

[Fig.1A-B]

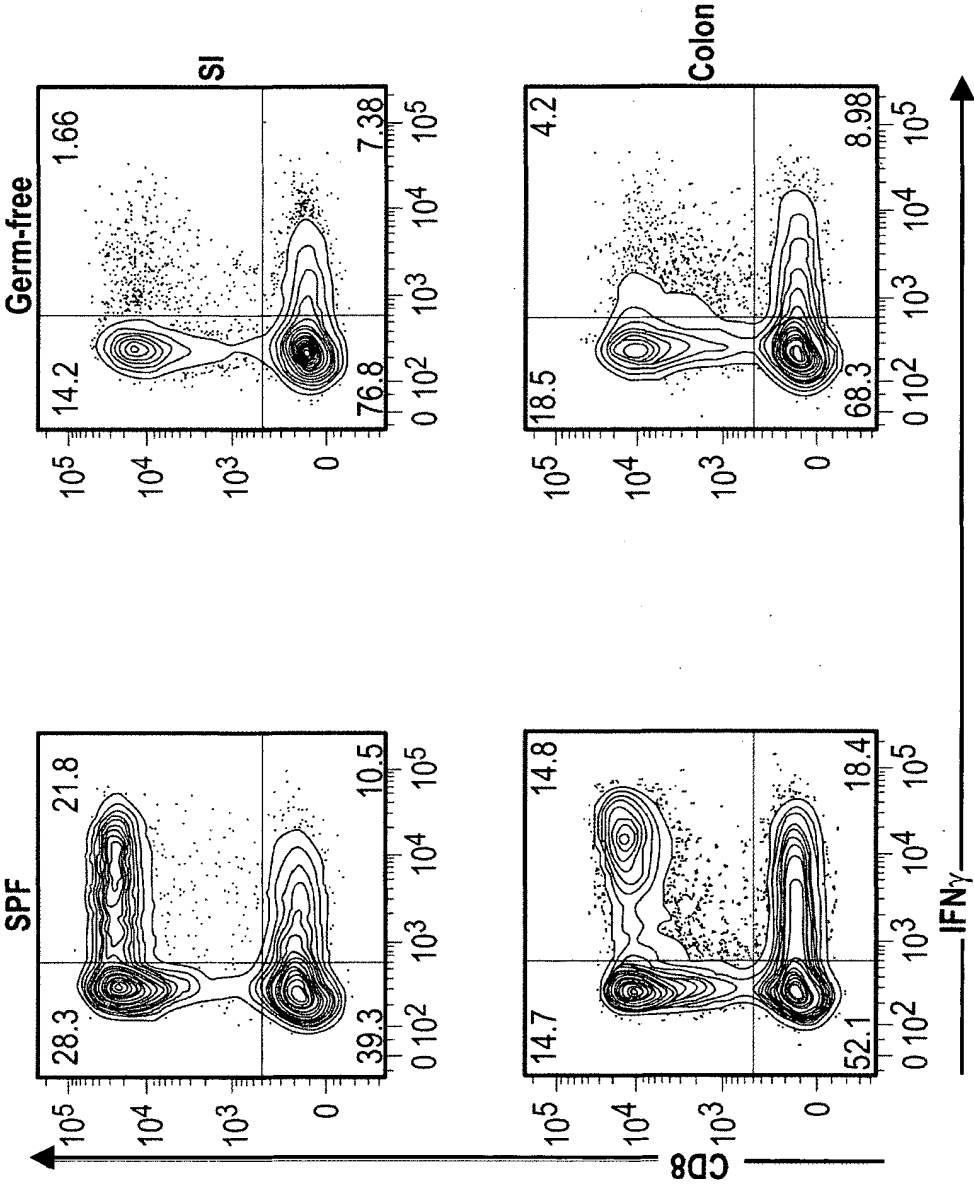


Fig. 1A

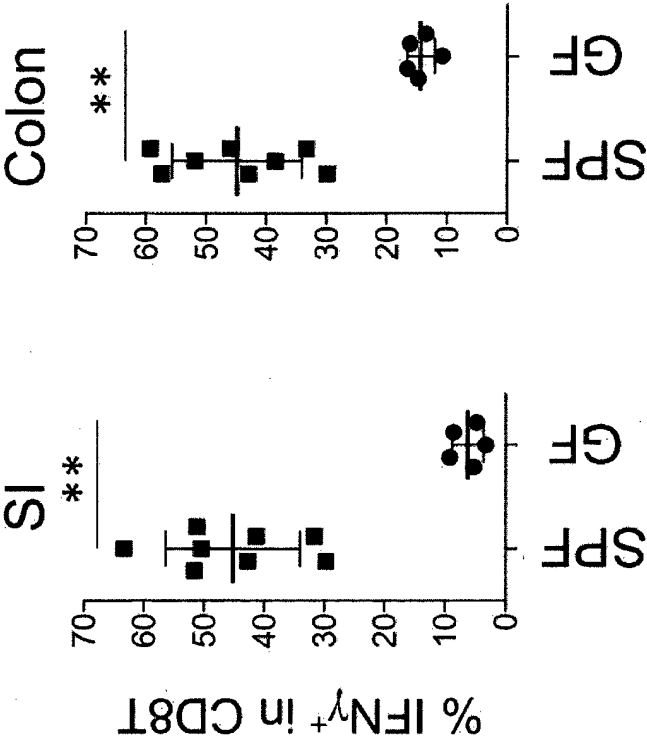


Fig. 1B

[Fig. 2A-B]

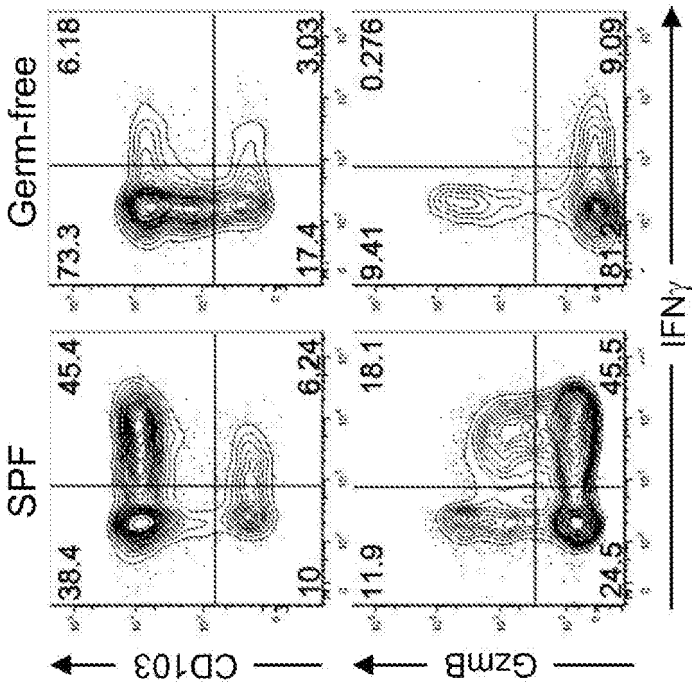


Fig. 2A

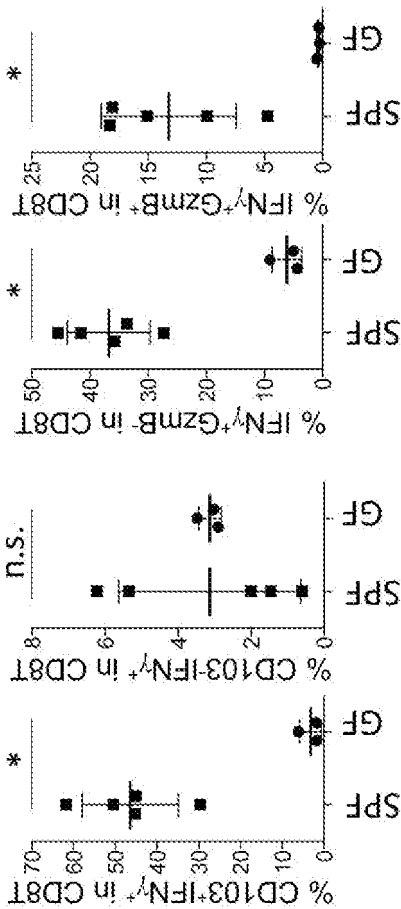


Fig. 2B

[Fig. 3A-B]

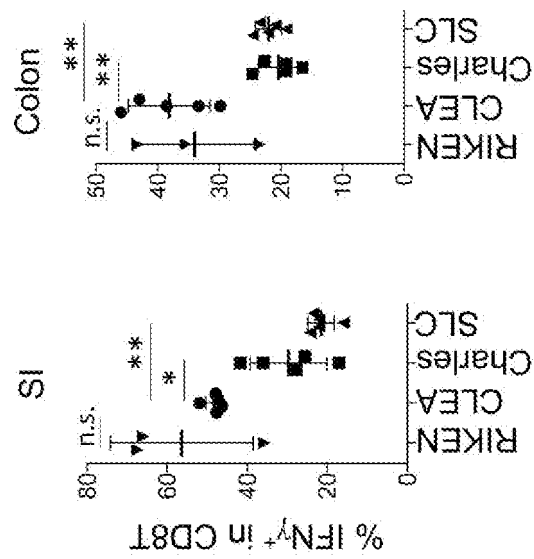


Fig. 3B

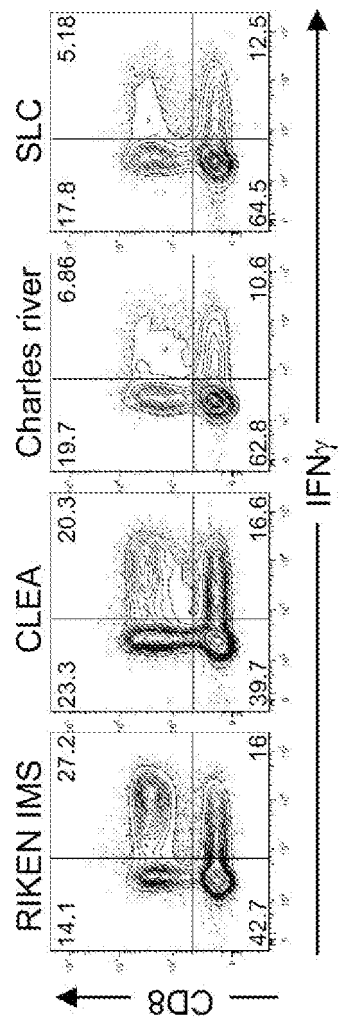


Fig. 3A

[Fig. 4A-B]

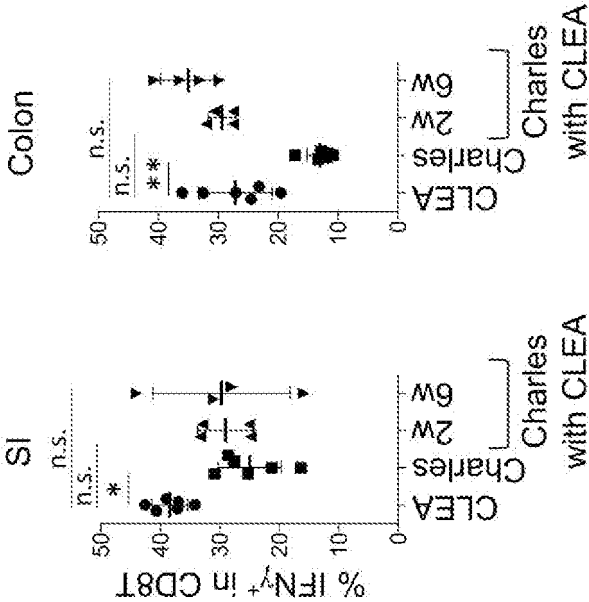


Fig. 4B

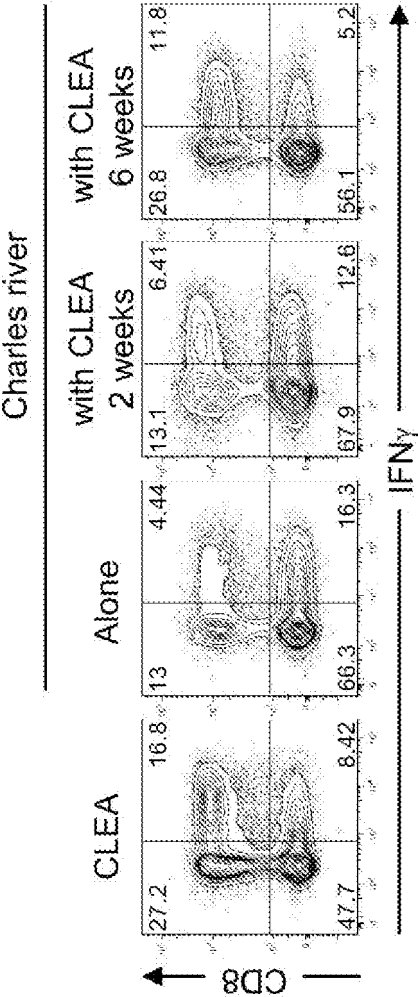


Fig. 4A

[Fig. 5A-B]

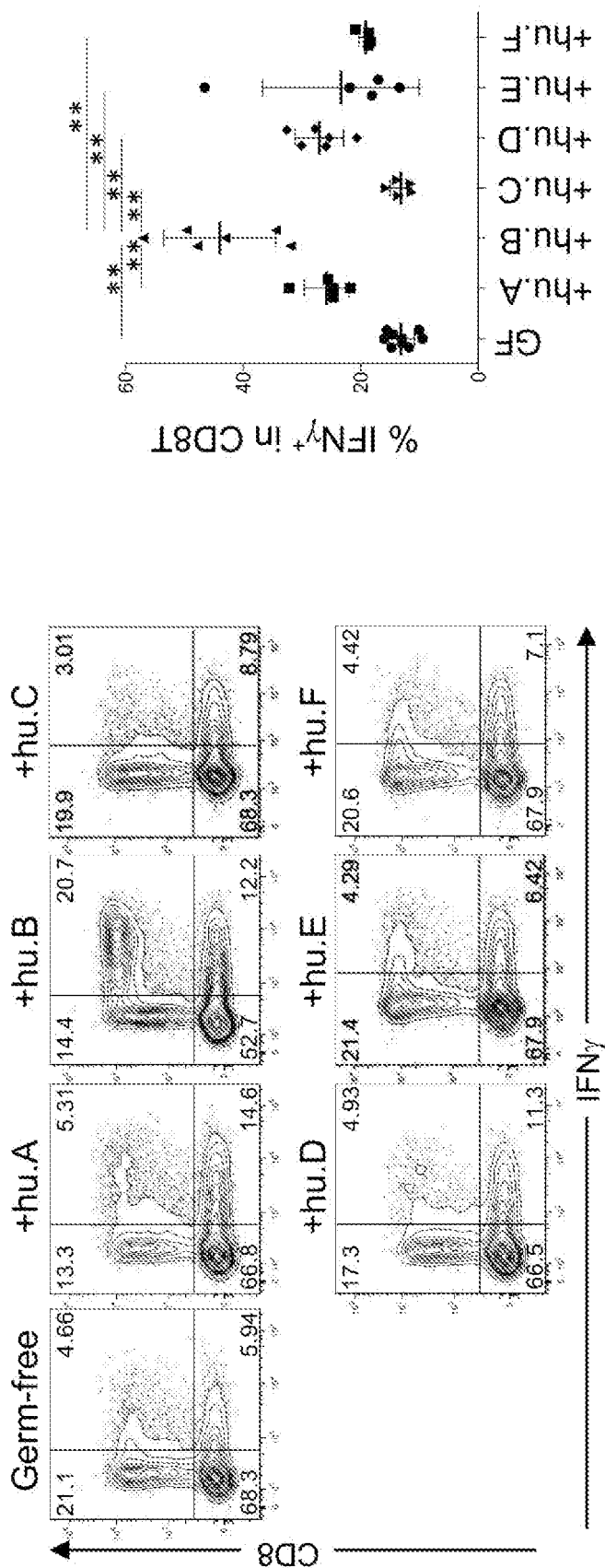


Fig. 5B

Fig. 5A

[Fig.6A-B]

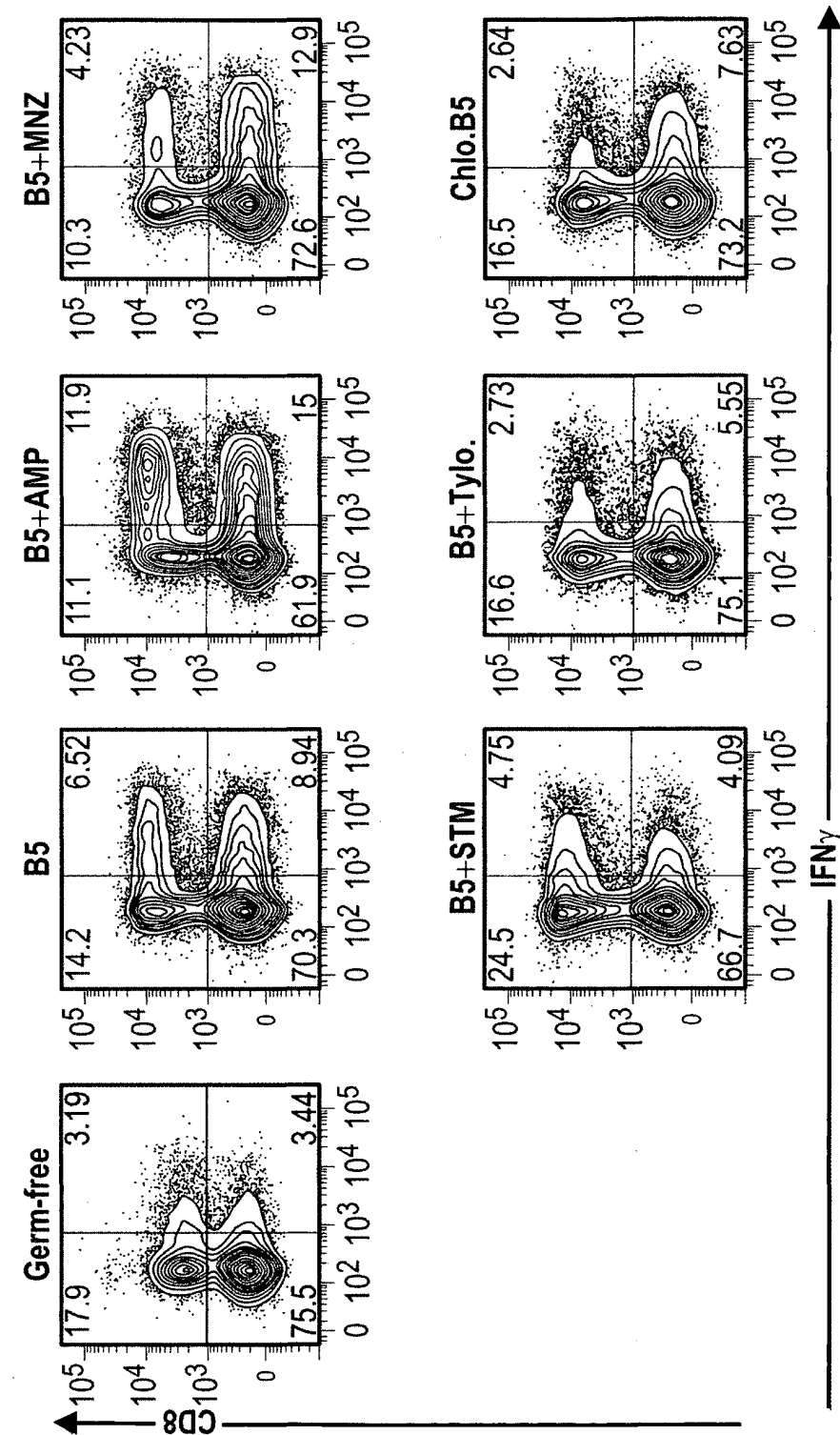


Fig. 6A

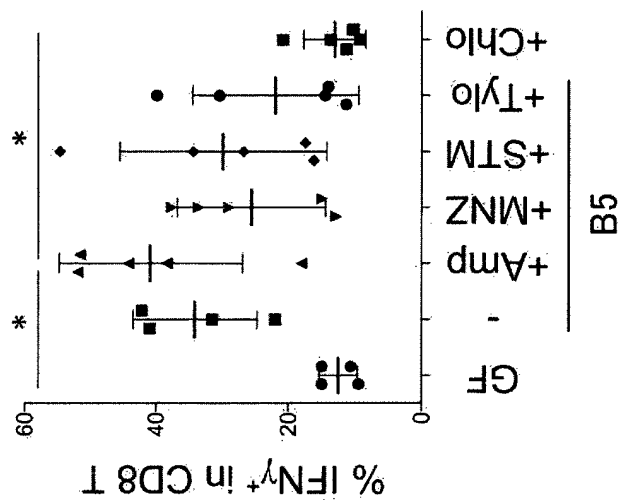


Fig. 6B

[Fig. 7A-B]

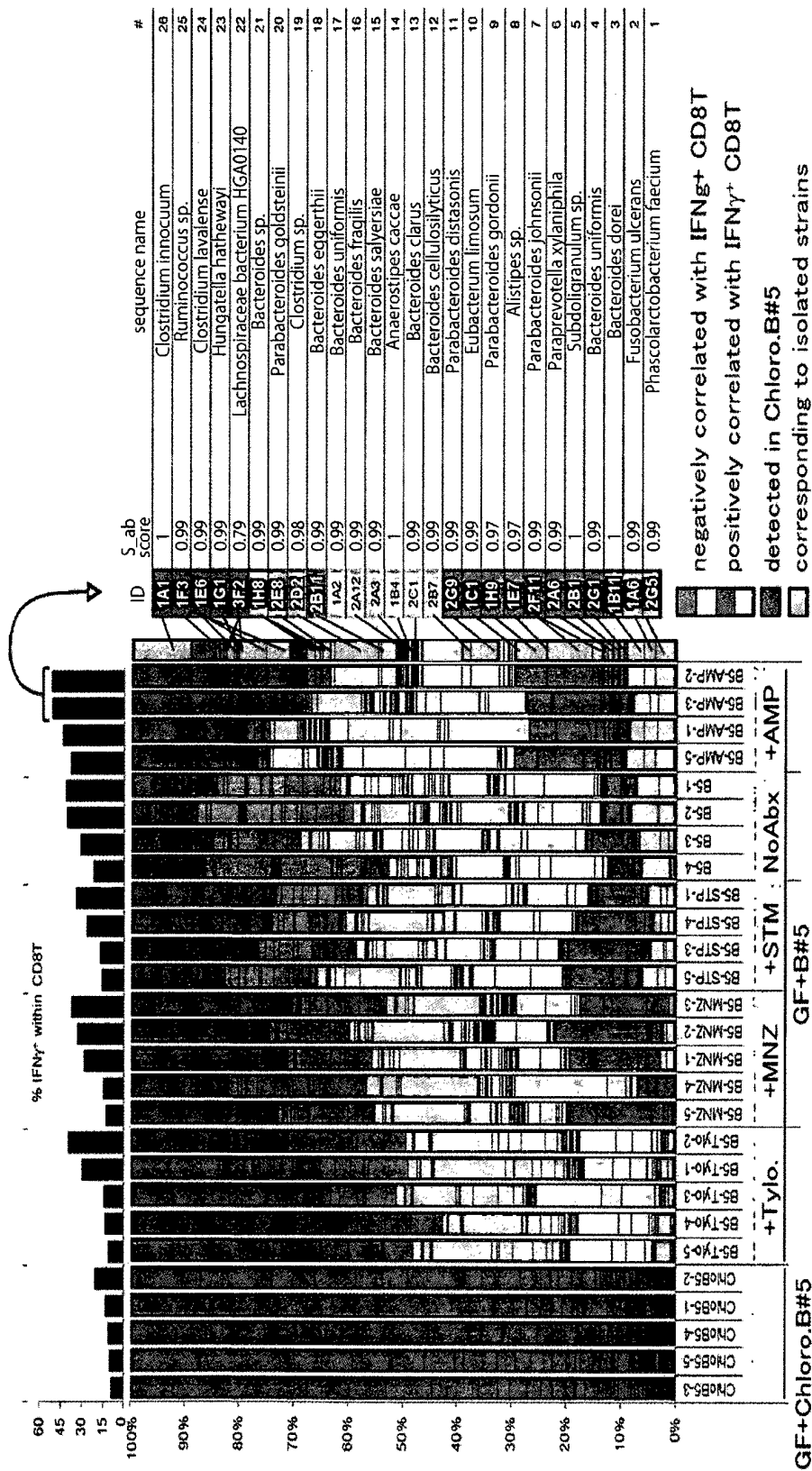


Fig. 7B

Fig. 7A

[Fig.8A-B]

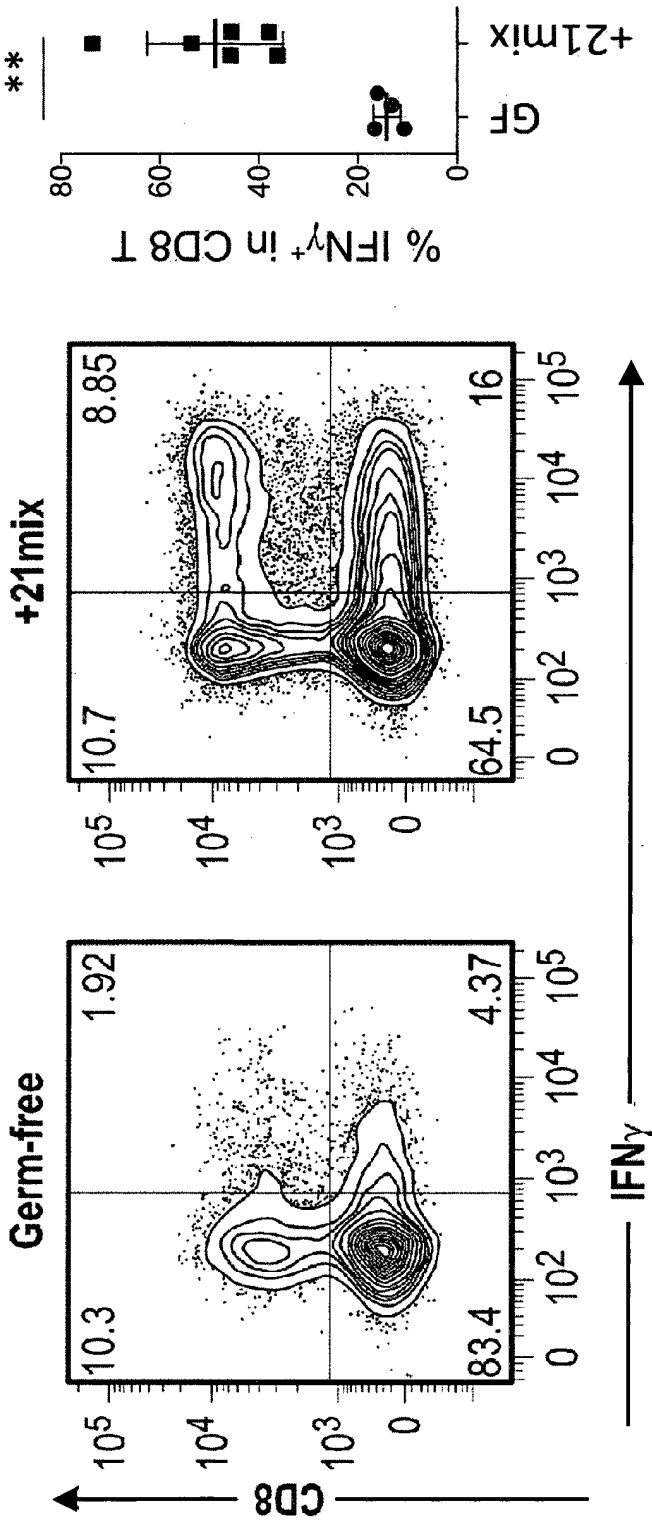


Fig. 8B

Fig. 8A

[Fig. 9A-B]

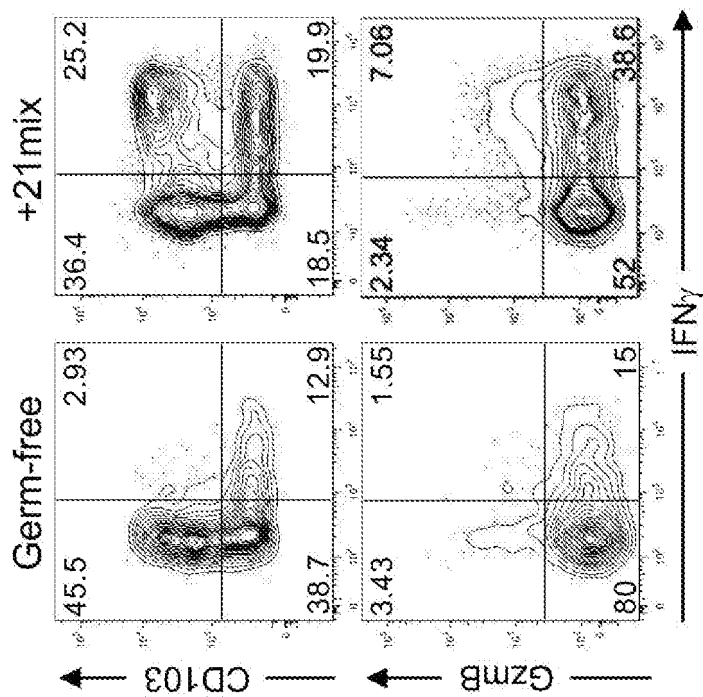


Fig. 9A

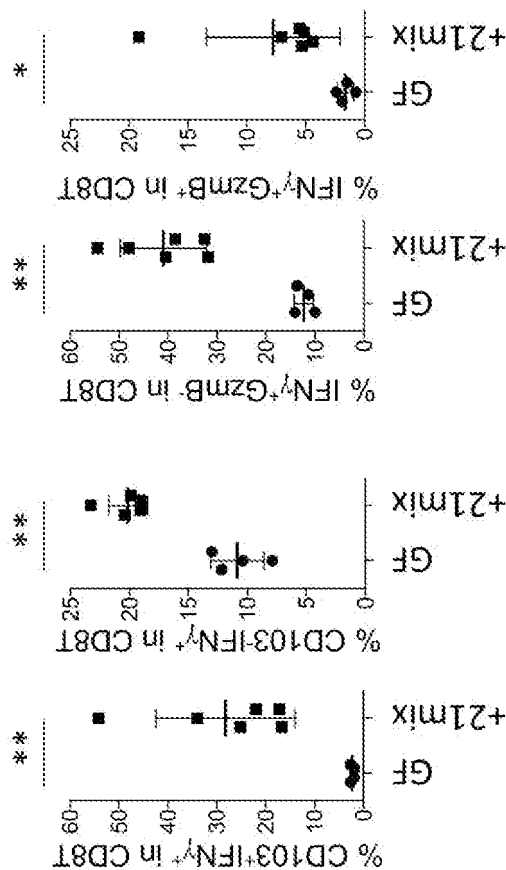


Fig. 9B

[Fig.10A-B]

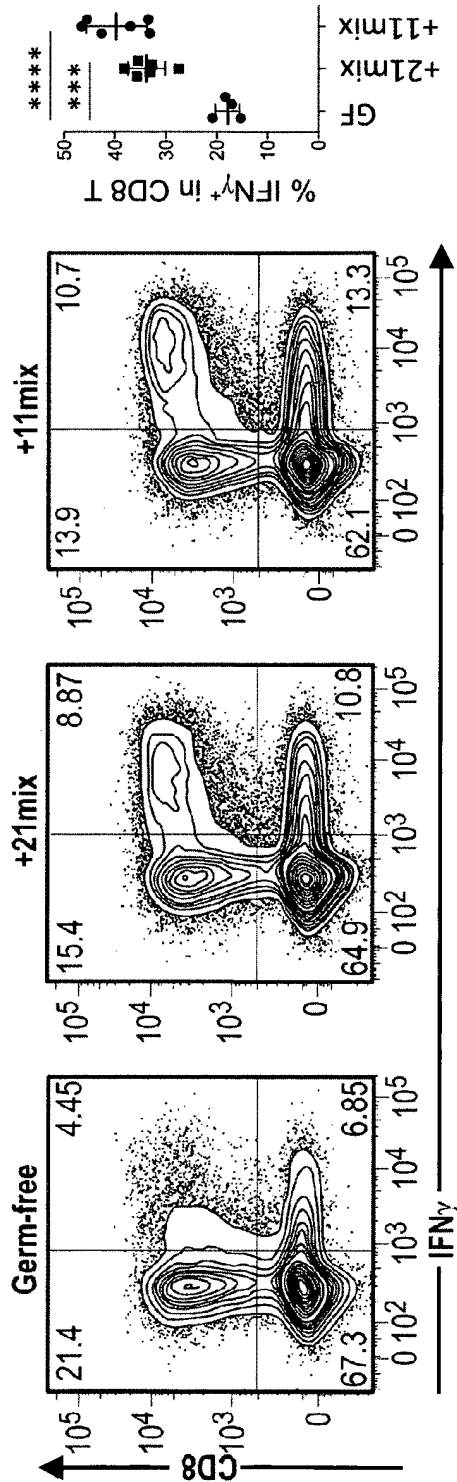


Fig. 10B

Fig. 10A

[Fig.11]

	ID	S_ab score	Closest sequence	#
Detected in Chloro.B#5	81A1	1	Clostridium innocuum	26
	81F3	0.99	Ruminococcus sp.	25
	81E6	0.99	Clostridium lavalense	24
	81G1	0.99	Hungatella hathewayi	23
	83F2	0.79	Lachnospiraceae bacterium HGA0140	22
10-mix	81H8	0.99	Bacteroides sp.	21
	82E8	0.99	Parabacteroides goldsteinii	20
	82D2	0.98	Clostridium sp.	19
	82B11	0.99	Bacteroides eggerthii	18
	81A2	0.99	Bacteroides uniformis	17
	82A12	0.99	Bacteroides fragilis	16
	82A3	0.99	Bacteroides salyersiae	15
	81B4	1	Anaerostipes caccae	14
	82C1	0.99	Bacteroides clarus	13
	82B7	0.99	Bacteroides cellulosilyticus	12
11-mix	82G9	0.99	Parabacteroides distasonis	11
	81C1	0.99	Eubacterium limosum	10
	81H9	0.97	Parabacteroides gordonii	9
	81E7	0.97	Alistipes sp.	8
	82F11	0.99	Parabacteroides johnsonii	7
	82A6	0.99	Paraprevotella xylaniphila	6
	82B1	1	Subdoligranulum sp.	5
	82G1	0.99	Bacteroides uniformis	4
	81B11	1	Bacteroides dorei	3
	81A6	0.99	Fusobacterium ulcerans	2
	82G5	0.99	Phascolarctobacterium faecium	1

[Fig.12A-B]

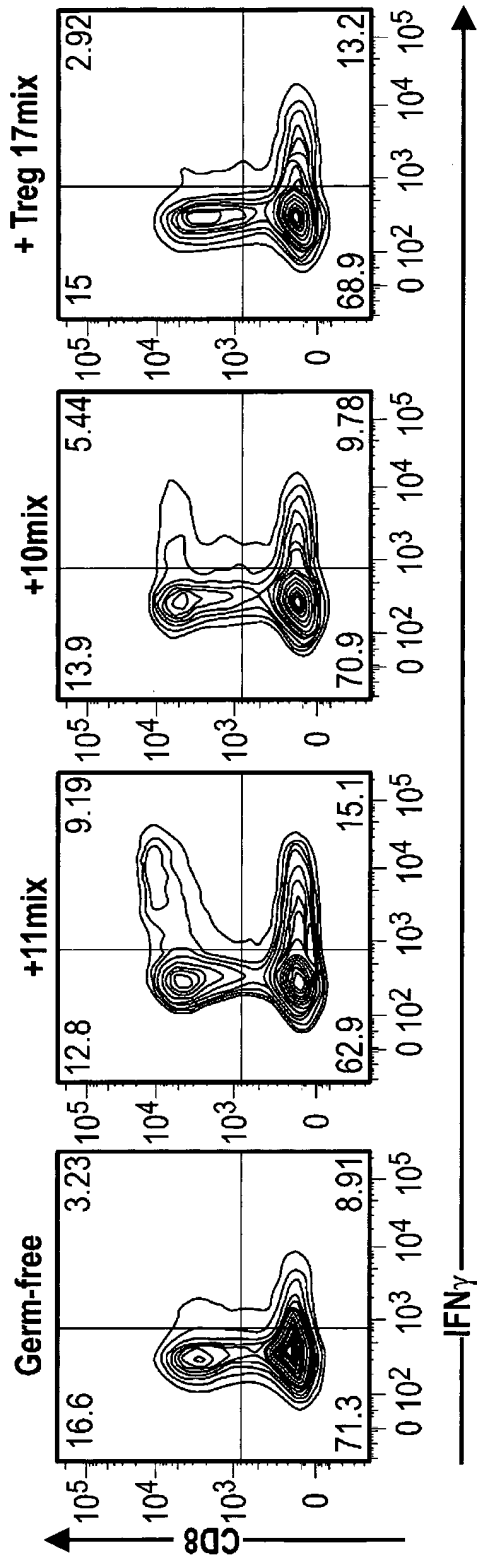


Fig. 12A

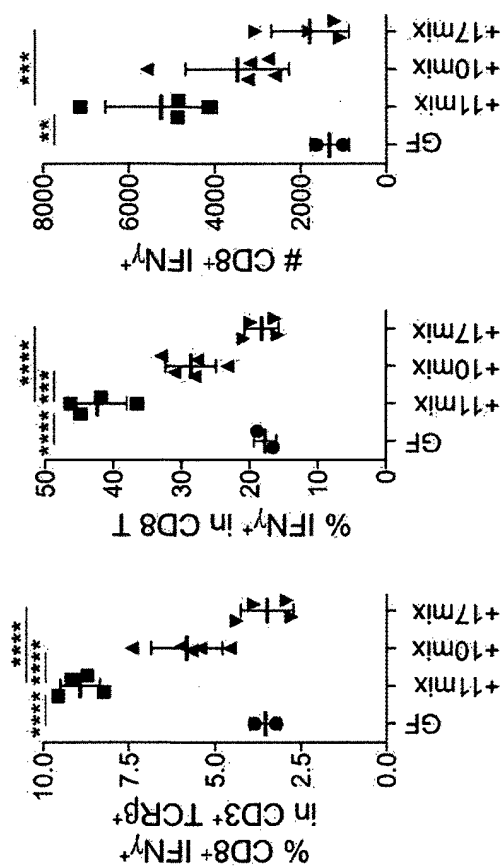


Fig. 12B

[Fig.13]

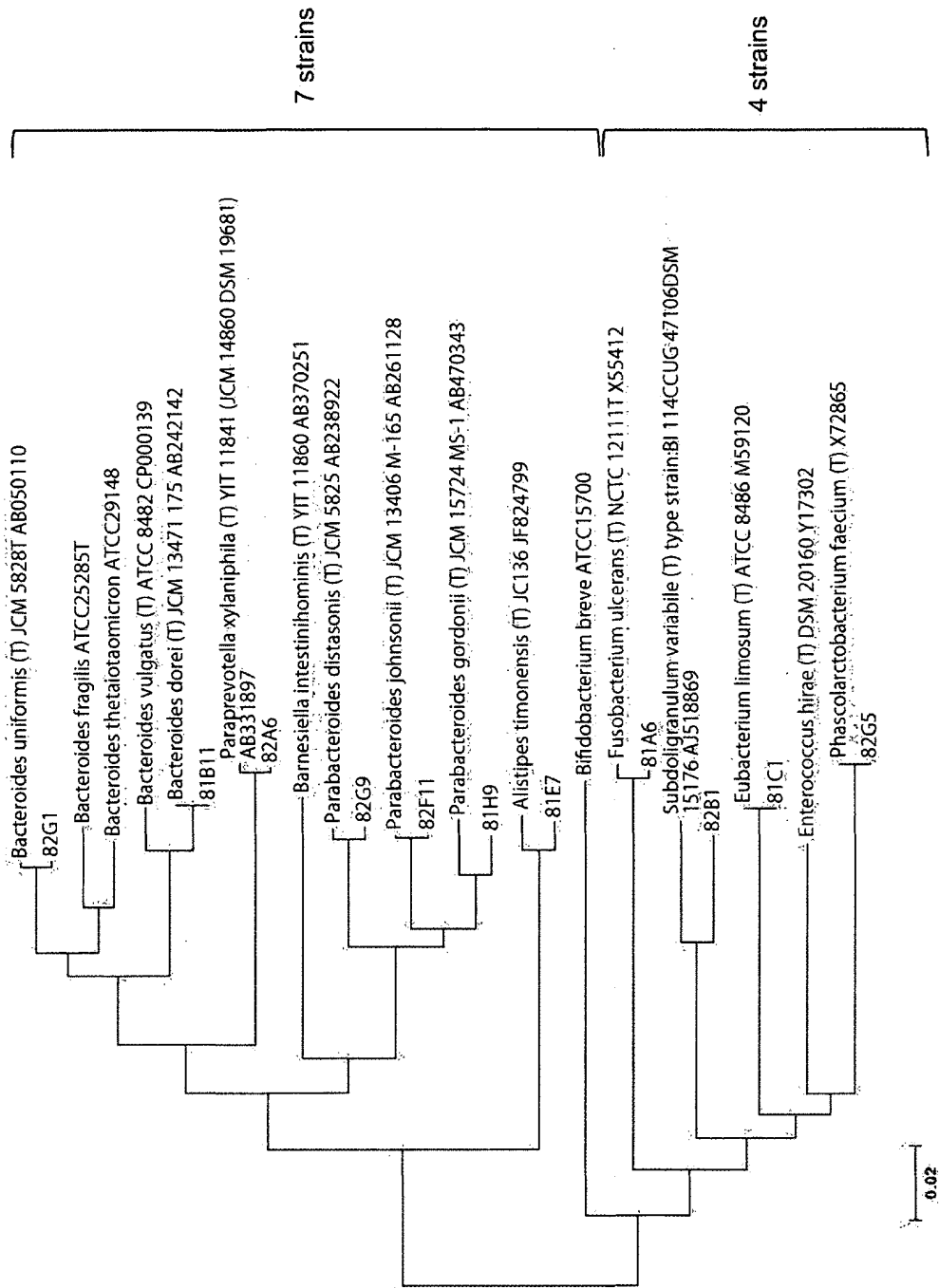


Fig. 13

[Fig.14A-B]

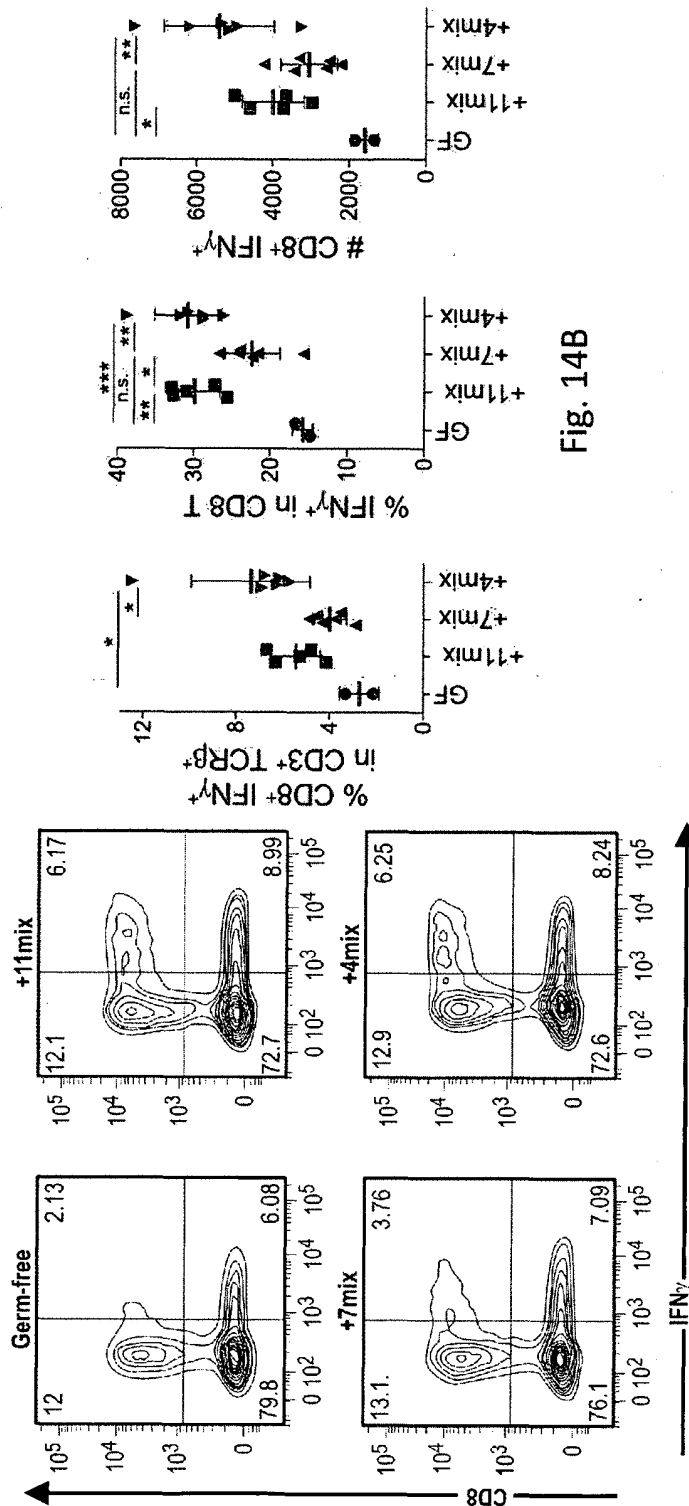


Fig. 14B

Fig. 14A

[Fig. 15]

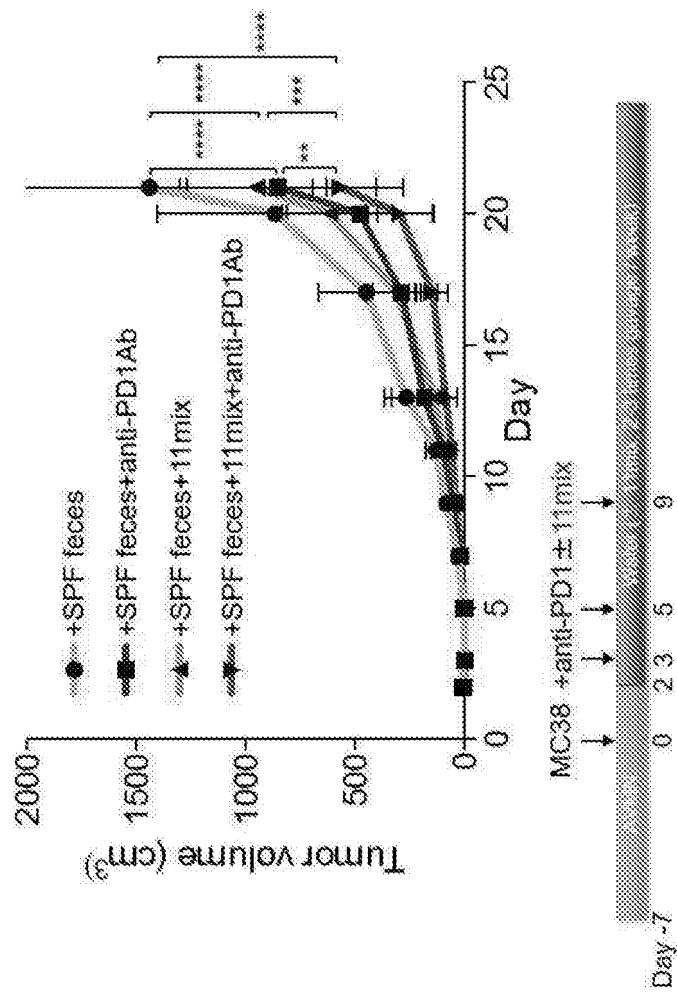


Fig. 15

[Fig.16A-B]

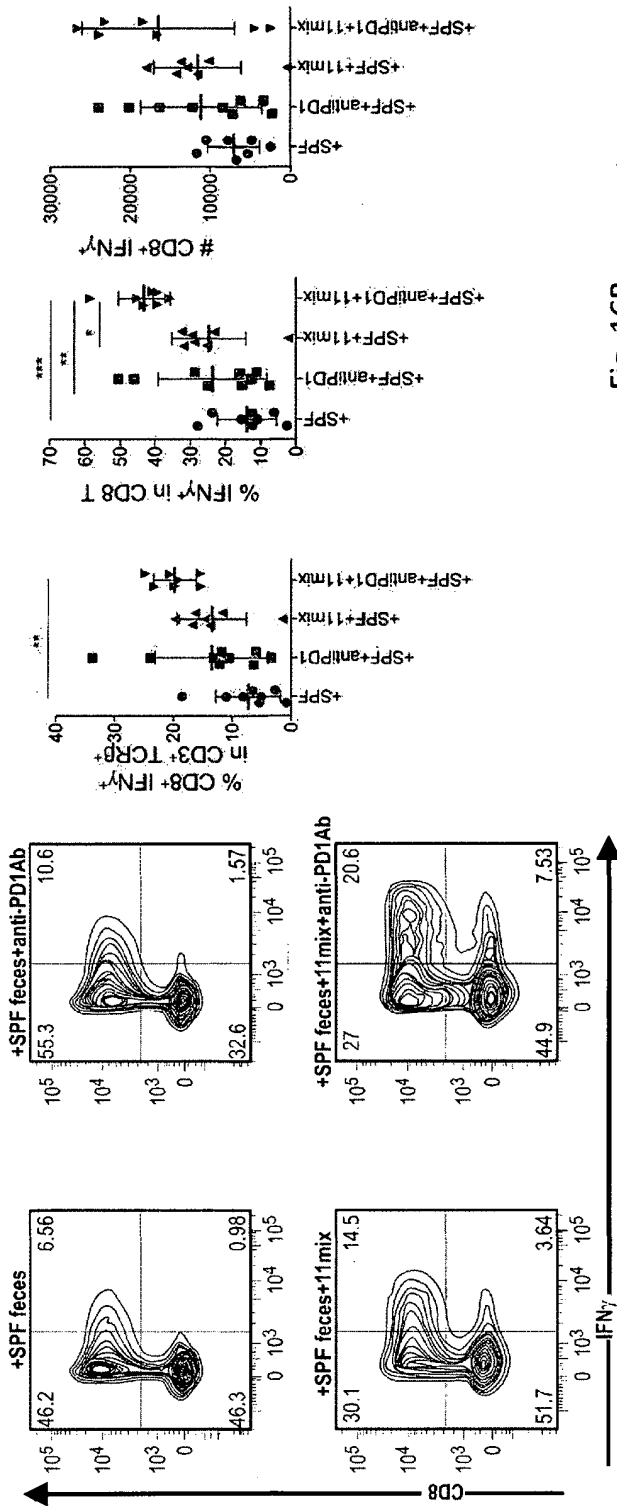


Fig. 16B

Fig. 16A

[Fig.17A-B]

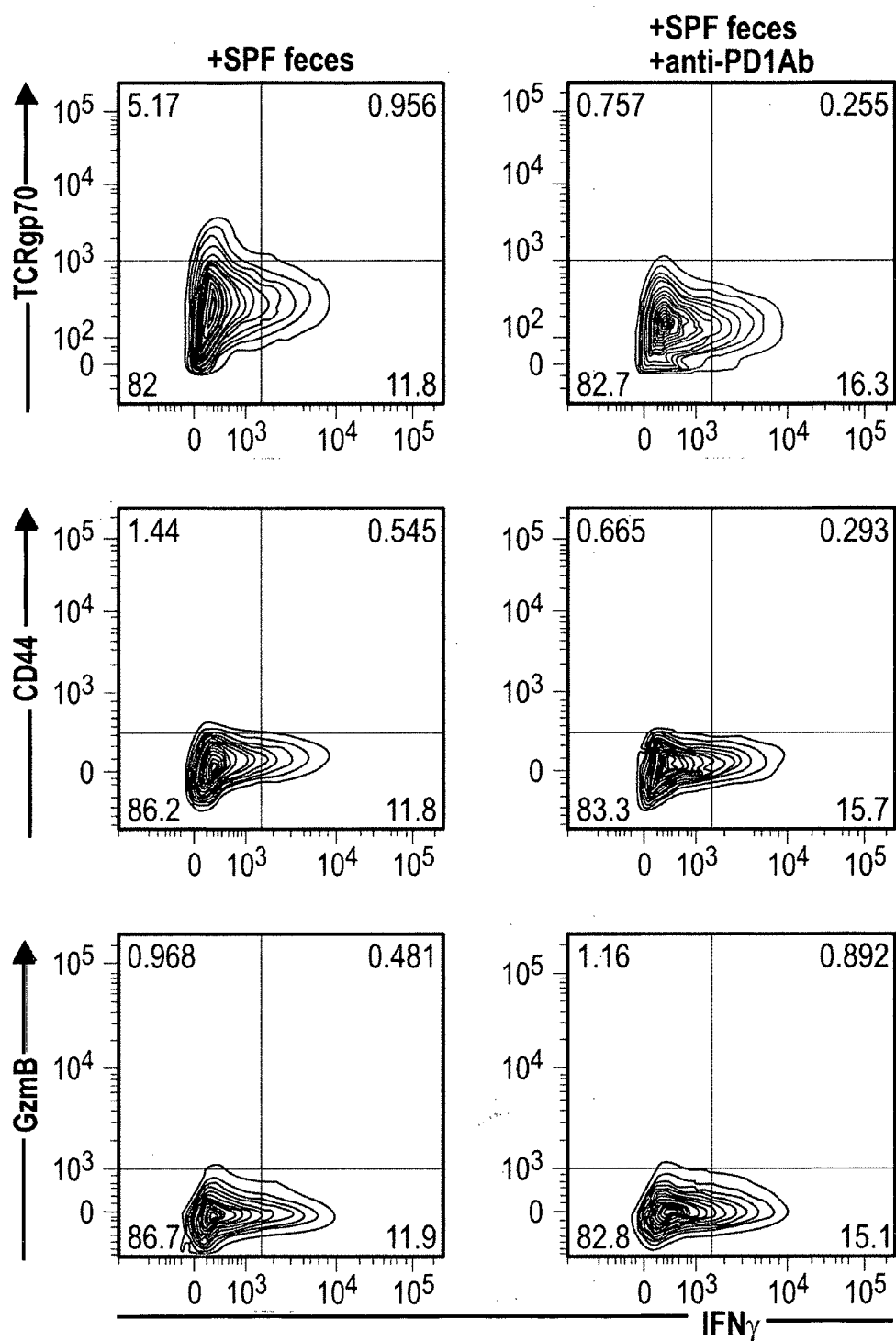
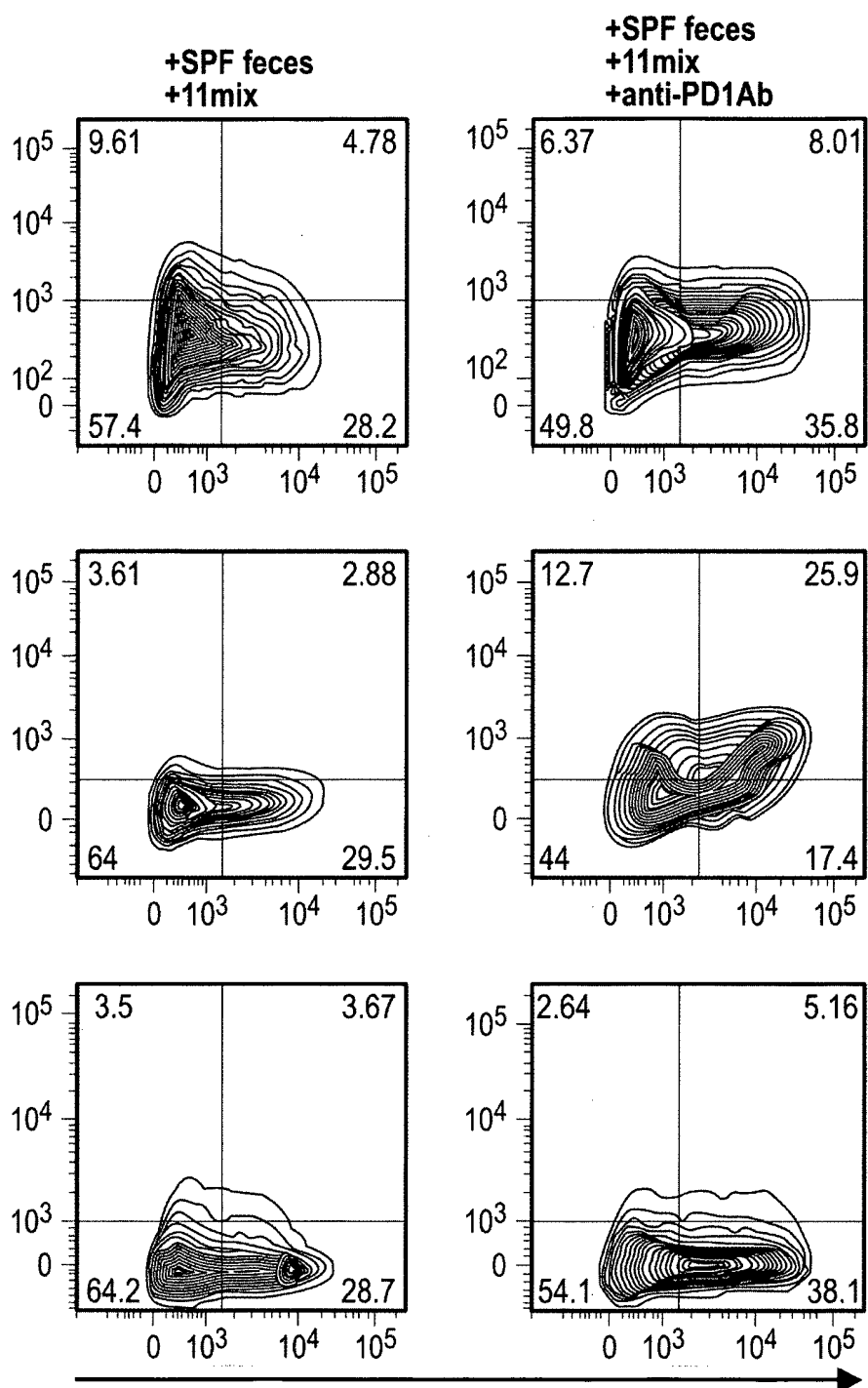


Fig. 17A



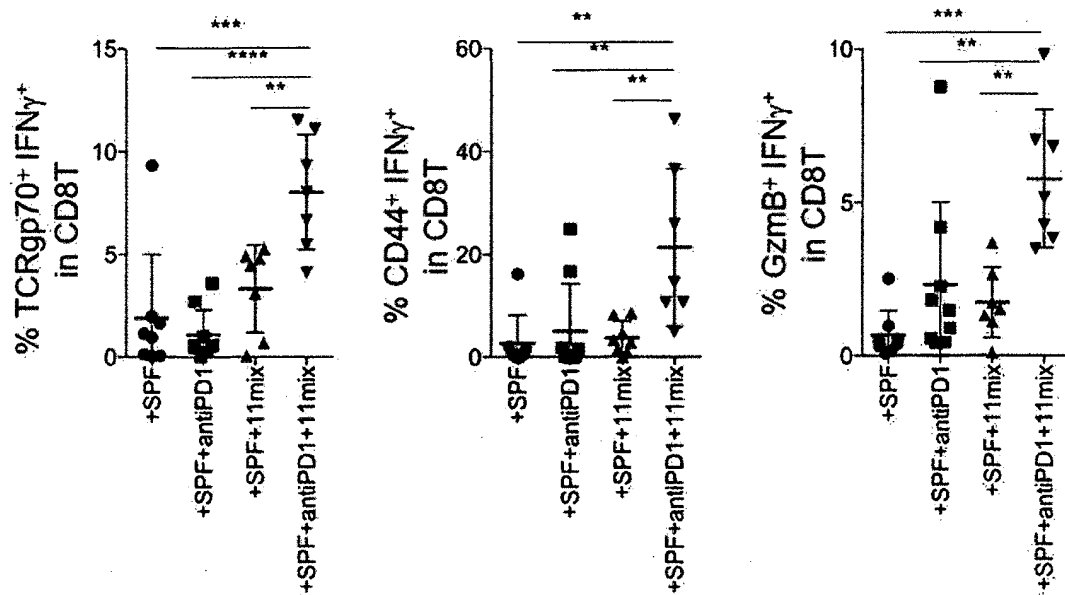


Fig. 17B

[Fig.18]

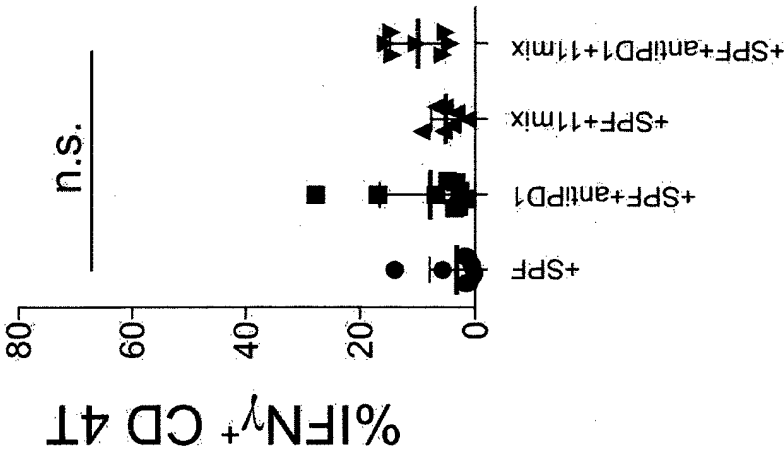


Fig. 18

[Fig.19]

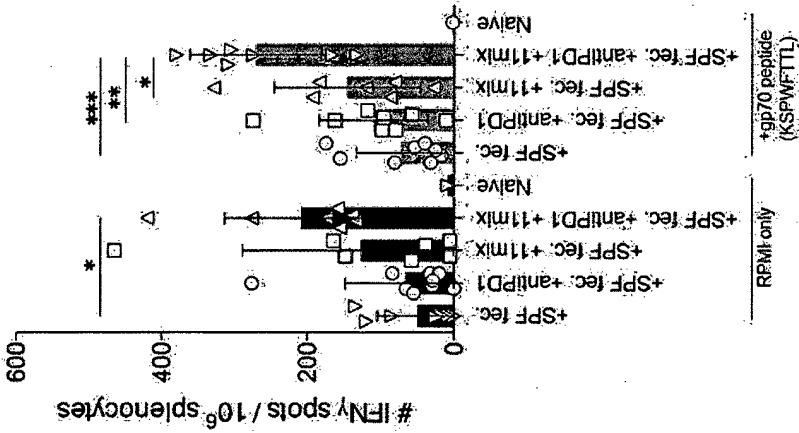


Fig. 19

[Fig.20]

Selected 11 strains			
ID	S_ab score		#
1A1	1	Erysipelotrichaceae bacterium	26
1F3	0.978	bacterium P1A6	25
1E6	0.979	Clostridium lavalense	24
1G1	1	Hungateella hathewayi	23
3F2	0.791	Lachnospiraceae bacterium	22
1H8	1	bacterium NLAE	21
2E8	1	Parabacteroides goldsteinii	20
2D2	0.946	Firmicutes bacterium	19
2B11	0.985	Bacteroides eggerthii	18
1A2	0.996	Bacteroides uniformis	17
2A12	0.993	Bacteroides sp. 1AL	16
2A3	0.986	Bacteroides salyersiae	15
1B4	1	Anaerostipes caecae	14
2C1	0.973	Bacteroides clarus	13
2B7	0.995	Bacteroides sp.	12
2G9	0.987	Parabacteroides distasonis	11
1C1	0.995	Eubacterium limosum	10
1H9	0.903	Parabacteroides gordonii	9
1E7	0.979	Bacteroides sp.	8
2F11	0.989	Parabacteroides johnsonii	7
2A6	0.966	Paraprevotella xylaniphila	6
2B1	1	Ruminococcaceae bacterium	5
2G1	0.995	bacterium IARFR67	4
1B11	1	Bacteroides dorei	3
1A6	1	Fusobacterium sp.	2
2G5	0.985	Phascolarctobacterium faecium	1

Fig. 20

[Fig.21]

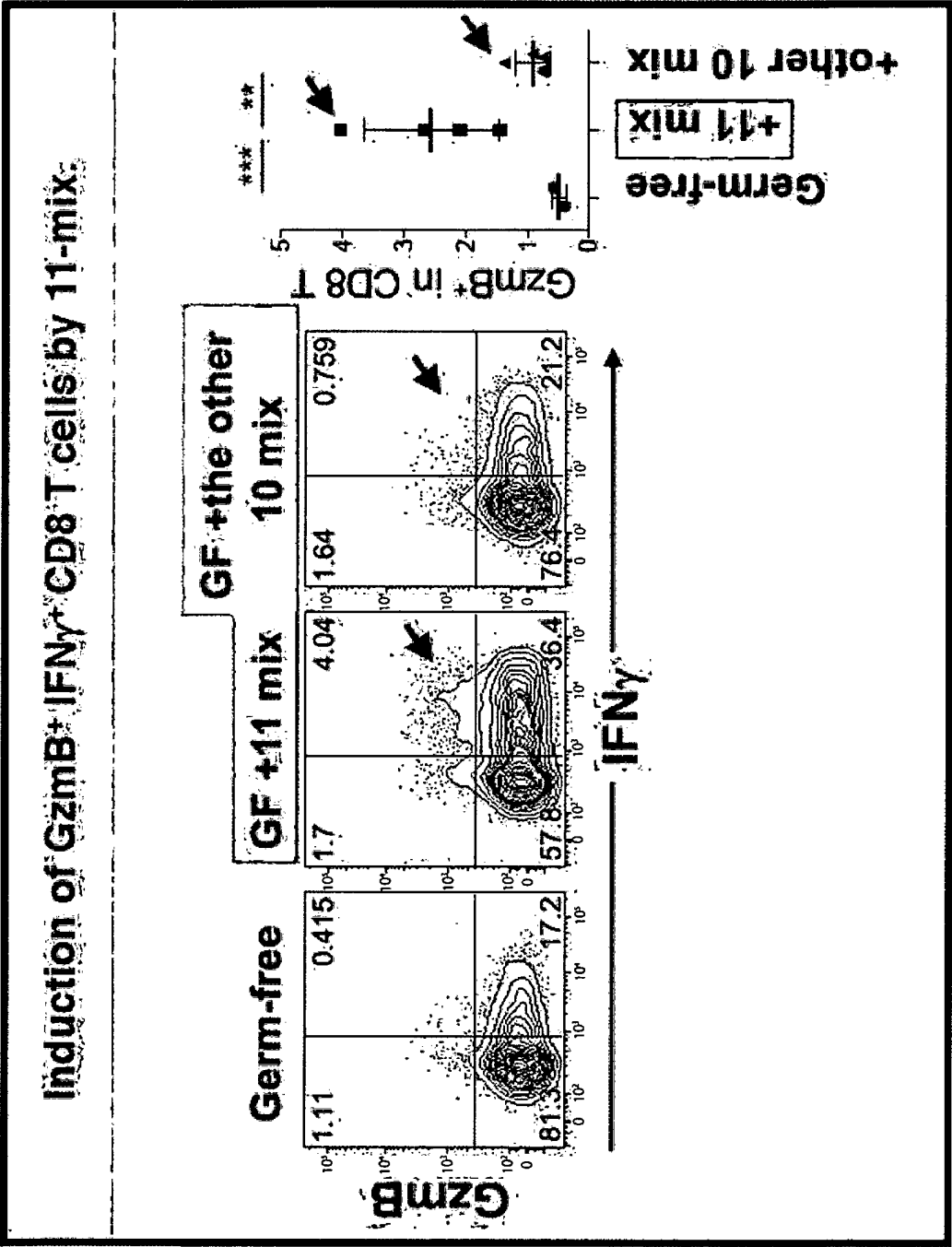


Fig. 21

[Fig.22]

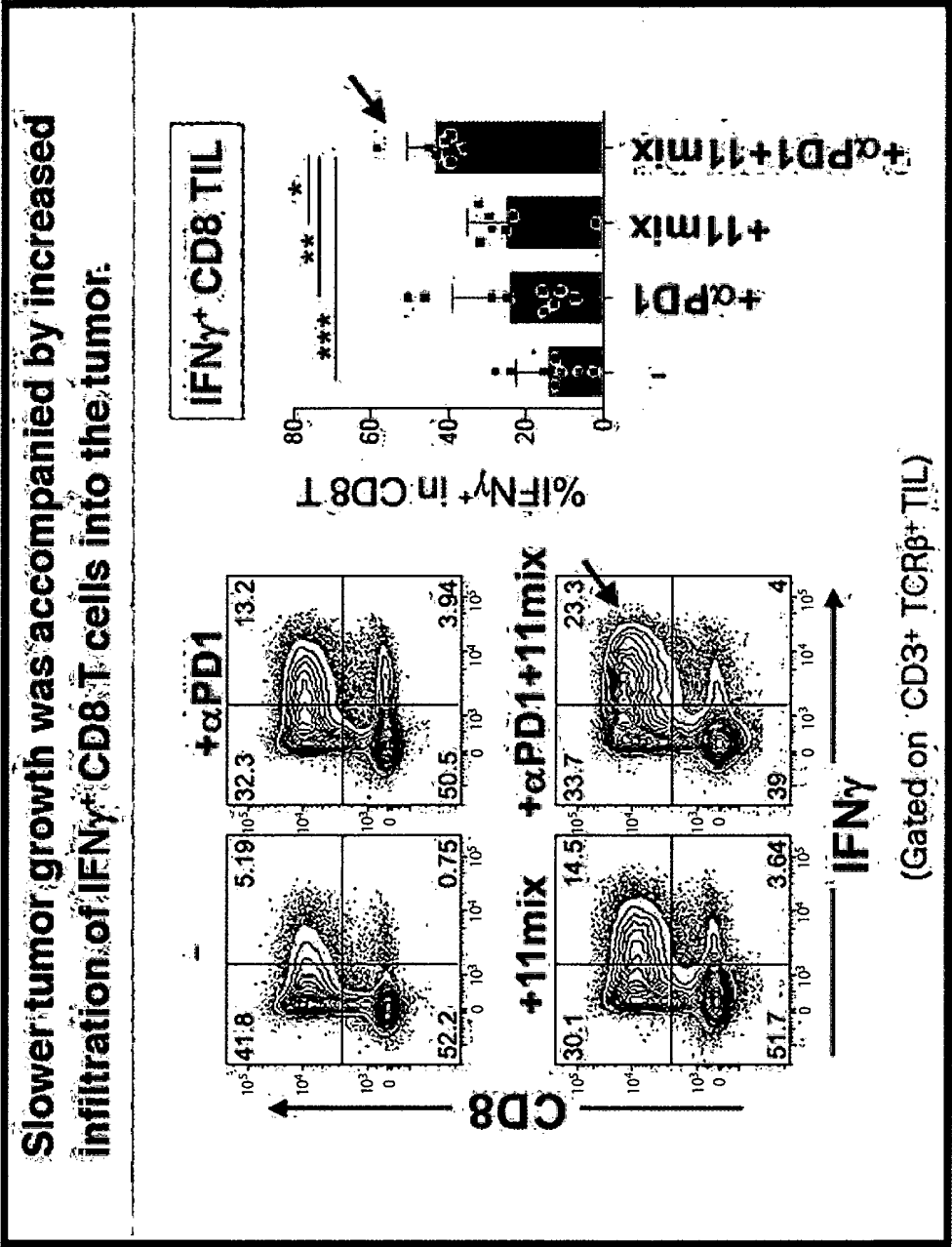


Fig. 22

[Fig.23]

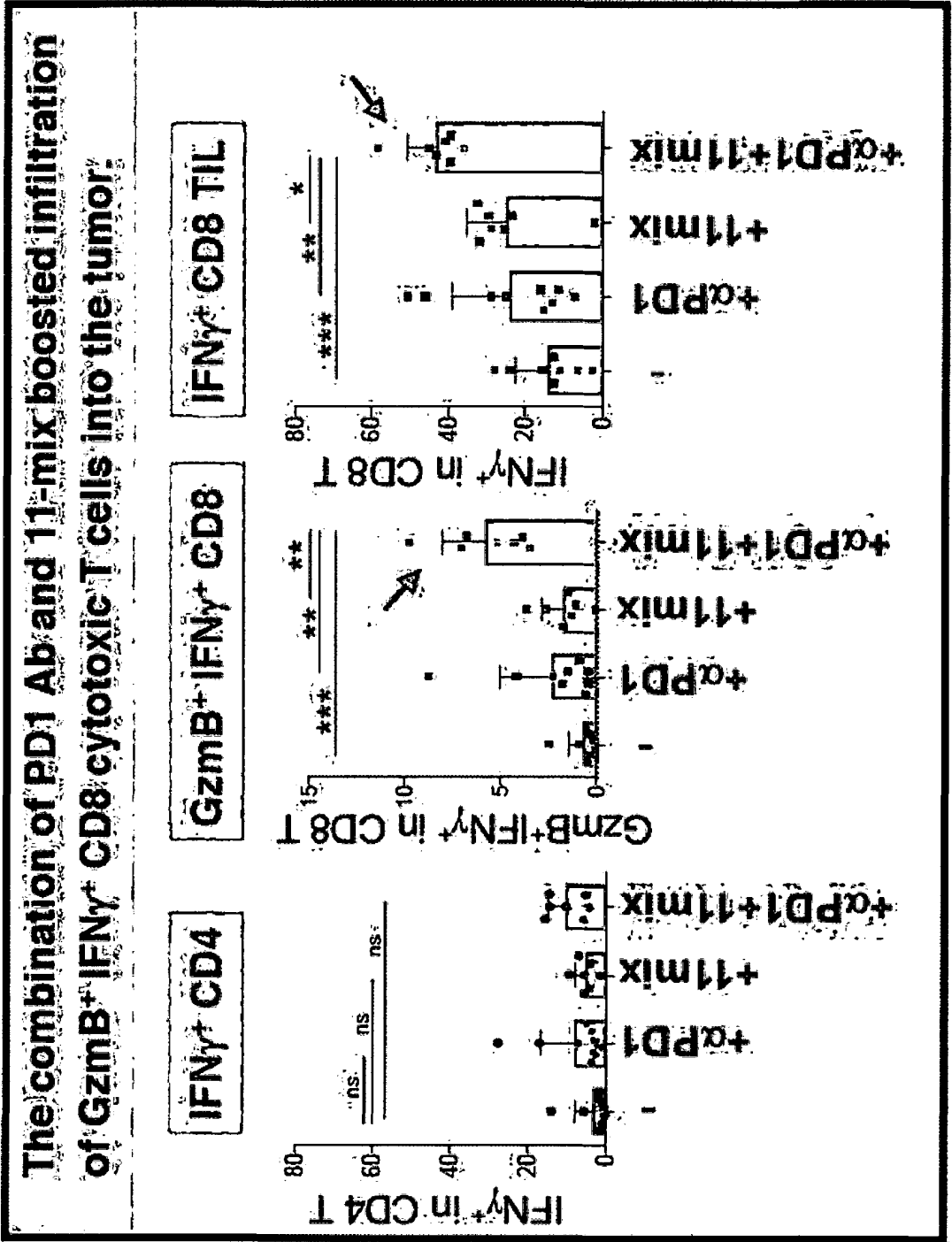


Fig. 23

[Fig.24]

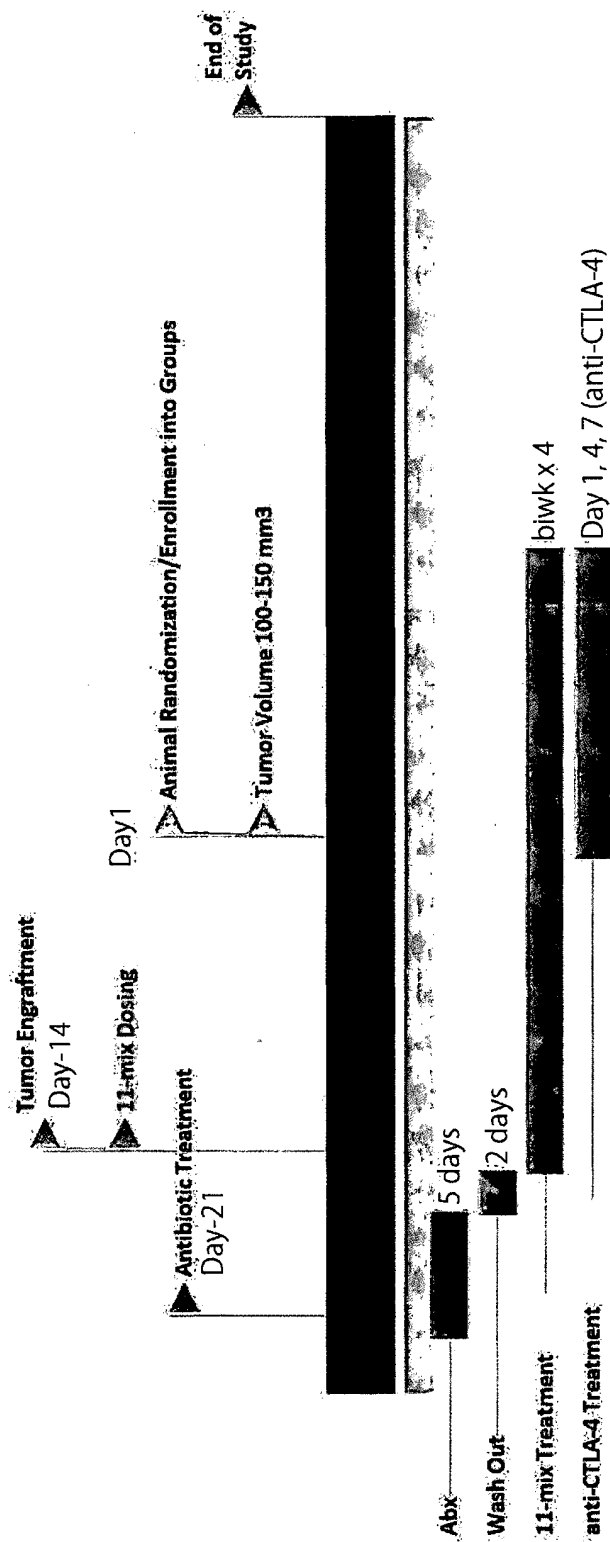


Fig. 24

[Fig. 25]

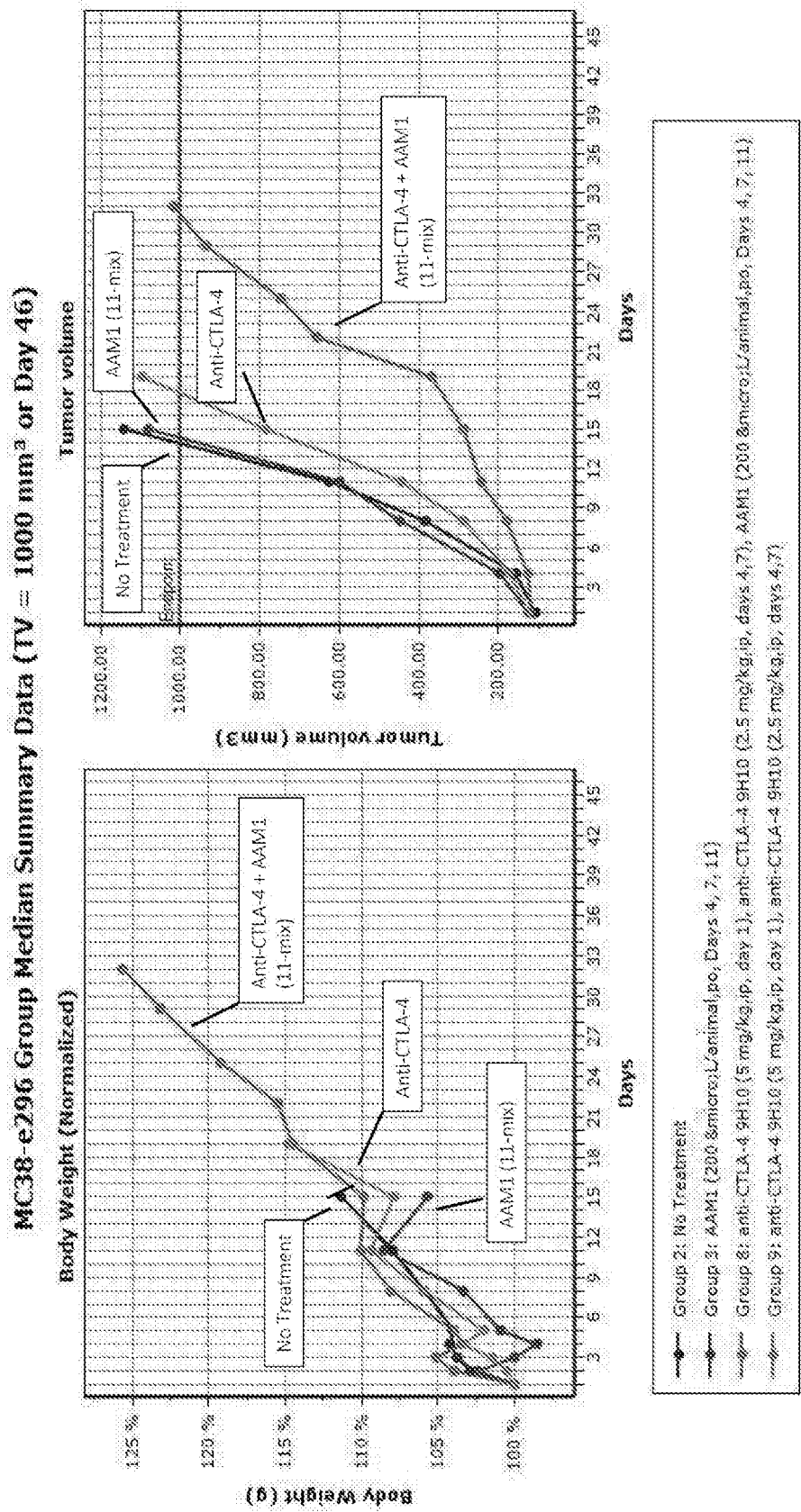


Fig. 25

[Fig. 26]

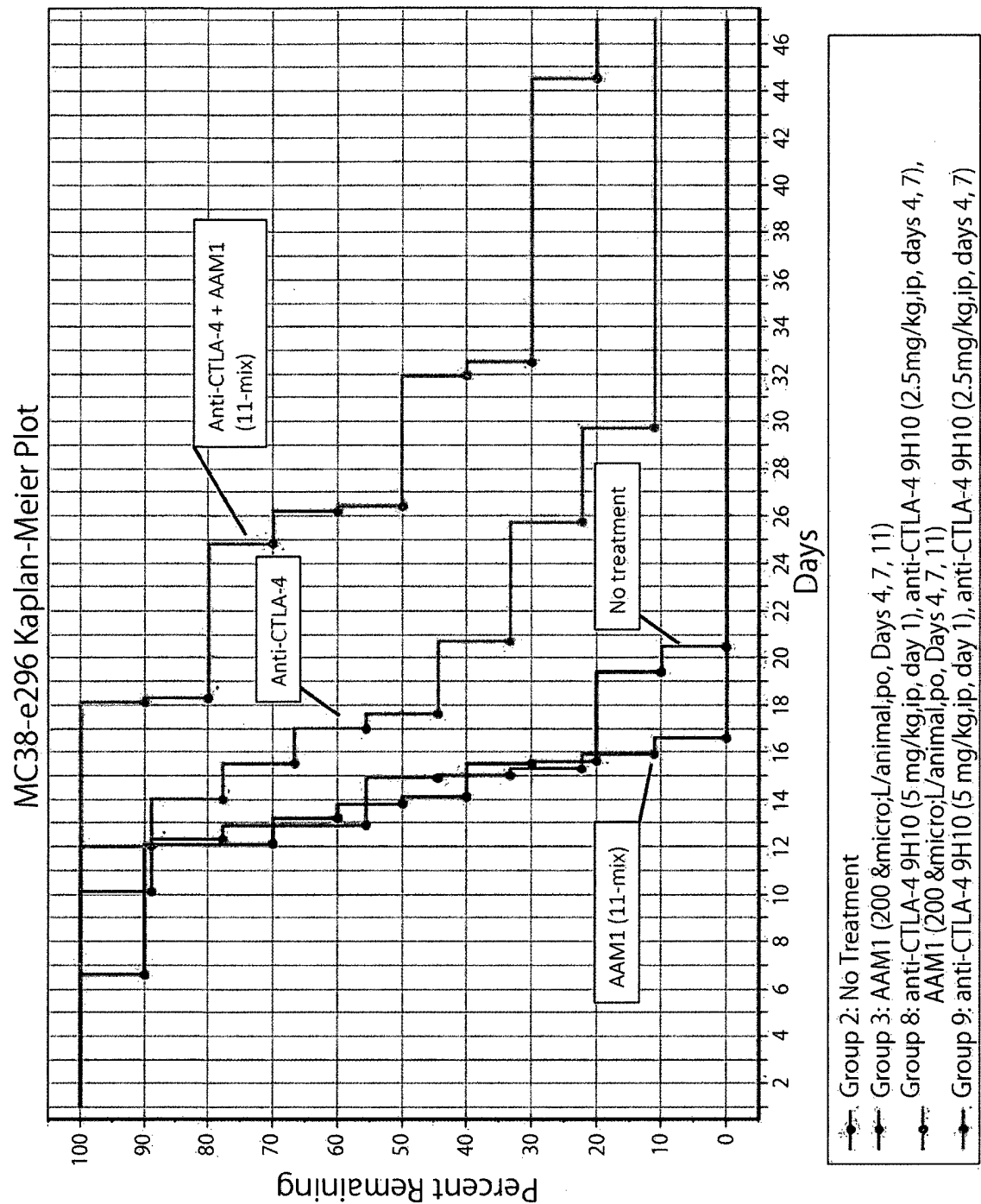


Fig. 26

[Fig.27]

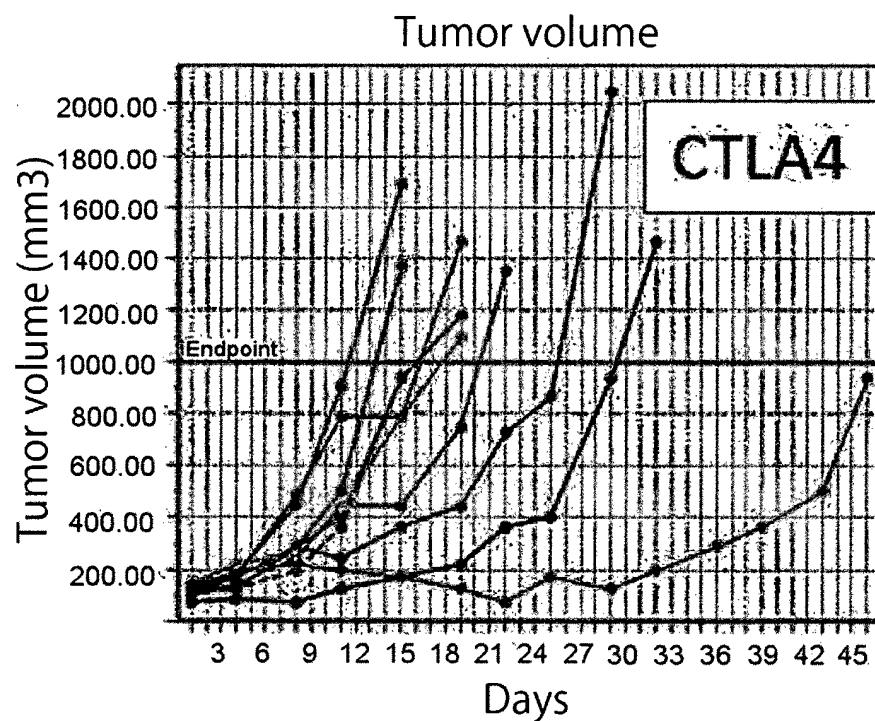
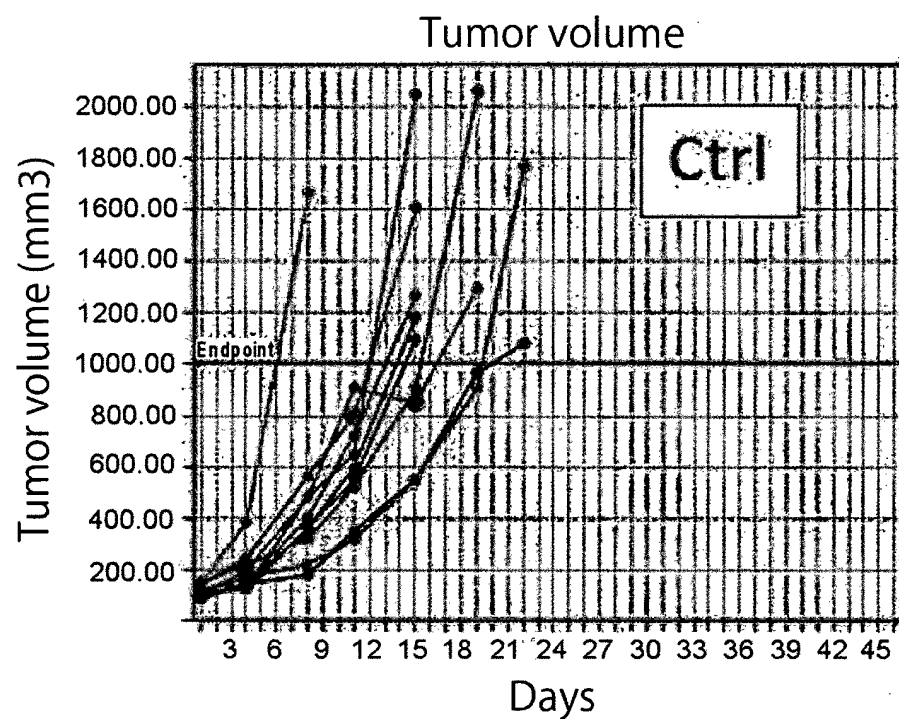
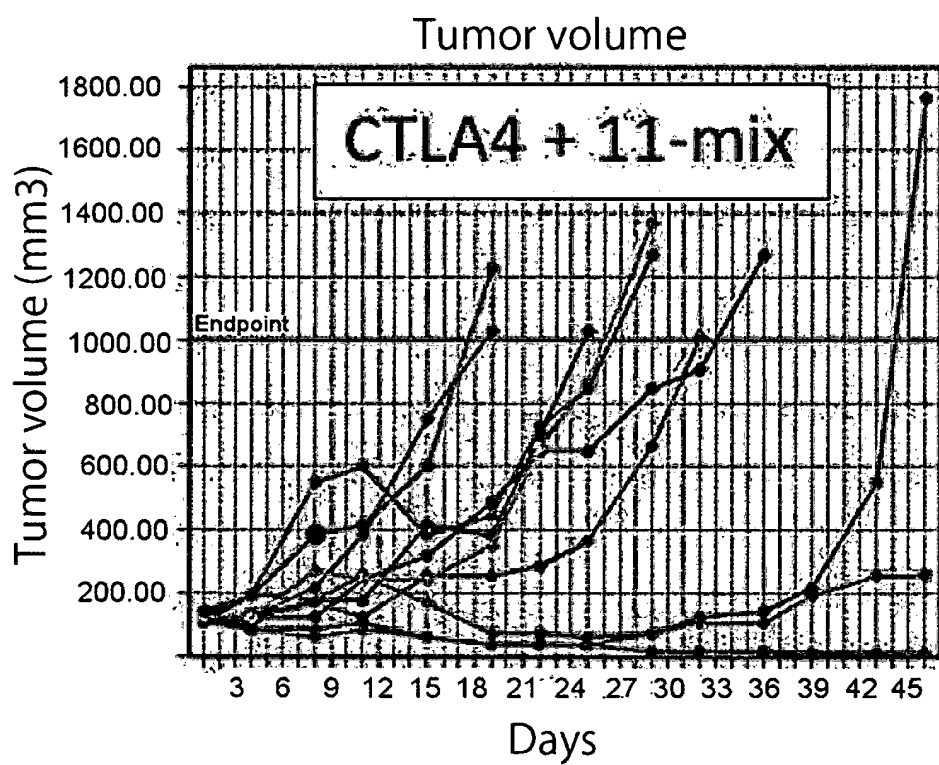
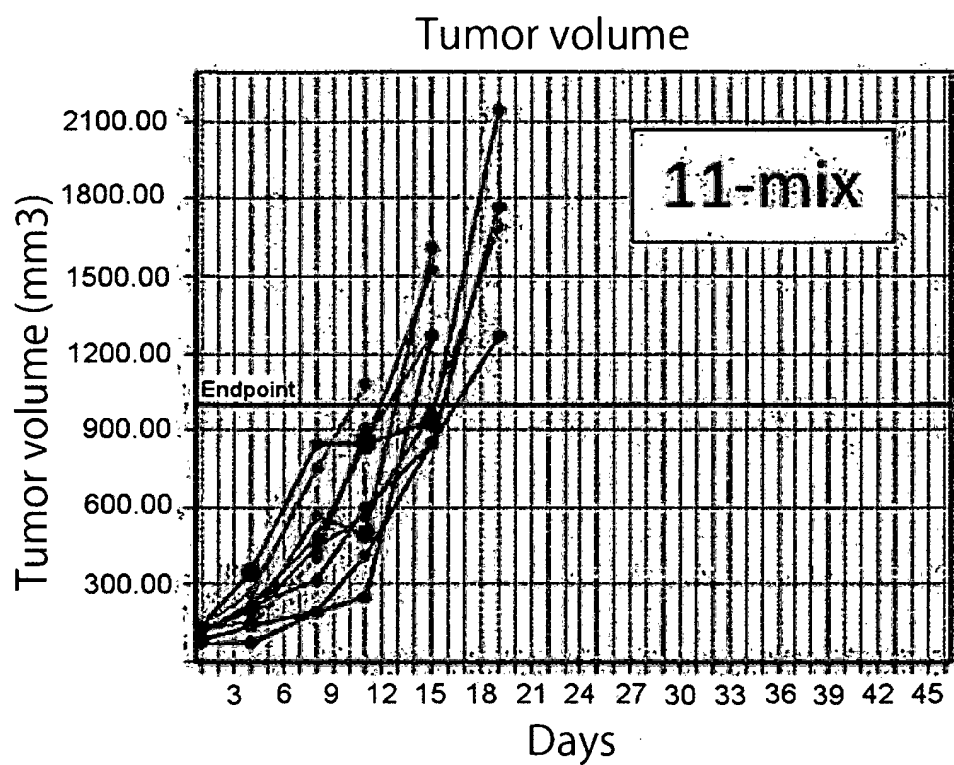


Fig. 27



[Fig. 28]

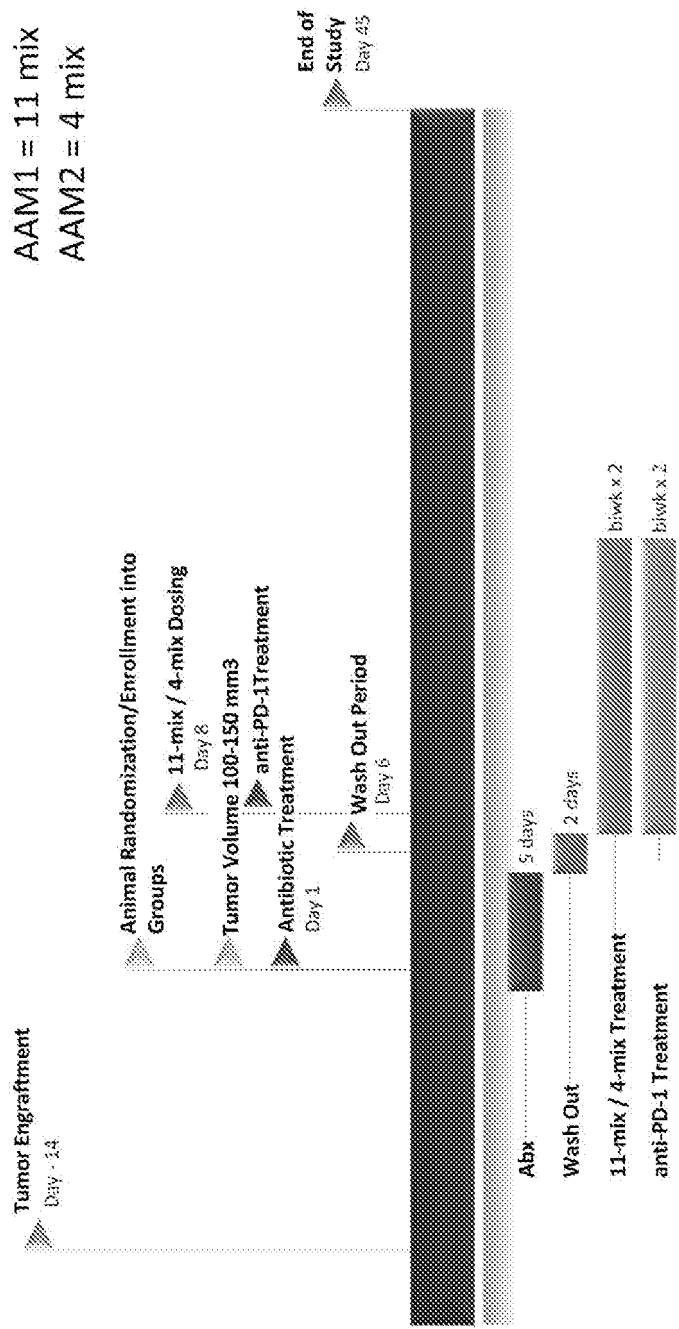


Fig. 28

[Fig. 29]

MC38-e297 Group Median-Summary Data (TV=1000mm³ or Day 46)
AAM1 = 11 mix
AAM2 = 4 mix

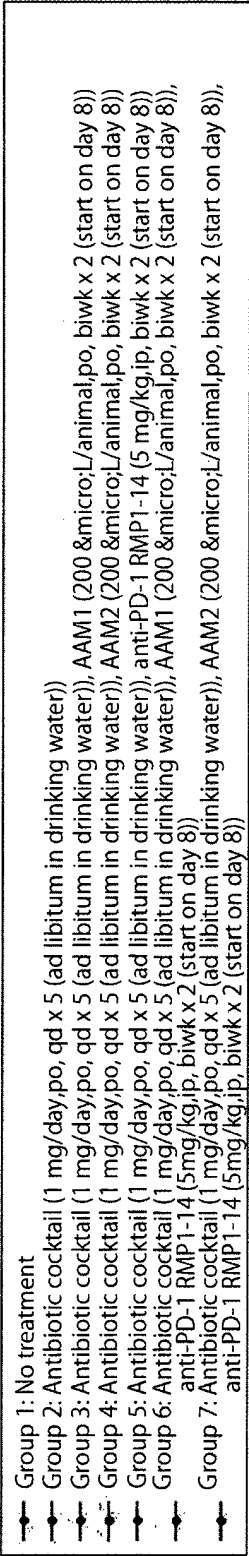
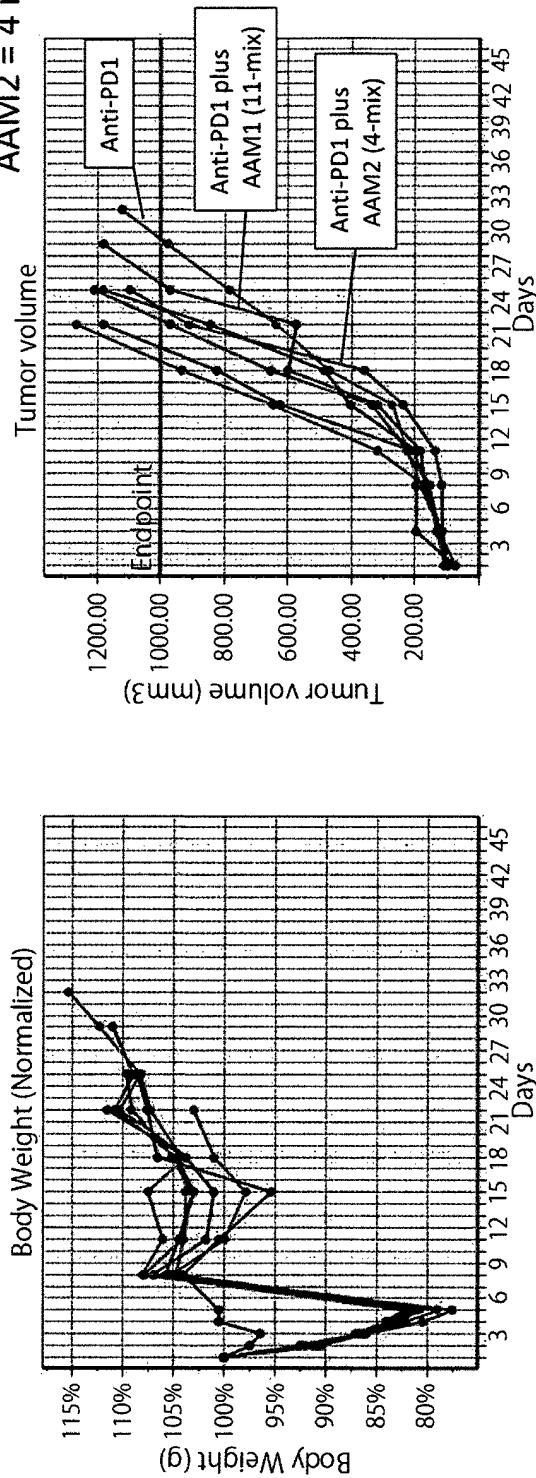


Fig. 29

[Fig.30]

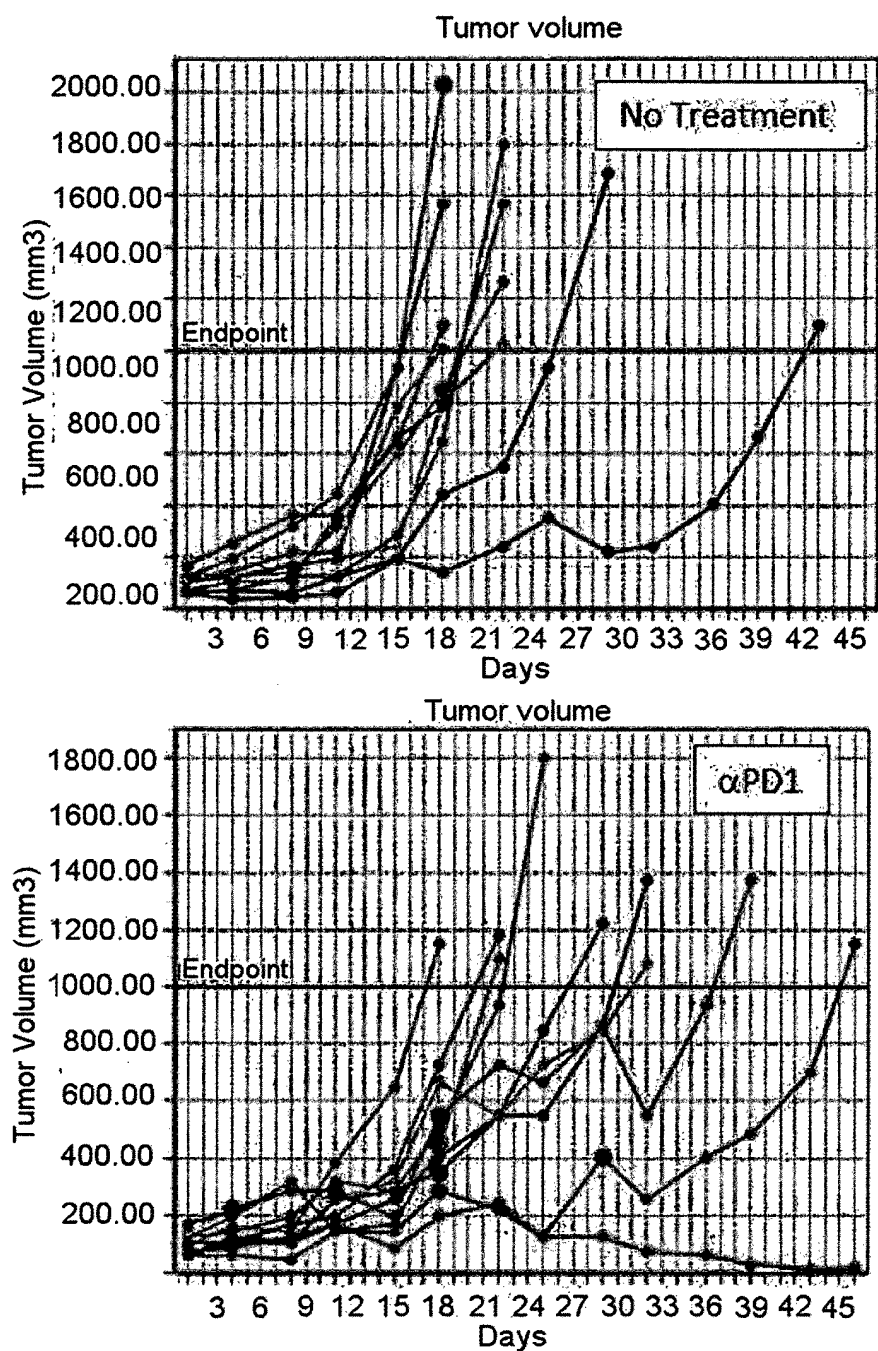
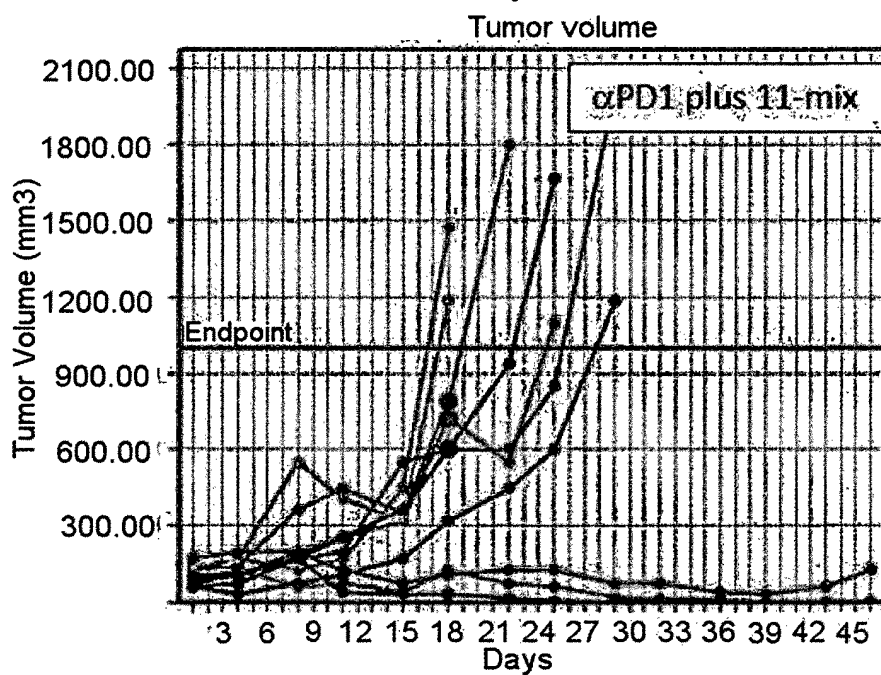
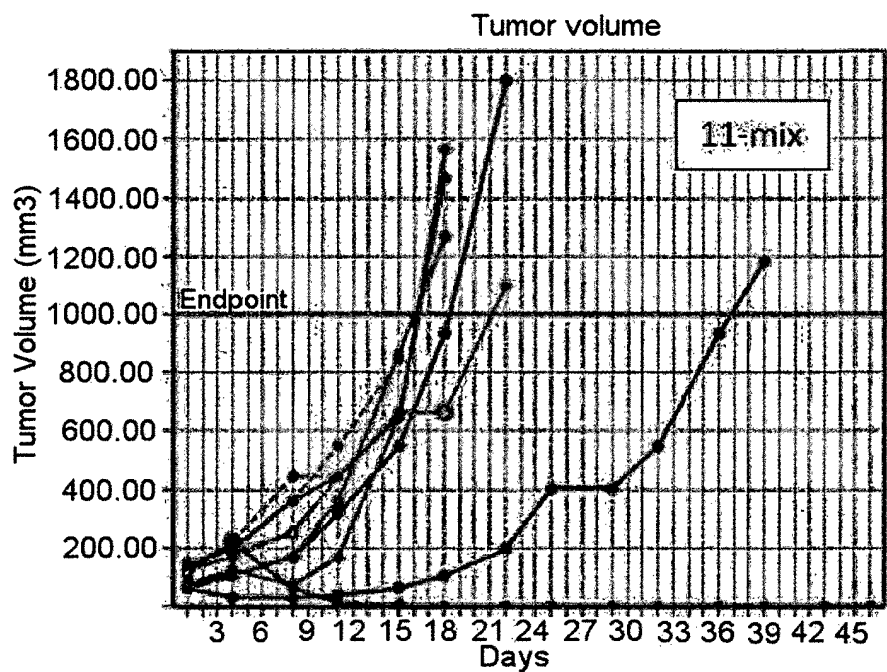


Fig. 30



[Fig.31]

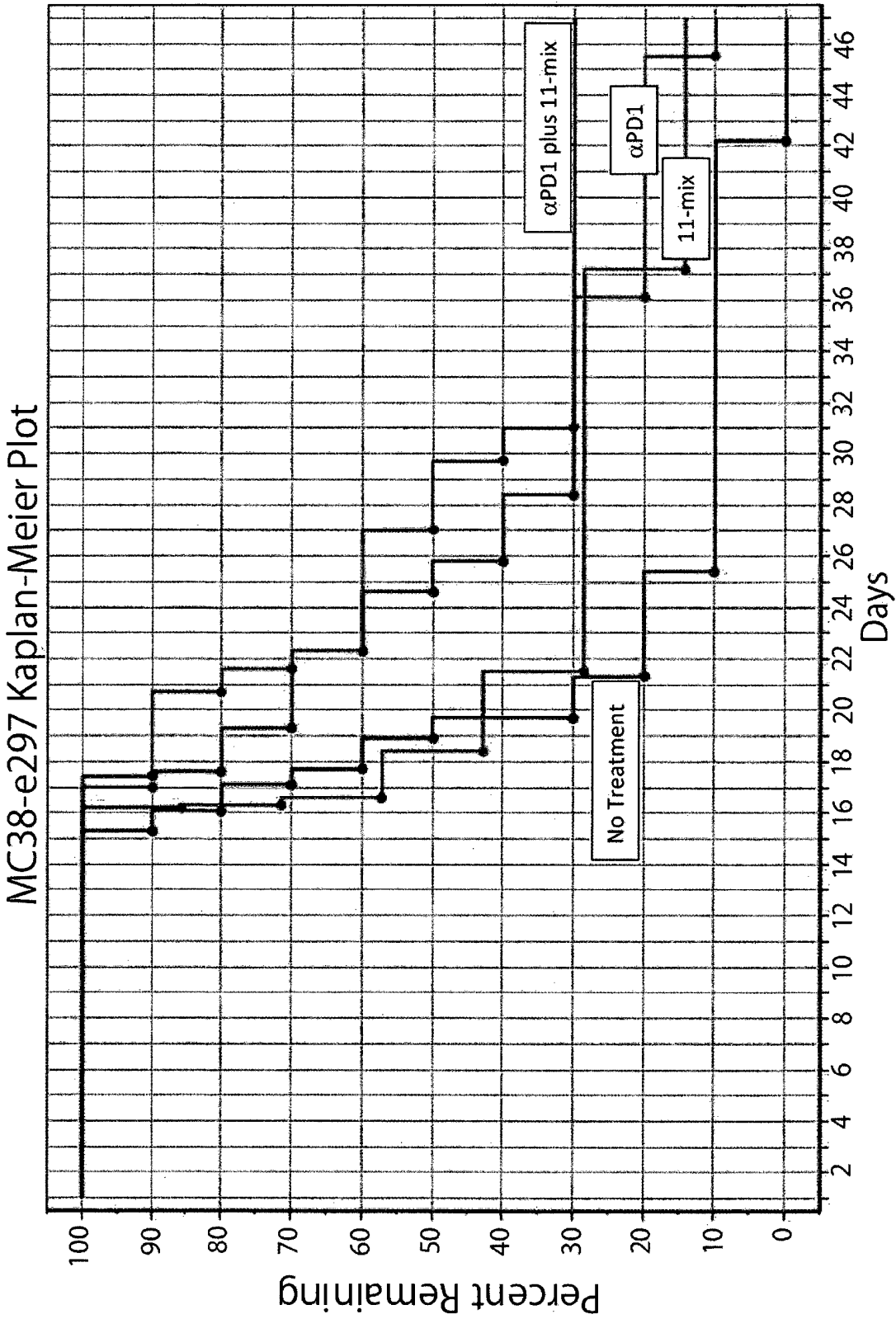


Fig. 31

[Fig.32]

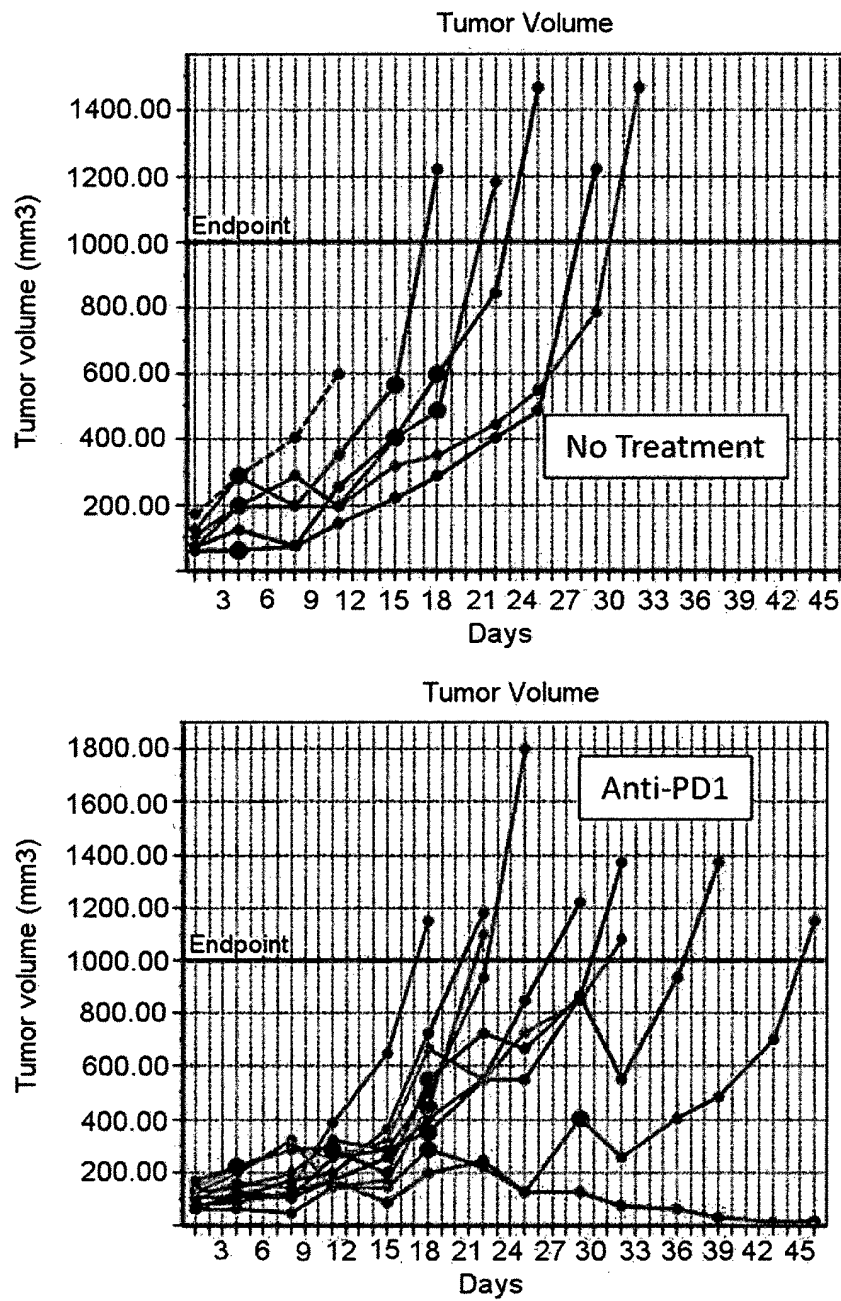
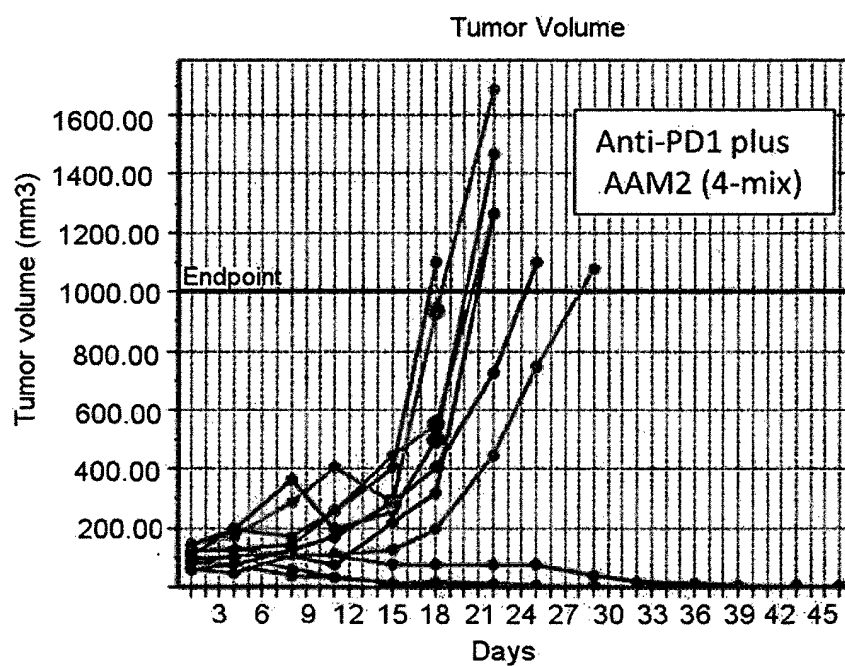
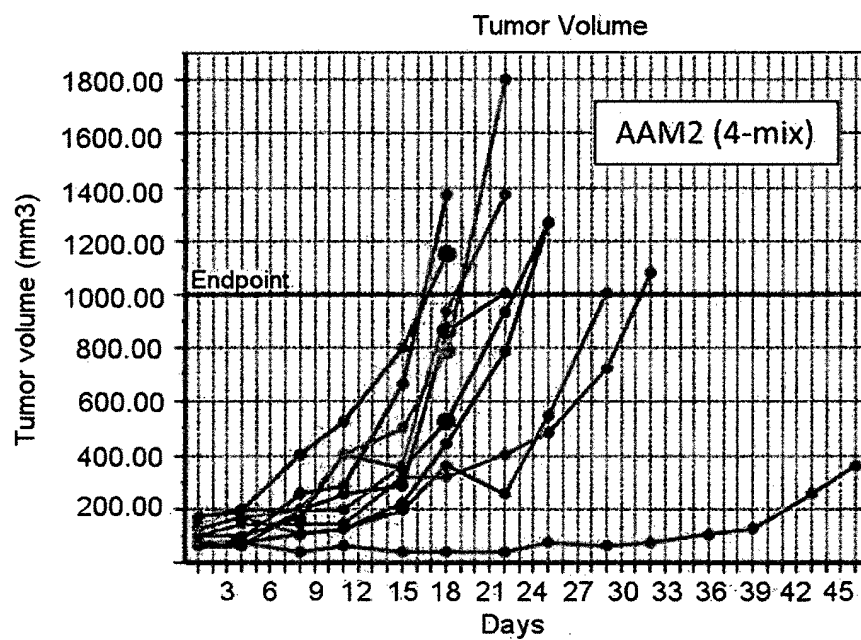


Fig. 32



[Fig.33]

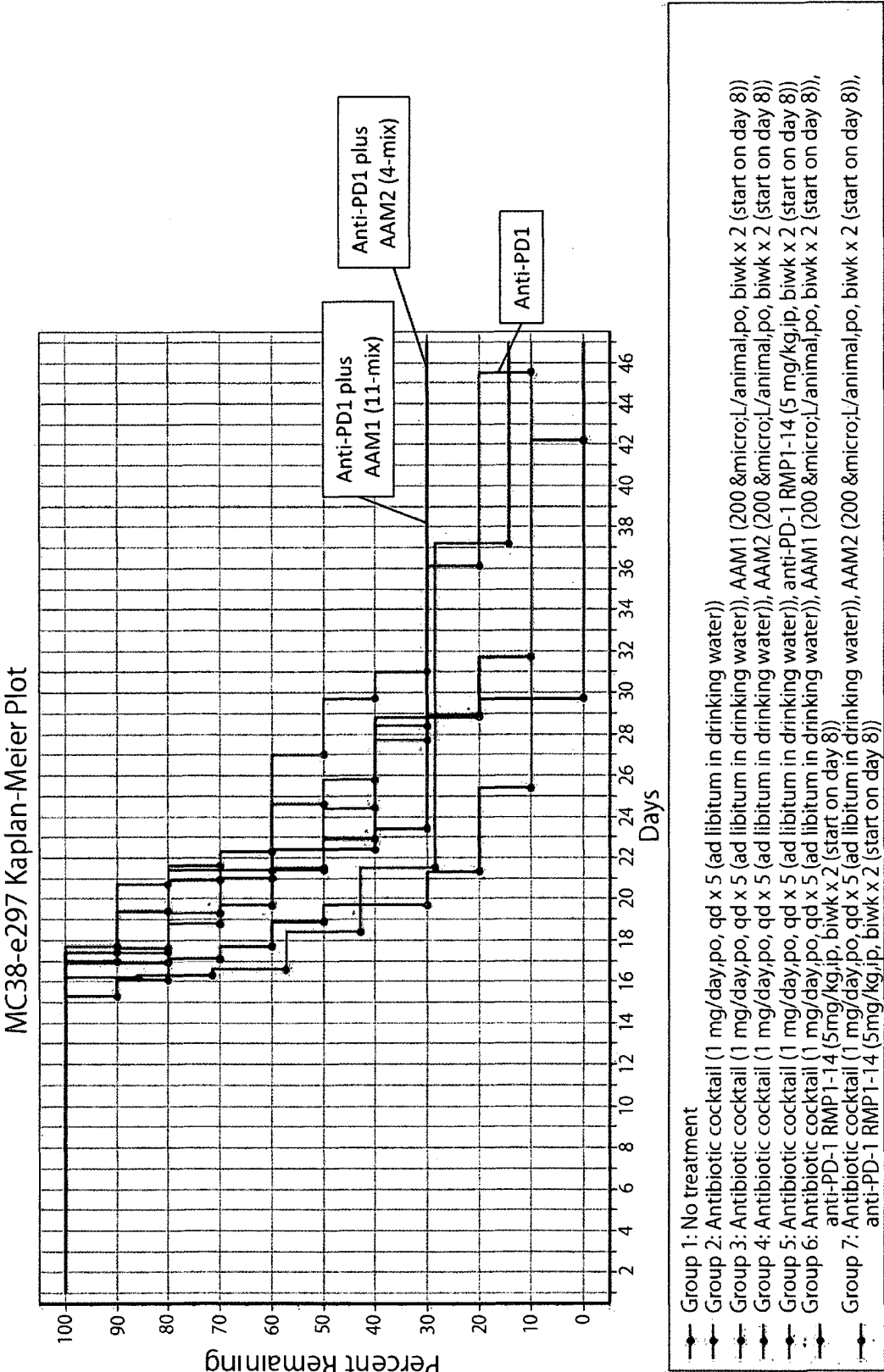
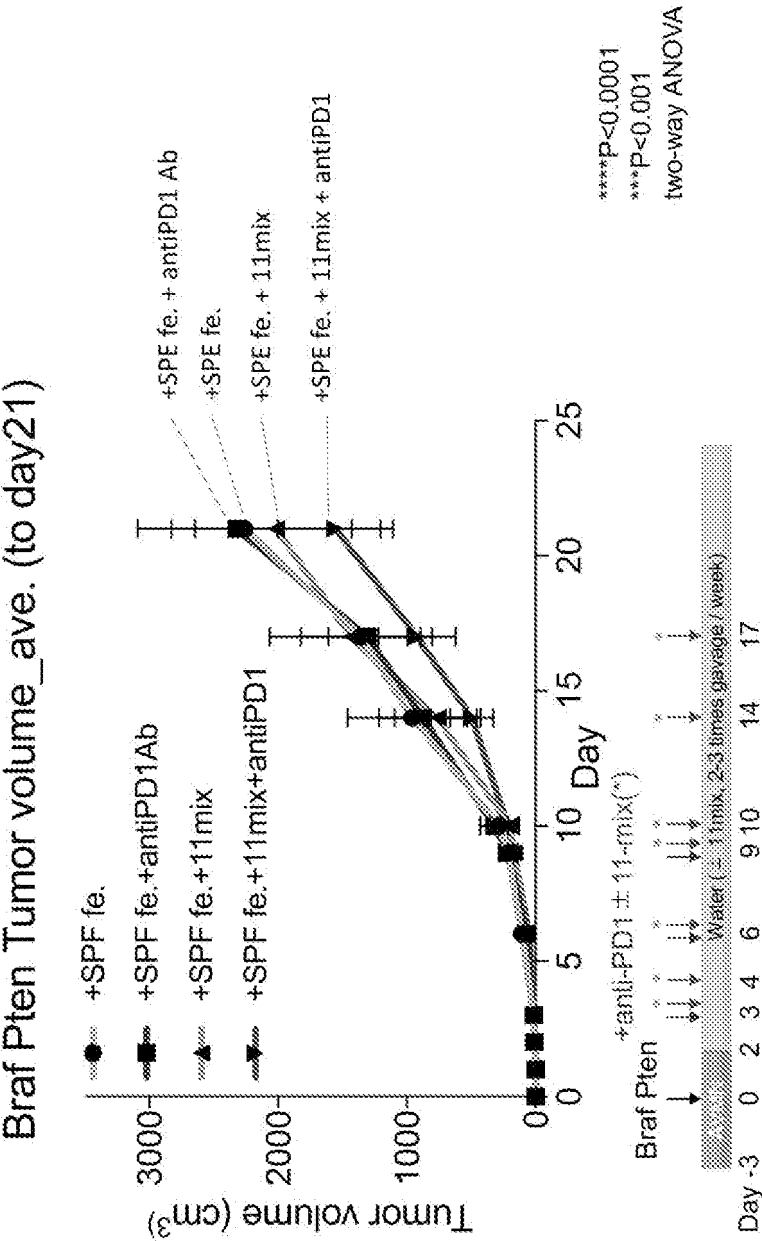


Fig. 33

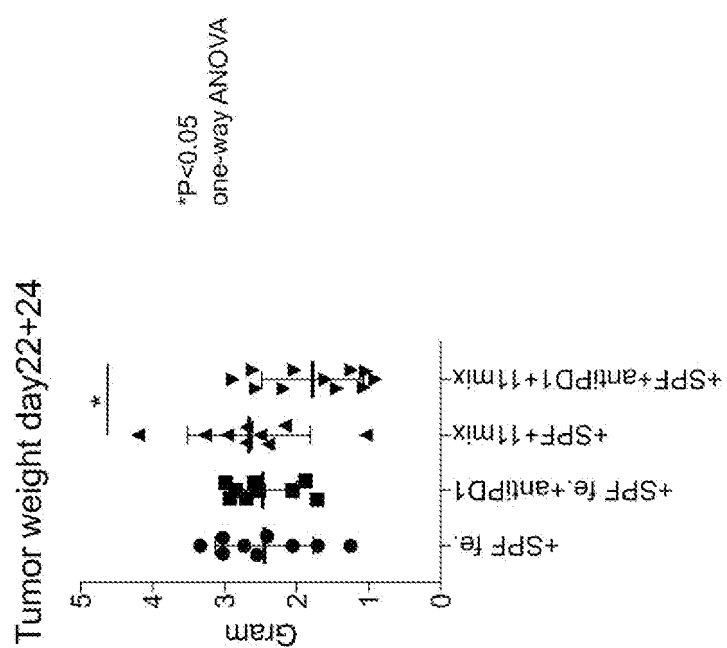
[Fig. 34]



Day-3~2 : AVMN
Day0 : Braf Pten 7x10⁵ cells
Day2~ : water
Day3,6,9 : +/- anti-PD1 200µg + SLC SPF feces +/- 11-mix
2 or 3 times/ week : +11mix

Fig. 34

[Fig. 36]



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[Fig. 37A-C]

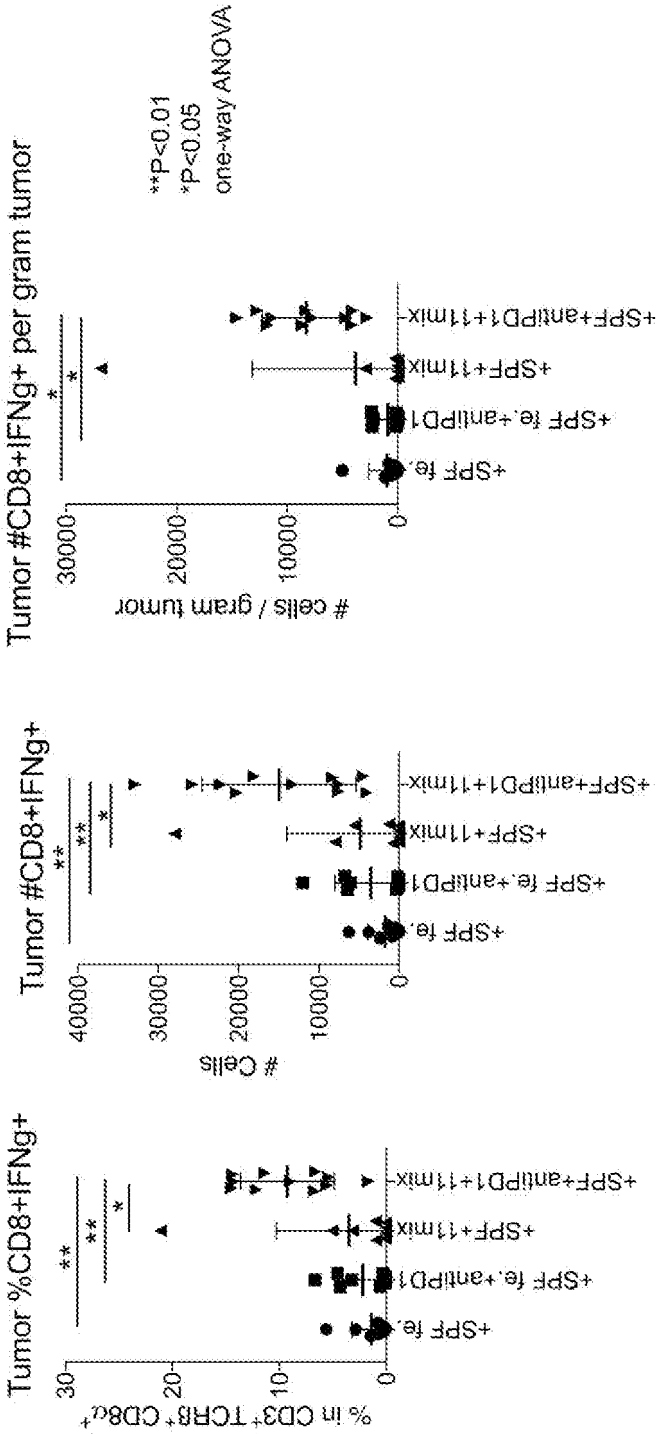


Fig. 37A

Fig. 37B

Fig. 37C

[Fig. 38]

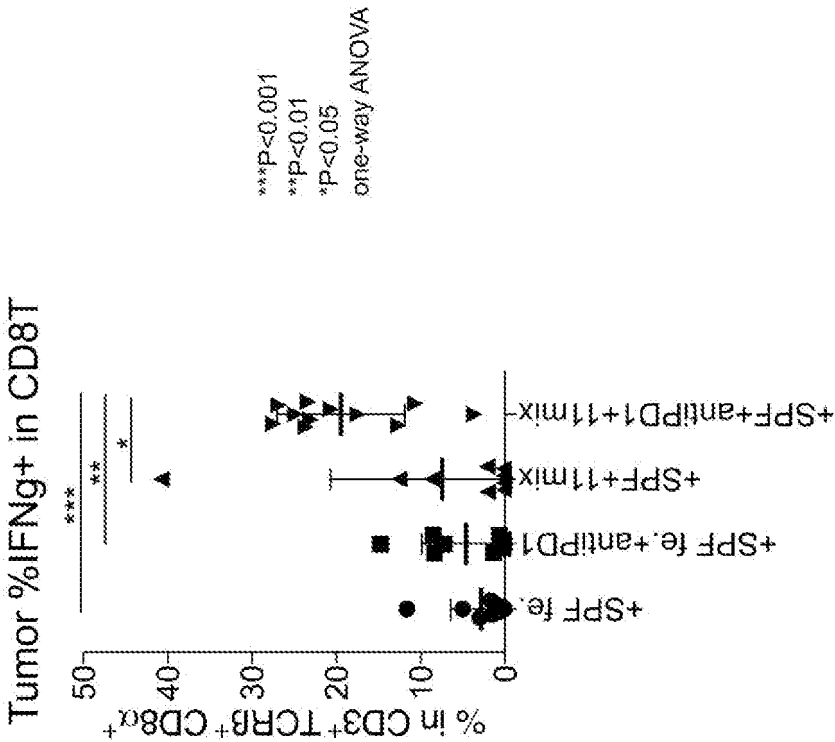


Fig. 38

[Fig. 39A-D]

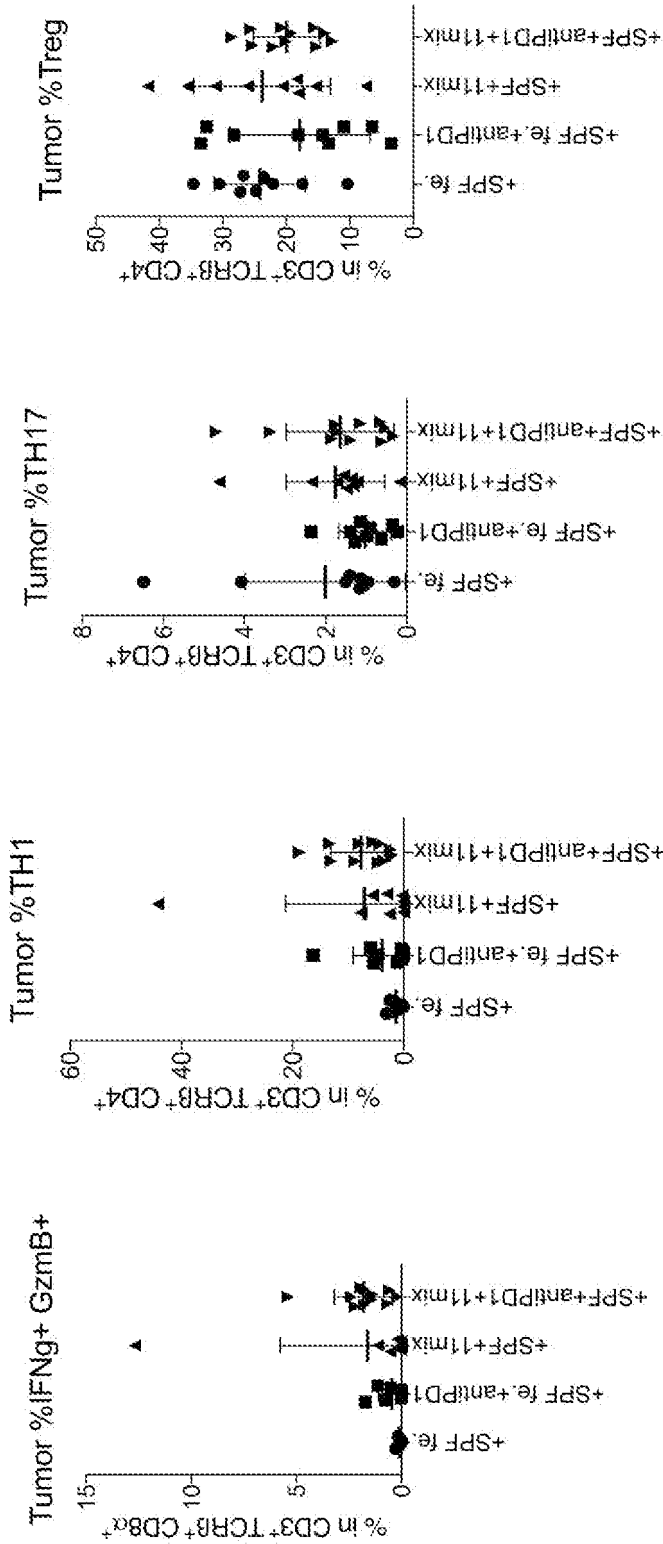


Fig. 39A

Fig. 39B

Fig. 39C

Fig. 39D

[Fig. 40]

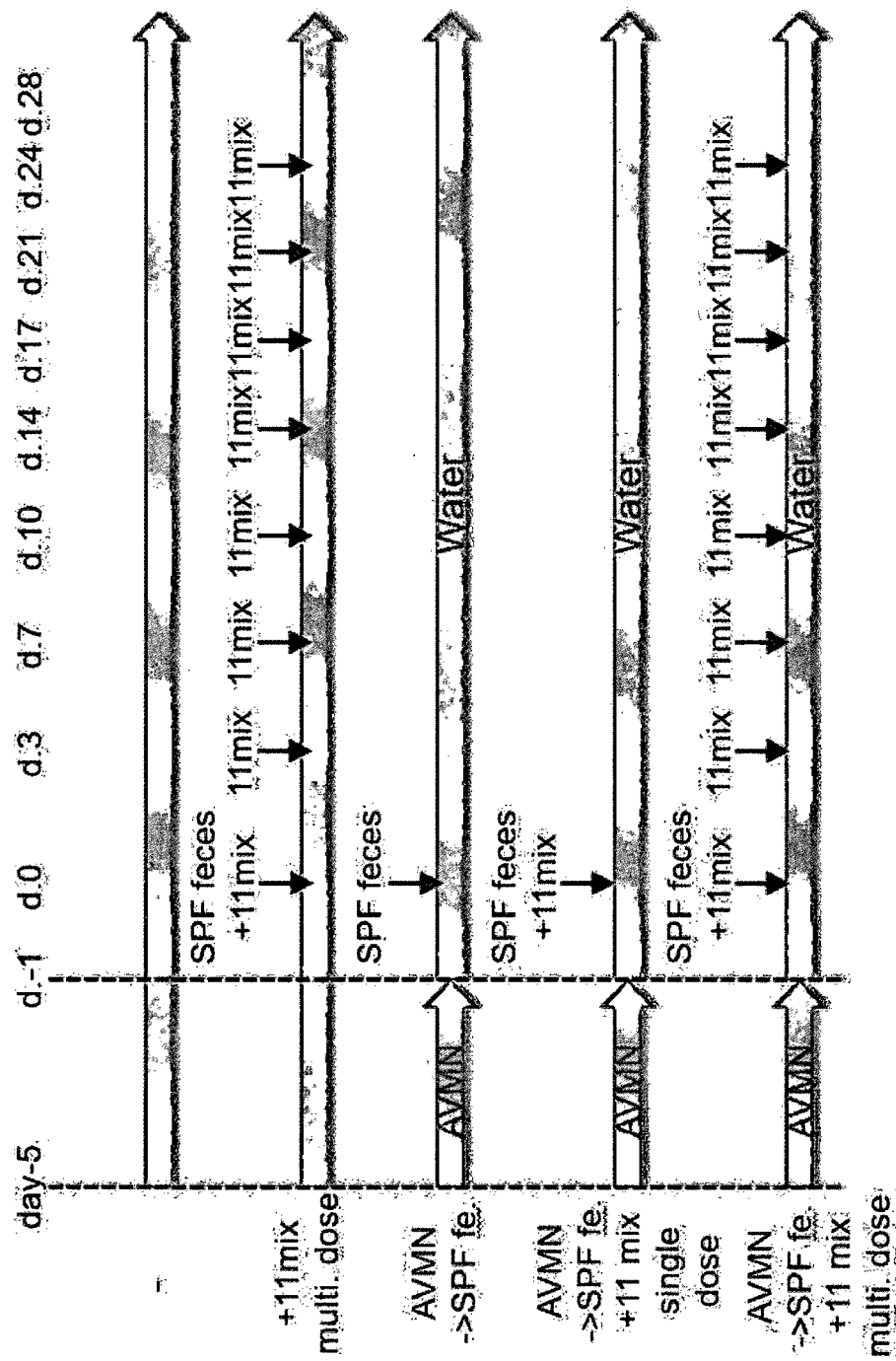


Fig. 40

[Fig. 41A-C]

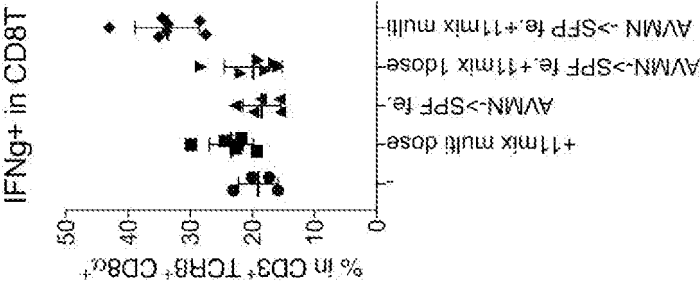


Fig. 41C

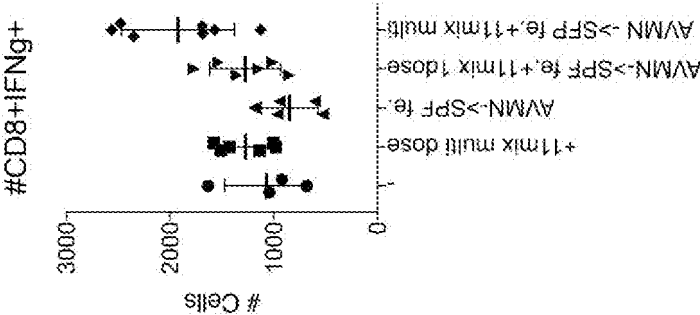


Fig. 41B

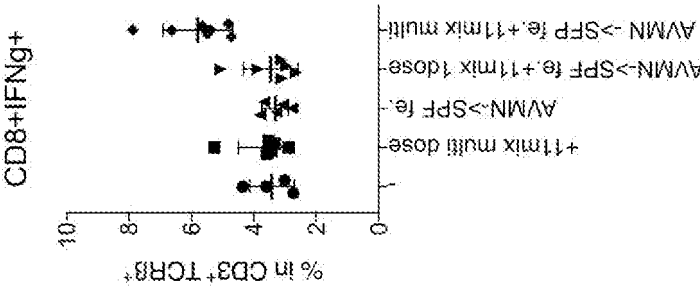


Fig. 41A

[Fig.42A-C]

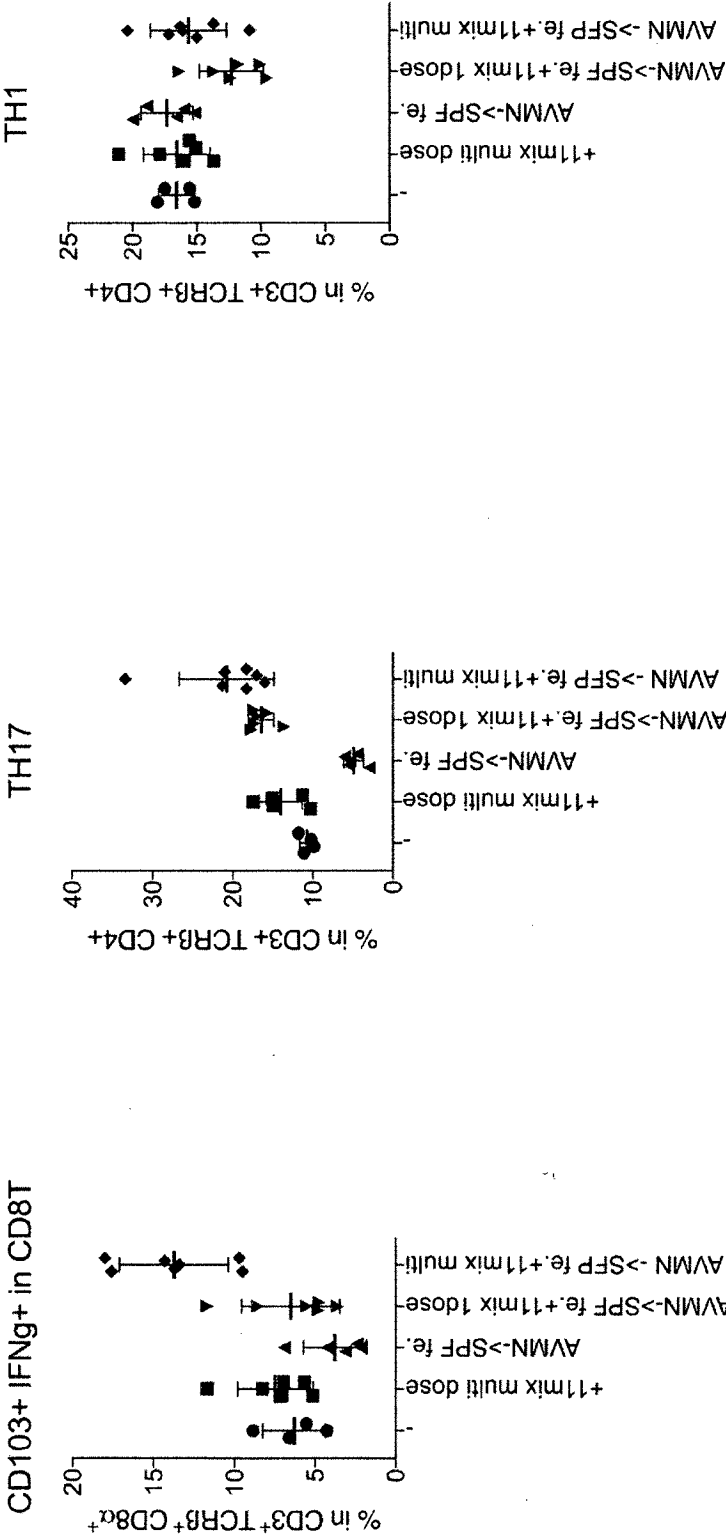


Fig. 42C

Fig. 42B

Fig. 42A

[Fig. 43A-C]

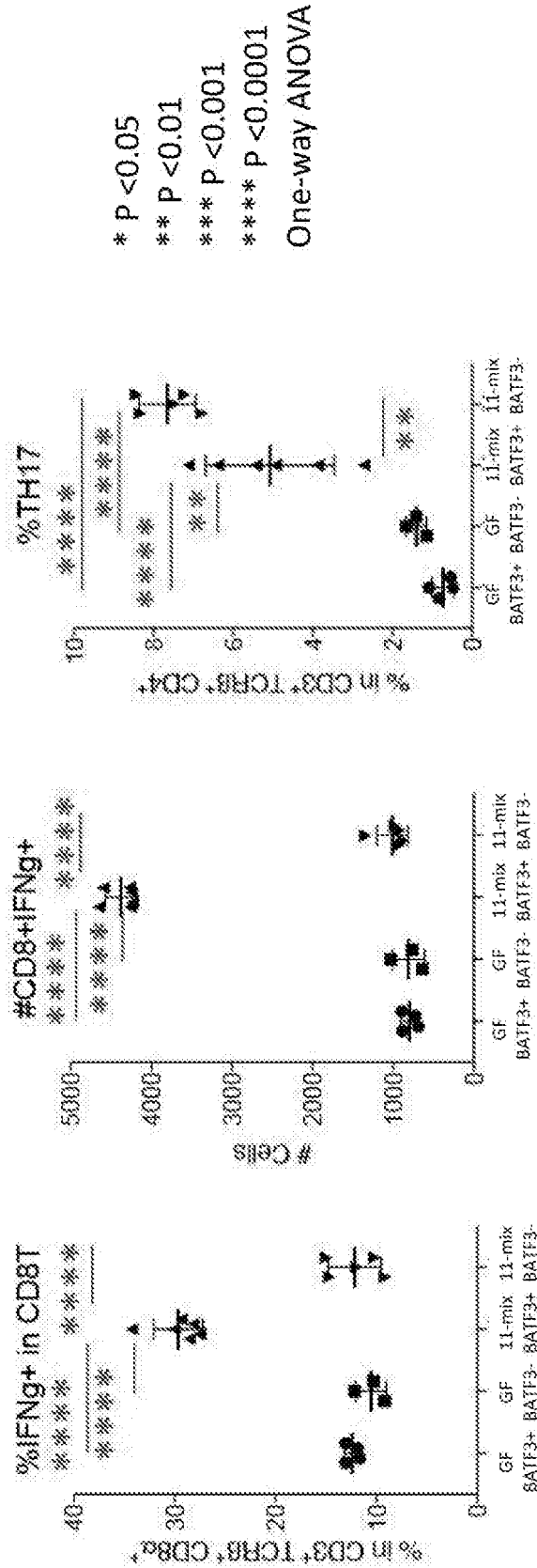


Fig. 43C

Fig. 43B

Fig. 43A

[Fig. 44A-B]

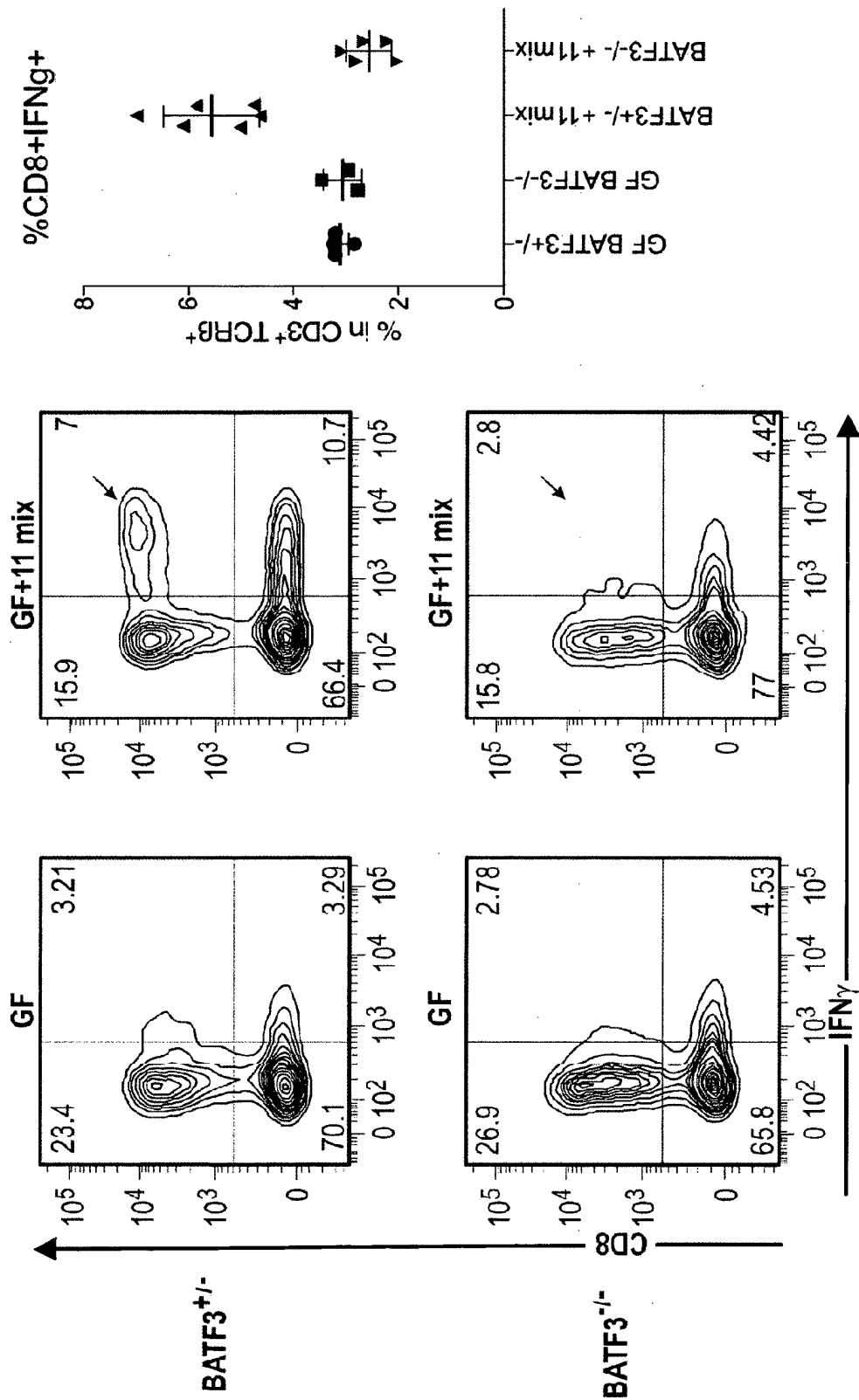


Fig. 44 B

Fig. 44A

[Fig. 45]

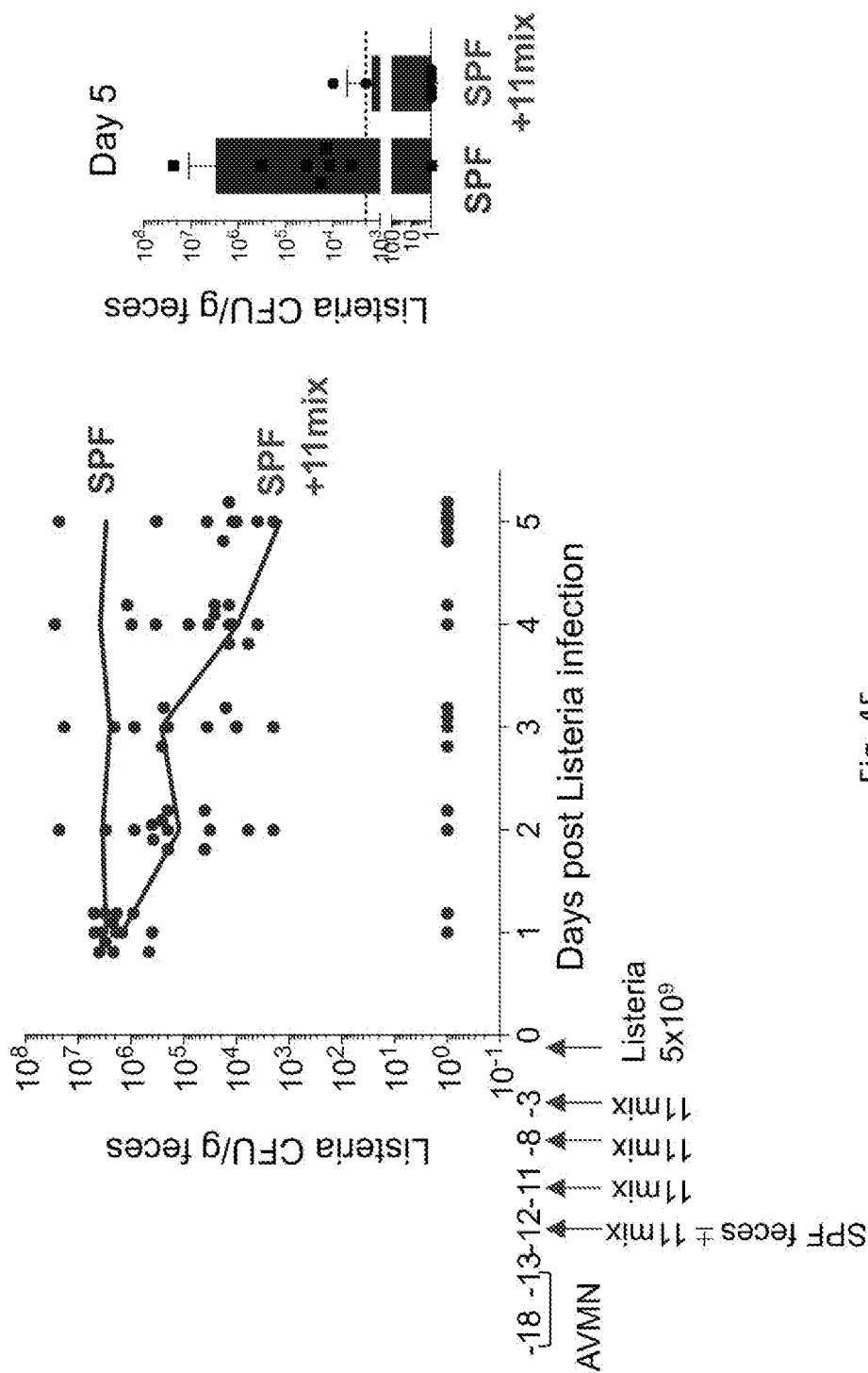
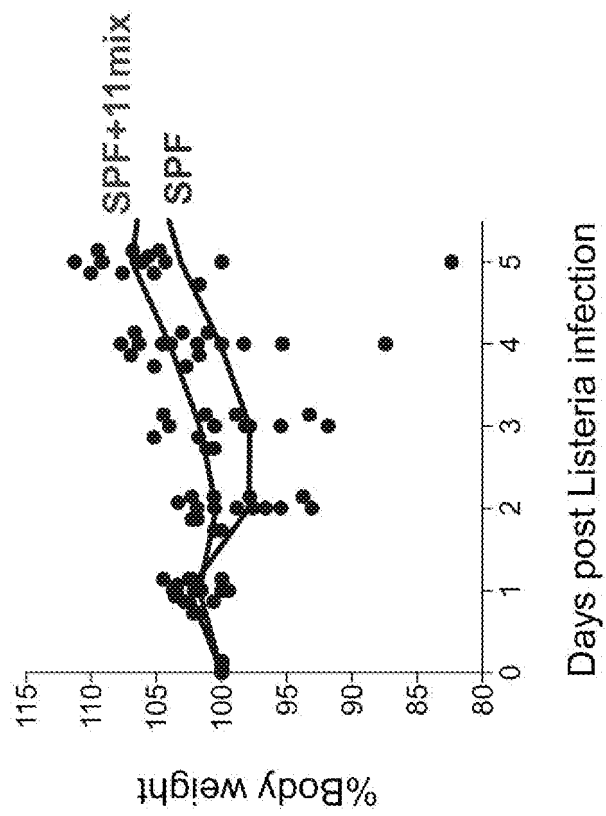


Fig. 45

[Fig. 46]



One mouse in SPF feces group (among 8 mice) died at day 6.
% BW of 11mix group is significantly ($P < 0.05$) higher than the other 2 groups at day 3-5.

Fig. 46

[Fig. 47A-B]

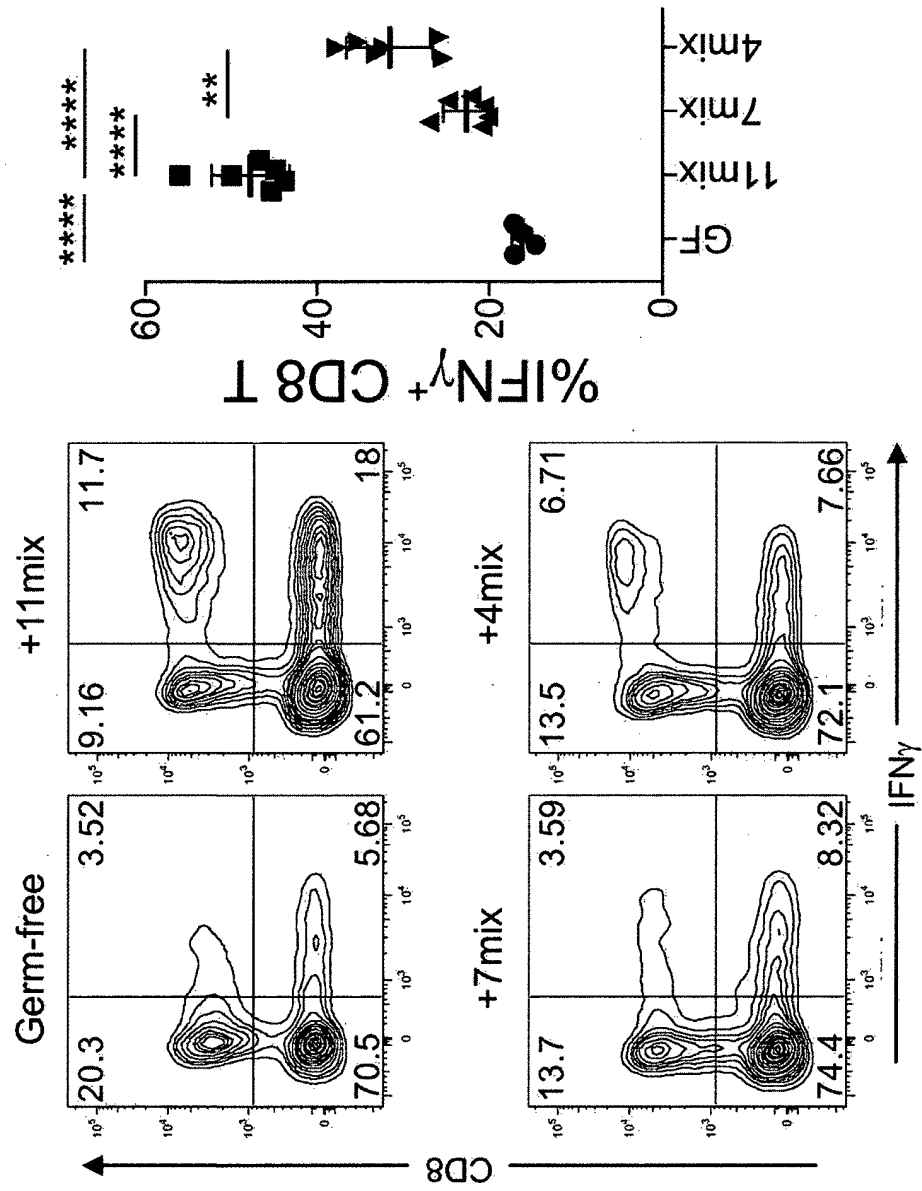


Fig. 47 B

Fig. 47 A

[Fig.48]

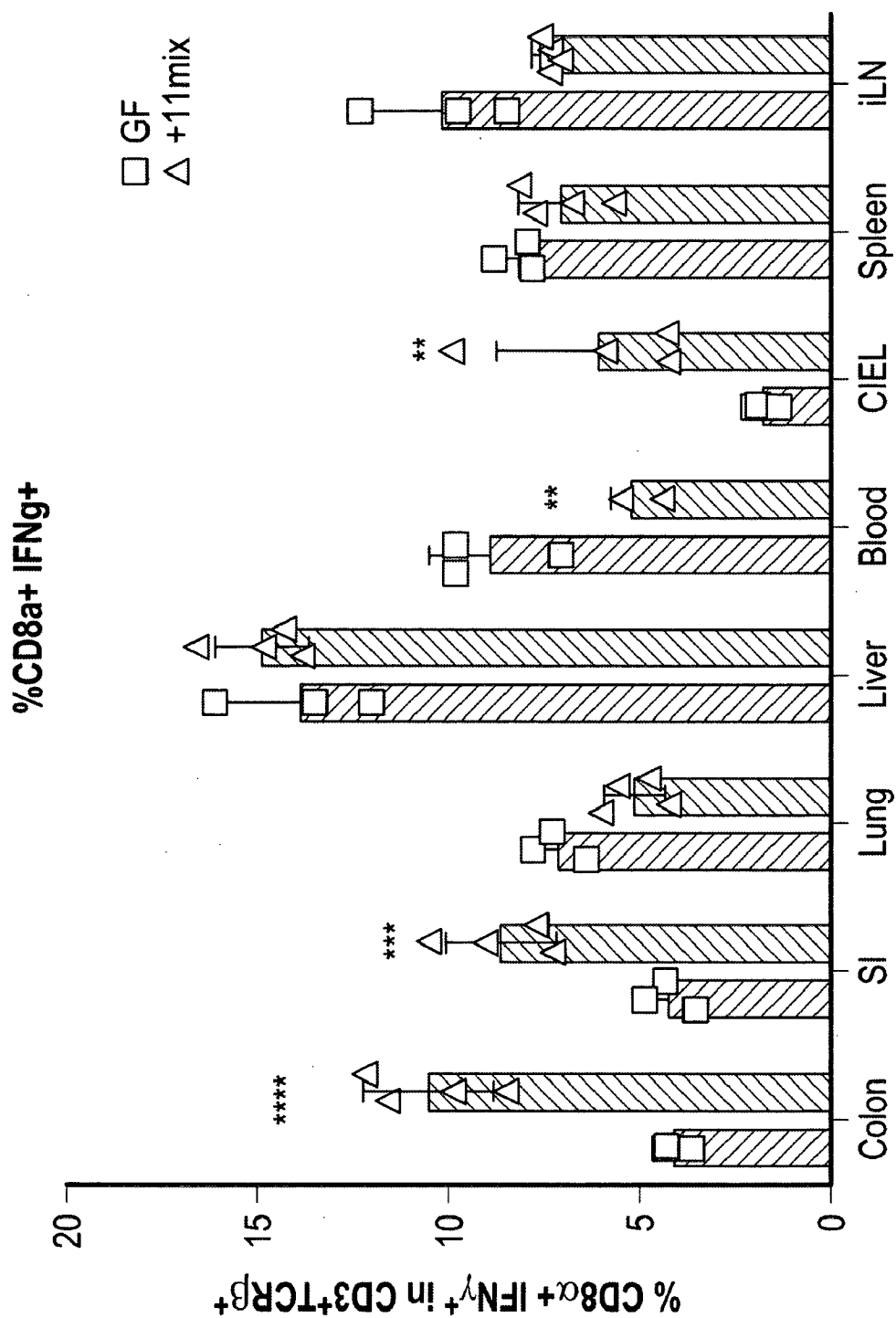
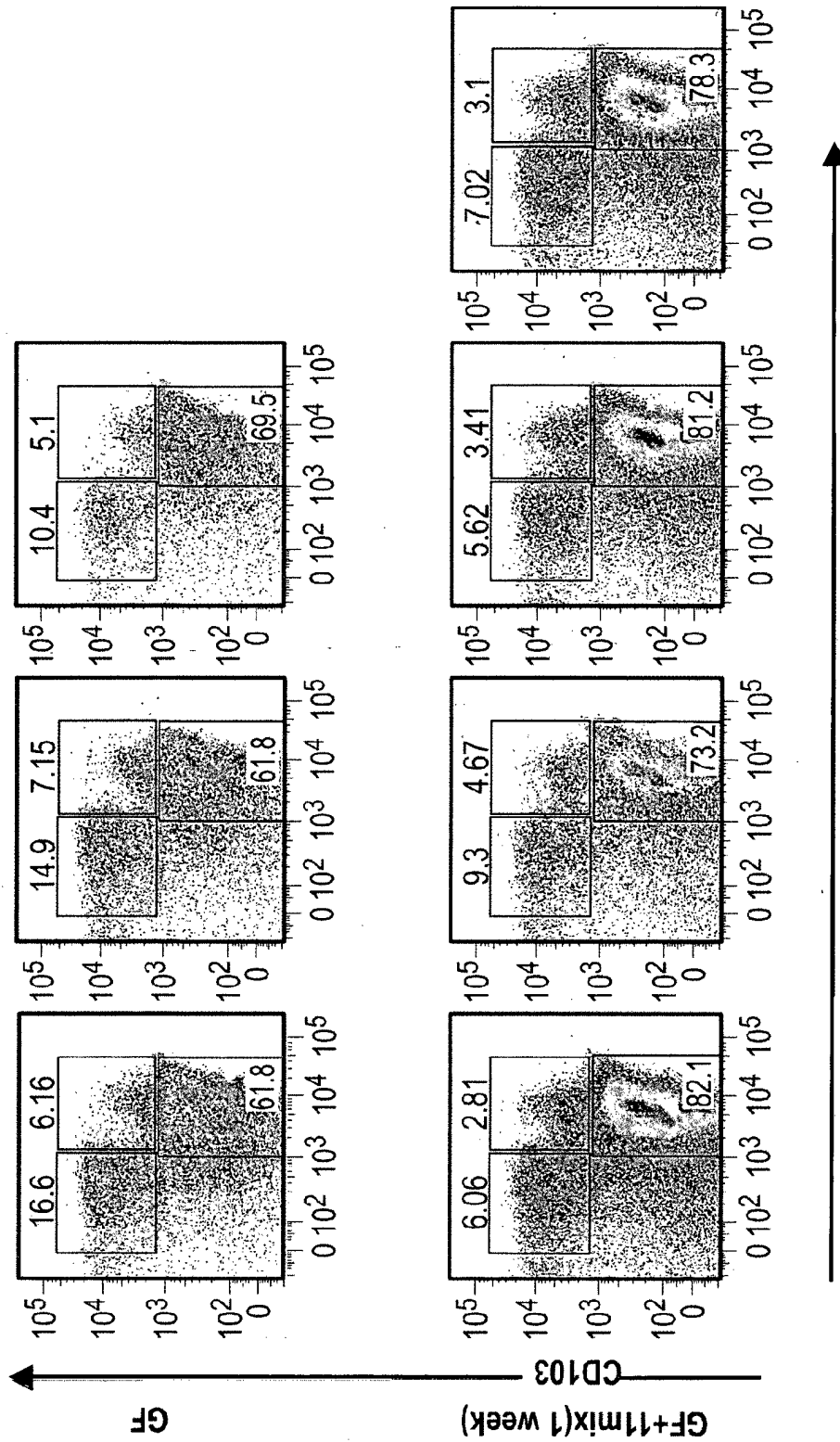


Fig. 48

[Fig.49]



[Fig.50]

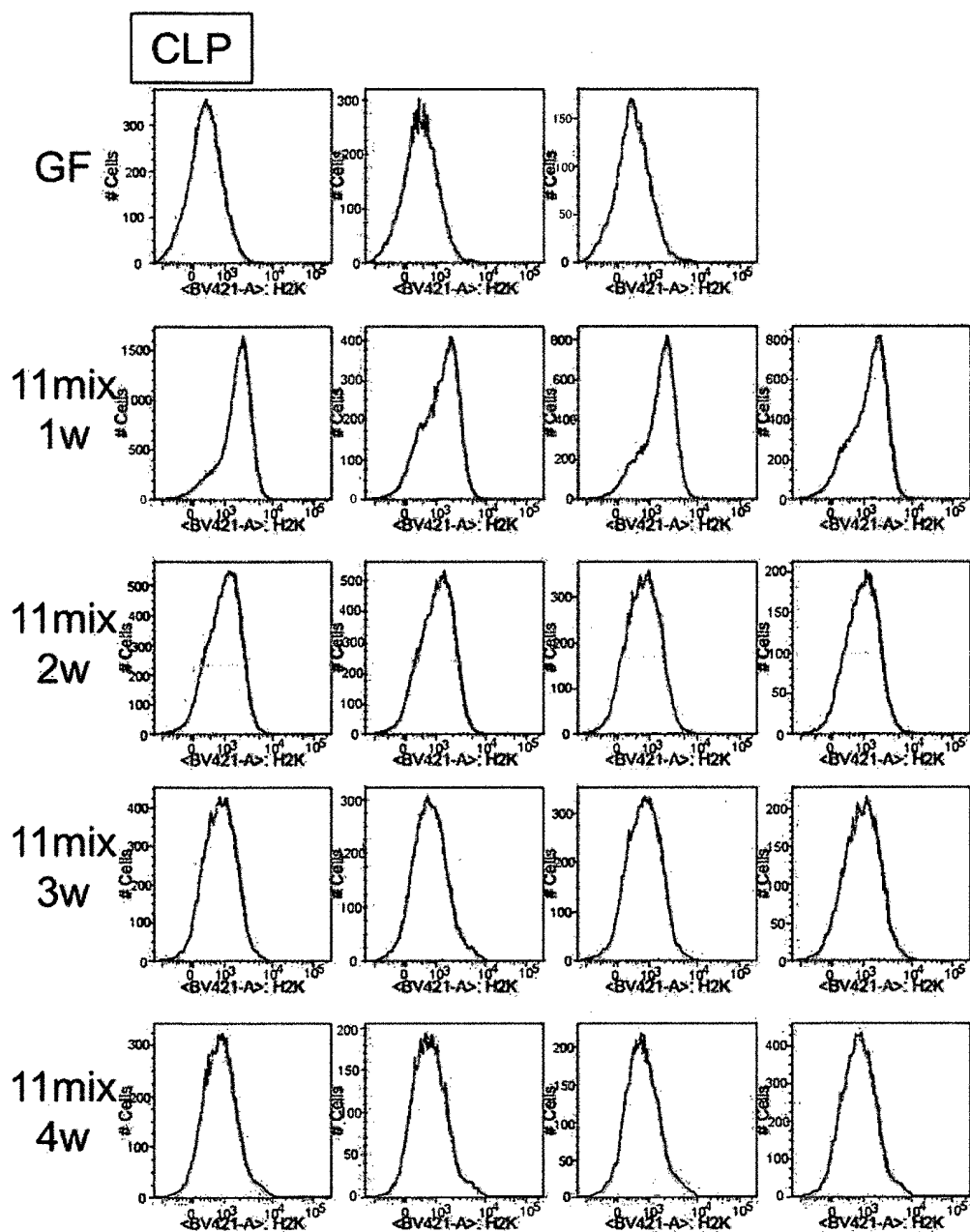
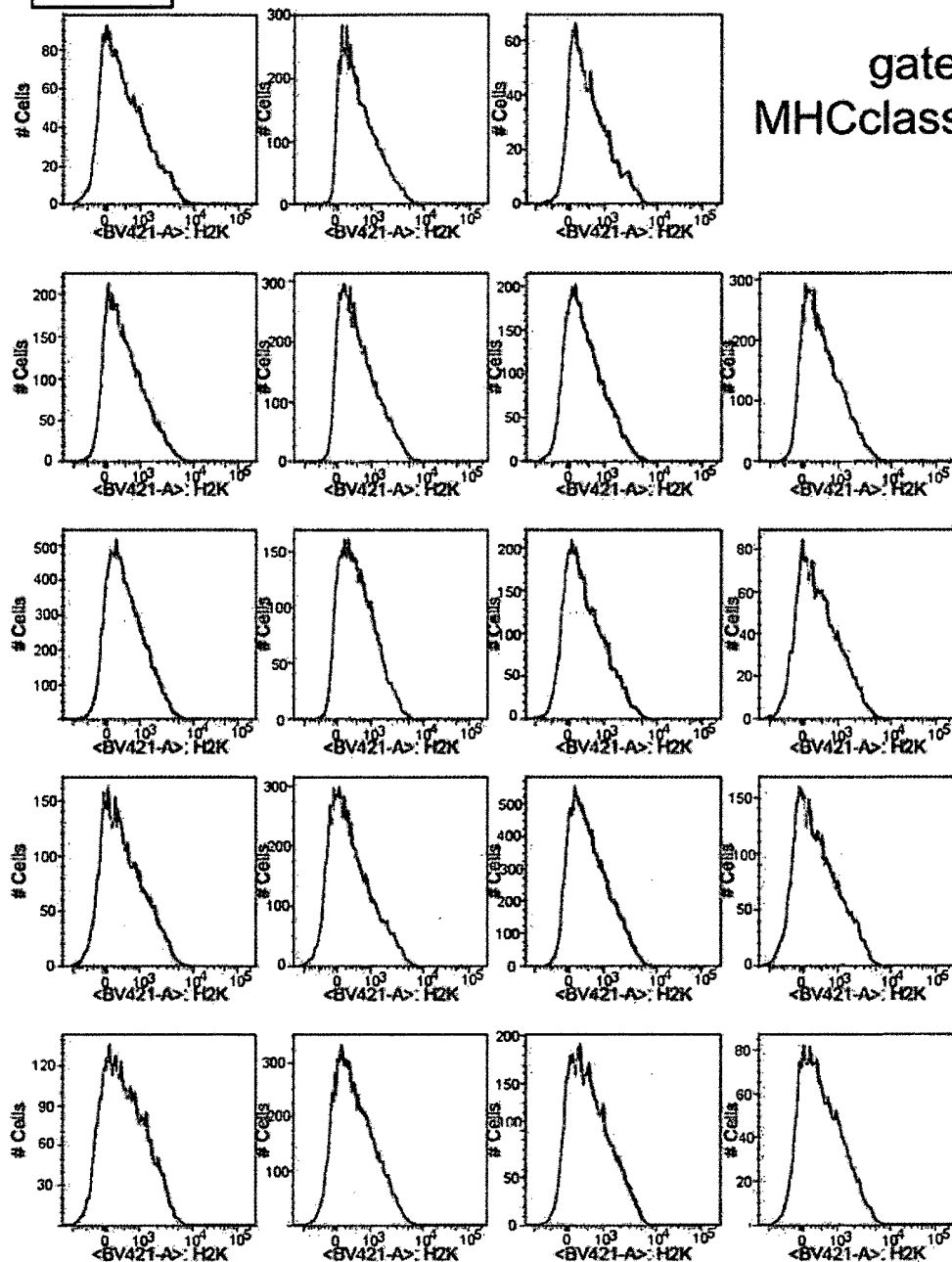


Fig. 50

gated on
MHCclassII⁺ CD11c⁺



[Fig.51]

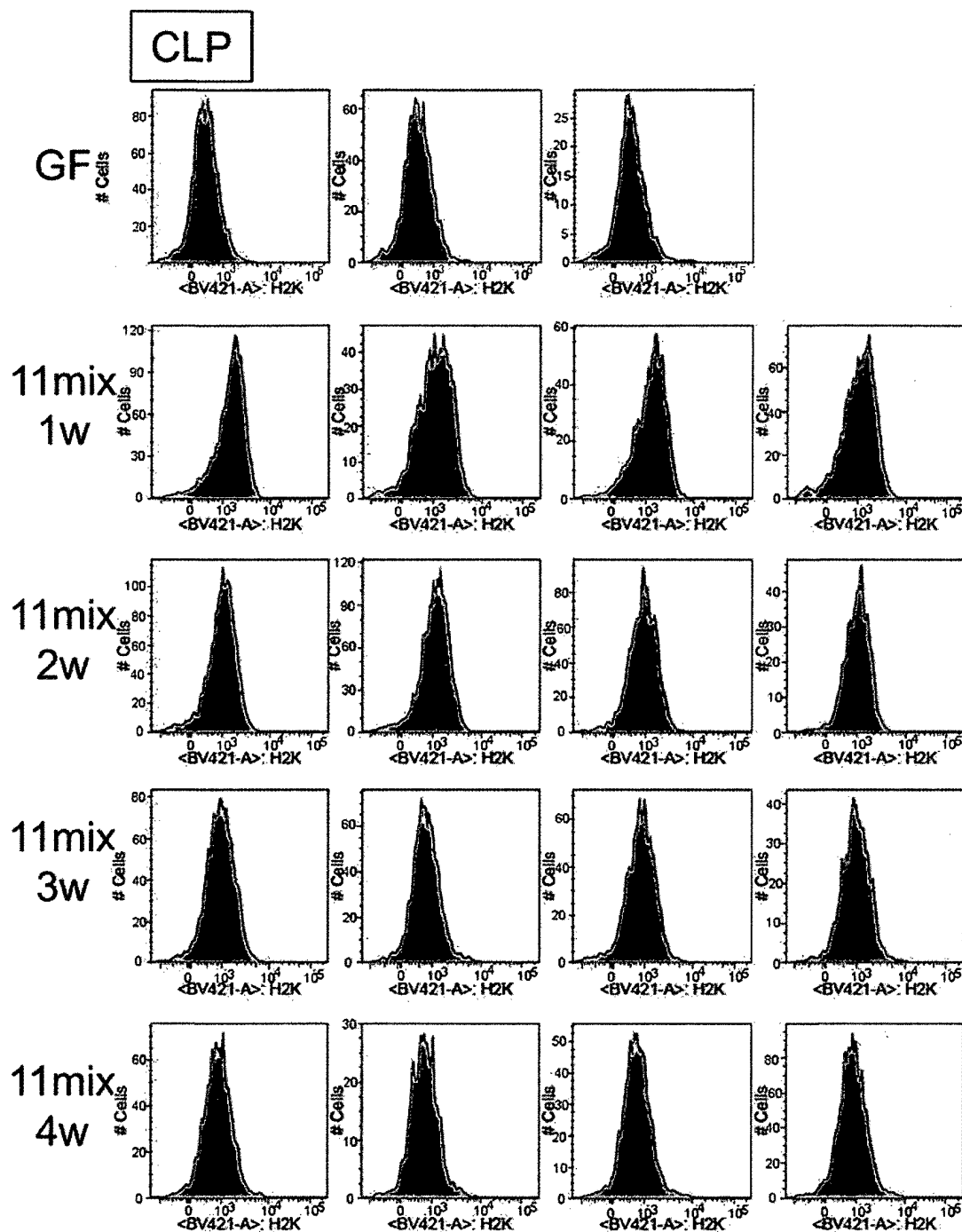
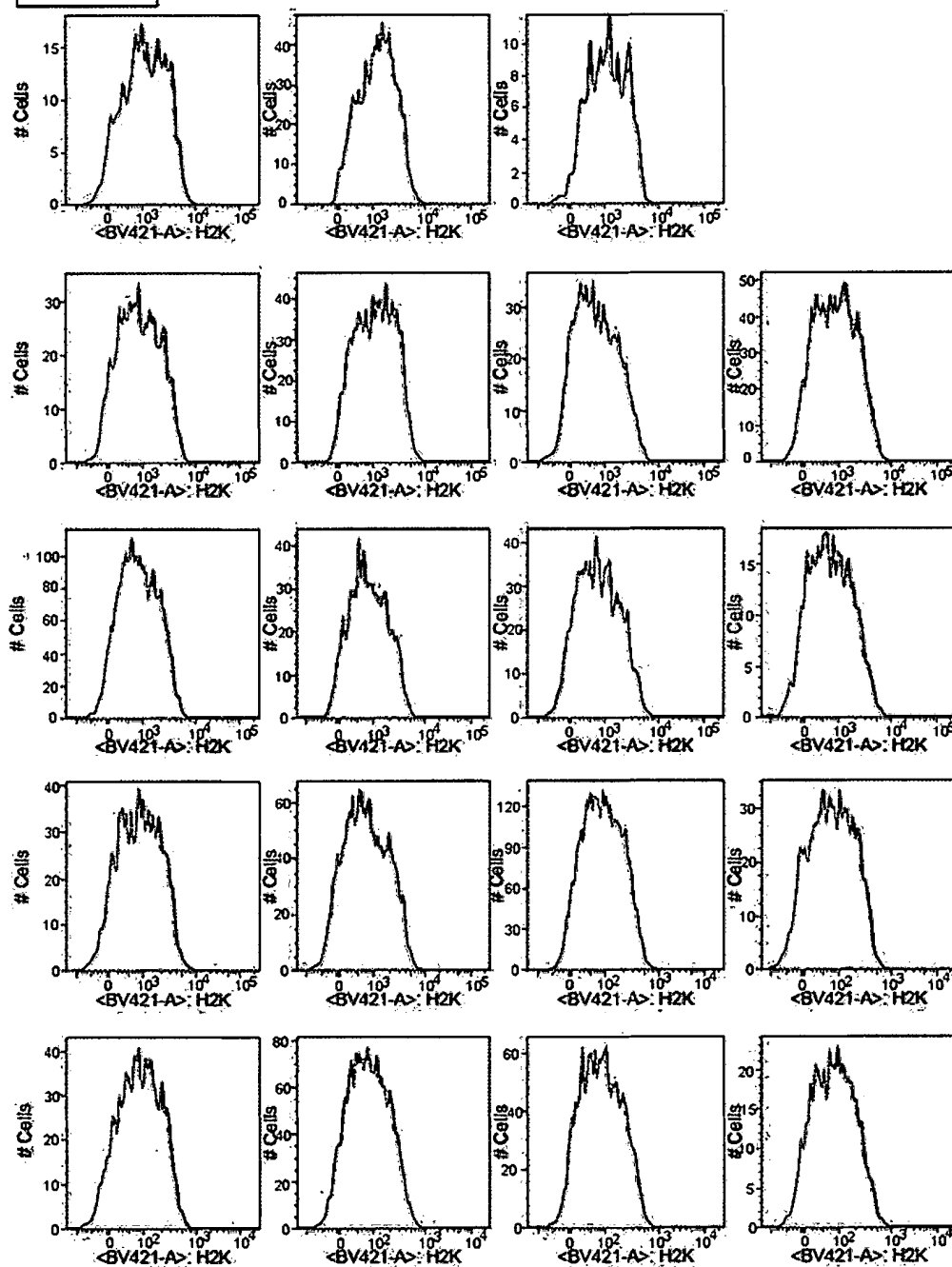


Fig. 51

MLN

gated on MHCclassII+
CD11c+CD103+CD11b-



[Fig. 52]

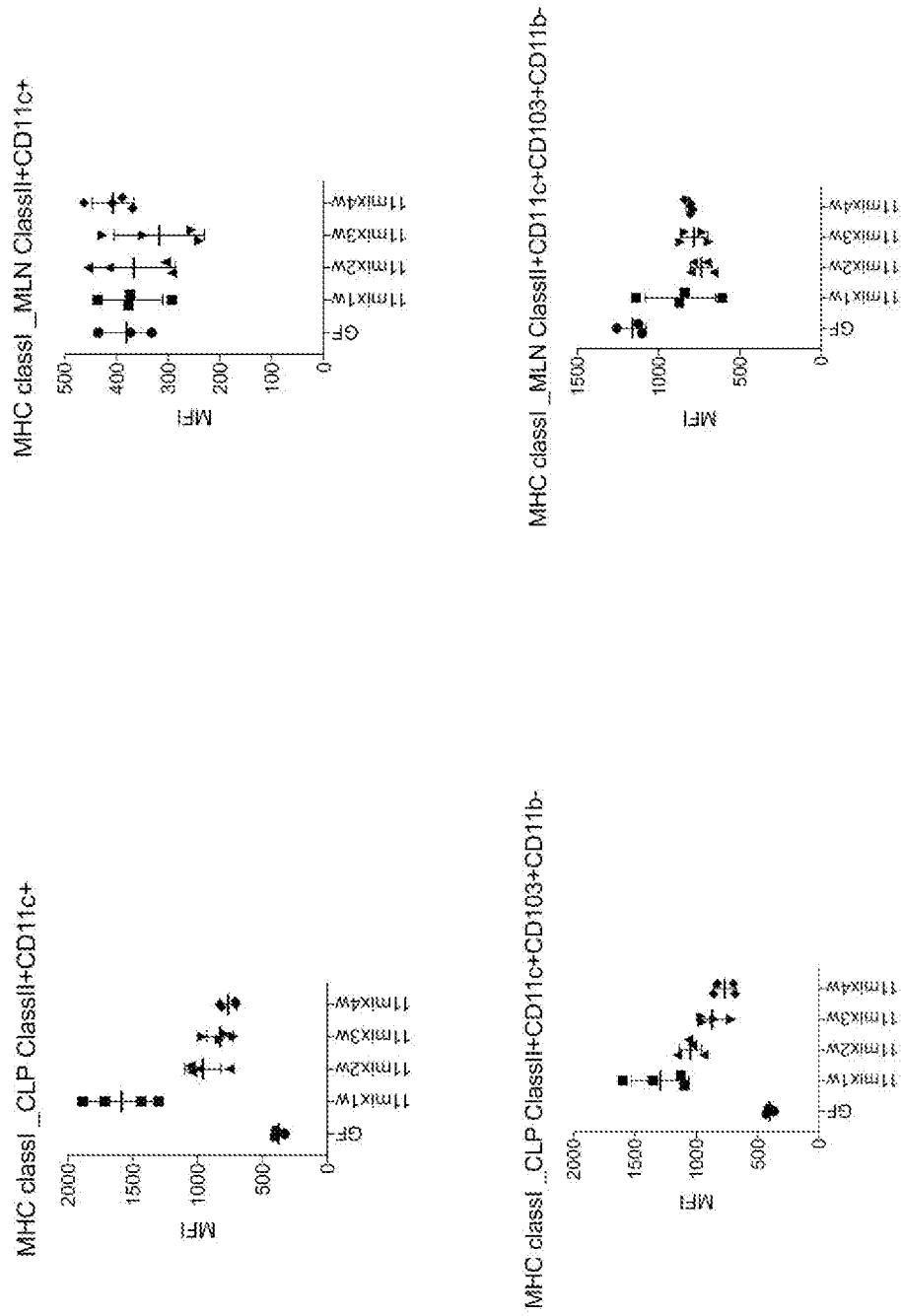


Fig. 52

[Fig.53]

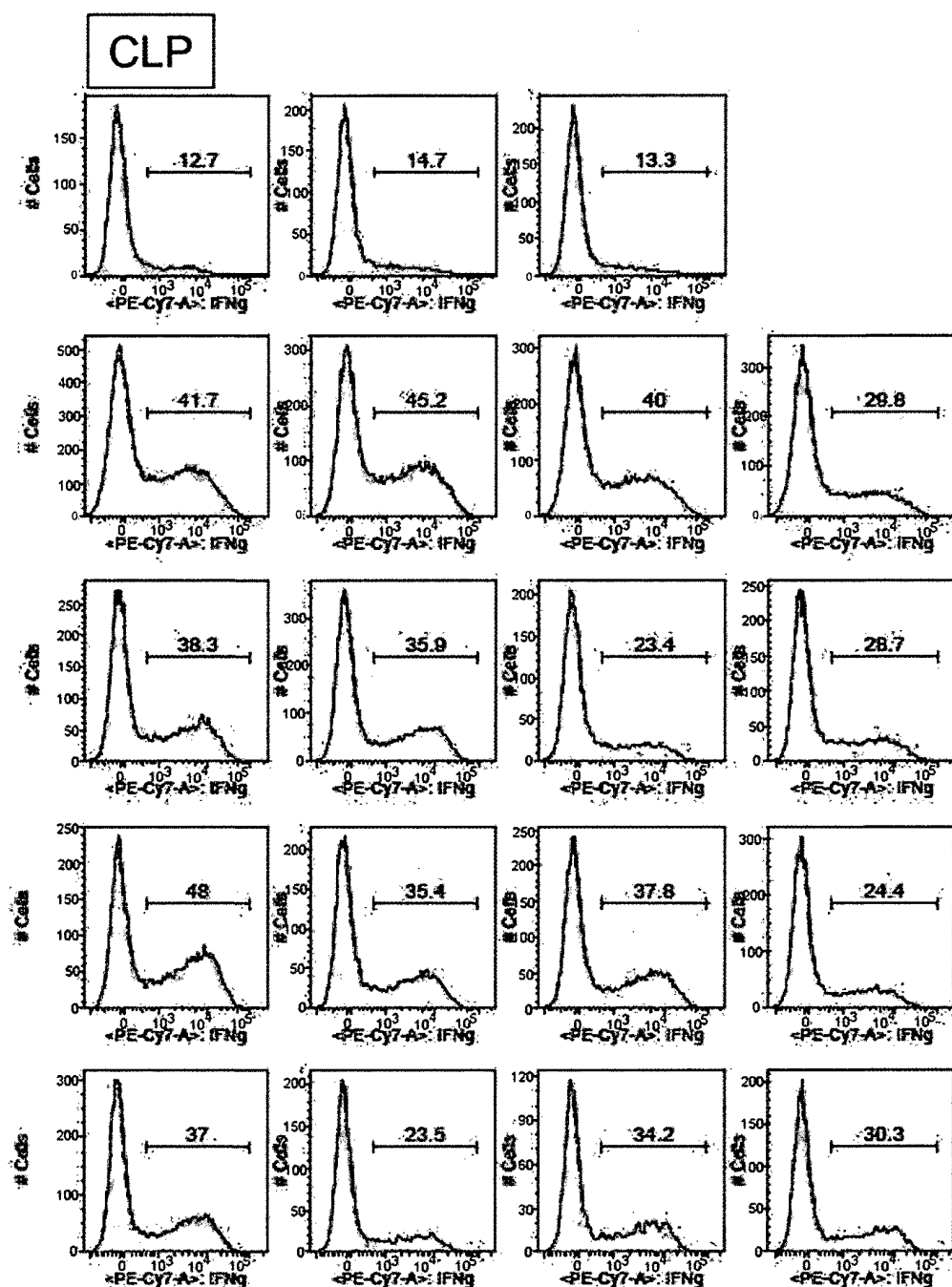
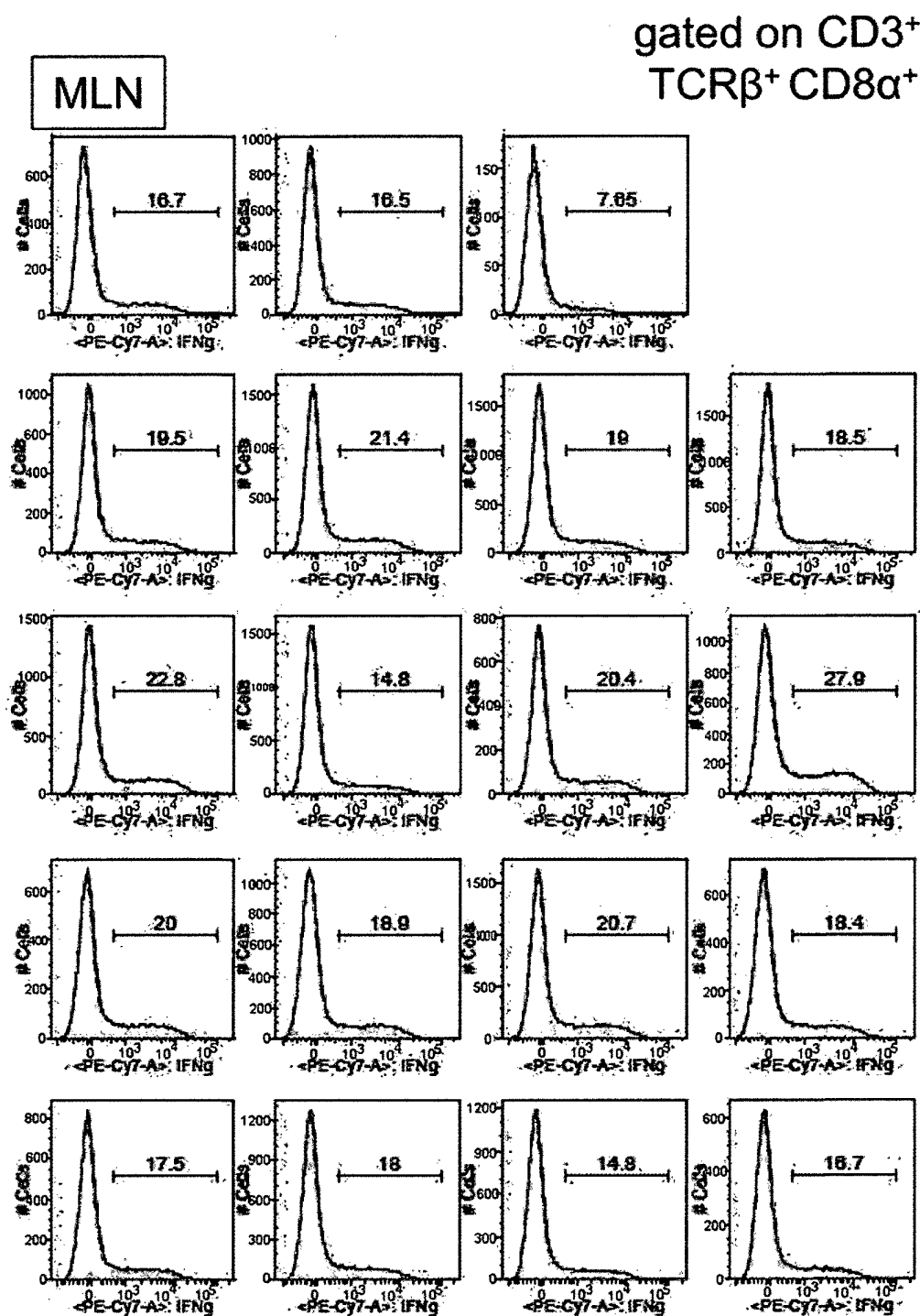


Fig. 53



[Fig. 54]

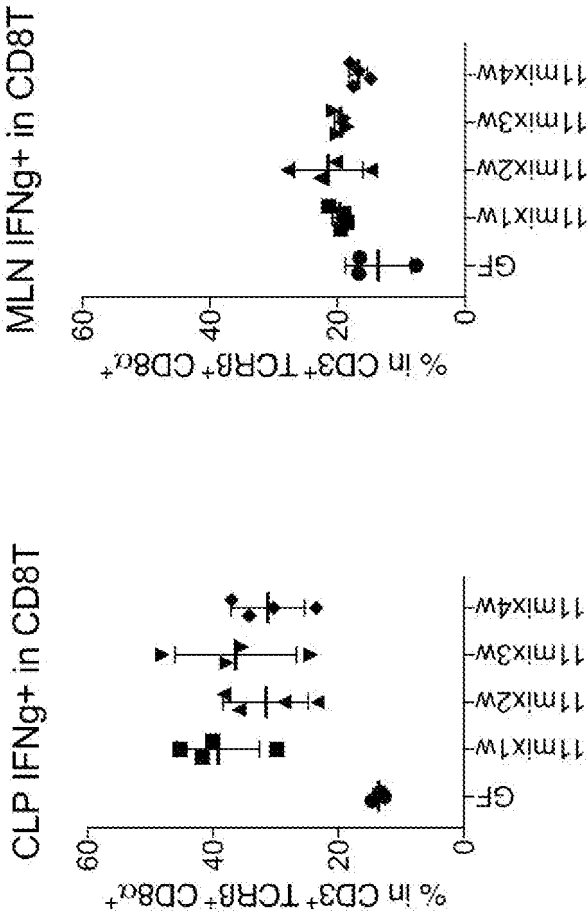


Fig. 54

[Fig. 55]

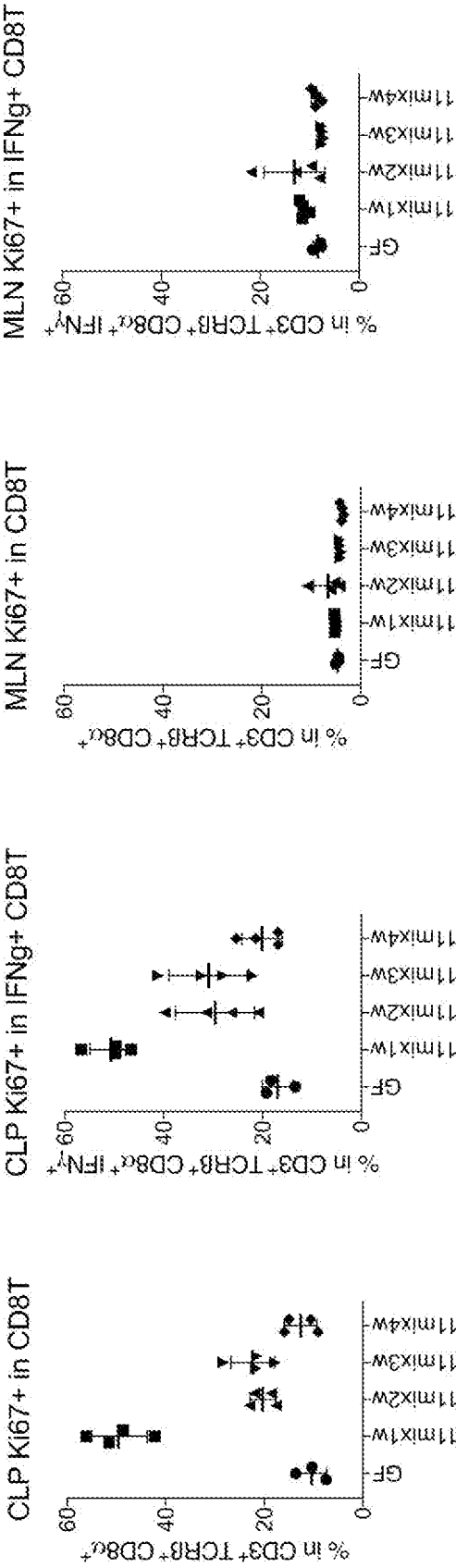


Fig. 55

[Fig.56]

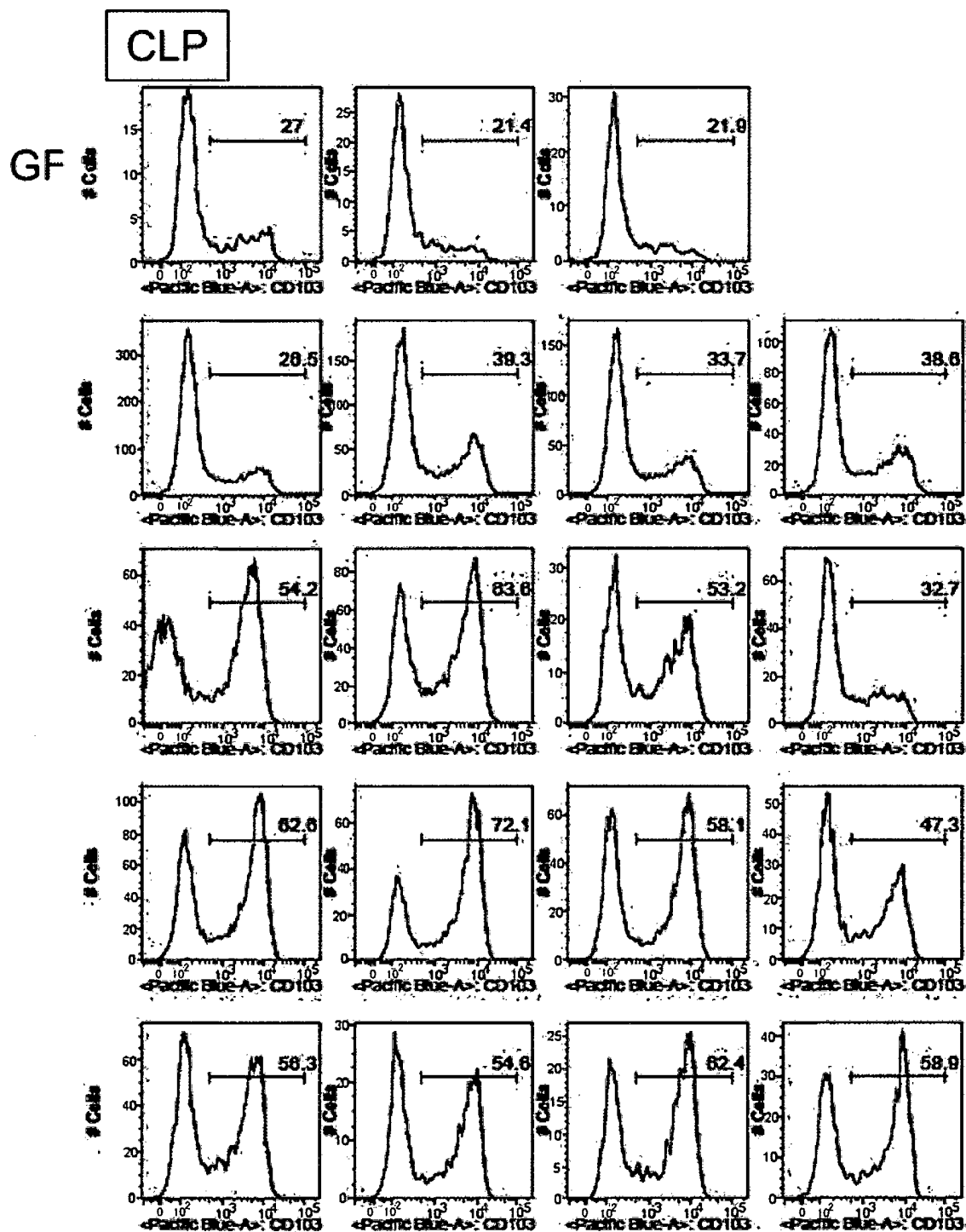
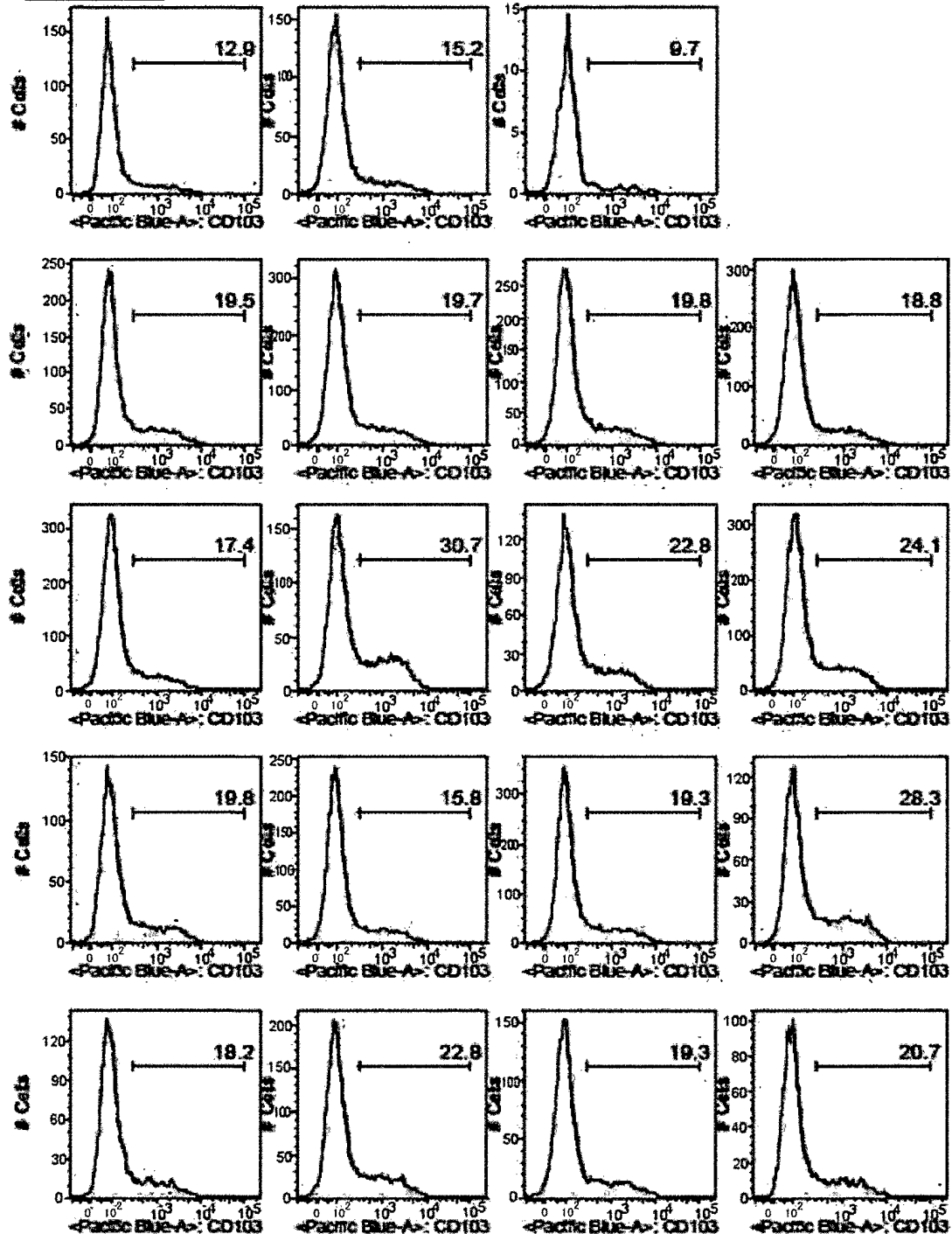


Fig. 56

MLNgated on CD3⁺ TCRβ⁺
CD8α⁺ IFNγ⁺

[Fig. 57]

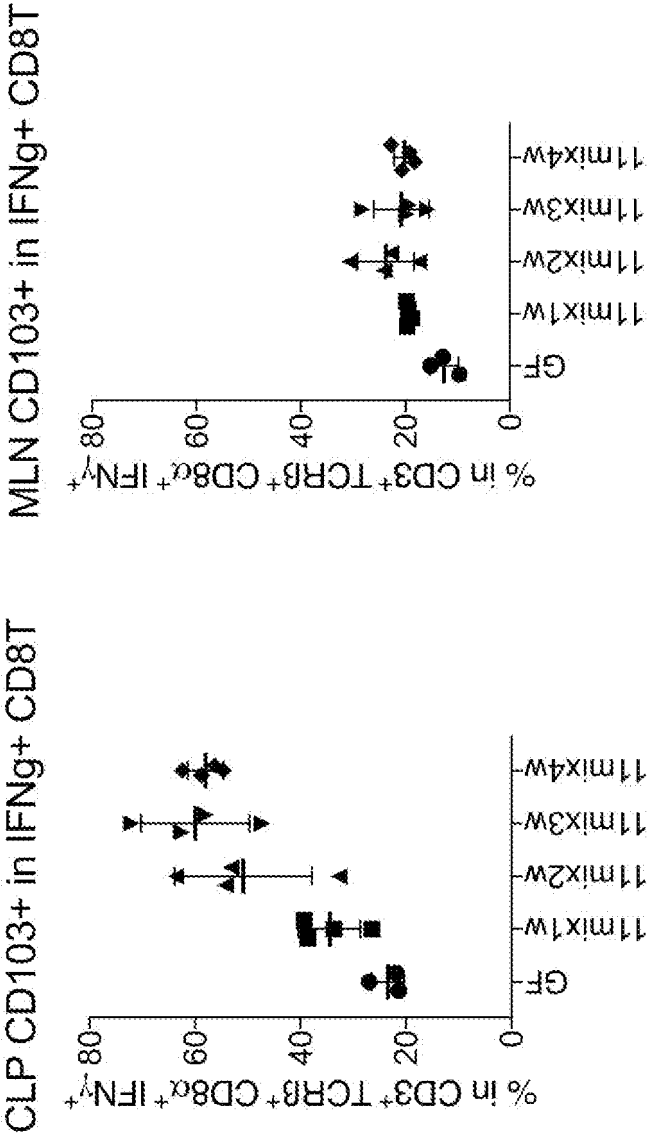


Fig. 57