

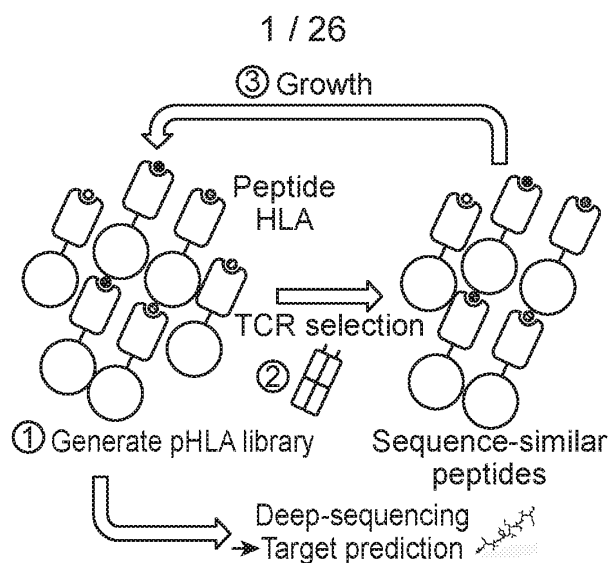


FIG. 1A

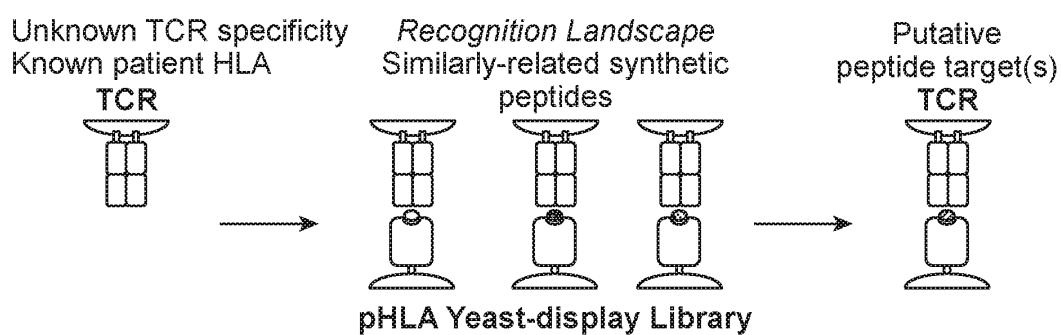


FIG. 1B

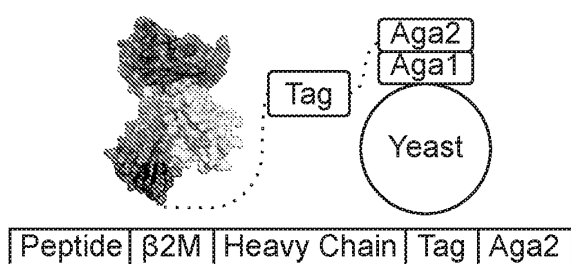


FIG. 1C

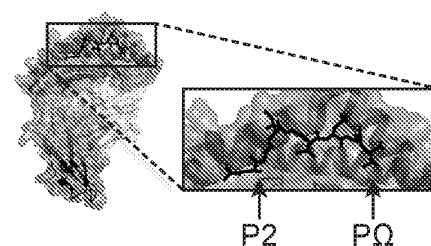


FIG. 1D

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	P1	P2	P3	P4	P5	P6	P7	P8
Library	X	L M	X	X	X	X	X	L M V
Codon	NNK	MTG	NNK	NNK	NNK	NNK	NNK	NTG

FIG. 1E

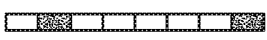
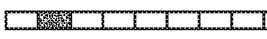
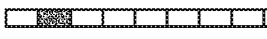
	P2	PQ	Epitope Tag	Theoretical Nucleotide Diversity	Functional Diversity
8mer			V5	8.59×10^9	8.0×10^7
9mer			Myc	2.75×10^{11}	1.2×10^8
10mer			HA	8.80×10^{12}	1.3×10^8
11mer			VSV	2.81×10^{14}	7.0×10^7

FIG. 1F

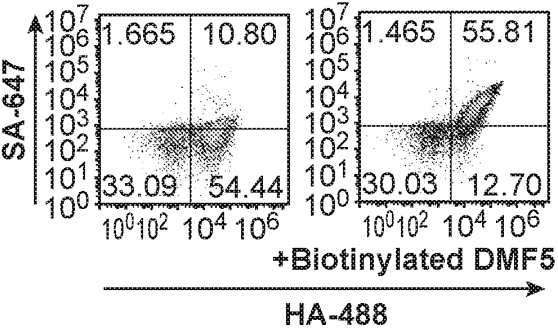


FIG. 2A

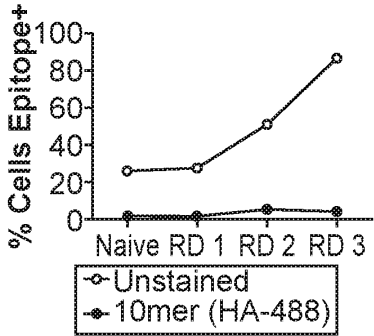


FIG. 2B

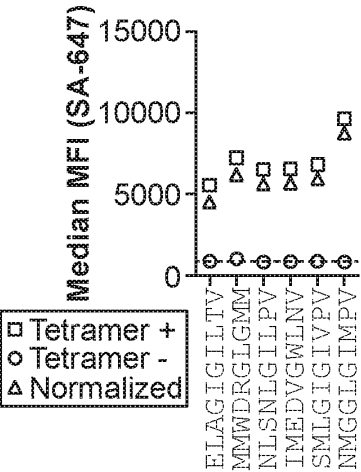


FIG. 2C

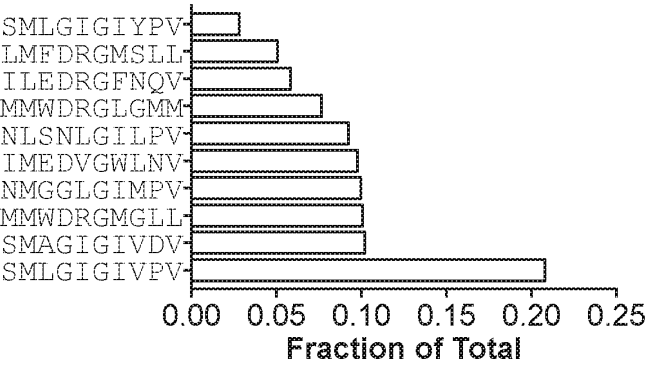


FIG. 2D

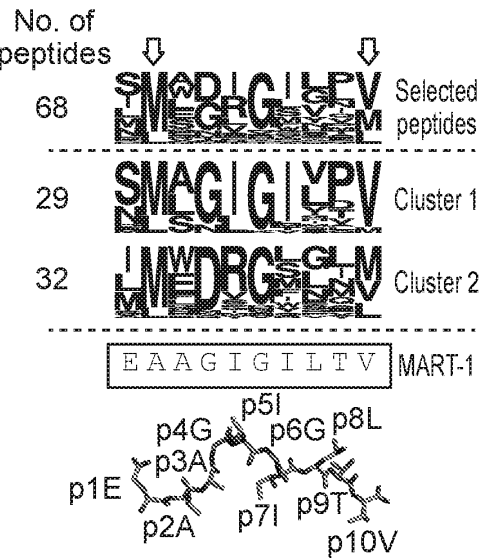


FIG. 2E

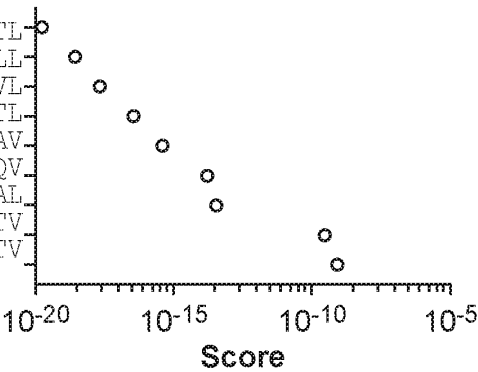


FIG. 2F

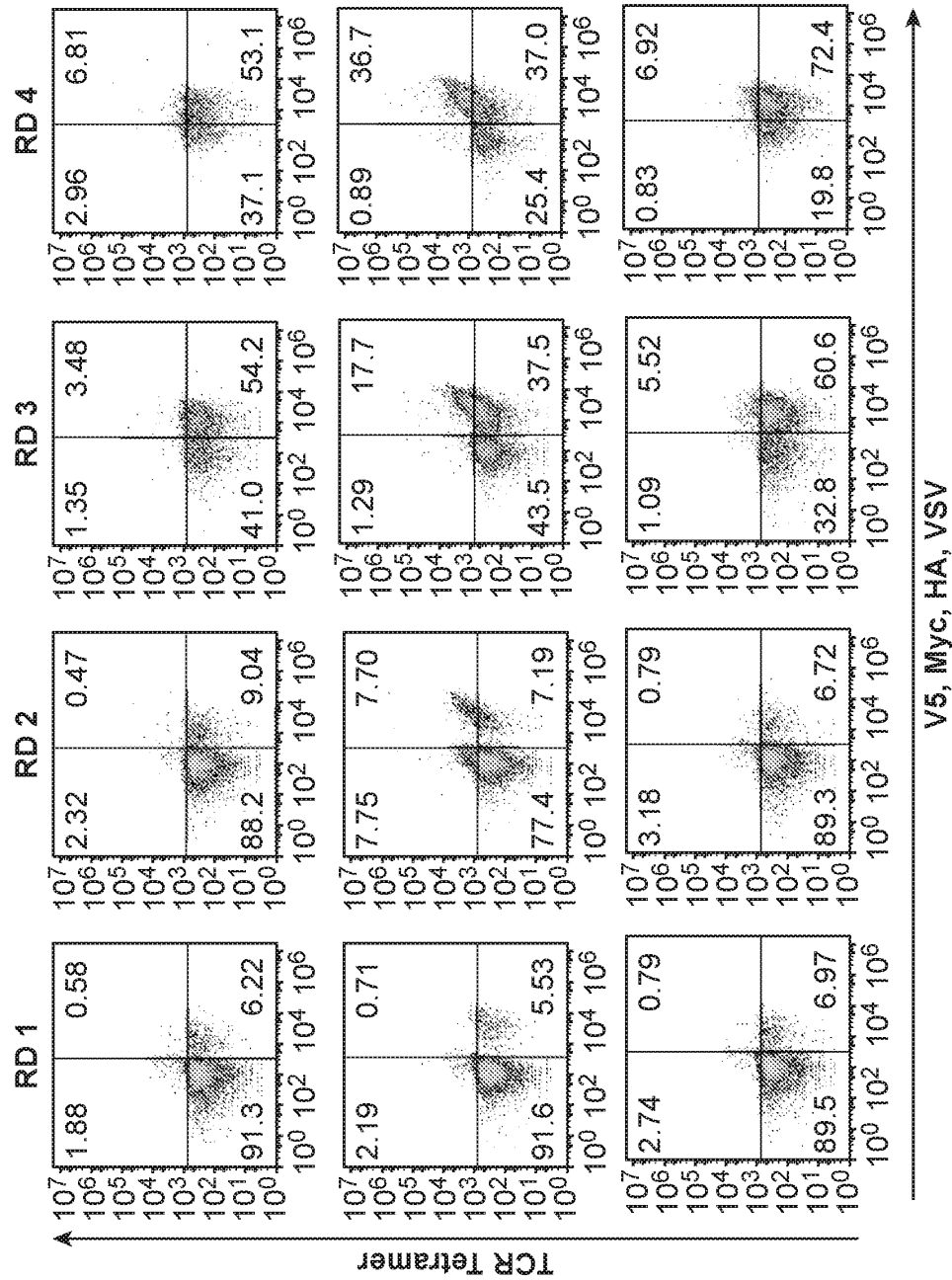


FIG. 3A

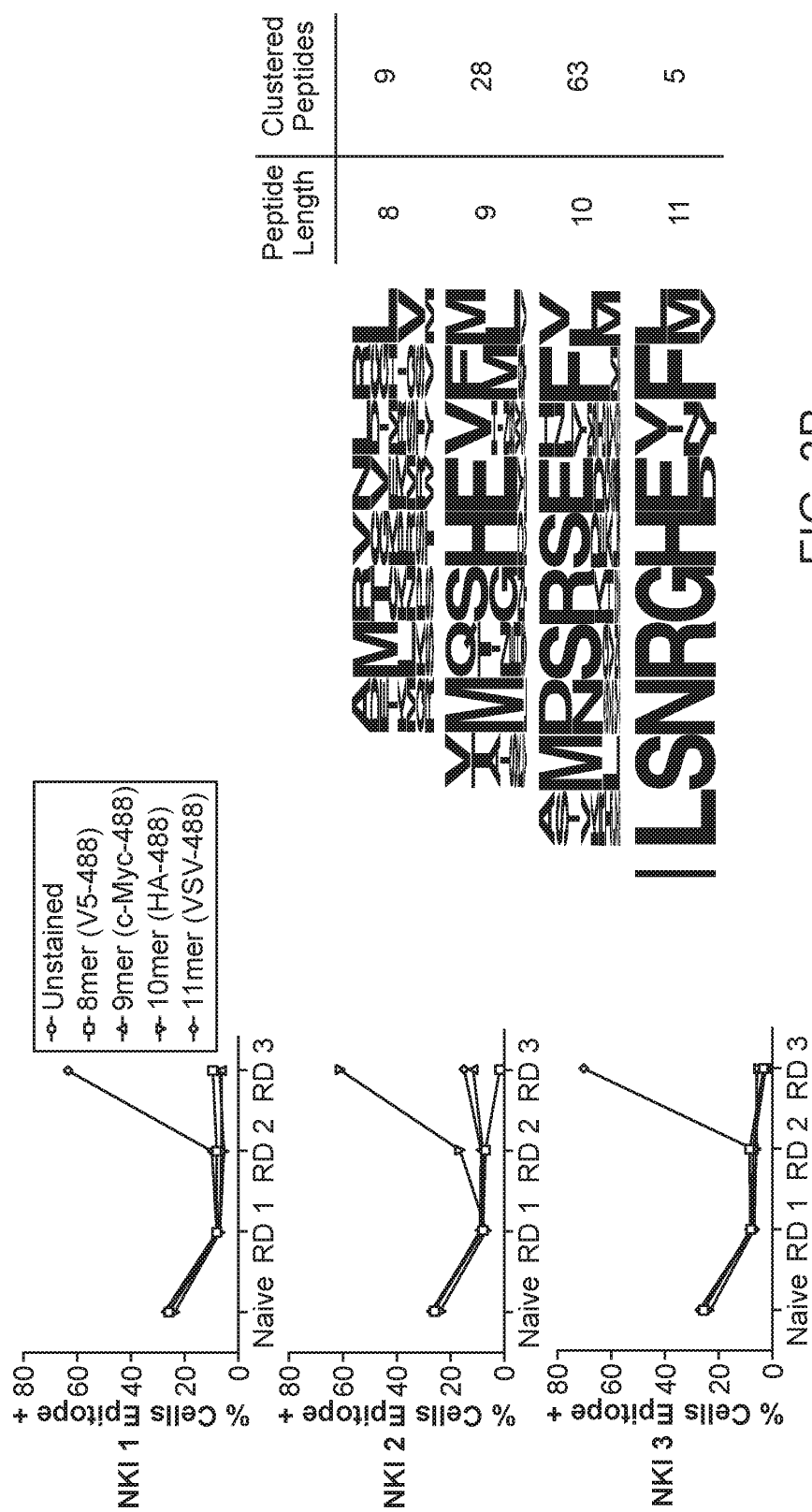
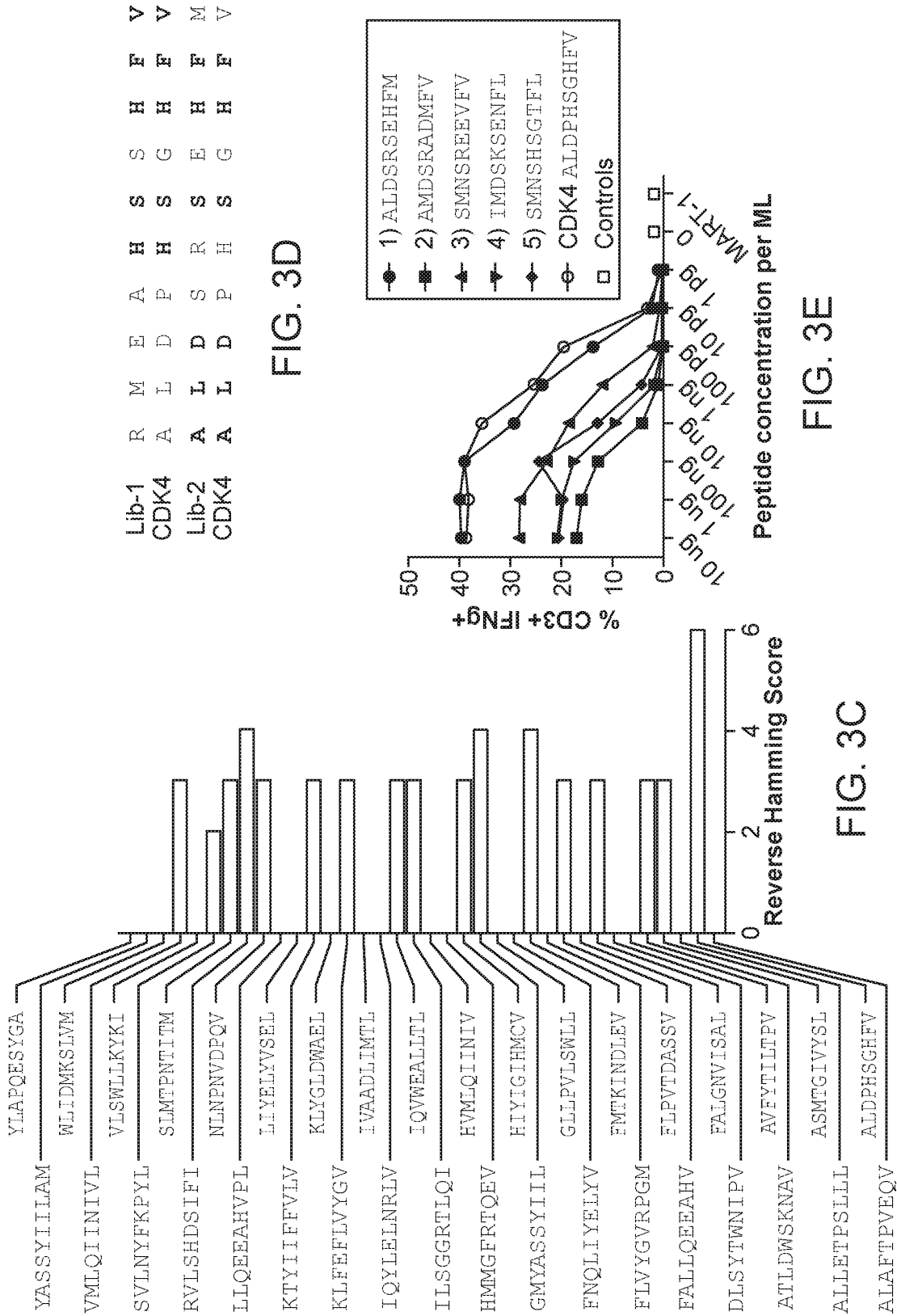


FIG. 3A (Cont.)



1) ALDSRSEHFV

2) AMDSRADMEV

3) SMNSREEVFV

4) IMDSKSENFV

5) SMNSHSGTFL

CDK4 ALDPHSGHFV

Controls

50

40

30

20

10

0

10 μ g

100 ng

100 pg

1000 pg

10000 pg

MART-1

Peptide concentration per ML

% CD3+TFNg+

FIG. 3E

Reverse Hamming Score

0

2

4

6

YIAPQESYGA

YASSYIIILAM

VMLQIINIVL

SVLNYFKPYL

RVLSHDSIFI

LLQEEAHVPL

KTYIIFFVLV

KLYGLDWAEL

KLFEFLVYGV

IQYLELNRLV

ILSGGRTLQI

HMMGERTQEV

GMVASSYIIL

FNQLIYELV

FLVYGVVRPGM

FALLQEEAHV

DLSYTNWIPV

ATLDWSKNAV

ALLETPSLLL

ALAFTPVEQV

FIG. 3C

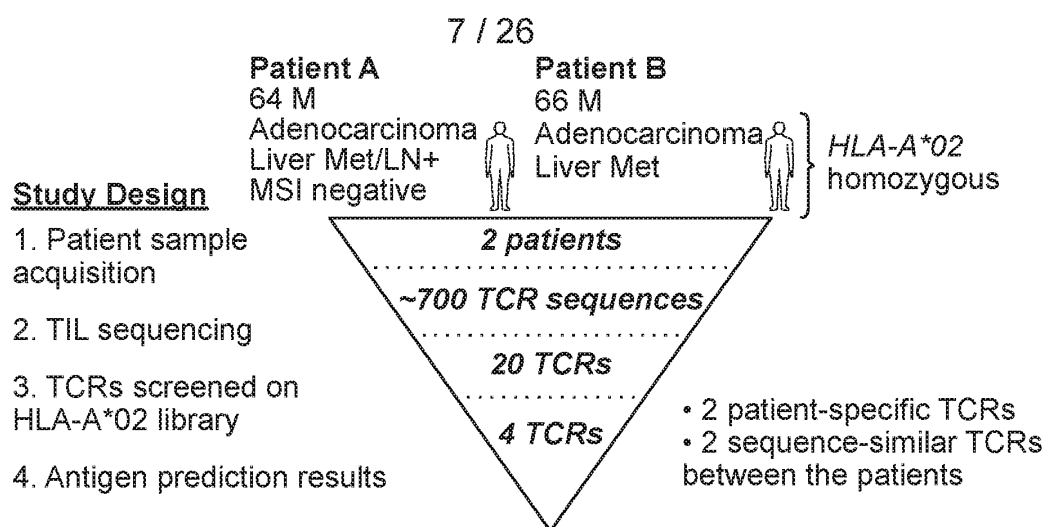


FIG. 4A

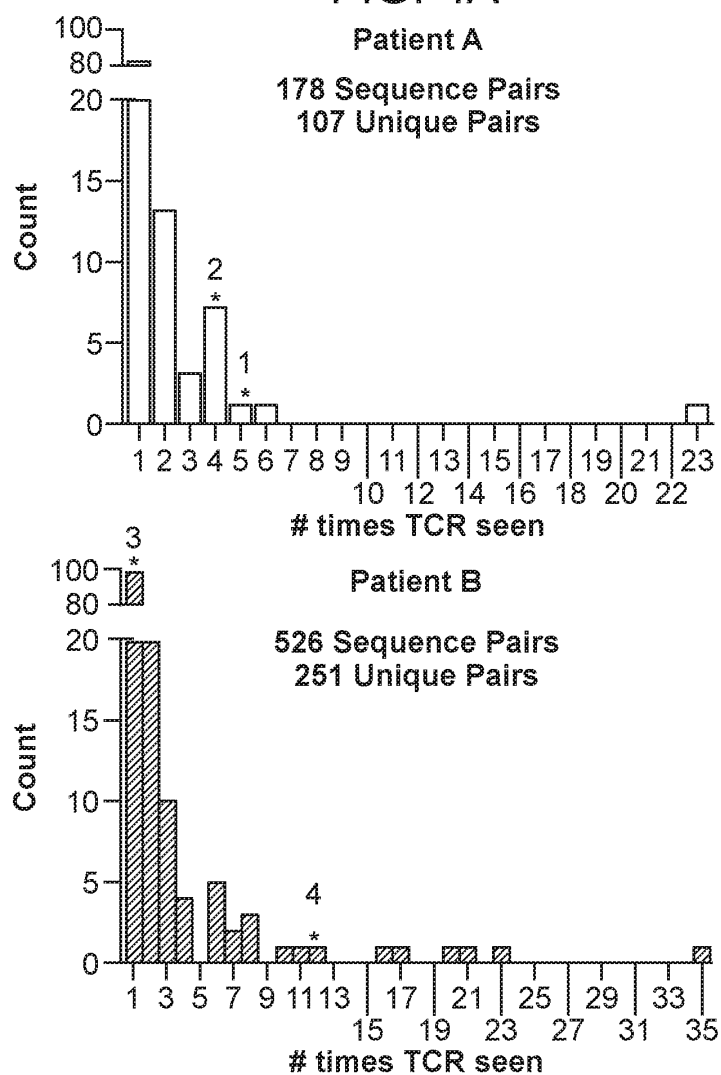


FIG. 4B

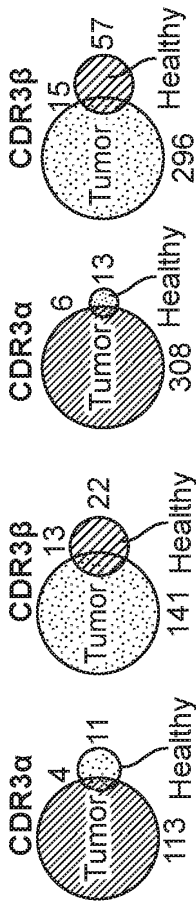


FIG. 4C

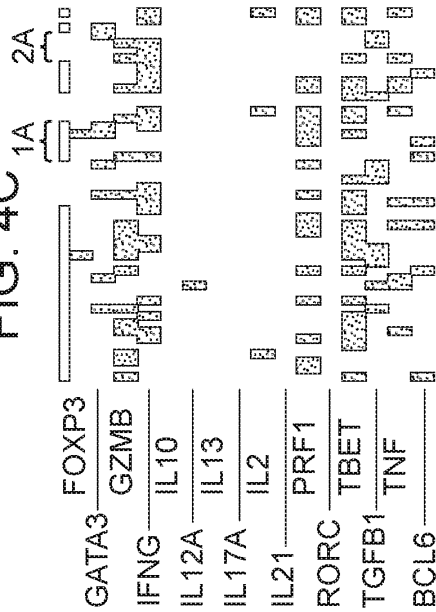
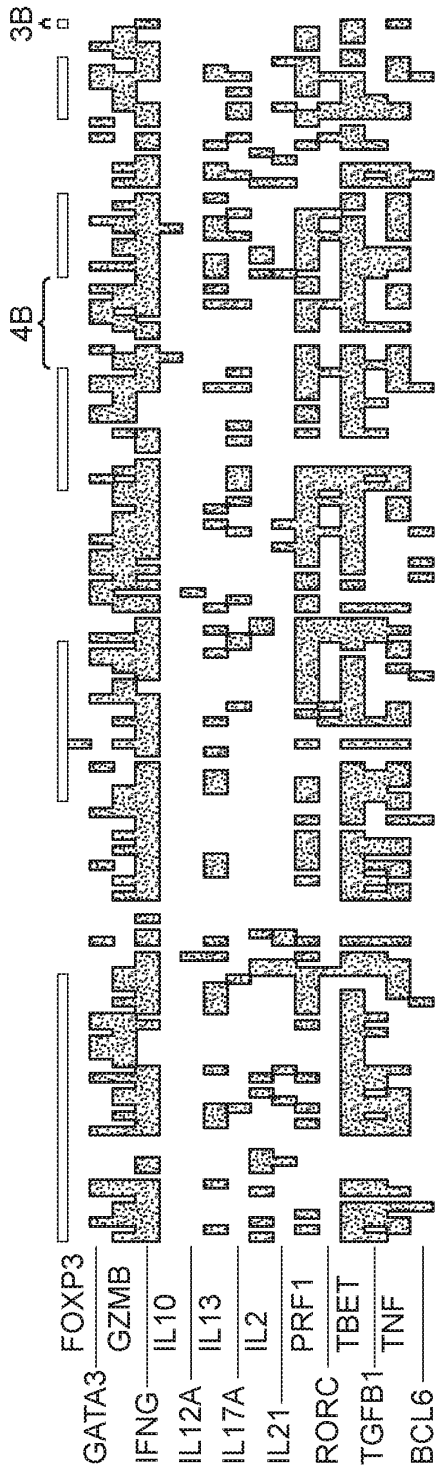


FIG. 4D

	V α	CDR3 α	J α	V β	CDR3 β	J β	Abundance
1A	TRAV19	CALSEAGMDSNYQLIW	TRAJ33	TRBV7-9	CASSLVNGLGYTF	TRBJ1-2	5/-
2A	TRAV19	CALSEARGGATNKLIF	TRAJ32	TRBV10-1	CASSRDTVNTEAFF	TRBJ1-1	4/-
3B	TRAV19	CALSEARGGATNKLIF	TRAJ32	TRBV10-1	CASSRDFVSNEQYF	TRBJ2-7	1/1
4B	TRAV19	CALSSRGSTILGRLYF	TRAJ18	TRBV11-3	CASSPSGLAGSNLGNEQFF	TRBJ2-1	12/-

FIG. 5A

2A	C	A	L	S	E	A	R	G	G	A	T	N	K	L	I	F
CDR3 α	TG	TC	CT	CT	GA	GT	GA	GG	CT	GA	GG	CT	GA	AG	CT	CA
3B	C	A	L	S	E	A	R	G	G	A	T	N	K	L	I	F
	TG	TC	CT	CT	GA	GT	GA	GG	CT	GA	GG	CT	GA	AG	CT	CA
2A	C	A	S	S	R	D	T	V	N	T	E	A	F	F		
CDR3 β	TG	CG	CC	AG	CA	GG	GA	CA	CT	GT	TA	AT	AC	TG	AA	AG
3B	C	A	S	S	R	D	F	V	S	N	E	Q	Y	F		
	TG	CG	CC	AG	CA	GT	CG	GT	CC	CA	AC	GA	GG	AG	TA	CT

FIG. 5B

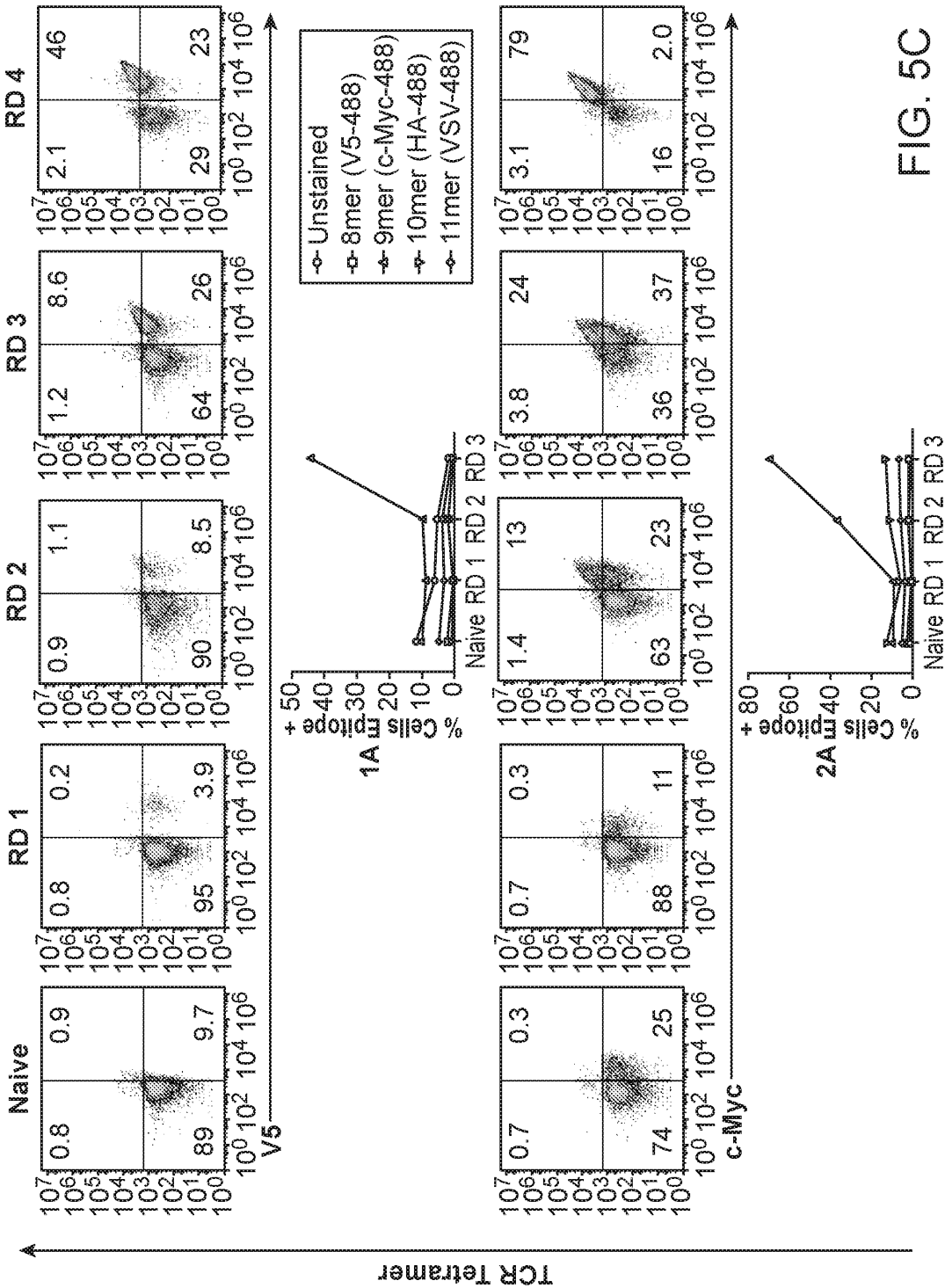


FIG. 5C

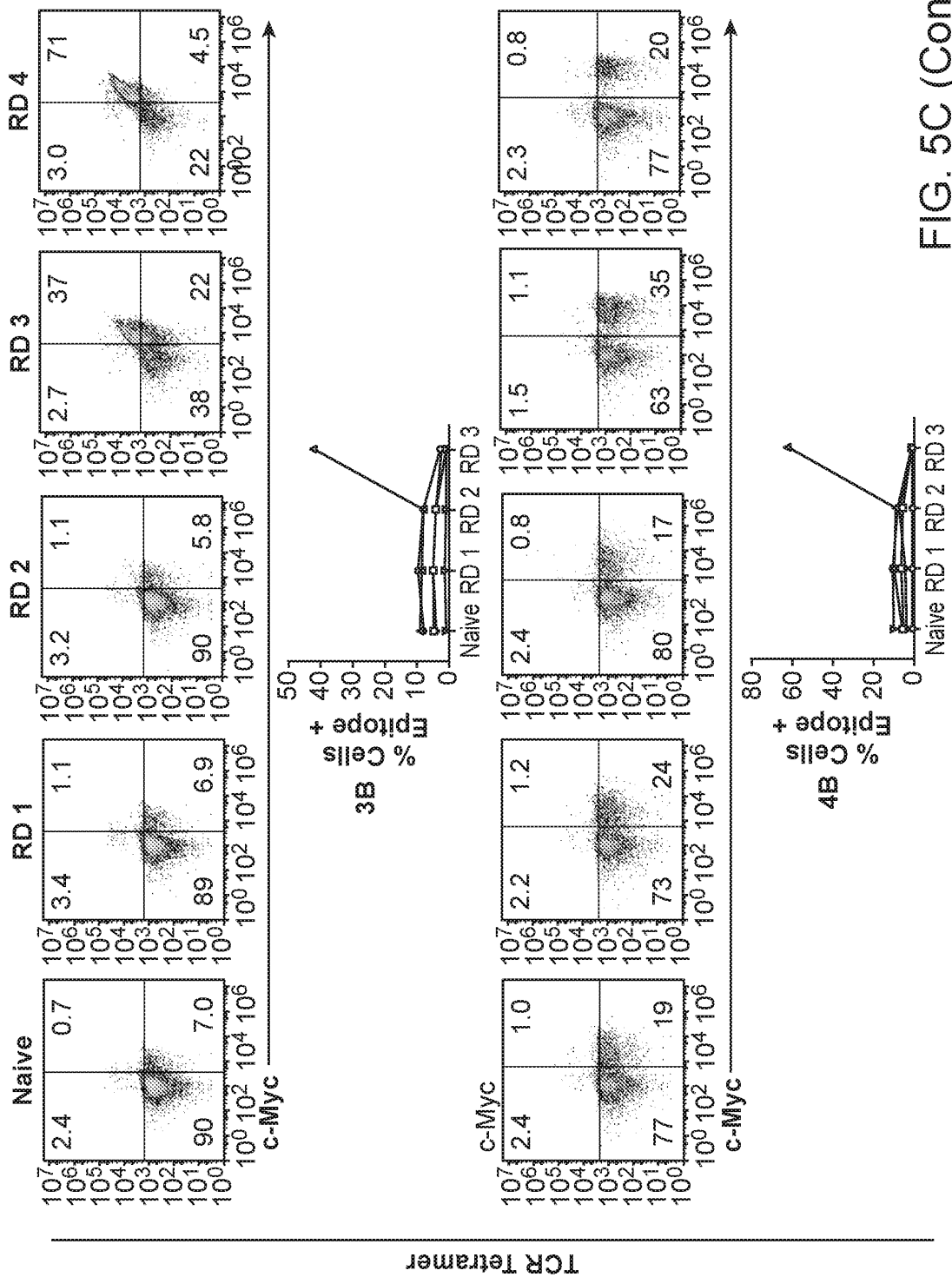




FIG. 6A

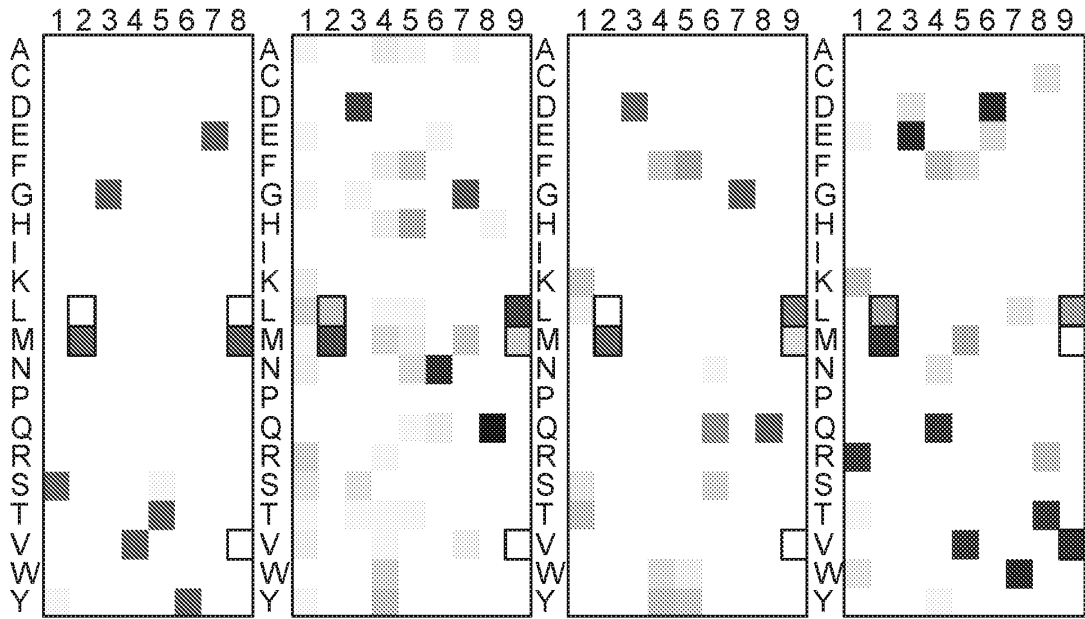


FIG. 6B

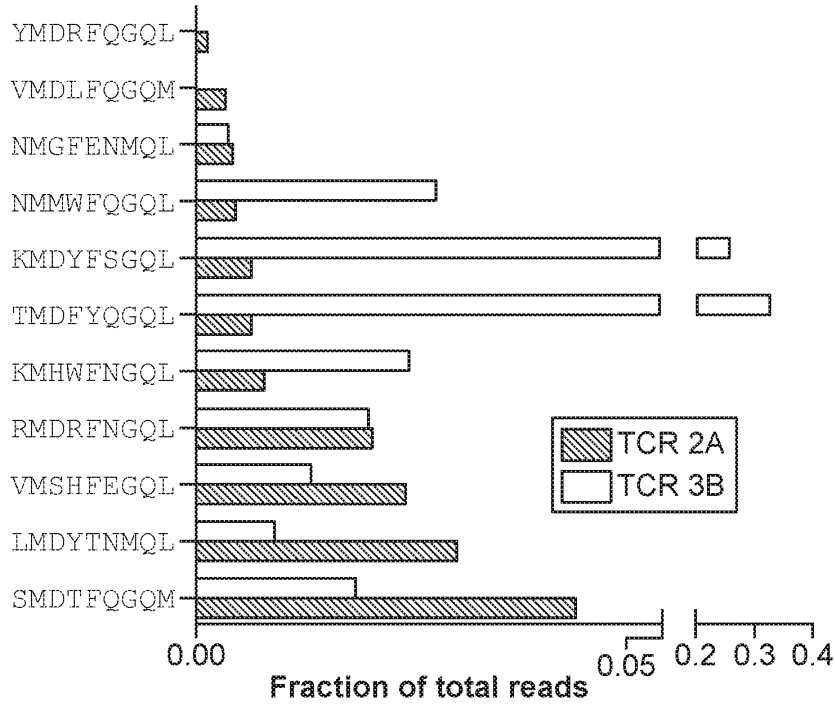


FIG. 6C

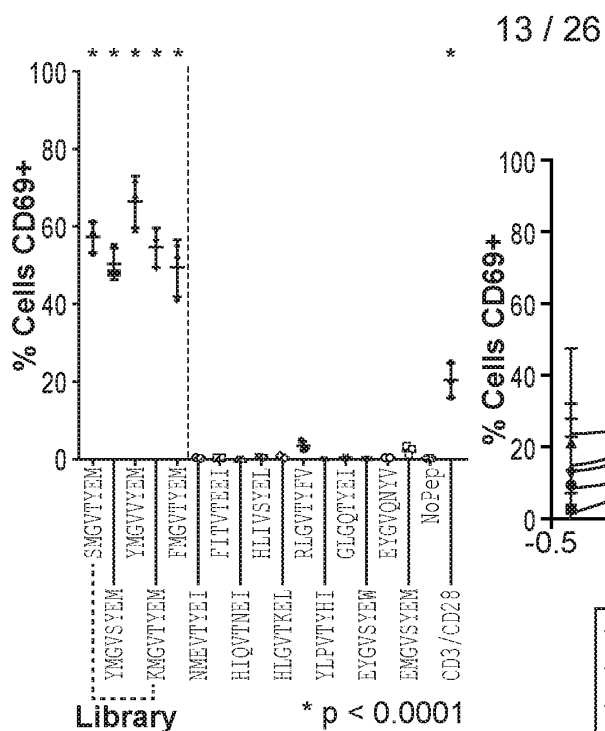


FIG. 7A

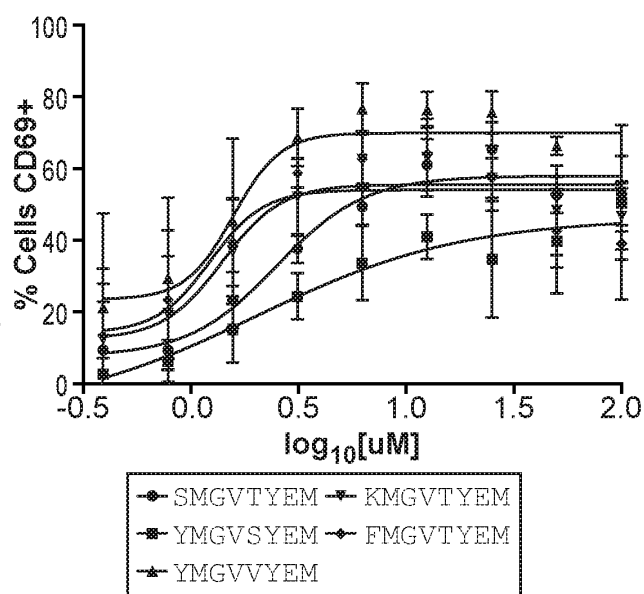


FIG. 7B

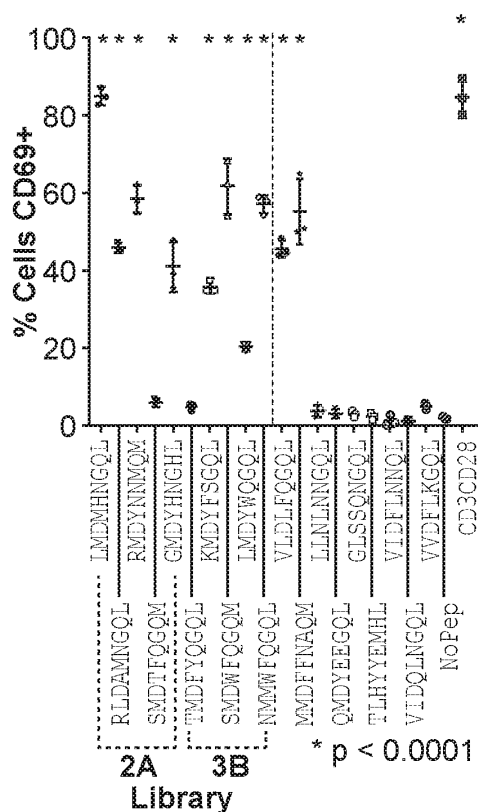


FIG. 7C

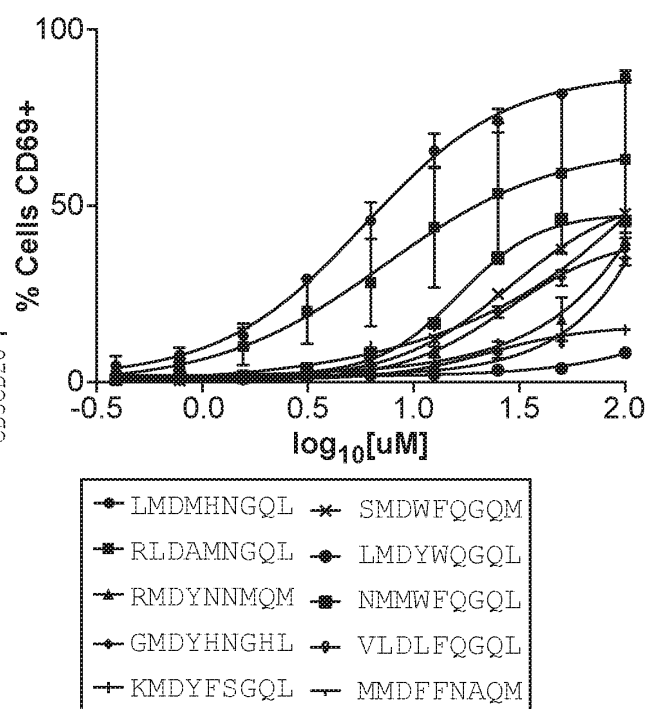


FIG. 7D

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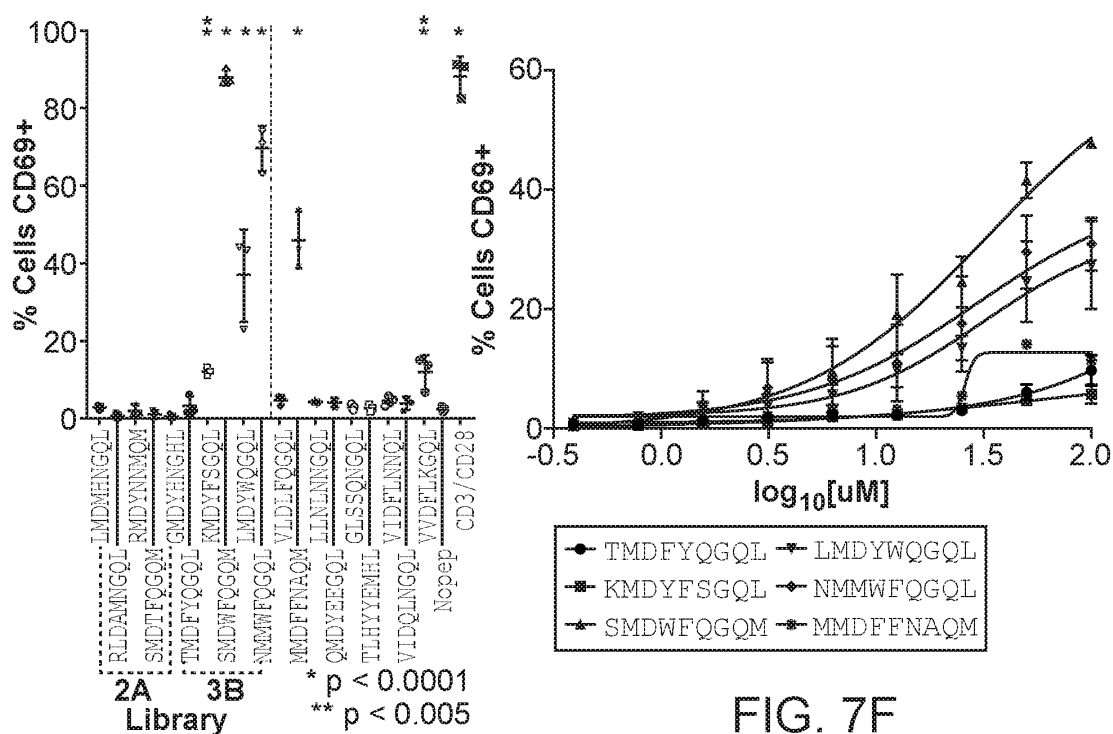


FIG. 7E

FIG. 7F

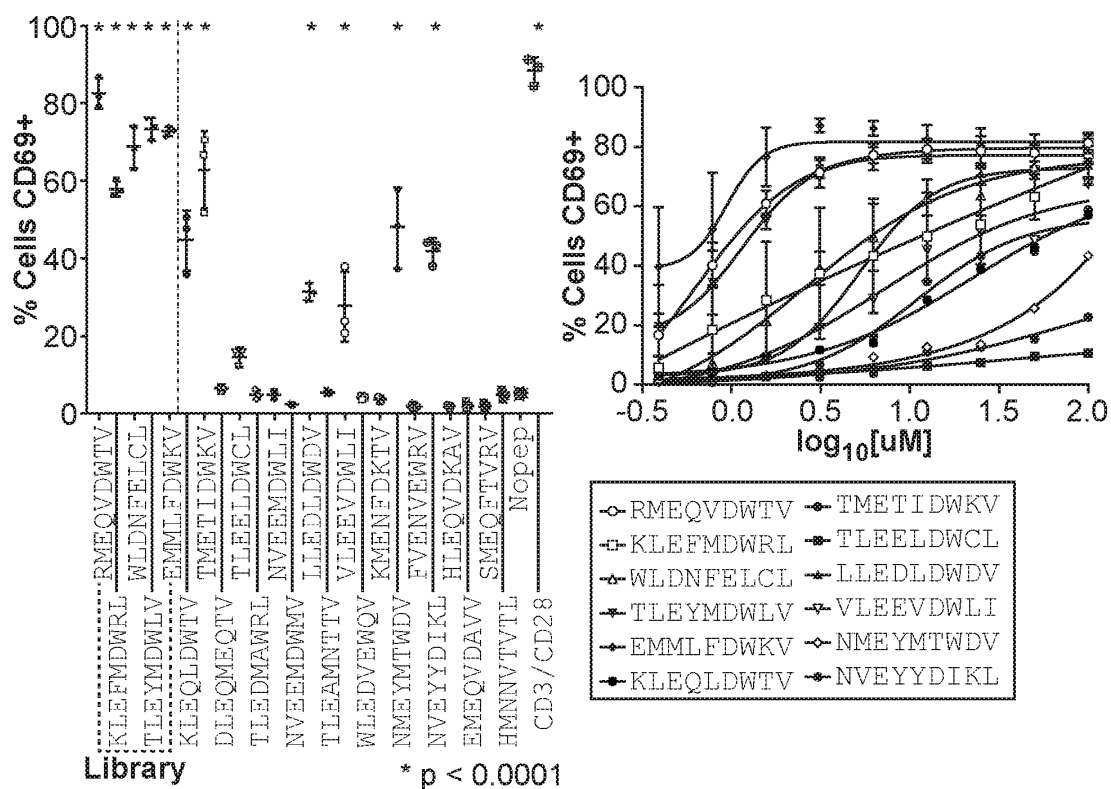
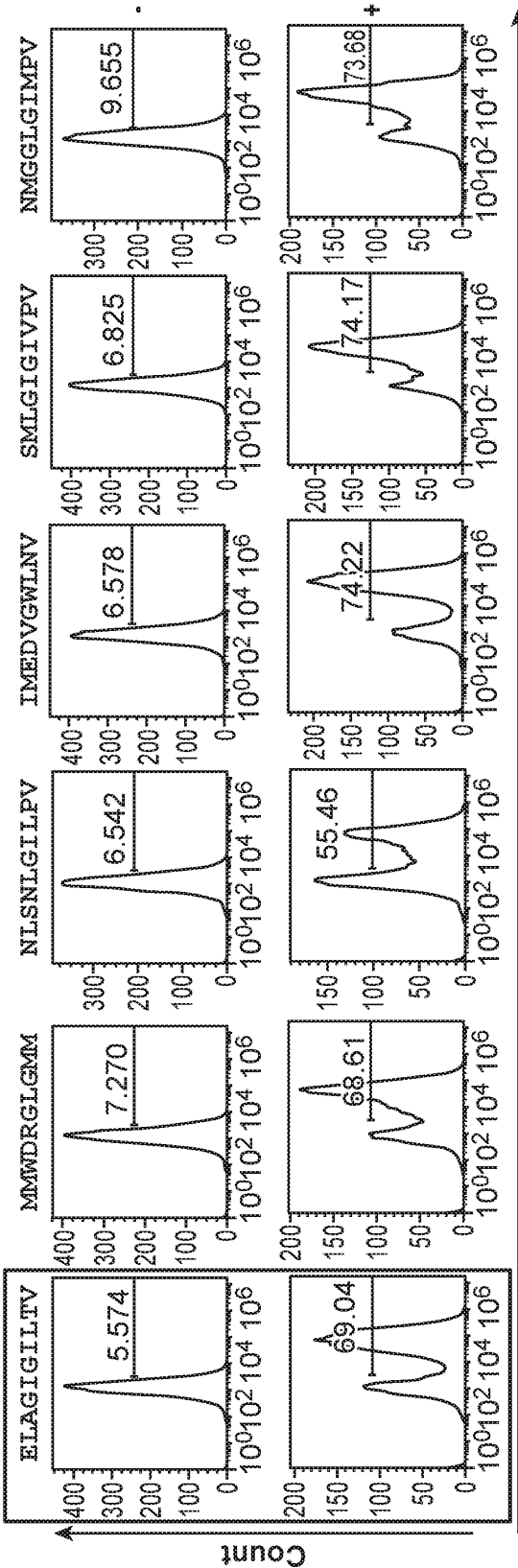


FIG. 7G

FIG. 7H



MA2.1 (488 secondary)

FIG. 8A

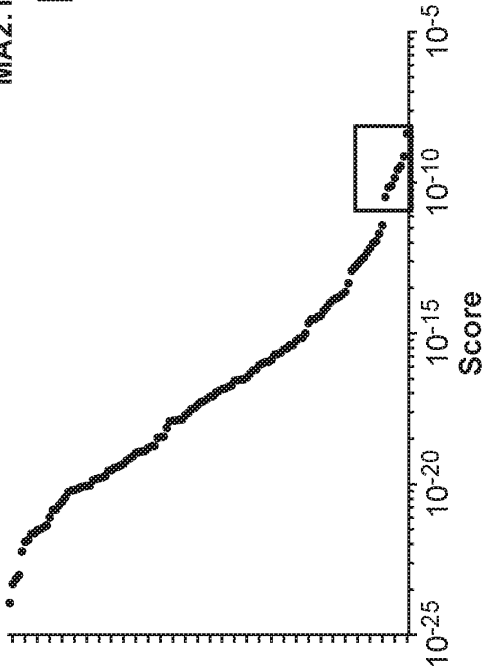


FIG. 8B

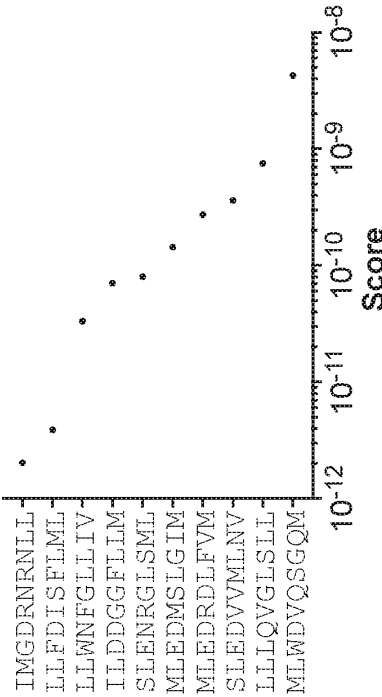
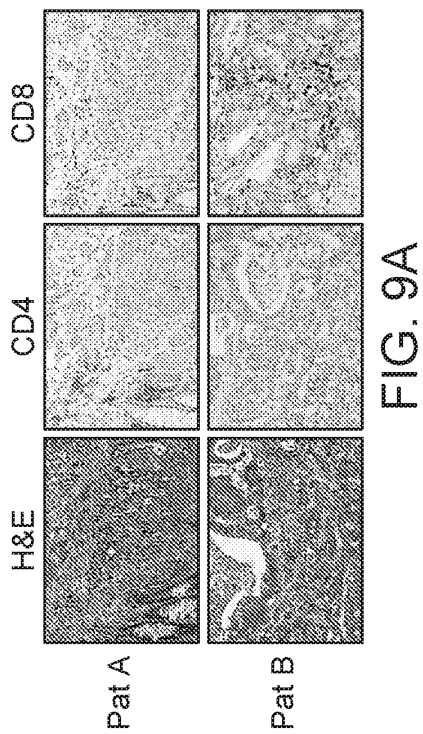
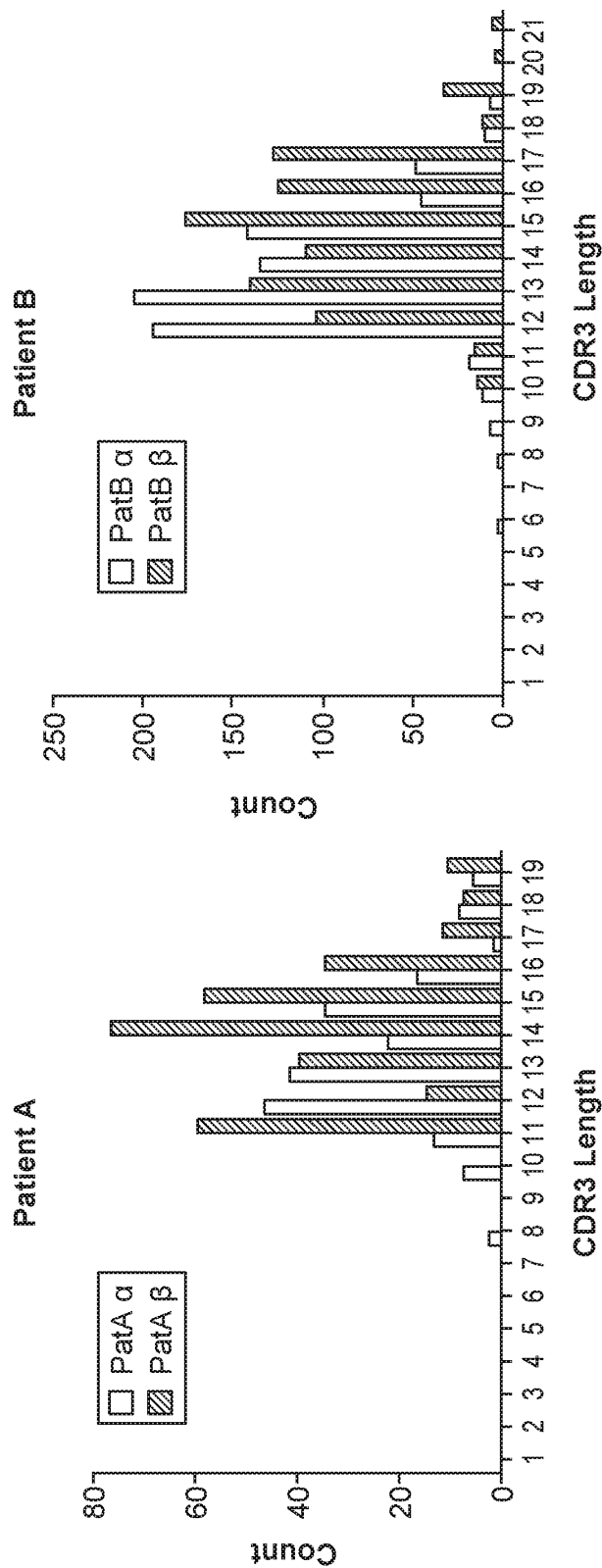
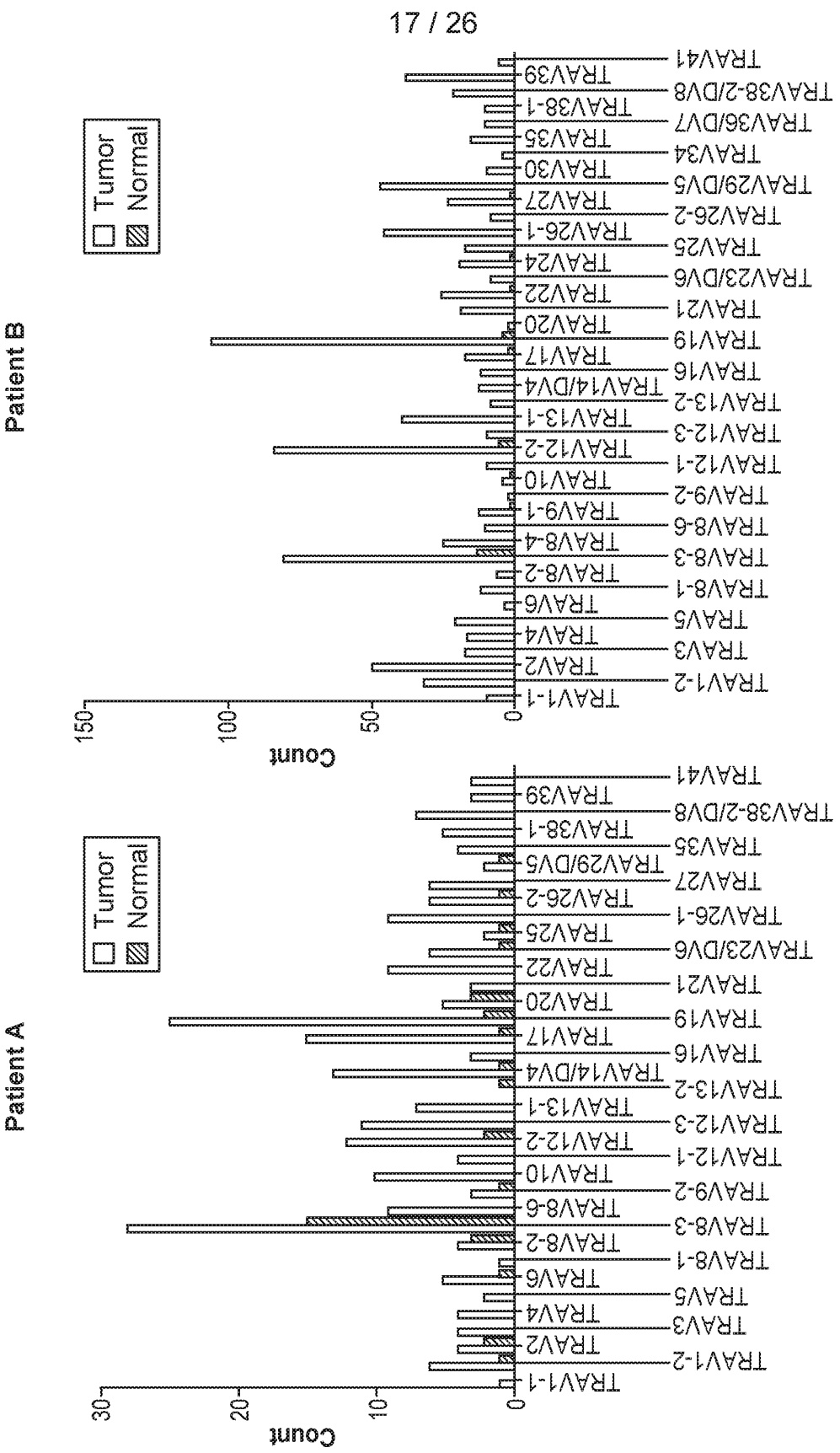


FIG. 8C





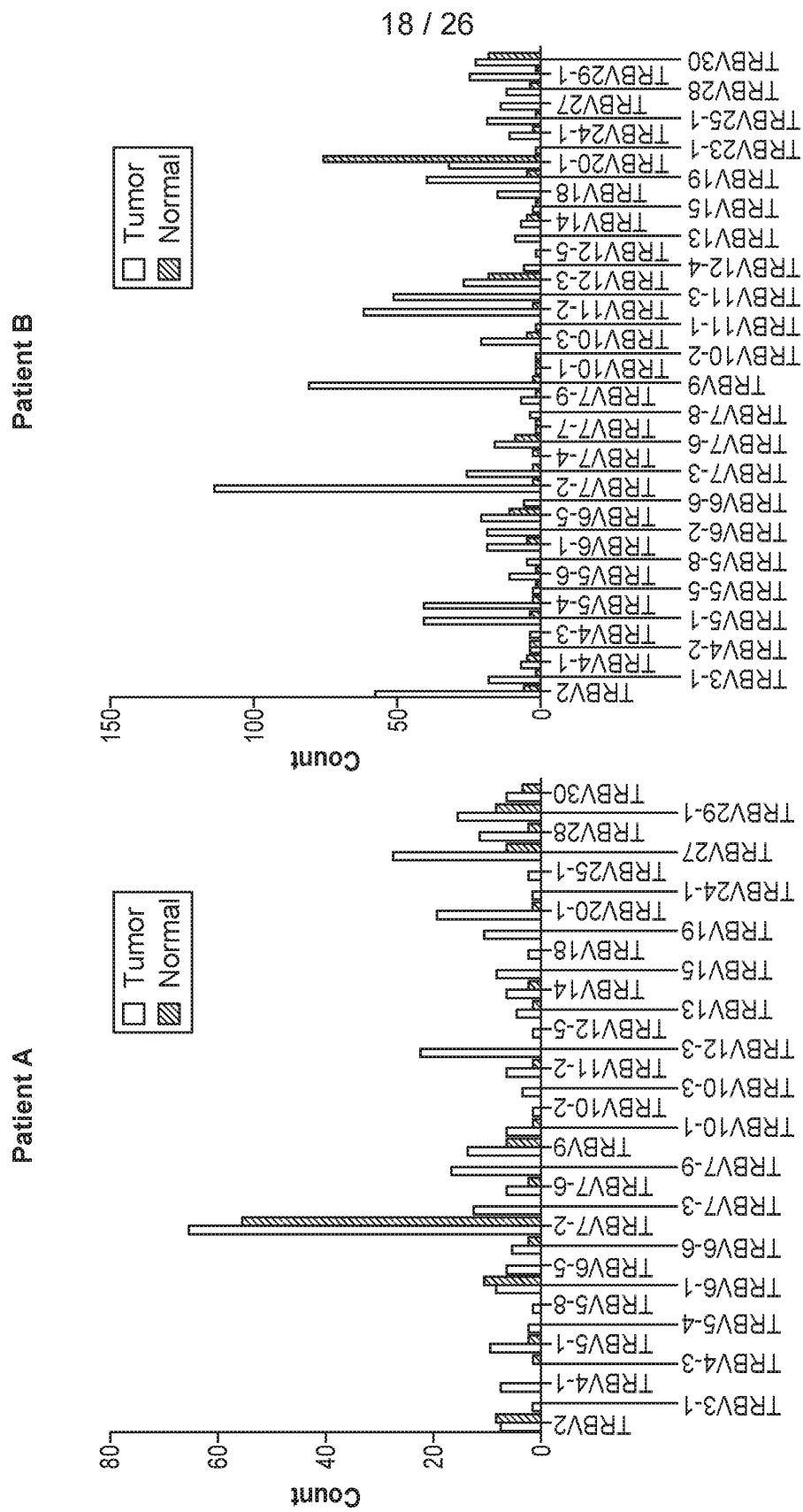


FIG. 9D

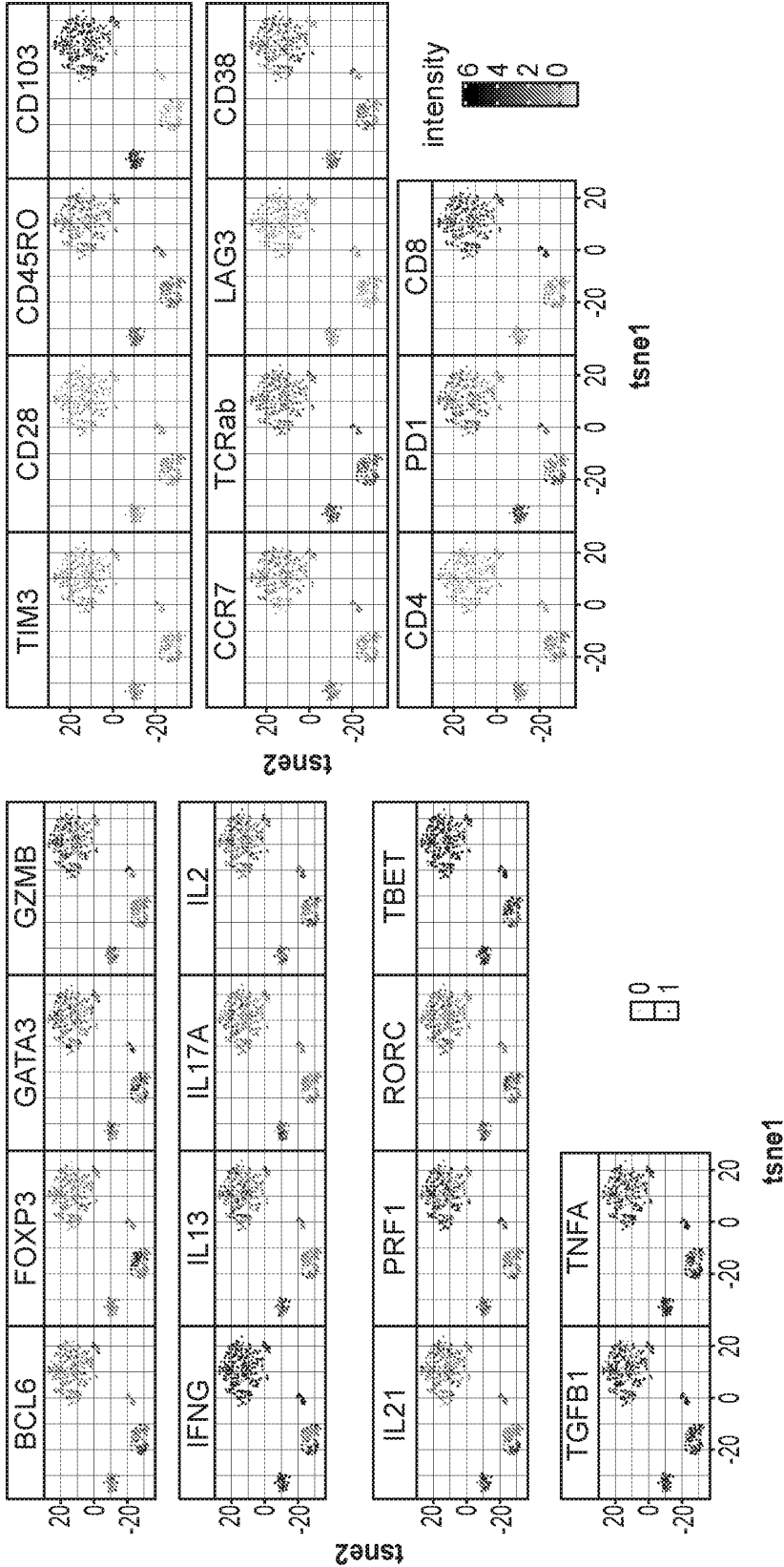
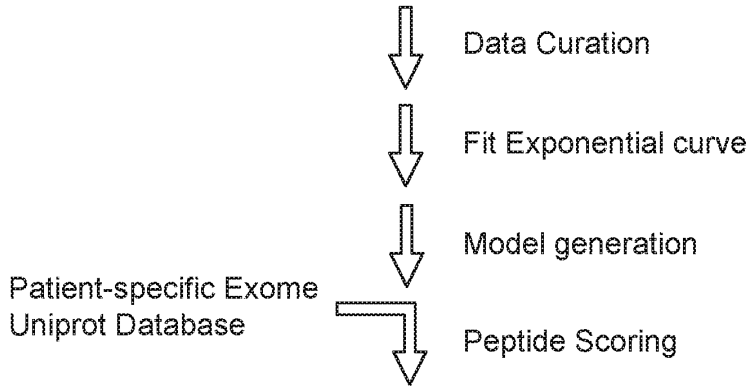


FIG. 9E

Peptide	Naive	RD 1	RD 2	RD 3	RD 4
SMGVITYEM	0	3	6744	71690	141732
YMGVSYEM	0	0	55	2430	1781
YMGVVYEM	0	1	158	1070	142
...	...	...	...	...	...



$C = K \cdot 2^{(F \cdot R)}$

C = counts
K = constant
F = fitness
R = round #

FIG. 10A

FIG. 10B

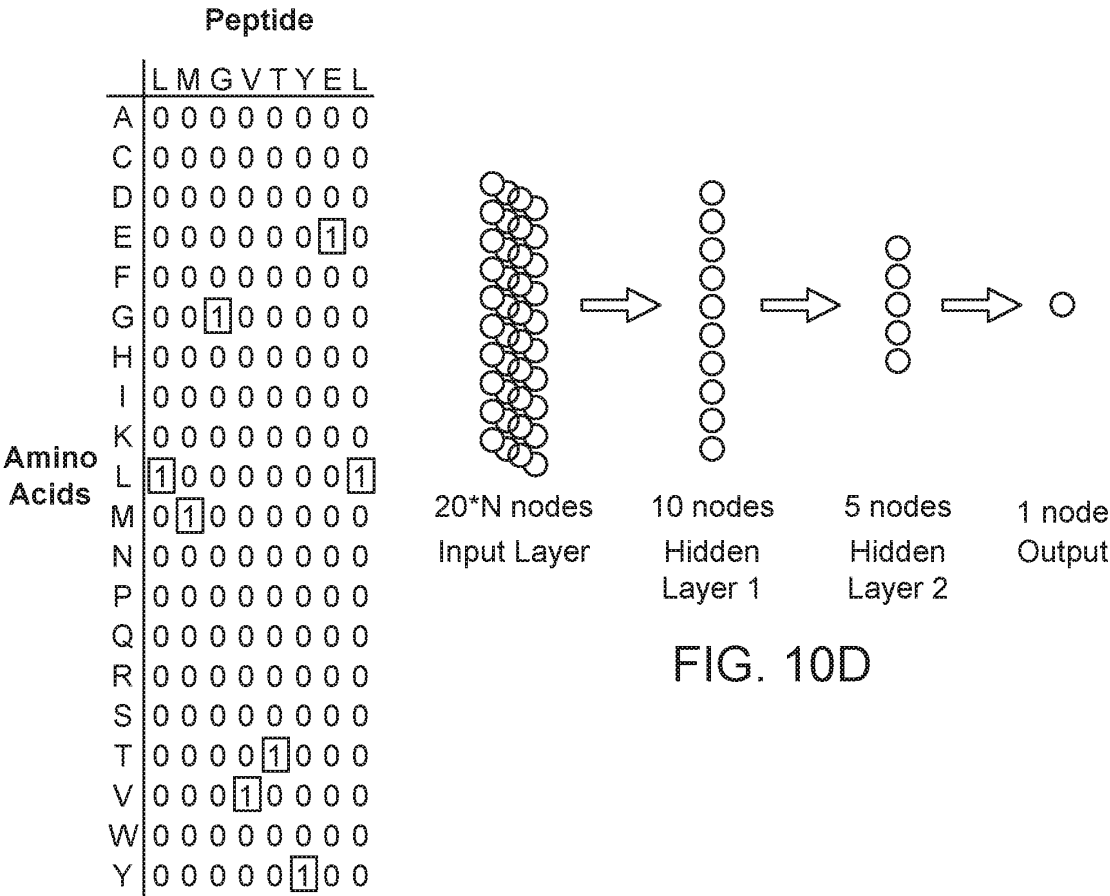


FIG. 10C

FIG. 10D

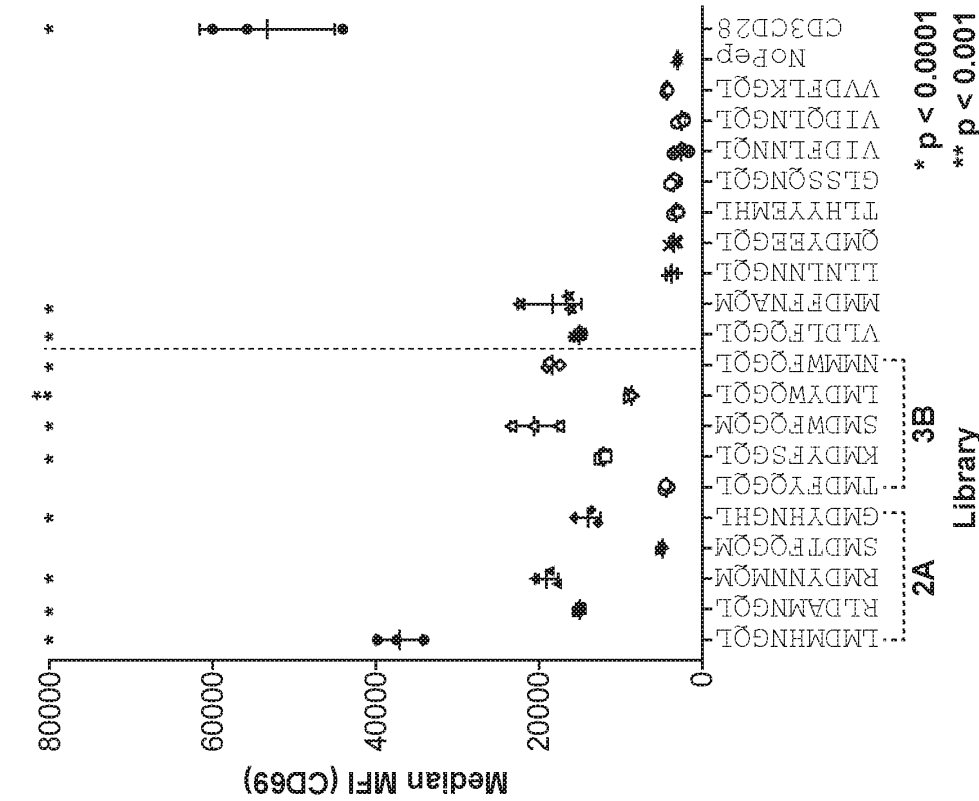


FIG. 11B

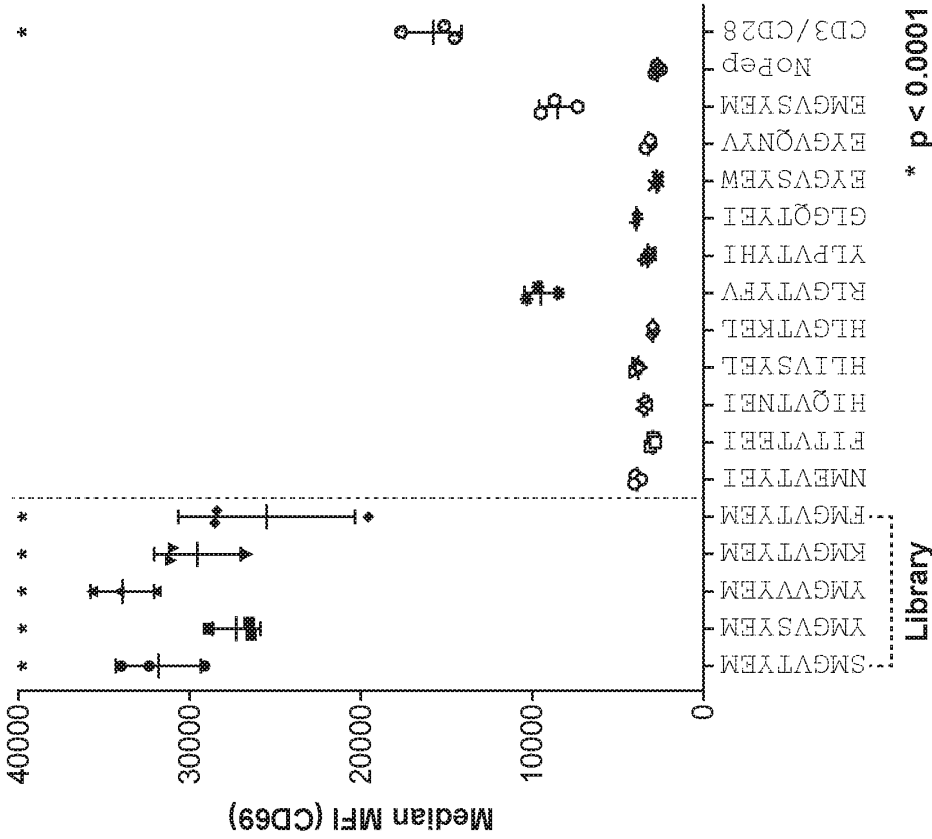


FIG. 11A

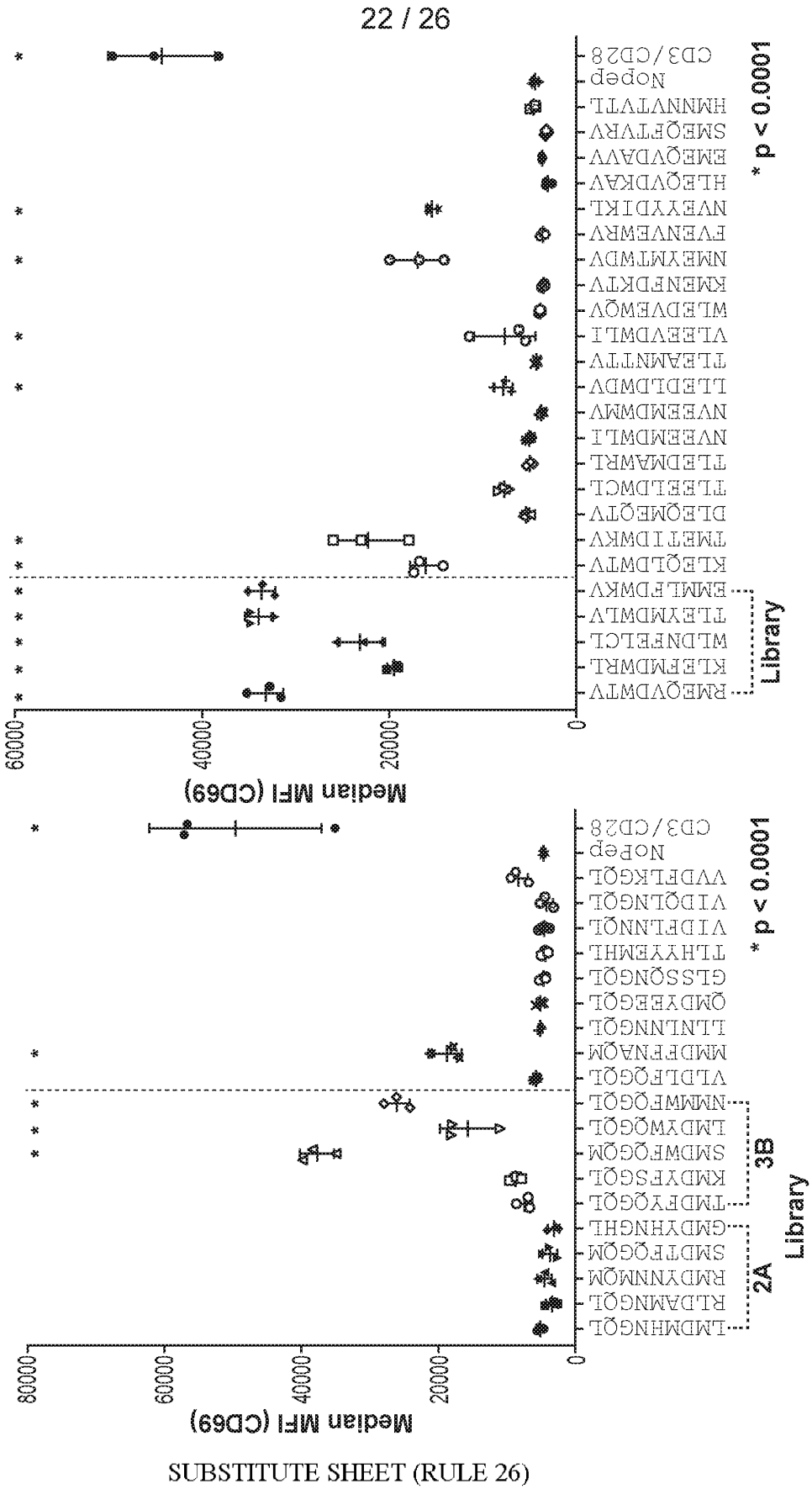


FIG. 11D

FIG. 11C

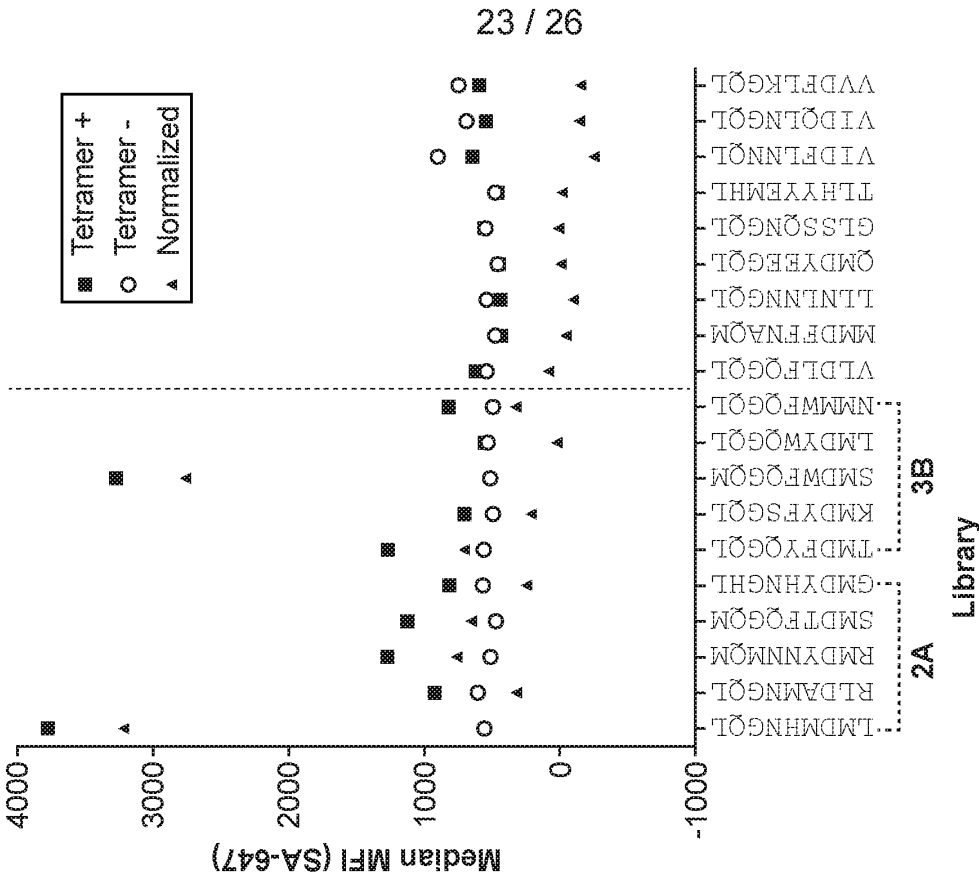


FIG. 11F

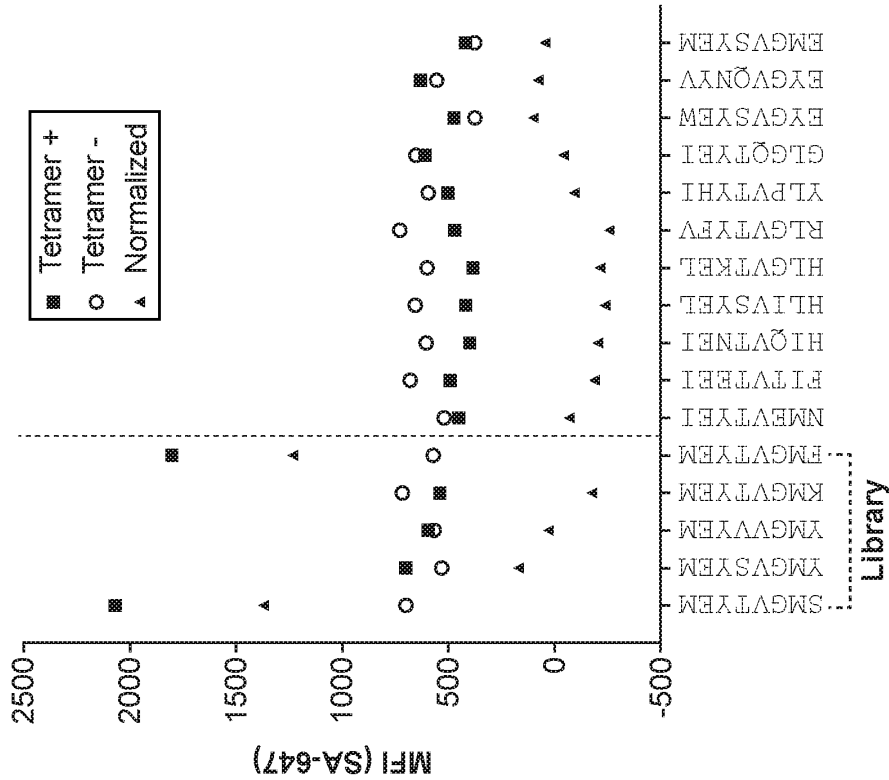
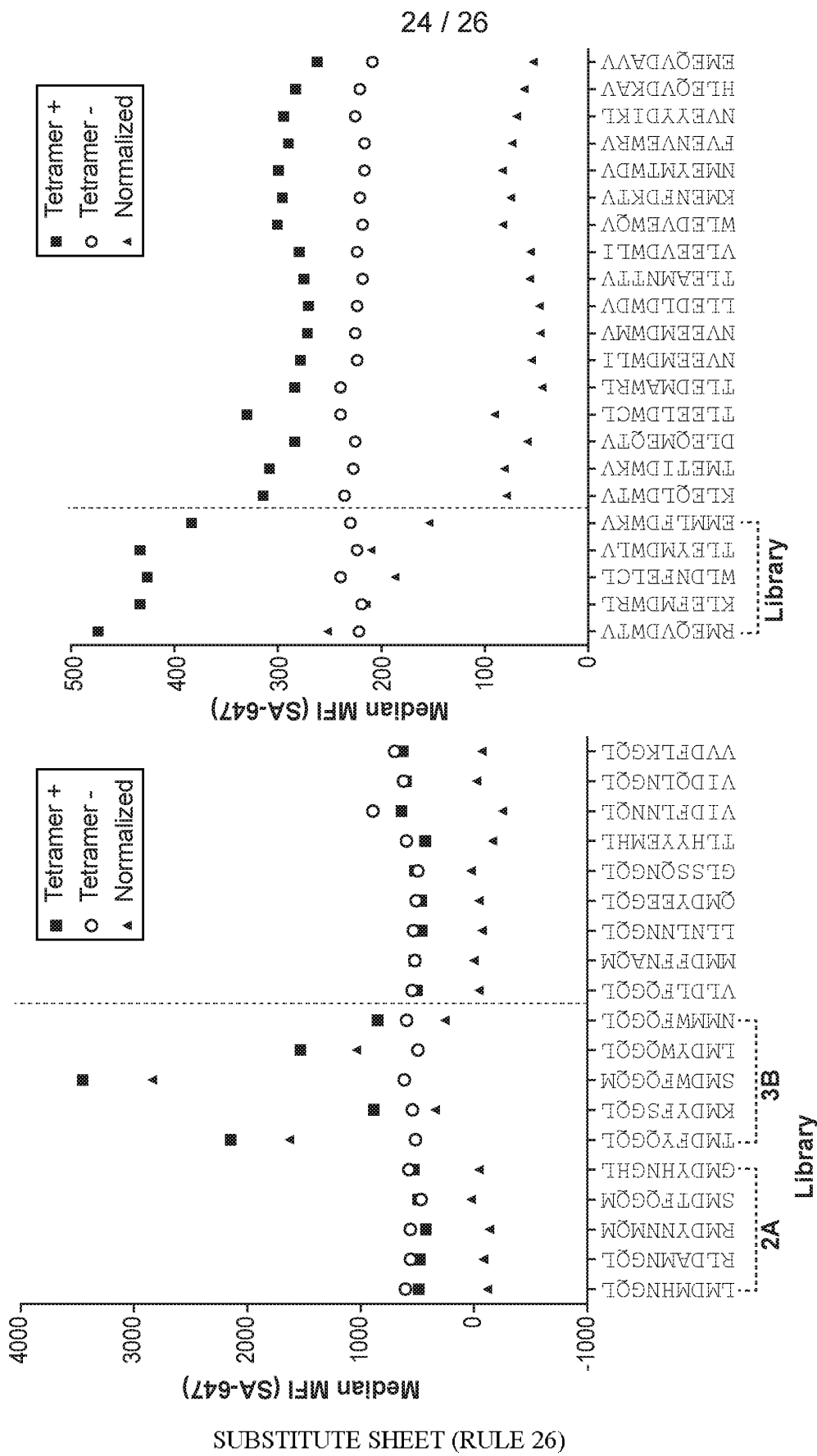


FIG. 11E



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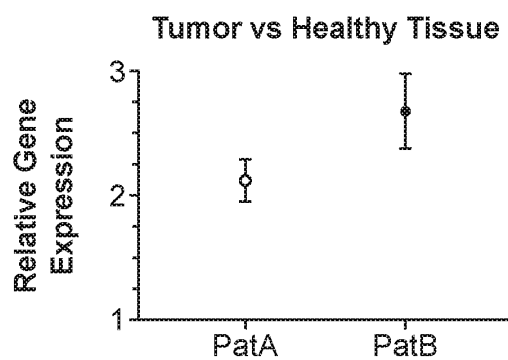


FIG. 12A

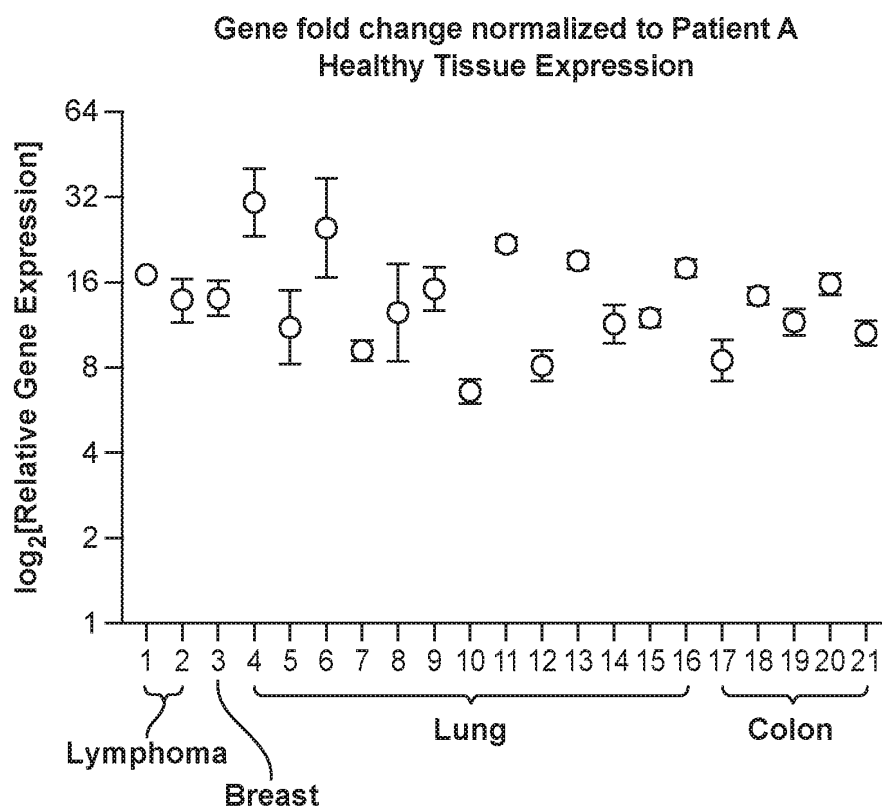


FIG. 12B

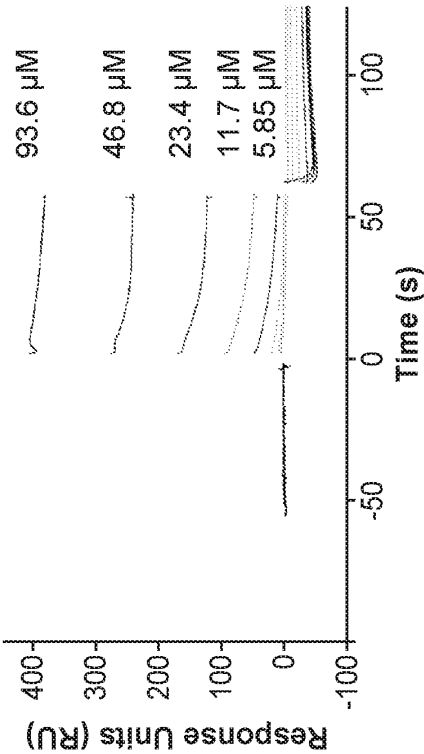


FIG. 12D

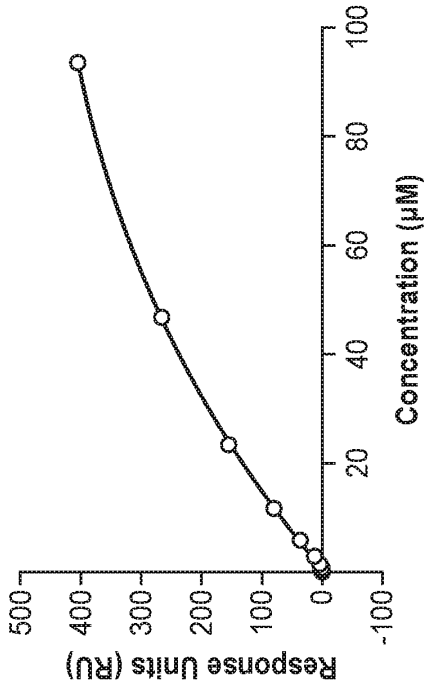


FIG. 12E

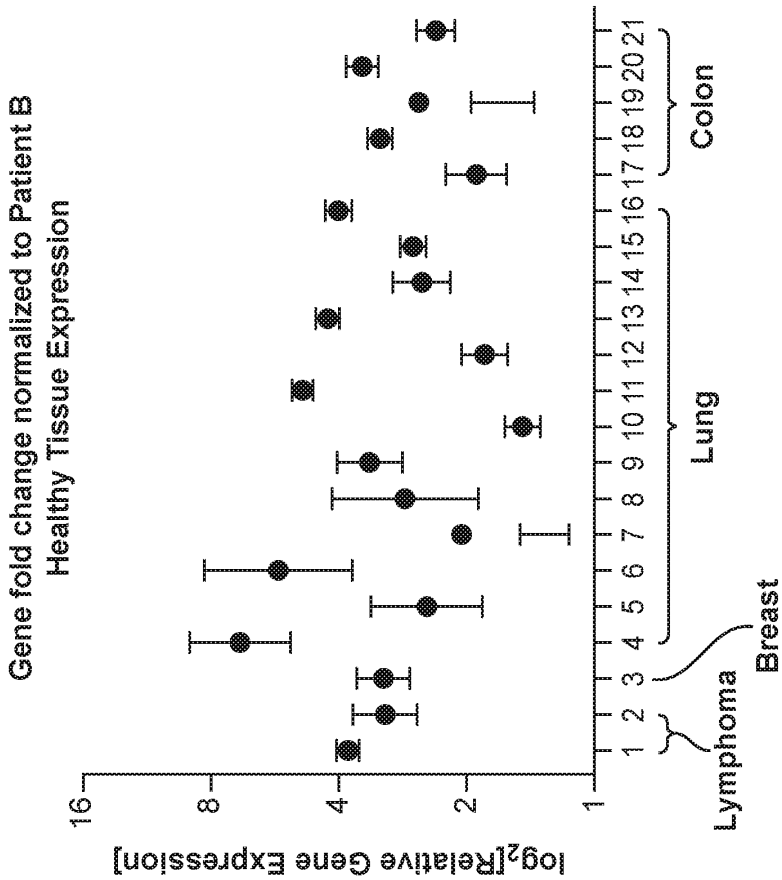


FIG. 12C