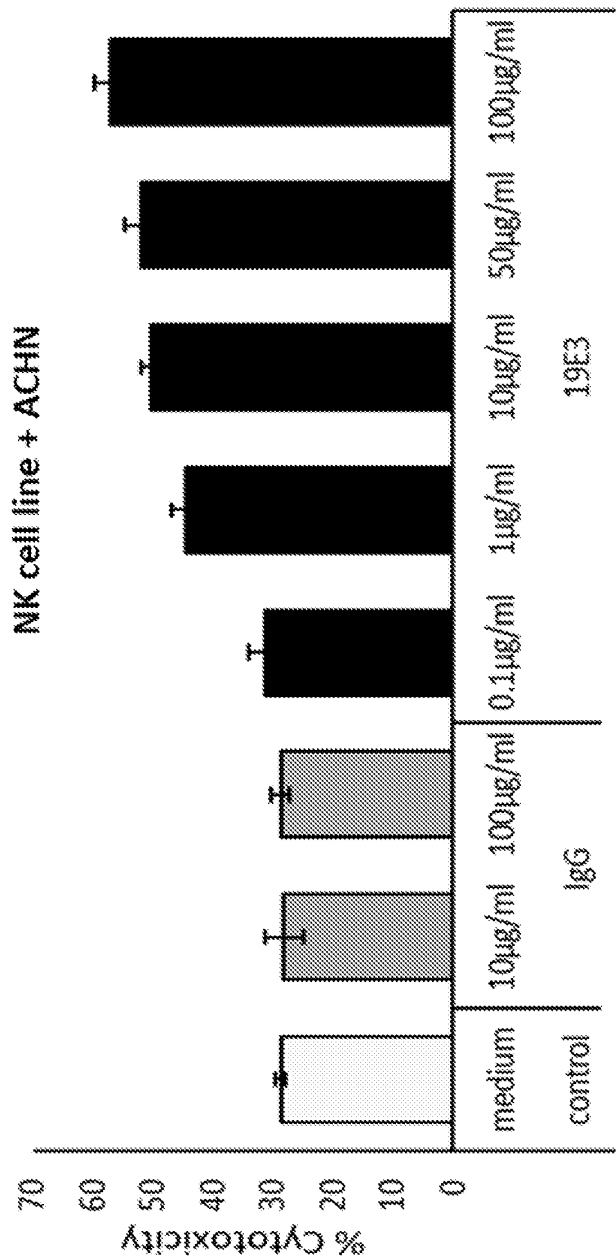


Fig. 11B

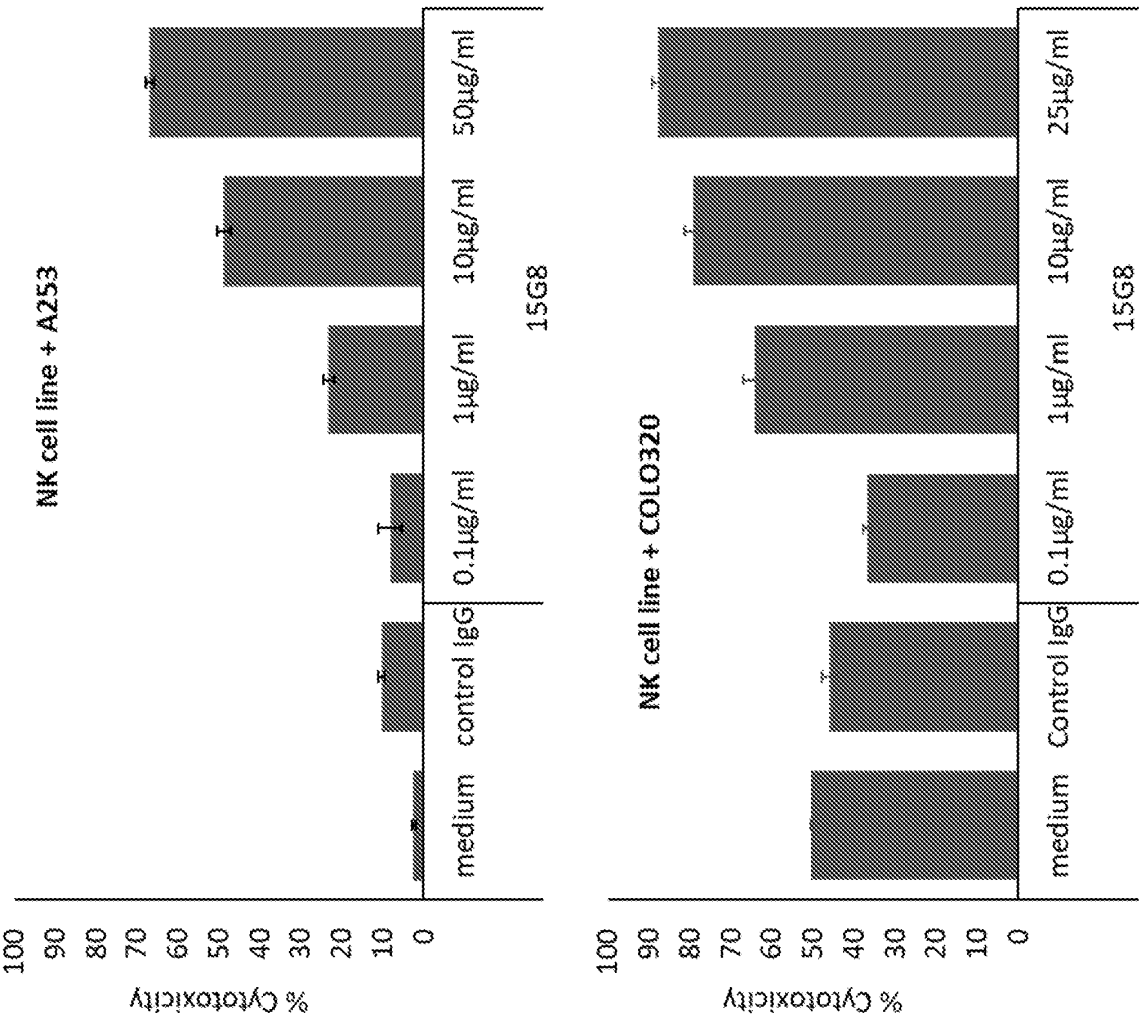


Fig. 11B
(cont.)

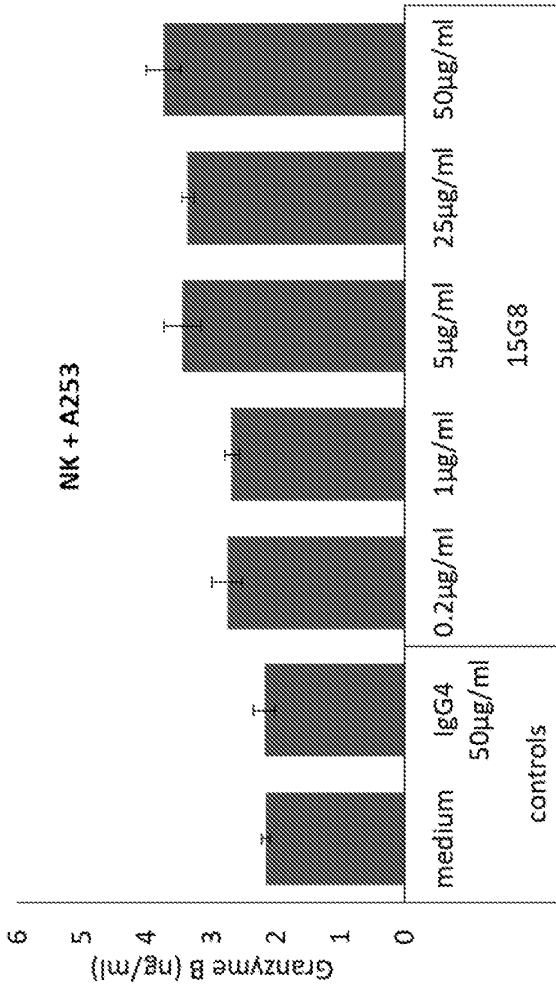


Fig. 11C

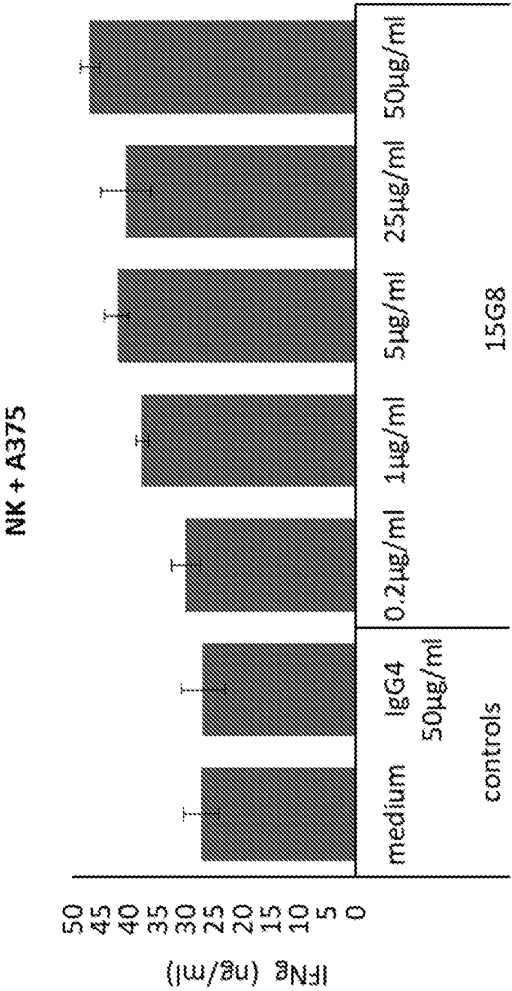


Fig. 11D

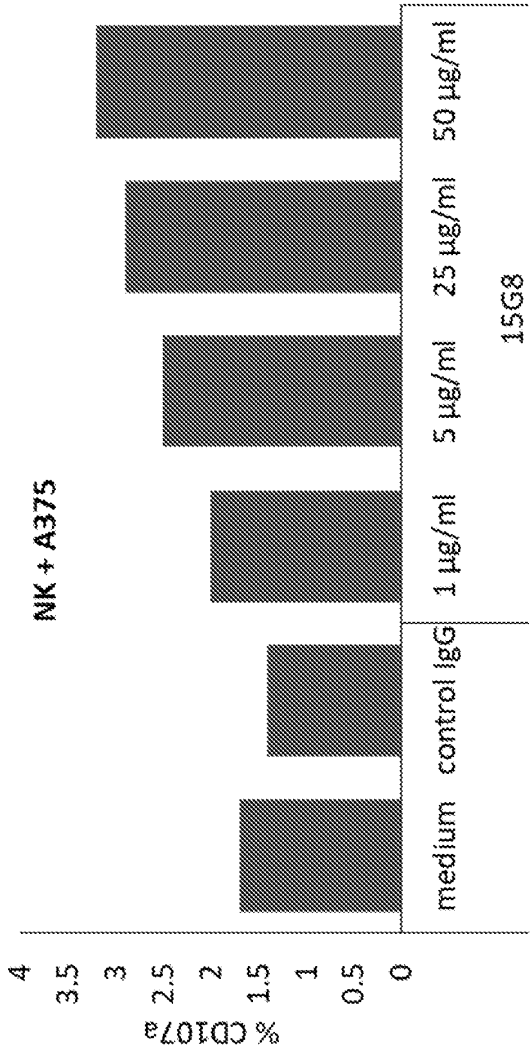
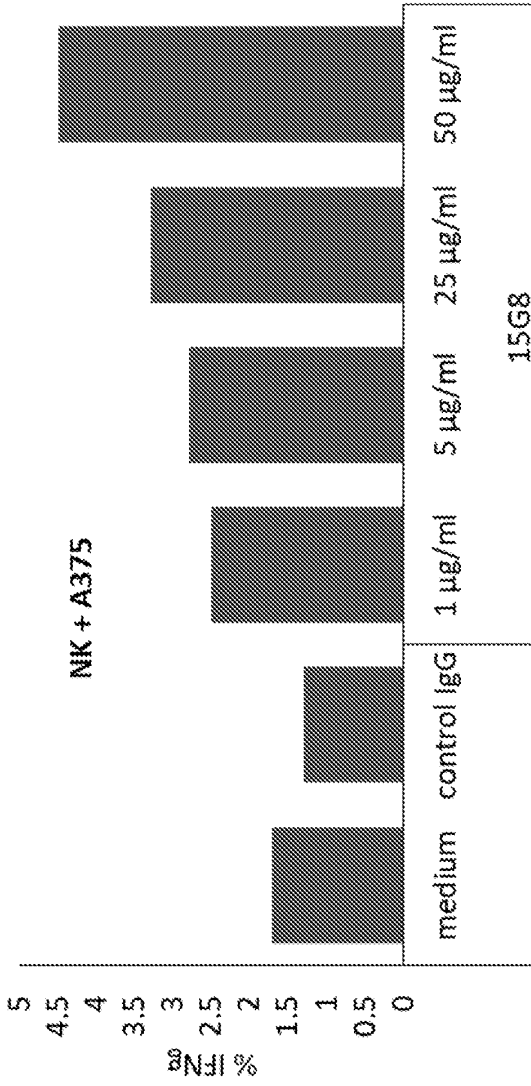


Fig. 11G

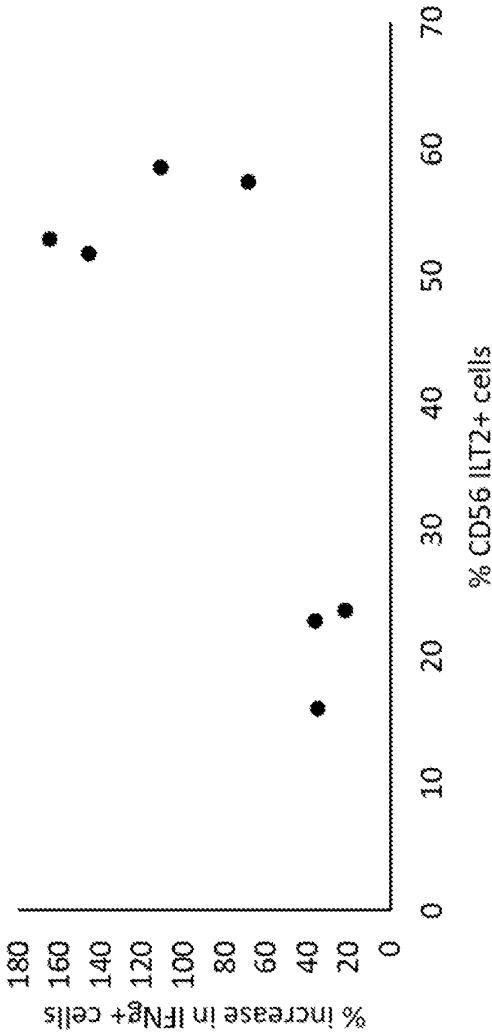
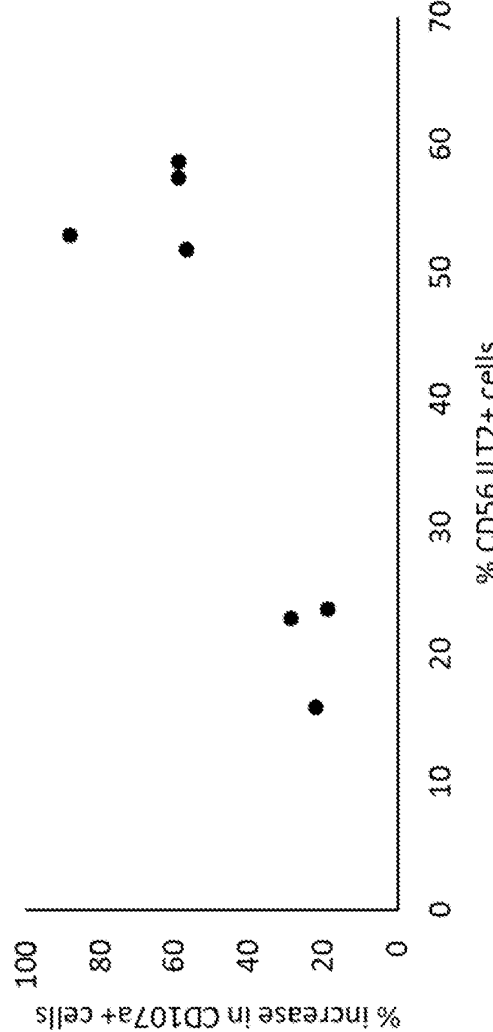


Fig. 11H



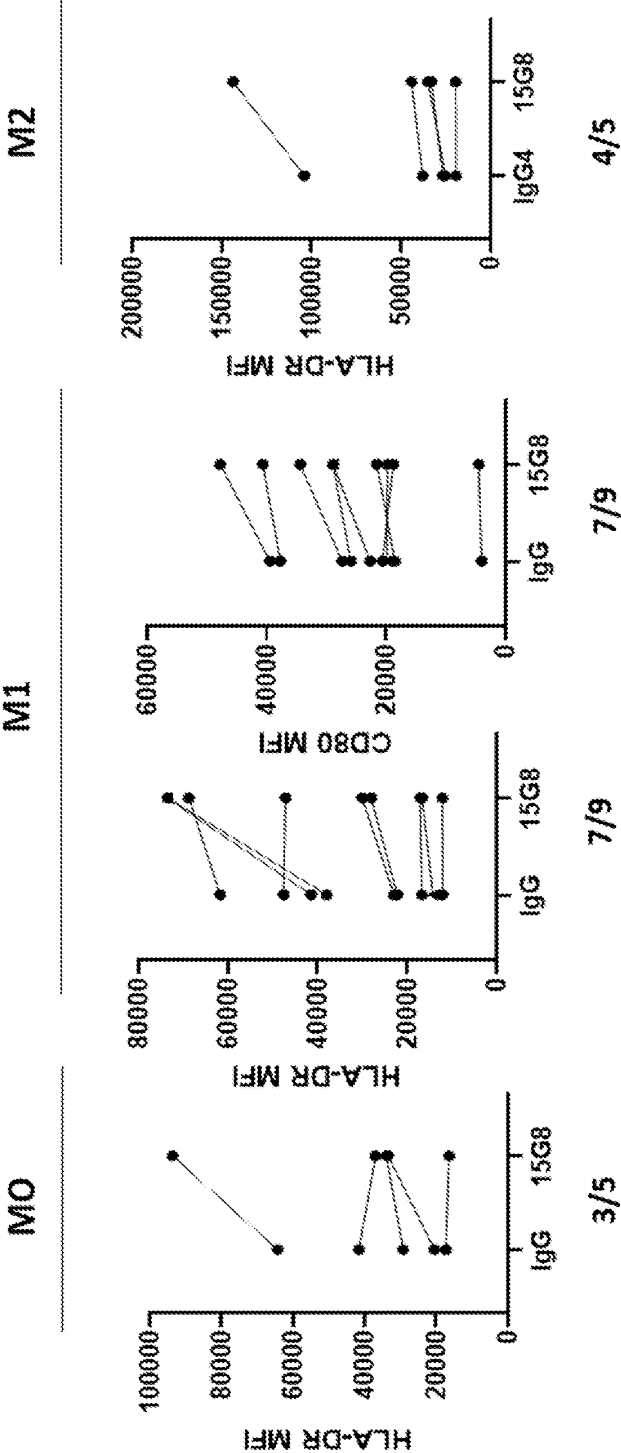


Fig. 12

Fig. 13A

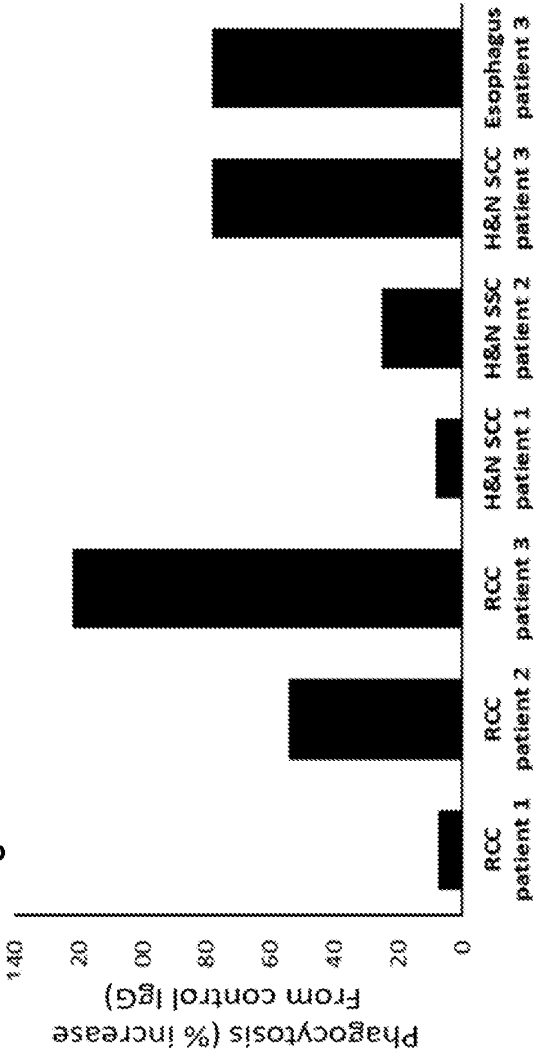


Fig. 13B

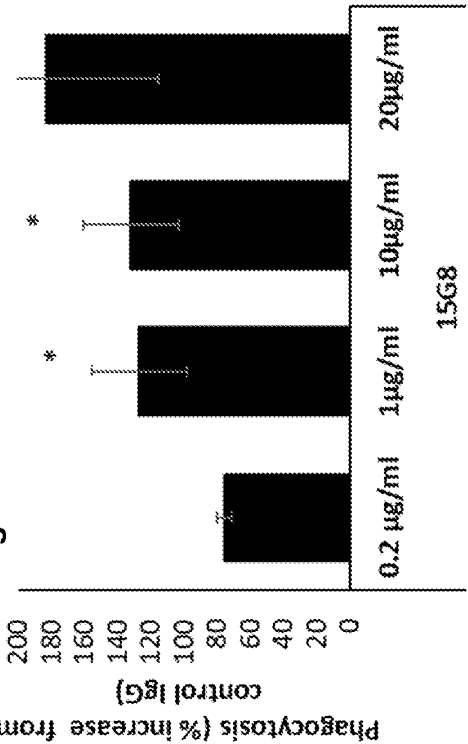
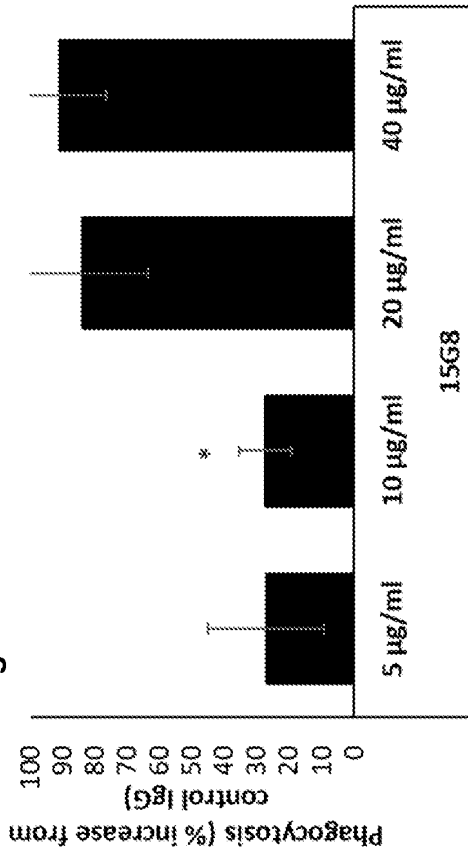


Fig. 13C



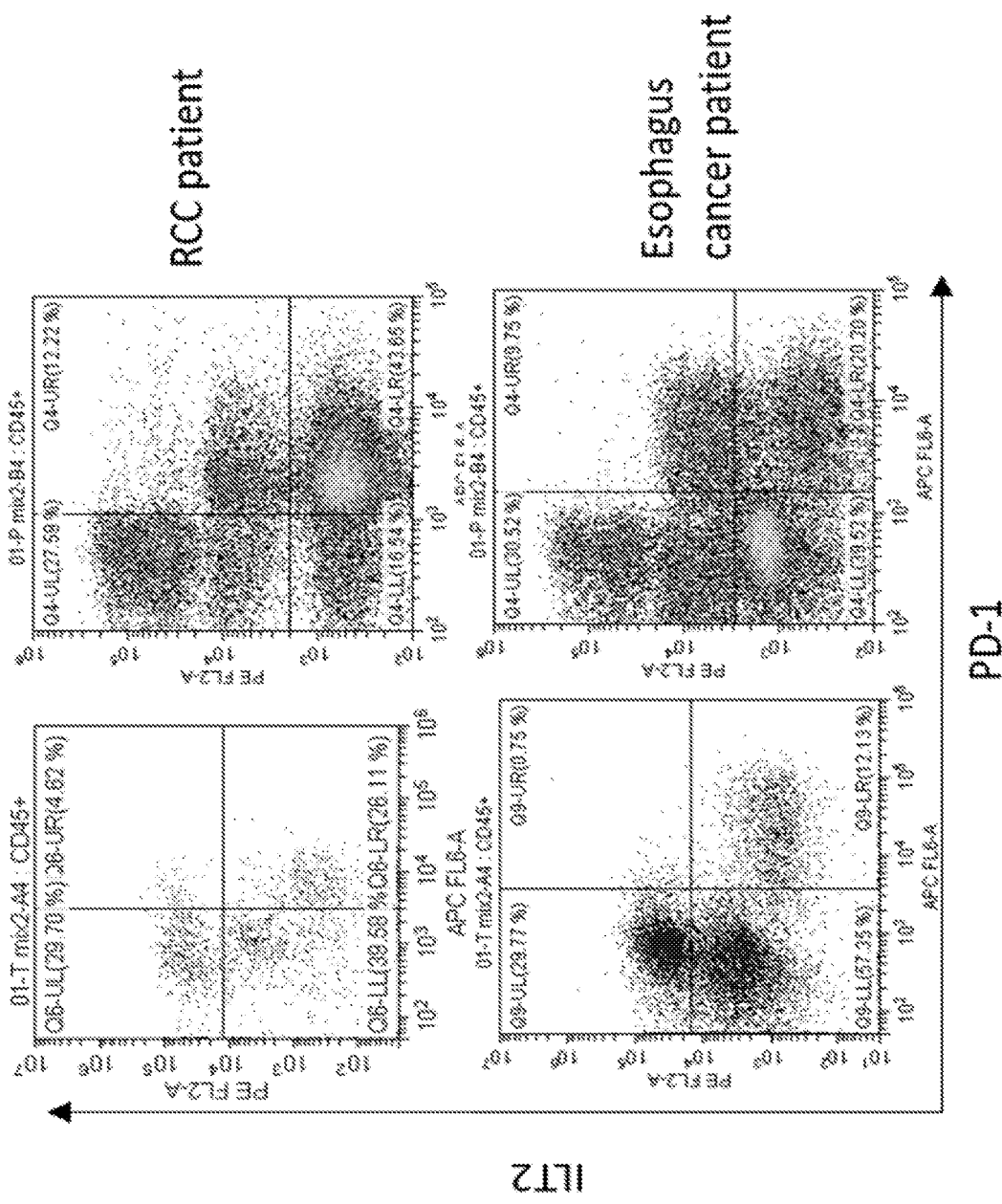


Fig. 14A

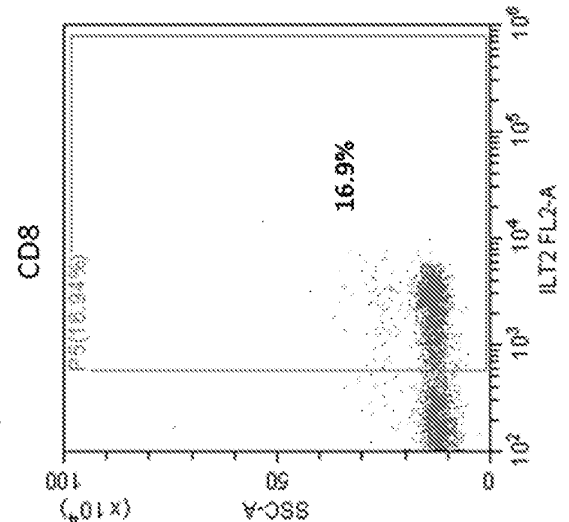
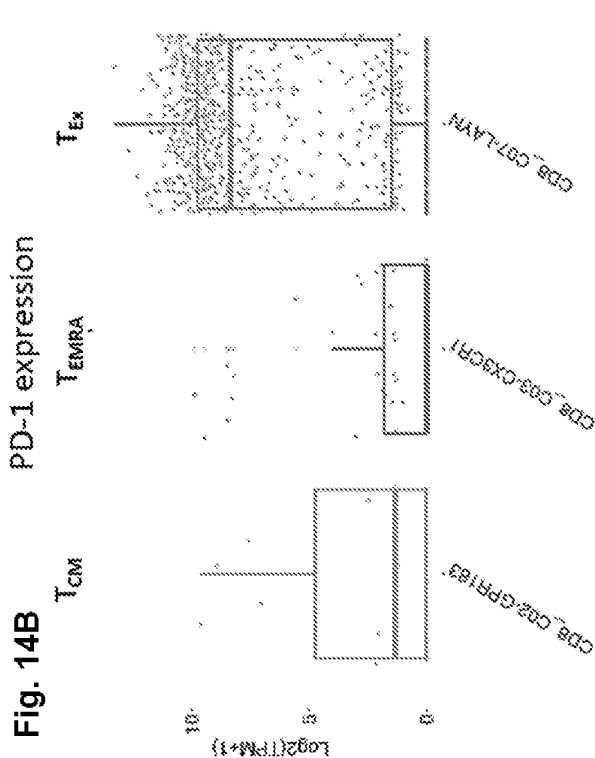
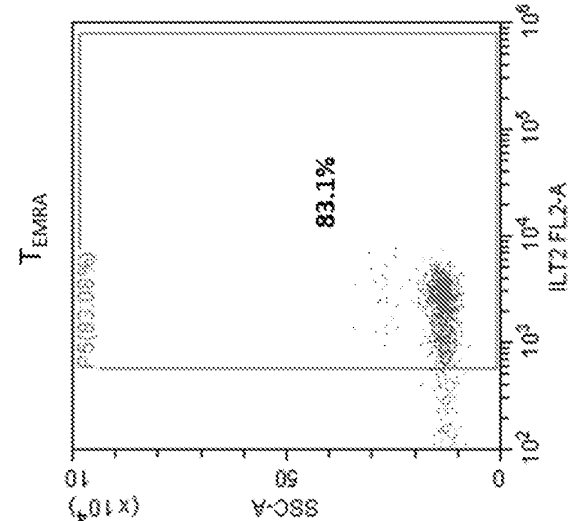
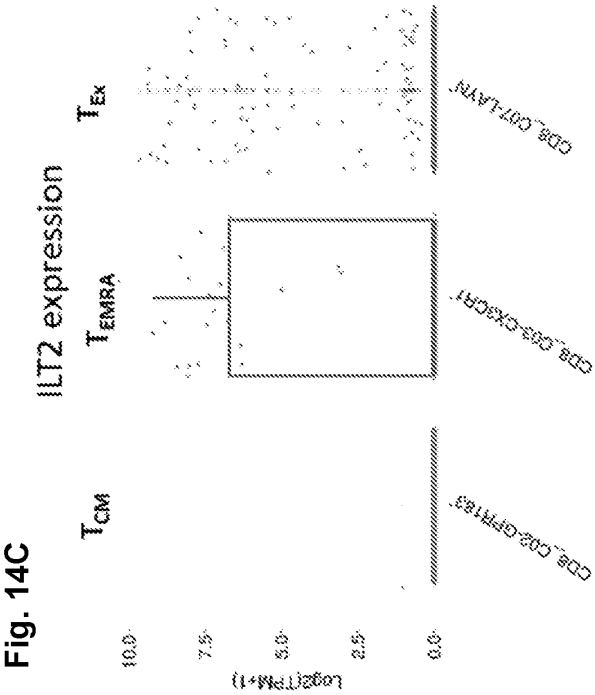


Fig. 14D

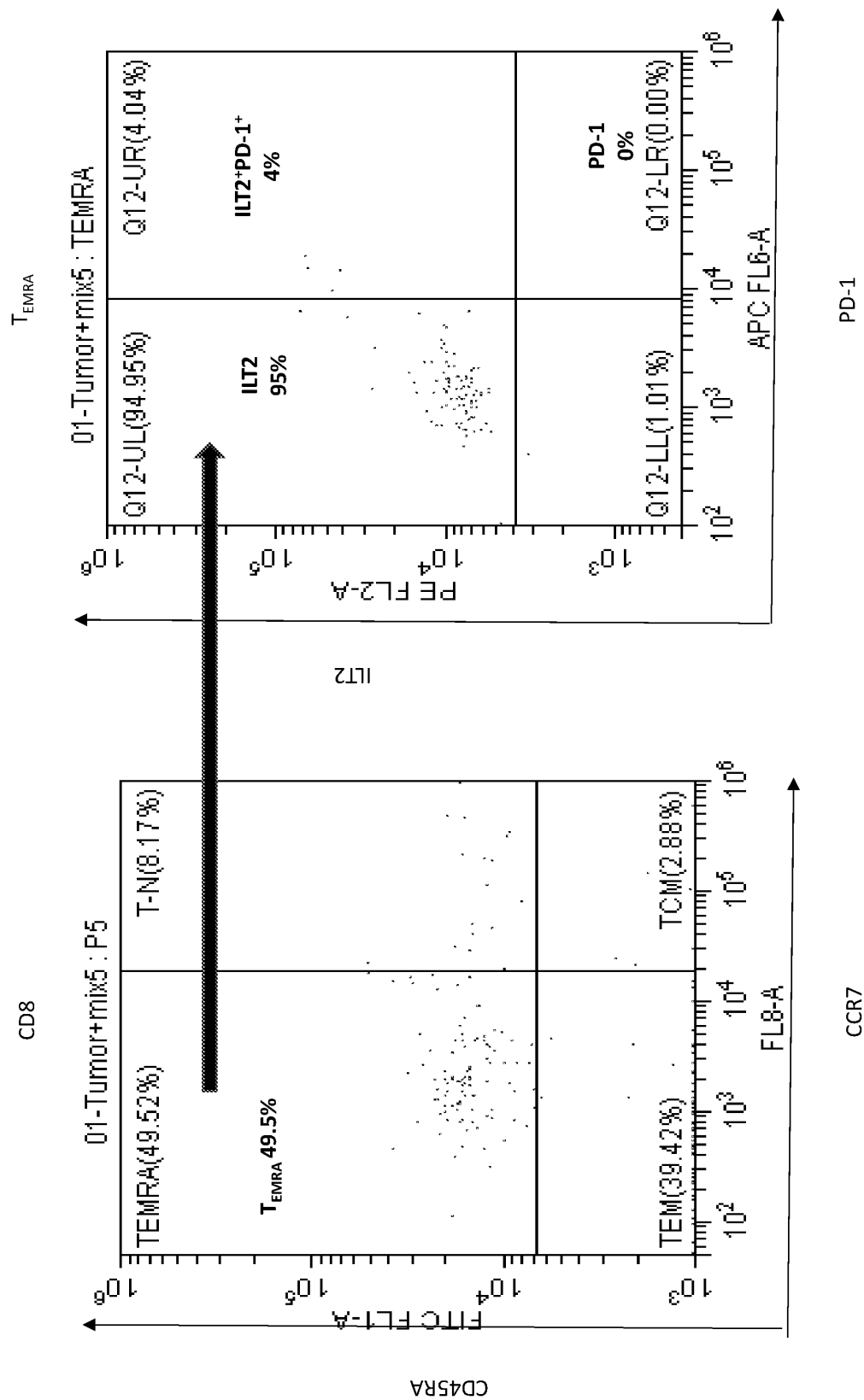


Fig. 14E

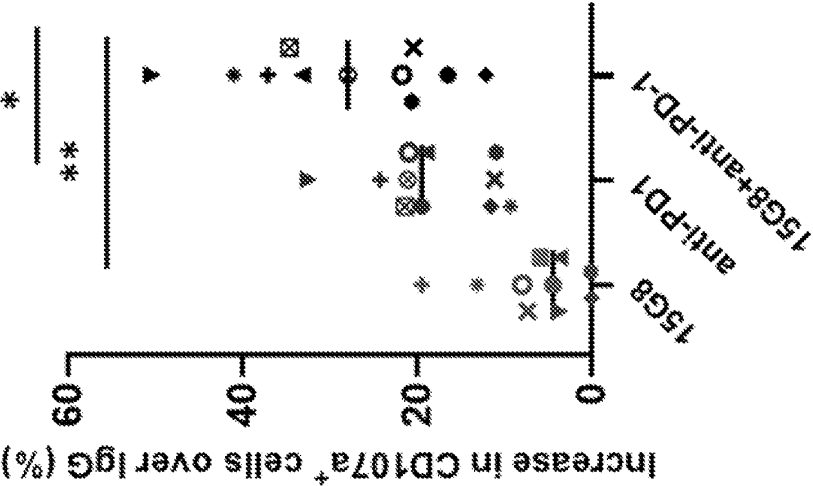


Fig. 14F

Fig. 14G

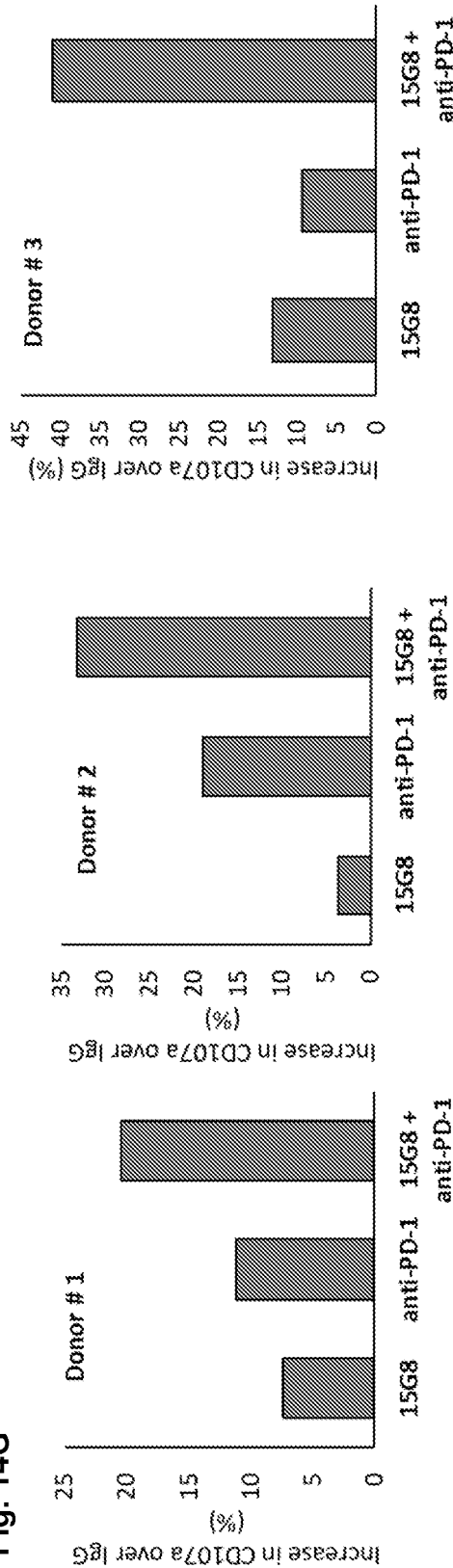
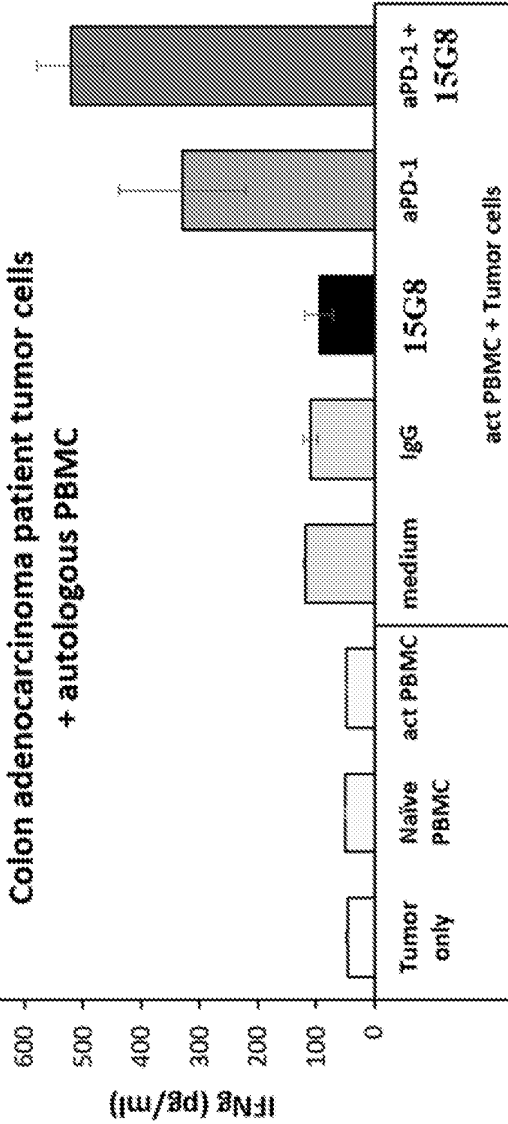


Fig. 14H



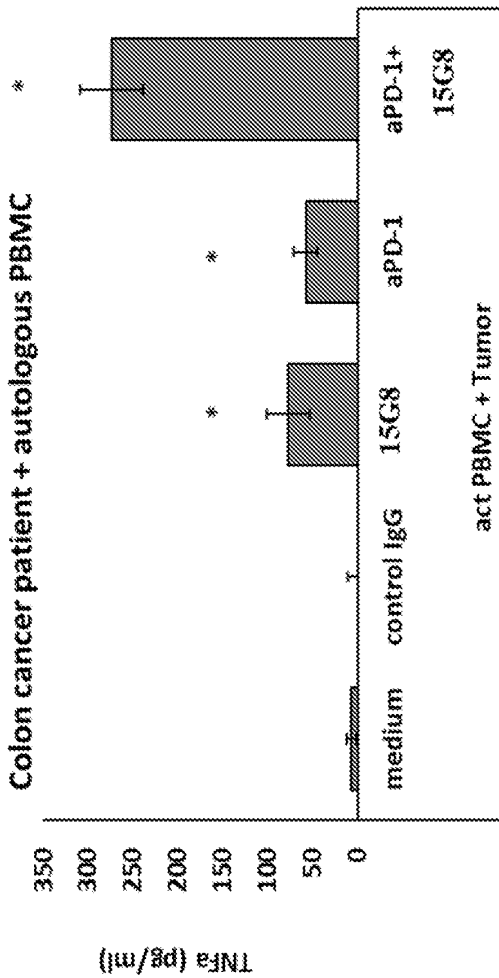


Fig. 14I

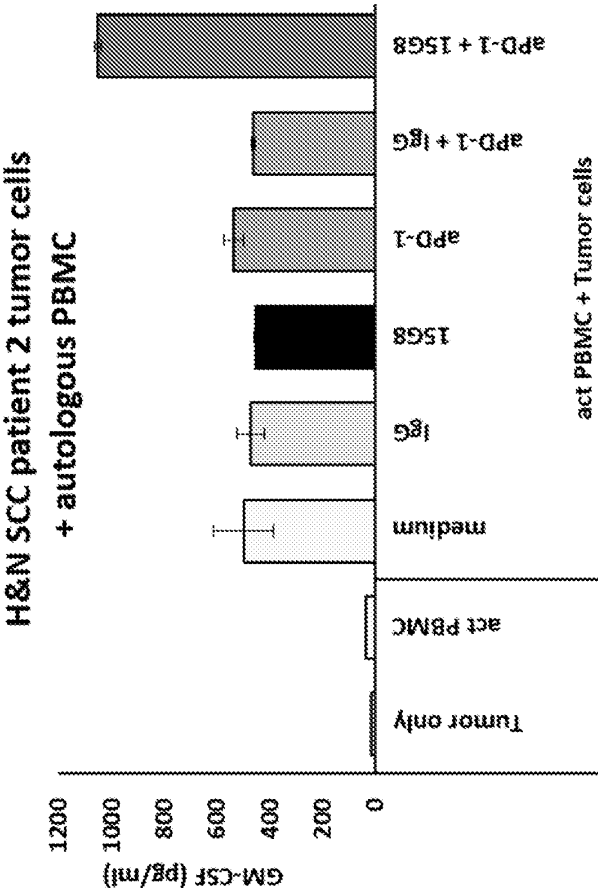


Fig. 14J

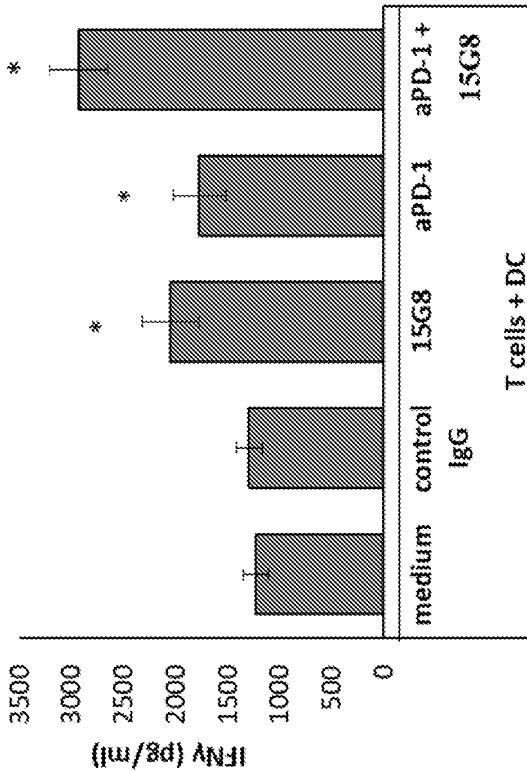


Fig. 14K

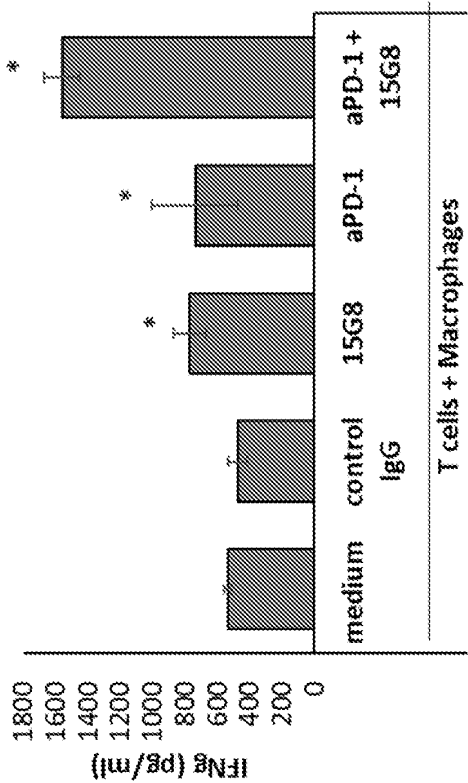


Fig. 14L

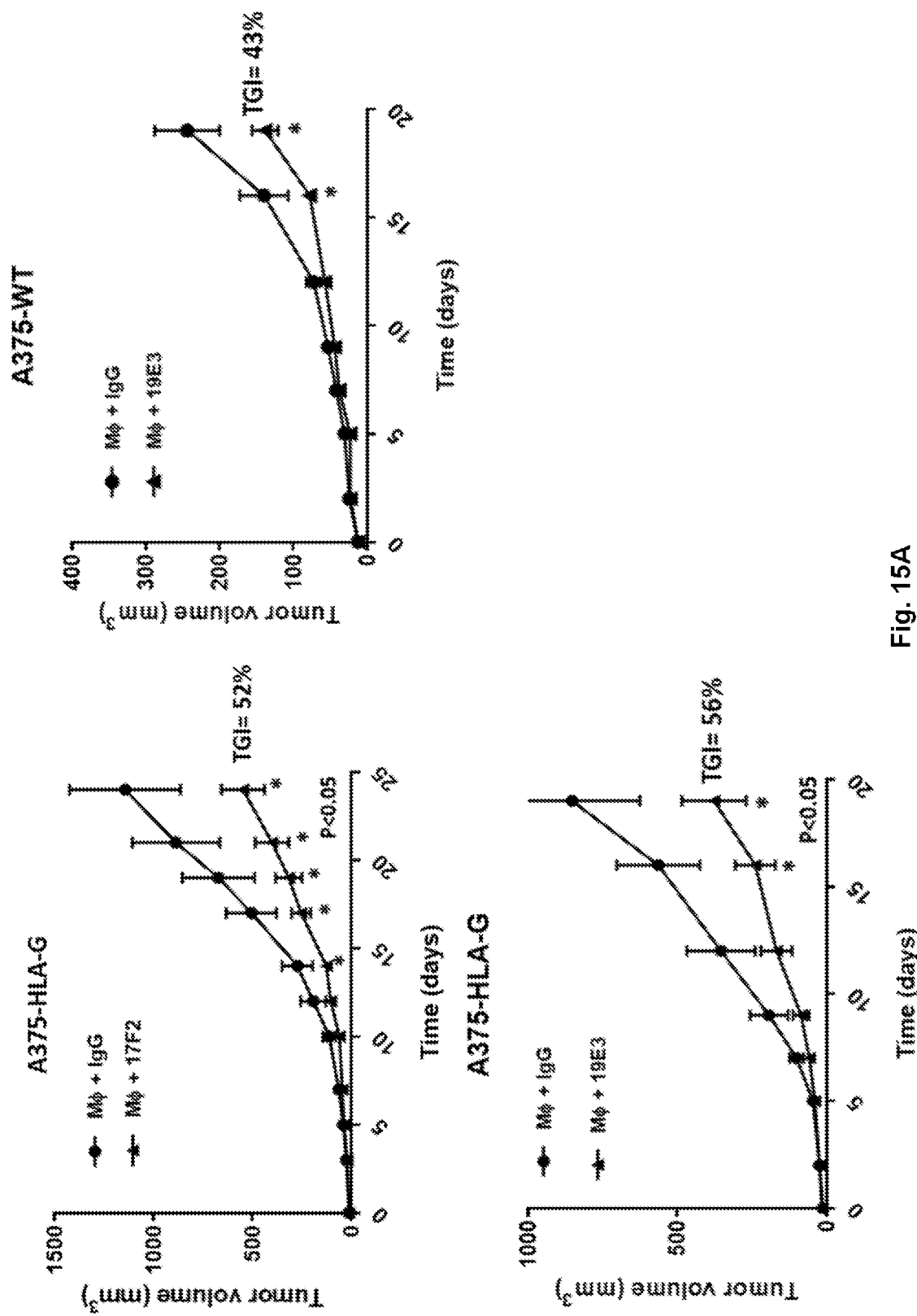


Fig. 15A

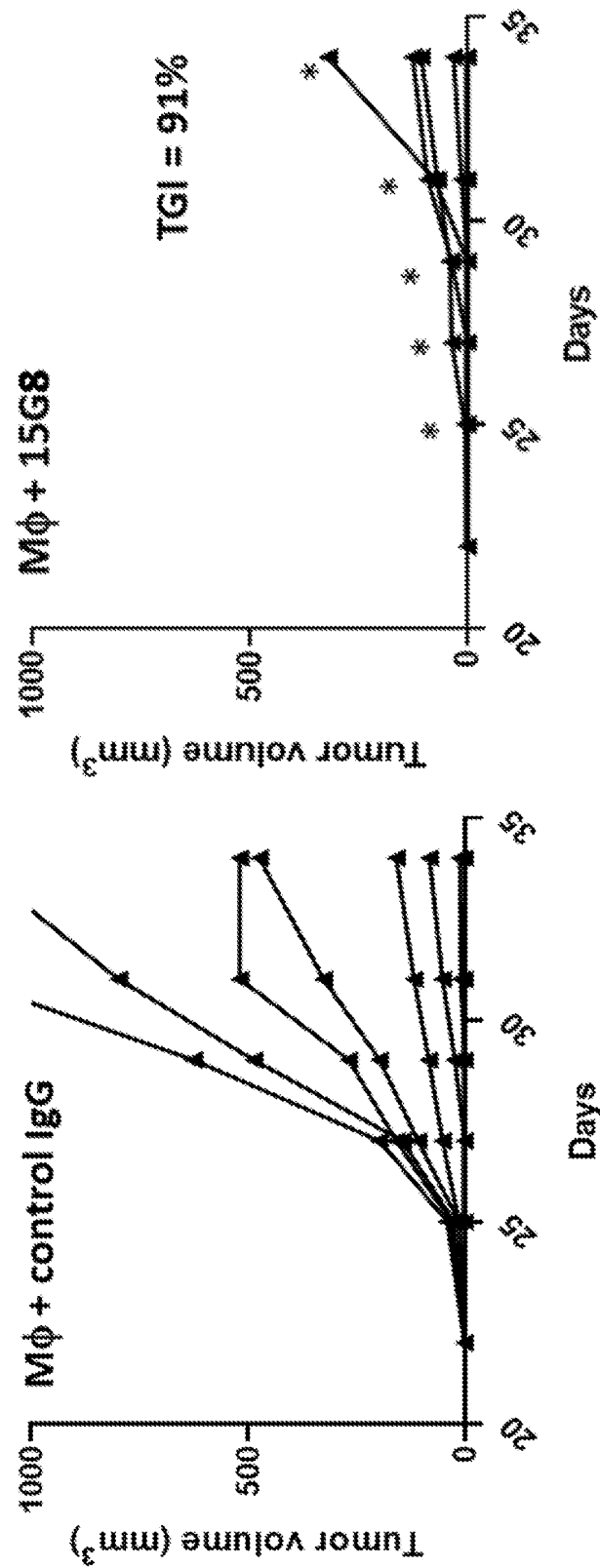
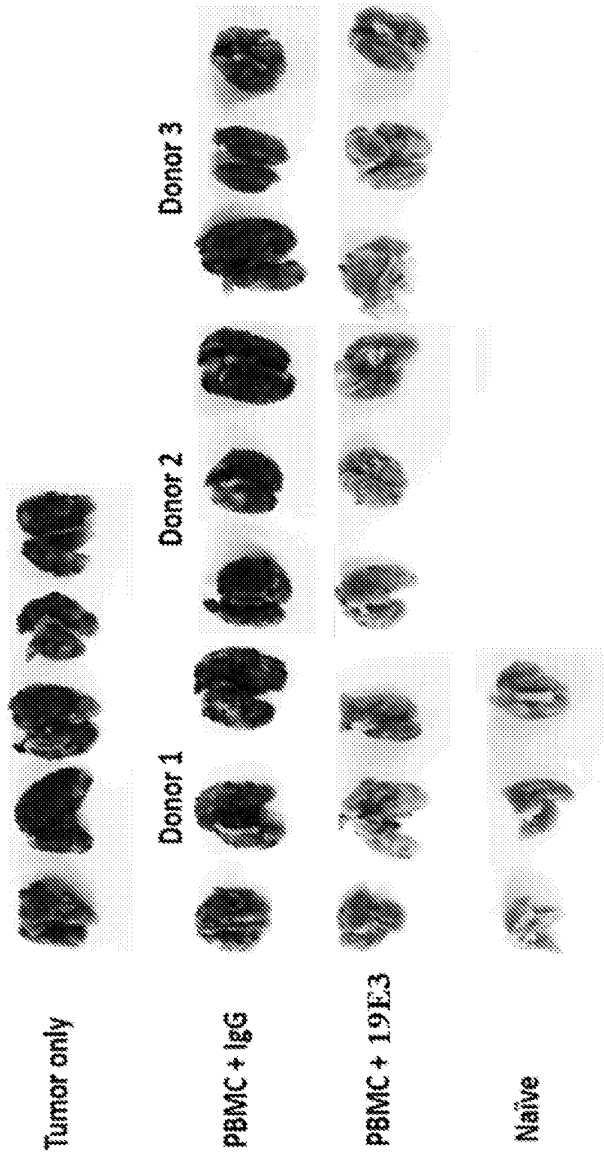
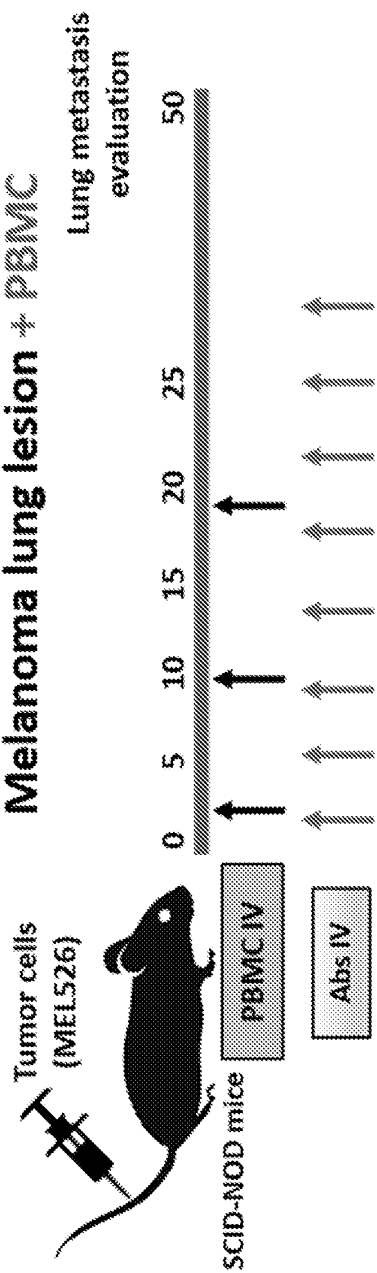


Fig. 15A (cont.)



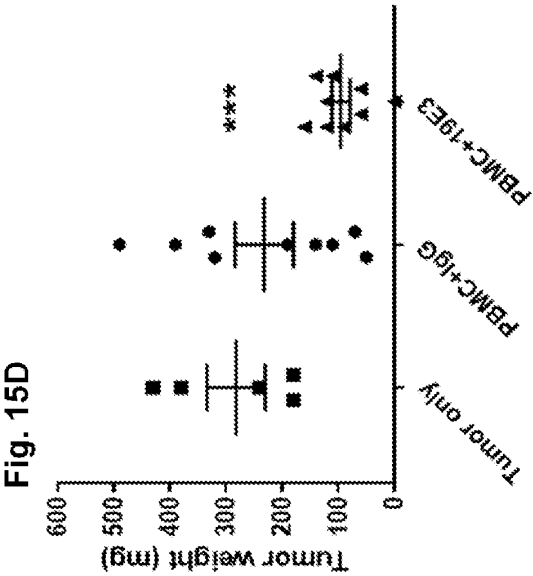


Fig. 15E

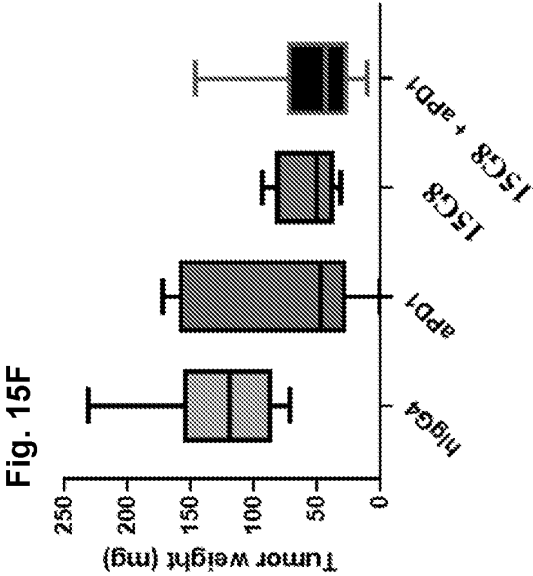
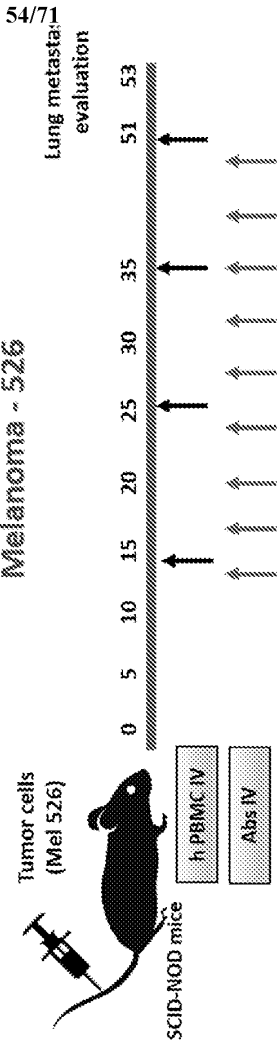


Fig. 16A

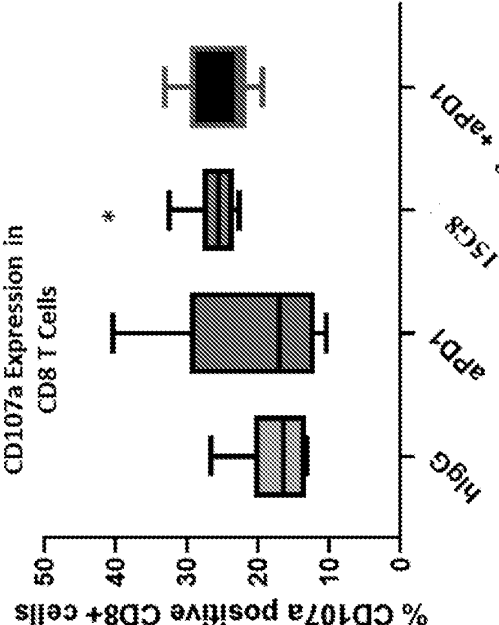


Fig. 16B

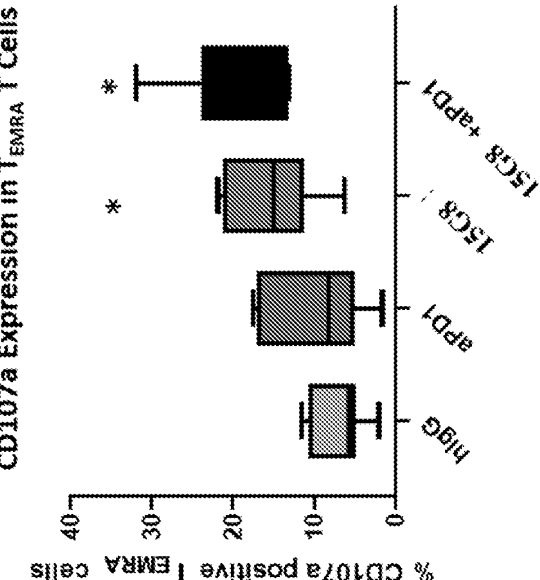


Fig. 16C

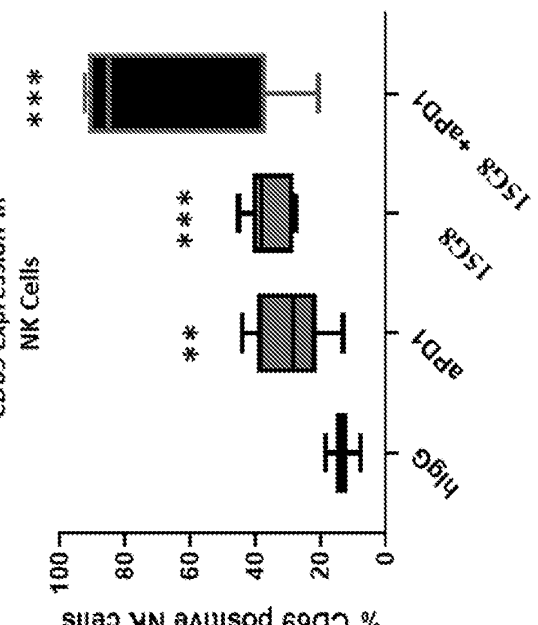
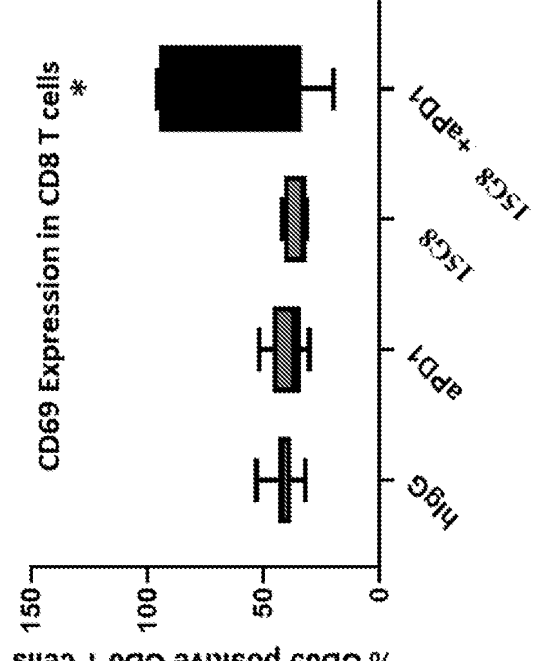


Fig. 16D



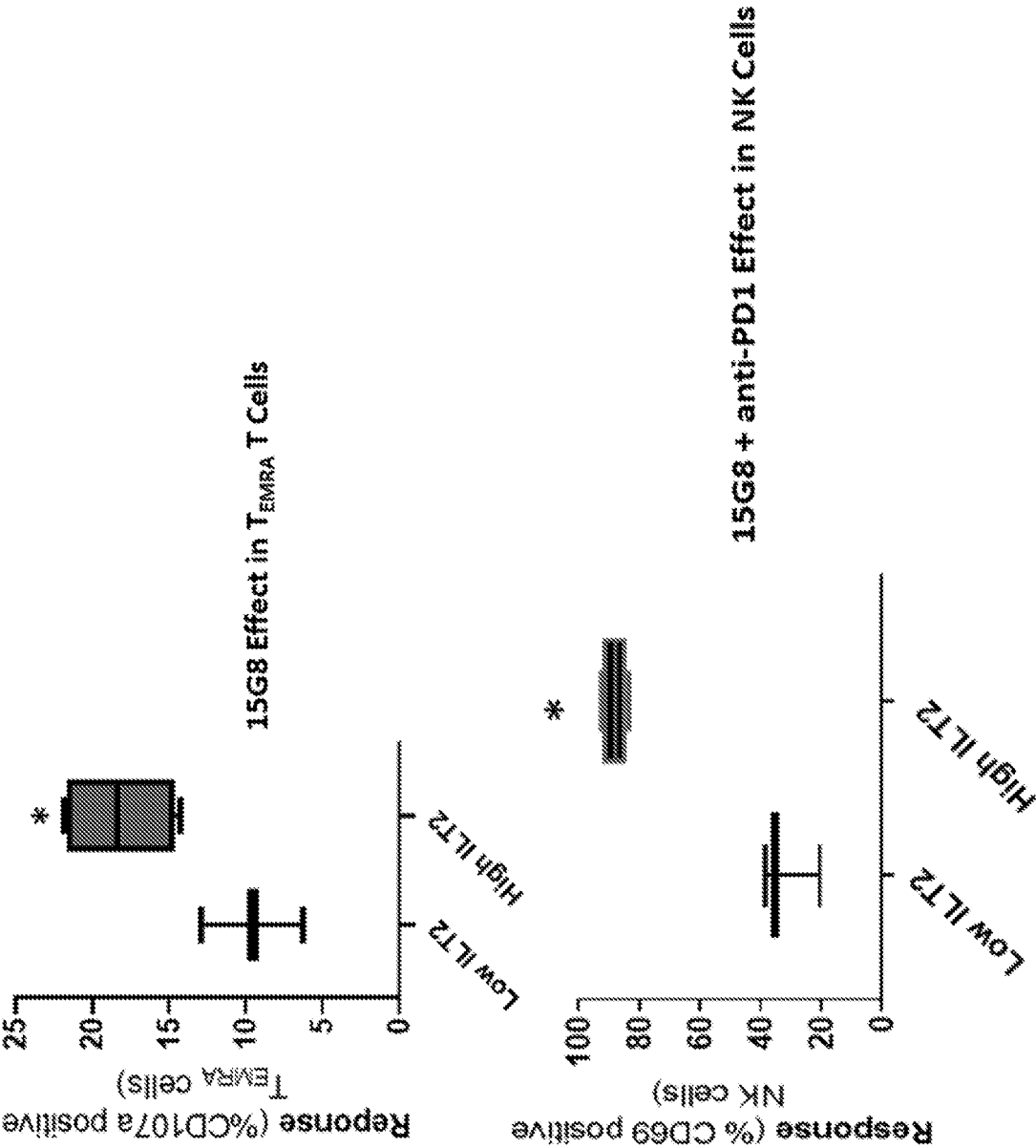


Fig. 16E

Fig. 16F

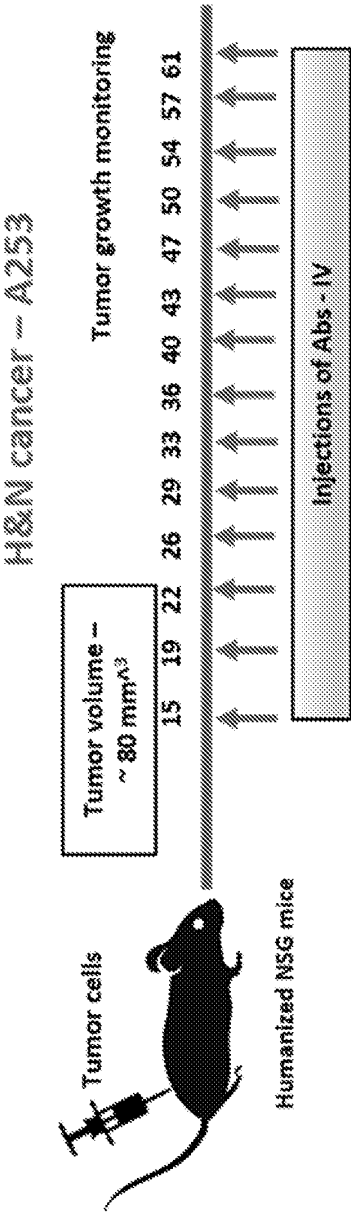


Fig. 17A

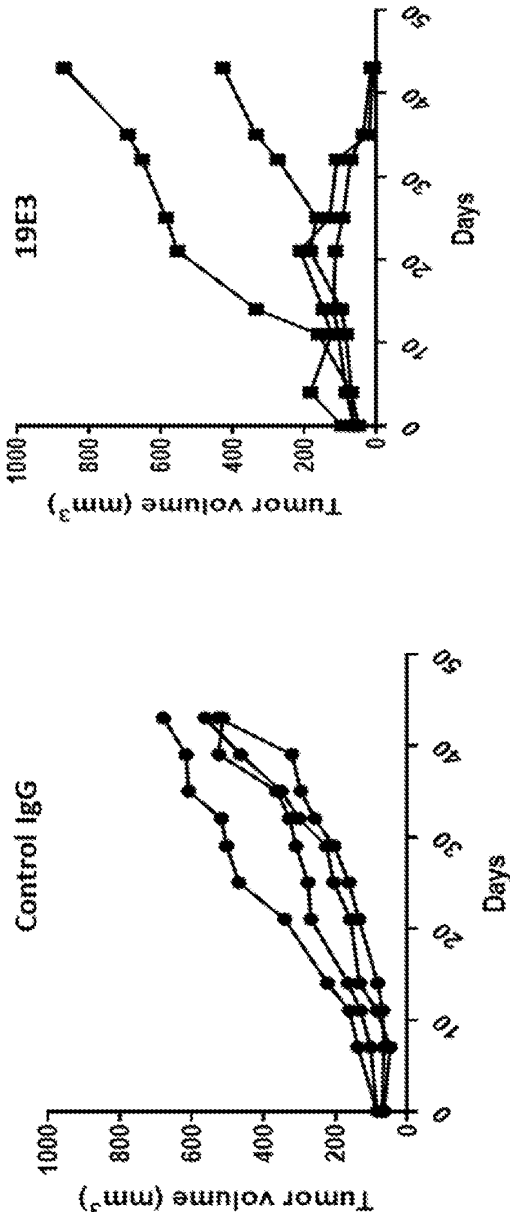
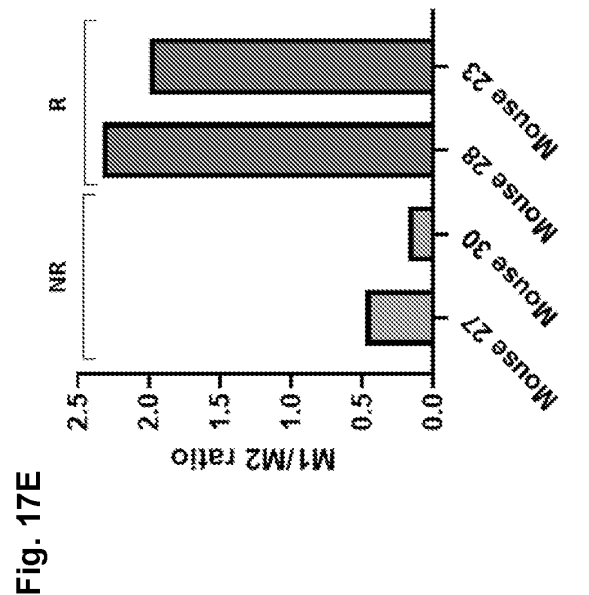
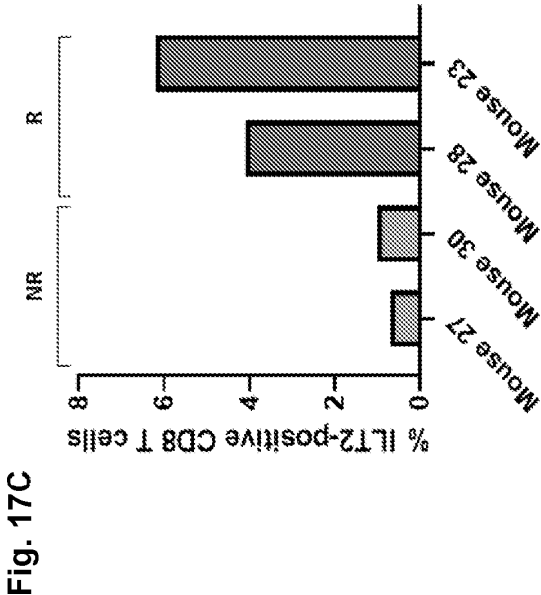
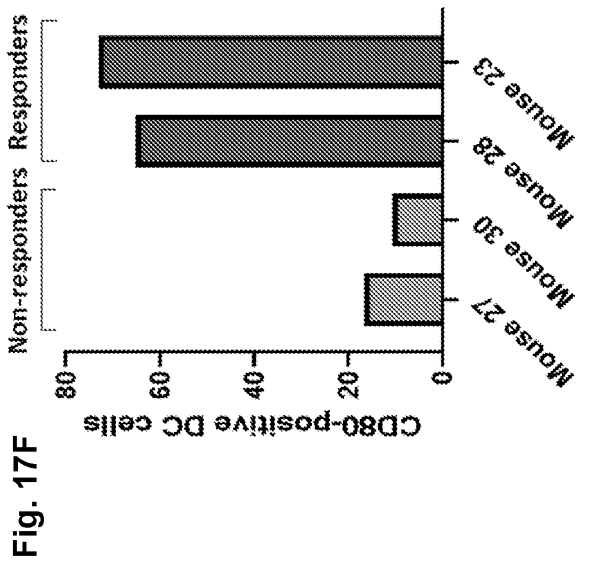
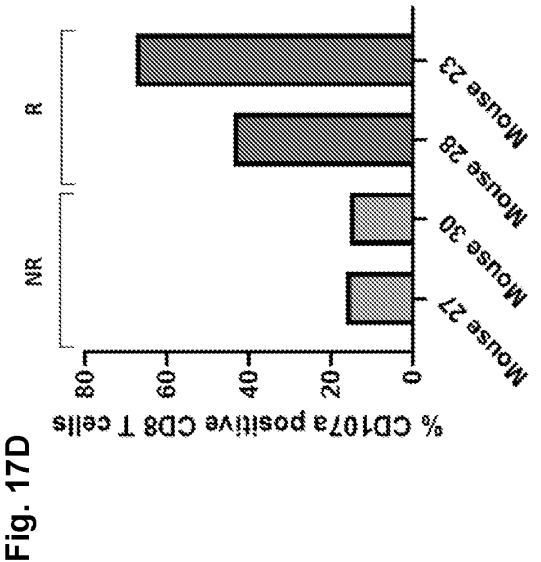


Fig. 17B



1 - HLPKPTLWAE PGSVITQGSP VTLRCQGGQE TQYRLYREK K TALWITRIP QELVKKGQFP * *

61 - IPSITWEHAG RYRCYIGSDT AGRSESDPL ELVVTGAYIK PTLAQPSPV VNSGGNVILQ * *
γδβαα *** * δααβ

121 - CDSQVAFDGE SLCKEGEDEH PQCLNSQPHA RGSSRAIFSV GPVSPSRWW YRCYAYDSNS * *
βγγγ β α γ

181 - PYEWSLPSDL LELLVLGVSK KPSLSVQPGP IVAPEETLTL QCGSDAGYNR FVLYKDGERR *

241 - FLQLAGAQPQ AGLSQANFTL GPVRSYGGQ YRCYGAHNLS SEWSAPSDPL DILIAGQFYD α

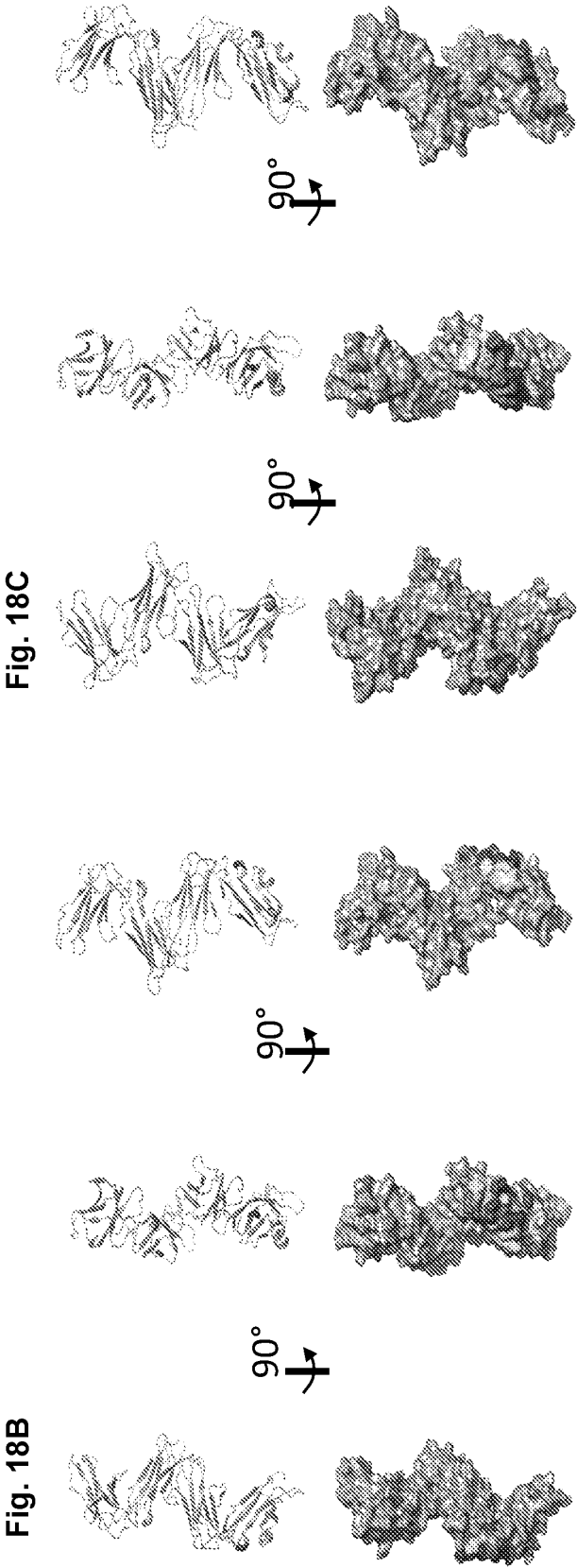
301 - RVSLSVQPGP TVASGENVTIL LCQSQGMQOT FLITKEGAD DPWRLRSTYQ SQKYQAEFFM

361 - GPVTSAHAGT YRCYGSQSSK PYLLTHPSDP LEL

Epitope residues	Interaction regions
α - Very highly probable	Region 1
β - Highly probable	Region 2
γ - Probable	Region 3
δ - Possible	Region 4

Fig. 18A

60/71



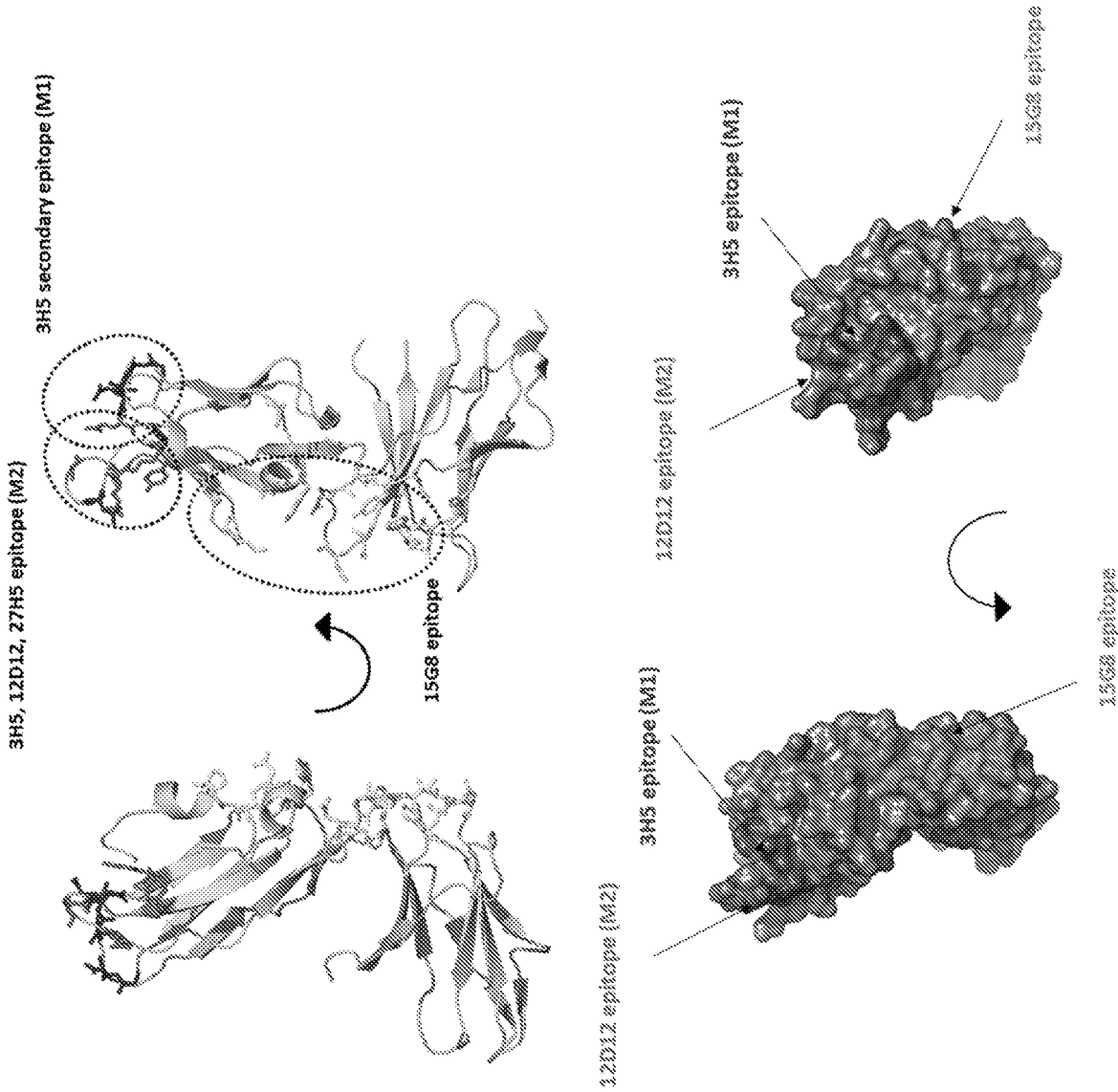


Fig. 18D

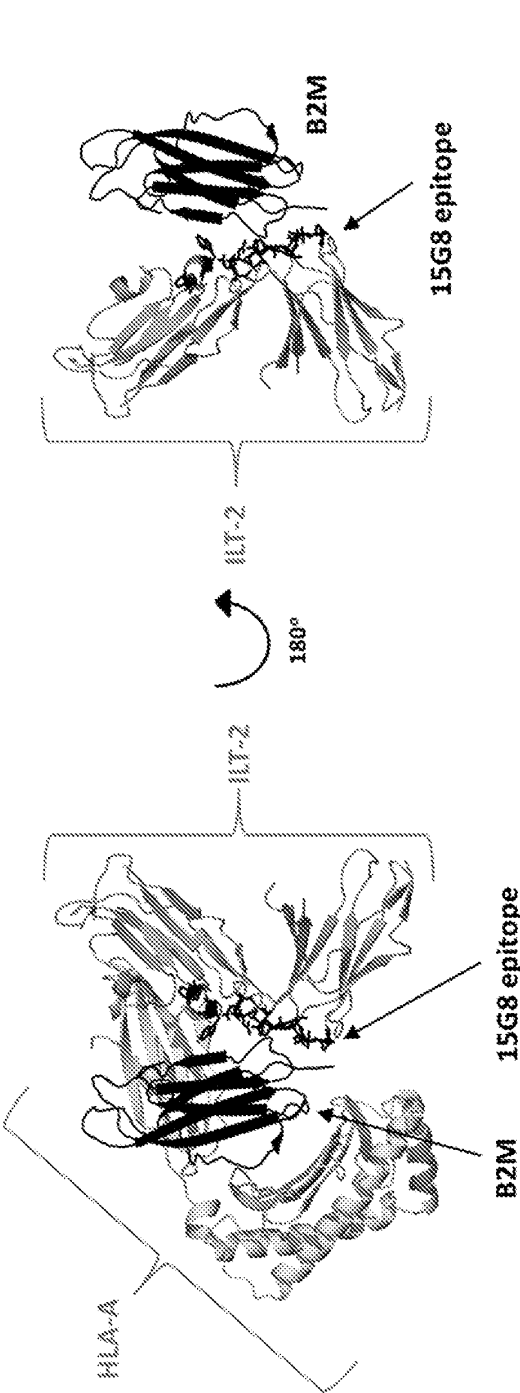


Fig. 18E

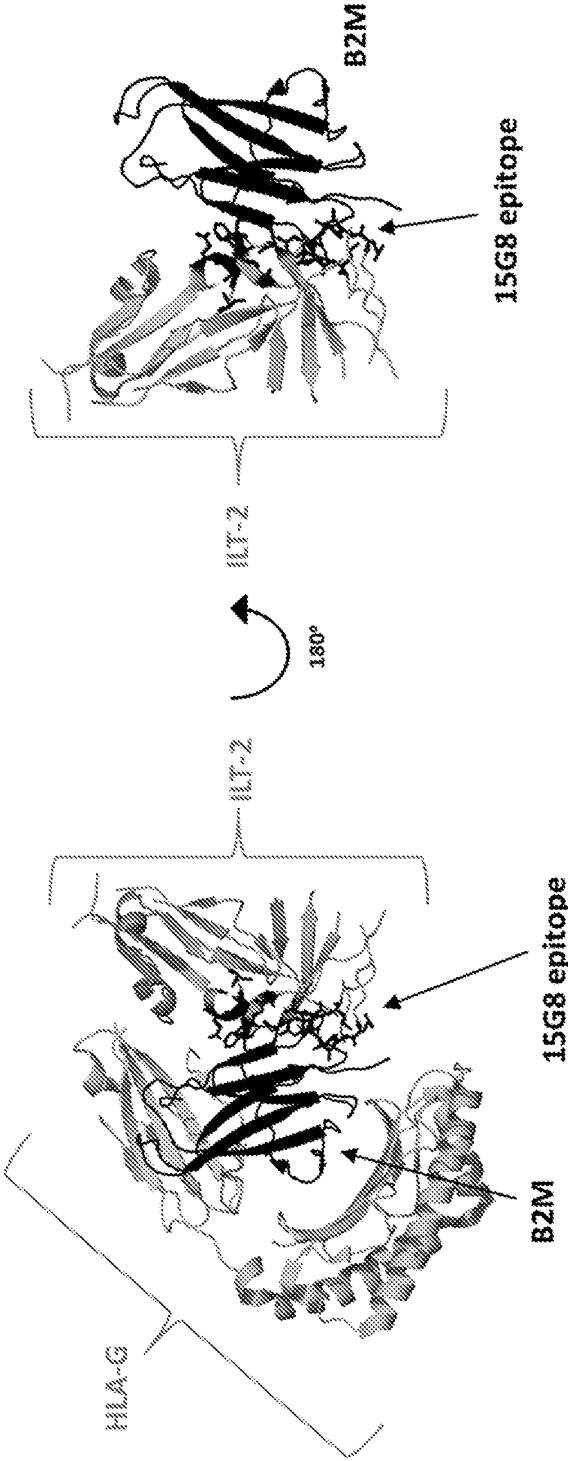


Fig. 18F

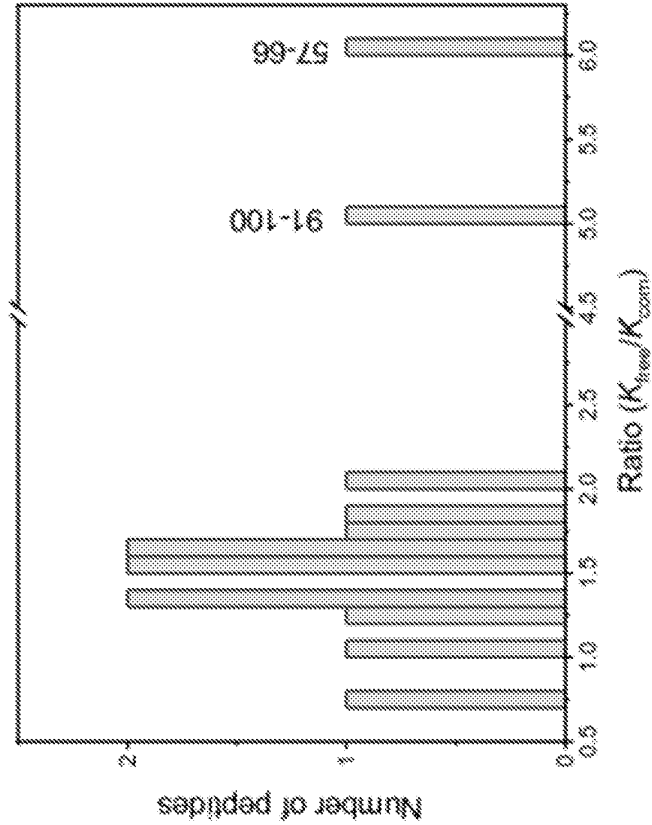


Fig. 19B

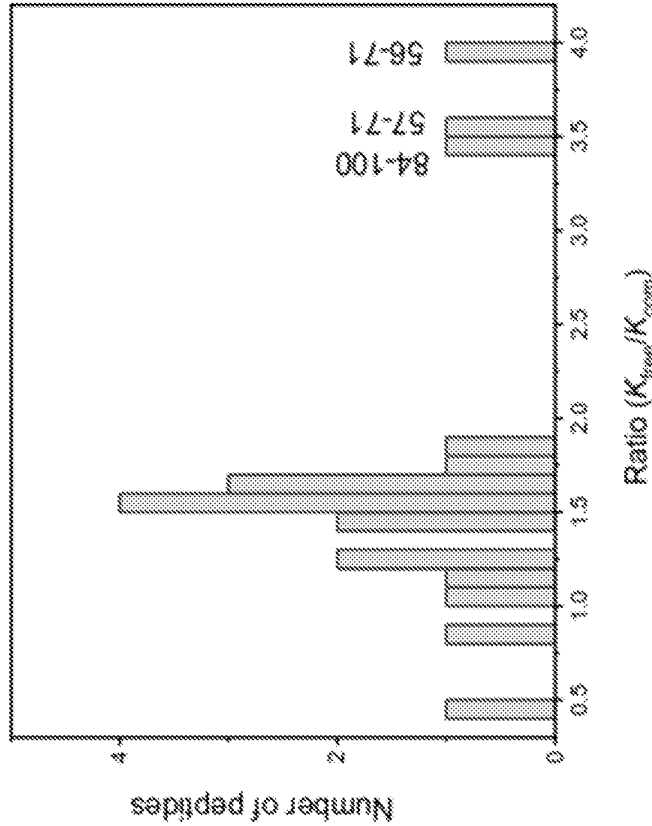
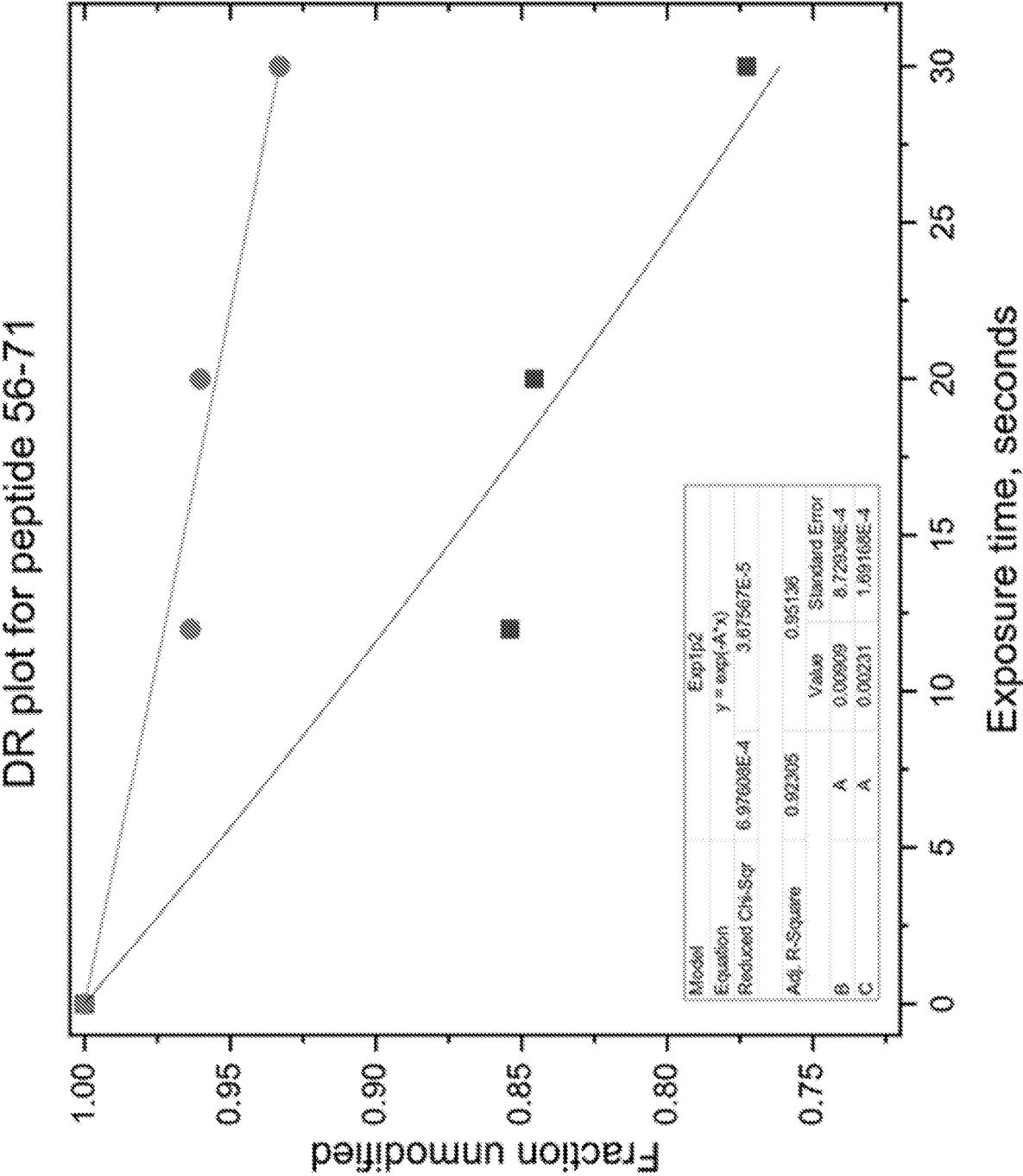
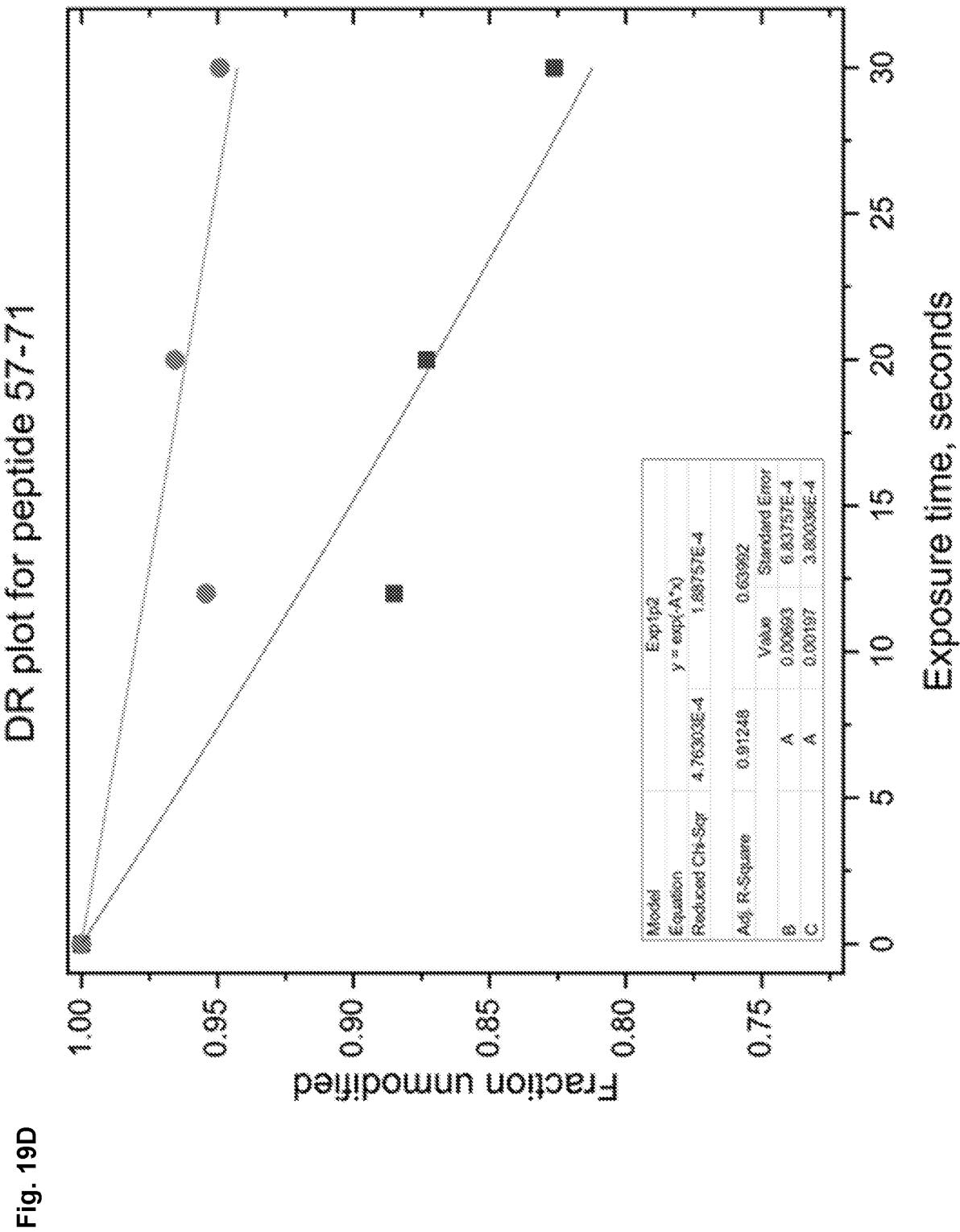


Fig. 19A

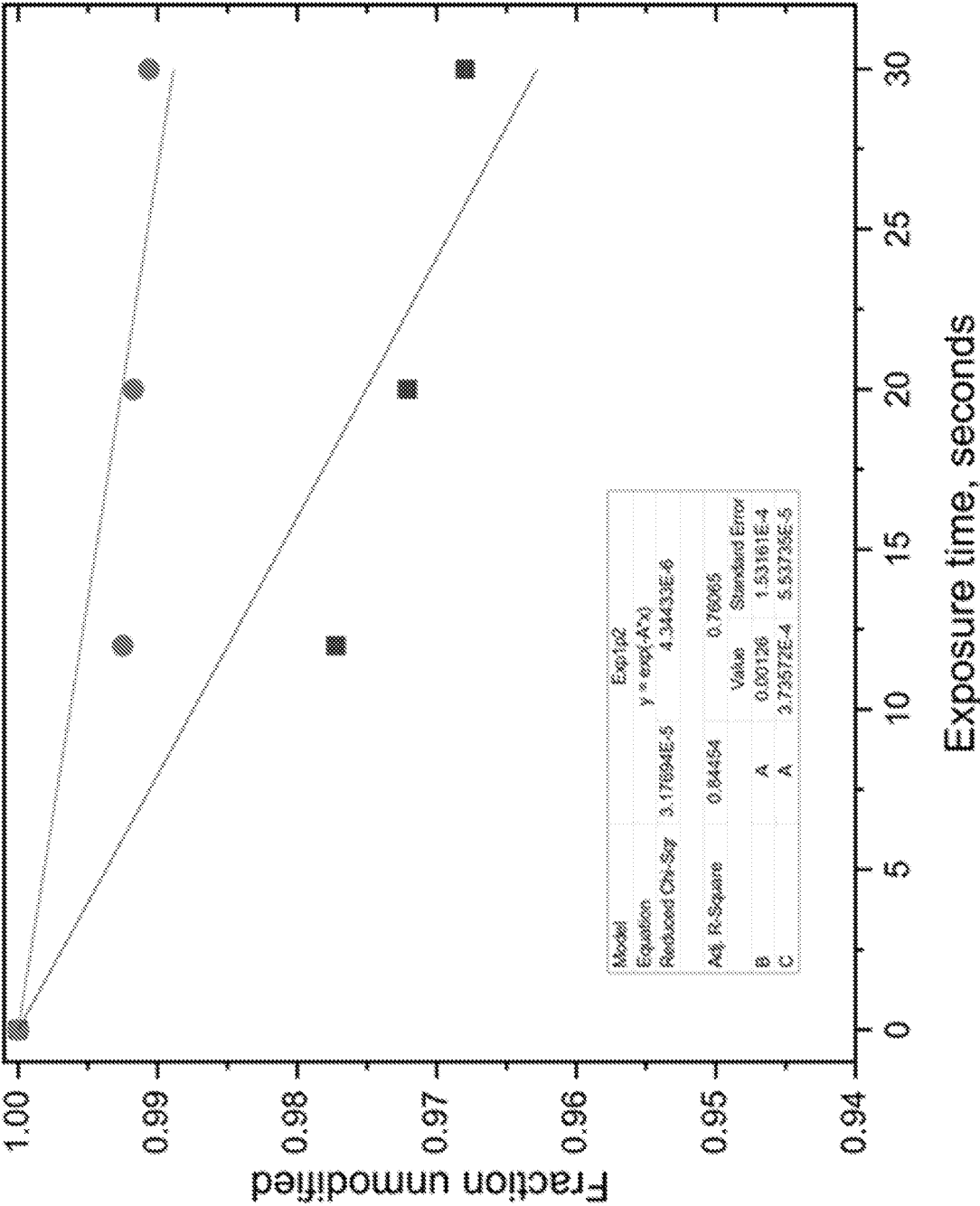
Fig. 19C





DR plot for peptide 84-100

Fig. 19E



DR plot for peptide 57-66

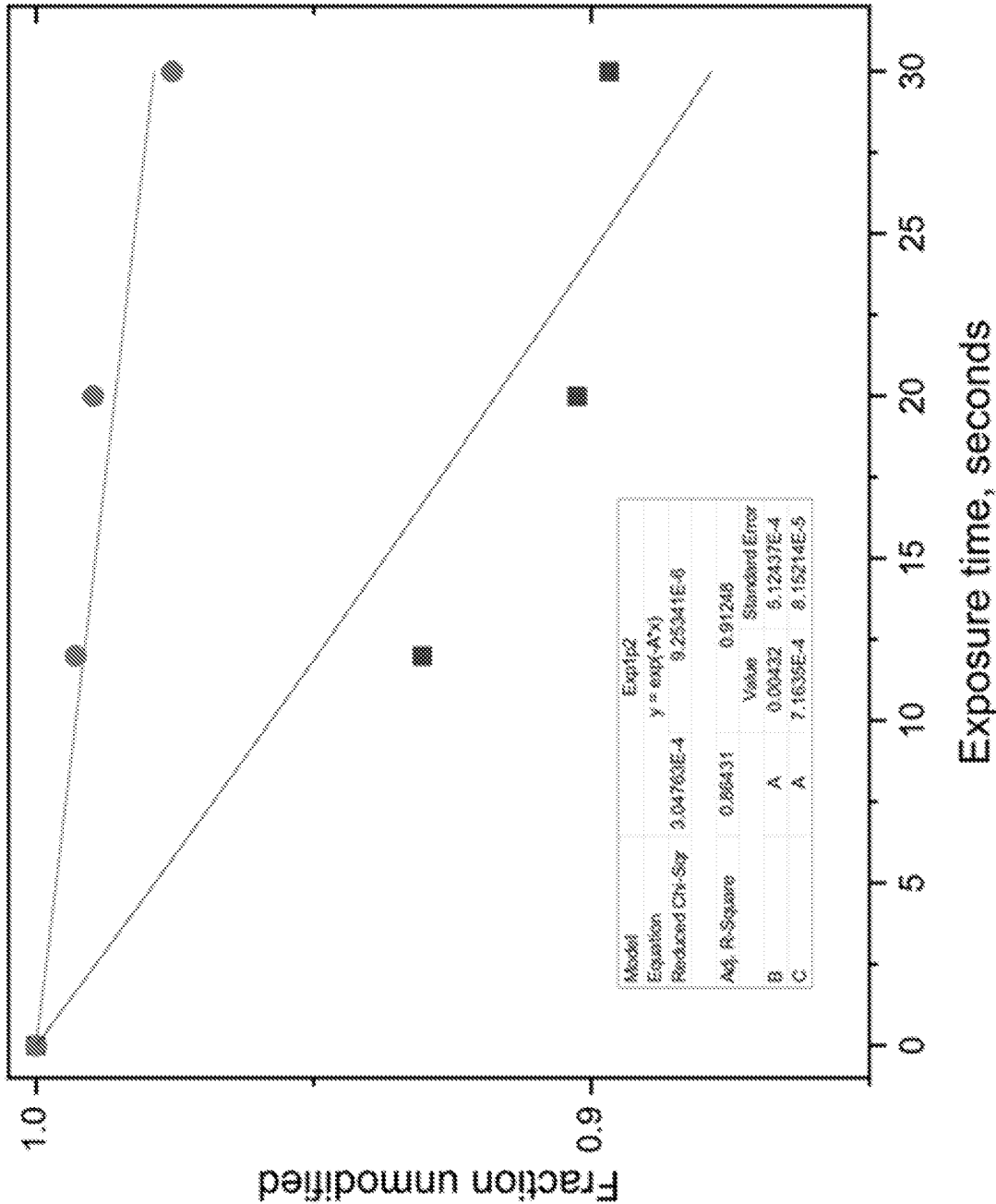
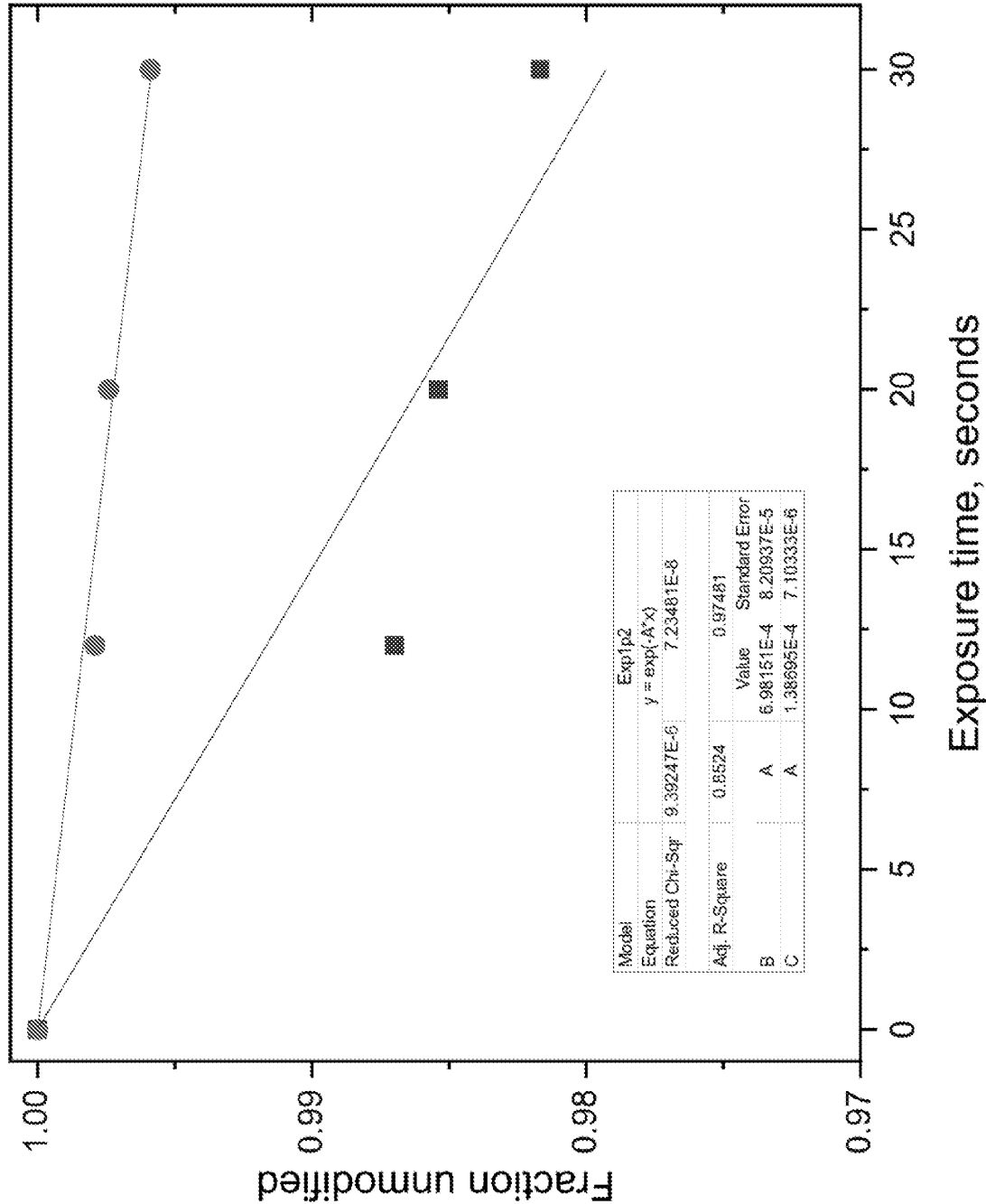


Fig. 19F

DR plot for peptide 91-100



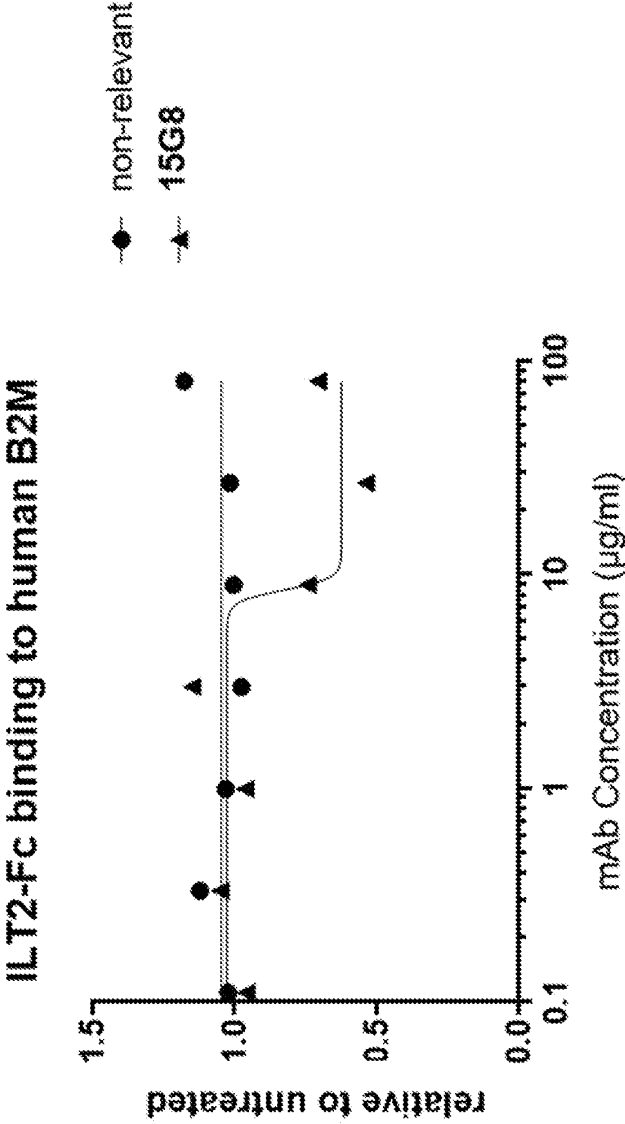


Fig. 20

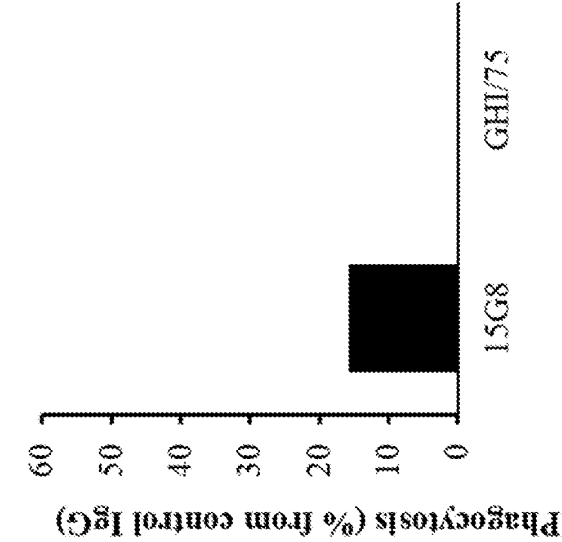


Fig. 21B

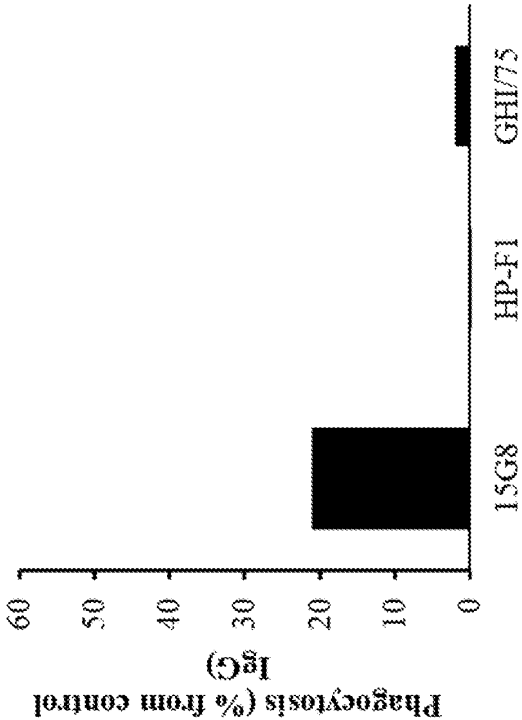


Fig. 21A

