

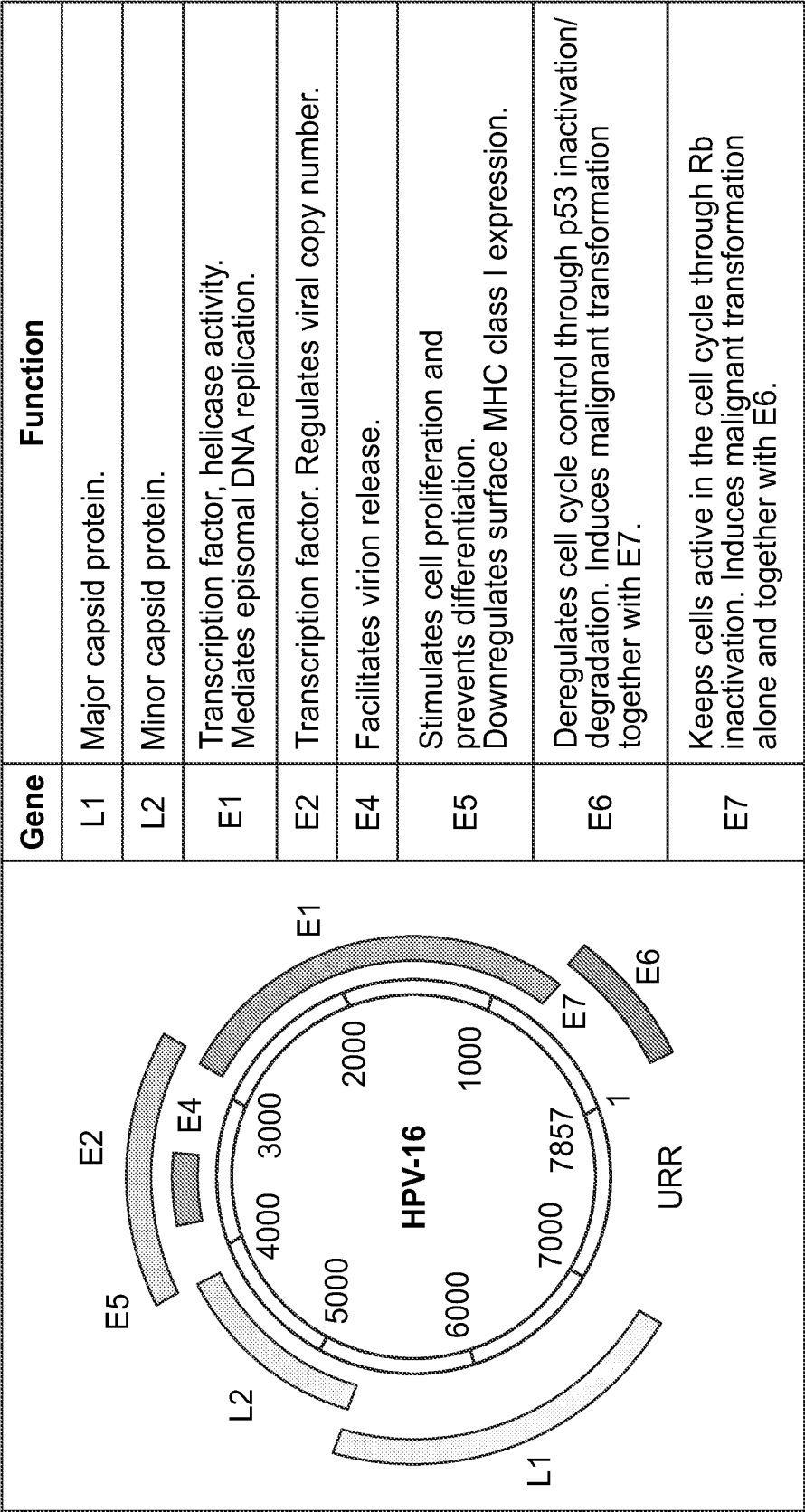


FIG. 1

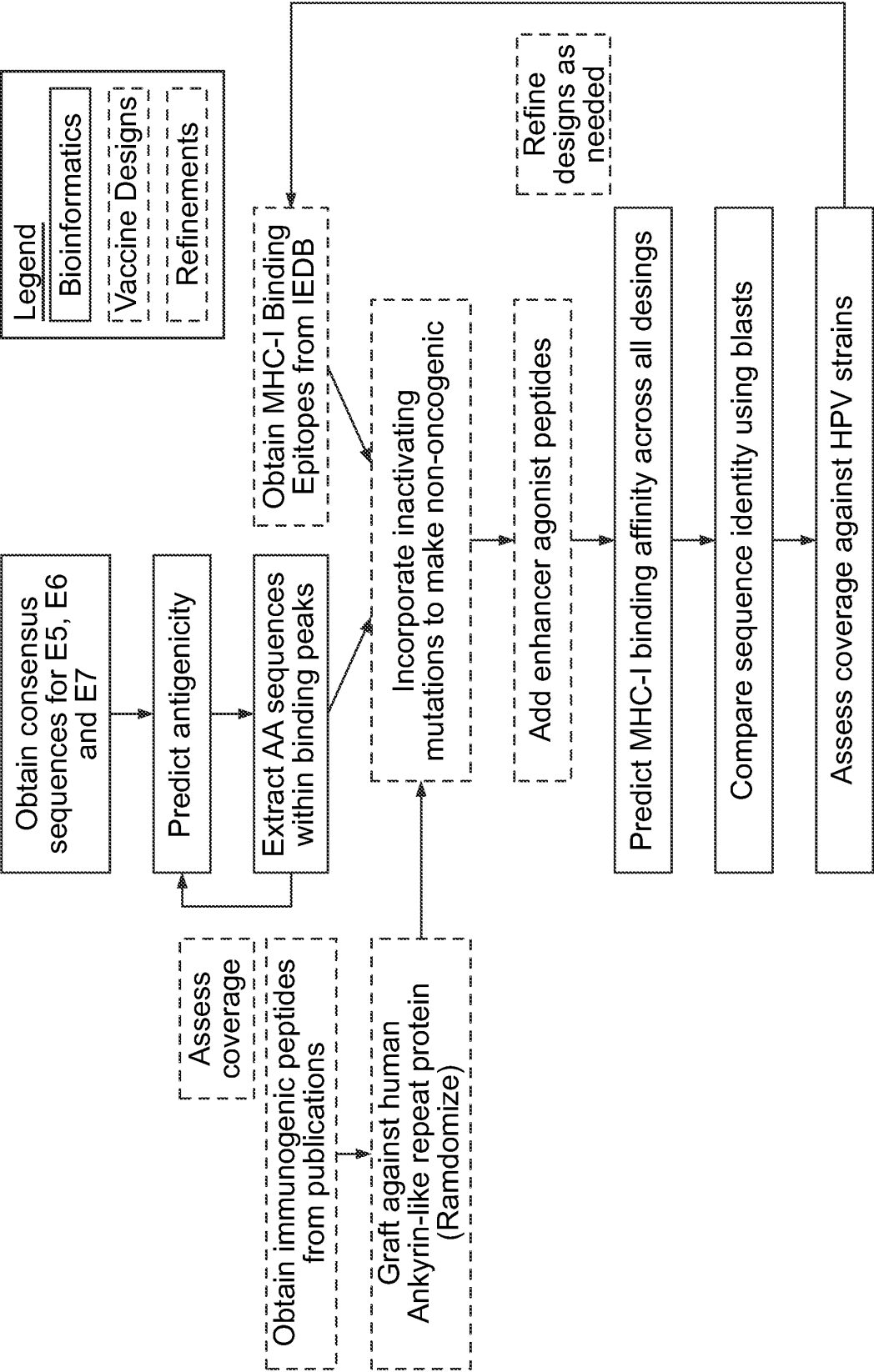


FIG. 2

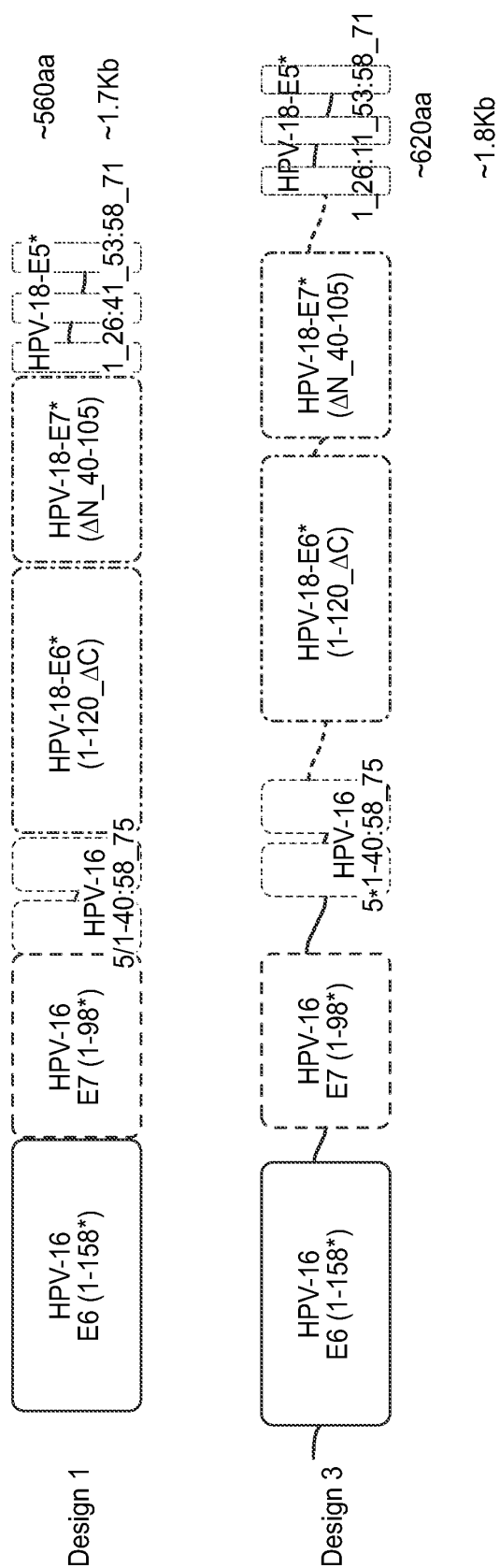


FIG. 3

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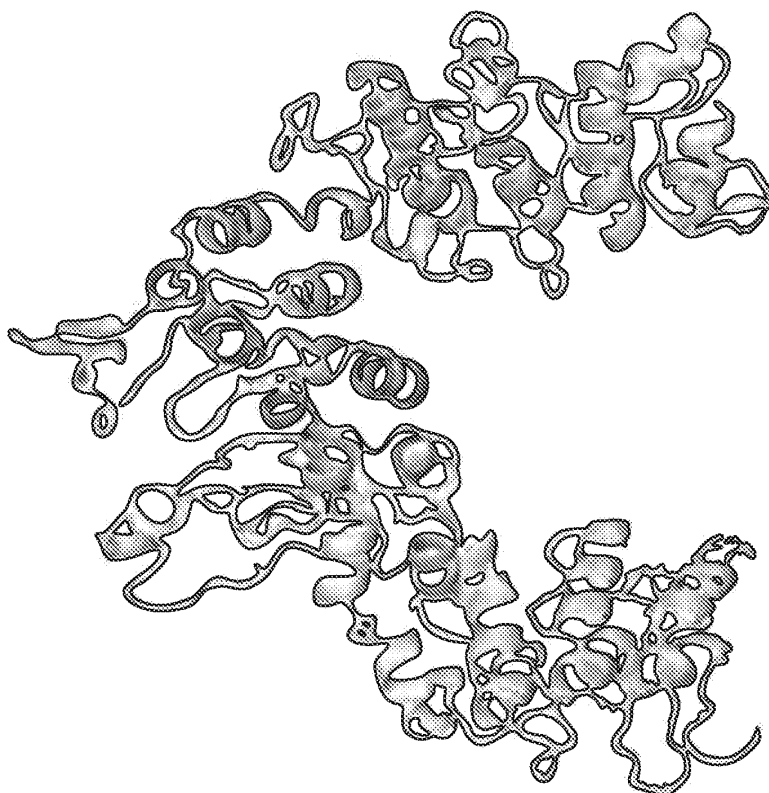


FIG. 4B

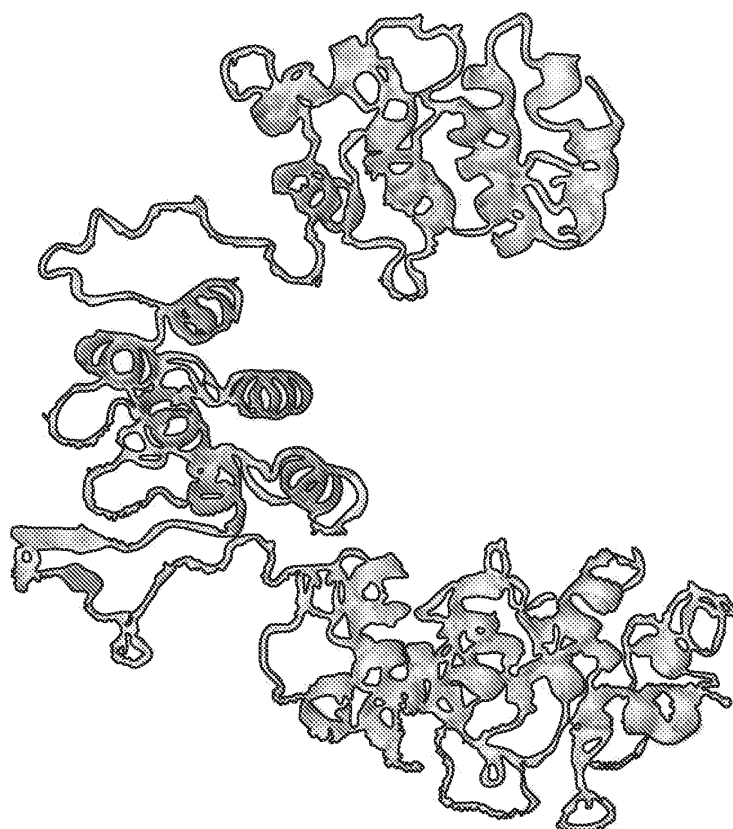


FIG. 4A

Score	Expect	Method	Identities	Positives	Gaps
585 bits(1507)	0.0	Compositional matrix adjust.	365/566(64%)	379/566(66%)	134/566(23%)
Query 4	RELTEVFEFAARYSRSDYIIFFVYIPLADAKLPQLCTEVDNMLLMGTLGIVPLHAAVSADT +ELTEVFEFA +Y IIFVYIP KLPQLCTEV LLMGTLGIV T				63
Sbjct 2	KELTEVFEFAKKY-----IIFVYIPLK-KKLPQLCTEVKK-LLMGTLGIV-----KKT				47
Query 64	LHEYMLDLNRNRTDLSEENDEIDGVNHQHLPARRMHDNLLIRCLRCPLILAARLAVLFL LHEYMLDL+ SEENDEIDGVNHQHLPARR NLLIRCLRC LFL				123
Sbjct 48	LHEYMLDLKK-----SEENDEIDGVNHQHLPARR-KKNLLIRCLRC-----KKLFL				93
Query 124	NTLSFVCPWCASHADVKCIDFYSRIDDLKLPDLCTELALHWAAAVNNVQLFNLTLSEVVG NTLSFVCPWCAS KCIDFYSRI KLPDLCTEL QLFNLTLSEV				183
Sbjct 94	NTLSFVCPWCASKK---KCIDFYSRIKK-KLPDLCTEL-----KKQLFNLTLSEV-				139
Query 184	ANKFQQLFNLTLNRRVYDFAFRDLPLFLAAREGSYEKLTNTGLYNLANRLCIVYRDGNPY KFQQLFNLTL +VYDFAFRDL +KLNTGLYNL +LCIVYRDGNPY				243
Sbjct 140	-KKFQQLFNLTLKKVYDFAFRDLK-----KKLTNTGLYNL-KKLCIVYRDGNPY				186
Query 244	AVCDDHMYMLDLQPETTPRDFAFRDLICIVIVRLLDLEVSQTSKLTRQTDRTLIGIVCP AVCD YMLDLQPETT + FAFRDLICIV +TLGIVCPI				303
Sbjct 187	AVCDKK-YMLDLQPETT-KKFAFRDLICIVY-----KKTLGIVCPIK				225
Query 304	ARYSRSDRTLEDLLMGVADATIHDIILECVDNMHLDKKQRFHNIPLHAAVSADTTLEQQY RTLEDLLMGV TIHDIILECV HLDKKQRFHNI TTLEQQY				363
Sbjct 226	K-----RTLEDLLMGVK-KTIHDIILECVKK-HLDKKQRFHNI-----KKTTLLEQQY				270
Query 364	NKPLCDLLRNRTDLCDSITRLCVMHDRWTGRCMSSCCPLILAARLAVSLQDIEITCVSHA NKPLCDLL+ CDSTLRLCV RWTGRCMSCC SLQDIEITCV				423
Sbjct 271	NKPLCDLLKK-----CDSTLRLCV-KKRWGRCMSCC-----KKSLQDIEITCVKK-				315
Query 424	DVLCVQSTHVDIDDLAHYNIIVTFCCCLHWAAAVNNVDDLRAFQQLFNLTLSEGANKISEYRH LCVQSTHVDI AHYNIIVTFCC DDLRAFQQLFNLTL KISEYRH				483
Sbjct 316	--LCVQSTHVDIKK-AHYNIIVTFCC-----KKDDLRAFQQLFNLTL--KKISEYRH				362
Query 484	YCYNRRKLPQLCTELPLFLAAREGSYEKTVLELTEVANRRRTLEDLLMGTFDMFAFKDLFV YCY +KLPQLCTEL +KTVLELTEV +RTLEDLLMGTFDMFAFKDLFV				543
Sbjct 363	YCY-KKKLPQLCTELK-----KKTVLELTEV-KKRTLEDLLMGTKK-FAFKDLFV				409
Query 544	VPRDQLYNKPLCDVIVRTLQDIVLHL 569				
Sbjct 410	V + QLYNKPLCDV +TLQDIVLHL 433				
	V-KKQLYNKPLCDV-KKTLQDIVLHL				

FIG. 5A

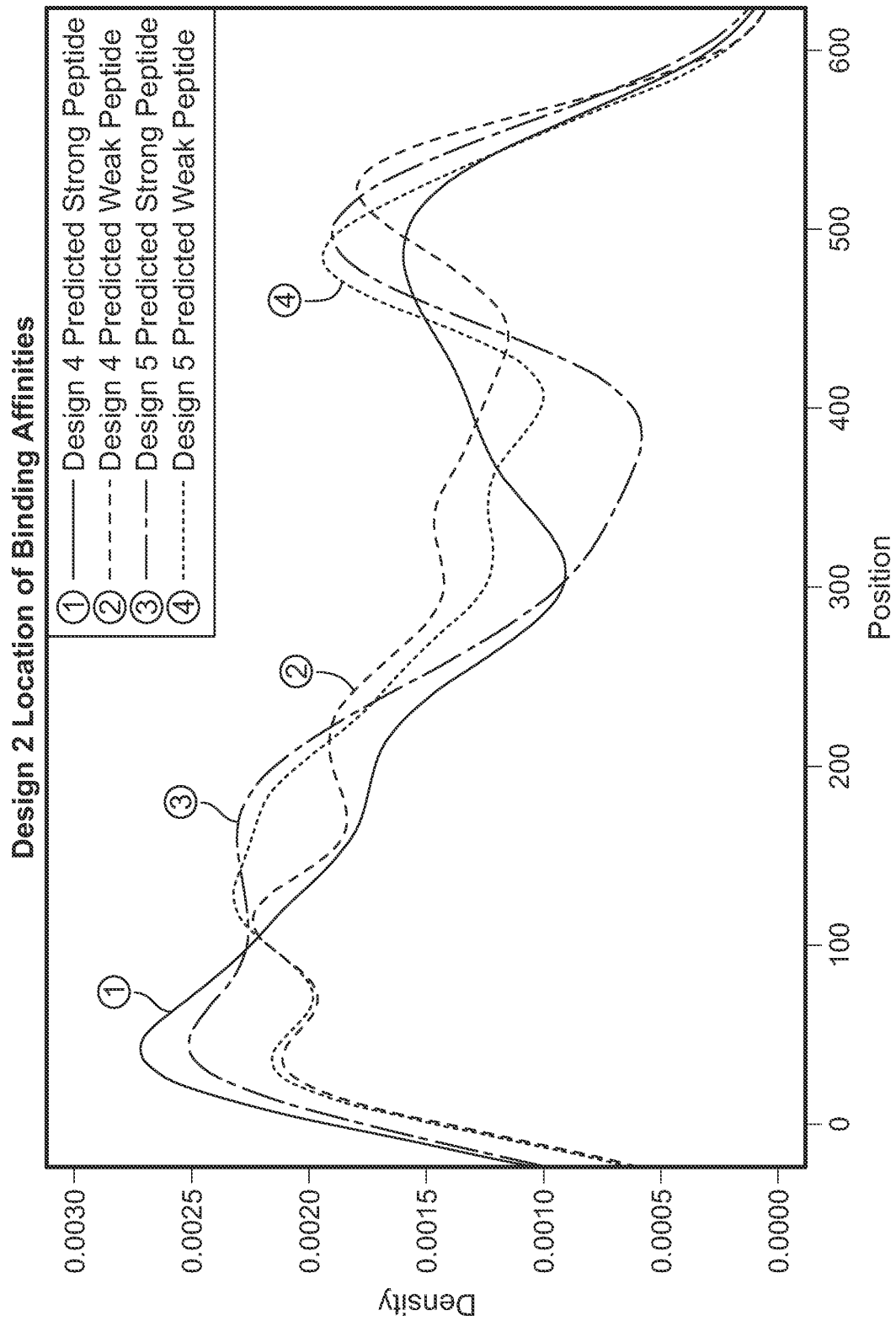


FIG. 5B

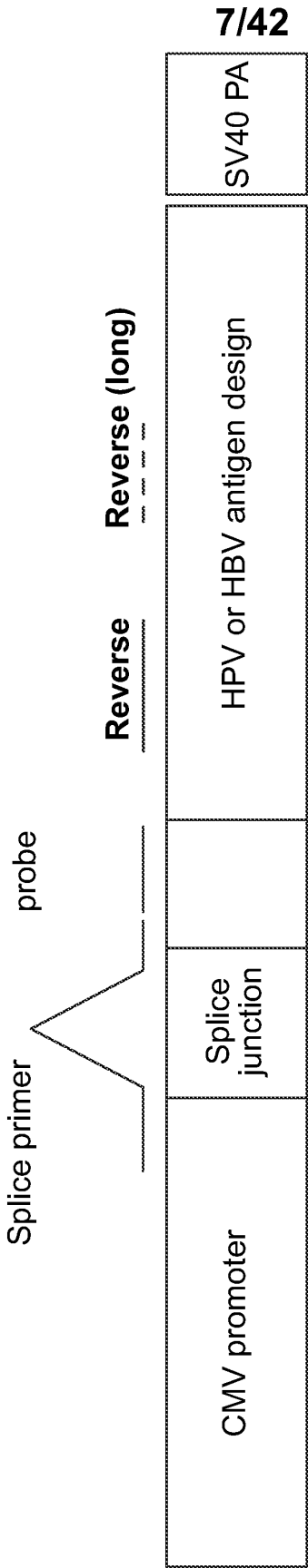


FIG. 6

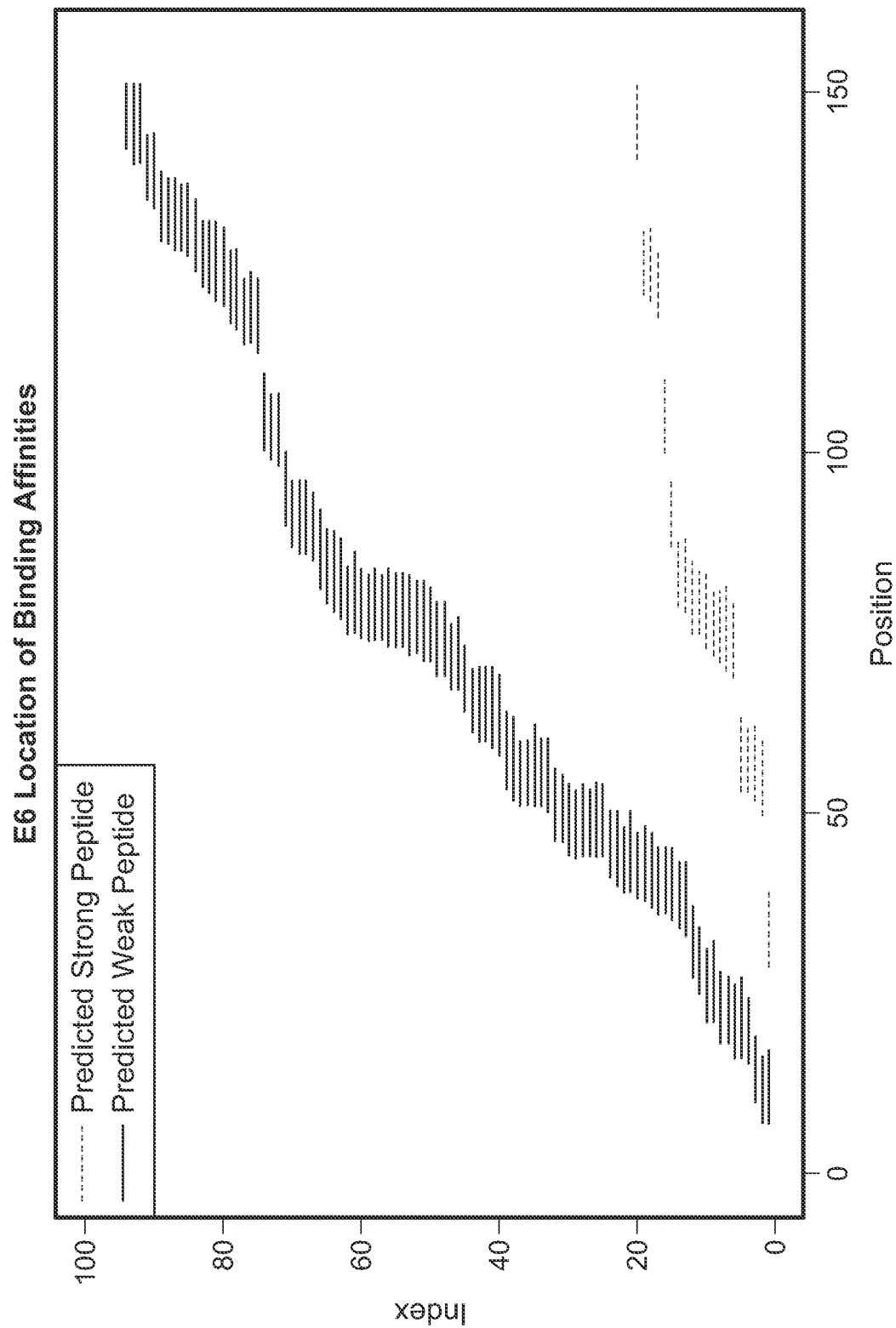


FIG. 7A

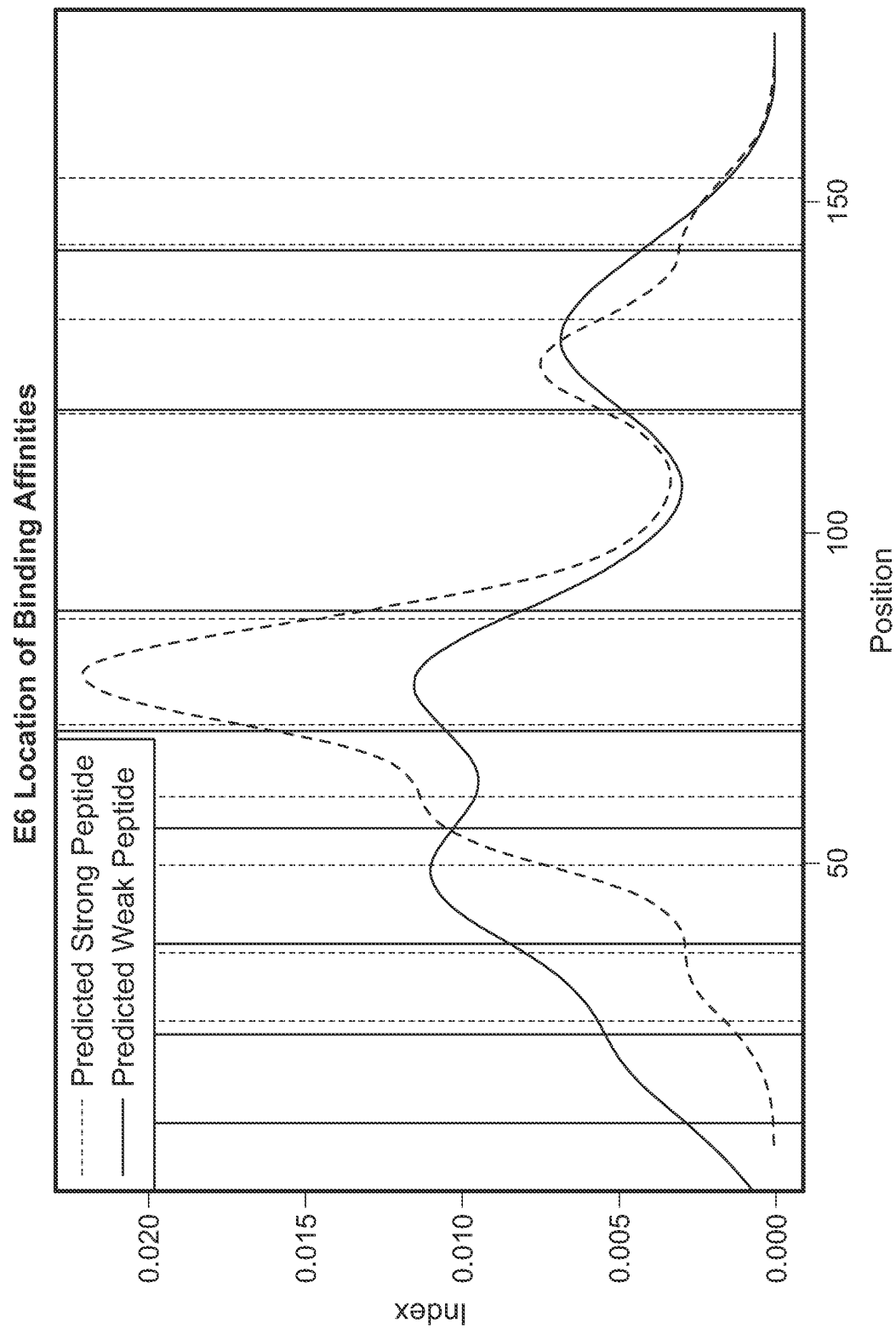


FIG. 7B

[illegible]

FIG. 7C

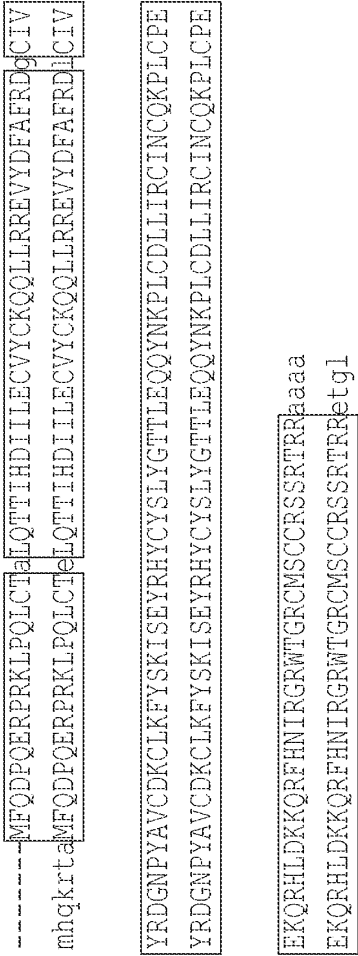
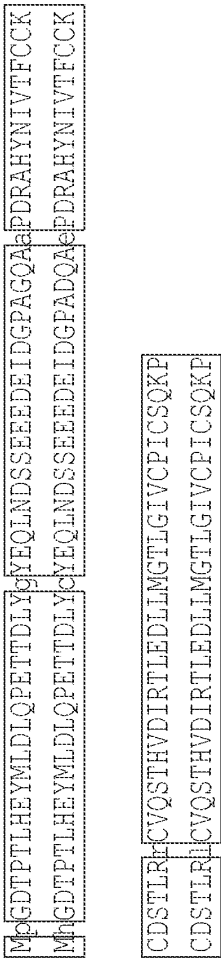


FIG. 9A



(MOD-1755805) HPV- 16 E7 (1-98) n
native seq

(MOD-1755805) HPV- 16 E7 (1-98) n
native seq

FIG. 9B

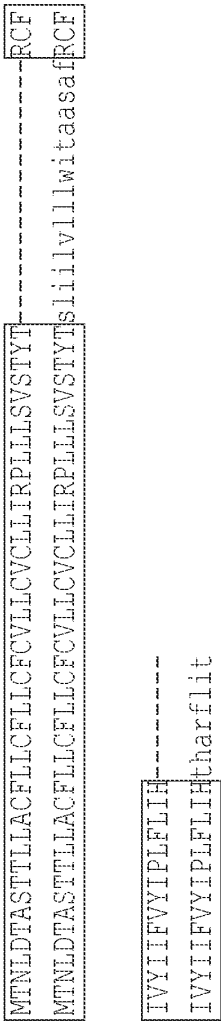


FIG. 9C

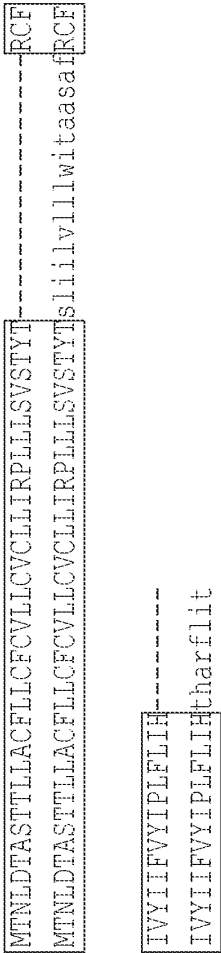


FIG. 10A

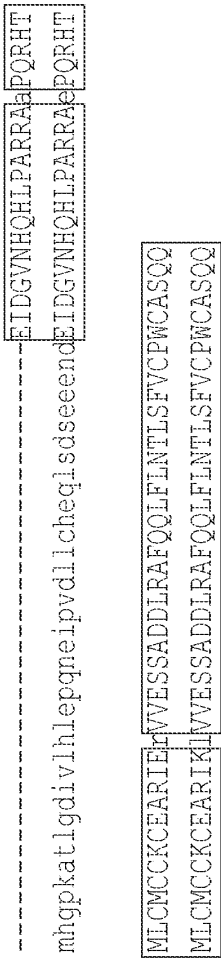


FIG. 10B

(MOD-1755809) HPV- 18 E5 (1-26:41
native seq

(MOD-1755809) HPV- 18 E5 (1-26:41
native seq

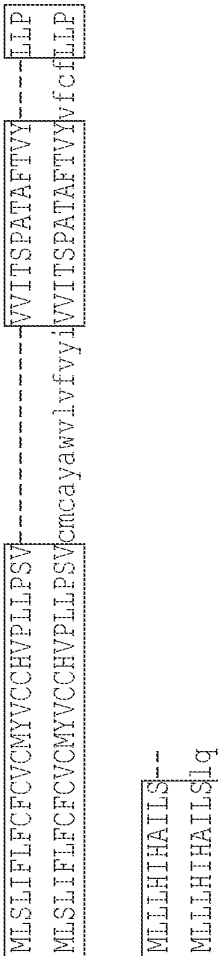


FIG. 10C

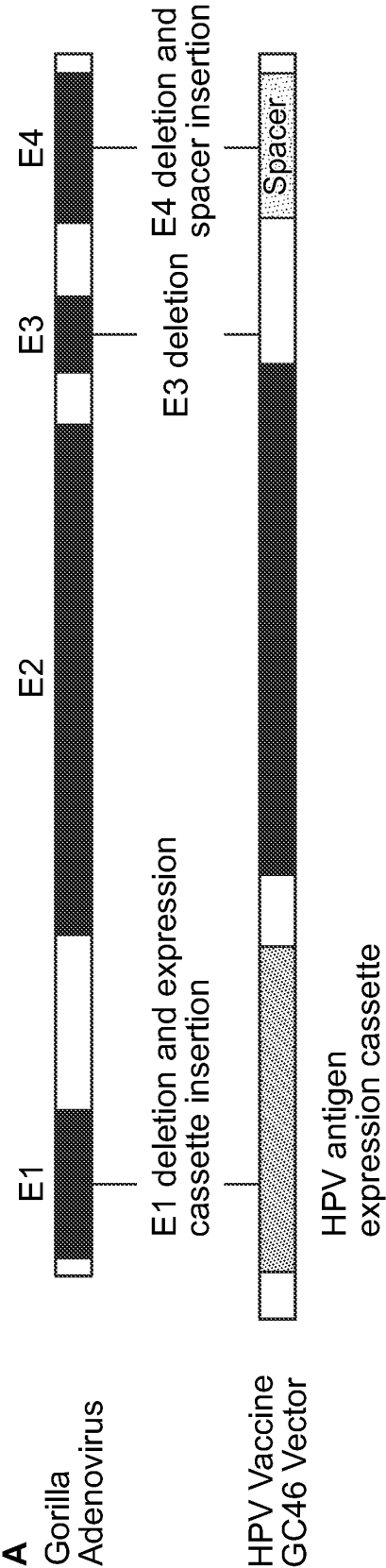


FIG. 11A

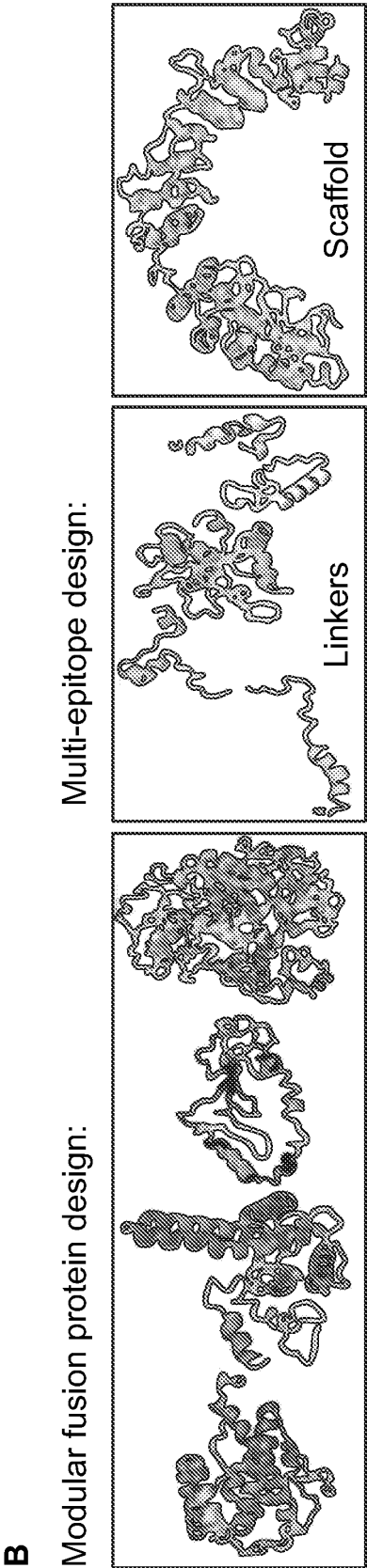


FIG. 11B

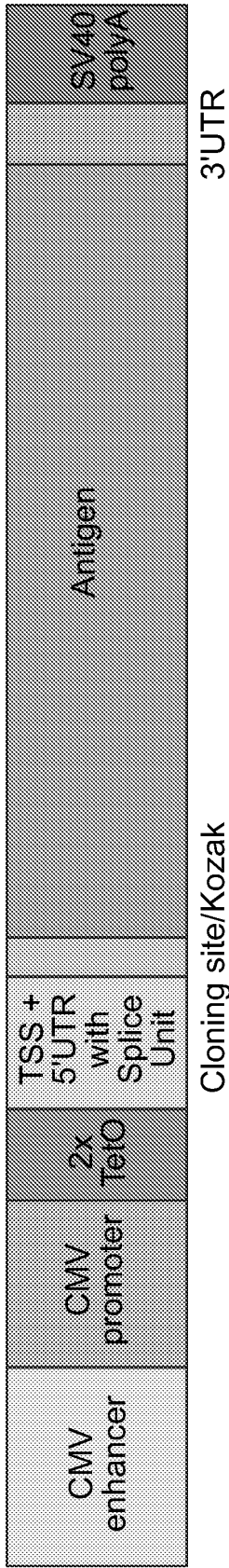
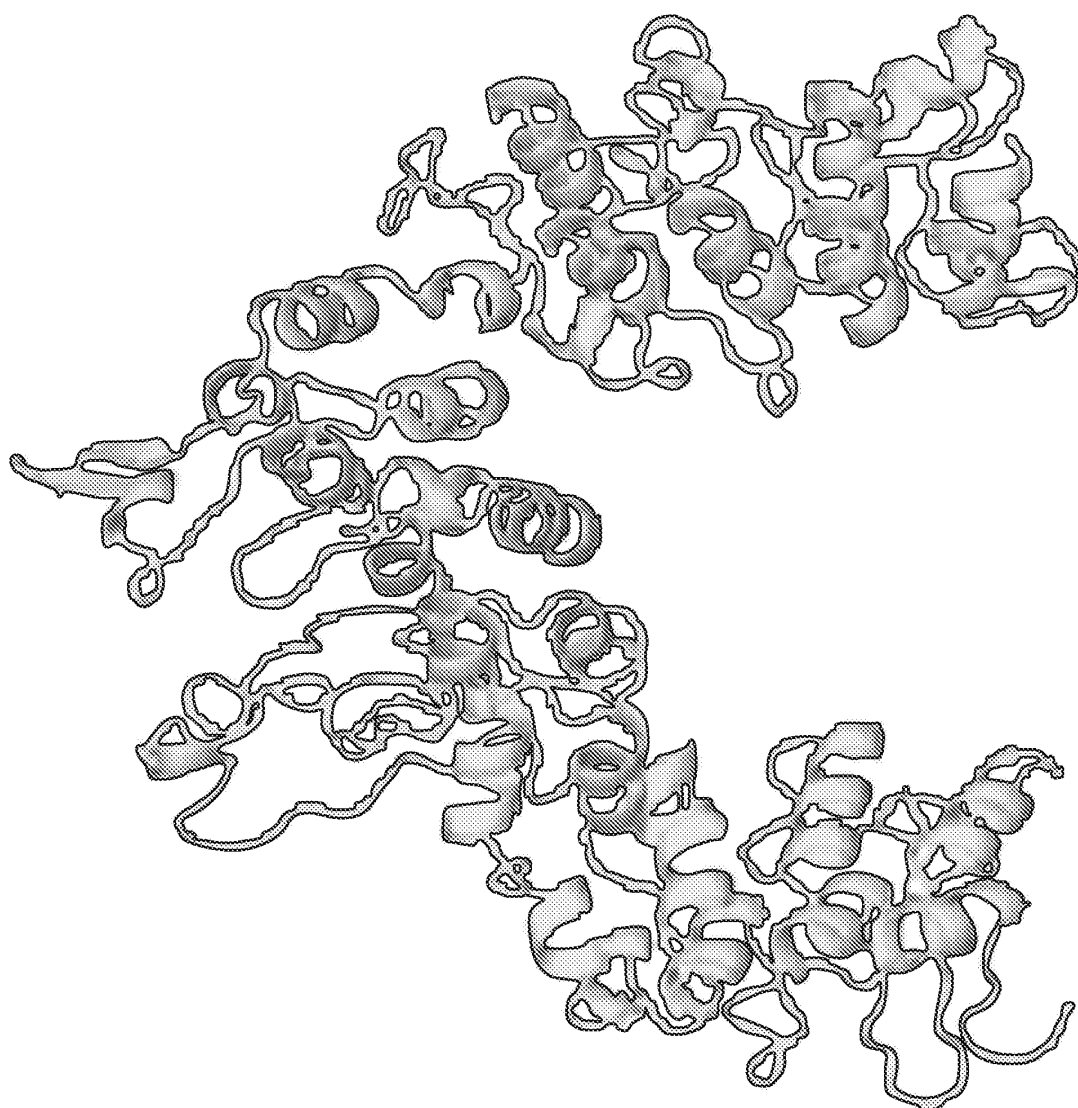


FIG. 12

FIG. 13A



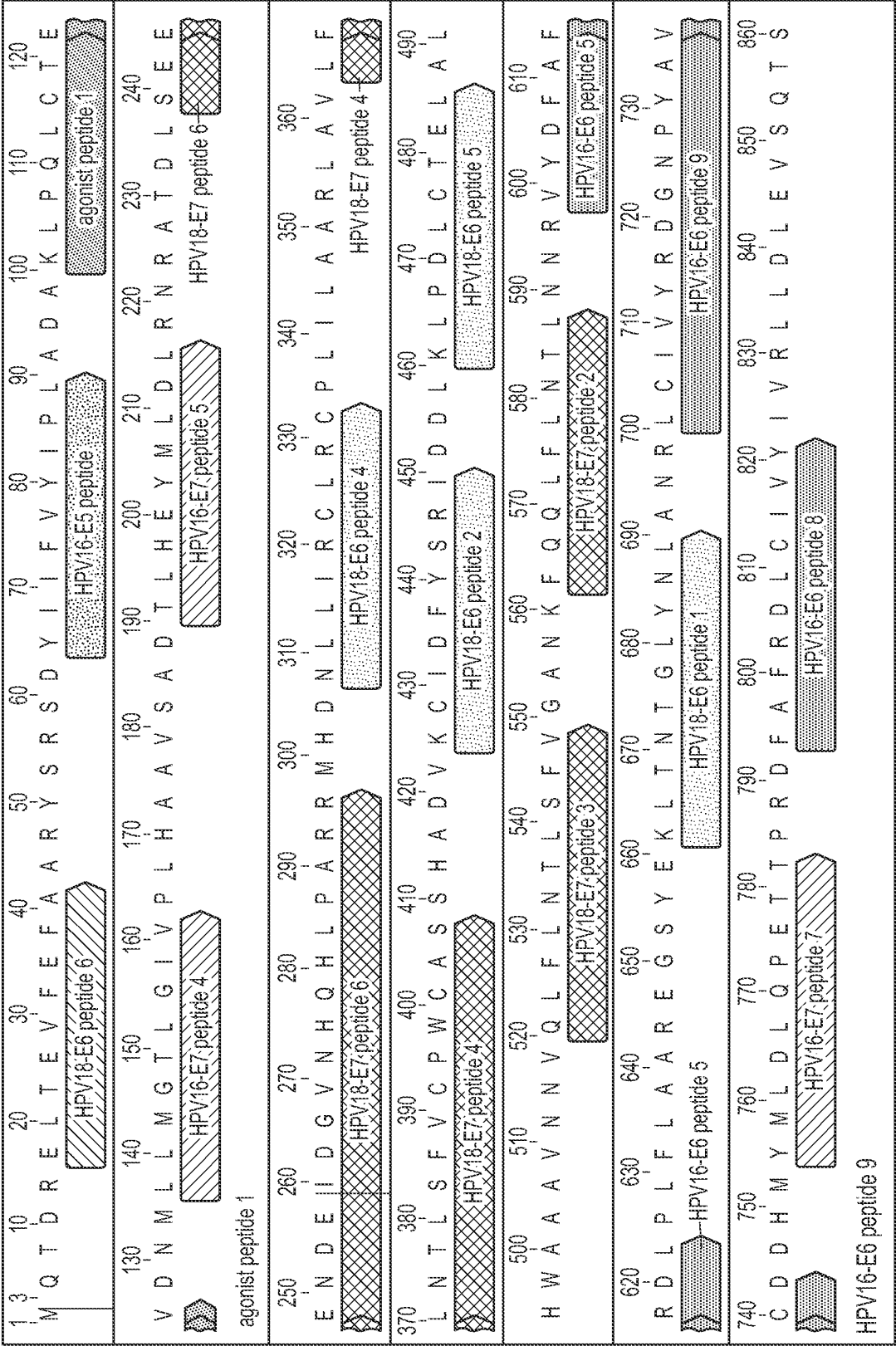


FIG. 13B

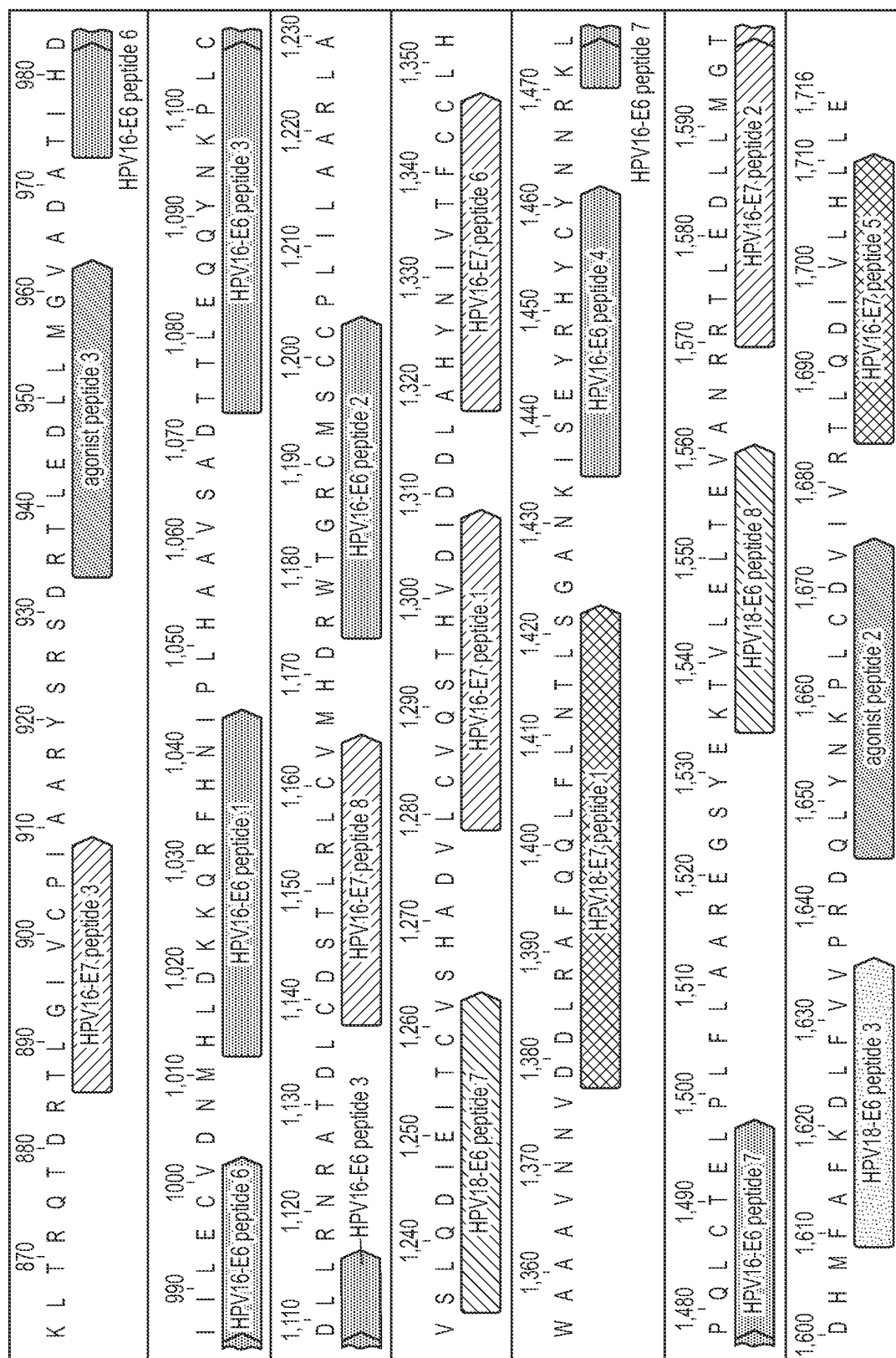
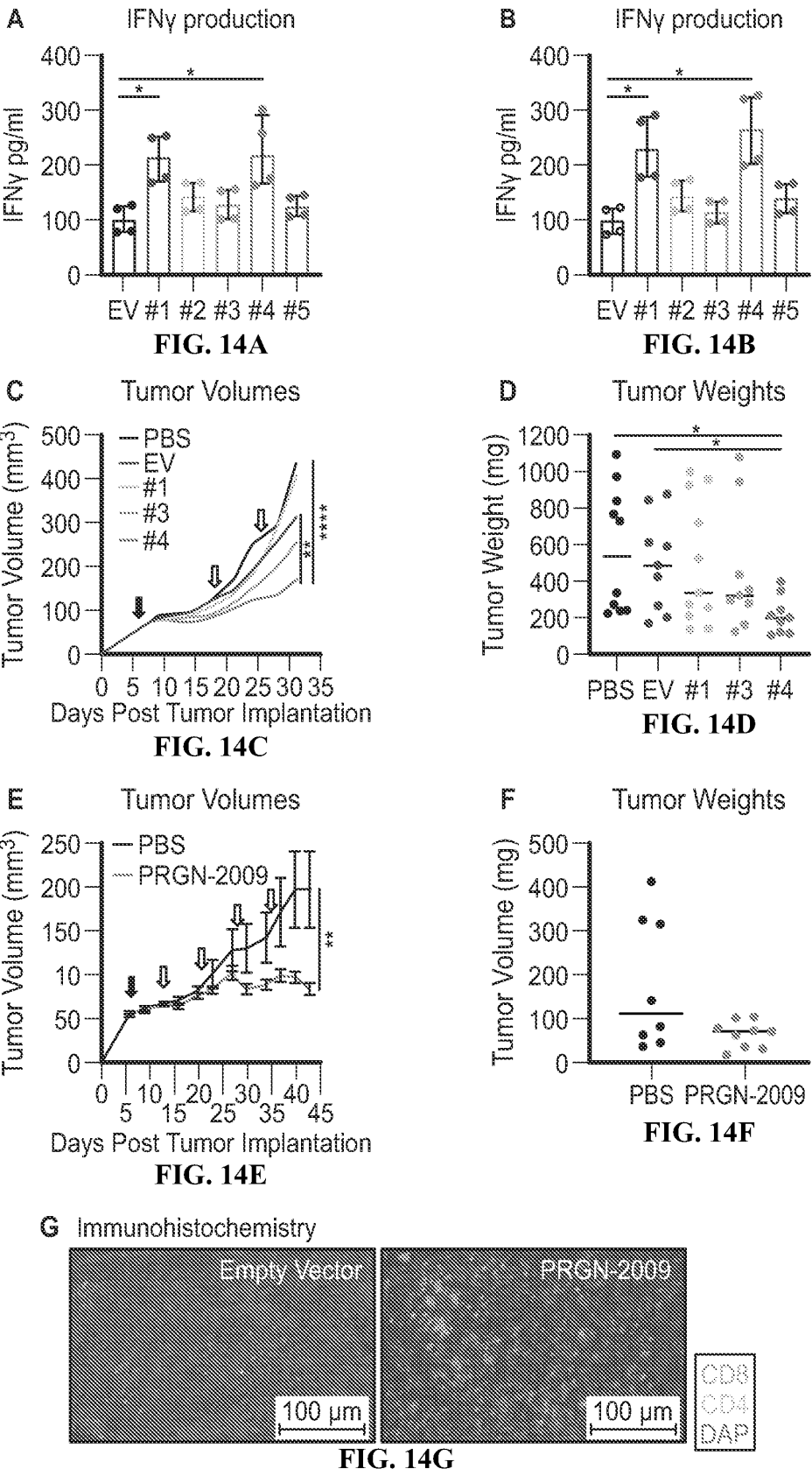


FIG. 13B (Cont.)



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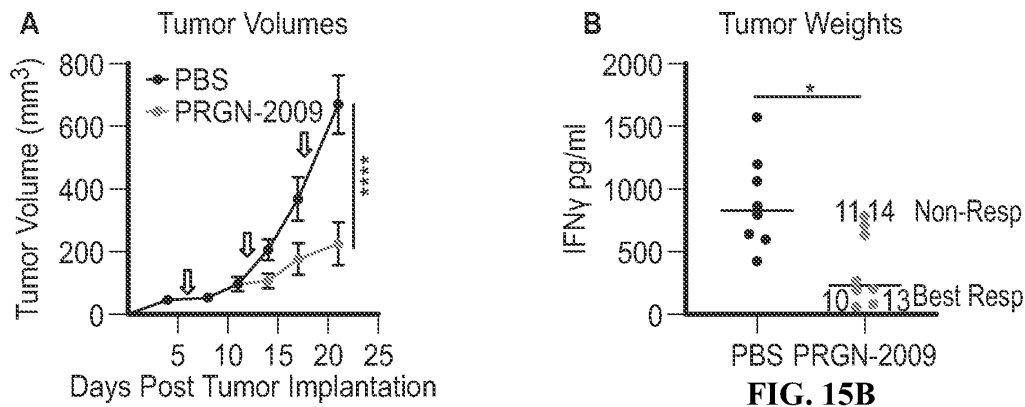


FIG. 15A

FIG. 15B

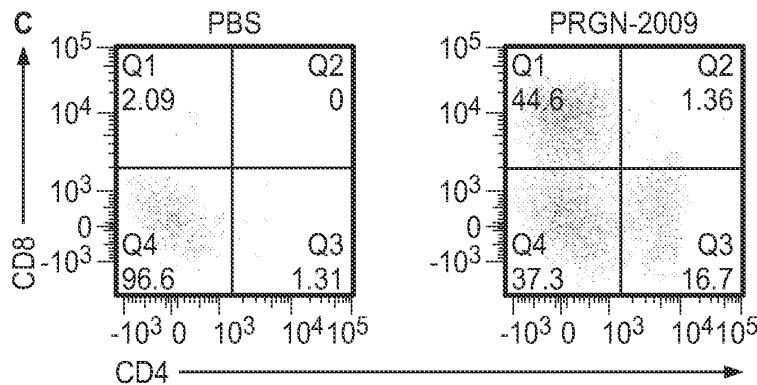


FIG. 15C

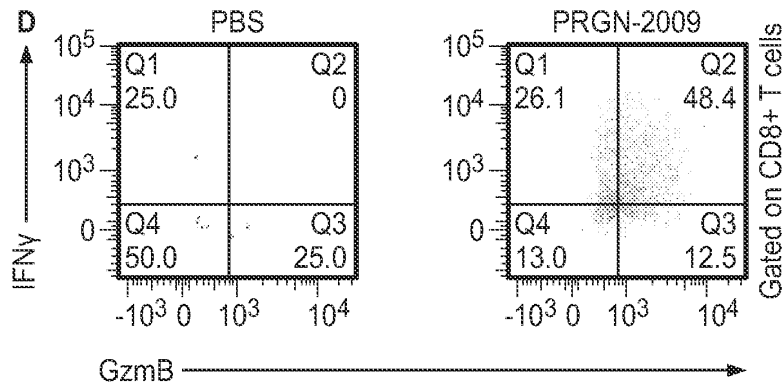


FIG. 15D

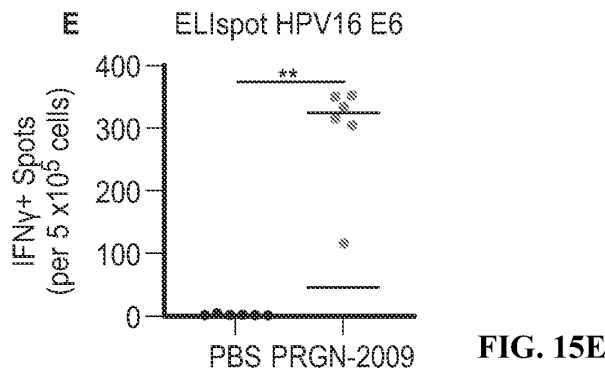
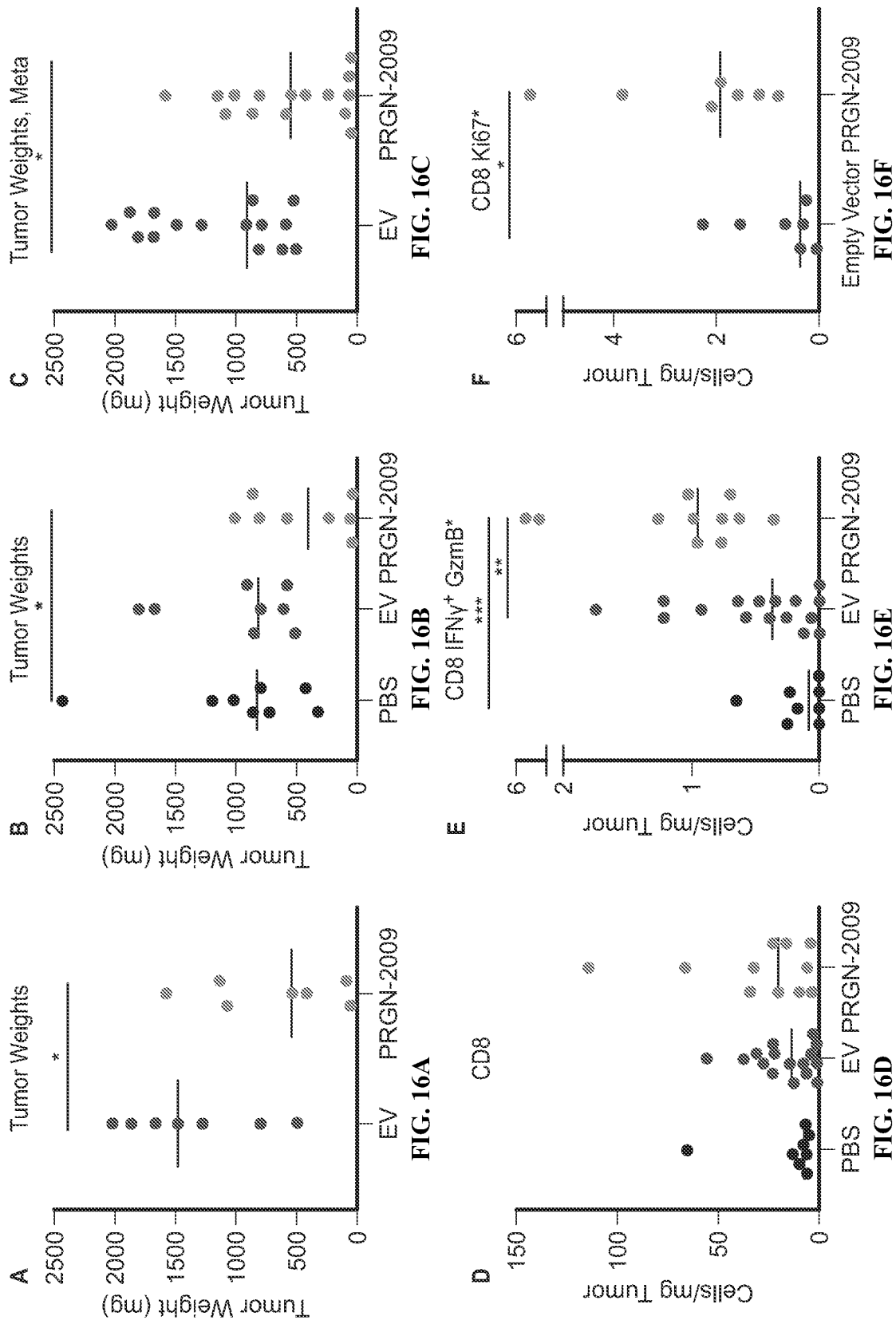
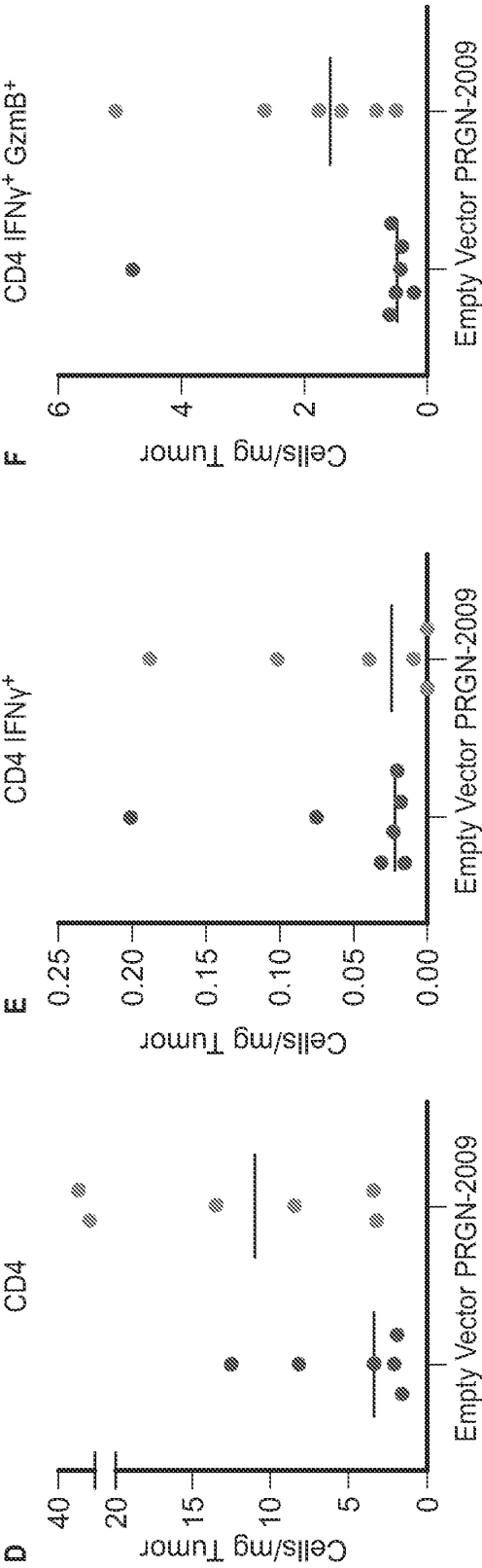
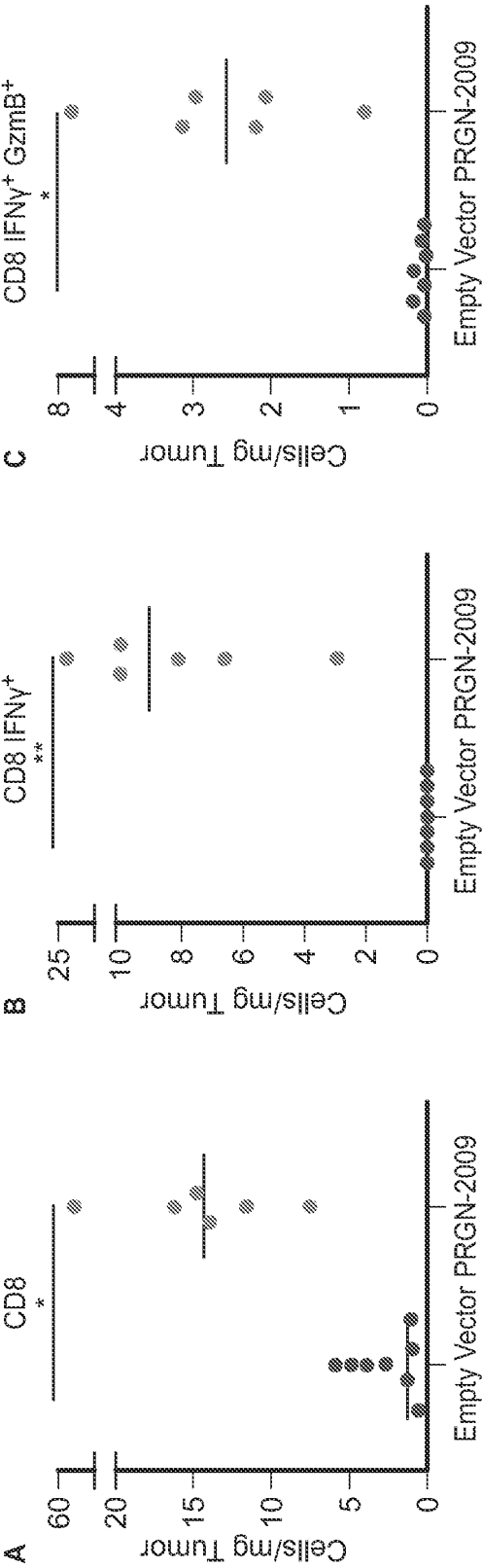
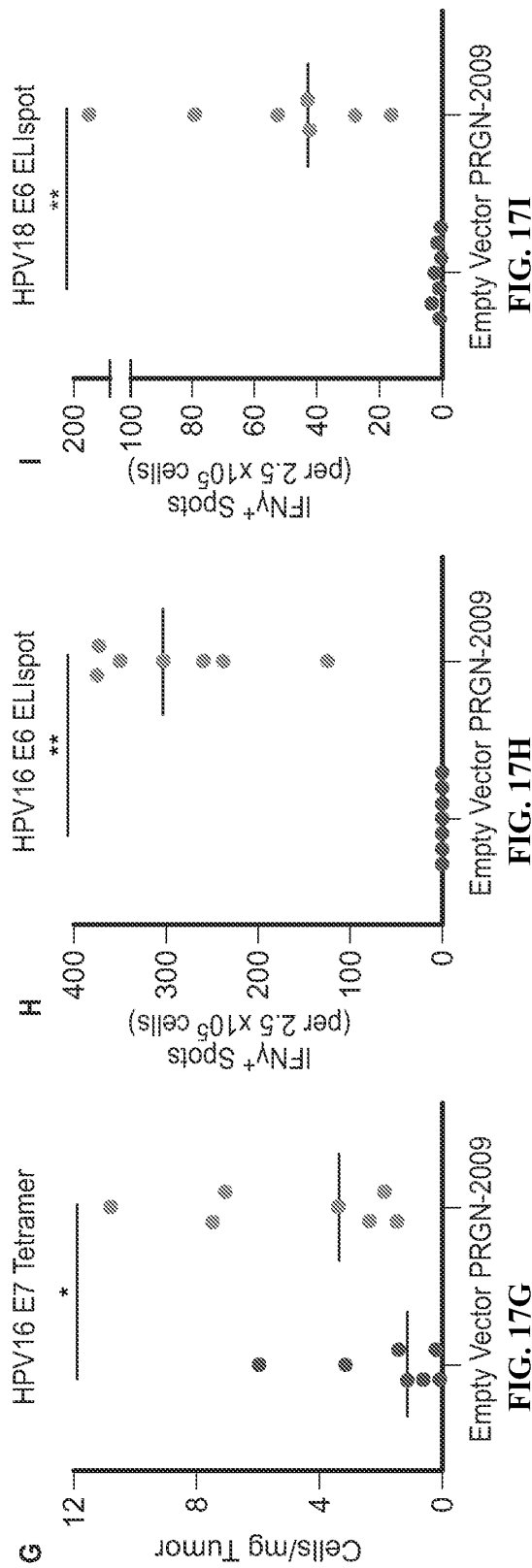


FIG. 15E







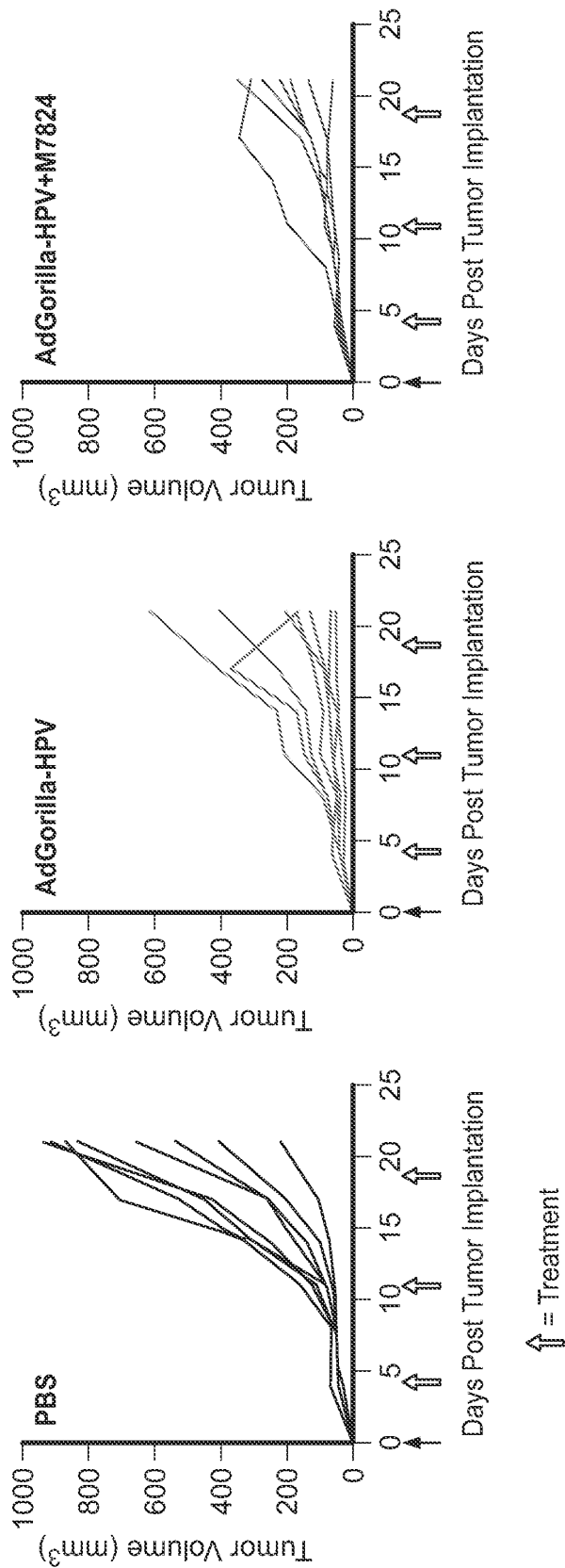


FIG. 18A

FIG. 18B

FIG. 18C

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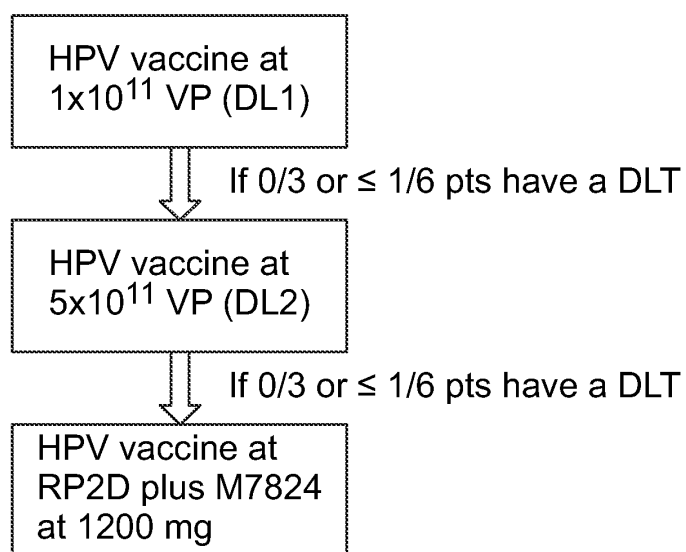
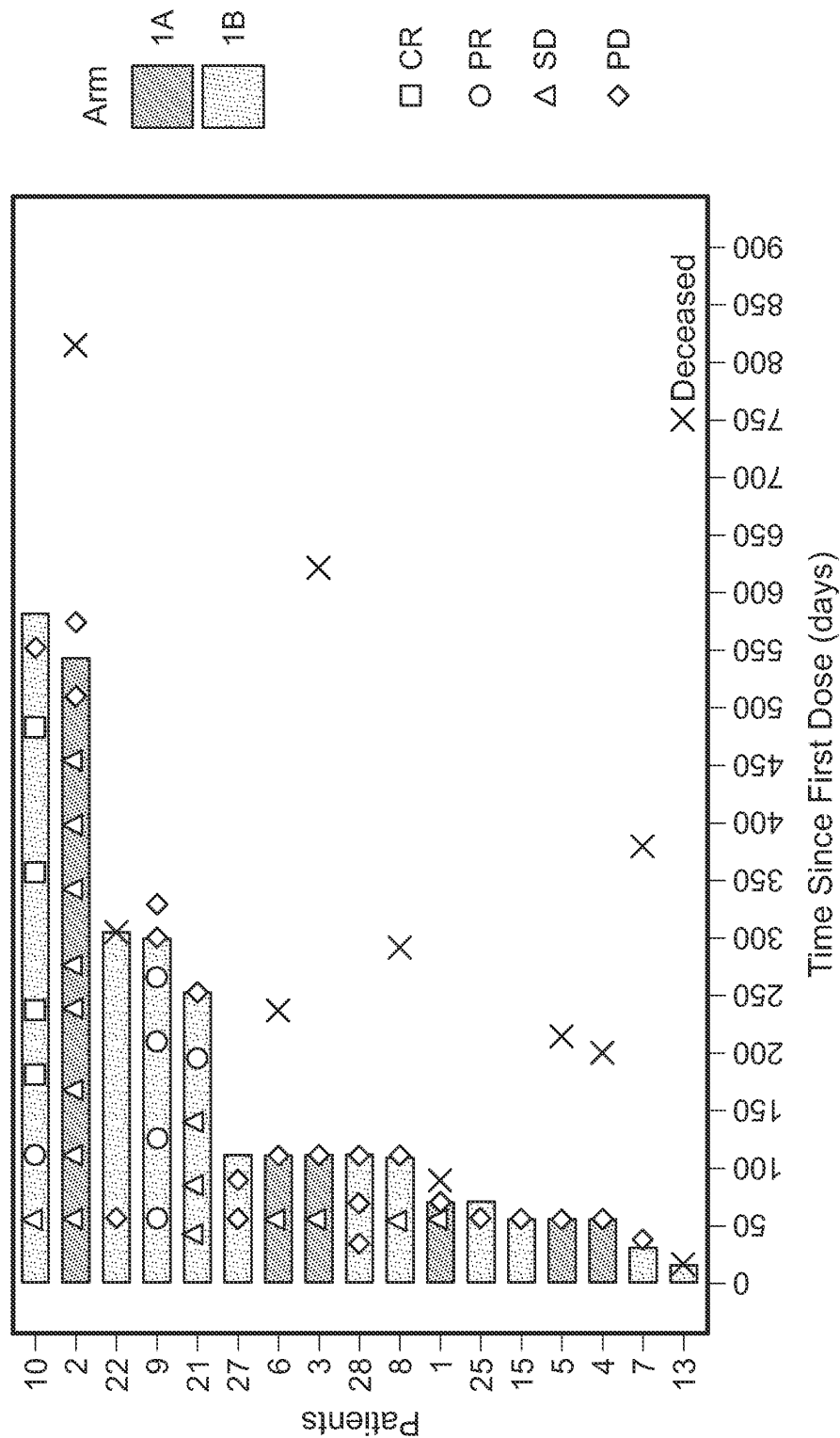


FIG. 19



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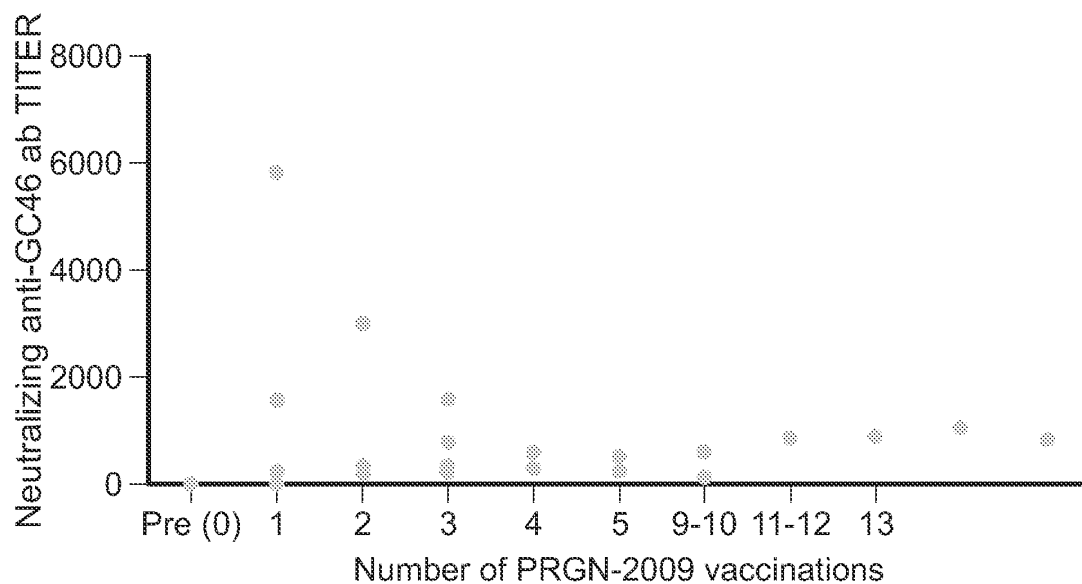


FIG. 21A

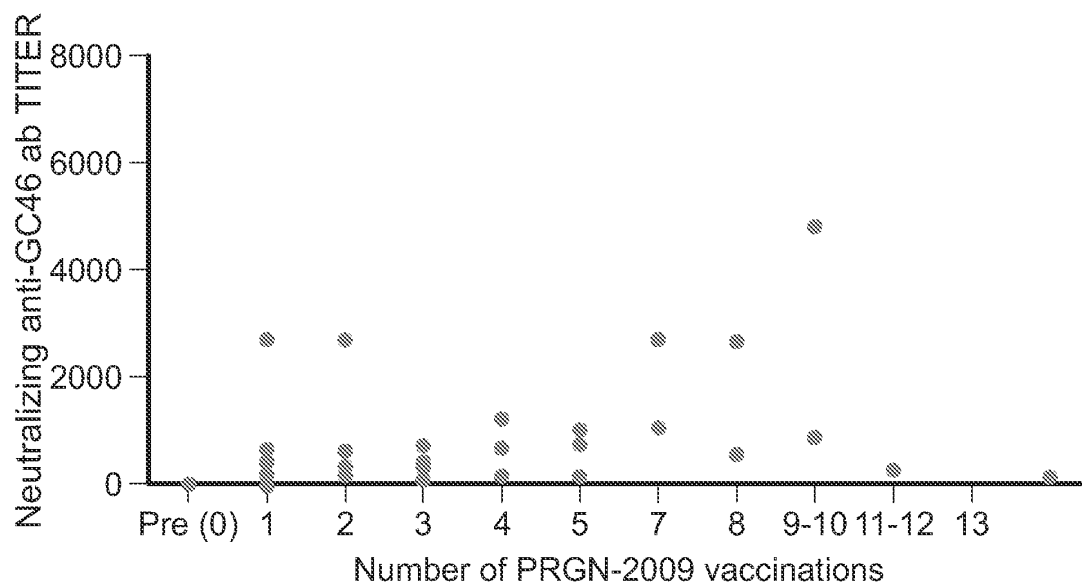


FIG. 21B

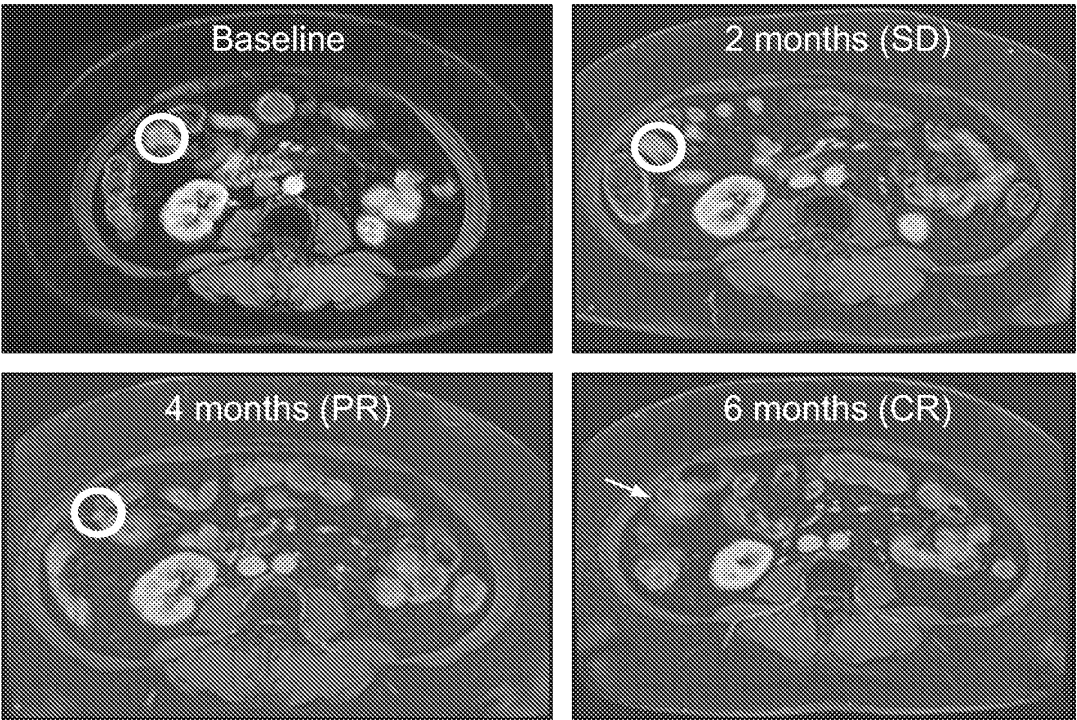


FIG. 22A

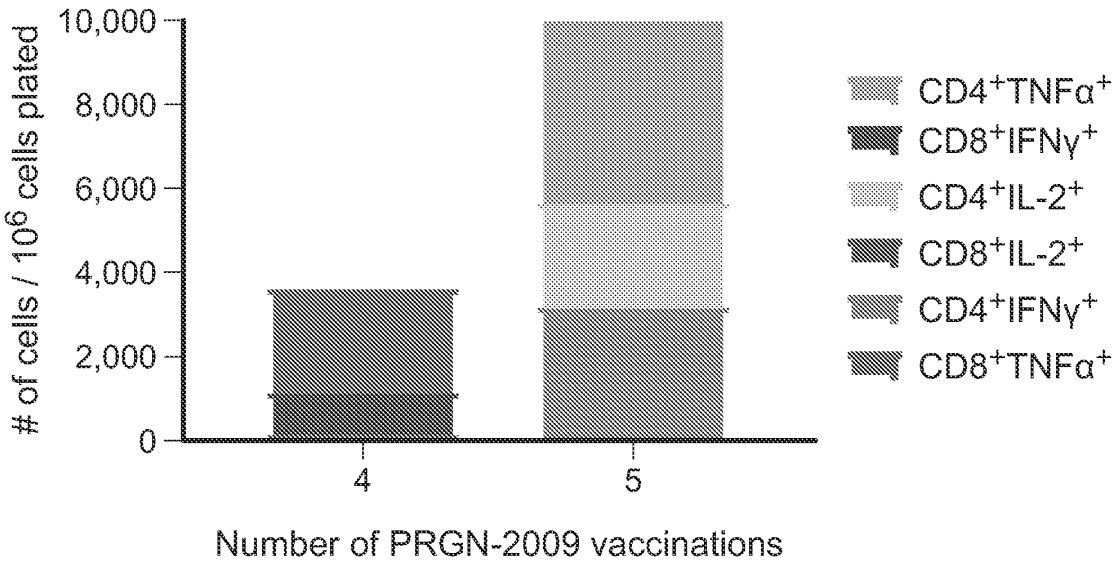


FIG. 22B

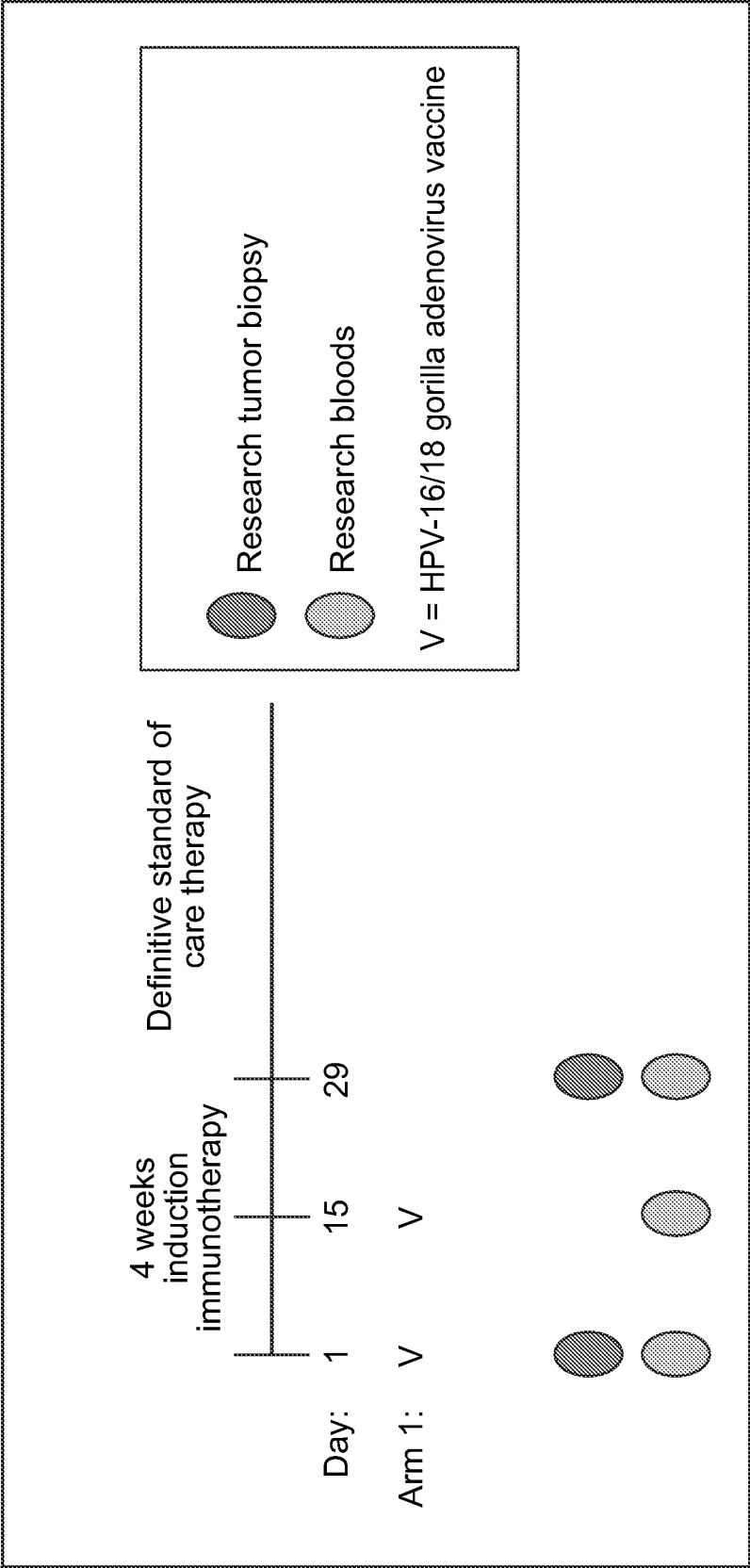


FIG. 23

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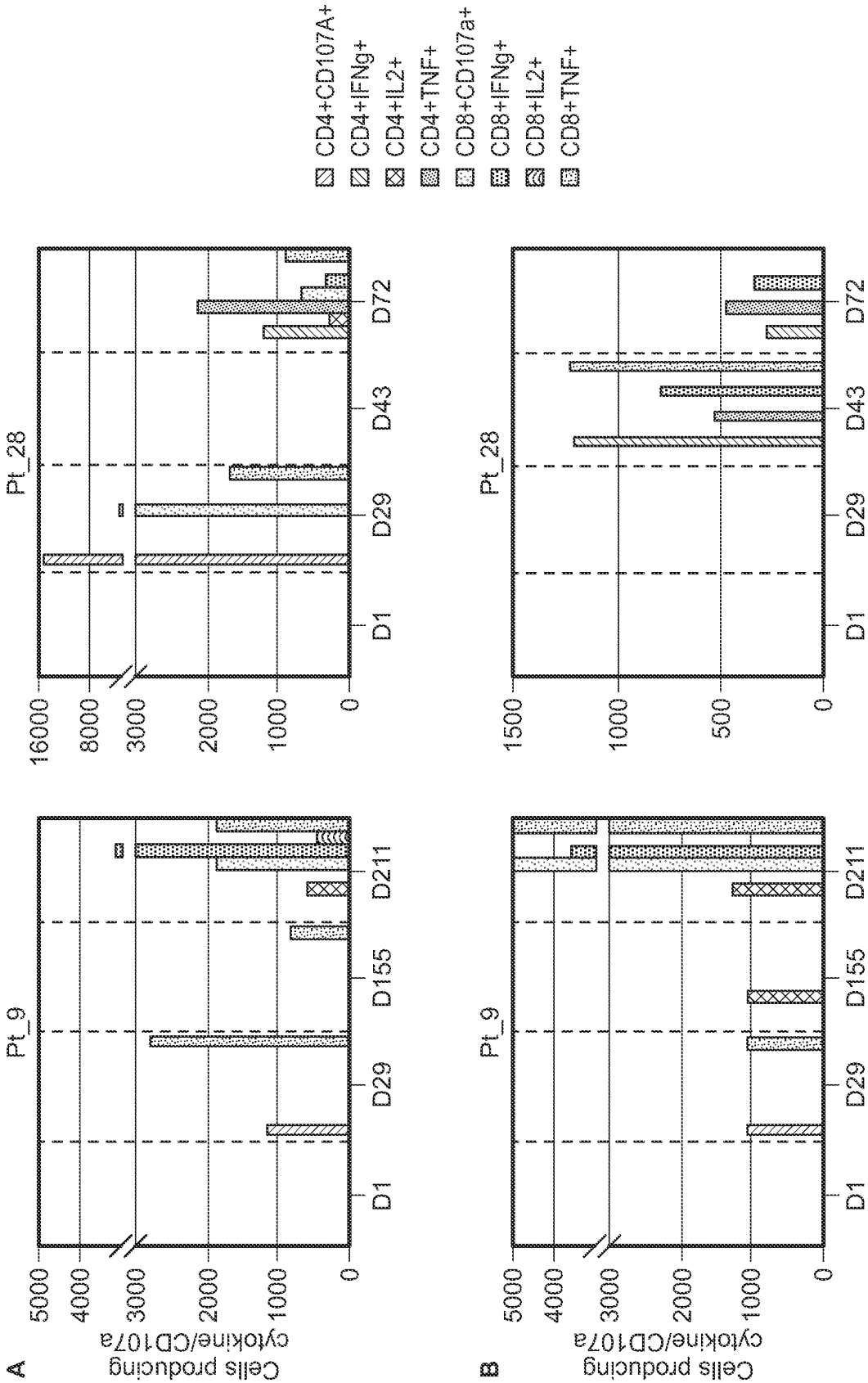


FIG. 24

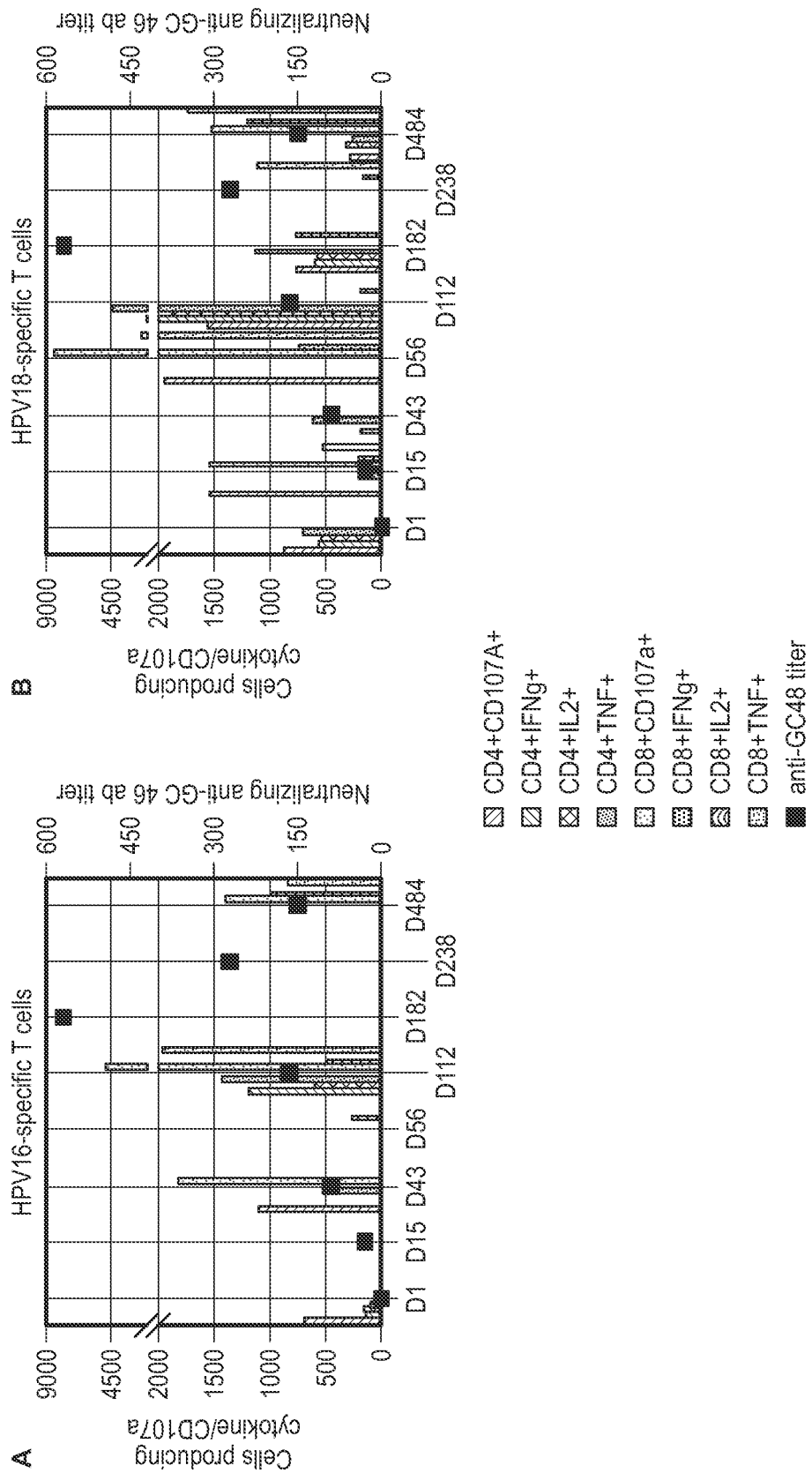


FIG. 25

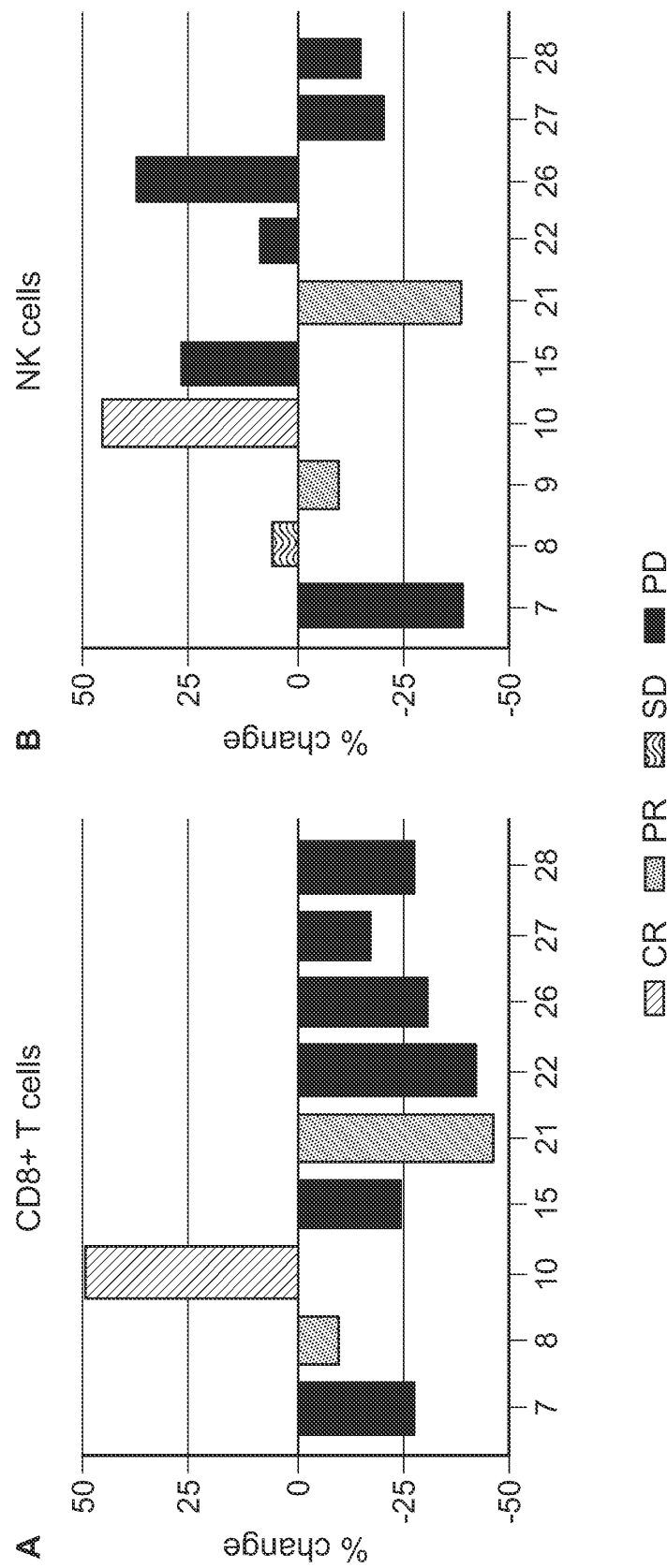


FIG. 26

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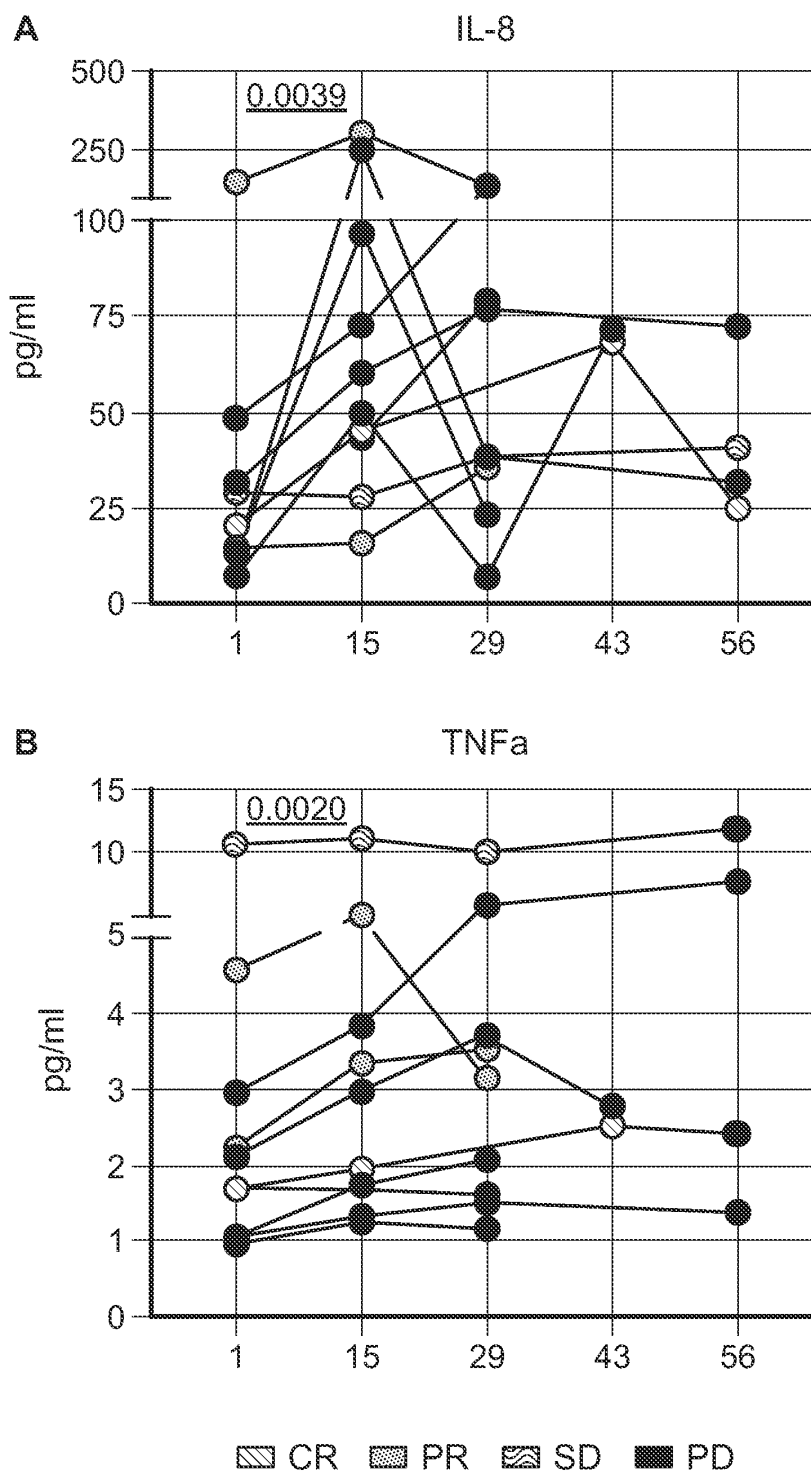


FIG. 27

SUBSTITUTE SHEET (RULE 26)

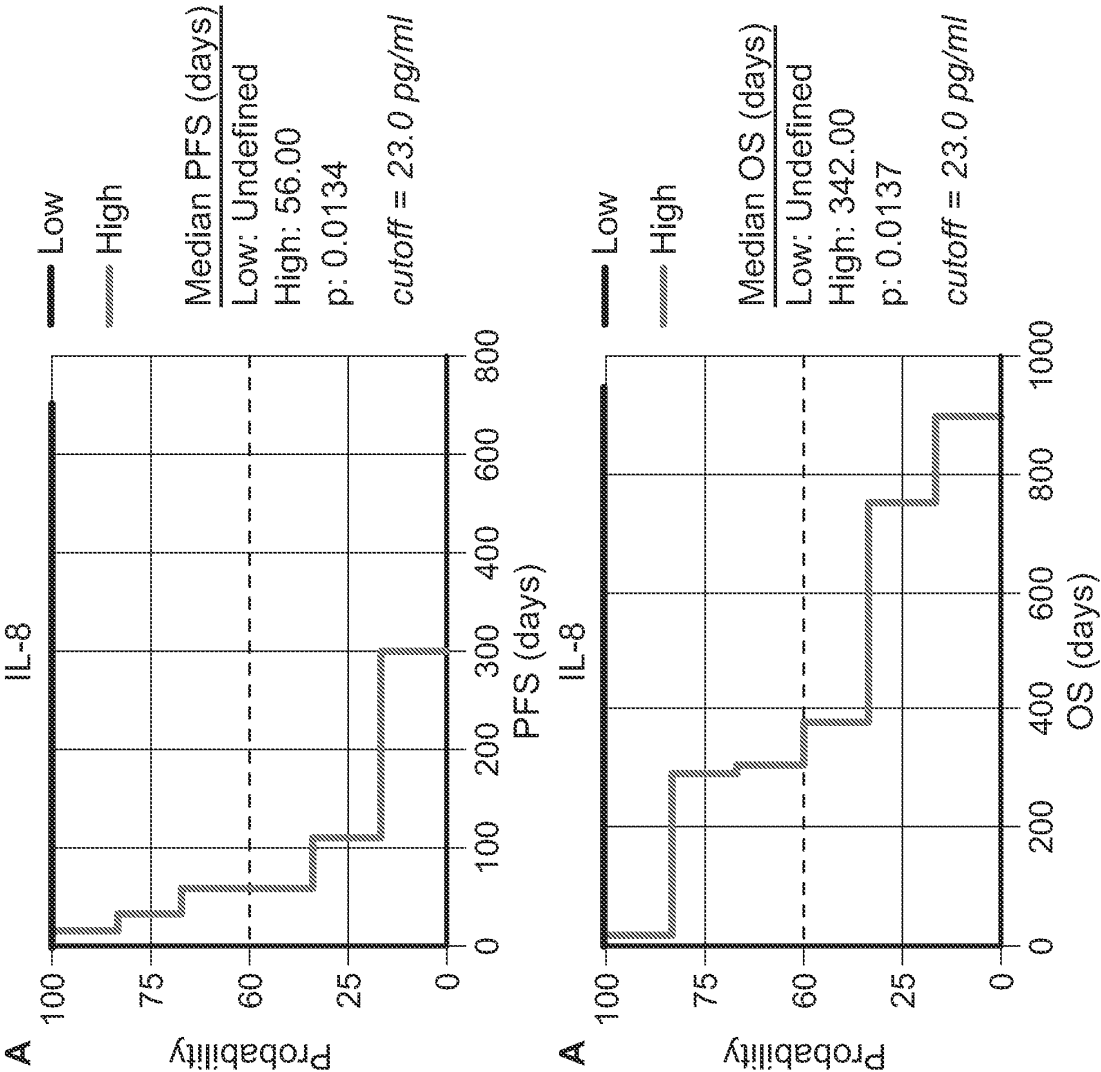
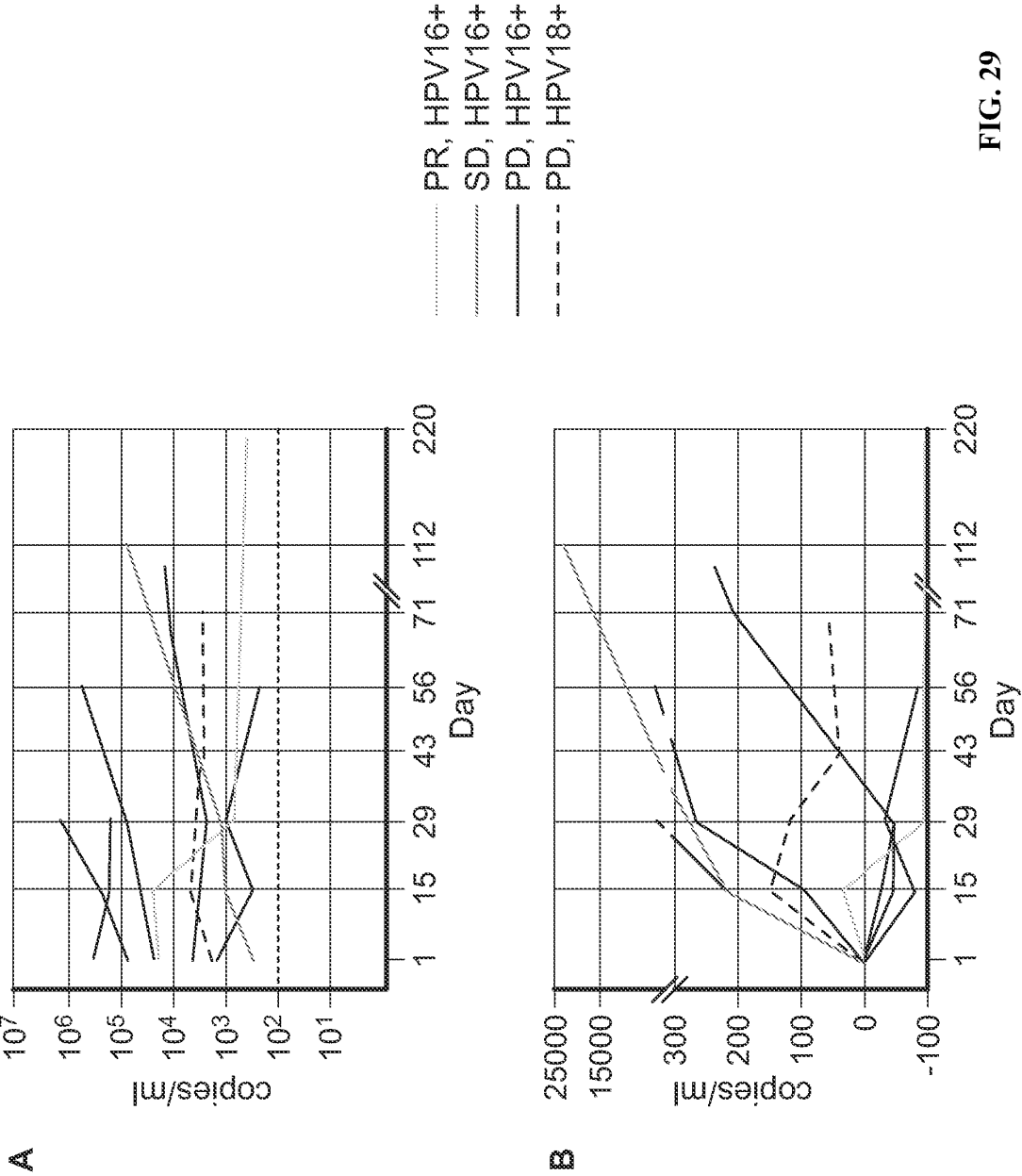


FIG. 28



*

FIG. 30

alignment position	11..... 21..... 31..... 41..... 51.....
HPV45-E7 (SEQ ID No: 326)	mhgpre TLQE IVLH lepqne ldpvdlllcyeqlse SEEND EADGVSHAQL PARR aepqgrh
HPV18-E7_pep1 (SEQ ID No: 226)	-----
HPV18-E7_pep2 (SEQ ID No: 194)	-----
HPV18-E7_pep3 (SEQ ID No: 192)	-----
HPV18-E7_pep4 (SEQ ID No: 186)	-----
HPV18-E7_pep5 (SEQ ID No: 240)	----- TLQD IVLHL -----
HPV18-E7_pep6 (SEQ ID No: 182)	----- SEEND EIDGVNHQHL PARR -----
	* * * *
alignment position	61..... 71..... 81..... 91..... 101....
HPV45-E7	kilcvckcd grieltvess a EDLRT LQQL FLSTLSFVCP WCA tnq
HPV18-E7_pep1	----- DDLR AFQQL FLNTLS -----
HPV18-E7_pep2	----- FQQL FLNTL -----
HPV18-E7_pep3	----- QL FLNTLSFV -----
HPV18-E7_pep4	----- L FLNTLSFVCP WCA s-----
HPV18-E7_pep5	-----
HPV18-E7_pep6	-----
	* * * *

FIG. 31

alignment position		1..... 11..... 21..... 31..... 41.....	
HPV45-E7	(SEQ ID No: 326)	1	
HPV18-E7_pep1	(SEQ ID No: 226)	1	
HPV18-E7_pep4	(SEQ ID No: 186)	1	
HPV18-E7_pep6	(SEQ ID No: 182)	1	
alignment position		51..... 61..... 71..... 81..... 91..... 101..	
HPV45-E7		1	
HPV18-E7_pep1		1	
HPV18-E7_pep4		1	
HPV18-E7_pep6		1	

FIG. 32