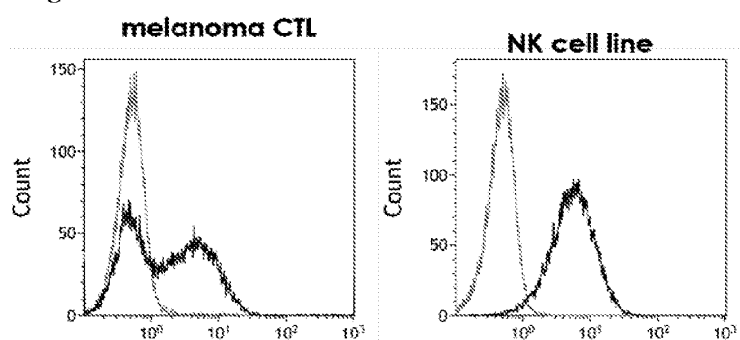
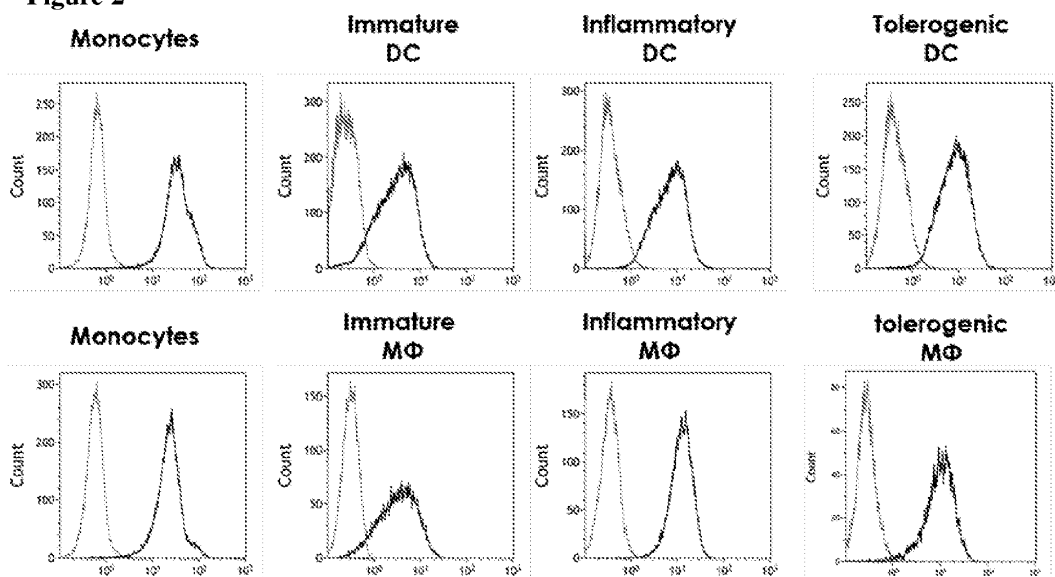


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Figure 1**Figure 2****Figure 3A**

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

Figure 3B

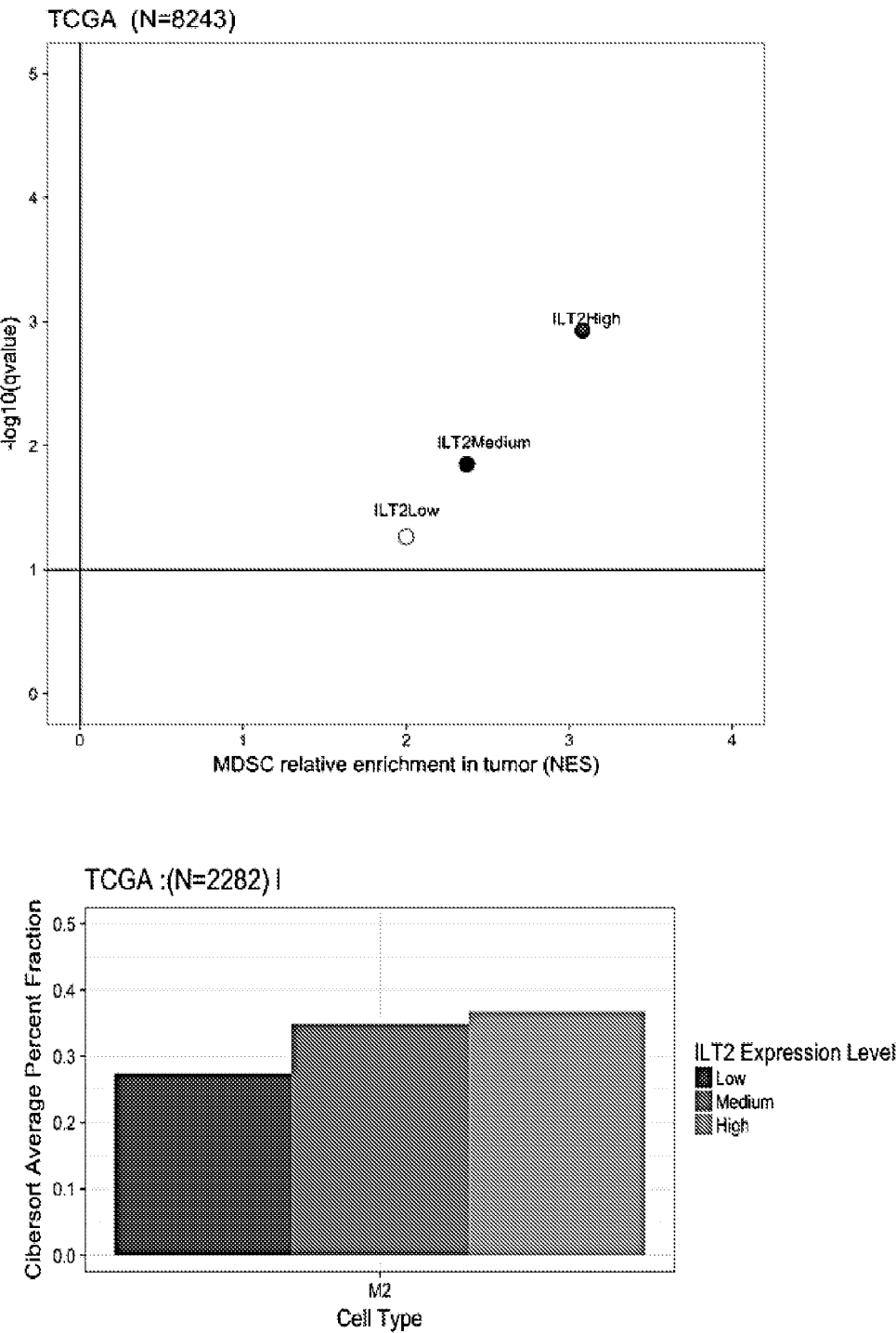


Figure 3C

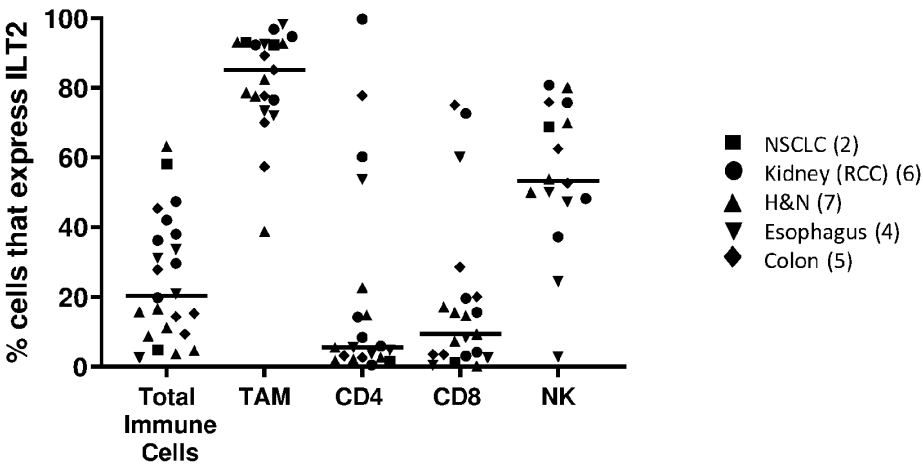


Figure 4A

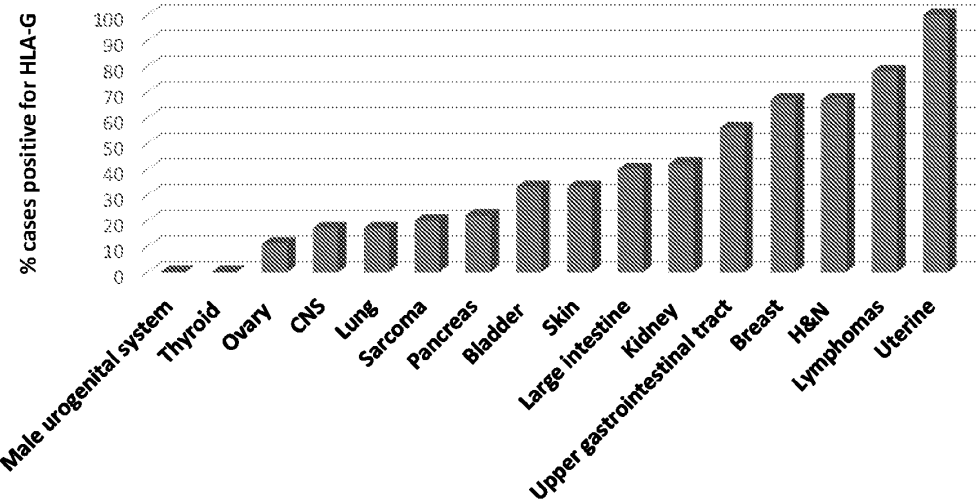


Figure 4B

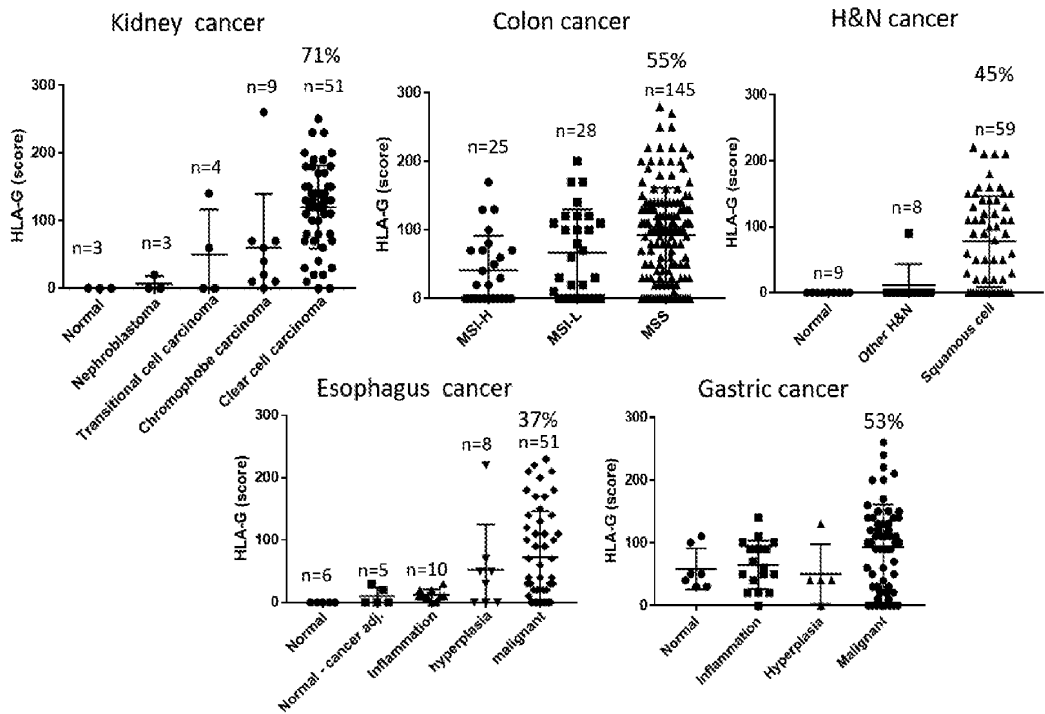
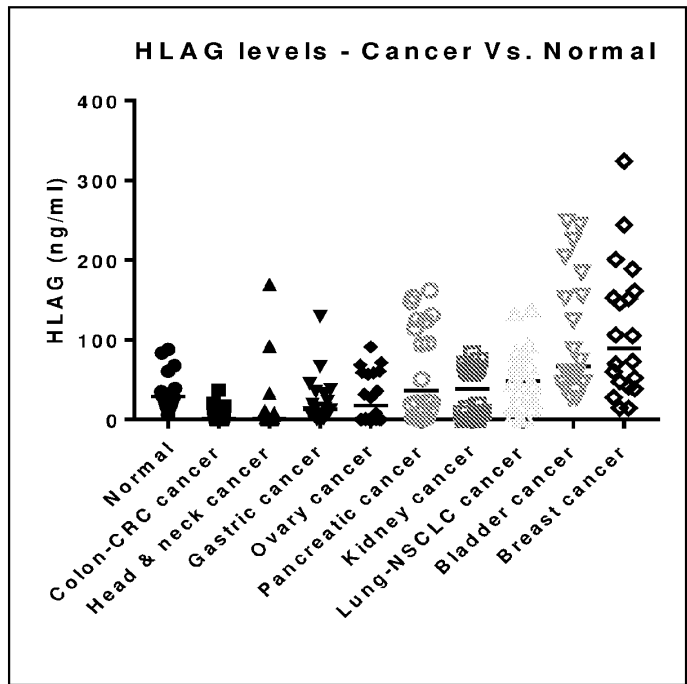


Figure 5



19E3 heavy chain variable region (Murine)

10	20	30	40	50	60	70	80	90	
CAGGTTCAAGCTGCAGCAGTCTGGAGCTGAGCTGGCGAGGCTGGGCTTCAGTGAAGCTGTCTGCAAGGCTTCTGGCTACACCTTCACAGCTATGGTA	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	33								
TAAGCTGGGTGAAGCAGAGAACTGGACAGGGCTTGGAGTGGGTTGGAGAGATTTAATCCCTGGGAAGTGGTAATTCTTACTACAAATGAGAGATTCAAGGGCAA	200								
S W V K Q R T G Q Q G L E W V G E I Y P G S G N S Y Y N E K F K G K	66								
GGCCACACTGACTGCAGACAAATCCTCCAGCAGACAGCGTACATGGAGCTCCGACGCTGACATCTGAGGACTCTGCGGTCATTCTCTGTGCAAGATCGAAT	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	99								
GATGGTTACCTGACTACTGGGCGCCAAAGSCACCACTCTCACAGTCTCTCA	351	SEQ ID NO: 35							
D G Y P D Y W G Q G T T L T V S S	117	SEQ ID NO: 21							

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19E3 light chain variable region (Murine)

10	20	30	40	50	60	70	80	90	
GACATCCAGATGACACAACTTCAATCTTACTTGTCTGTAICTCTAGGAGGCAGAGTCACCAATTACTTGCAGGGCAAGTGACCACATTAATAATGGTTAG	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 L A	33								
CCTGGTATCAGCAGAAACAGGAAATGCTCTAGGCTCTTAATATCTGGTGCACCAAGTTTGGAAACTGGGGTTCCTTTCAGGATTCAGTGGCAGTGGATC	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 G S	66								
TGGAAAGGATTACACTCTCAGCATTACCAAGTCTTCAGACTGAAGATGTTGCTACTTATTACTGTCAACAGTATTGGAGTACTCCGTGGACGTTCCGGTGGGA	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	99								
GGCACCAAGCTGGAAATCAAA	321	SEQ ID NO: 39							
G T K L E I K	107	SEQ ID NO: 22							

Figure 6

15G8 heavy chain variable region (Murine)

10	20	30	40	50	60	70	80	90
GATGTACAGCTTCAGGGGTGAGGACCTGGCCCTCGTGAACCTTCTCAGTCTGTCTCTCACCTGCTGTGCTACTGGCTACTCCATCACCAGTGGTTATT								
100								
D V Q L Q G S G P G L V K P S Q S L S L T C S V T G Y S I T S G Y Y								
33								
ACTGGAACTGGATCCGGCAGTTTCCAGGAAACAAACTGGAAATGGATGGGCTACATAAGCTACGATGGTAGCAATAACTACAACCCATCTCTCAAAAATCG								
200								
W N W I R Q F P G N K L E W M G Y I S Y D G S N N Y N P S L K N R								
66								
AATCTCCATCACTCGTGACACATCTAAGGAACCCAGTTTTCCTGAAGTTGAATTCGTGACTTCTGAGGACACAGCCACATATTACTGTGCCCATGGTTAC								
300								
I S I T R D T S K N Q F F L K L N S V T S E D T A T Y Y C A M G Y								
99								
TCATATTACTATGCTATGGACTGCTGGGGTCAAGGAACCTTCAGTCAACGCTCTCTCA								
357								
SEQ ID NO: 33								
S Y Y Y A H D C W G Q G T S V T V S S								
119								
SEQ ID NO: 30								

15G8 light chain variable region (Murine)

10	20	30	40	50	60	70	80	90
GATATCCAGATGACACAGACTACATCTCCCTGTGCTGCTCTCTGGGAGACAGAGTCAACCATCAGTTCAGGACAGTCAAGTCAATTATTAA 100								
D I Q H T Q T T S S L S A S L G D R V T I S C R T S Q D I S N Y L N 33								
ACTGGTATCAGCAGAAACCCAGATGGAACTGTGTTAAACTCTTGATCTCTTACACATCAAGATTGCACTCAGGAGTCCCAATCAAGGTTTCAGTGGCAGTGGGTC 200								
N Y Q Q K P D G T V K L L I S Y T S R L H S G V P S R F S G S G S 66								
TGGAAACAGATTATTCTCACCATTAGCAACCTGGAGCAAGAGATATTGGCACTTACTTTTGGCAACAGGGTAATACGCTTCCACAGTTCCGGCTCGGGG 300								
G T D Y S L T I S N L E Q E D I A T V F C Q Q G N T L P T F G S G 99								
ACAAAGTTGGAAATAAAA 318 SEQ ID NO: 37								
T K L E I K 106 SEQ ID NO: 45								

Figure 6 continued

15G8 heavy chain variable region (Human)

10	20	30	40	50	60	70	80	90	
GATGTCAGCTGCAAGGCTCTGGCCCTGGACTGGTTAAGCCTTCCGAGACACTGTCCCTGACCTGCTCTGTGACCGGGTACTCTATCACCCTCCGGCTACT	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	33								
ACTGGAACTGGATCAGACAGTTCCTCCGGCAAGAAACTGGAAATGGATGGGCTACATCTCCCTACGACGGCTCCAAACAATACAAACCCAGCTGGAAGAACCG	200								
W N W I R Q F P G K K L E W M H G Y I S Y D G S N N Y N P S L K N R	66								
GATCACCATCTCTGGGACACCTCCAAAGAACCAAGTTCTCCCTGAAGCTGAACCTCCGTGACCGCTGCCGATACCCGCTACCTACTACTGTGCTCAGCGCTAC	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	99								
TCCTACTACTACGCCATGGATGCTTGGGGCCAGGGCACATCTGTGACAGTGTCTCT	357								
S Y Y Y A M D A W G Q G T S V T V S S	119								
SEQ ID NO: 34									
SEQ ID NO: 28									

SUBSTITUTE SHEET (RULE 26)

15G8 light chain variable region (Human)

10	20	30	40	50	60	70	80	90	
GACATCCAGATGACCCAGTCTCCATCTCTGTCTGCTGCTGCGGCGACAGAGTGACCAATCACCTGTGCGGACCTCTCAGGACATCTCCAACTACCTGA	100								
D I Q M 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	33								
ACTGGTATCAGCAGAAACCCGGCAAGGCCGTGAAGCTGCTGATCTCTCTACACCTCCAGACTGCACTCTGGCGTGGCTCCAGATTTTCTGGCTCTGGATC	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 G S	66								
TGGCACCAGACTACACCCCTGACCATCAGTTCTCTGCAGCCTTGAGGACTTCGCCACTACTACTGTGACAGGGGCAACACCTCGCTACCTTTGGCCAGGGC	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	99								
ACCAAGCTGGAAATCAAG	318								
T K L E I K	106								
SEQ ID NO: 38									
SEQ ID NO: 24									

Figure 6 continued_1

17F2 light chain variable region (Murine)

310
300
290
280
270
260
250
240
230
220
210
200
190
180
170
160
150
140
130
120
110
100
90
80
70
60
50
40
30
20
10
0

Figure 6 continued_2

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Figure 7A

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

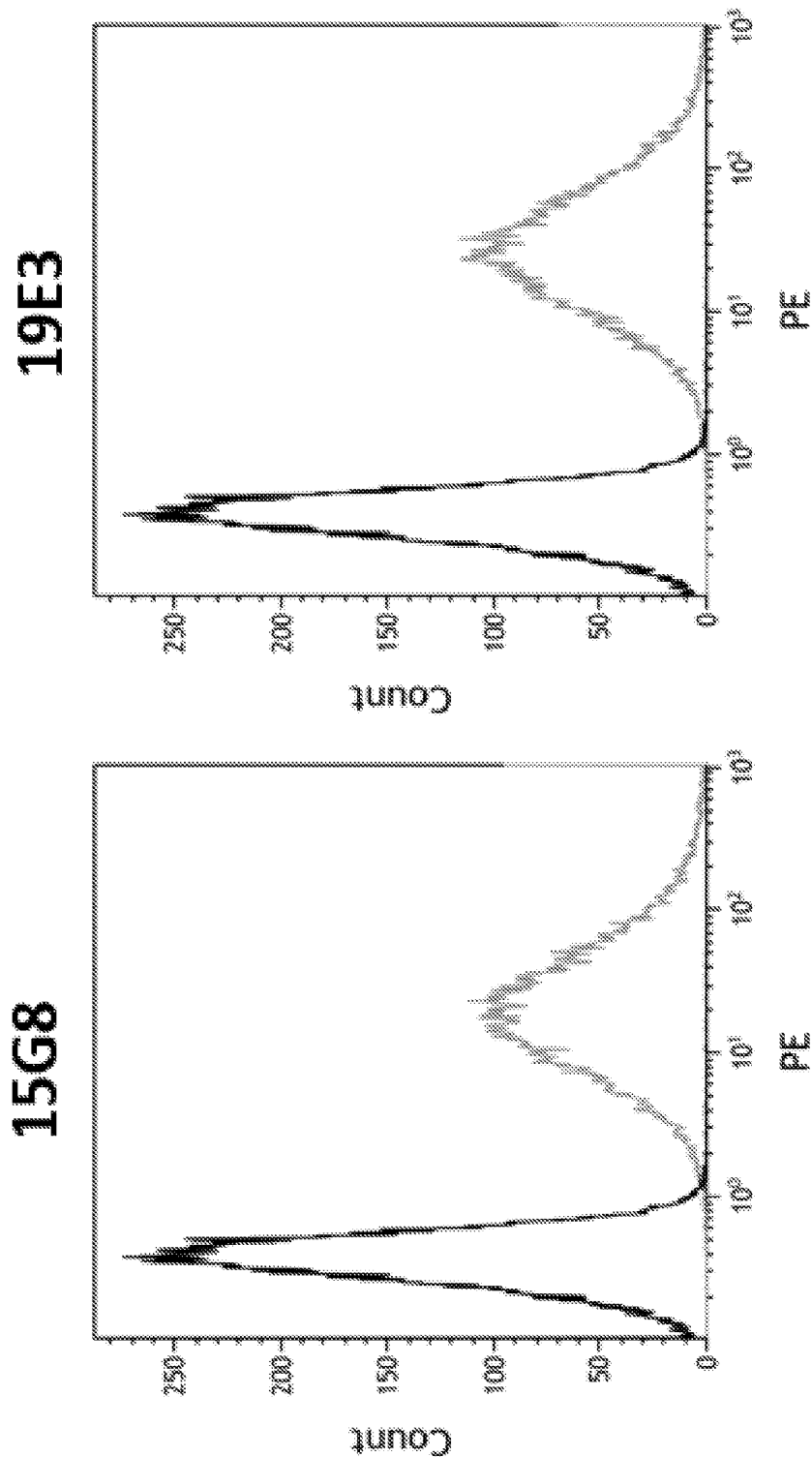


Figure 7B

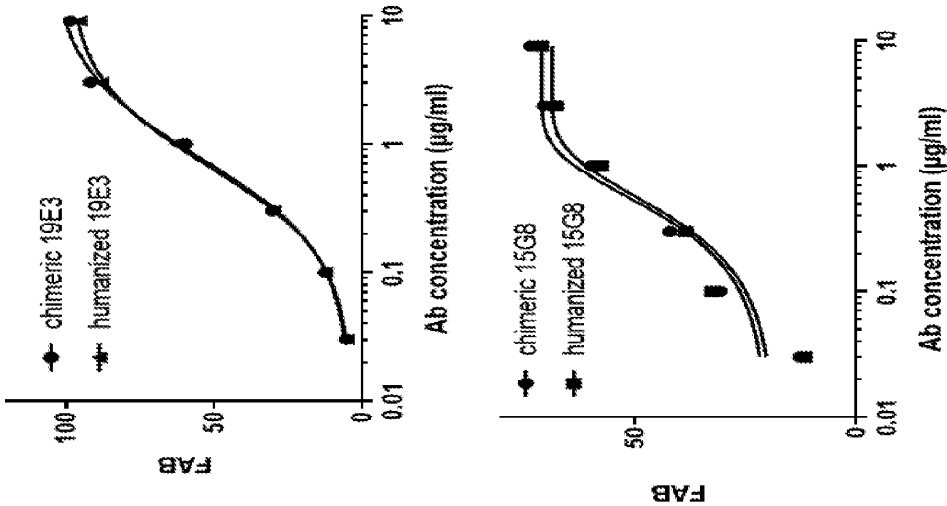


Figure 7C

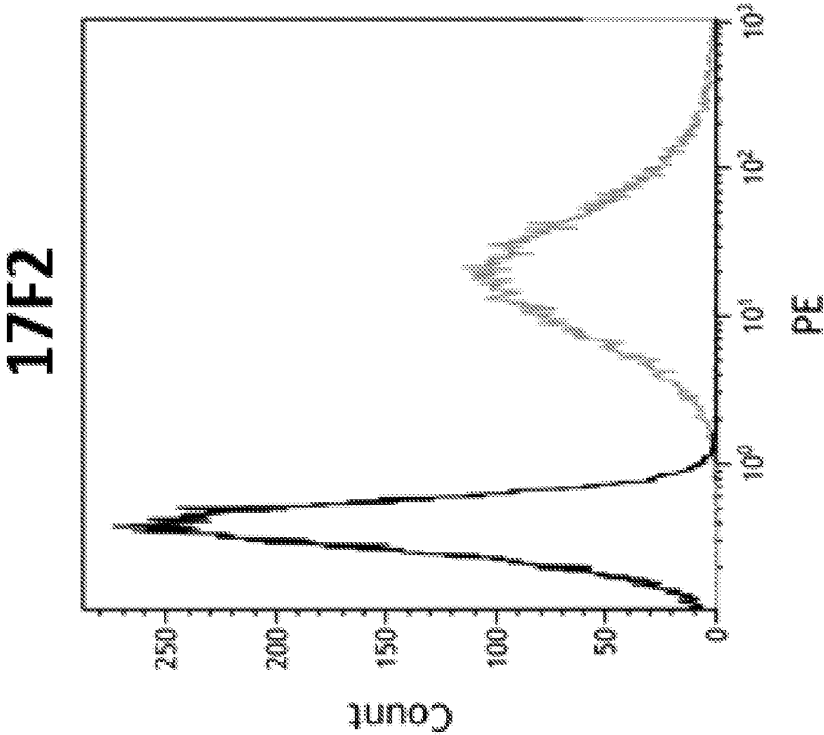


Figure 7B continued

Figure 7D

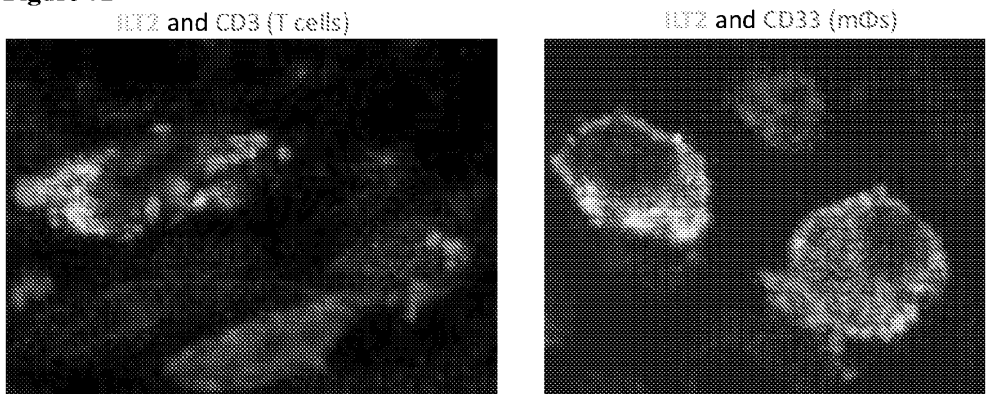


Figure 7E

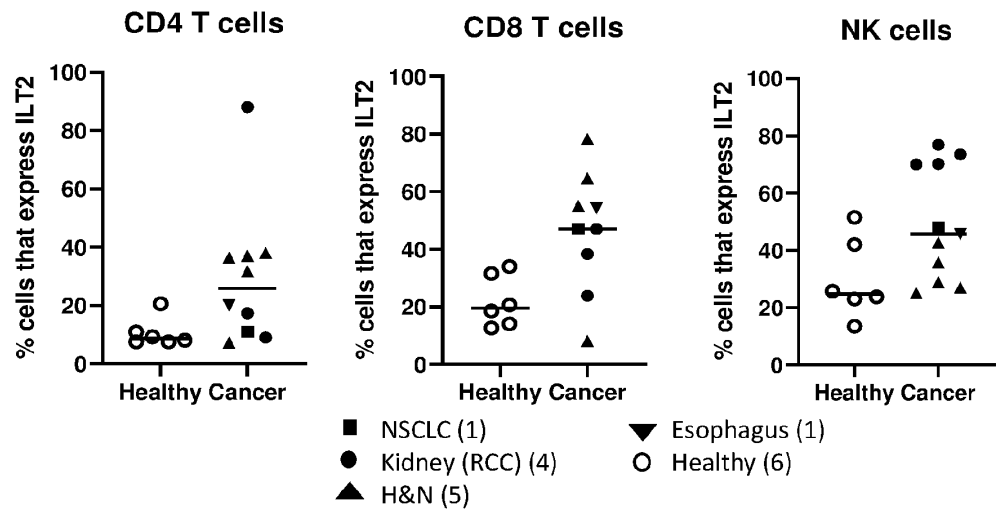


Figure 8A

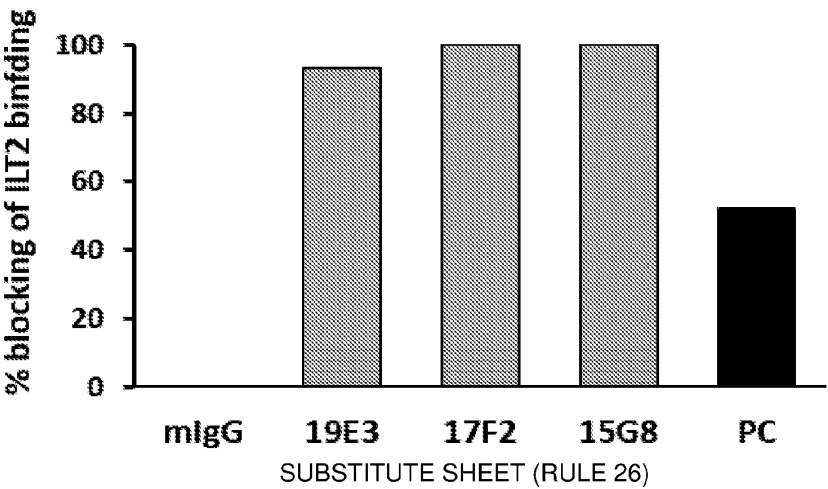


Figure 8B

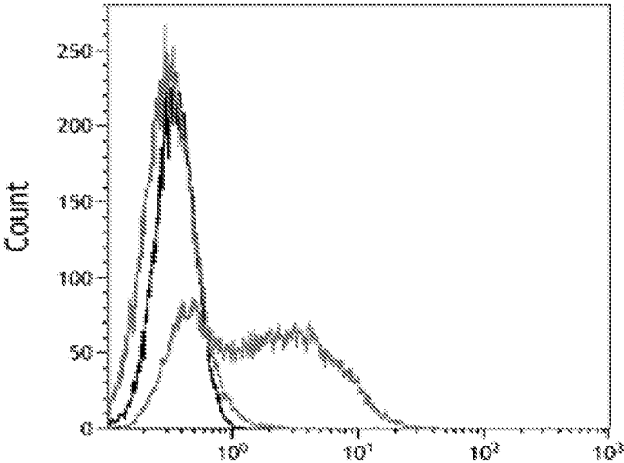


Figure 8C

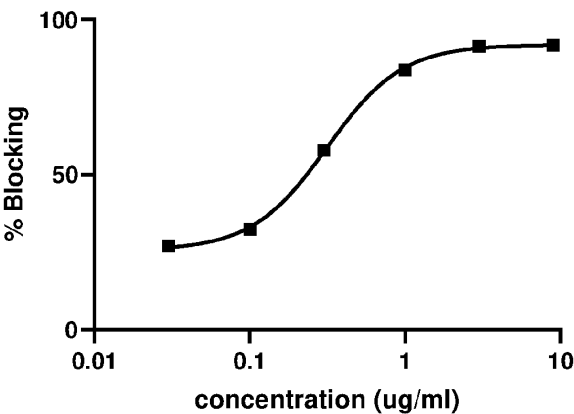


Figure 8D

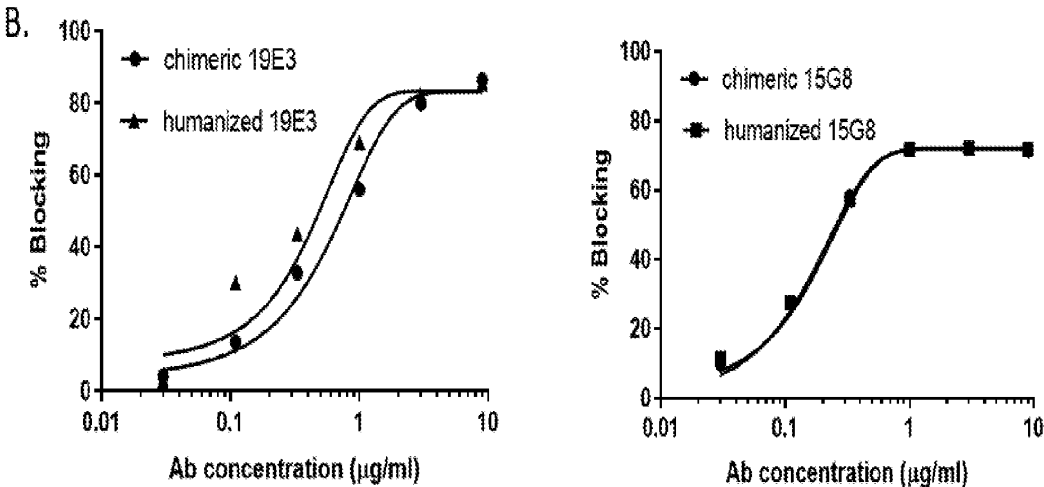


Figure 8E

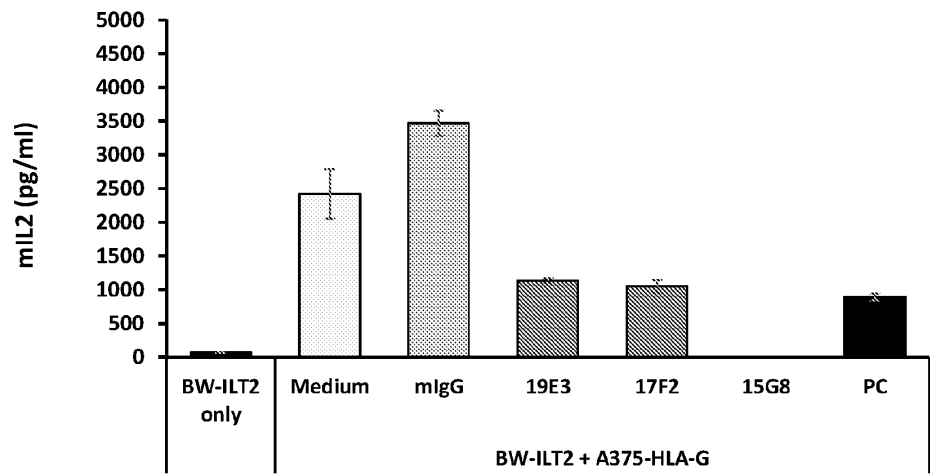


Figure 8F

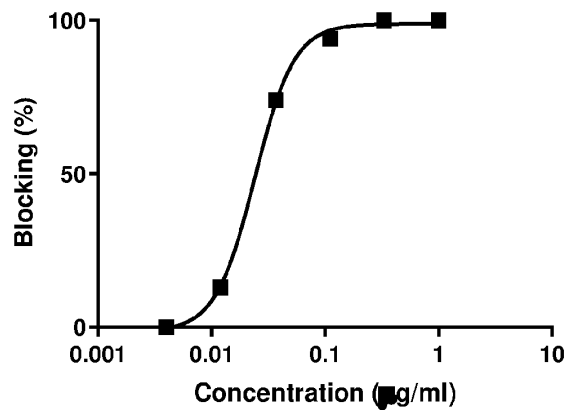
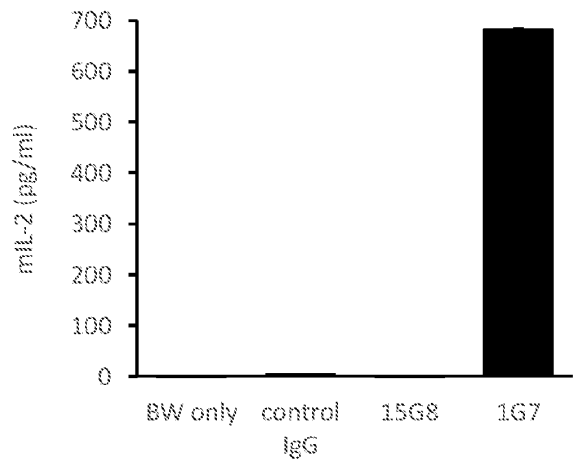


Figure 8G



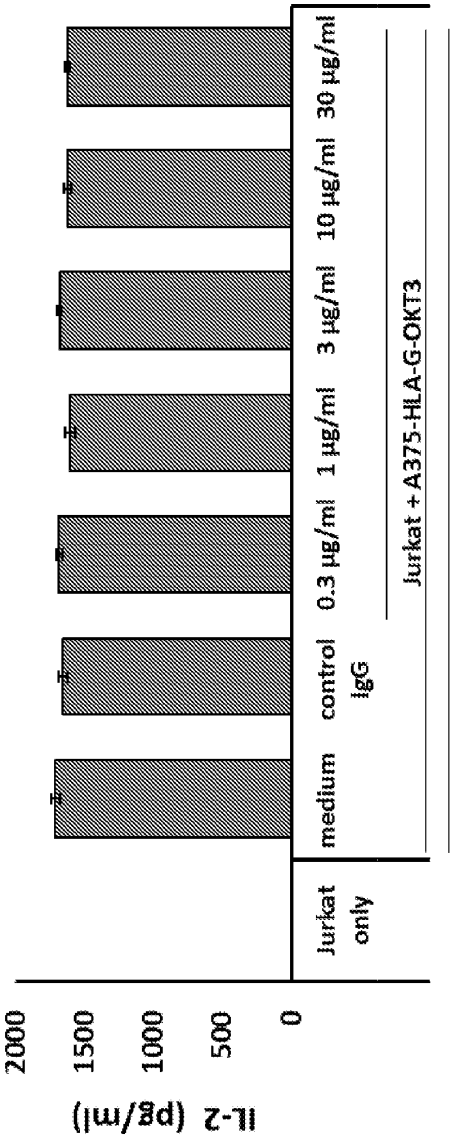


Figure 8H

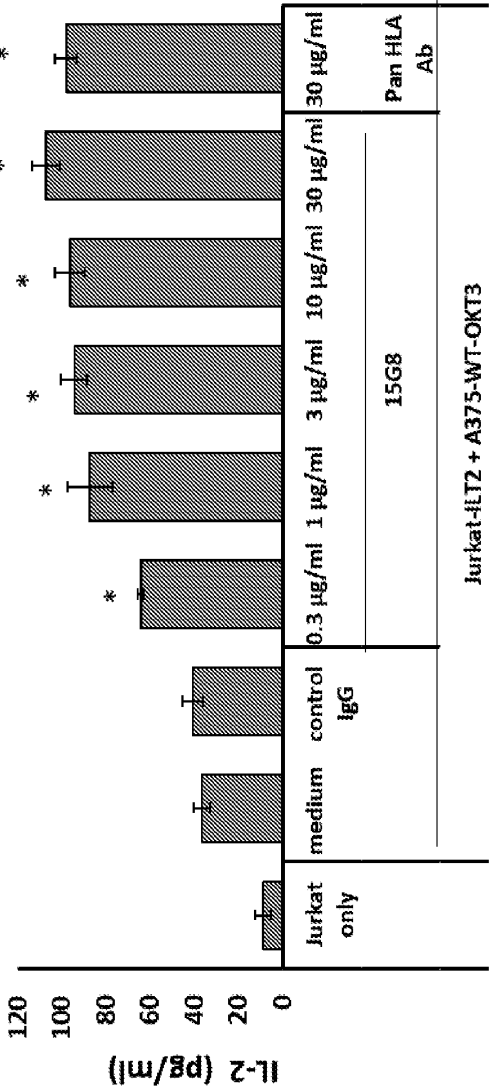


Figure 8I

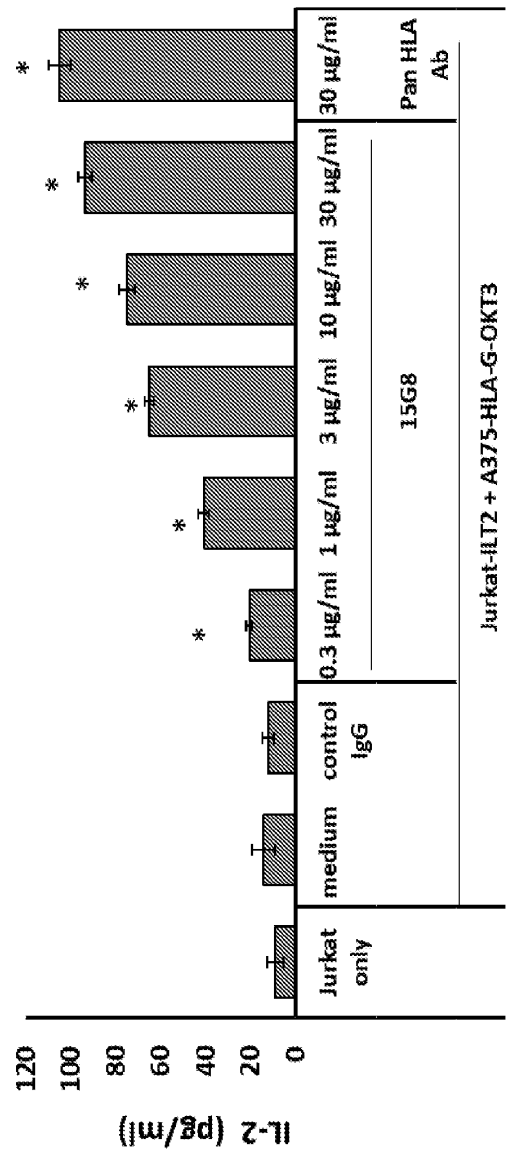


Figure 8J

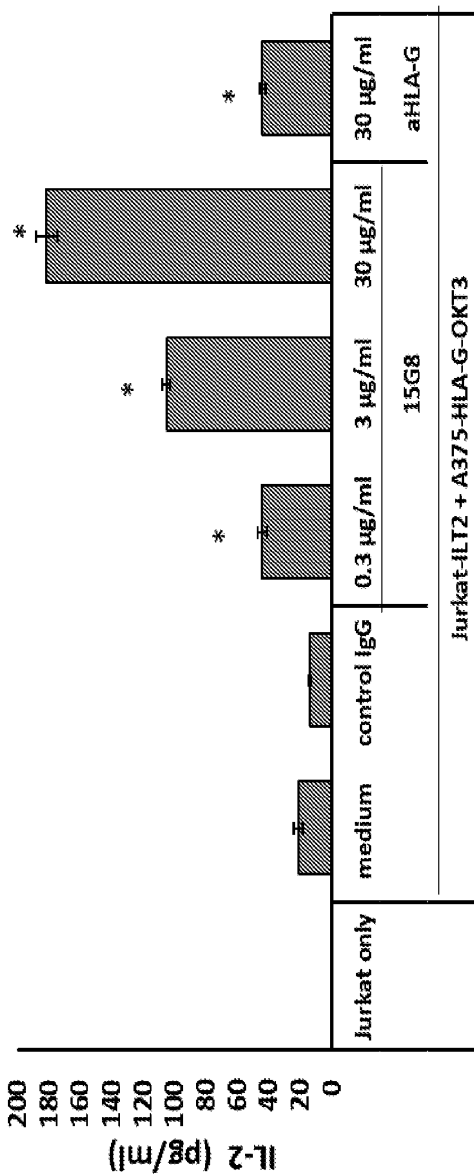


Figure 8K

Figure 8L

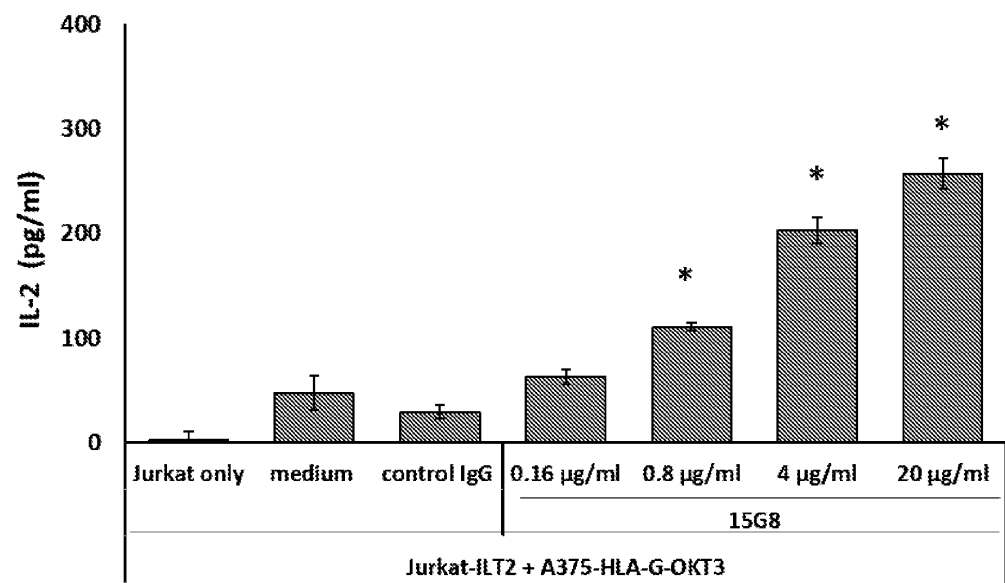


Figure 8M

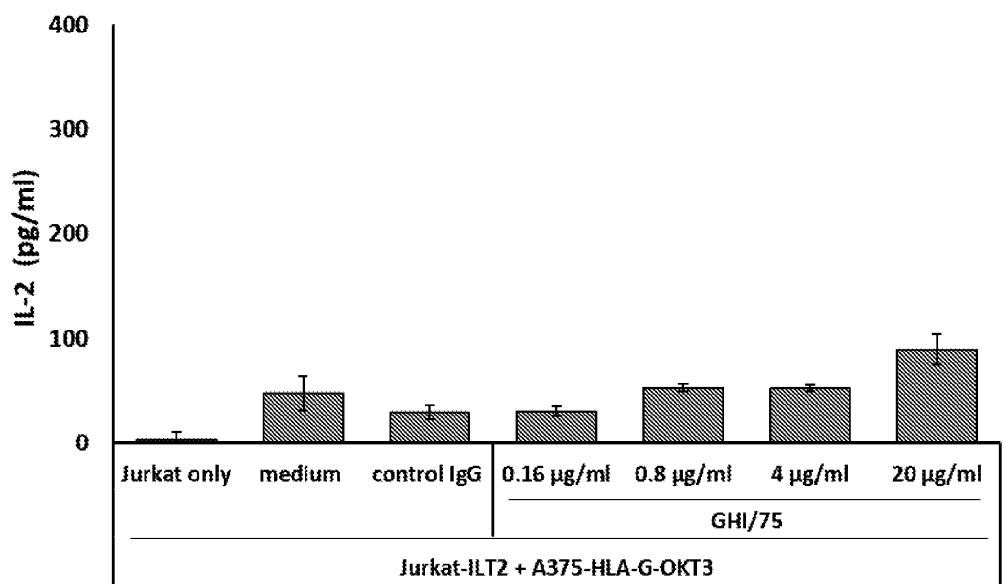


Figure 8N

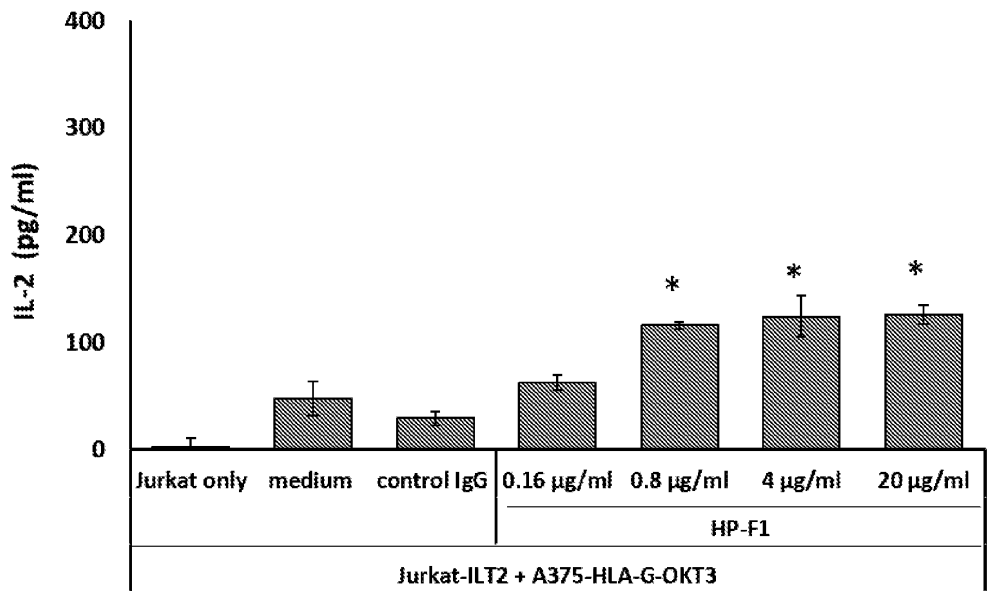


Figure 8O

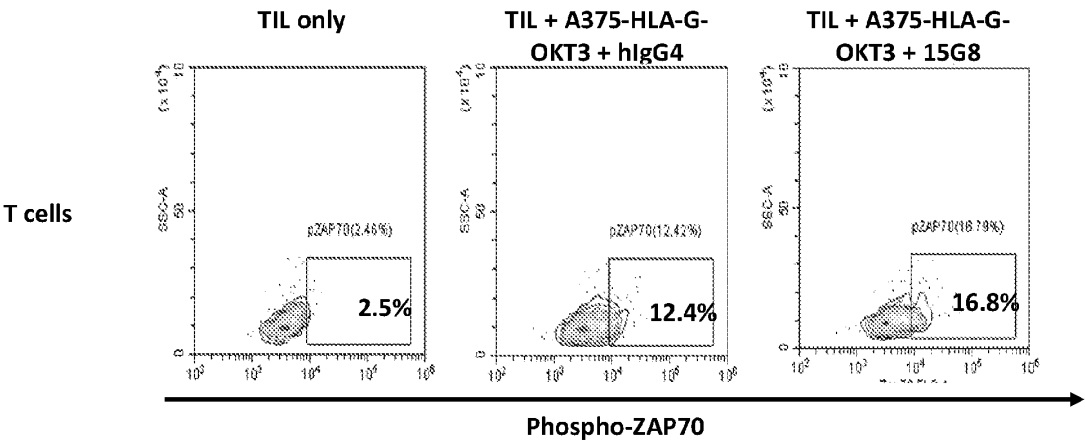


Figure 8P

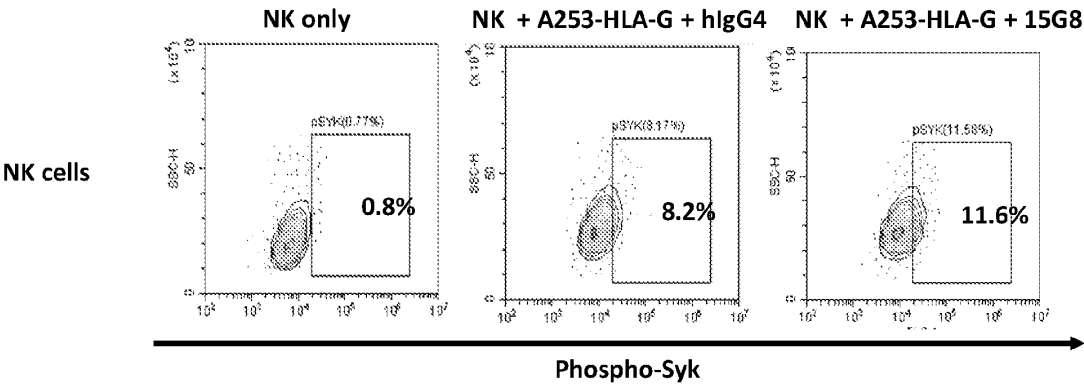
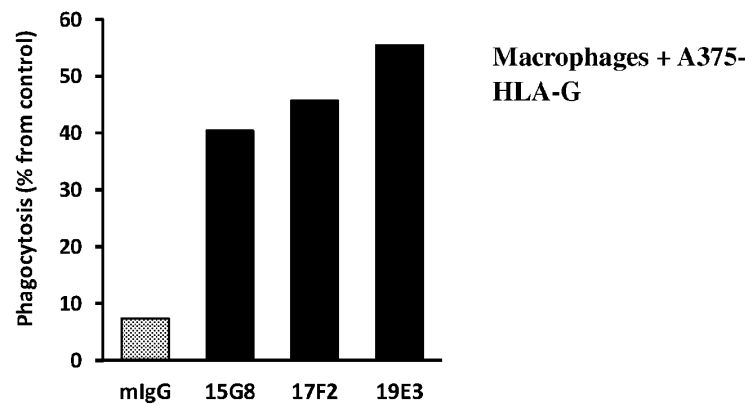


Figure 9A



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Figure 9B

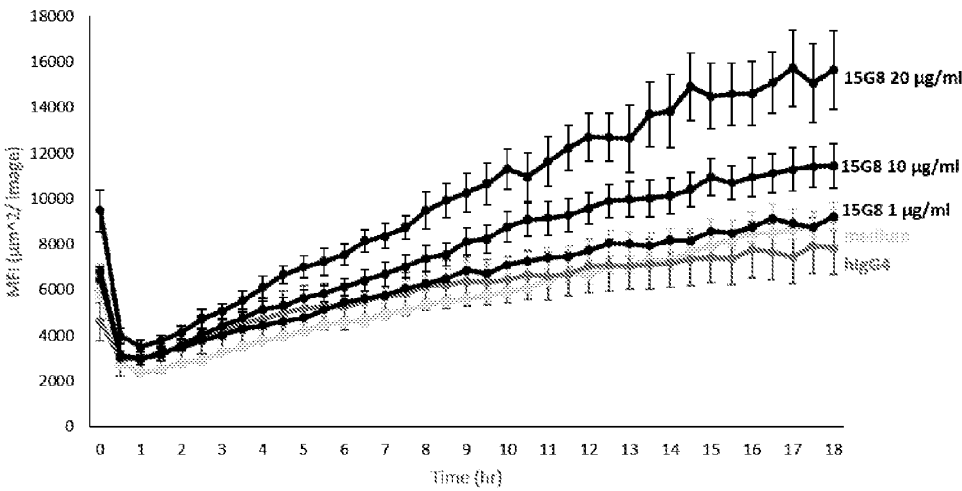


Figure 9C

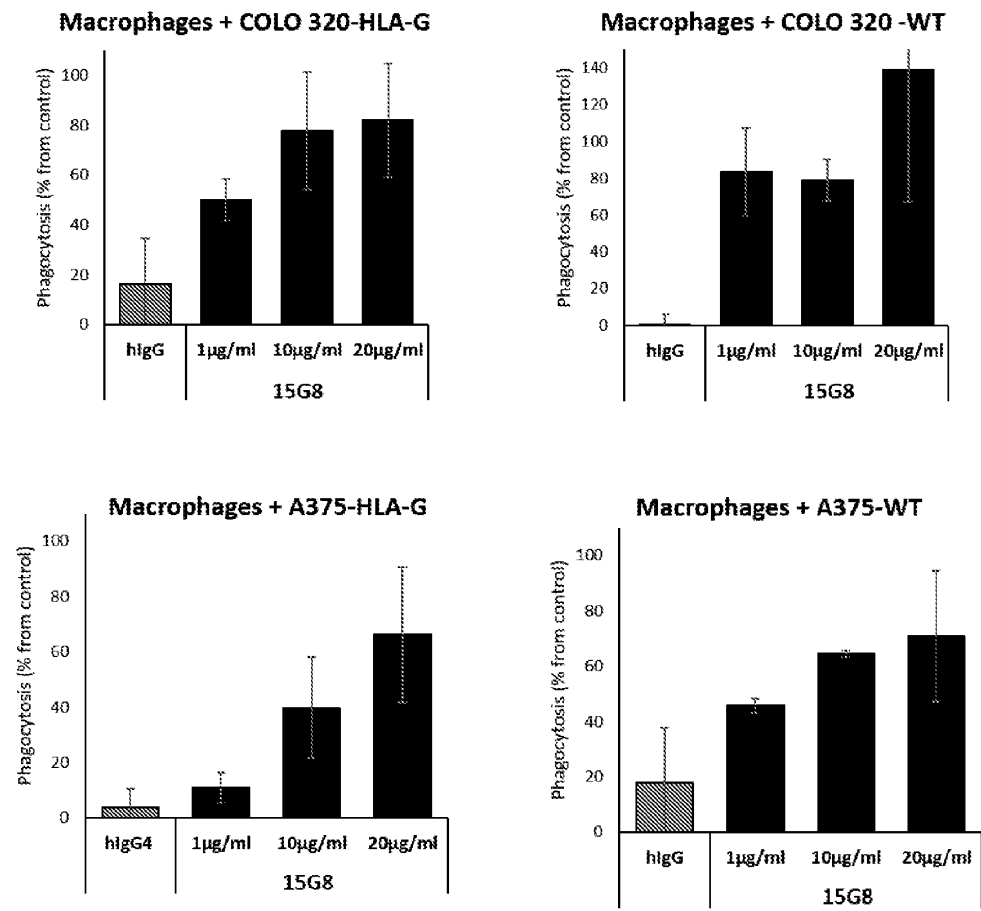


Figure 9D

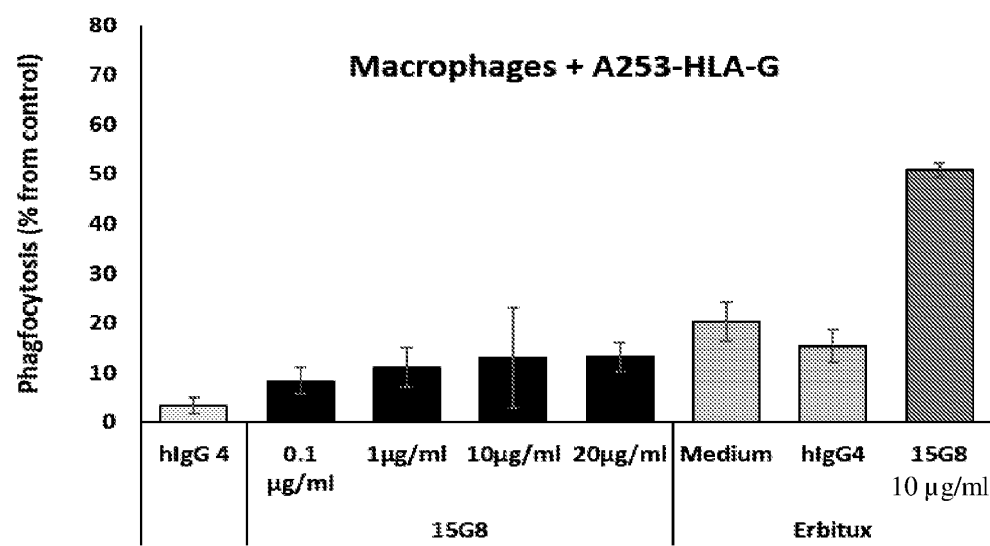
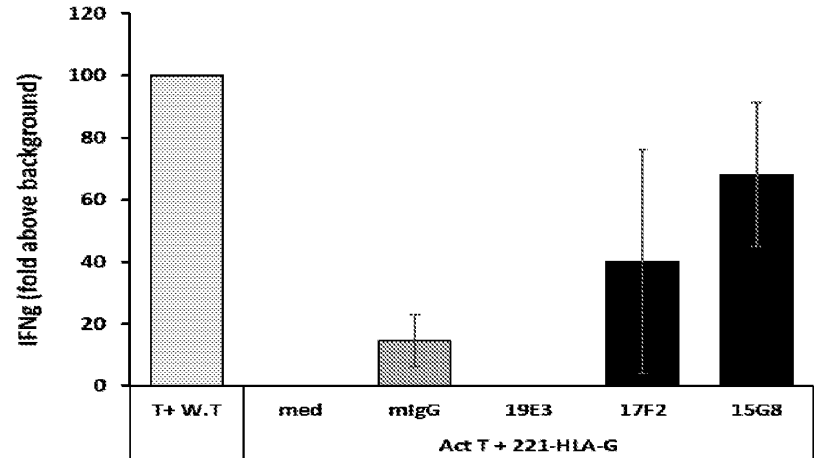


Figure 10A



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Figure 10B

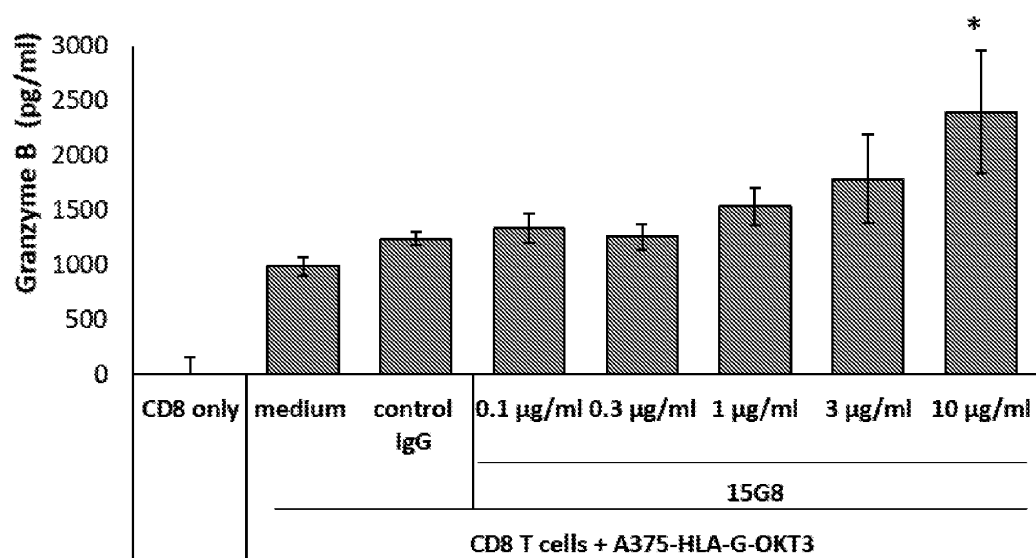


Figure 11A

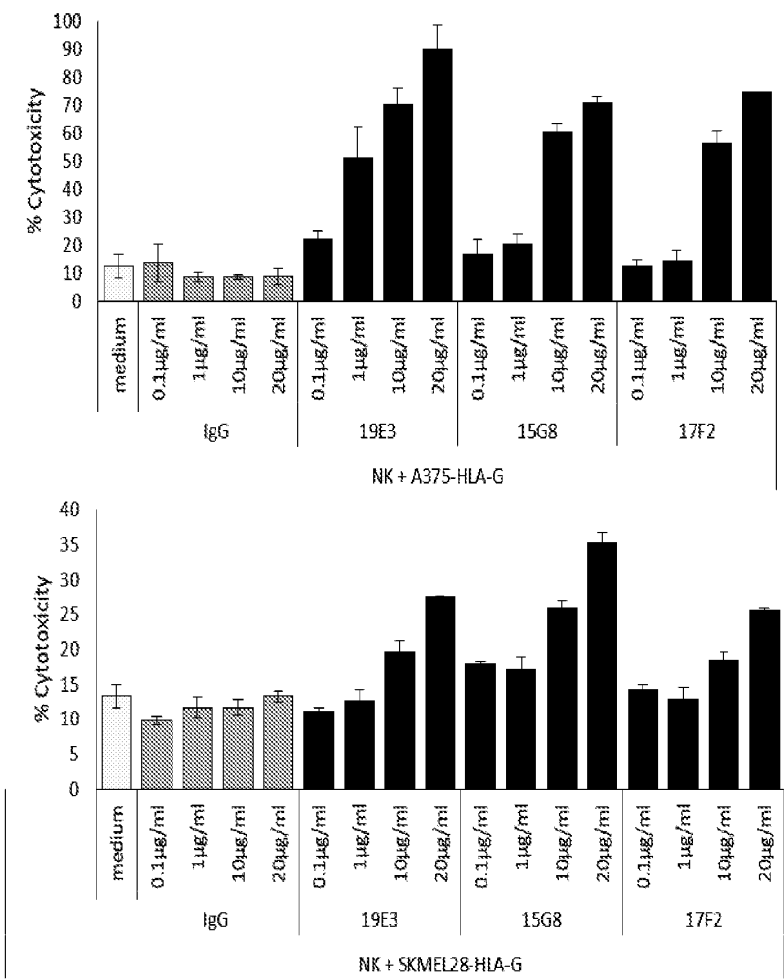
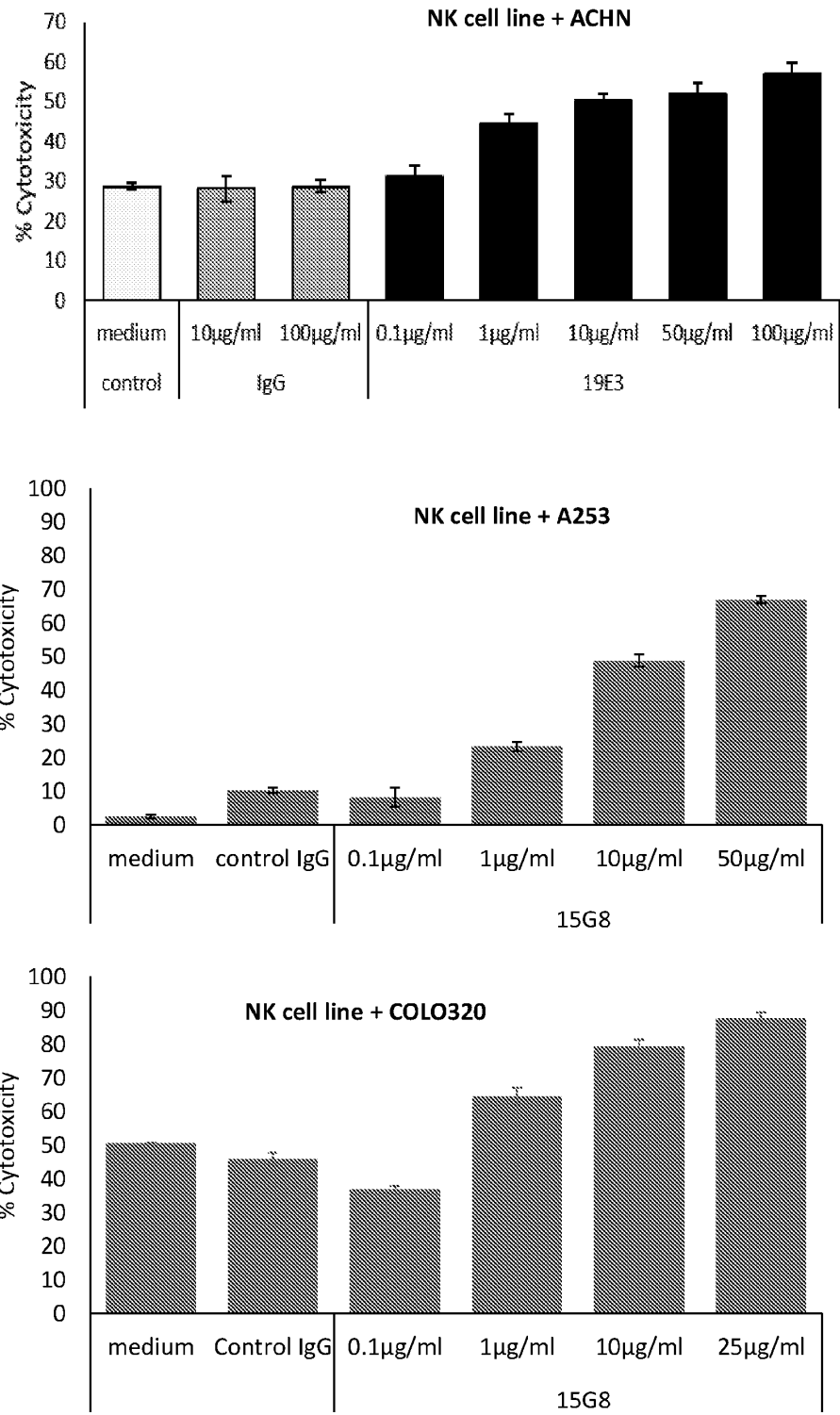


Figure 11B



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Figure 11C

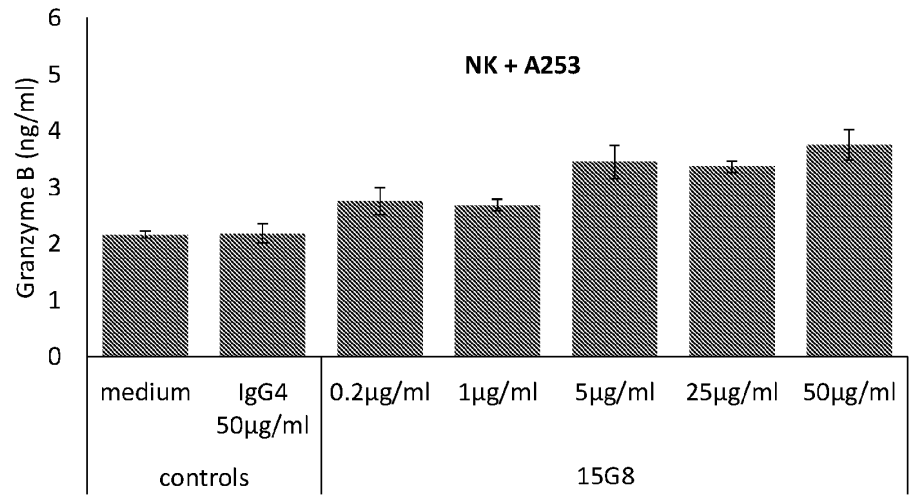


Figure 11D

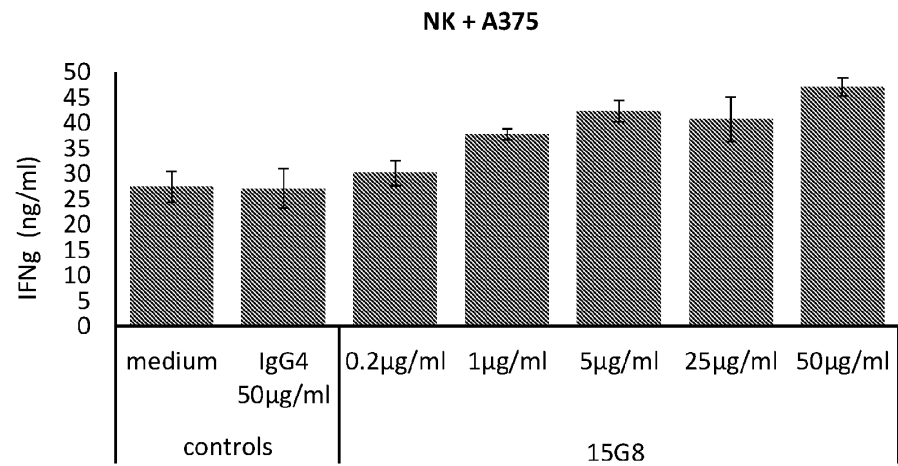


Figure 11E

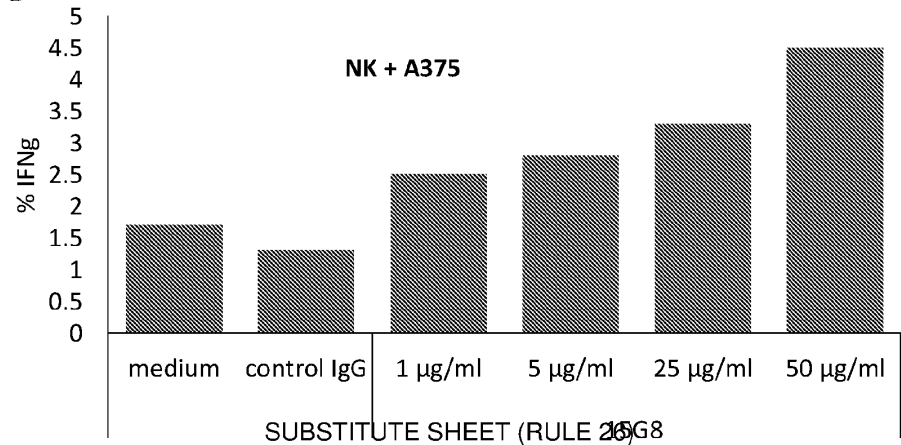


Figure 11F

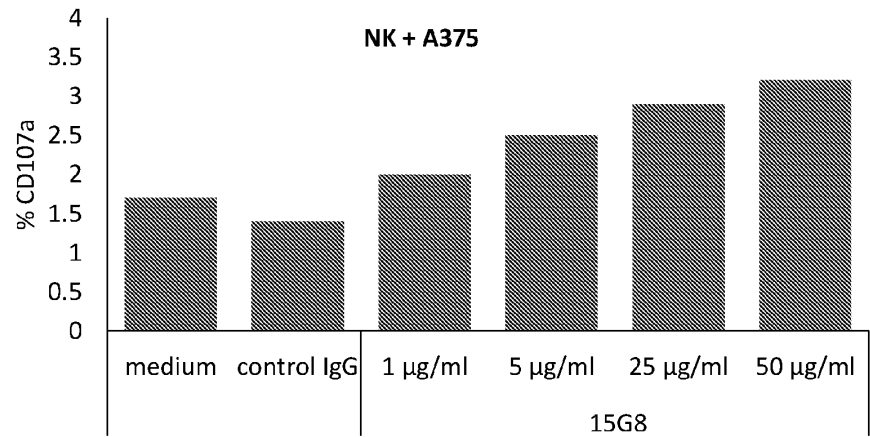


Figure 11G

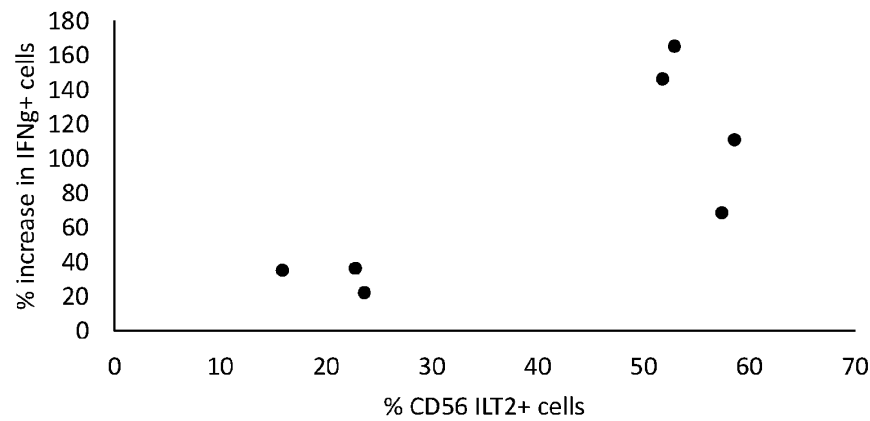


Figure 11H

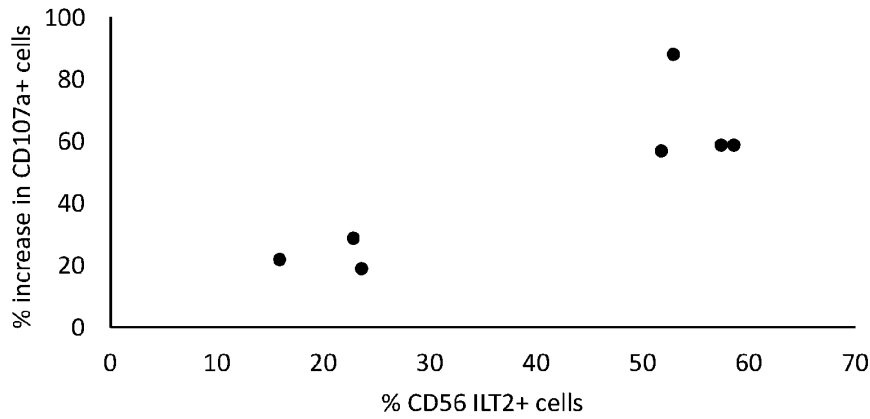


Figure 12

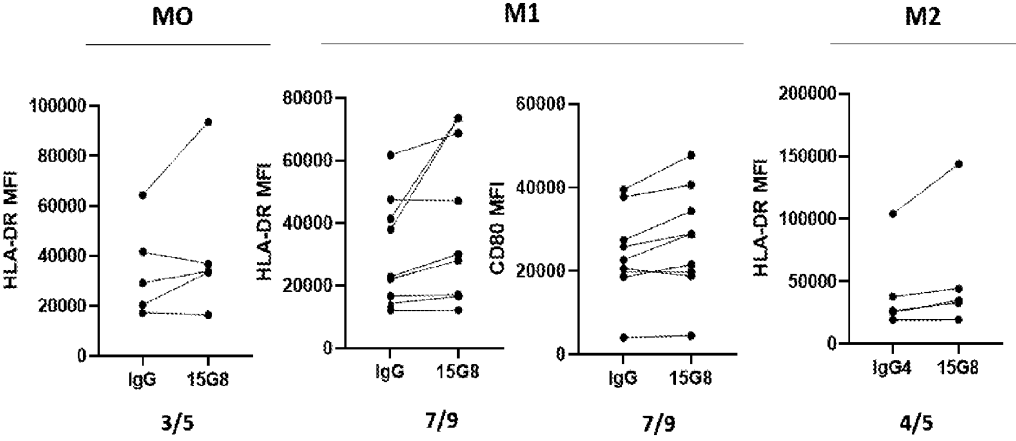
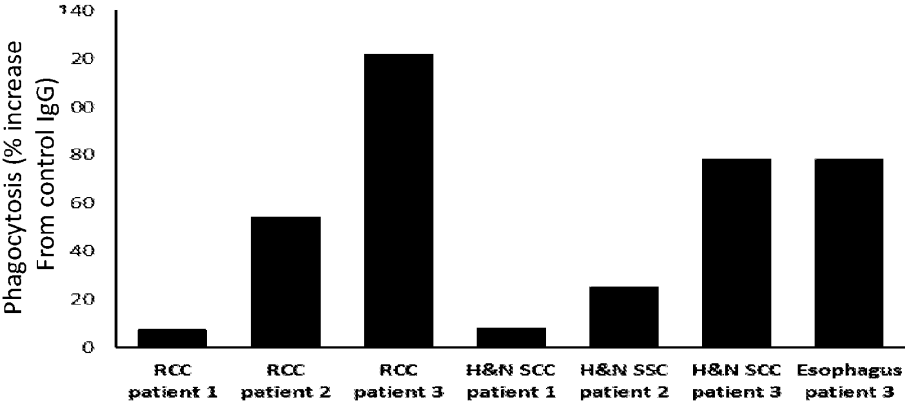


Figure 13A



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Figure 13B

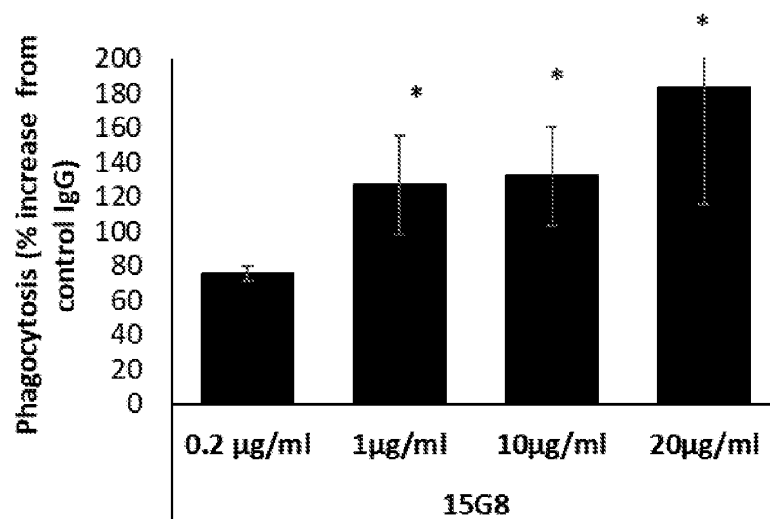


Figure 13C

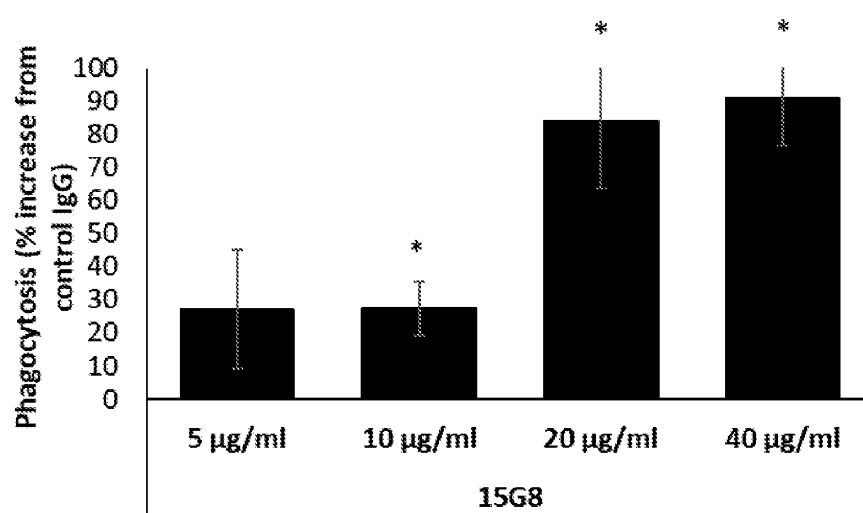


Figure 14A

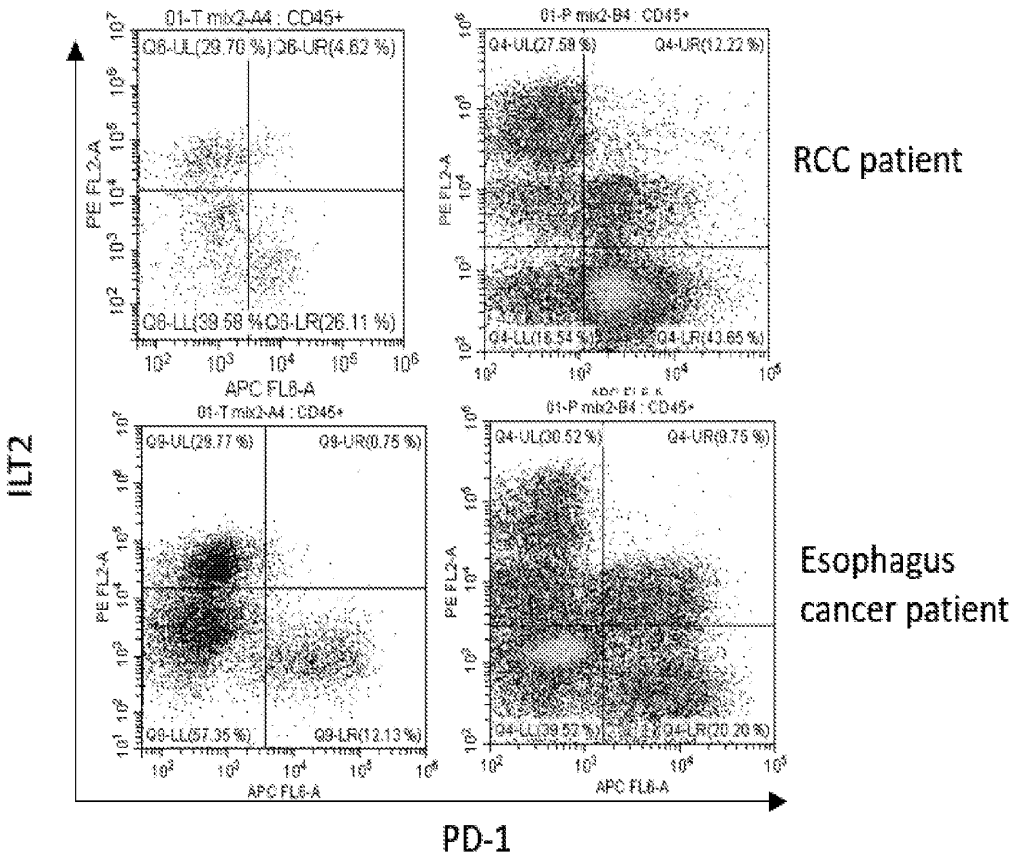


Figure 14B

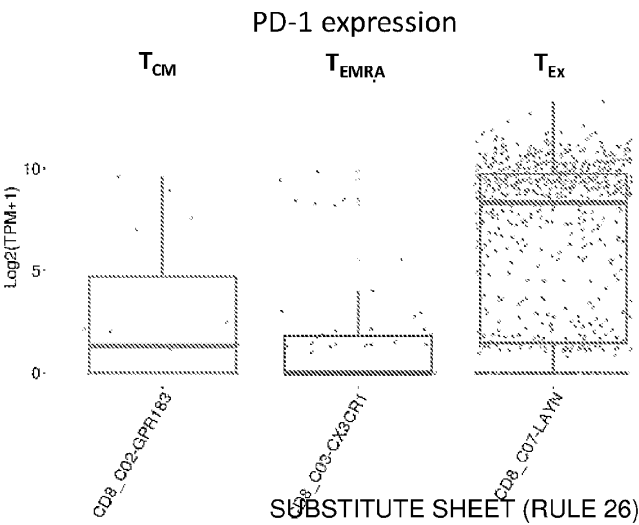


Figure 14C

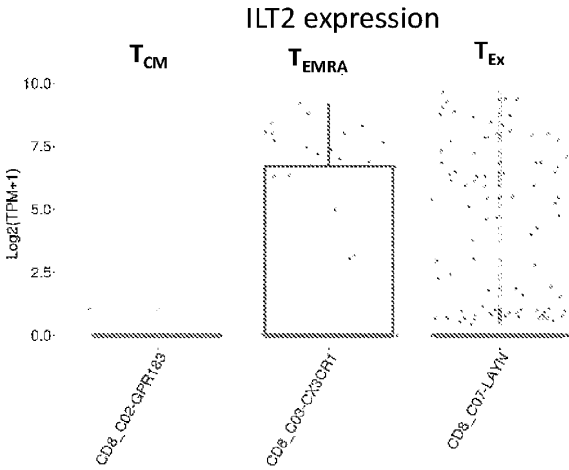
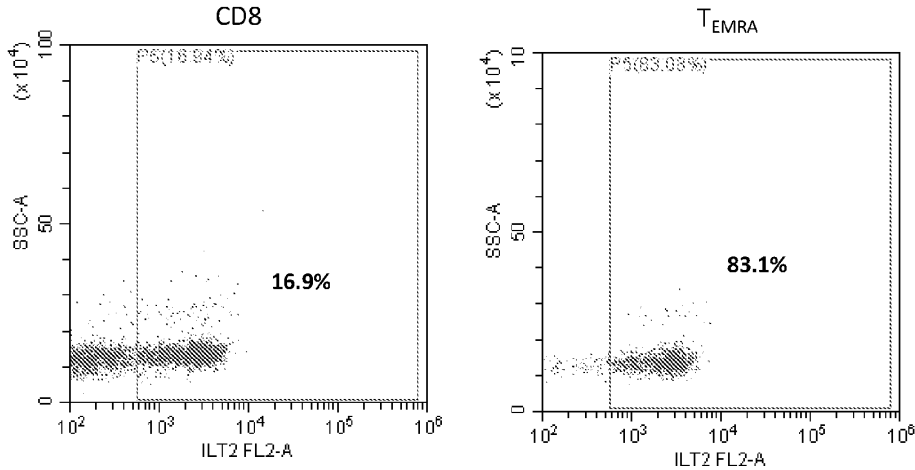


Figure 14D



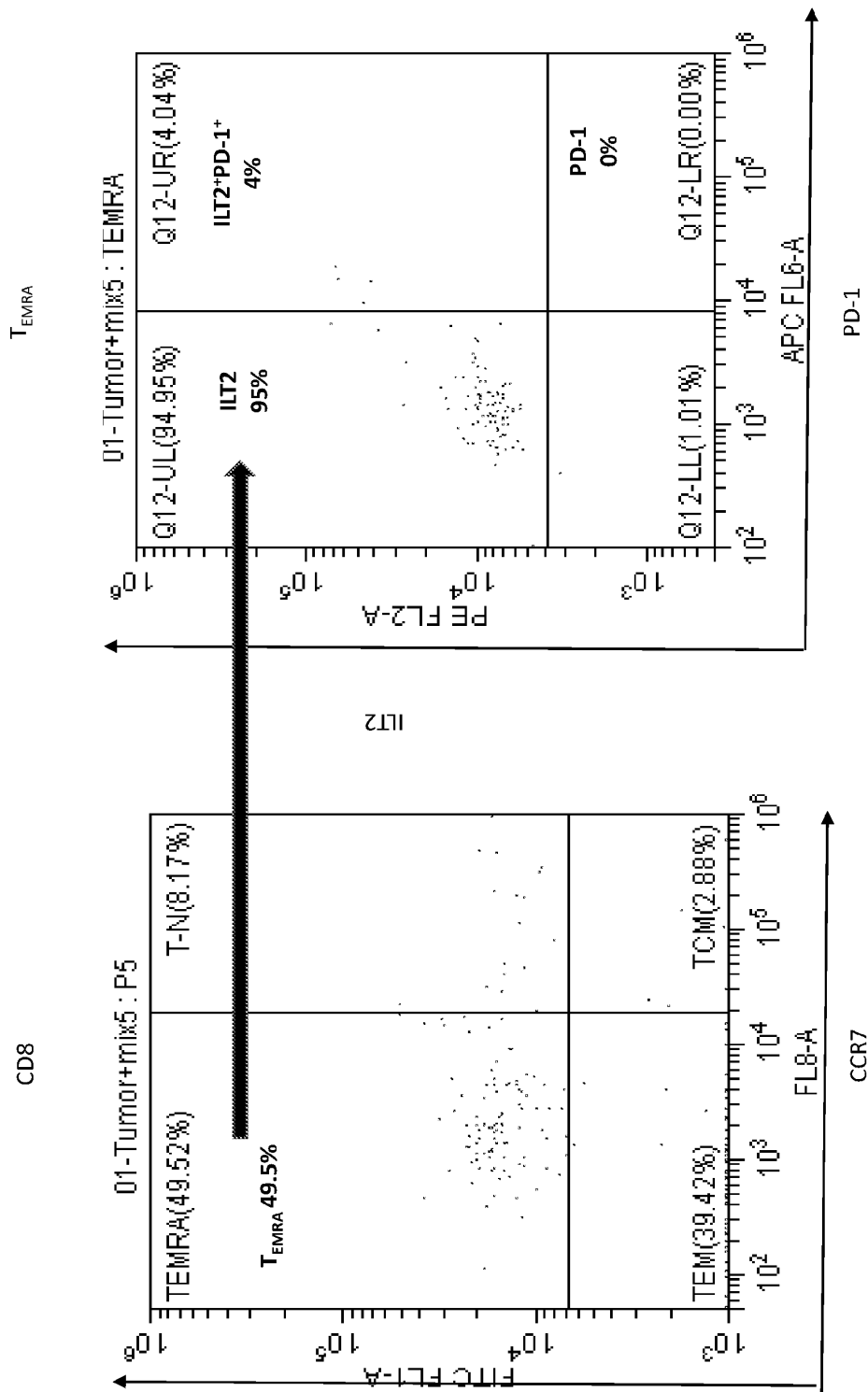


Figure 14E

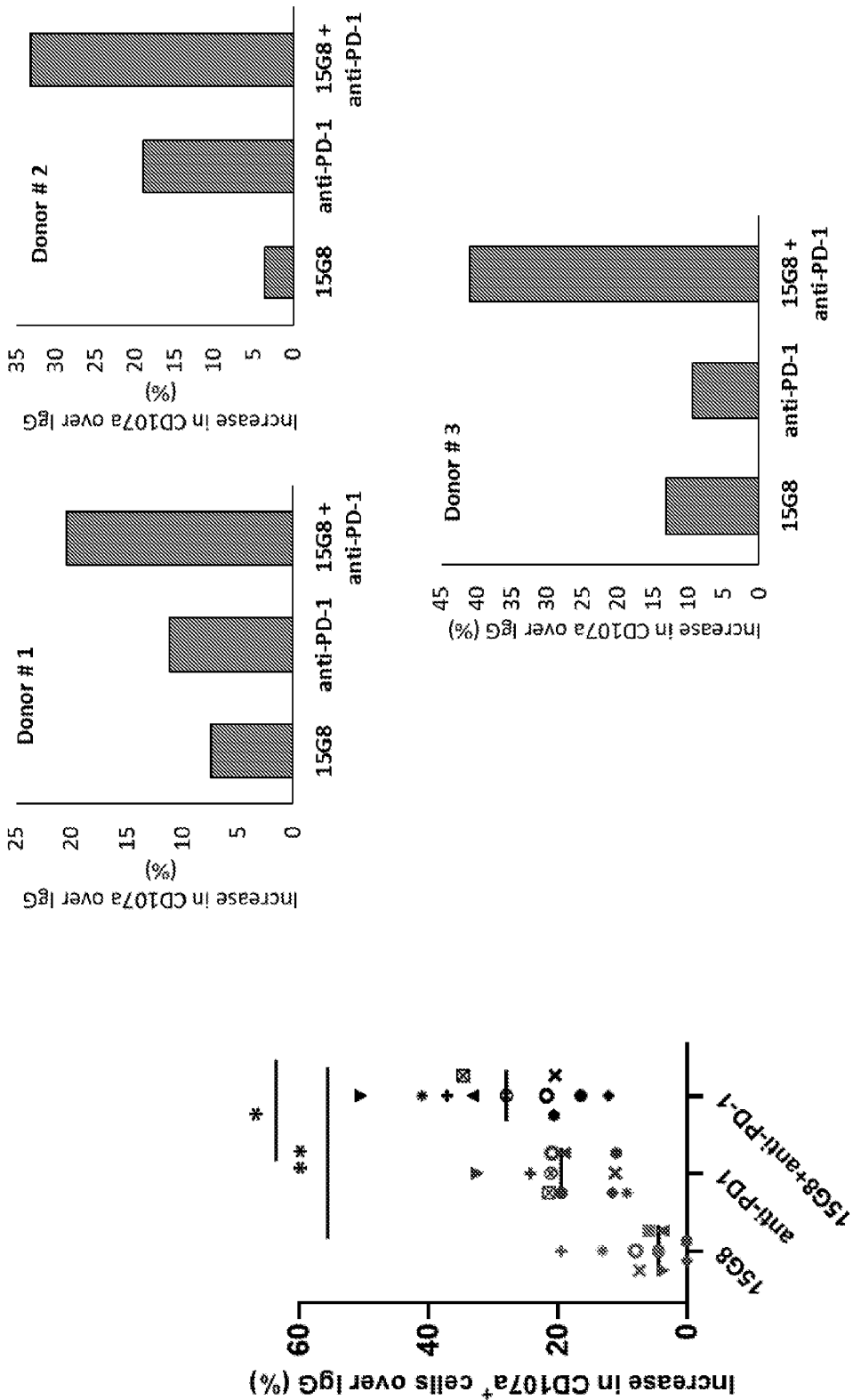


Figure 14G

Figure 14F

Figure 14H

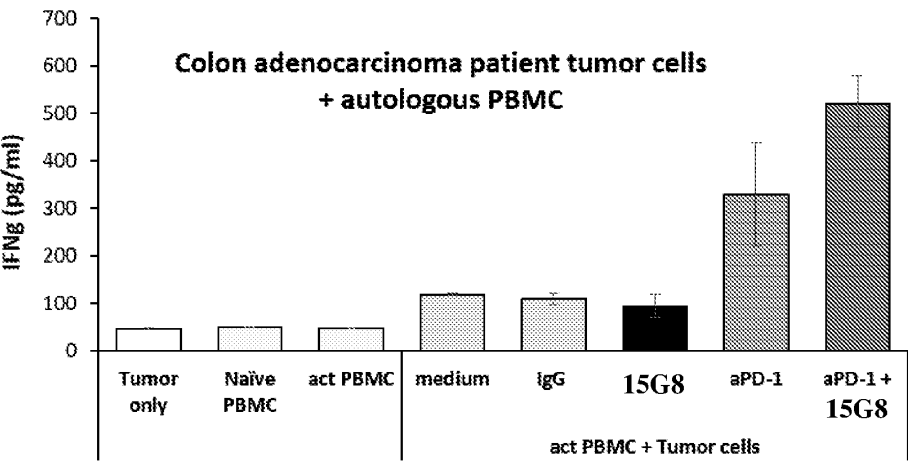


Figure 14I

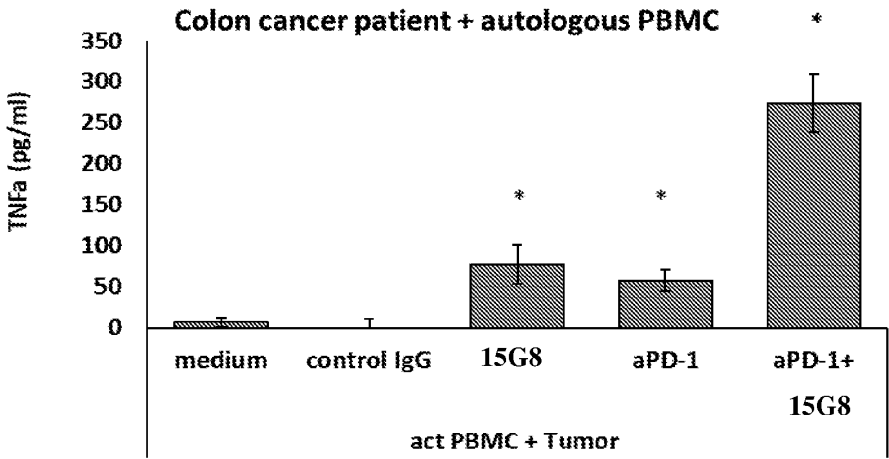
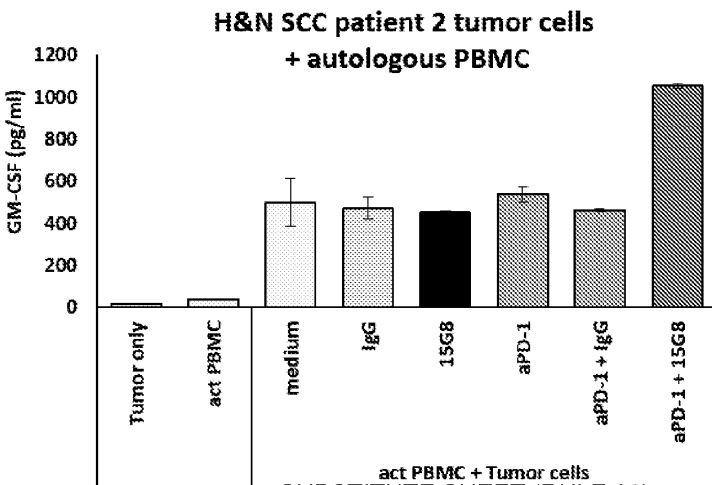
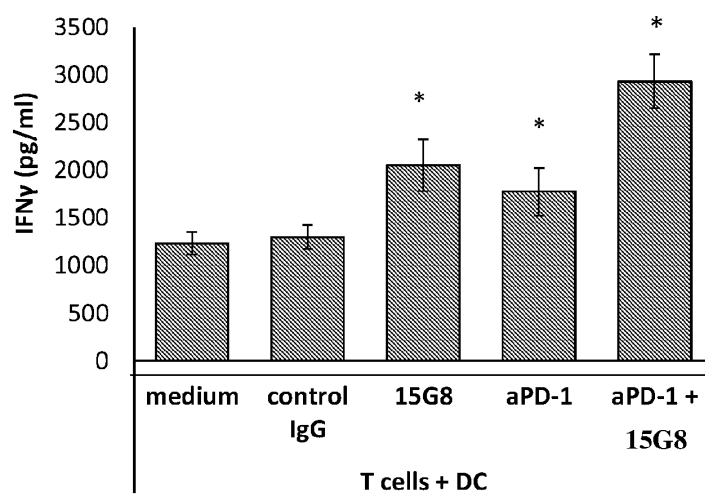
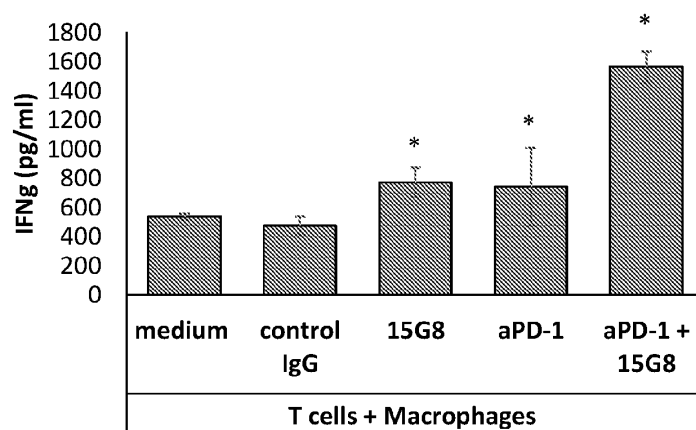


Figure 14J



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Figure 14K**Figure 14L**

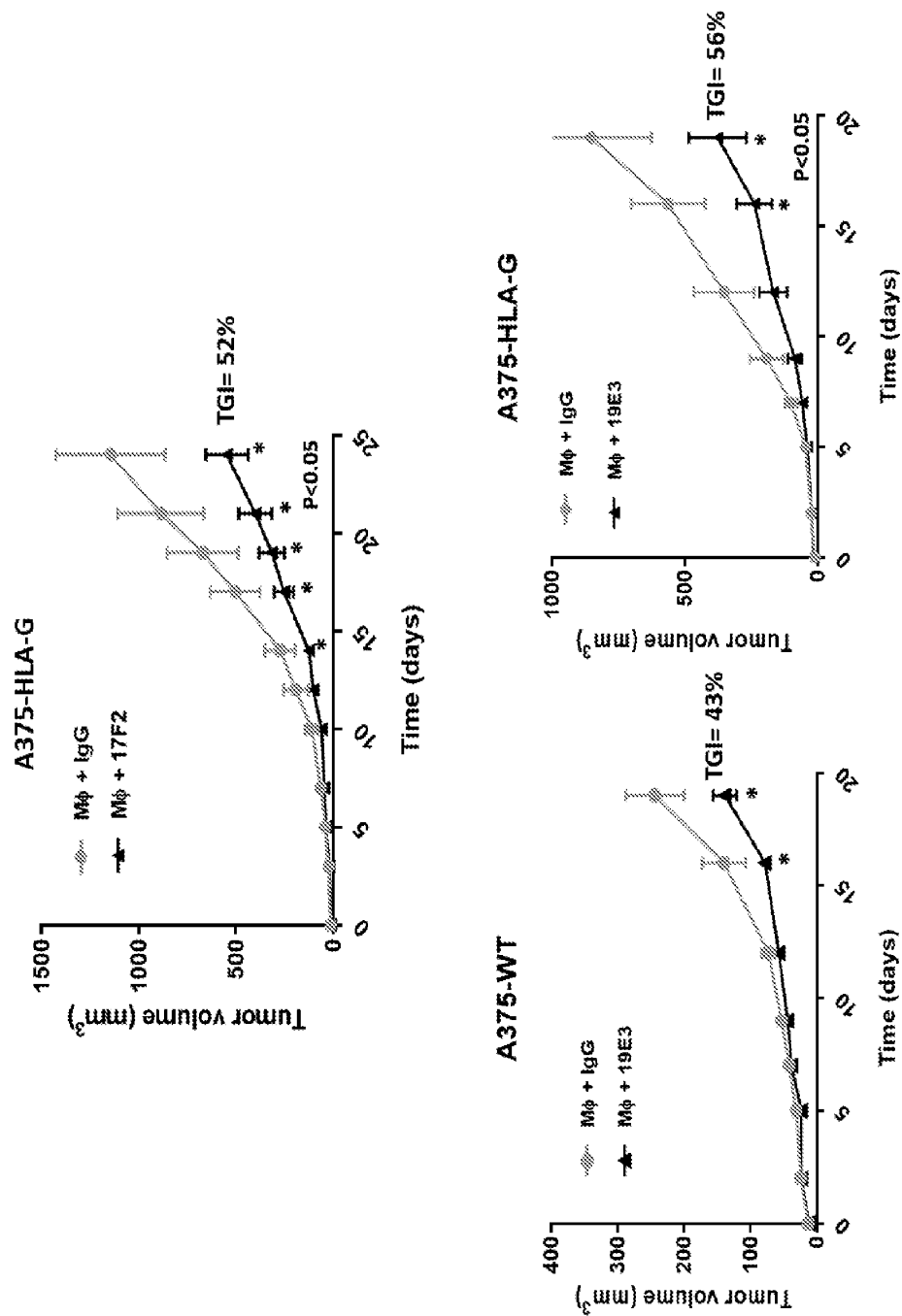


Figure 15A

Figure 15A continued

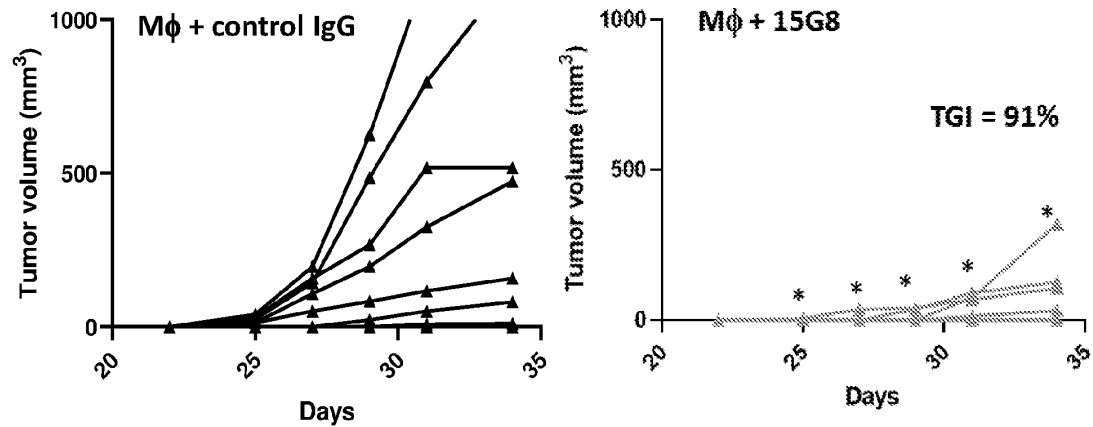


Figure 15B

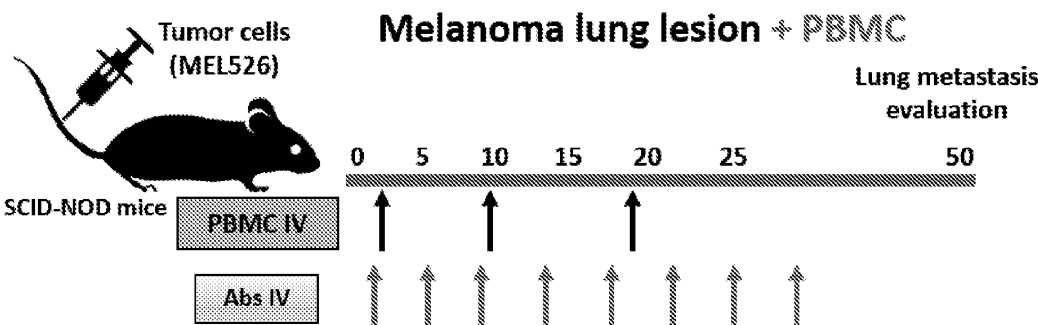


Figure 15C

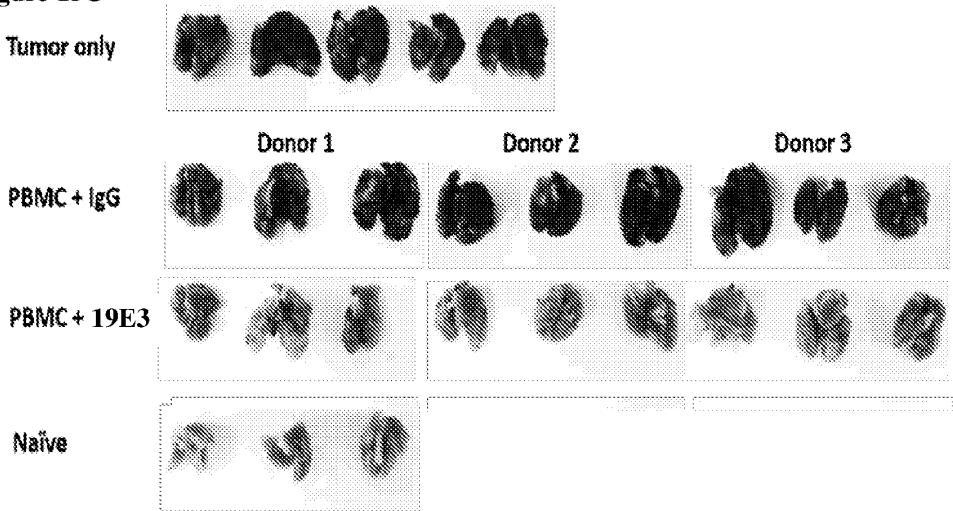


Figure 15D

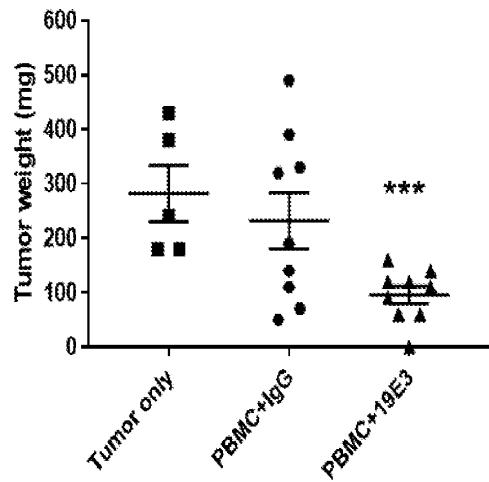


Figure 15E

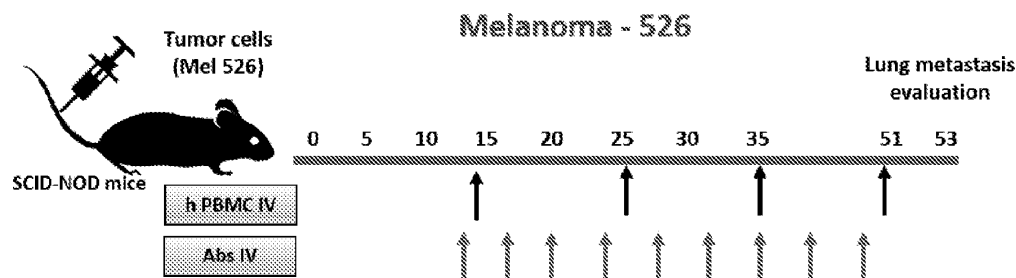
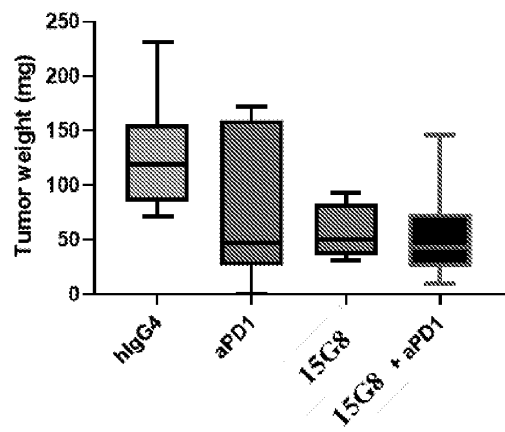


Figure 15F



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Figure 16A

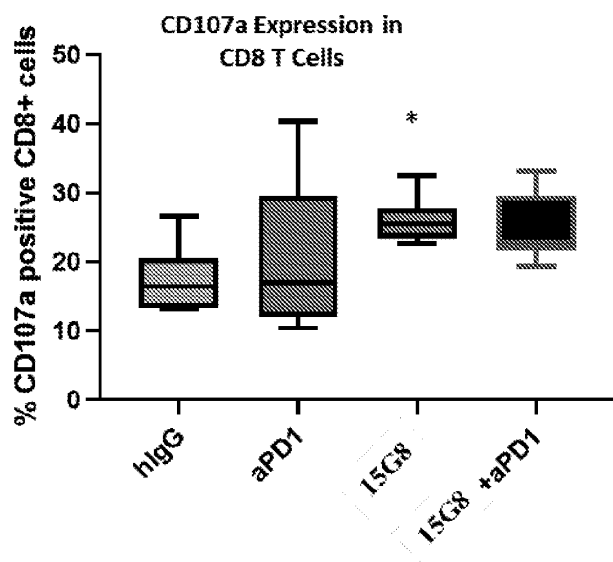
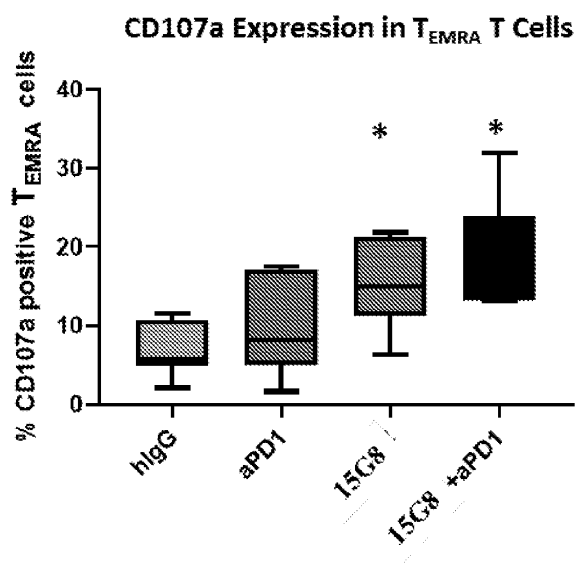


Figure 16B



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Figure 16C

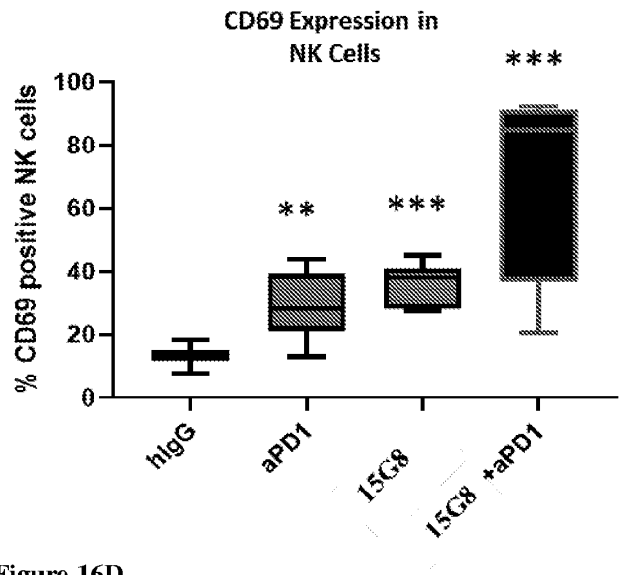


Figure 16D

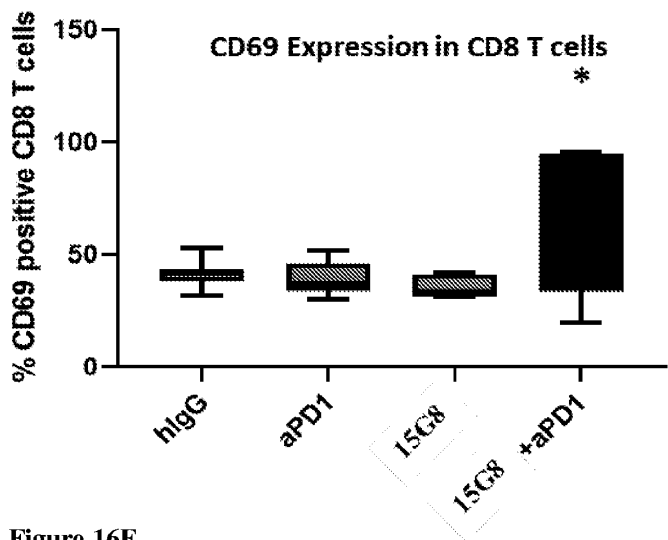


Figure 16E

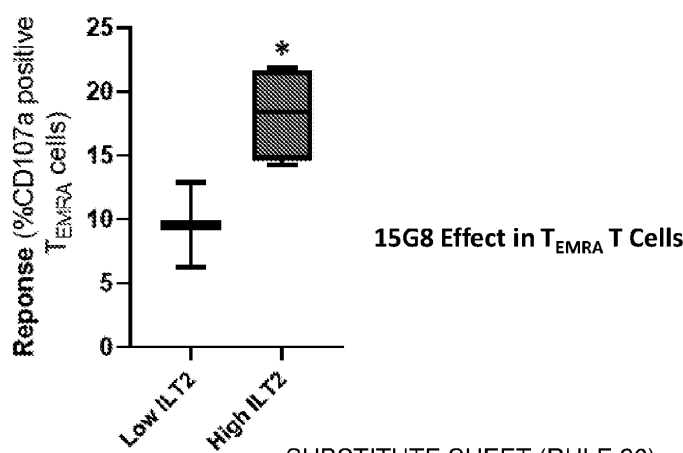


Figure 16F

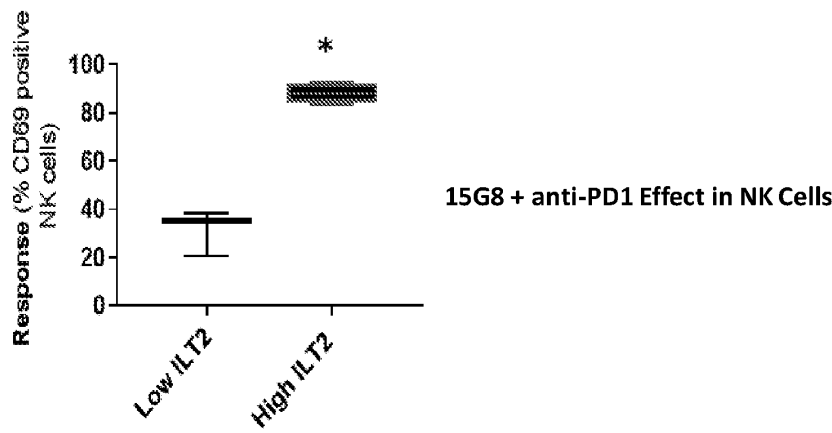


Figure 17A

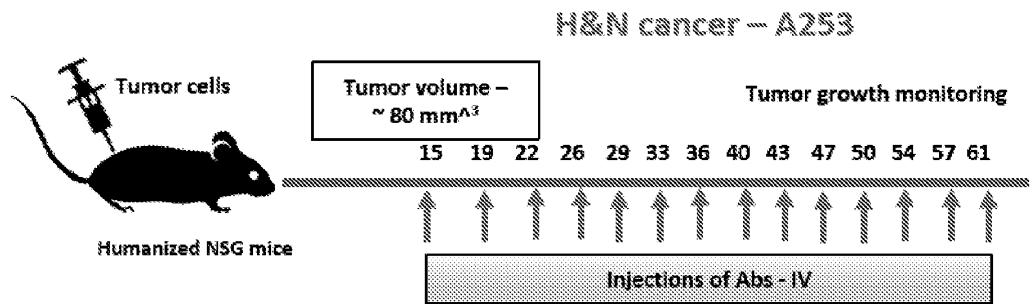


Figure 17B

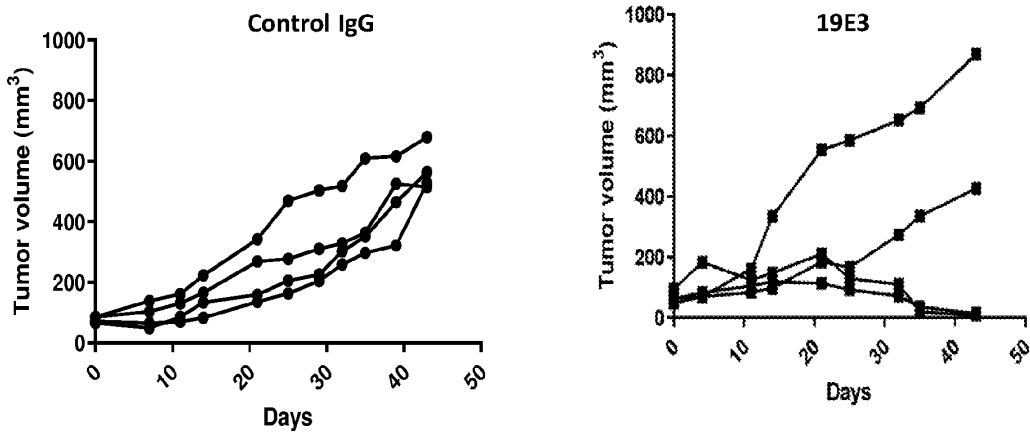


Figure 17C

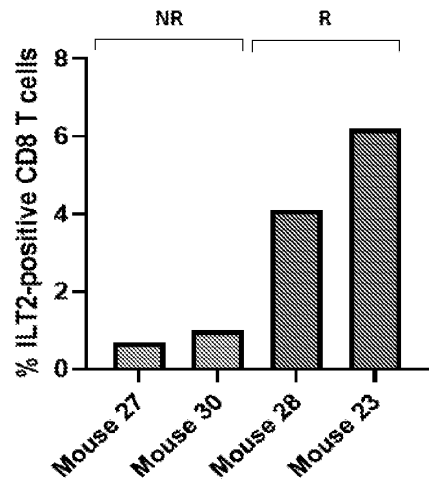


Figure 17D

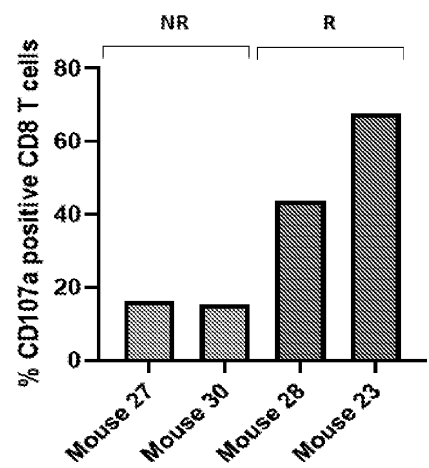
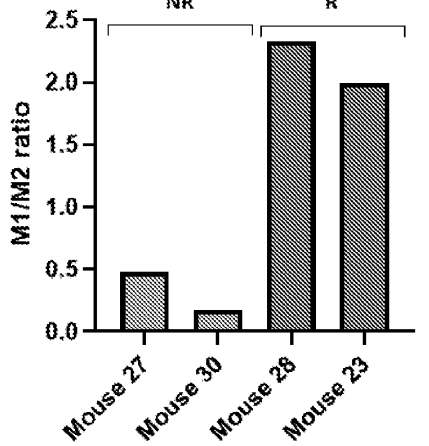
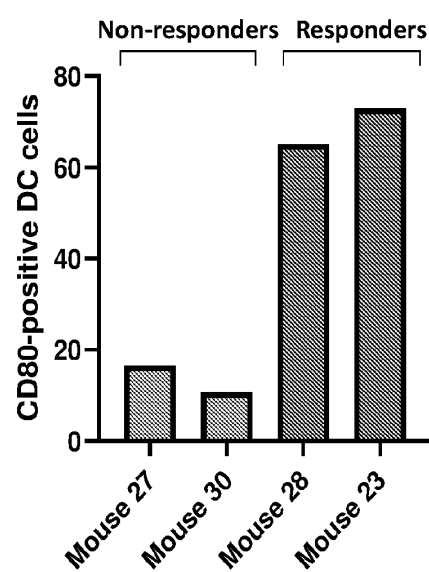


Figure 17E



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Figure 17F



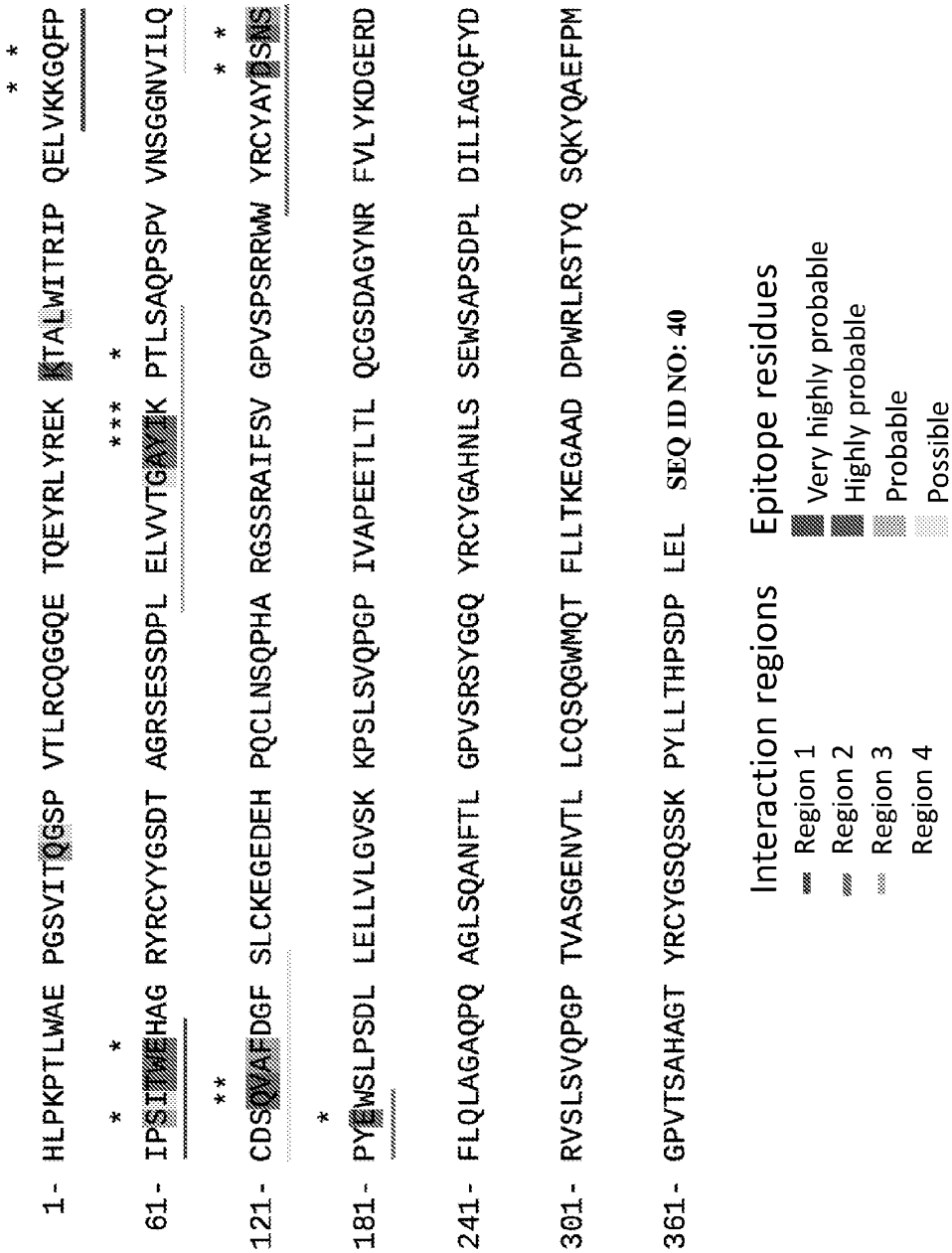


Figure 18A

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Figure 18B

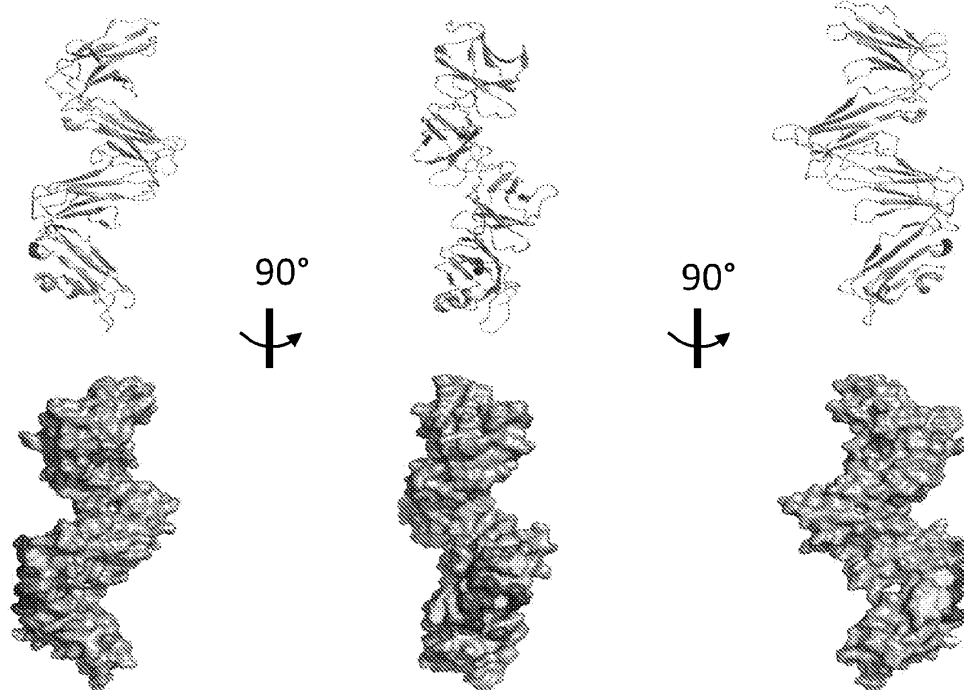
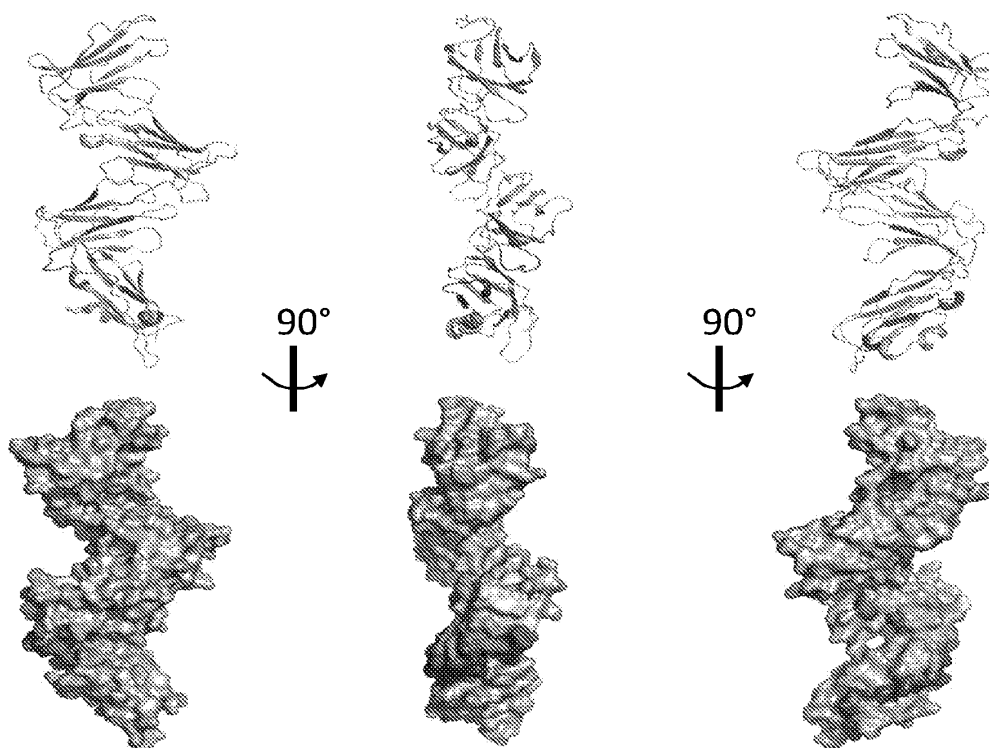


Figure 18C



SUBSTITUTE SHEET (RULE 26)

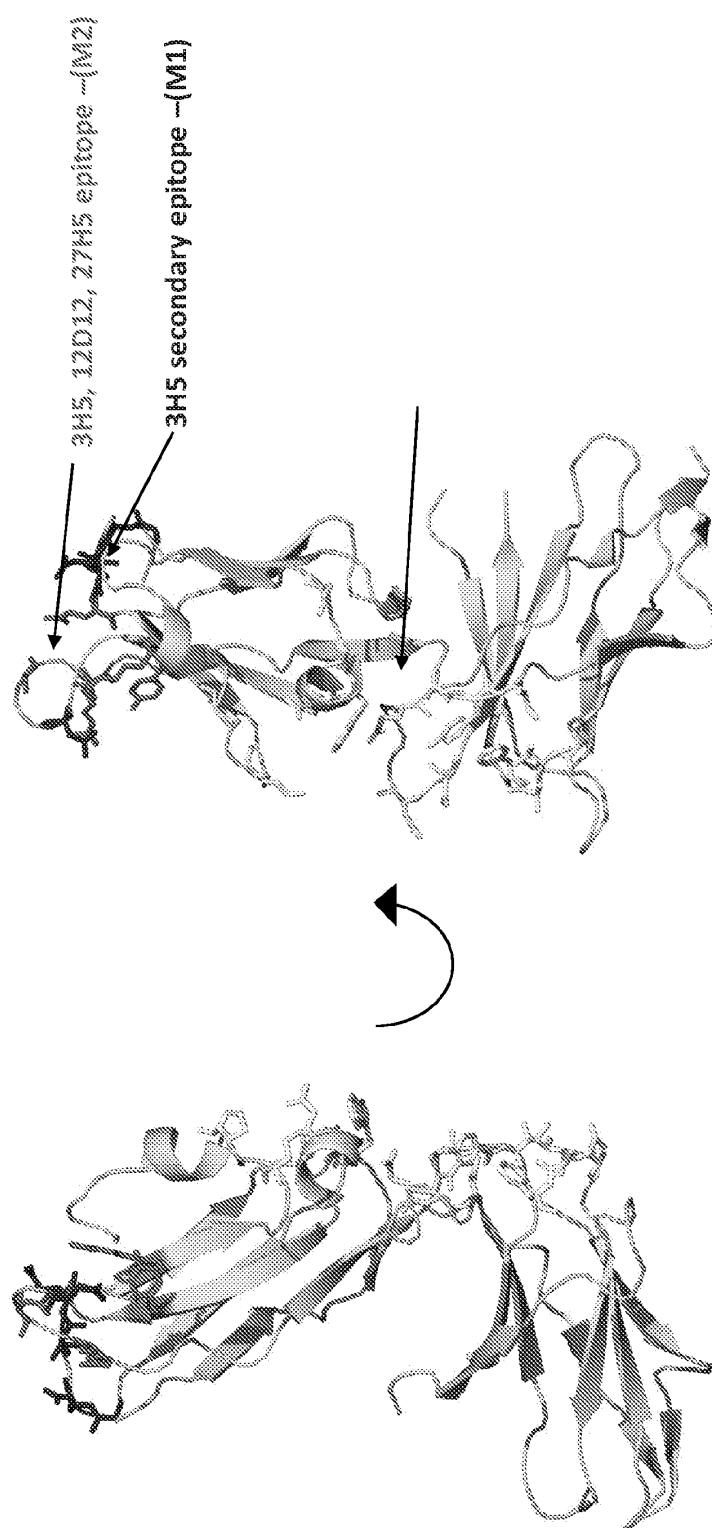


Figure 18D

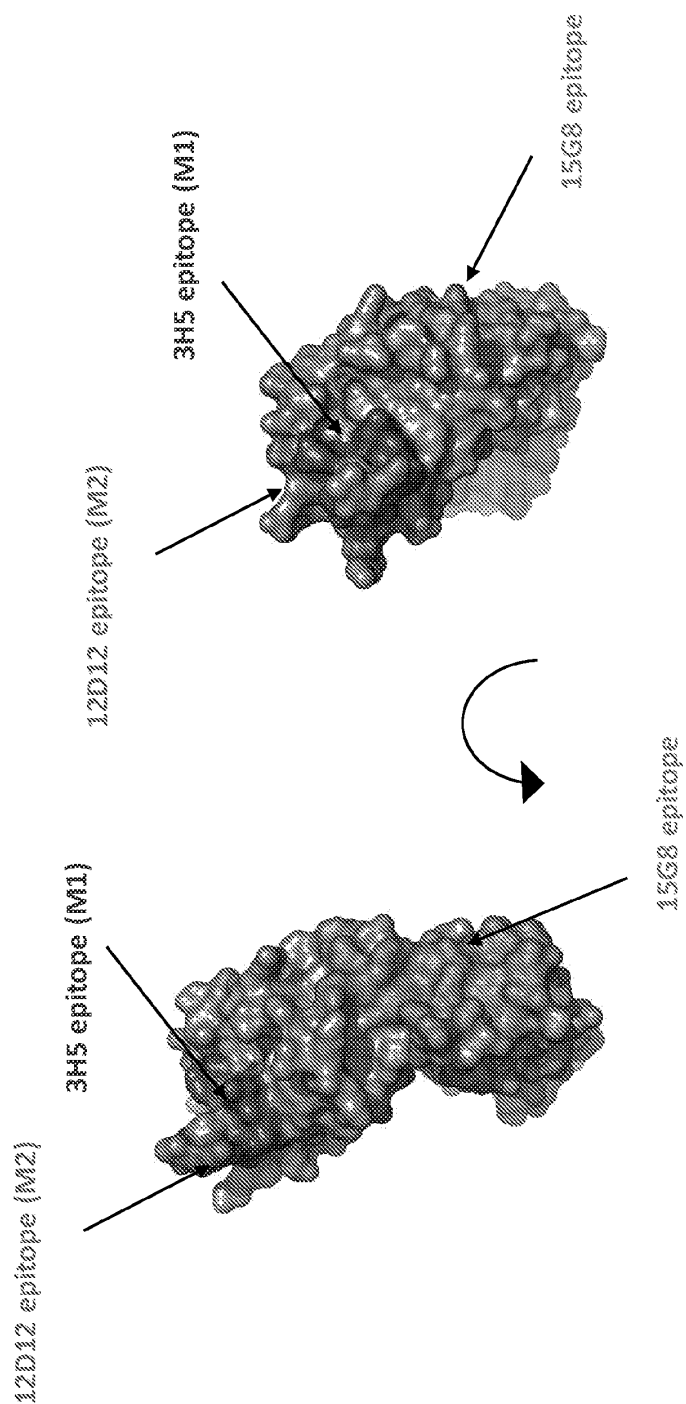


Figure 18D_continued

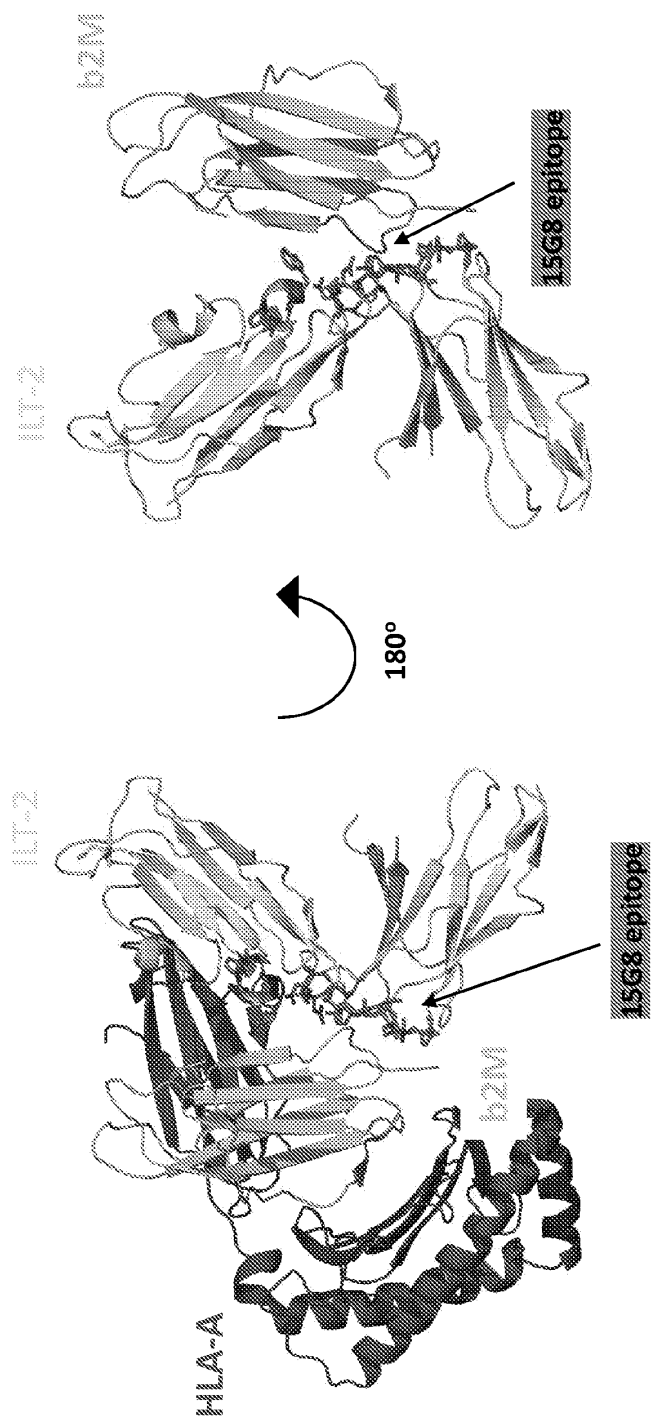


Figure 18E

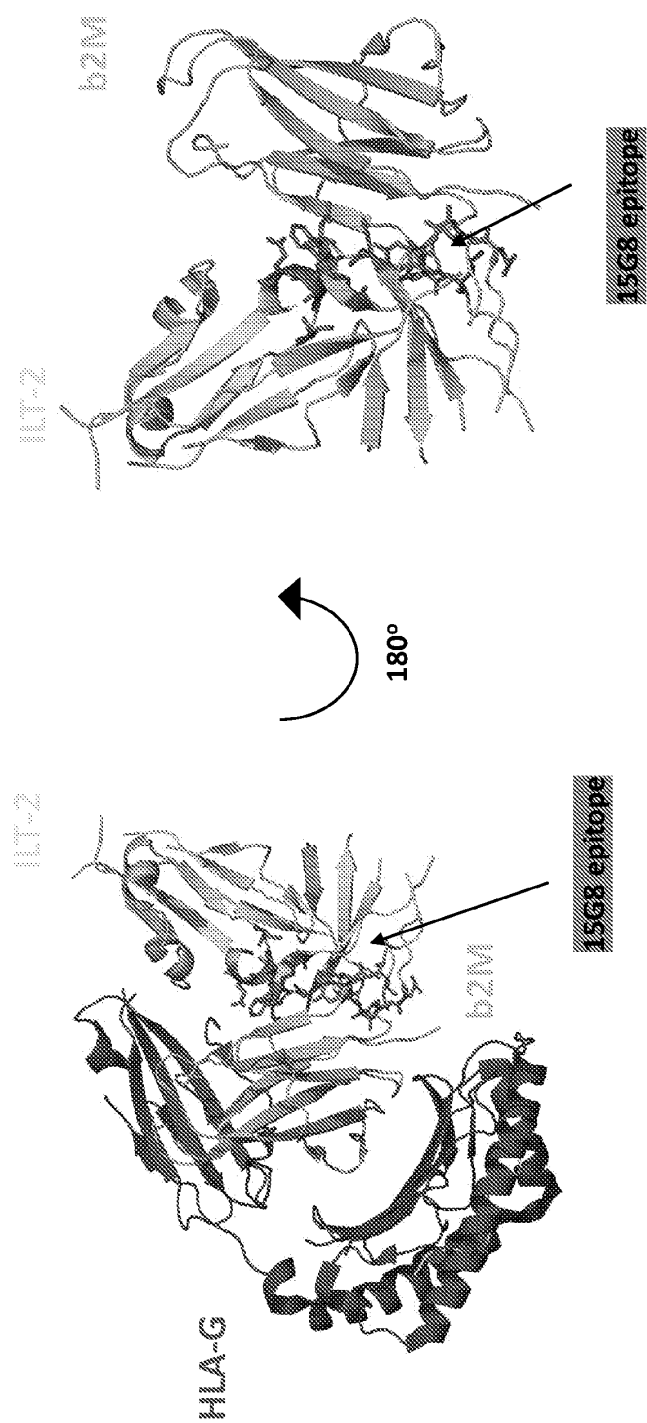


Figure 18F

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Figure 19A

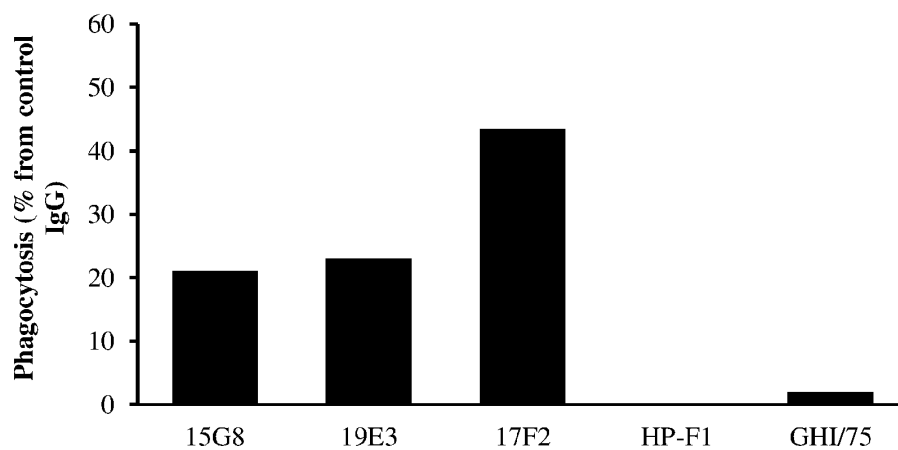
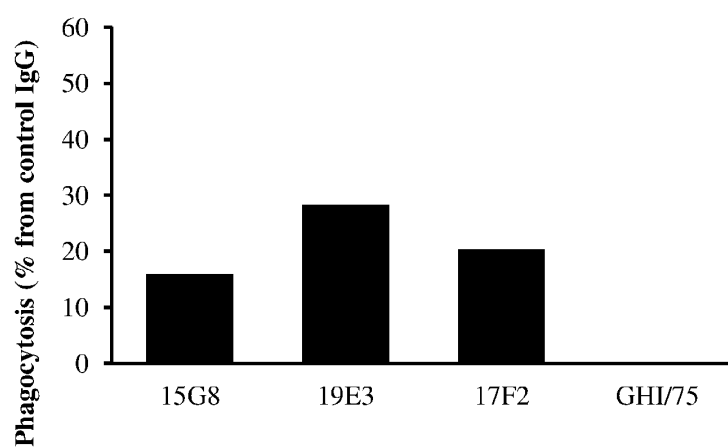


Figure 19B



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Figure 19C

