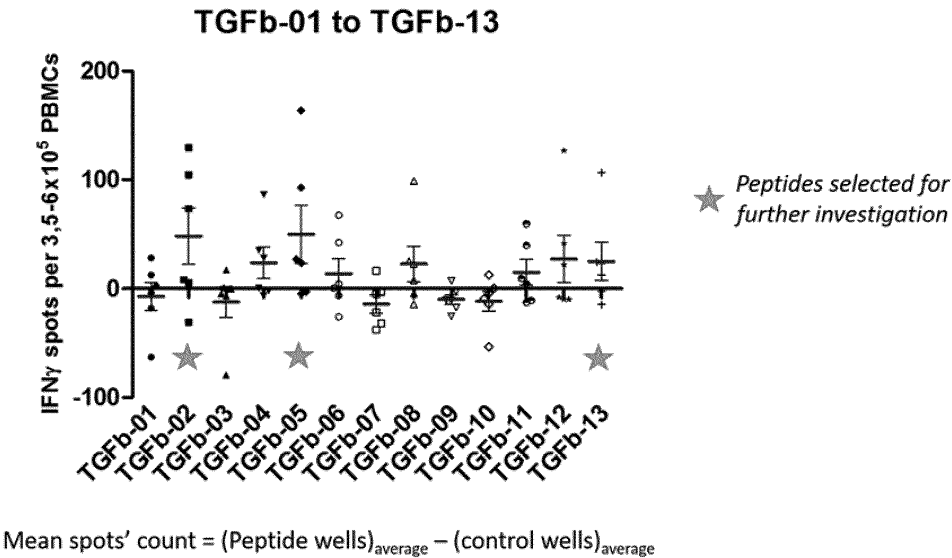


FIGURE 1

A

IFN γ spots count of all 20mers
from 3 Library Screenings (6 healthy subjects) (1)



B

IFN γ spots count of all 20mers from
3 Library Screenings (6 healthy subjects) (2)

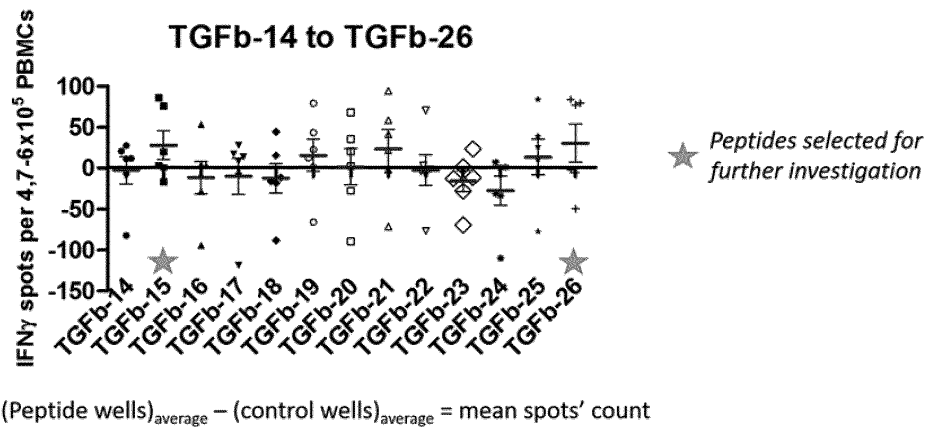
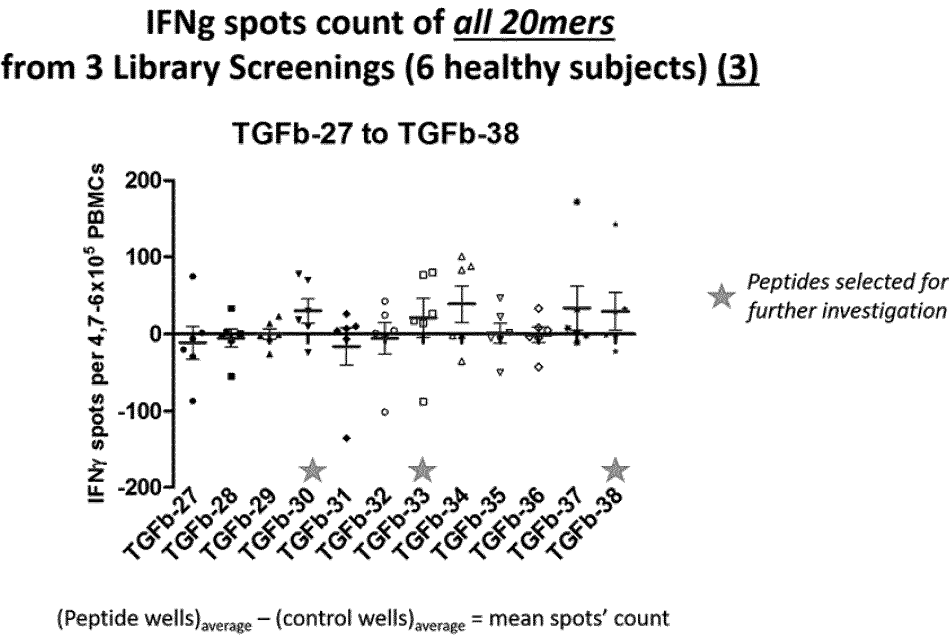


FIGURE 1 (CONT.)

C



D

			Best Peptides	Mean Spots number	Notes
Peptides selected for further investigation ★			TGFb-02	48,17	
			TGFb-05	49,78	
			TGFb-13	24,8	
			TGFb-15	27,94	
			TGFb-26	30,39	
			TGFb-30	28,67	
			TGFb-33	20,89	
			TGFb-38	28,33	
Good peptides but statistically inferior to the 8 first			TGFb-04	23,5	No DFRx2 response (two DFR responses)
			TGFb-12	27	No DFR response
			TGFb-34	38,67	3 DFR responses
			TGFb-37	31	1 DFRx2 response

FIGURE 1 (CONT.)

E

10	20	TGFb-02	30	40	TGFb-05	50
MPPSGLRLLL	LLLPLLWLLV	LTPGRPAAGL	STCKTIDMEL	VKRKRIEAIR		
60	70	80	90	100		
GQILSKRLRLA	SPPSQGEVPP	GPLPEAVLAL	YNSTRDRVAG	ESAEPEPEPE		
110	120	130	TGFb-13	140	TGFb-15	150
ADYYAKEVTR	VLMVETHNEI	YDKFKQSTHS	IYMFFNTSEL	REAVPEPVLL		
160	170	180	190	200		
SRAELRLLRL	KLKVEQHVEL	YQKYSNNSWR	YLSNRLLAPS	DSPEWLSFDV		
210	220	230	240	250		
TGVVRQWLSR	GGEIEGFRLS	AHCSCDSRDN	TLQVDINGFT	TGRRGDLATI		
260	TGFb-26	270	280	290	TGFb-30	300
HGMNRPFLLL	MATPLERAQH	LQSSRHRRAL	DTNYCFSSTE	KNCCVRQLYI		
310	320	330	TGFb-33	340	350	
DFRKDLGWKW	IHEPKGYHAN	FCLGPCPYIW	SLDTQYSKVL	ALYNQHNPGA		
360	370	380	TGFb-38	390		
SAAPCCVPQA	LEPLPIVYYV	GRKPKVEQLS	NMIVRSCKCS			

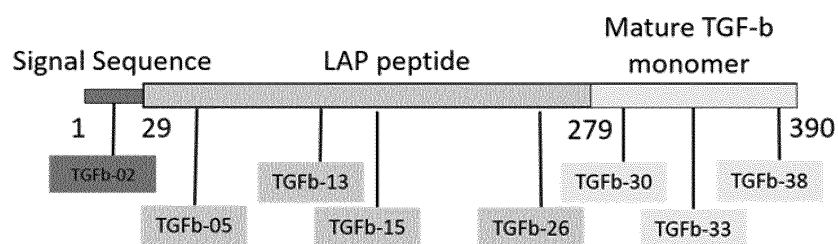


FIGURE 2

A

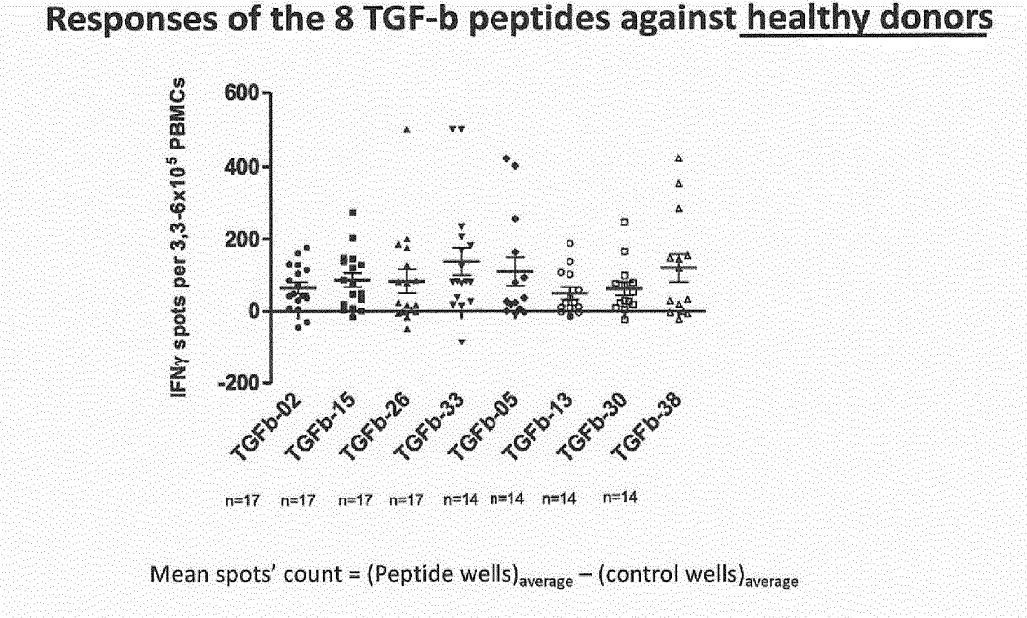


FIGURE 2B

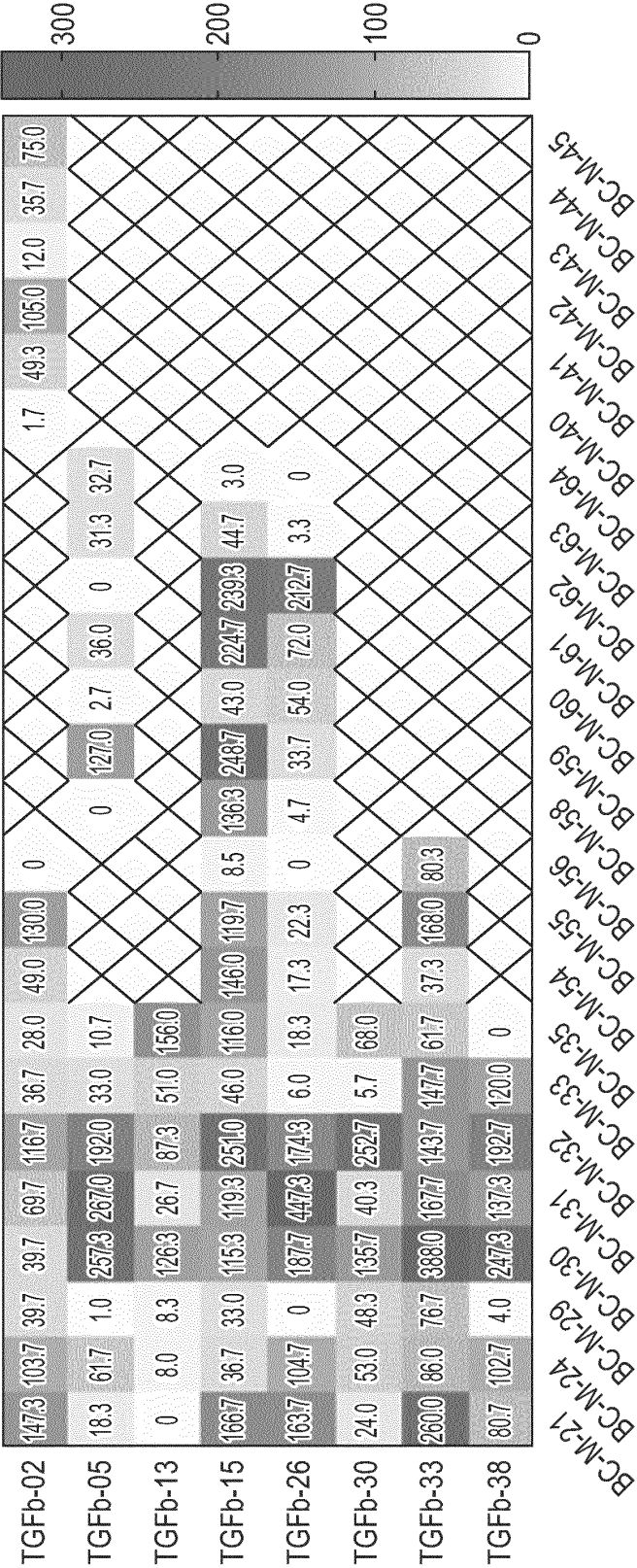


FIGURE 2B (CONT.)

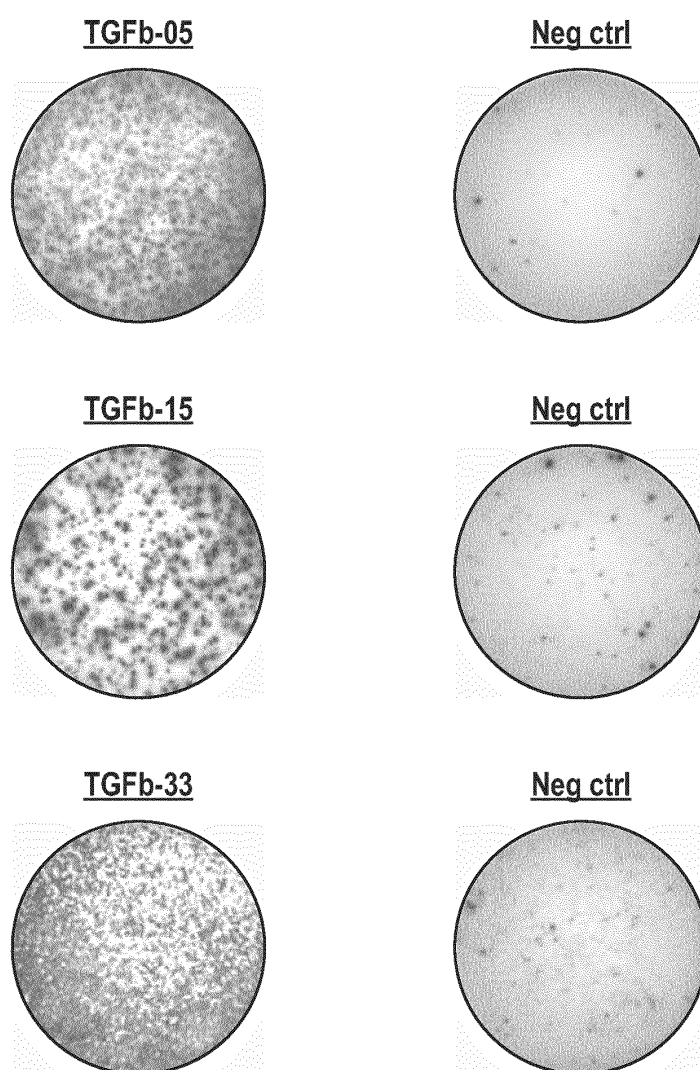


FIGURE 3

A

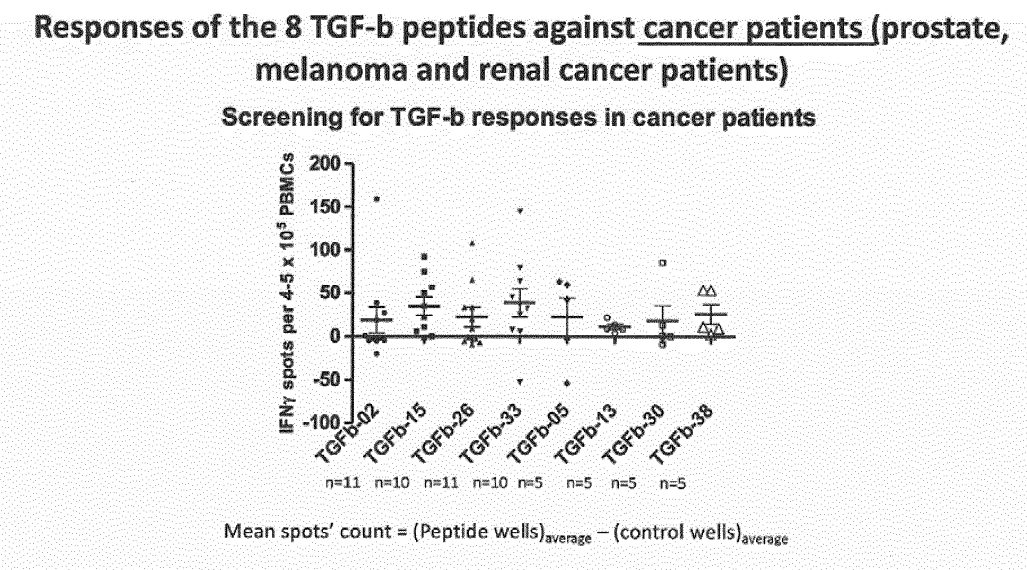
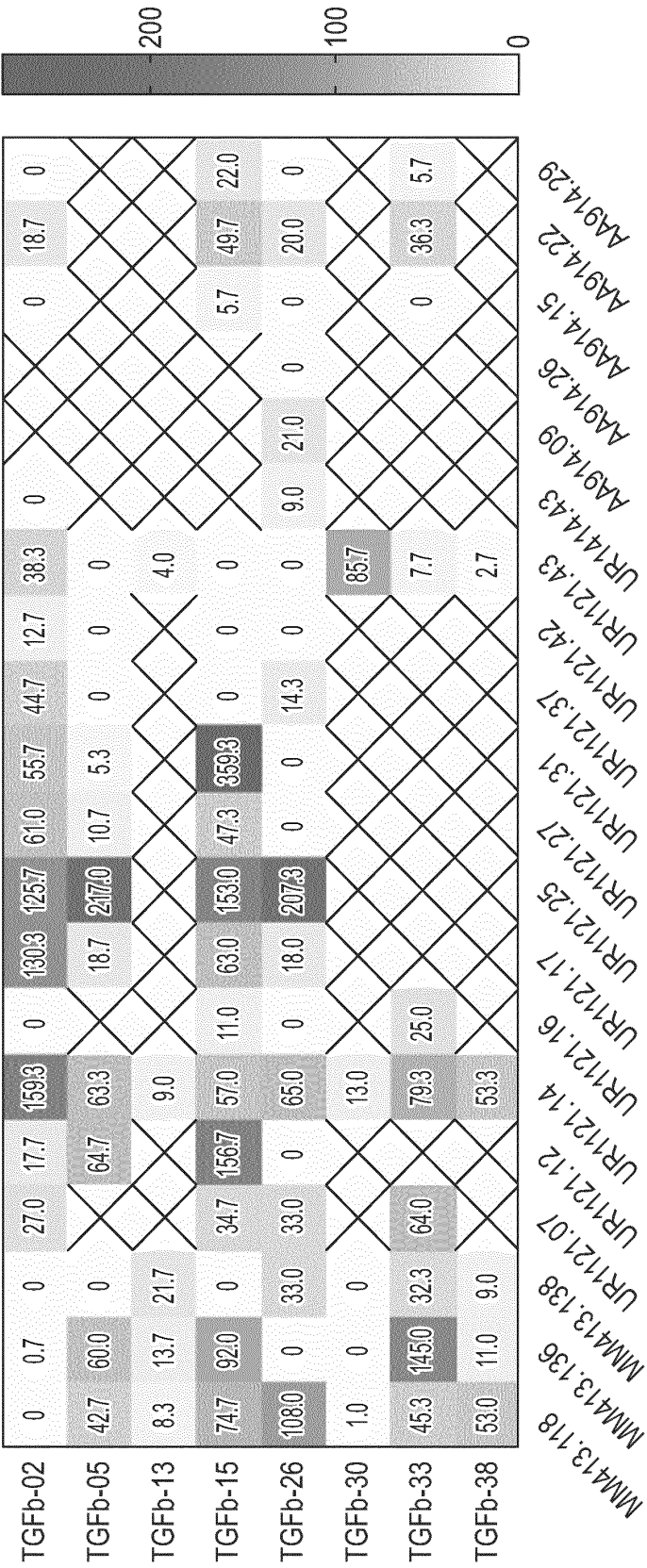


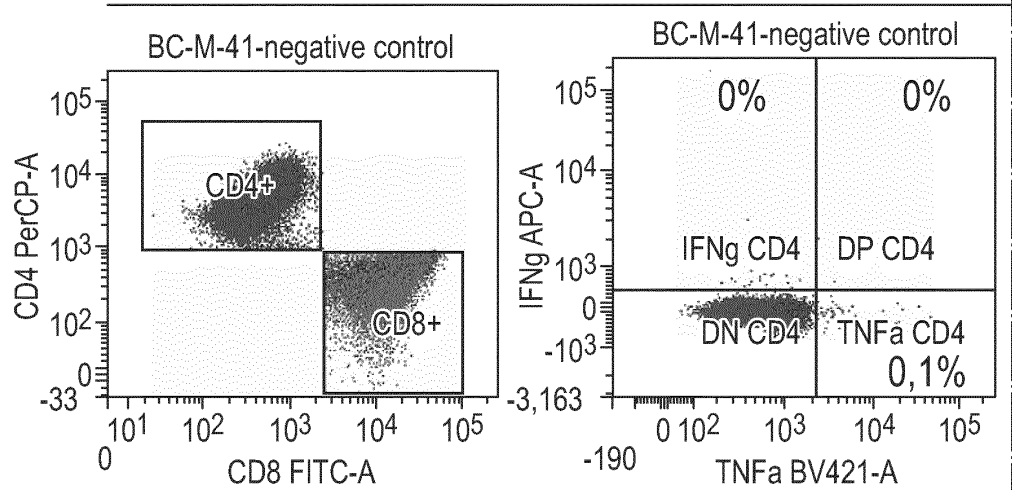
FIGURE 3B



Cytokine analysis of TGFbeta reactive culture by intracellular cytokine staining. Example shown here from a healthy subject (BC-M-41)

BC-M-41 vs. TGFb-02

Negative control



Response against TGFb-02

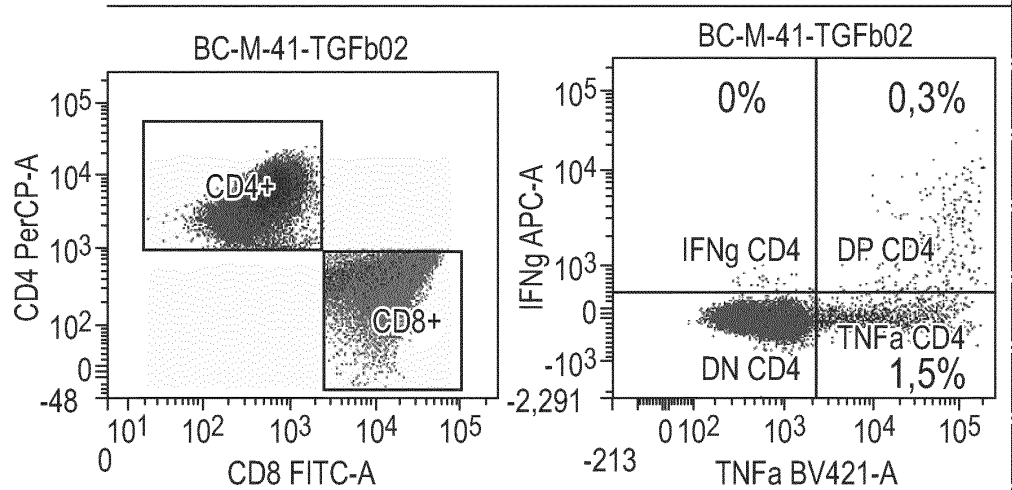


FIGURE 4

FIGURE 4 (CONT I.)

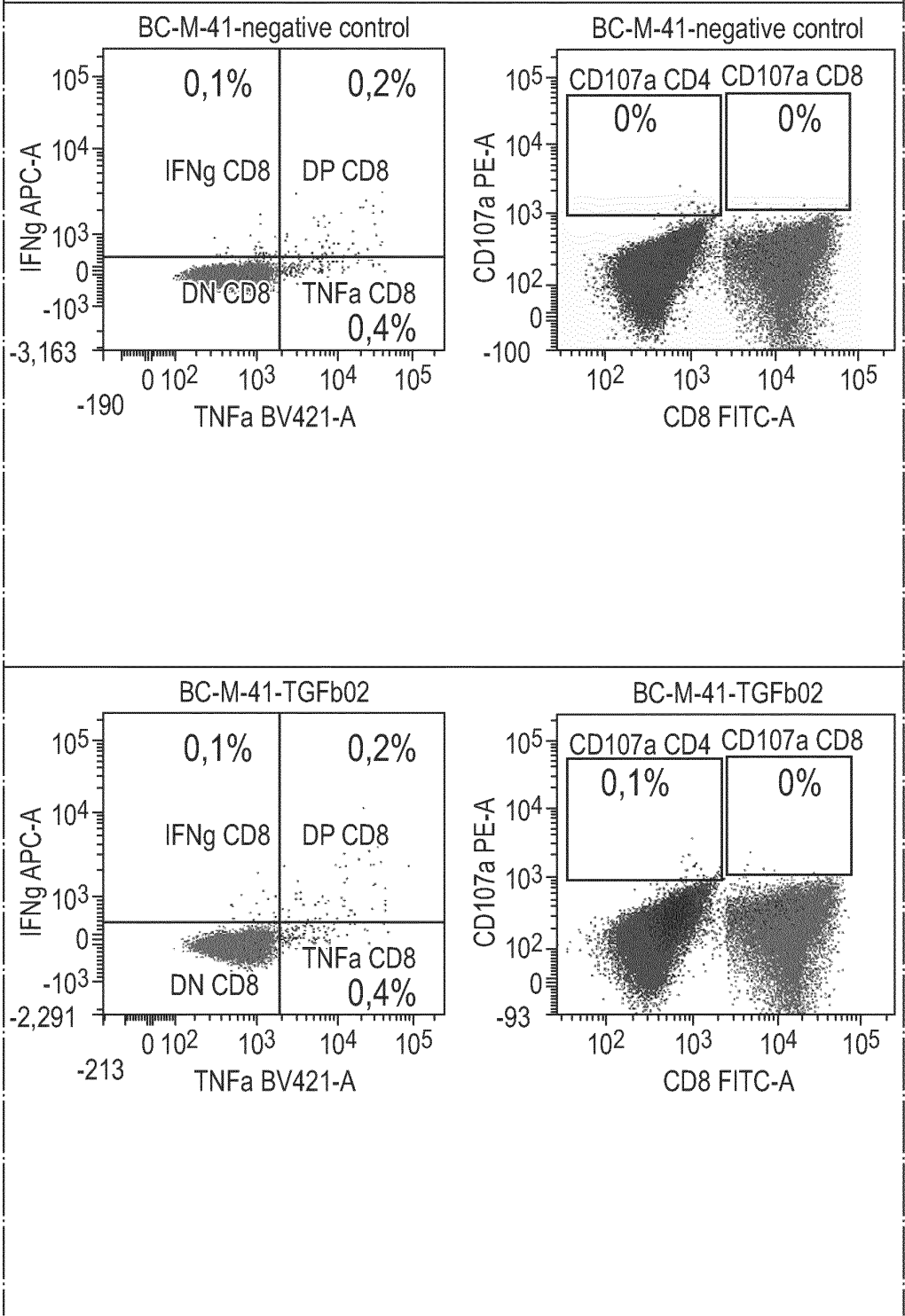


FIGURE 4 (CONT II.)

Tube: negative control

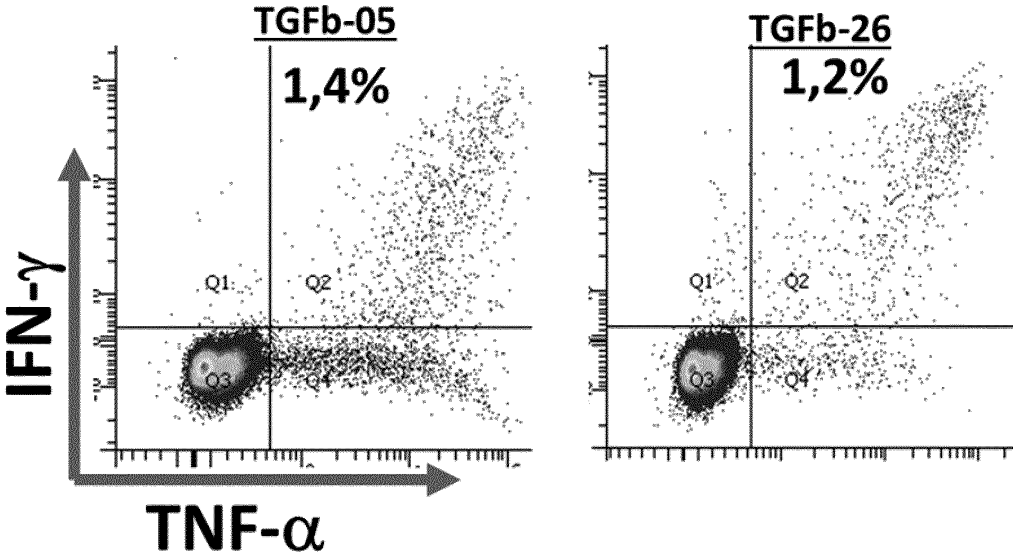
Population	#Events	%Parent	%Total
■ All Events	147,224	####	100.0
■ PBMC	124,780	84.8	84.8
■ Singlets	123,106	98.7	83.6
■ Live	122,805	99.8	83.4
■ CD3+	105,129	85.8	71.5
■ CD4+	75,129	71.3	51.5
■ IFNγ CD4	22	0.0	0.0
■ DP CD4	2	0.0	0.0
☒ DN CD4	75,059	99.9	51.0
■ TNFα CD4	46	0.1	0.0
■ CD107a CD4	31	0.0	0.0
■ CD8+	25,224	23.9	17.1
■ IFNγ CD8	34	0.1	0.0
■ DP CD8	50	0.2	0.0
☒ DN CD8	25,028	99.2	17.0
■ TNFα CD8	112	0.4	0.1
■ CD107a CD8	11	0.0	0.0

Tube: TGFb02

Population	#Events	%Parent	%Total
■ All Events	163,576	####	100.0
■ PBMC	126,201	77.2	77.2
■ Singlets	123,953	98.2	75.8
■ Live	123,498	99.6	75.5
■ CD3+	104,668	84.8	64.0
■ CD4+	73,372	70.1	44.9
■ IFNγ CD4	26	0.0	0.0
■ DP CD4	242	0.3	0.1
☒ DN CD4	72,031	98.2	44.0
■ TNFα CD4	1,073	1.5	0.7
■ CD107a CD4	45	0.1	0.0
■ CD8+	25,788	24.6	15.8
■ IFNγ CD8	19	0.1	0.0
■ DP CD8	55	0.2	0.0
☒ DN CD8	25,599	99.3	15.6
■ TNFα CD8	115	0.4	0.1
■ CD107a CD8	10	0.0	0.0

FIGURE 5

A



B

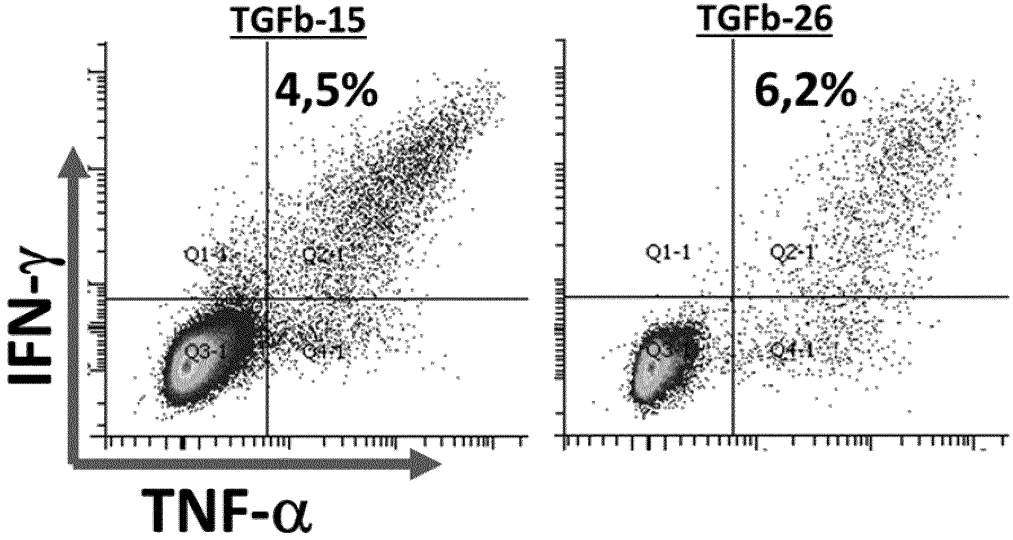


FIGURE 6

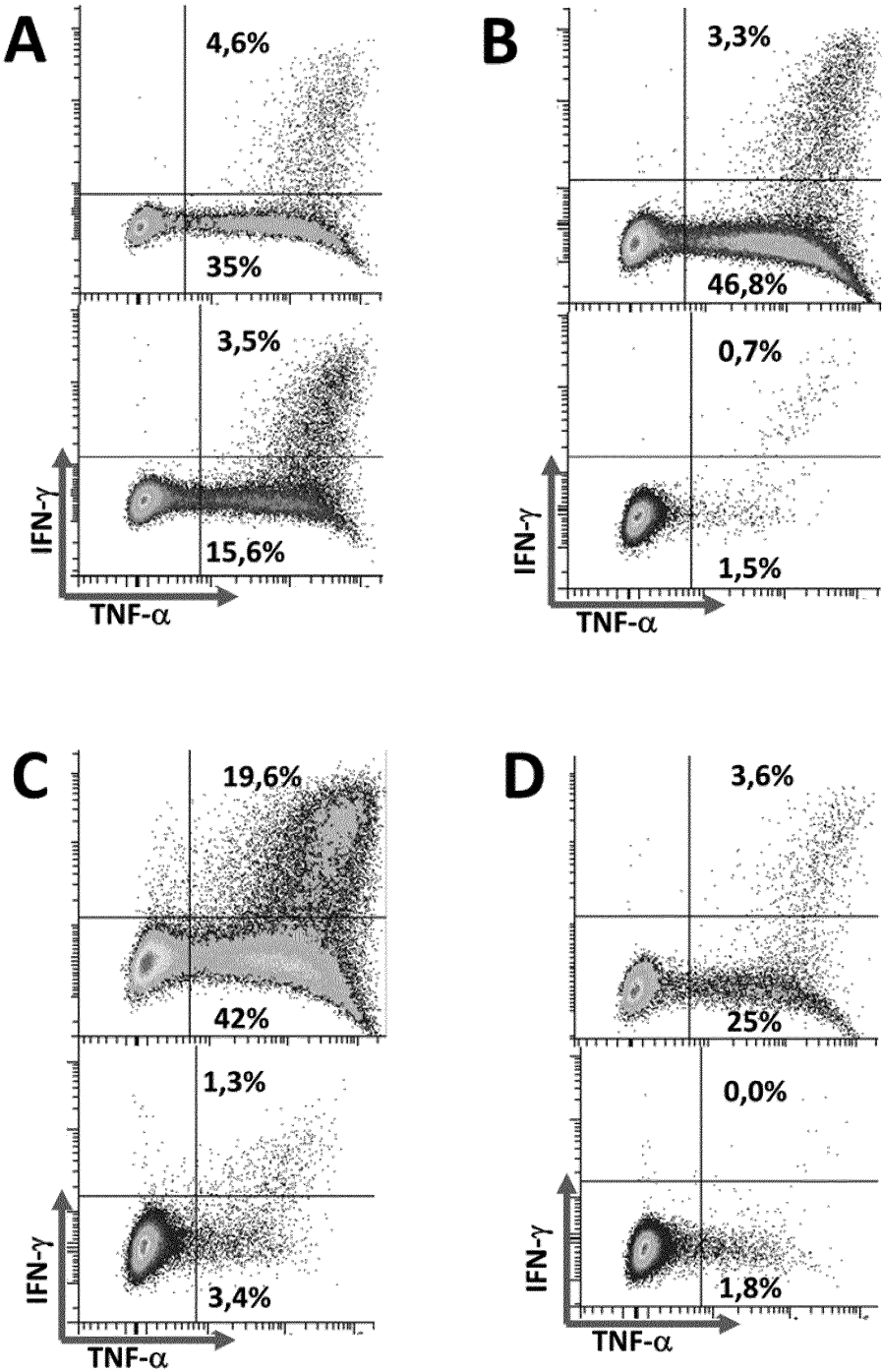
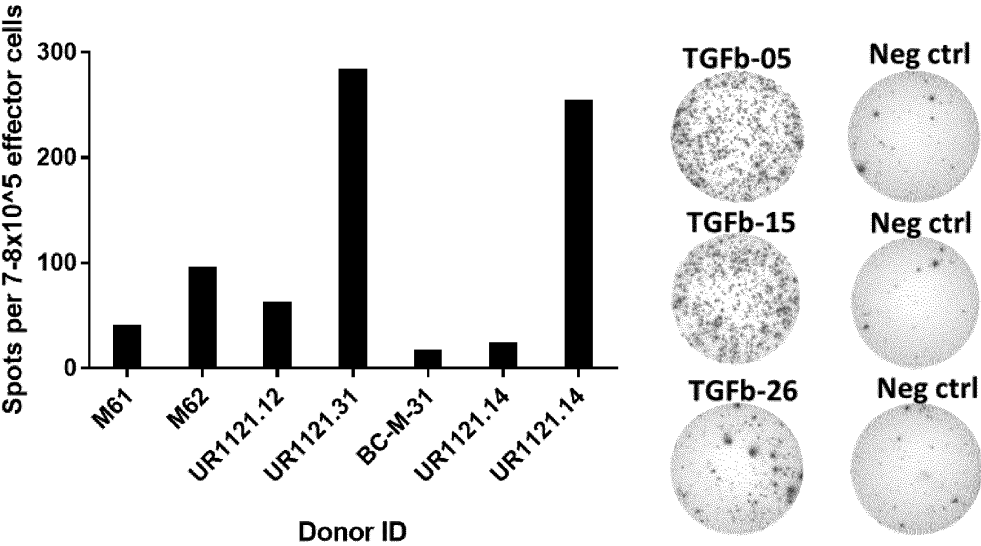


FIGURE 7

A



B

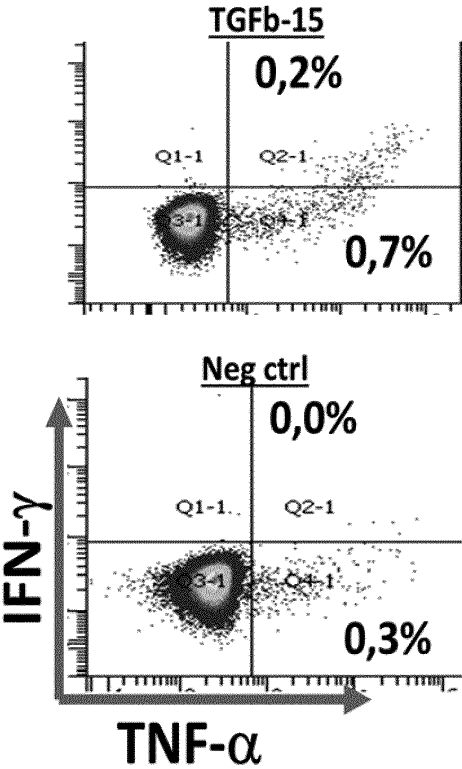
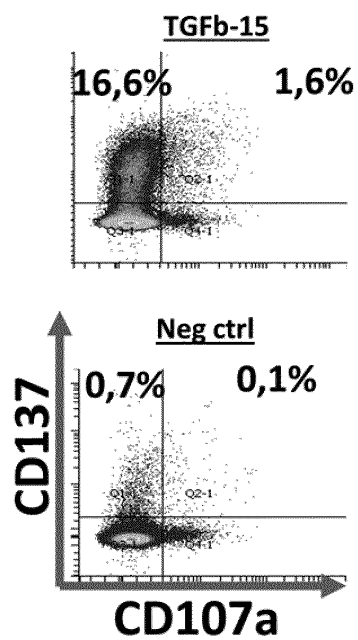


FIGURE 8

A



B

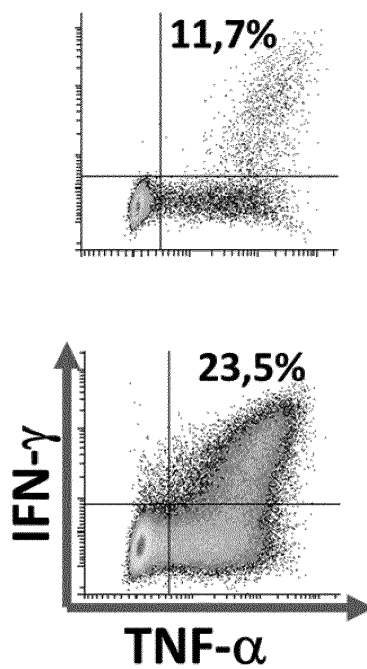


FIGURE 9

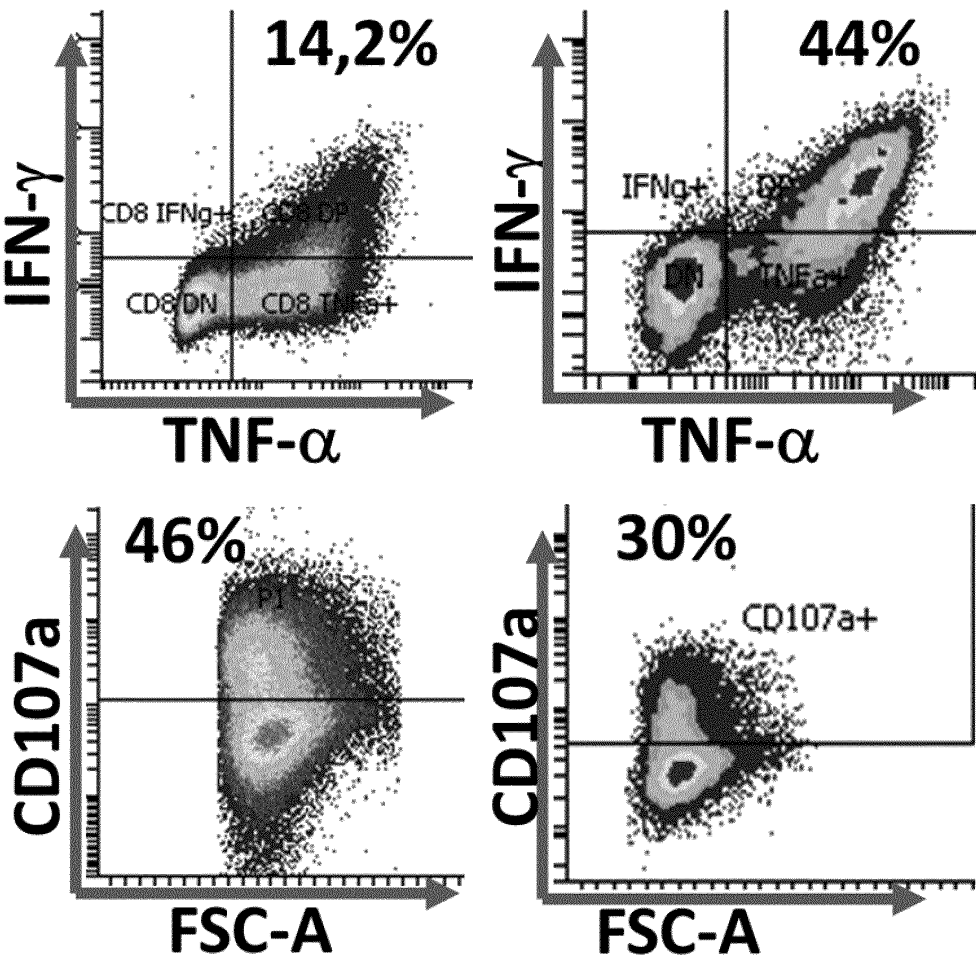


FIGURE 10

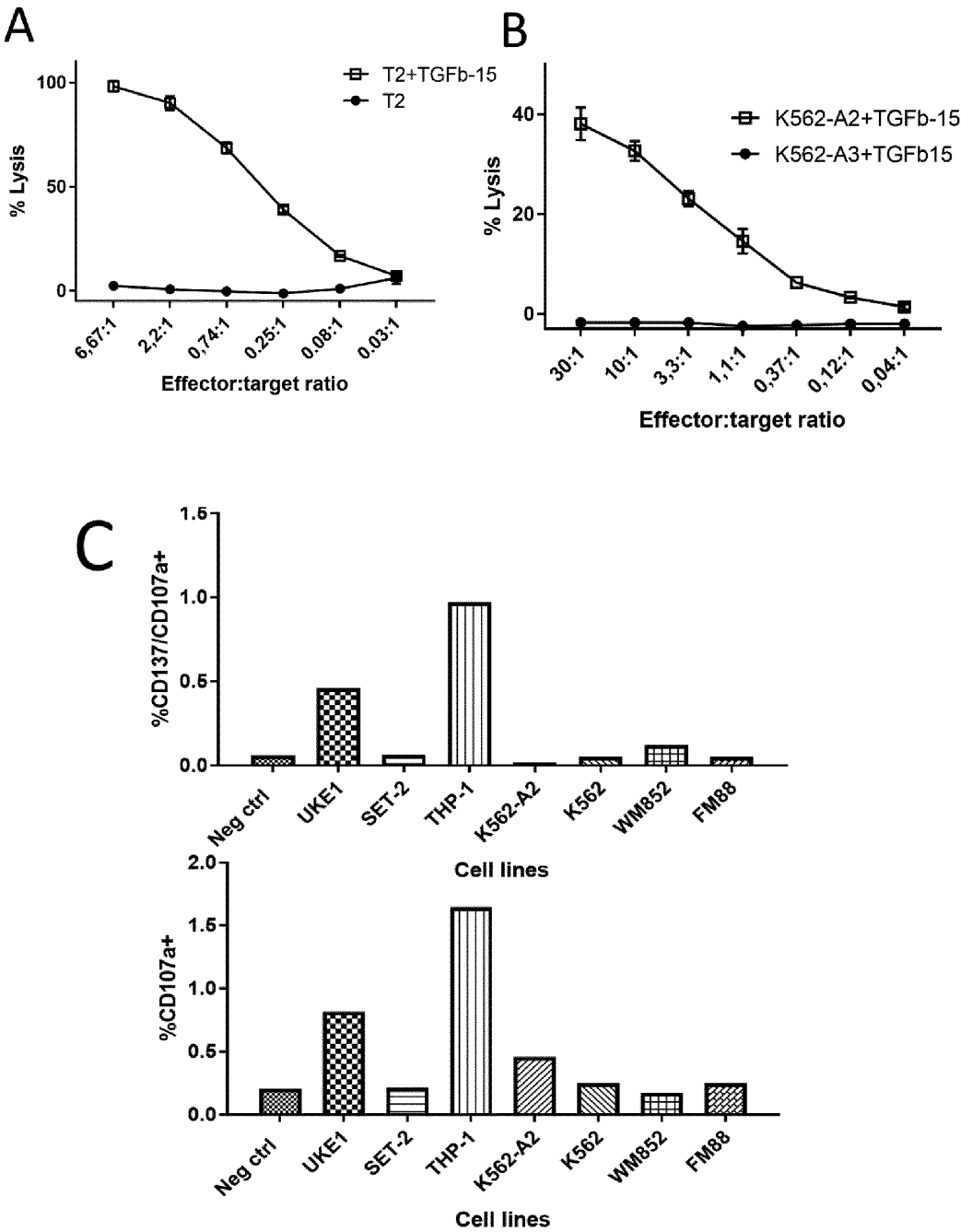


FIGURE 10 (CONT.)

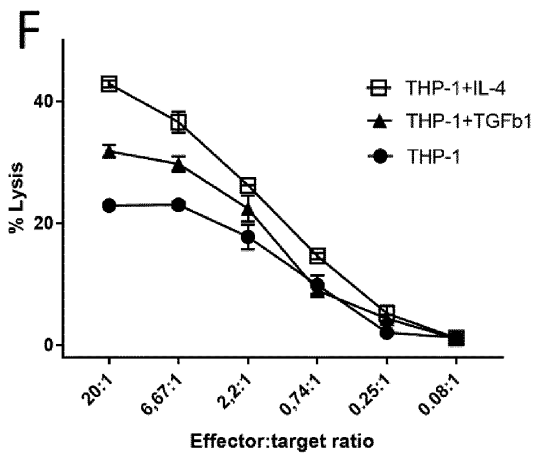
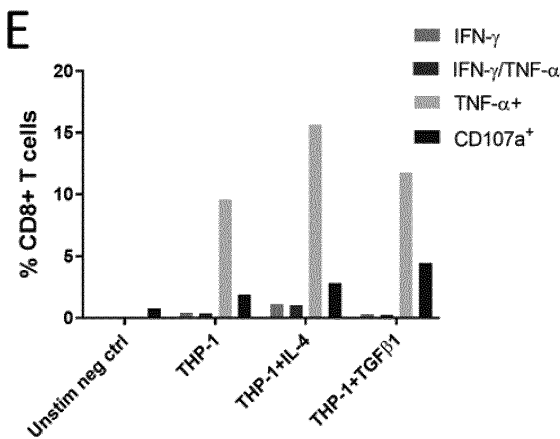
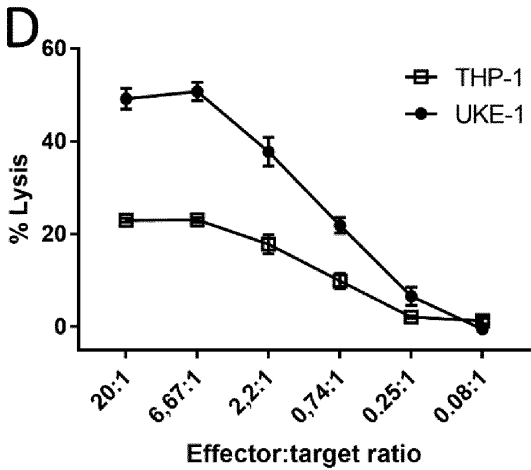


FIGURE 11

A

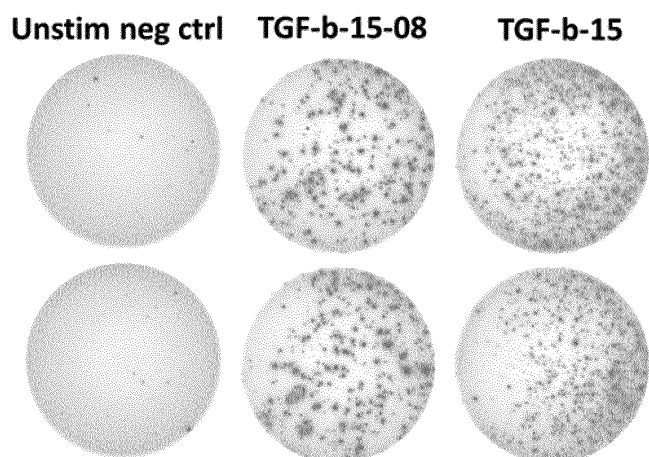
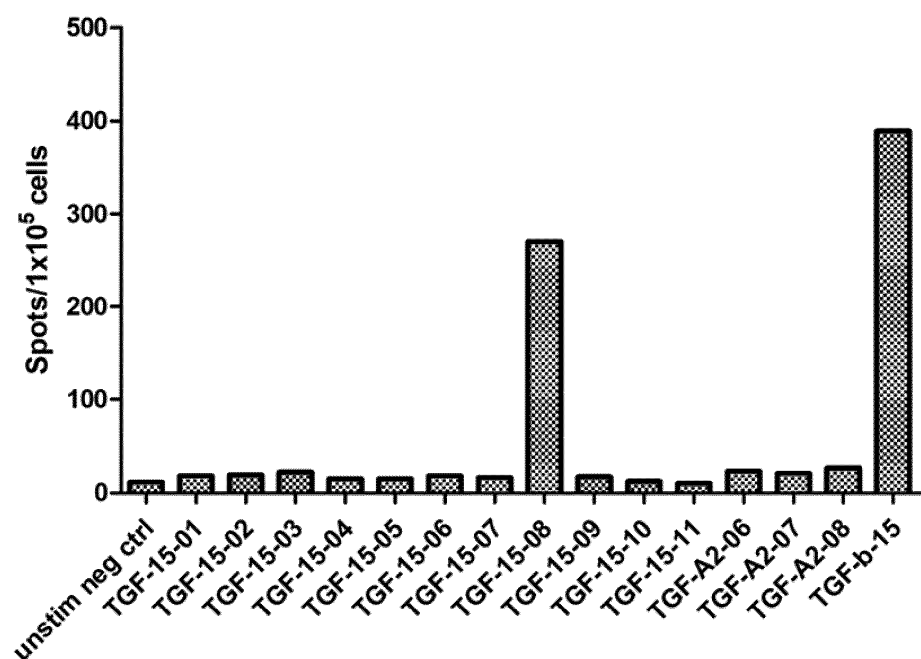


FIGURE 11 (CONT.)

B

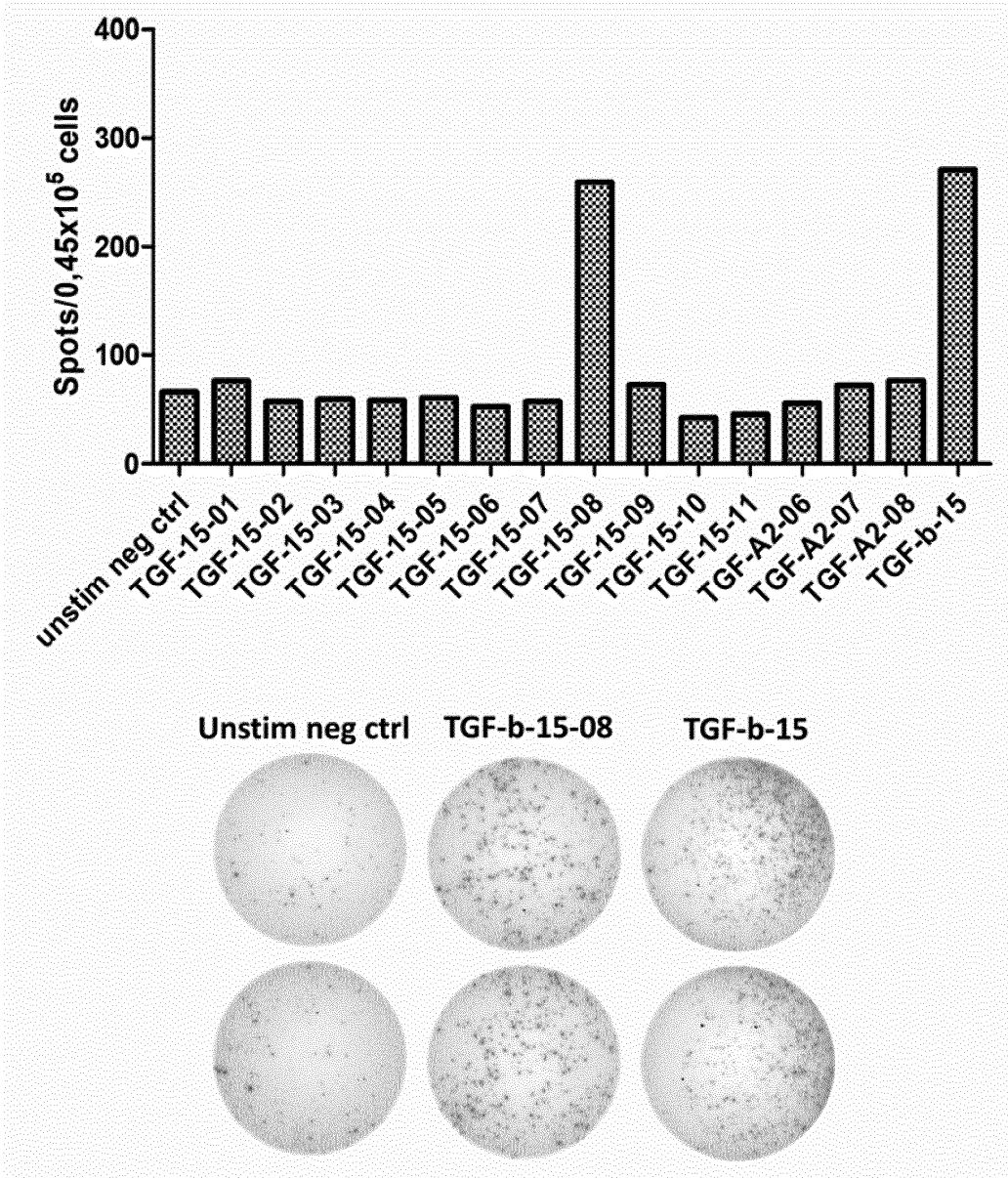


FIGURE 12

A

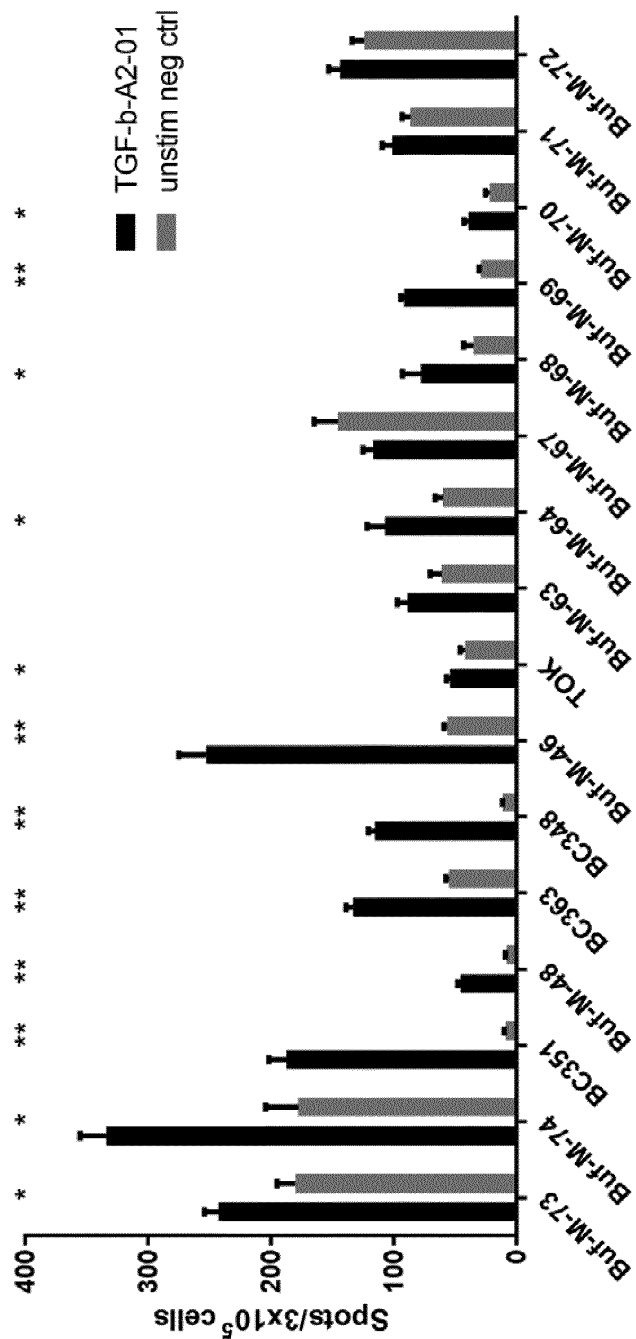


FIGURE 12 (CONT.)

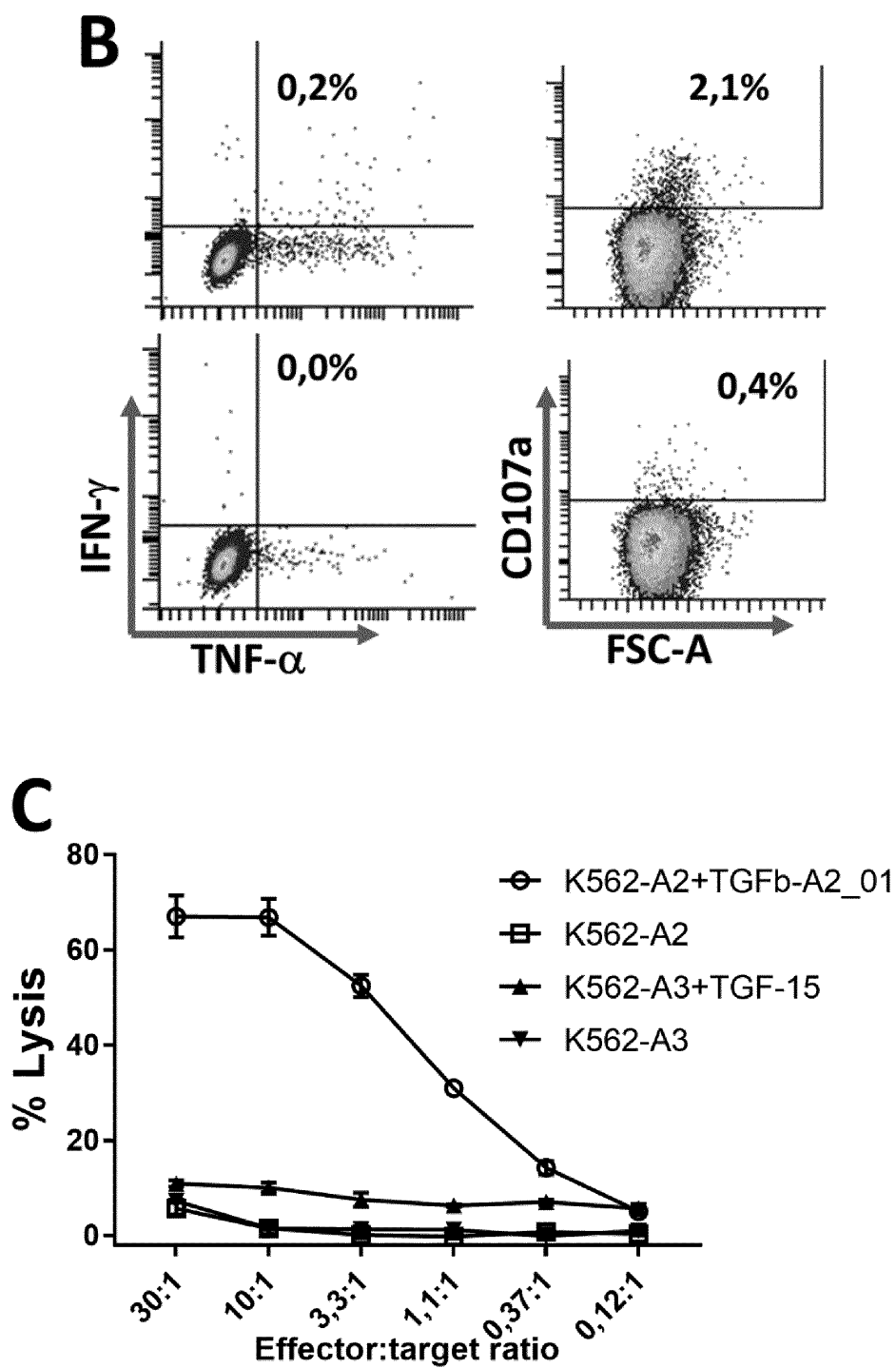


FIGURE 12 (CONT.)

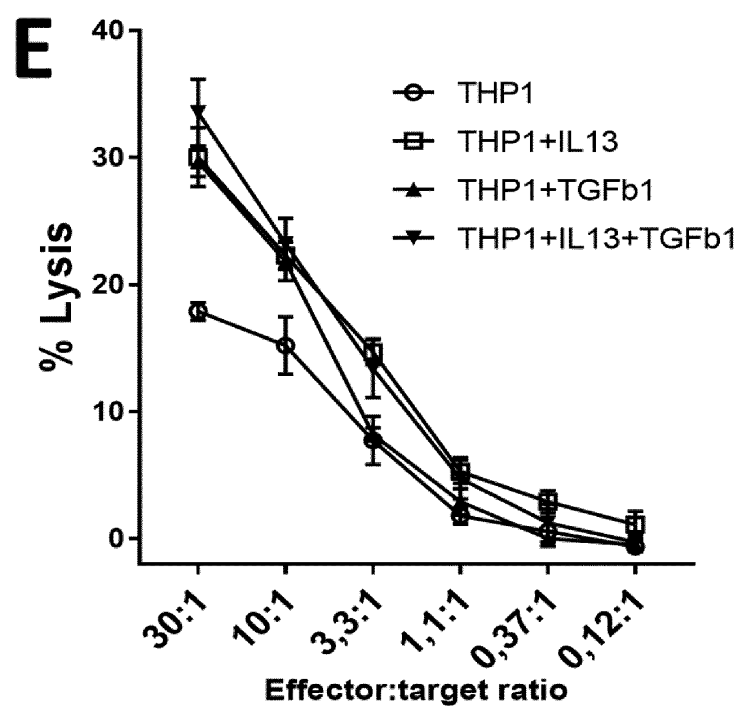
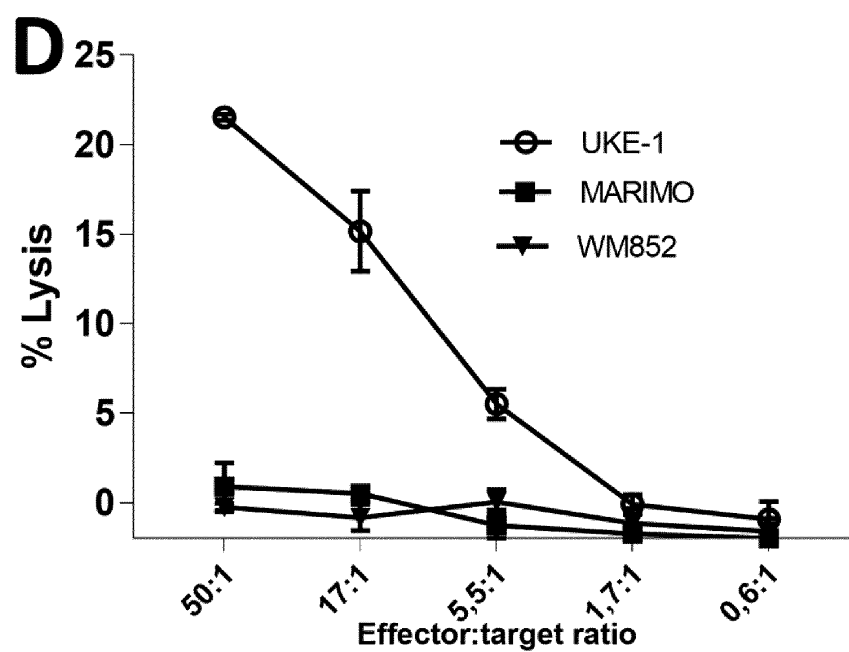


FIGURE 13

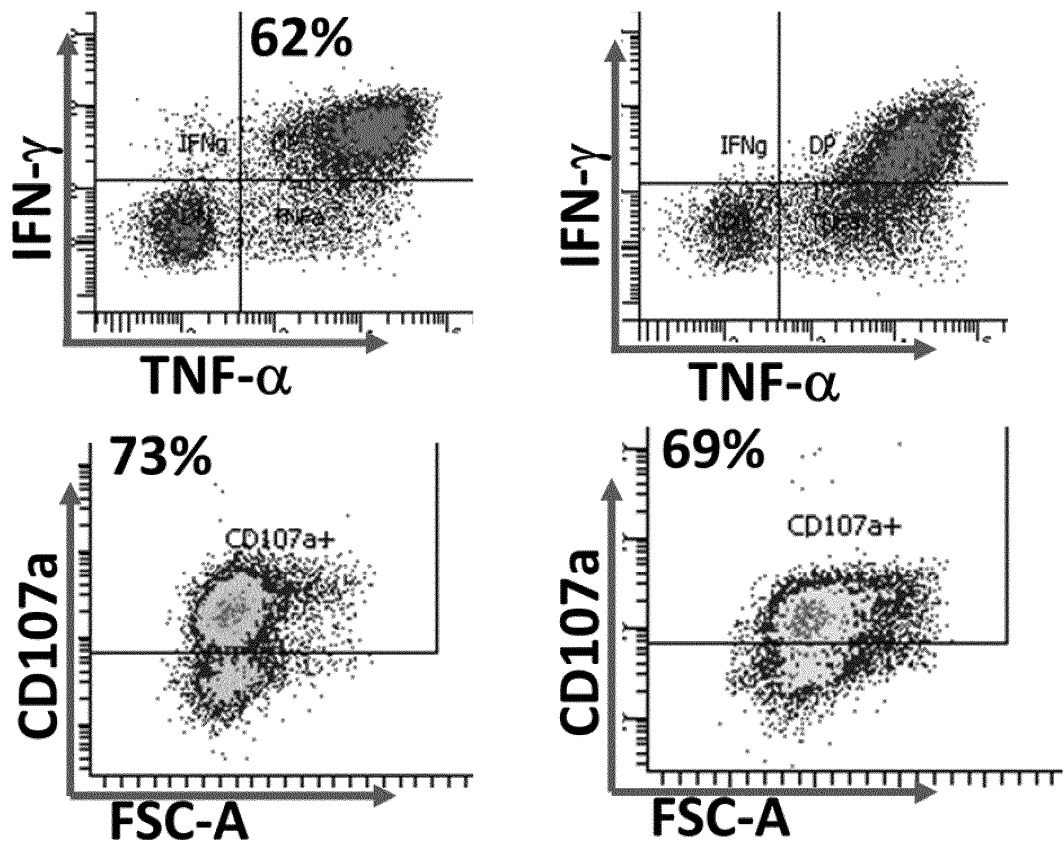


FIGURE 14

TGfb-01: MPPSGLRLLLLLLPLLWLLV
TGfb-02: LLLPLLWLLVLTGGRPAAGL
TGfb-03: LTPGRPAAGLSTCKTIDMEL
TGfb-04: STCKTIDMELVKRKRIEAIR
TGfb-05: VKRKRIEAIRGQILSKRLRLA
TGfb-06: GQILSKRLRLASPPSQGEVPP
TGfb-07: SPPSQGEVPPGPLPEAVLAL
TGfb-08: GPLPEAVLALYNSTRDRVAG
TGfb-09: YNSTRDRVAGESAEPEPEPE
TGfb-10: ESAEPEPEPEADYYAKEVTR
TGfb-11: ADYYAKEVTRVLMVETHNEI
TGfb-12: VMVETHNEIYDKFKQSTHS
TGfb-13: YDKFKQSTHSIYMFFNTSEL
TGfb-14: IYMFFNTSELREAVPEPVLL
TGfb-15: REAVPEPVLLSRAELRLRL
TGfb-16: SRAELRLRLKLKVEQHVEL
TGfb-17: KLKVEQHVELYQKYSNNSWR
TGfb-18: YQKYSNNSWRYLSNRLAPS
TGfb-19: YLSNRLAPSDSPEWLSFDV
TGfb-20: DSPEWLSFDVTGVVRQWLSR
TGfb-21: TGVVRQWLSRGGEIEGFRLS
TGfb-22: GGEIEGFRLSAHCSCDSRDN
TGfb-23: AHCSCDSRDNTLQVDINGFT
TGfb-24: TLQVDINGFTTGRRGDLATI
TGfb-25: TGRRGDLATIHGMNRPFLLL
TGfb-26: HGMNRPFLLLMTPLERAQH
TGfb-27: MATPLERAQHLQSSRHRRAL
TGfb-28: LQSSRHRRALDTNYCFSSTE
TGfb-29: DTNYCFSSTEKNCCVRQLYI
TGfb-30: KNCCVRQLYIDFRKDLGWKW
TGfb-31: DFRKDLGWKWIHEPKGYHAN
TGfb-32: IHEPKGYHANFCLGPCPYIW
TGfb-33: FCLGPCPYIWSLDTQYSKVL
TGfb-34: SLDTQYSKVLALYNQHNPQA
TGfb-35: ALYNQHNPQASAAPCCVPQA
TGfb-36: SAAPCCVPQALEPLPIVYYV
TGfb-37: LEPLPIVYYVGRKPKVEQLS
TGfb-38: GRKPKVEQLSNMIVRSCKCS