

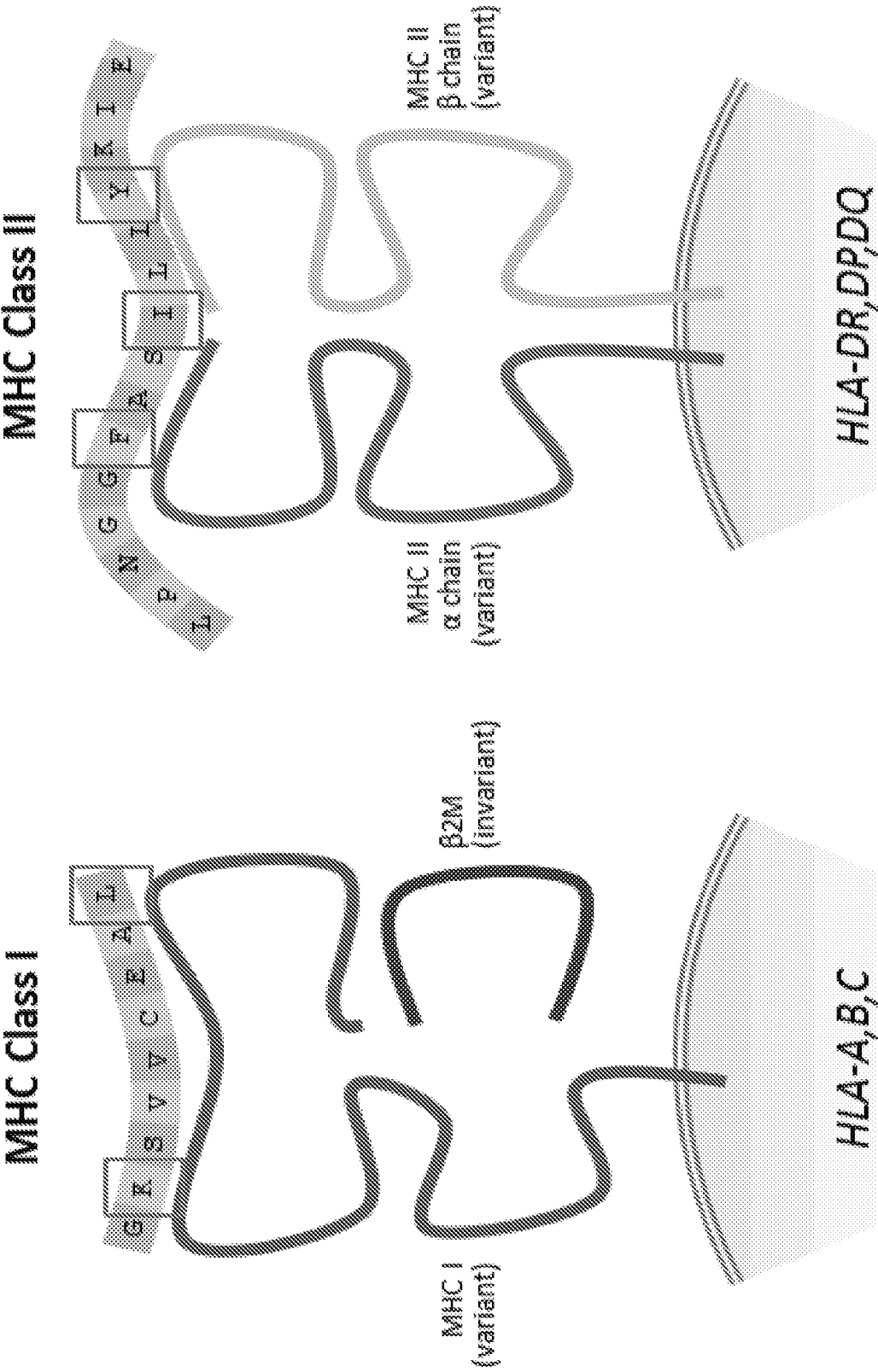


FIG. 1A

FIG. 1B

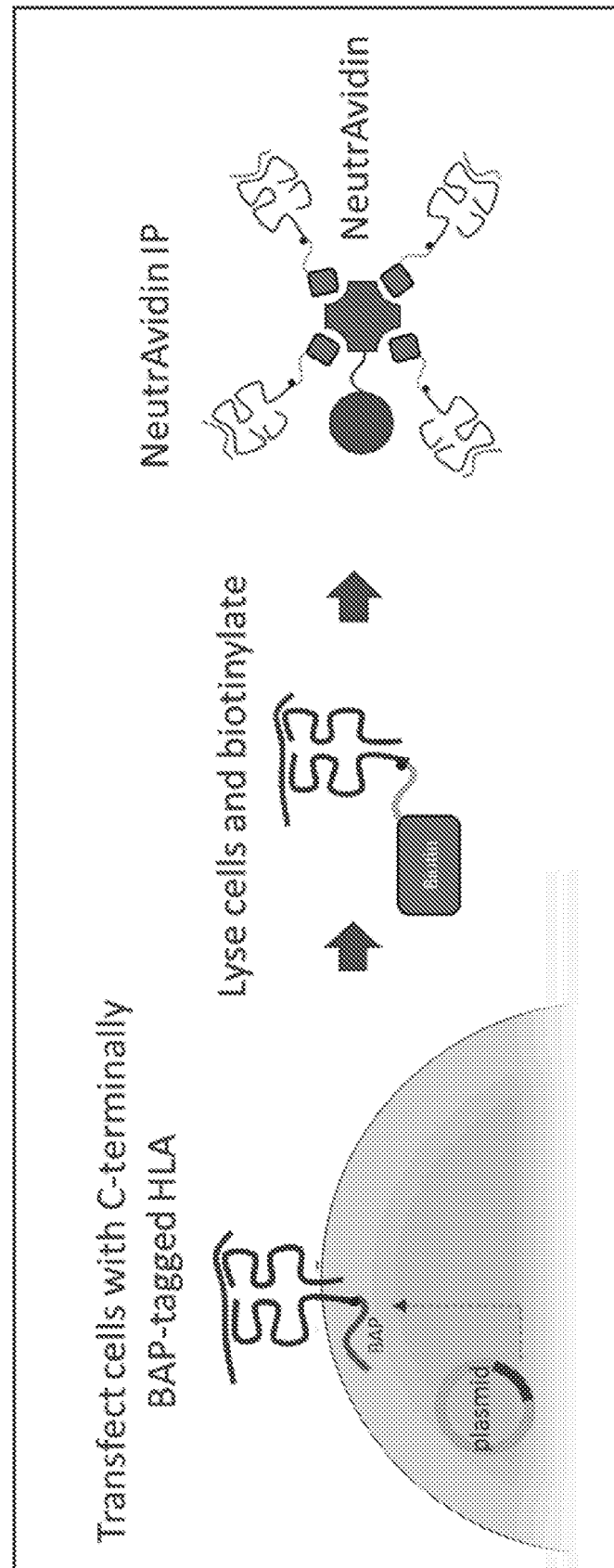
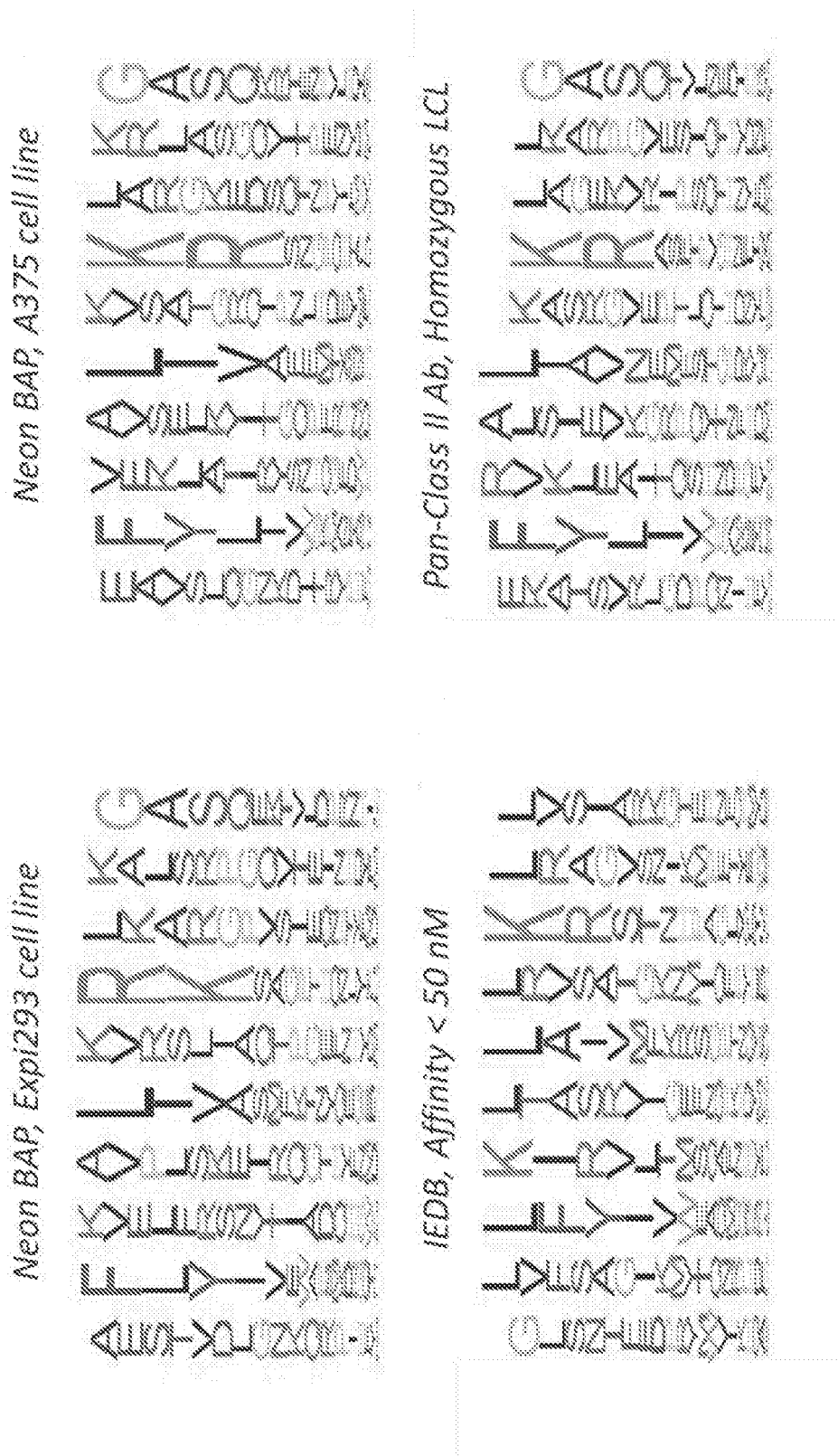


FIG. 2

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**FIG. 3**

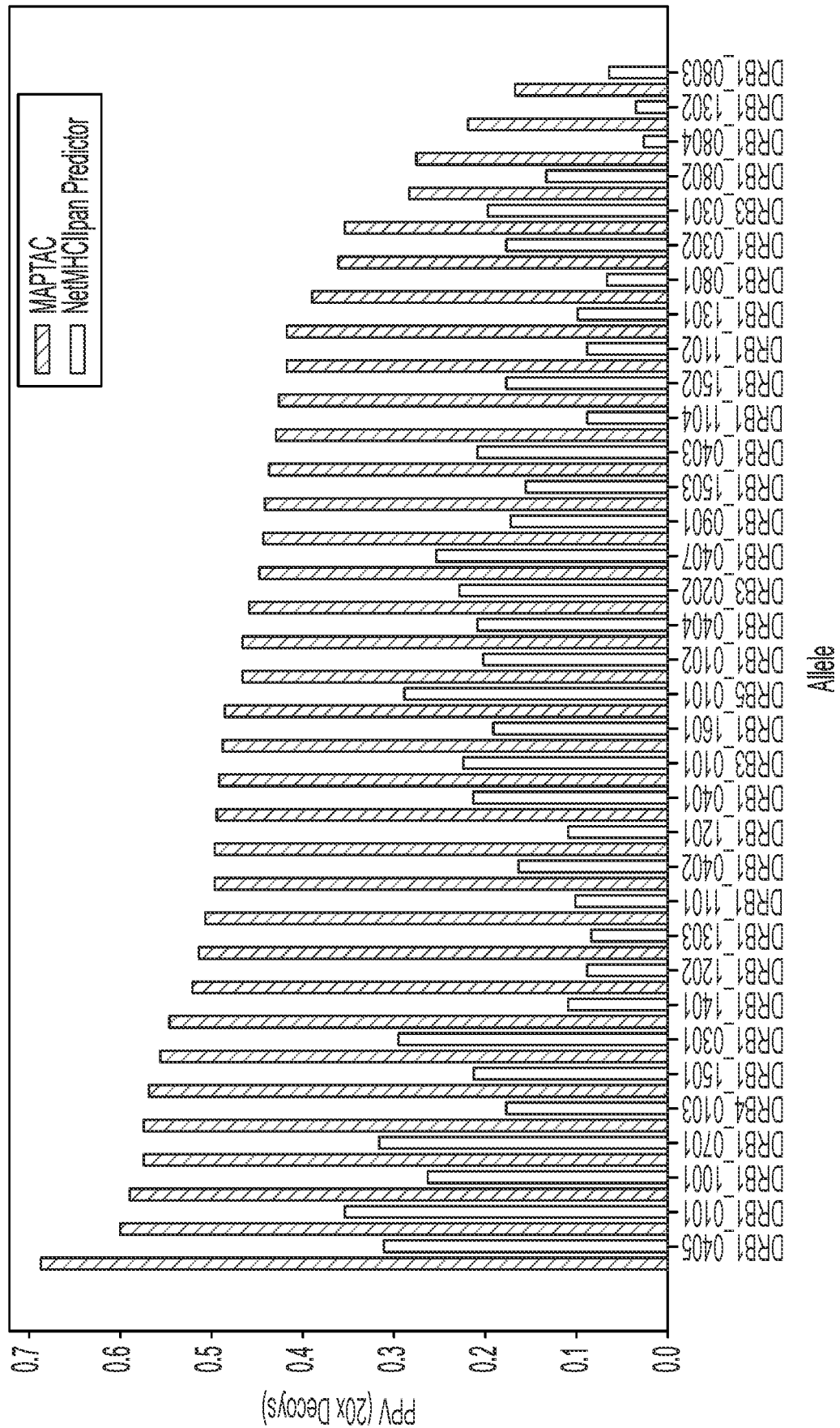


FIG. 4

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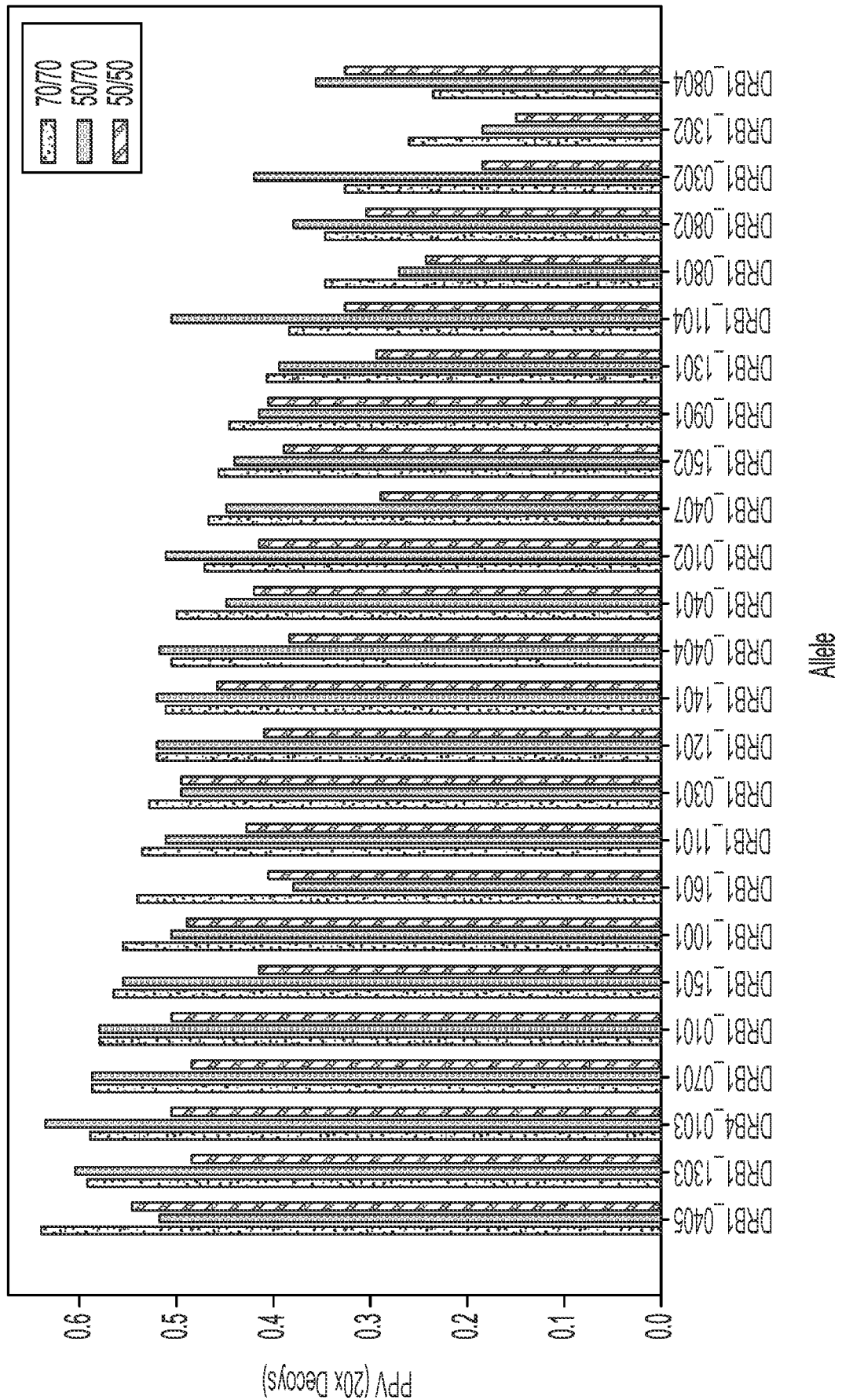


FIG. 5

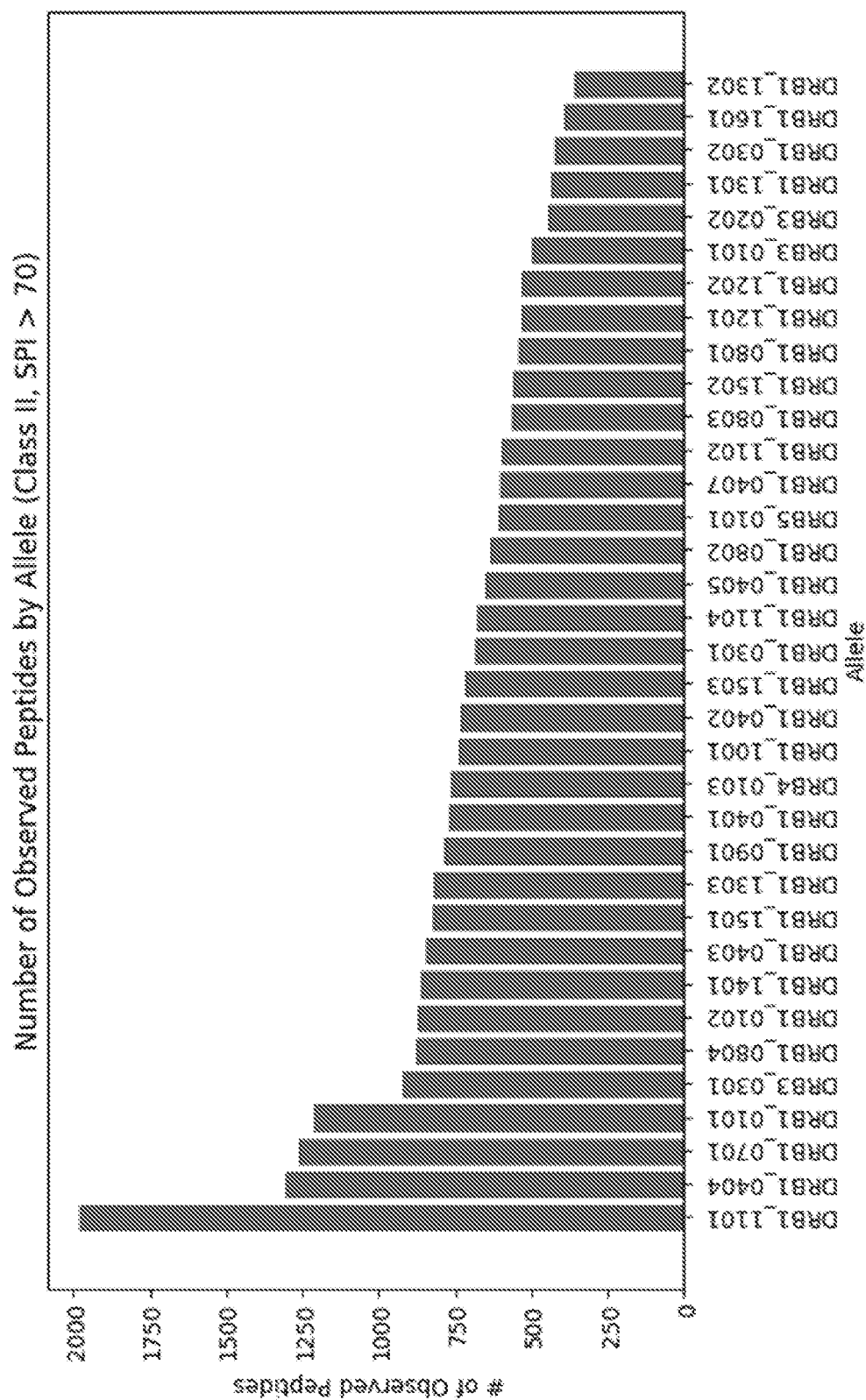
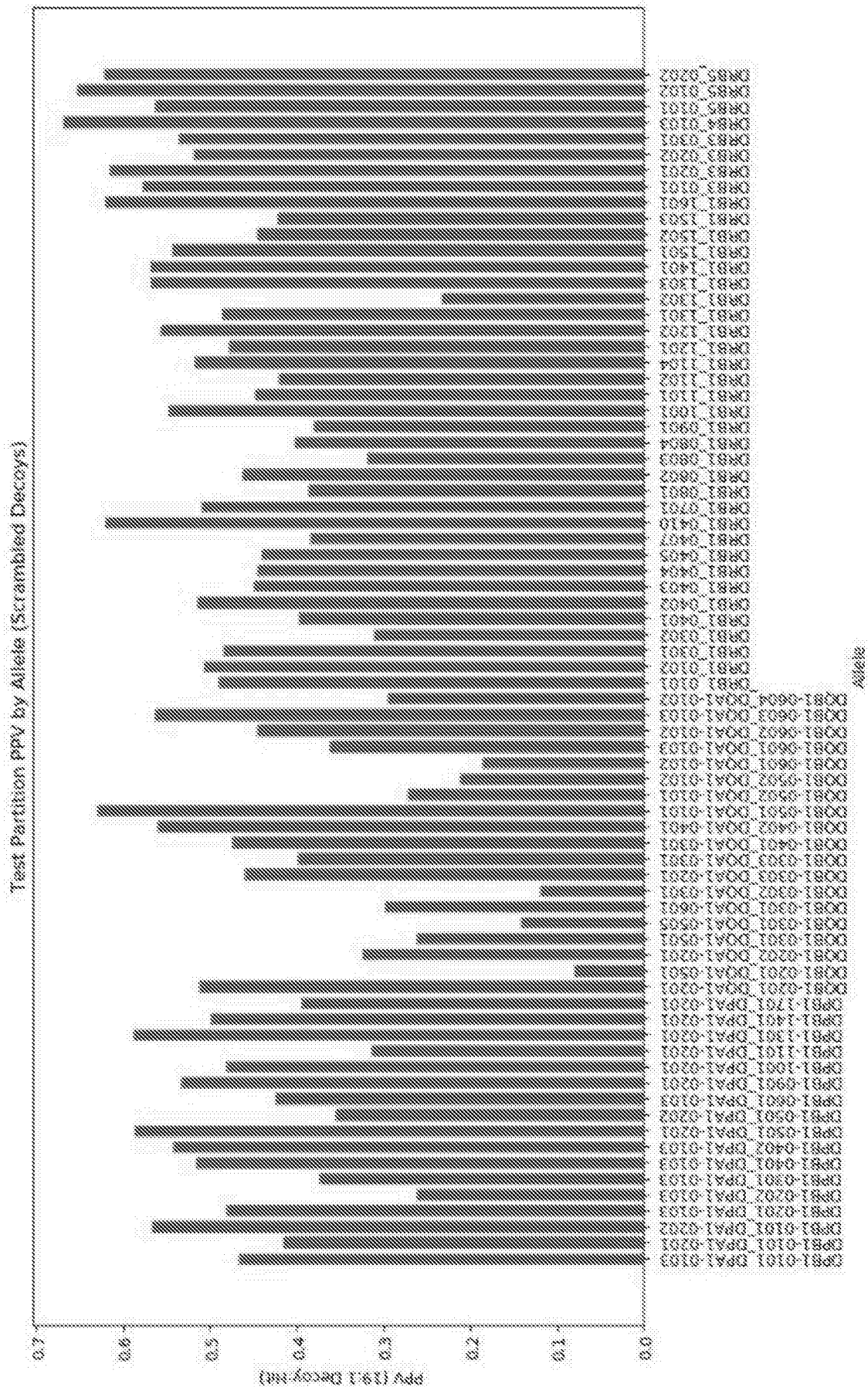
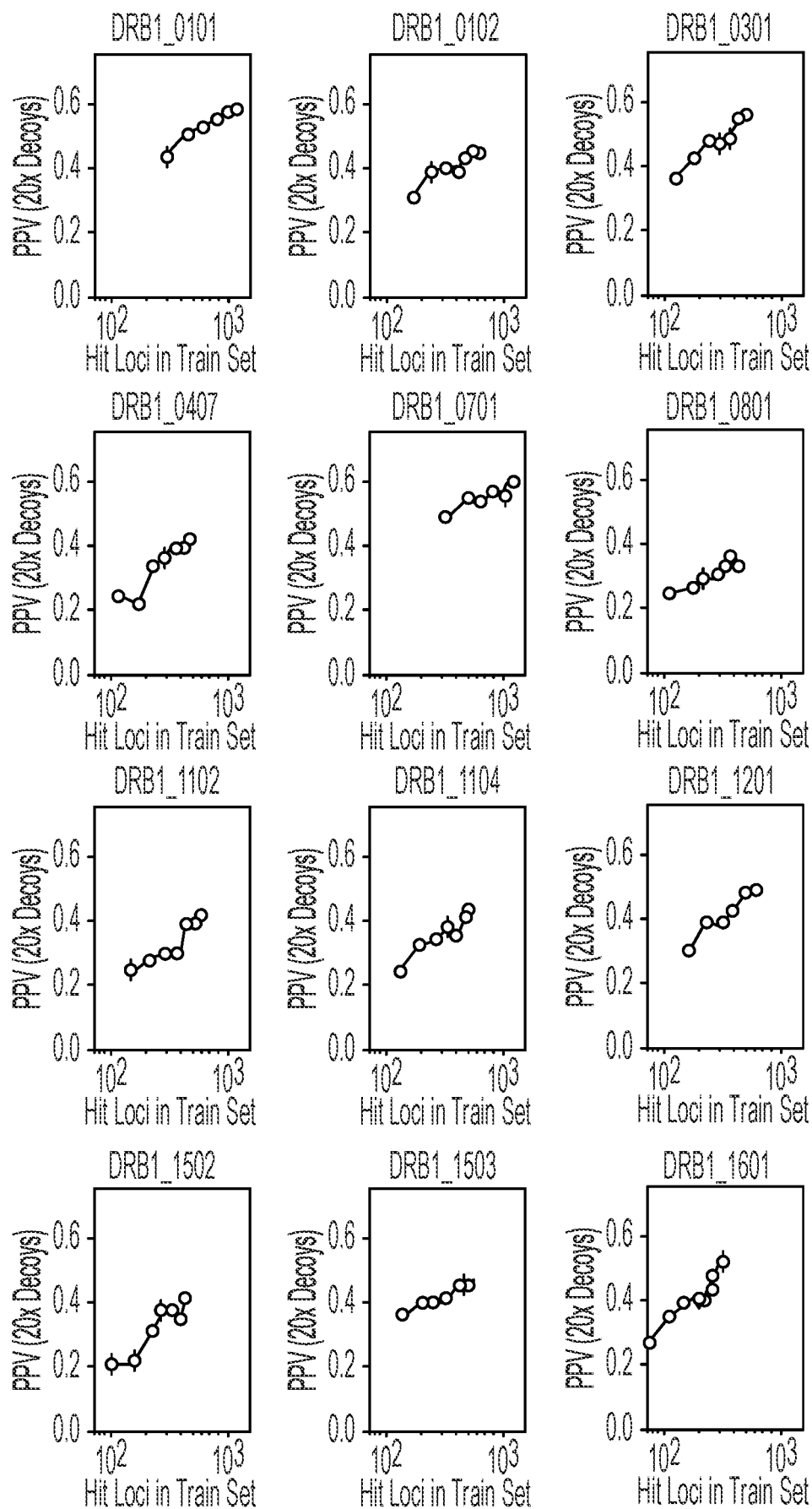


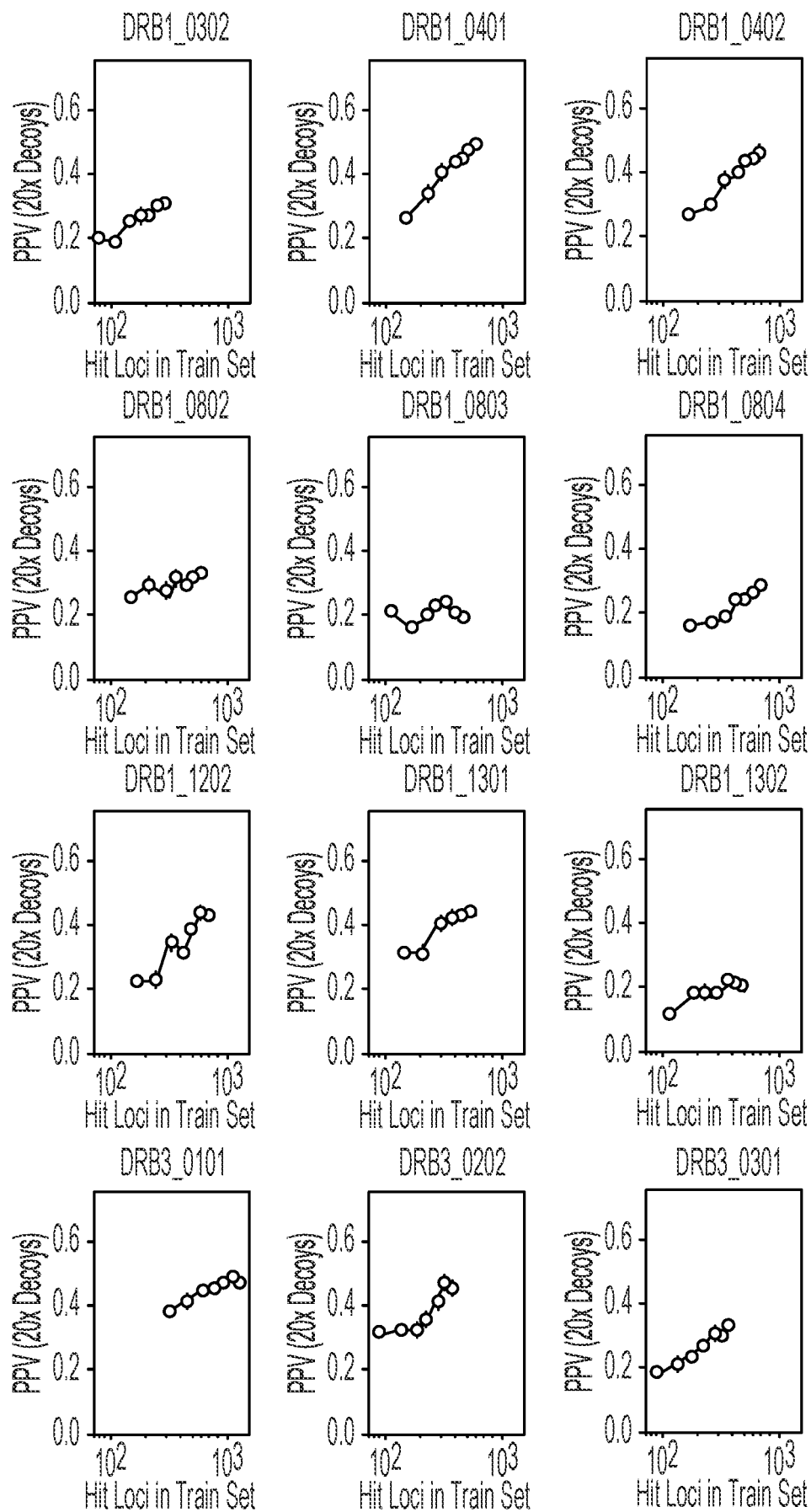
FIG. 6



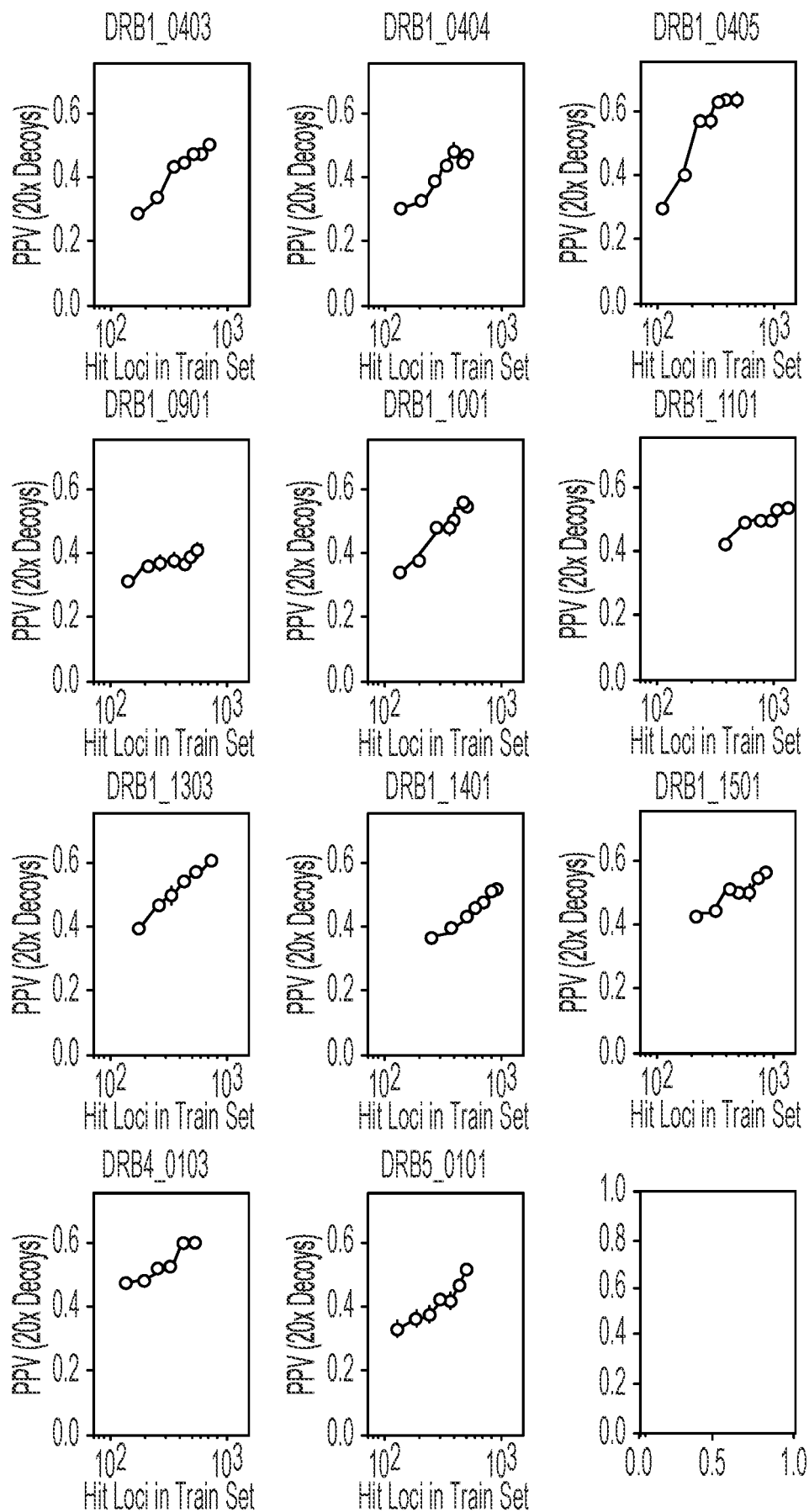
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**FIG. 7B**

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**FIG. 7B CONT.**

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**FIG. 7B CONT.**

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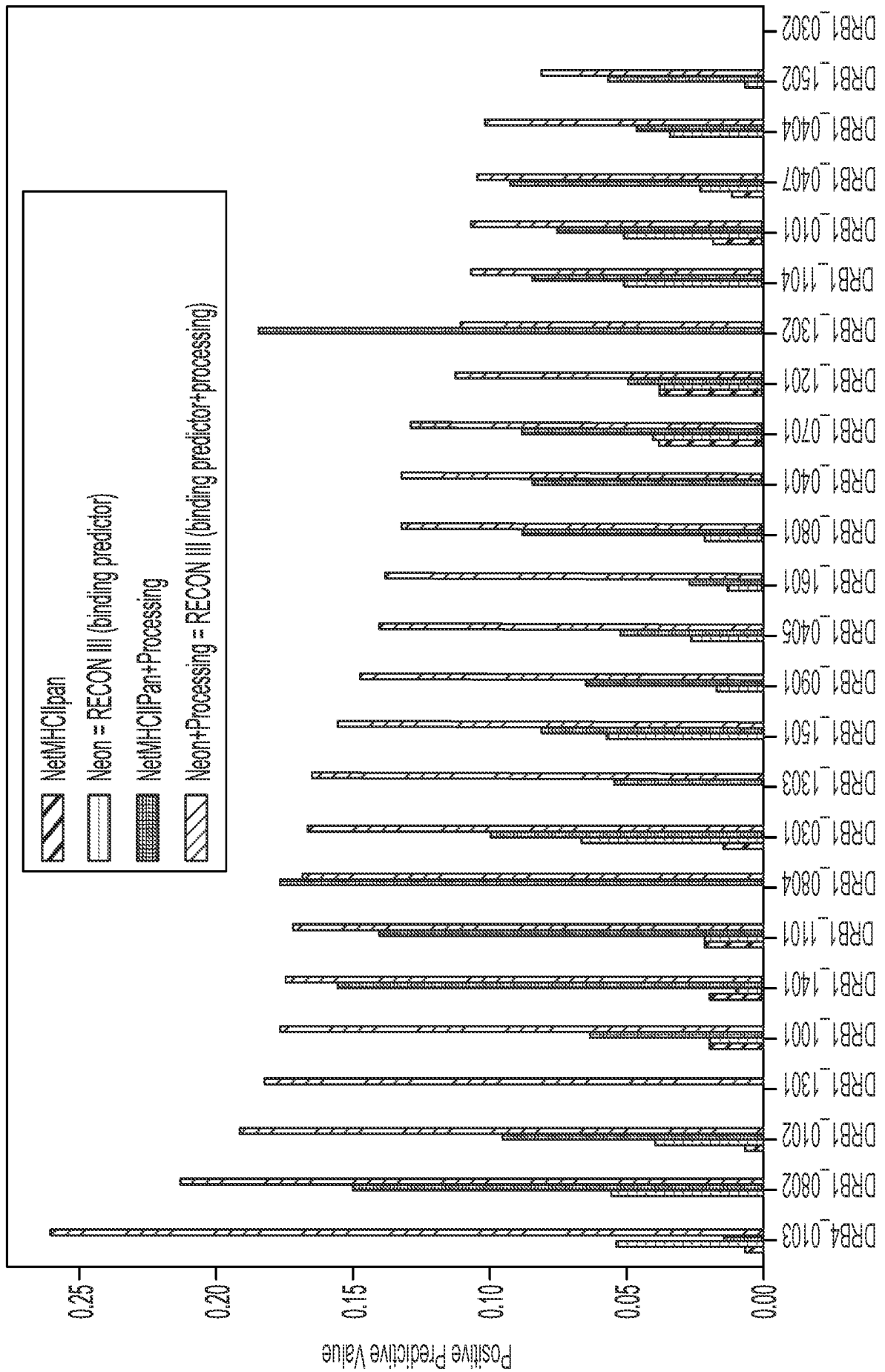
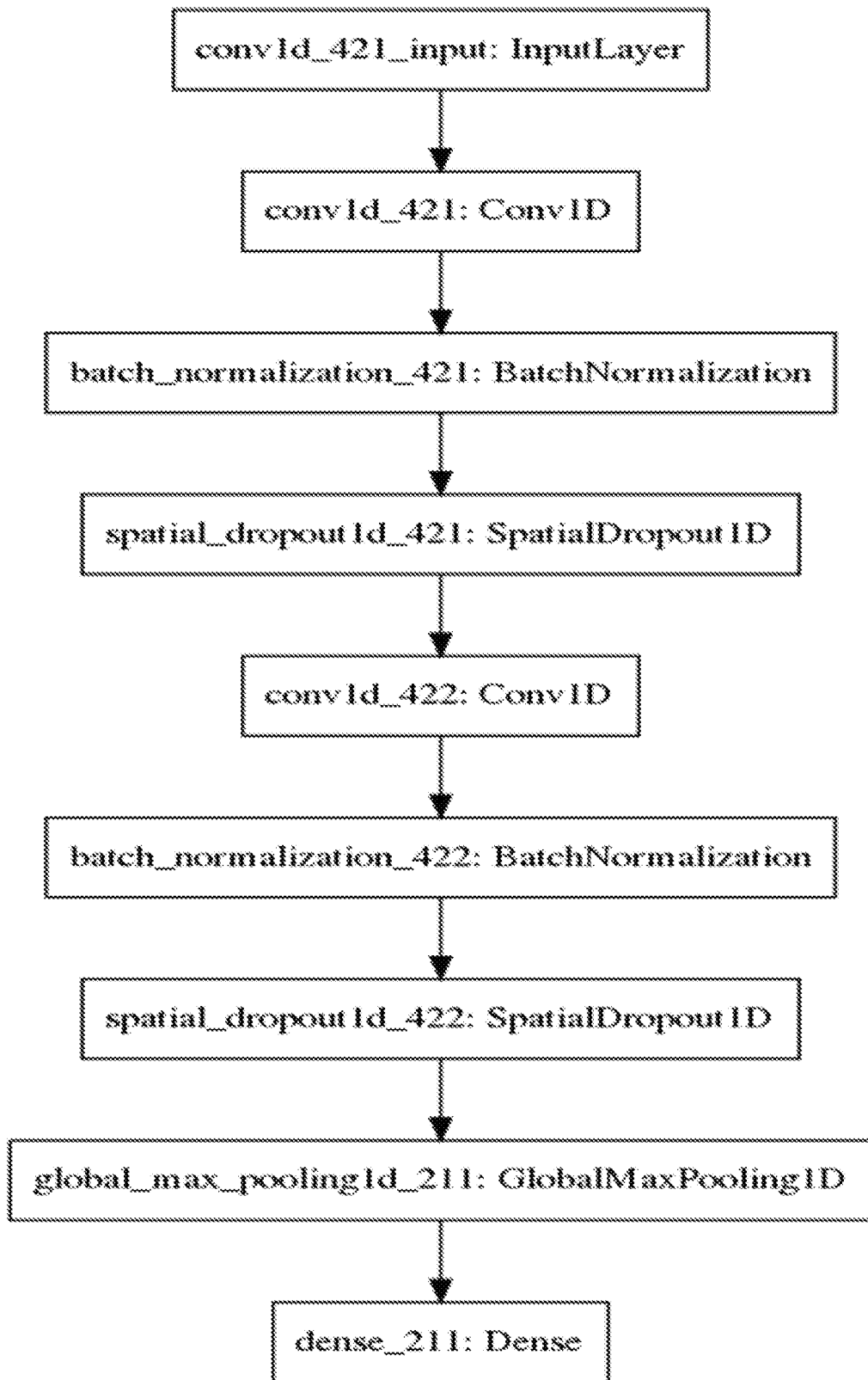


FIG. 8

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**FIG. 9**

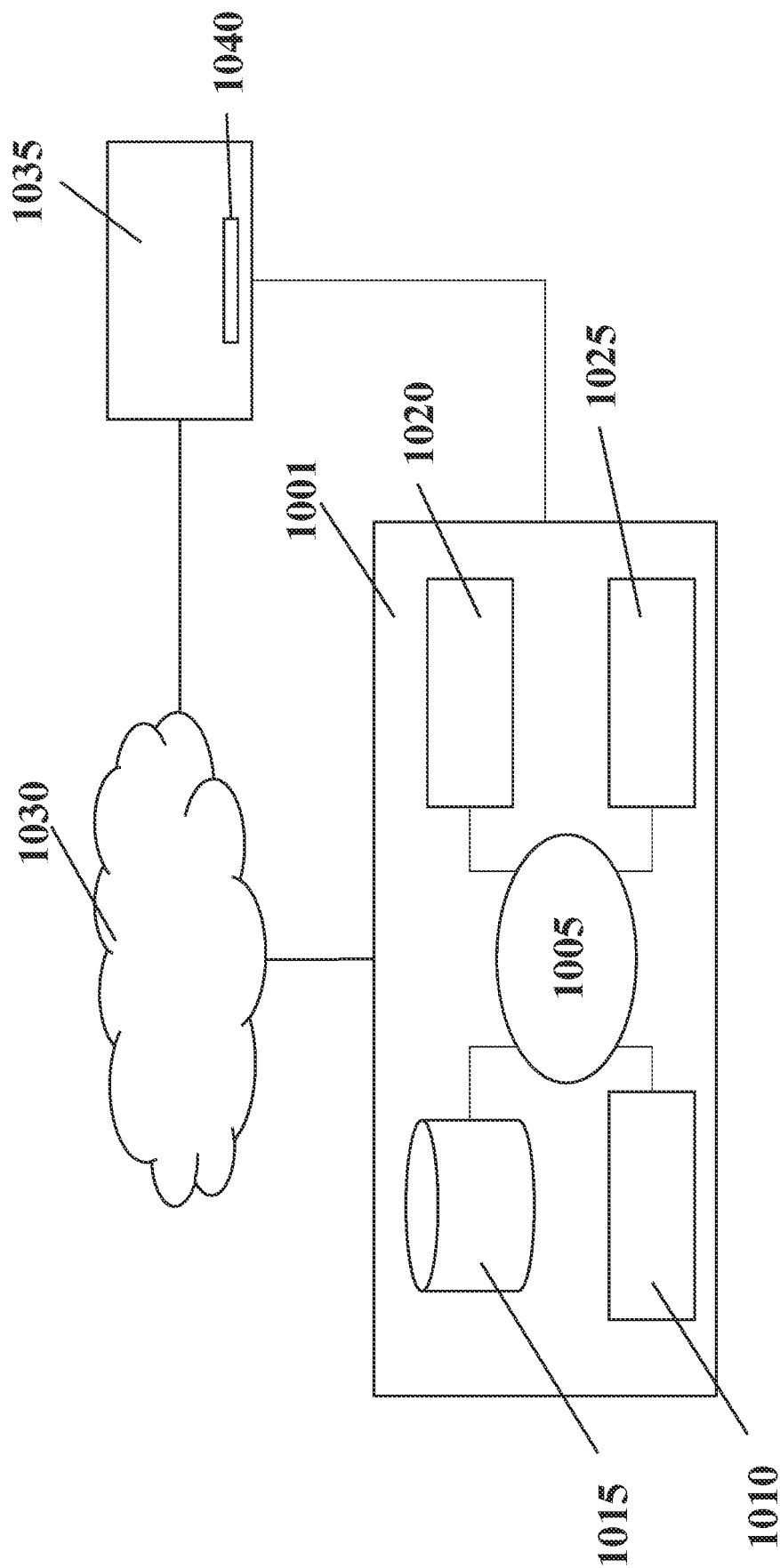
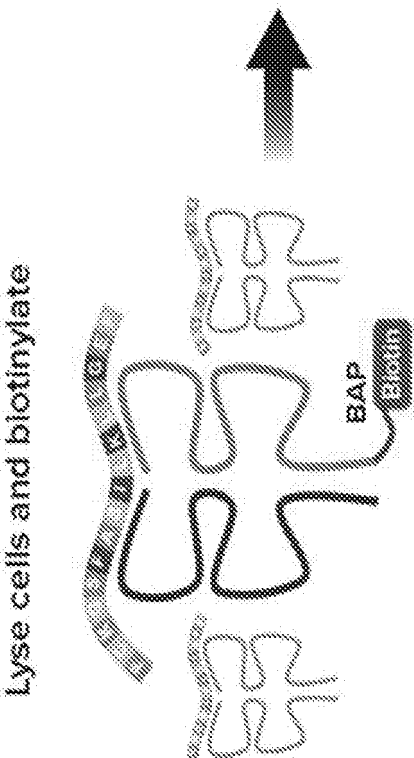
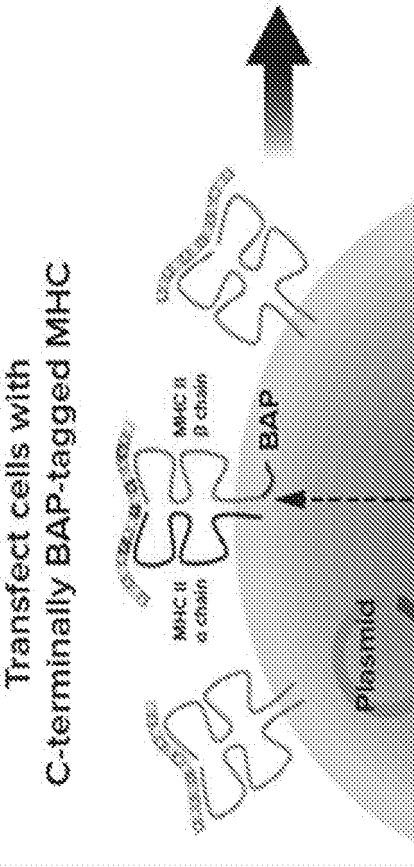


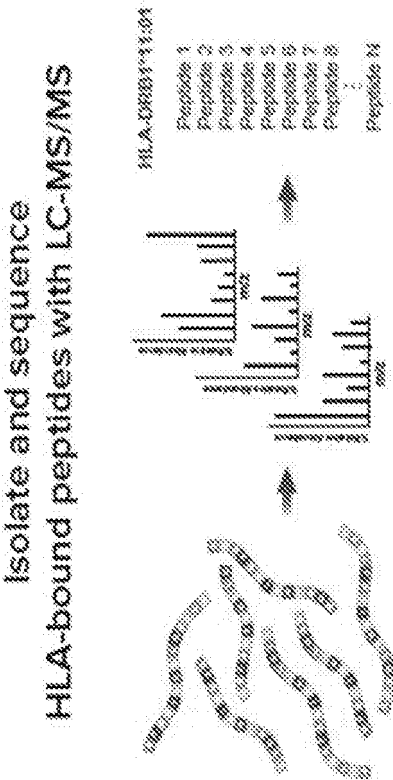
FIG. 10



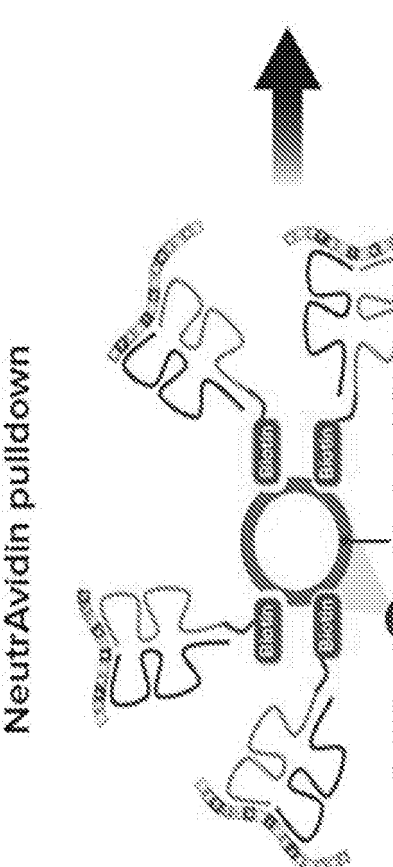
(1)



(2)



(3)



(4)

FIG. 11A

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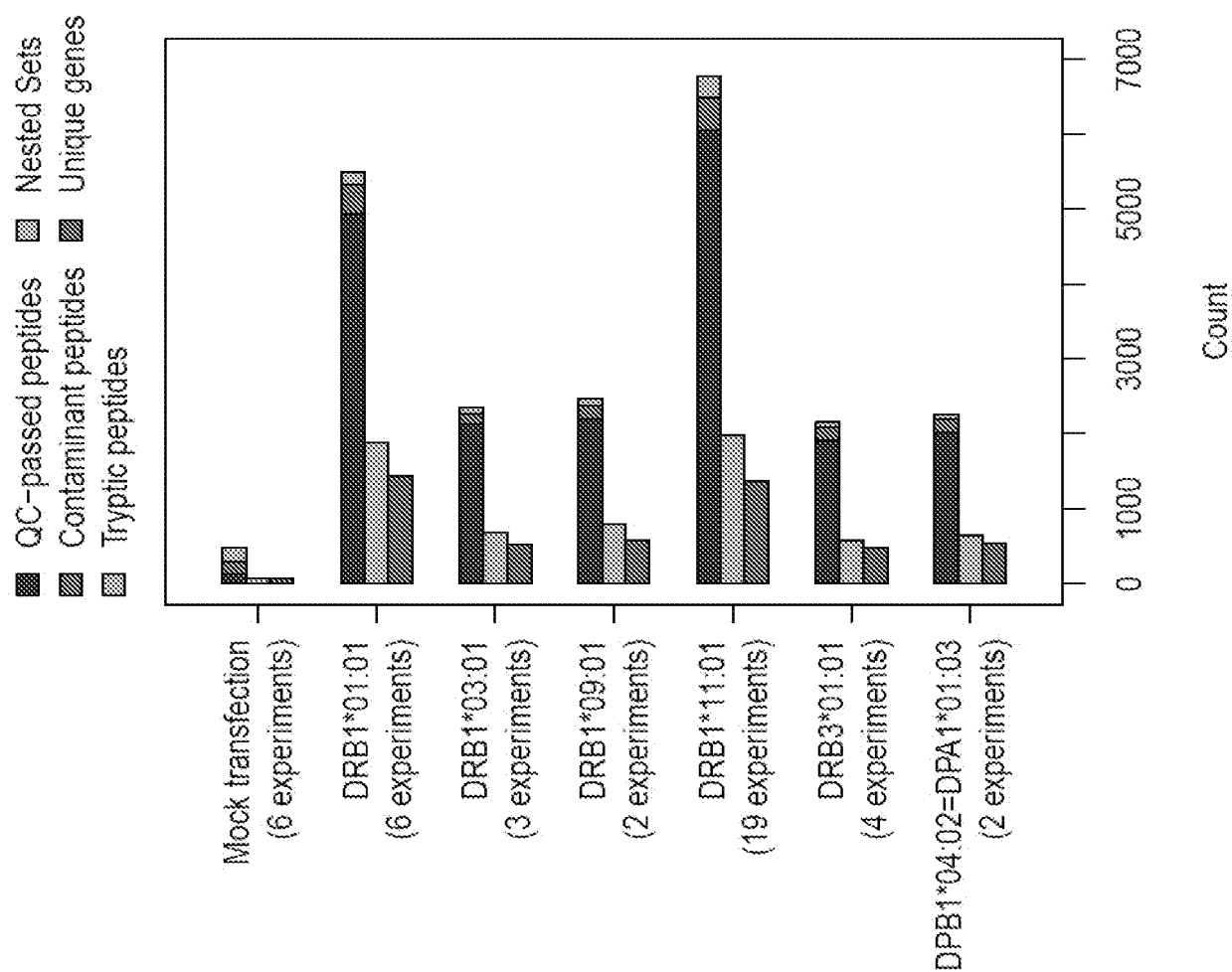
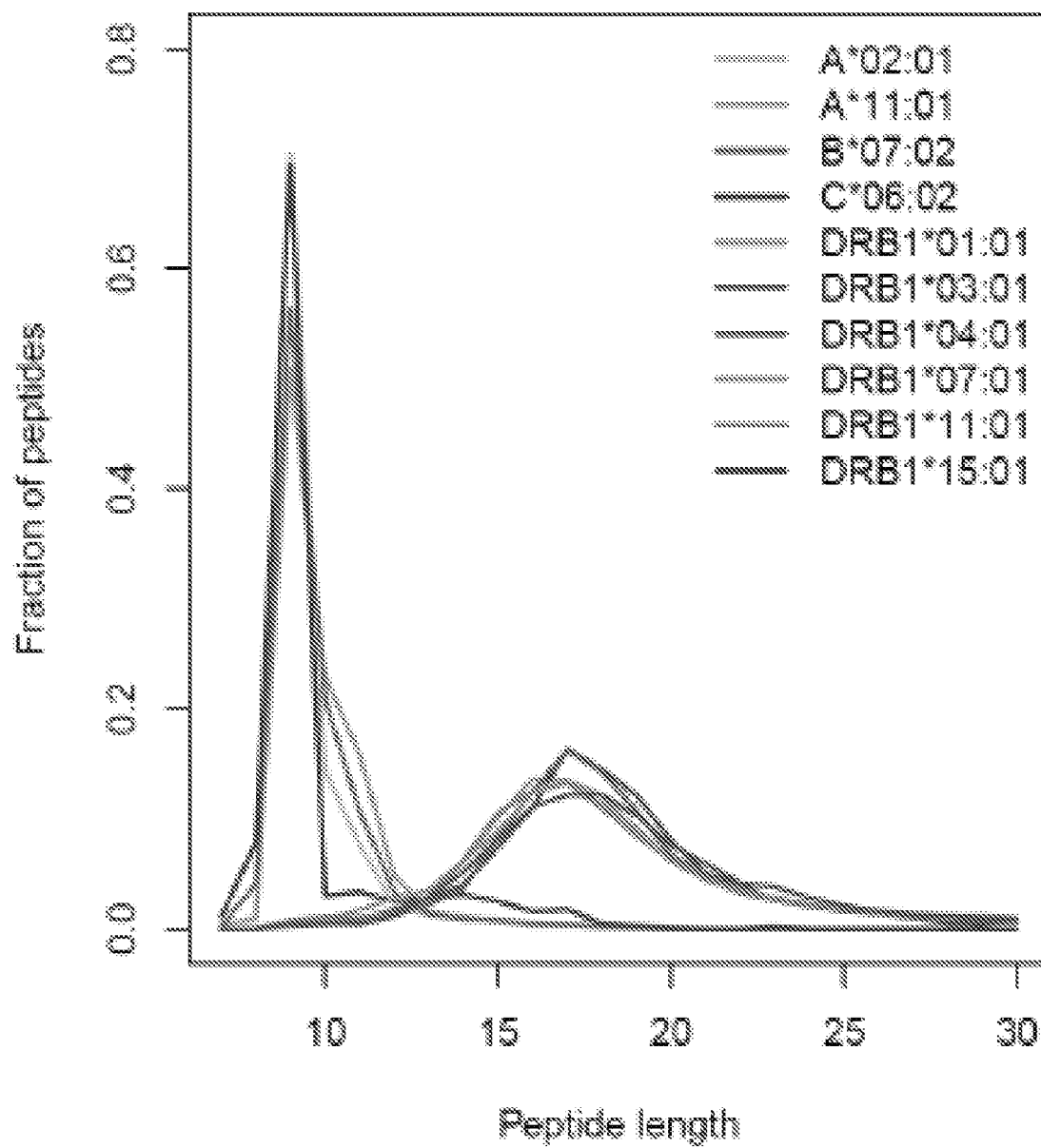
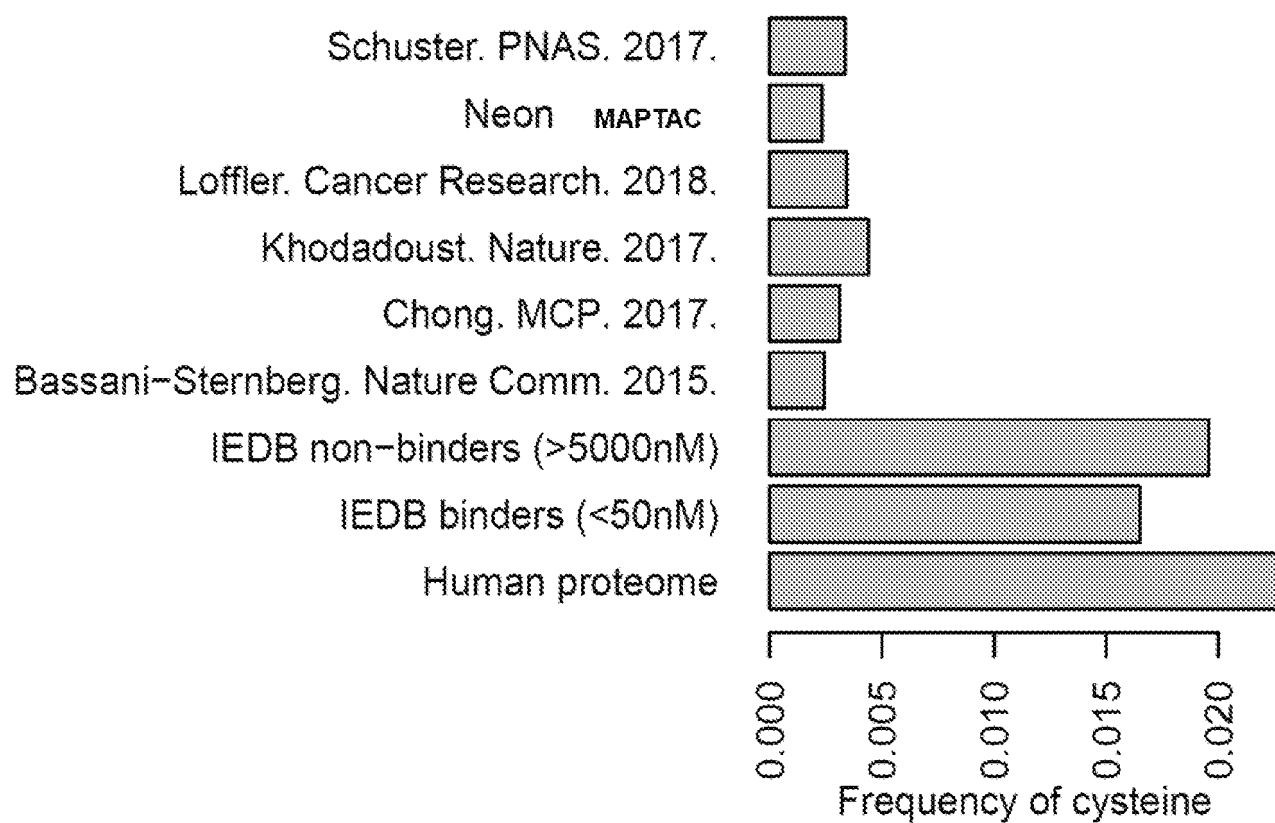


FIG. 11B

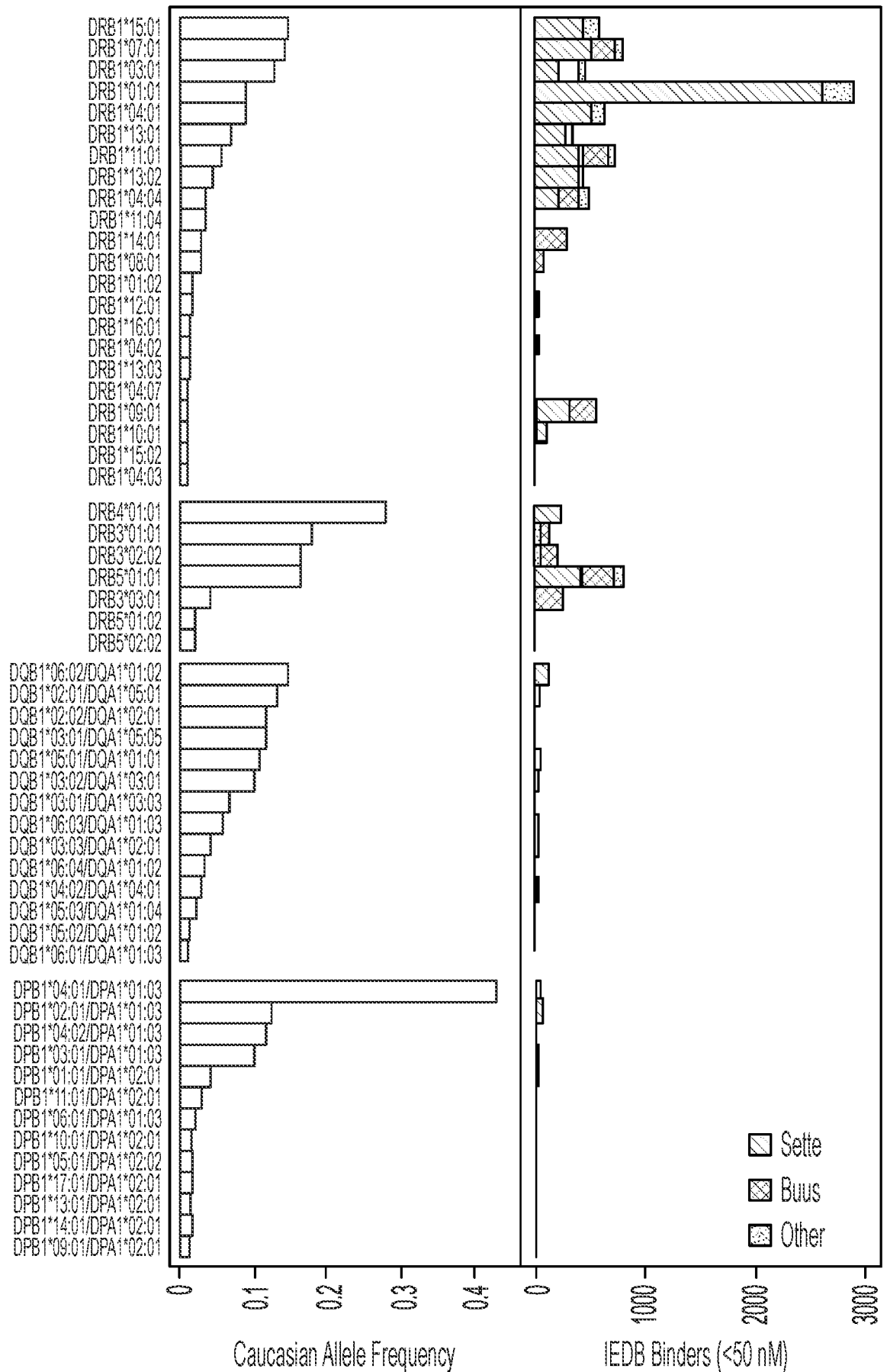
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*FIG. 11C*

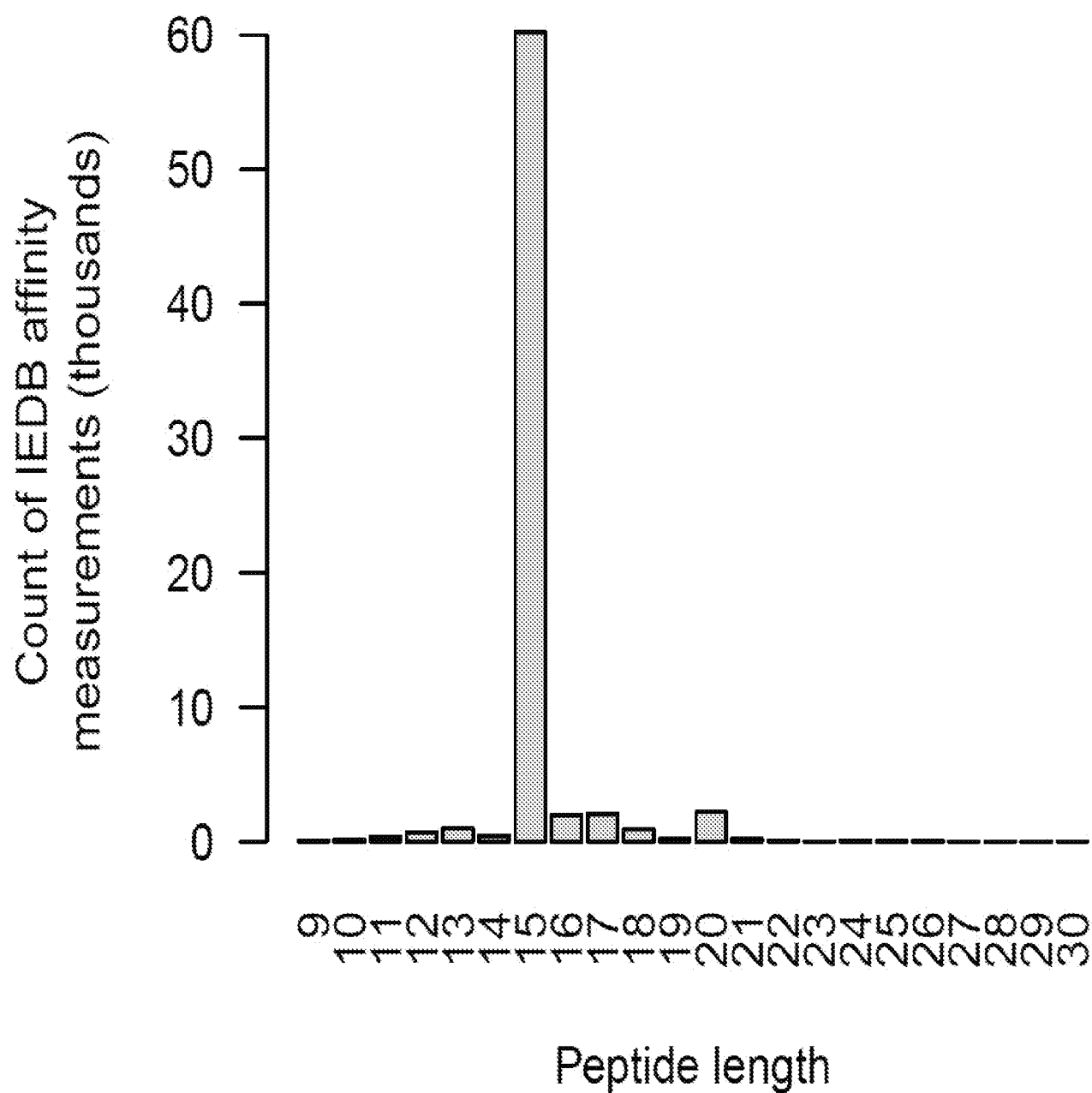
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**FIG. 11D**

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**FIG. 12A**

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*FIG. 12B*

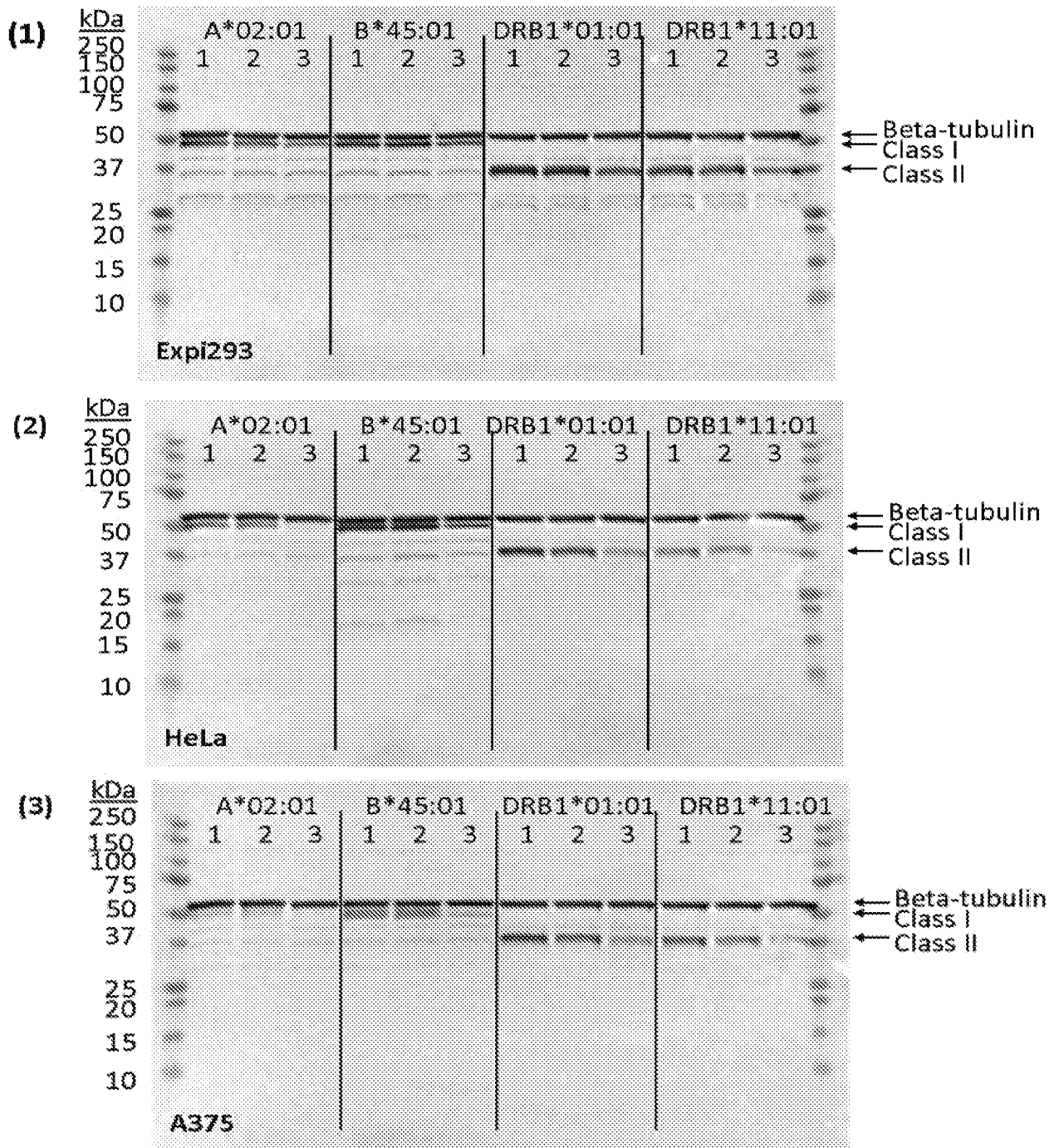


FIG. 12C

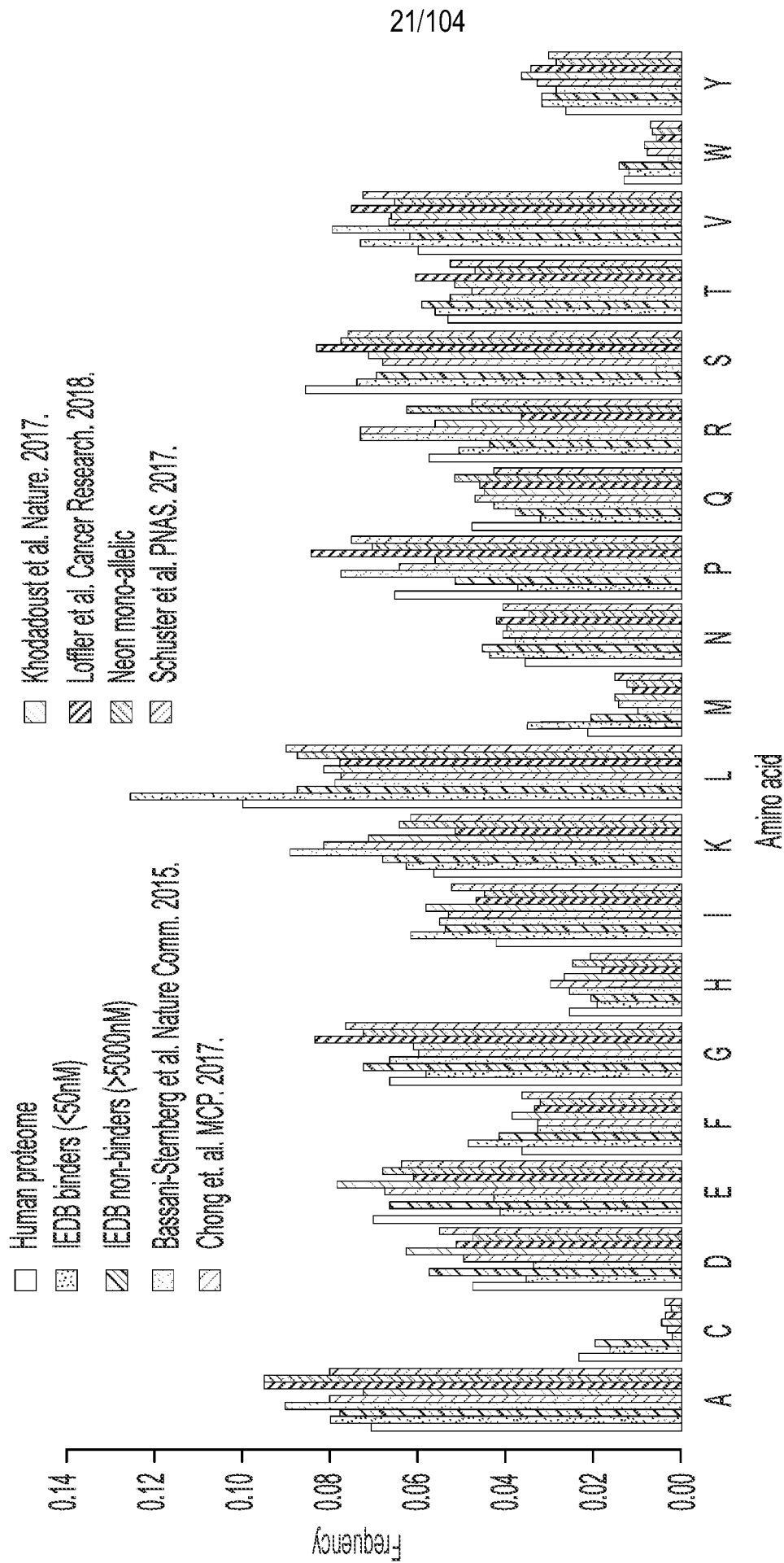


FIG. 12D

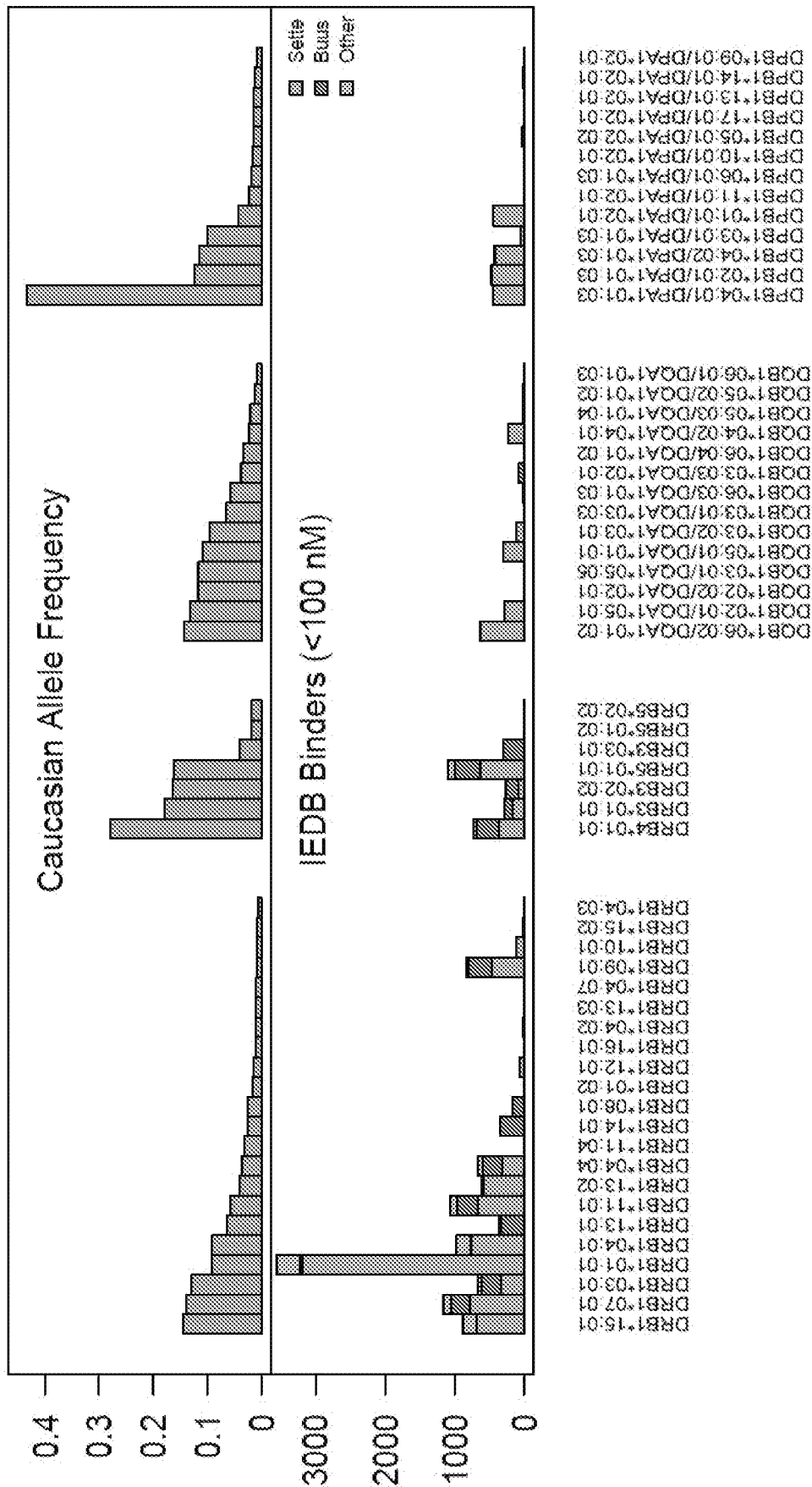


FIG. 12E

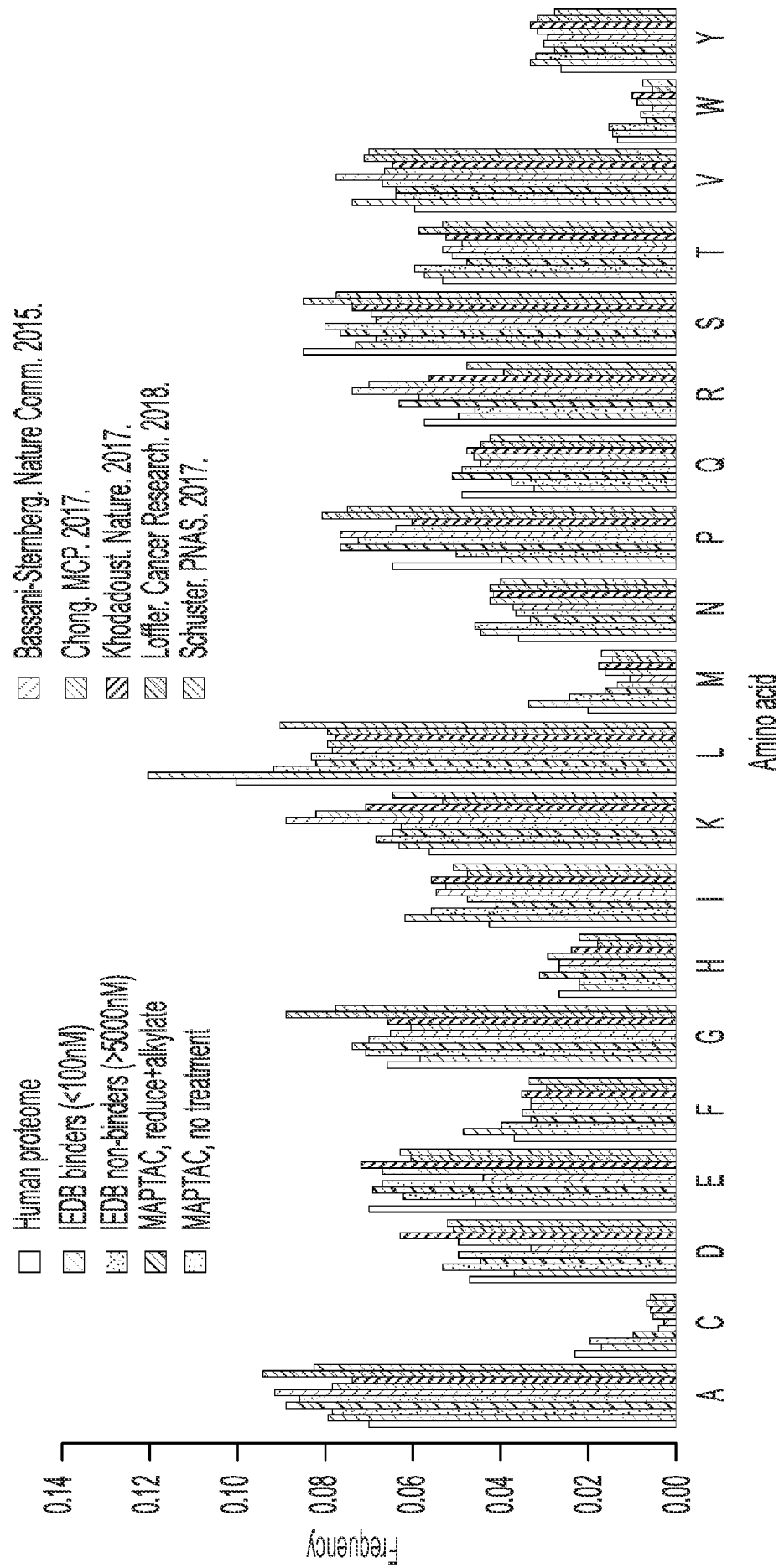


FIG. 12F

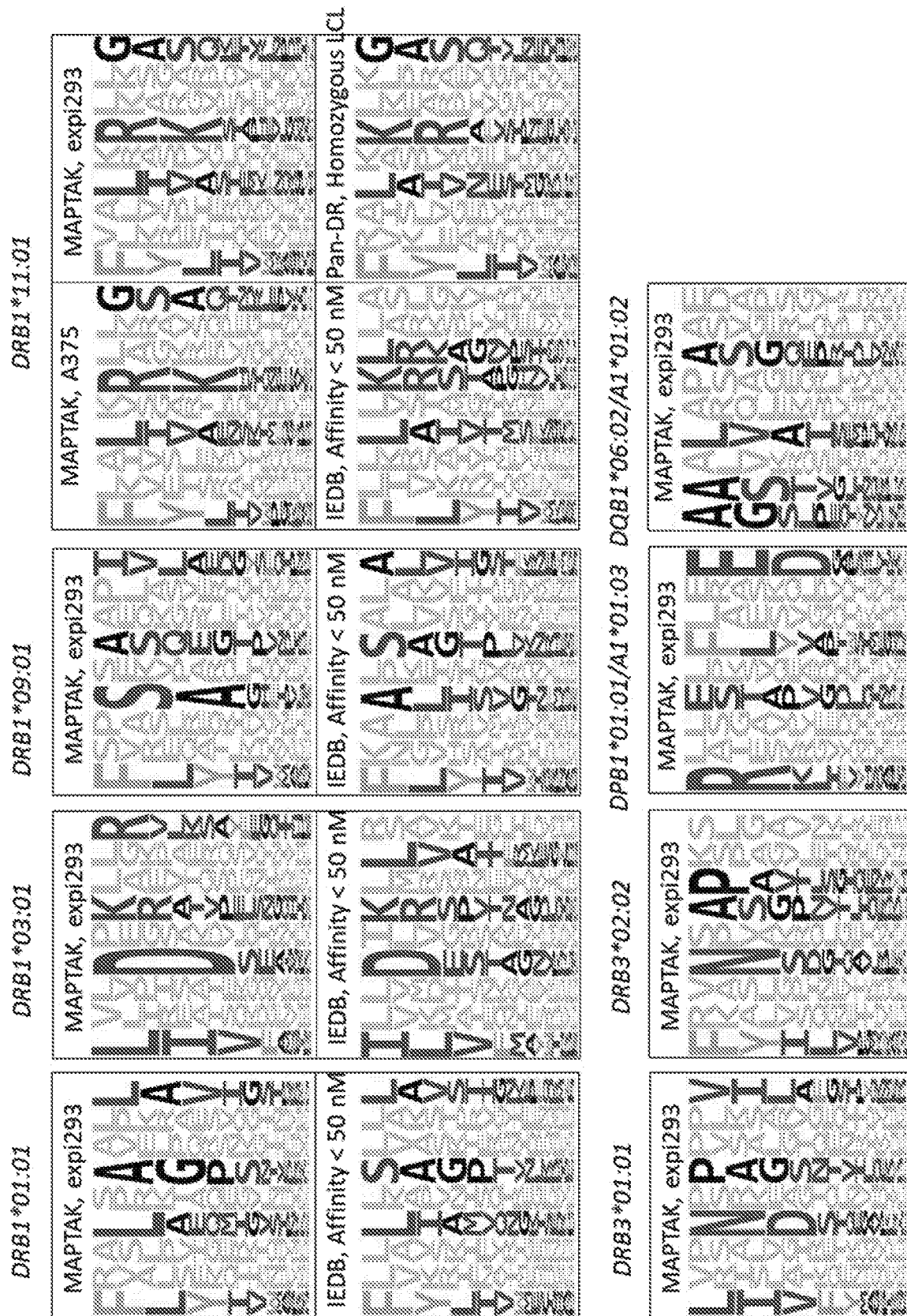


FIG. 13

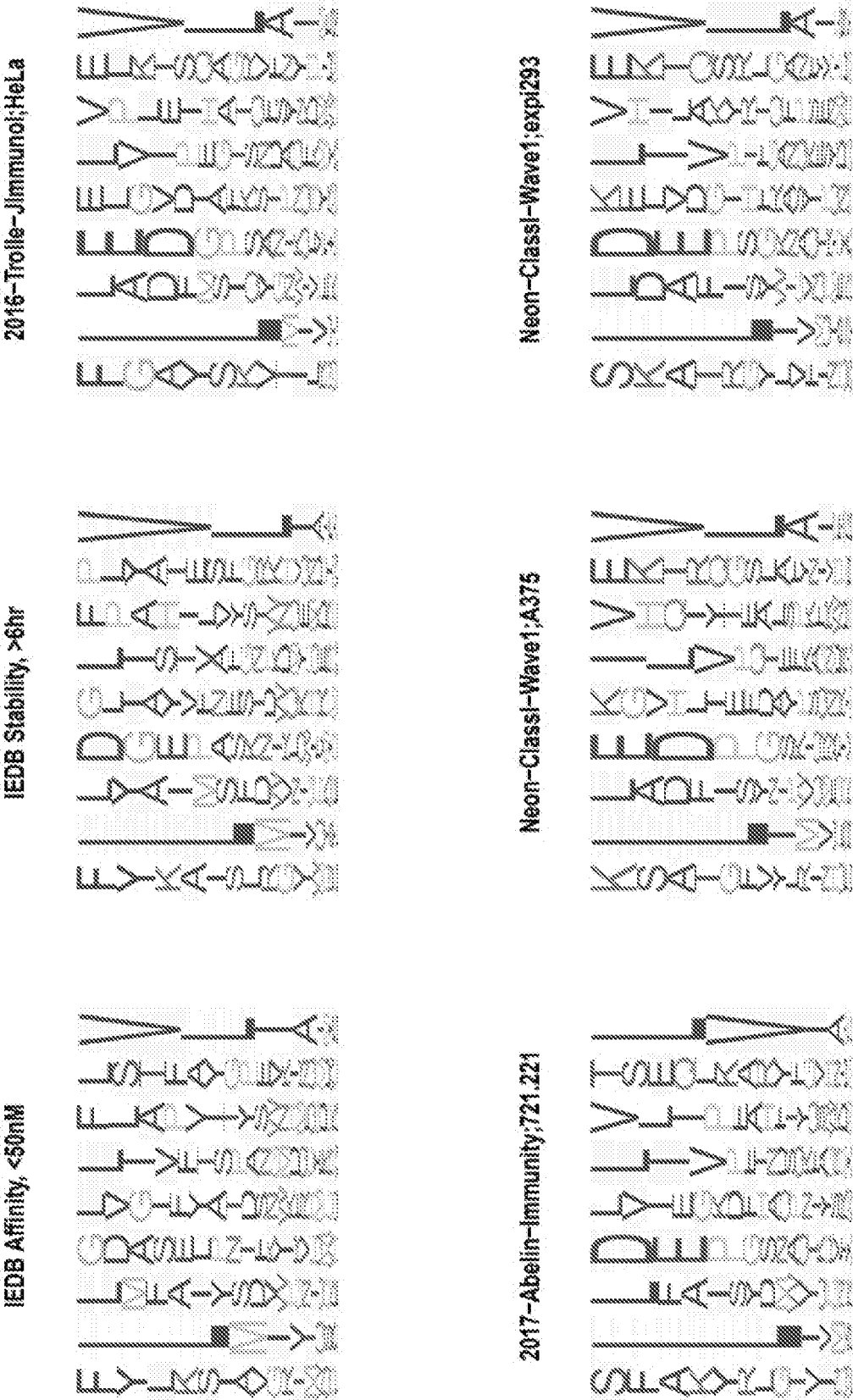


FIG. 14A

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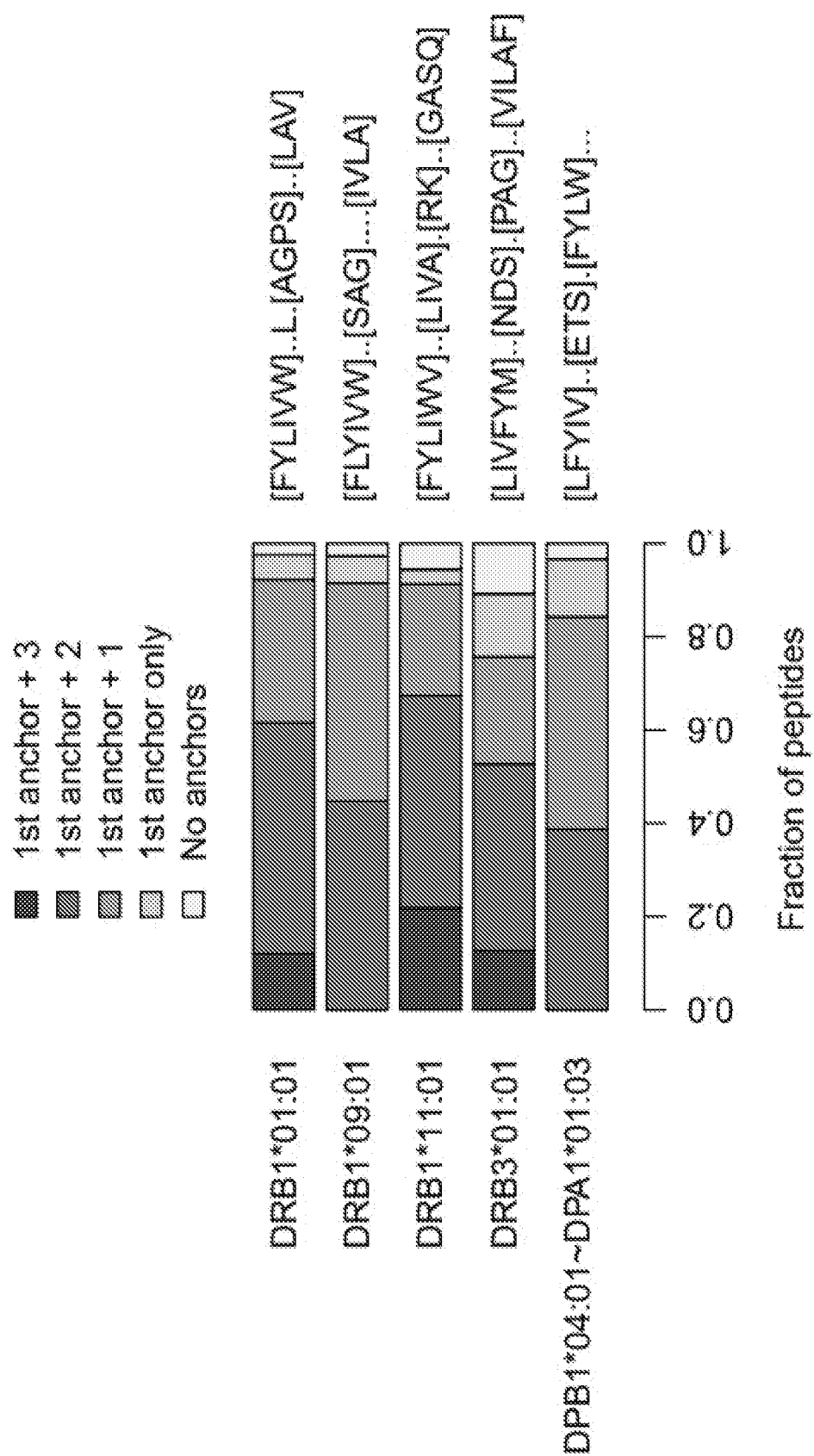


FIG. 14B

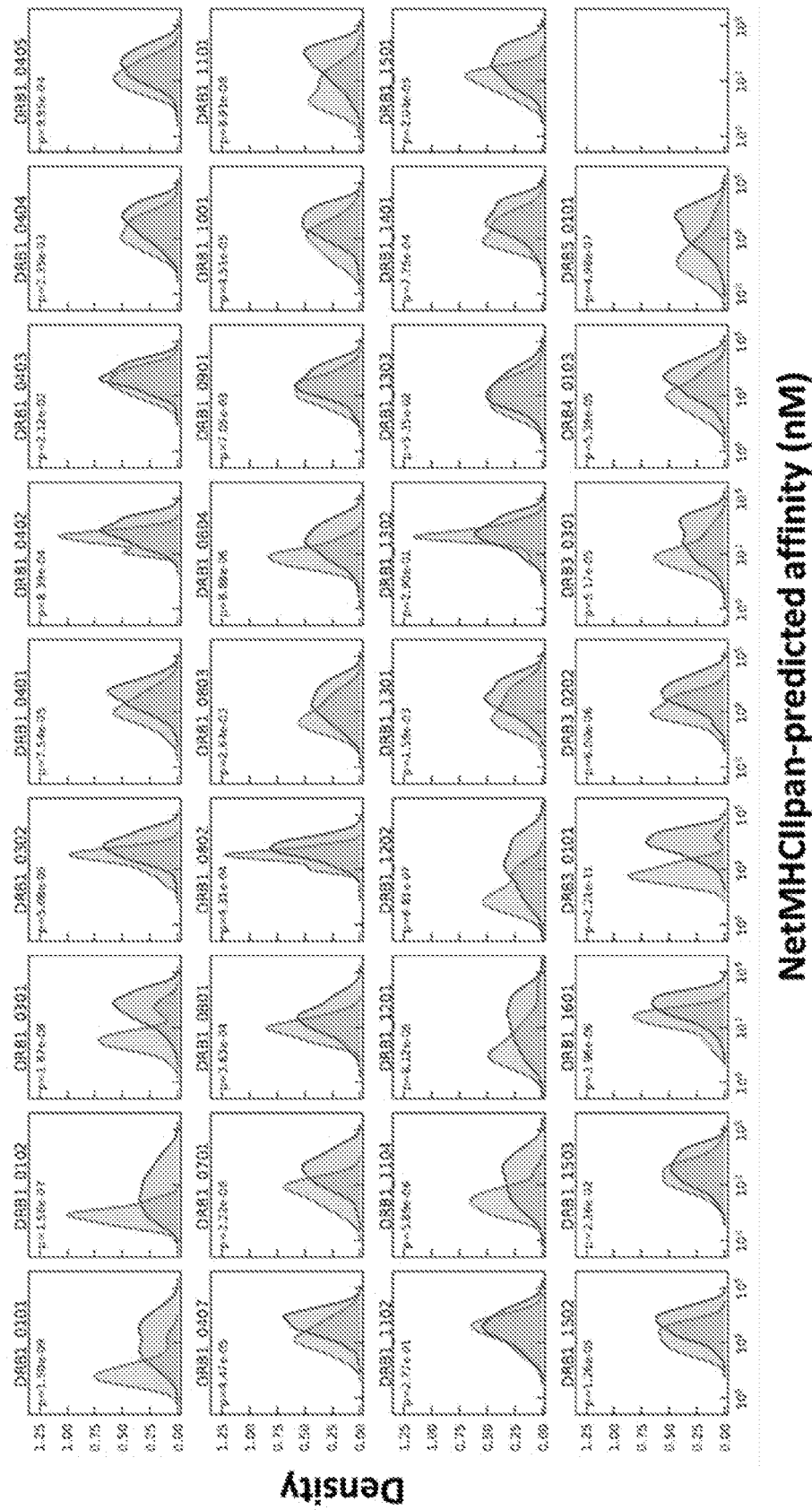


FIG. 14C

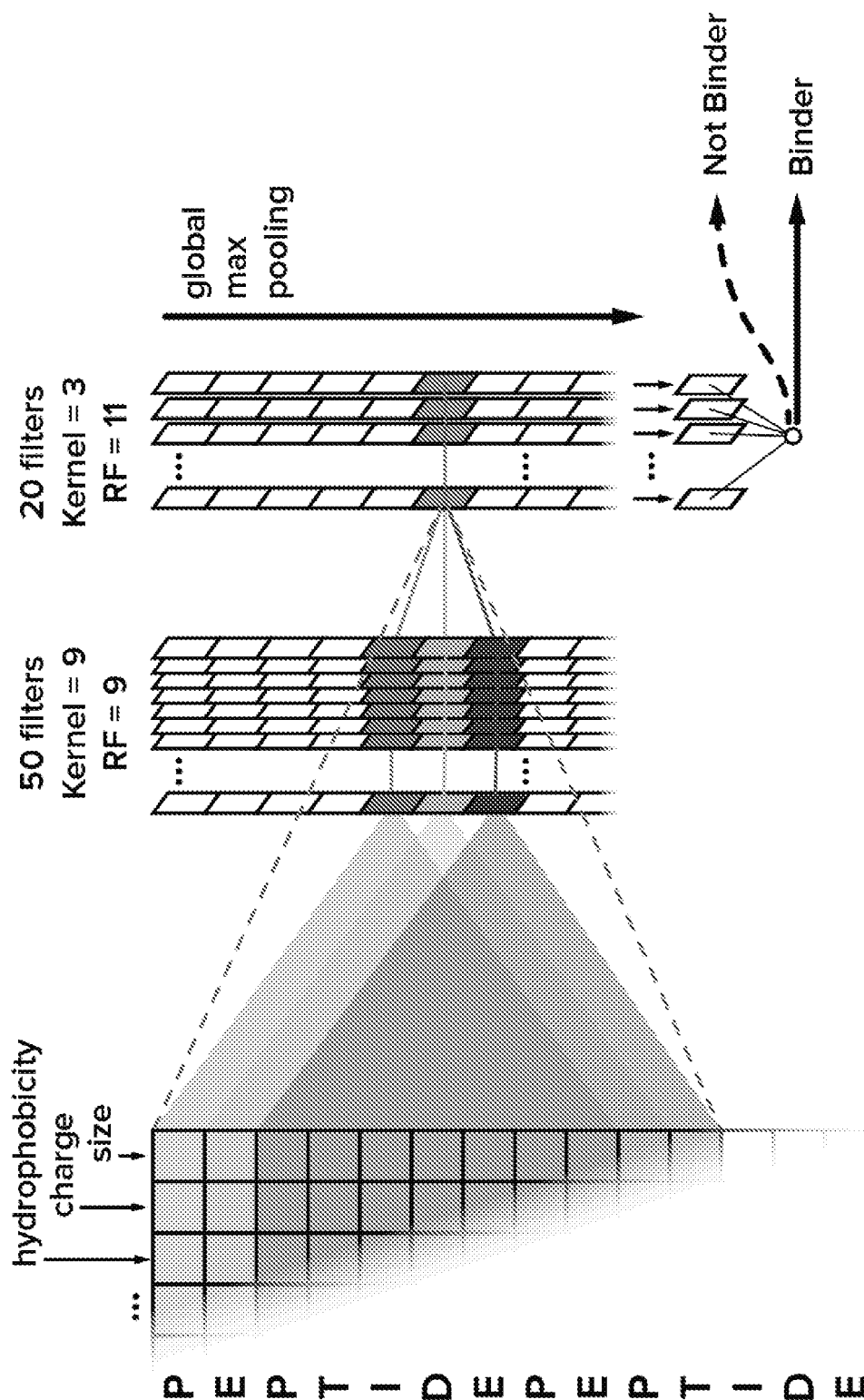


FIG. 15A

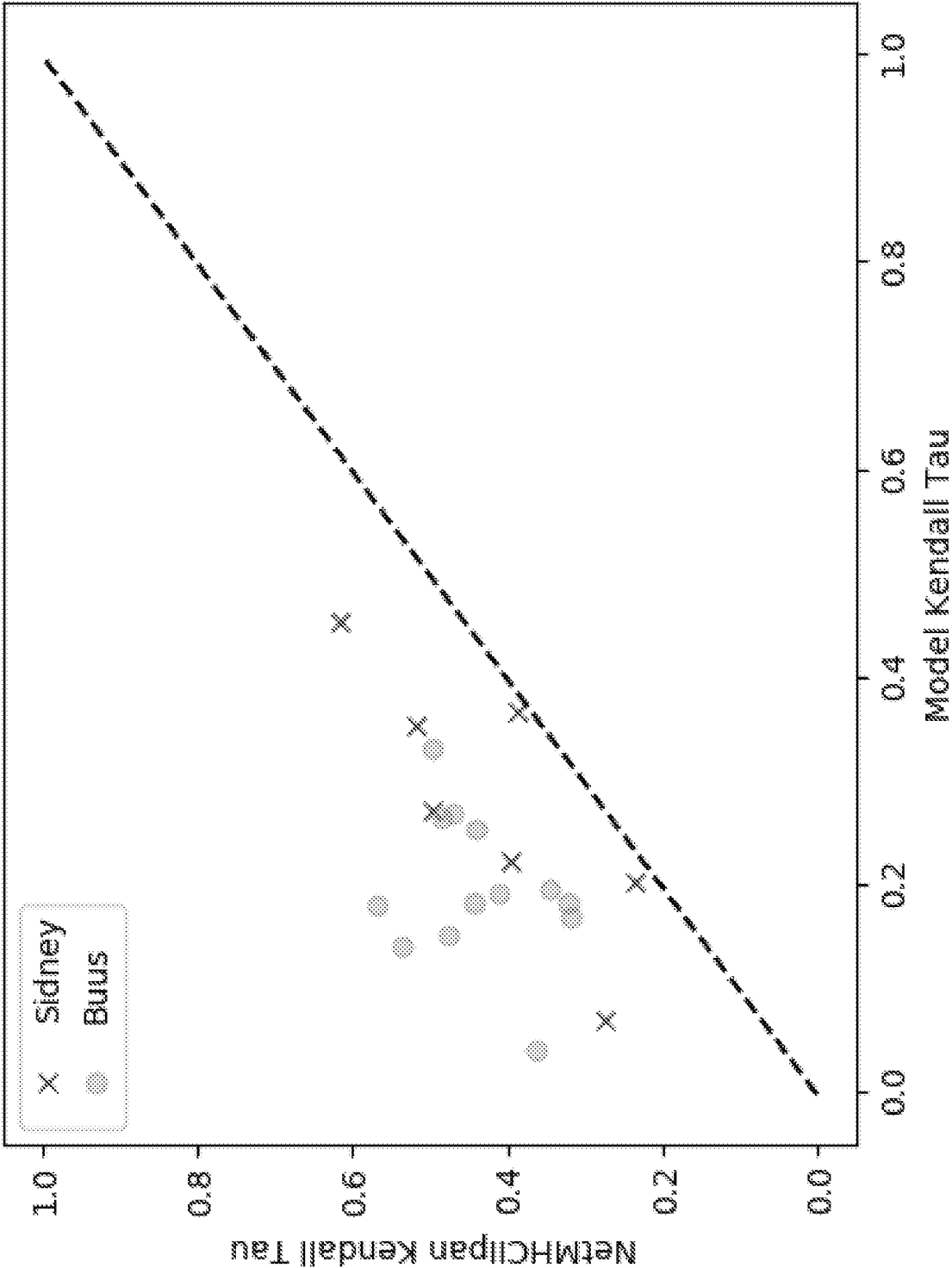


FIG. 15B



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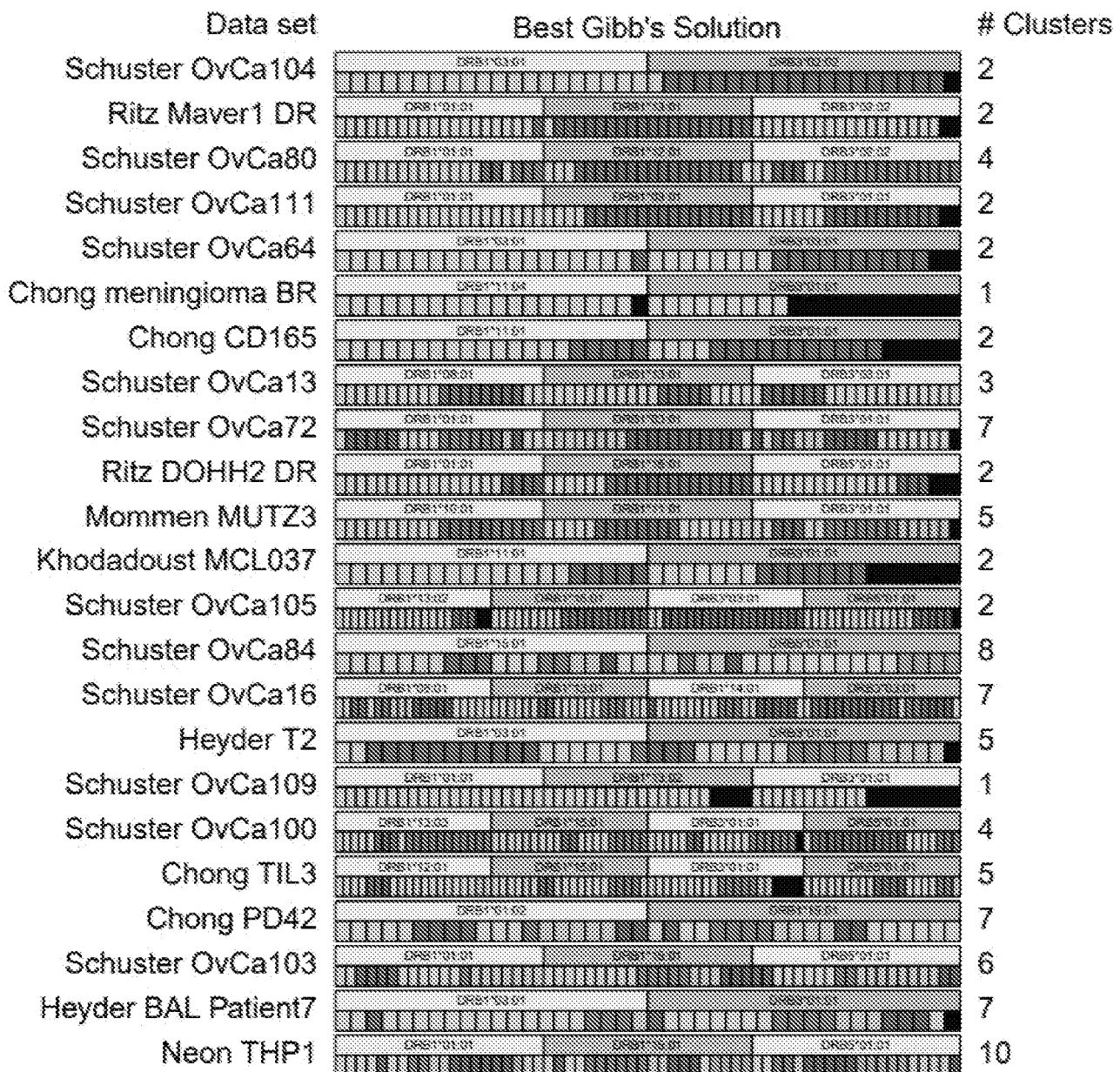
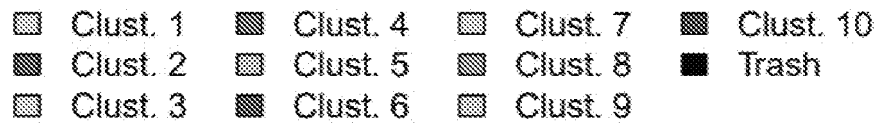
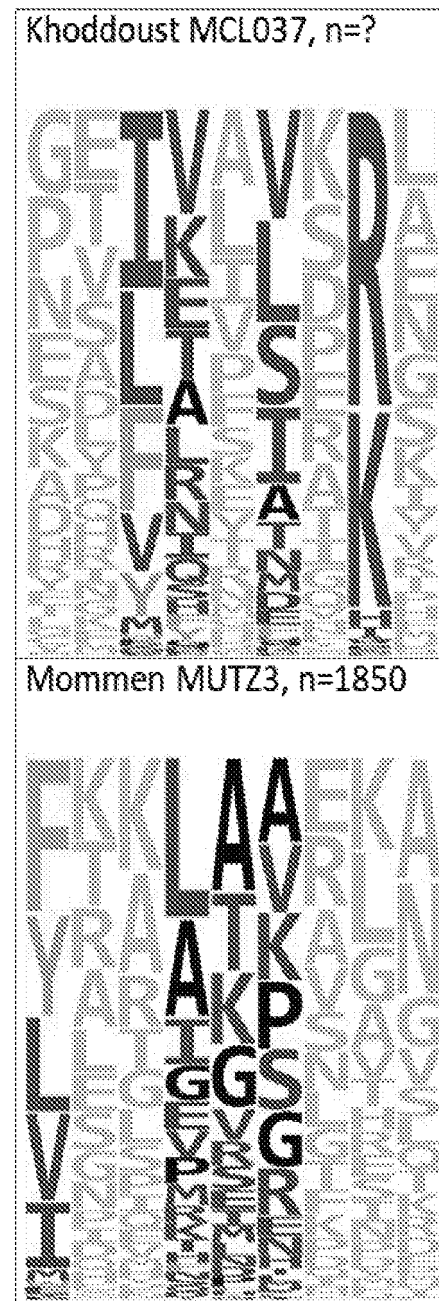
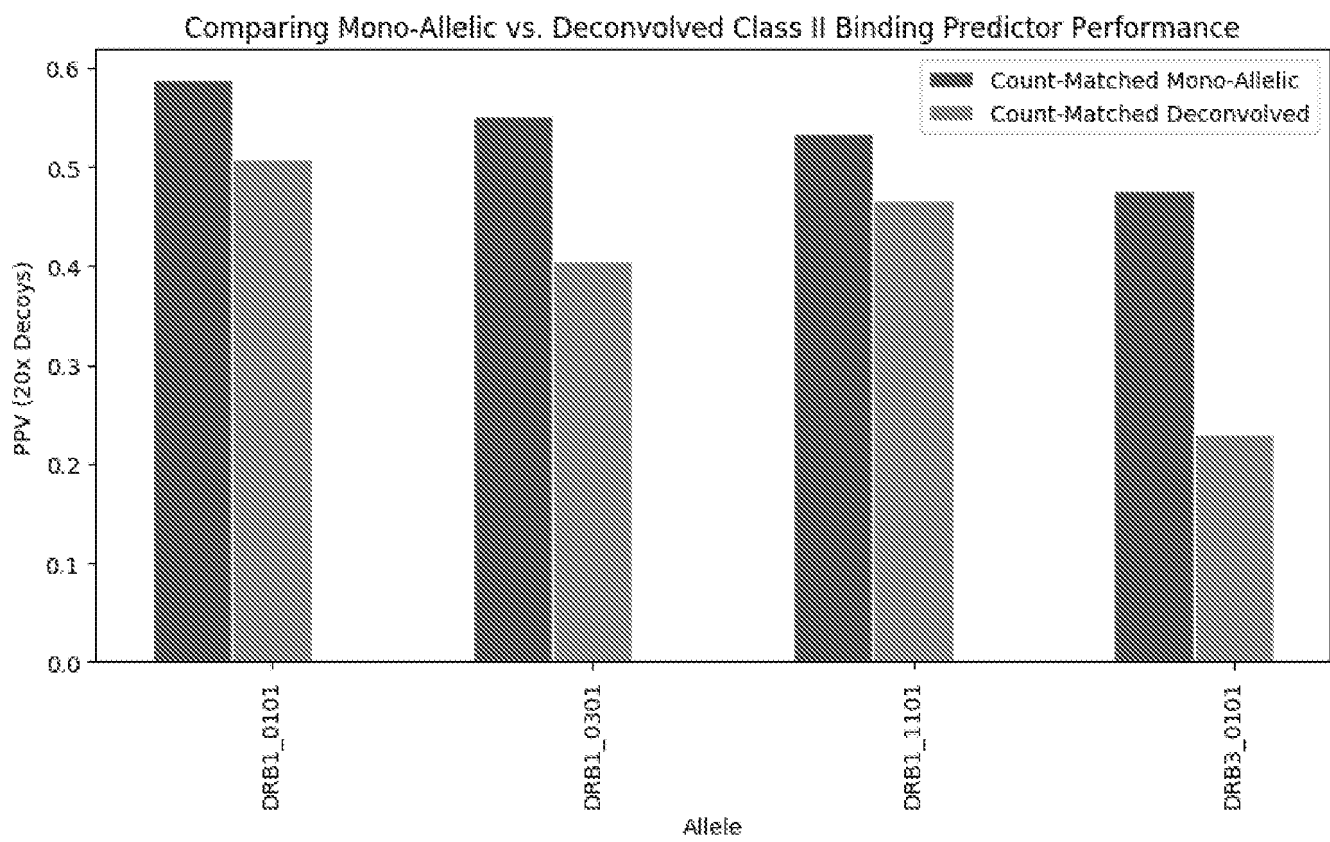


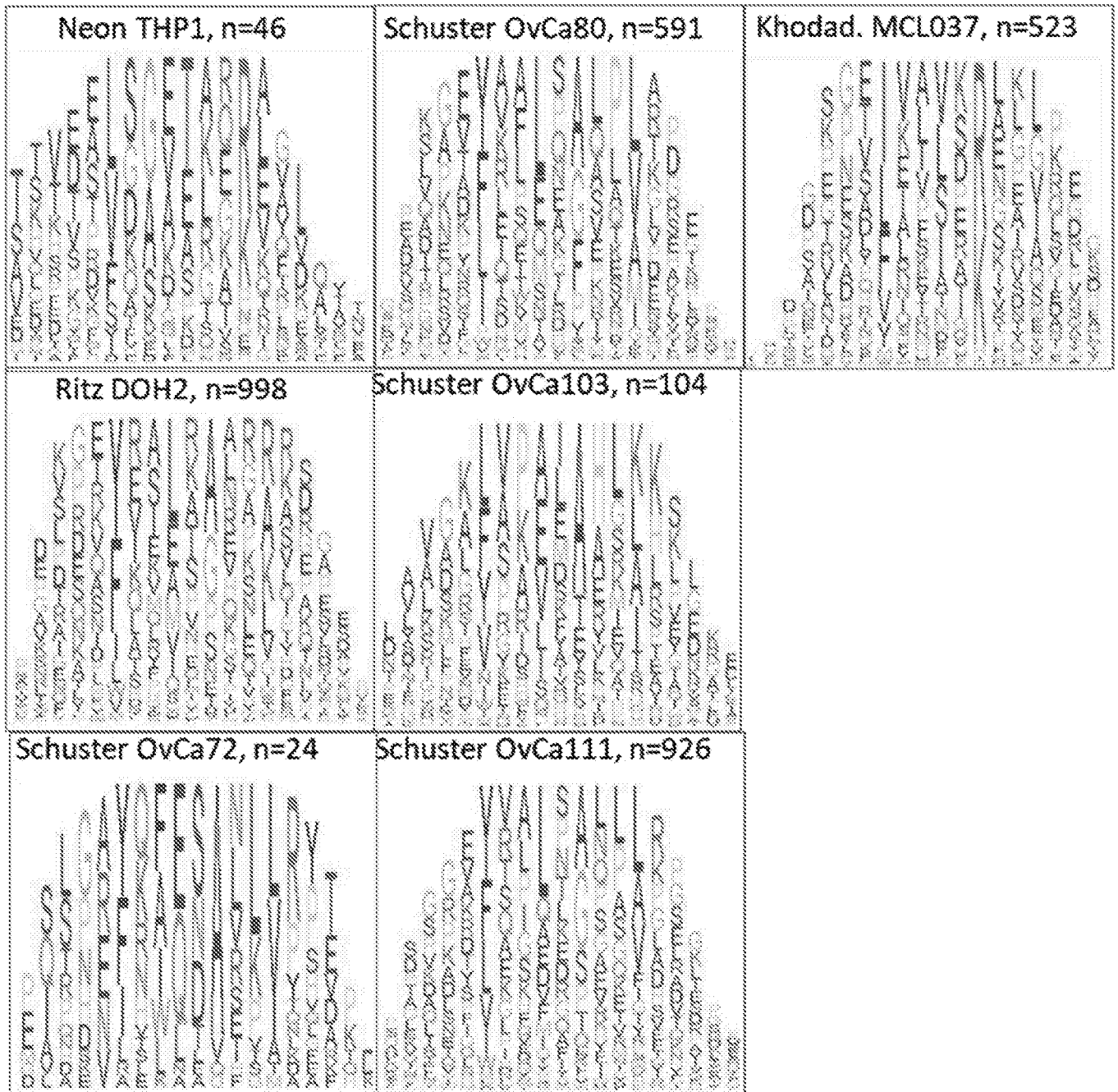
FIG. 17A

*DRB1*01:01**DRB1*11:01***FIG. 17B**

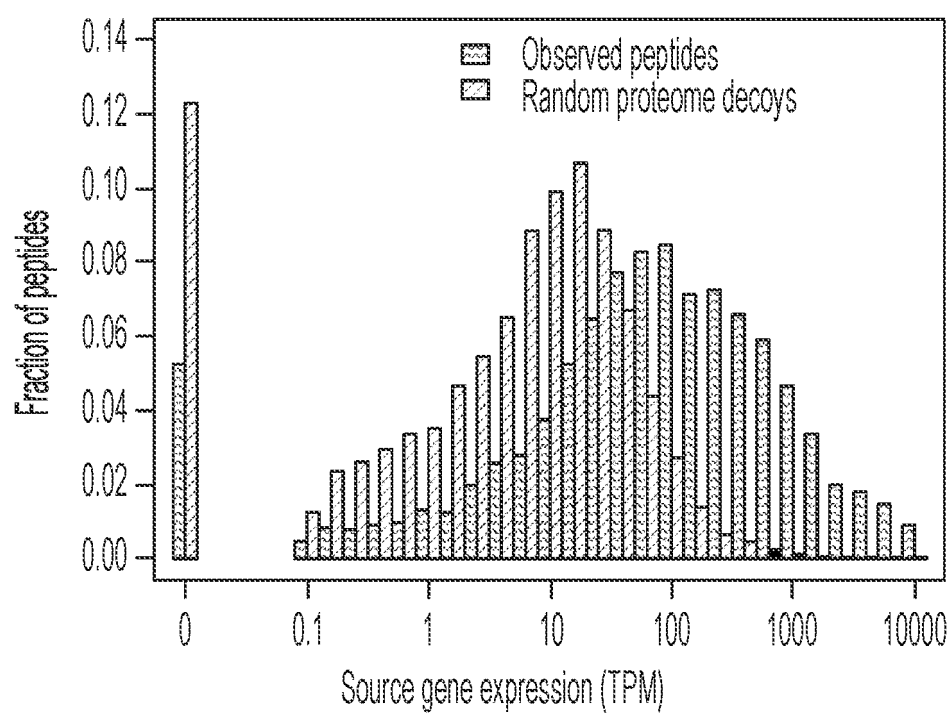
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**FIG. 17C**

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*DRB1*01:01**DRB1*01:01*
(continued)*DRB1*11:01***FIG. 17D**

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**FIG. 18A**

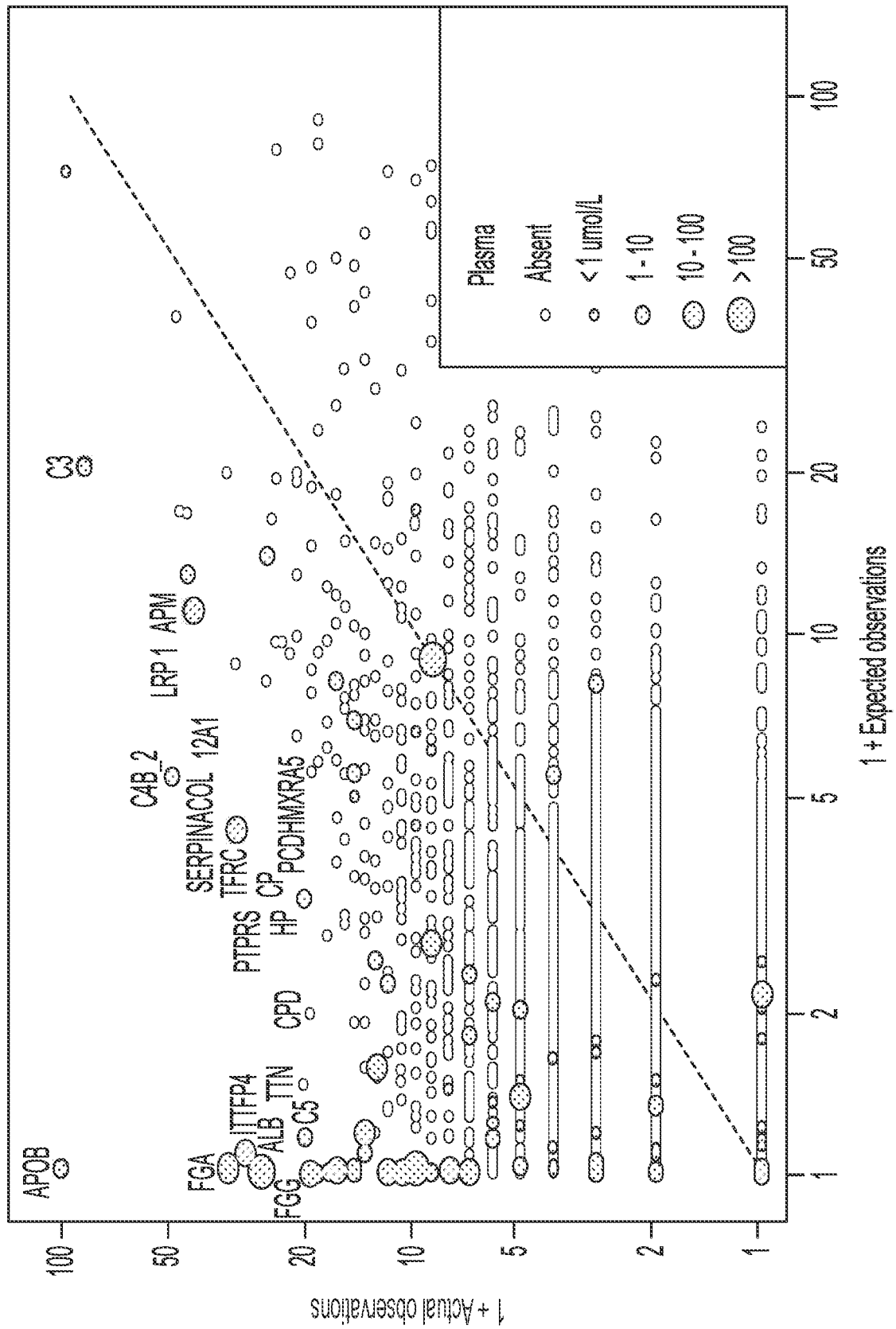
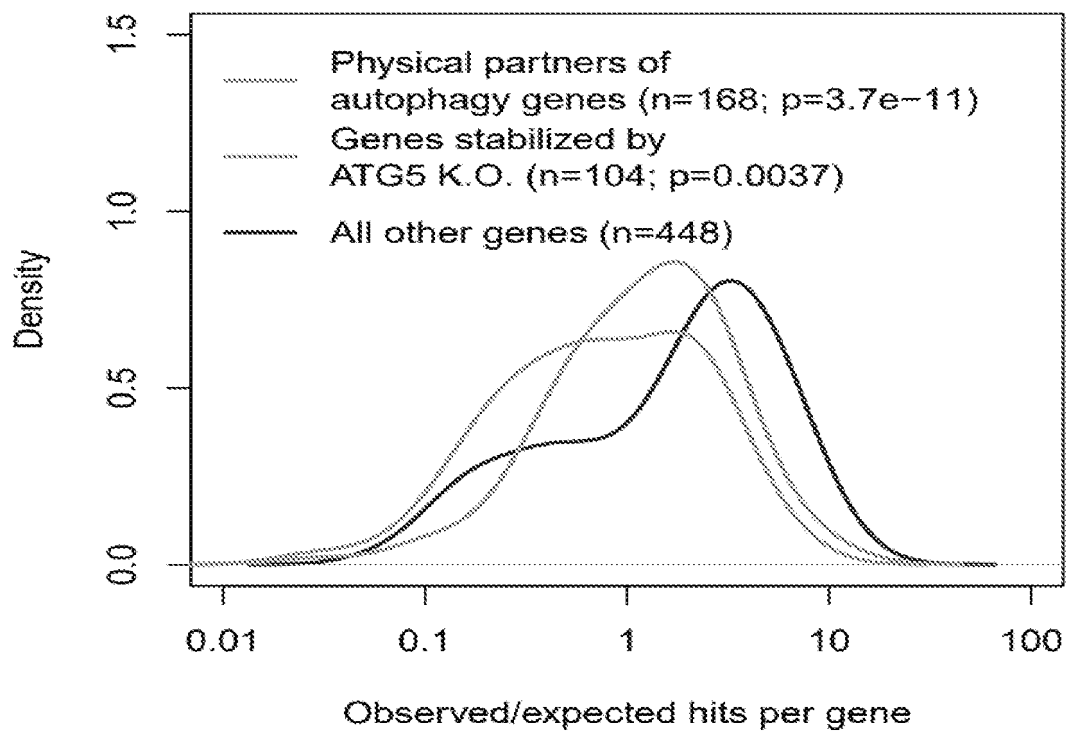
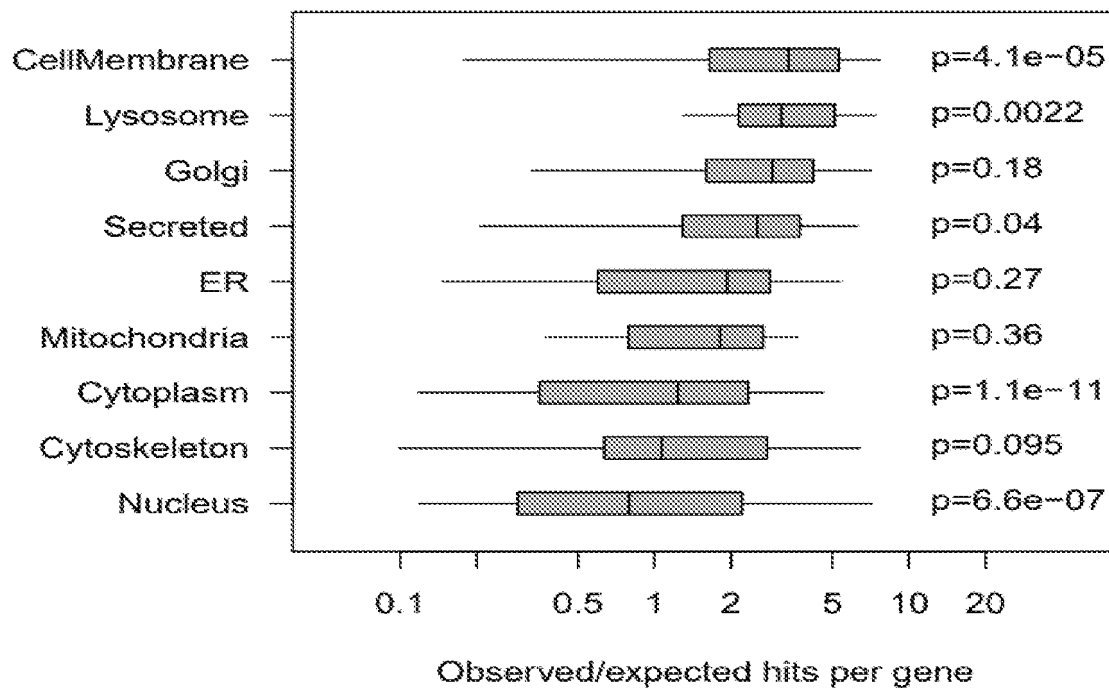
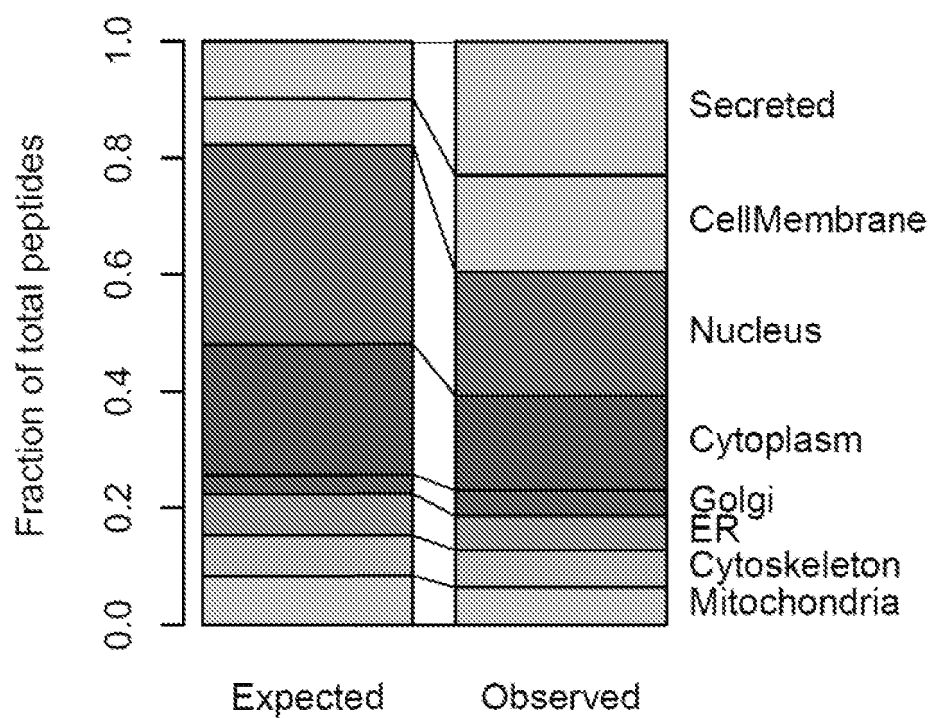


FIG. 18B

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*FIG. 18C**FIG. 18D*

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**FIG. 18E**

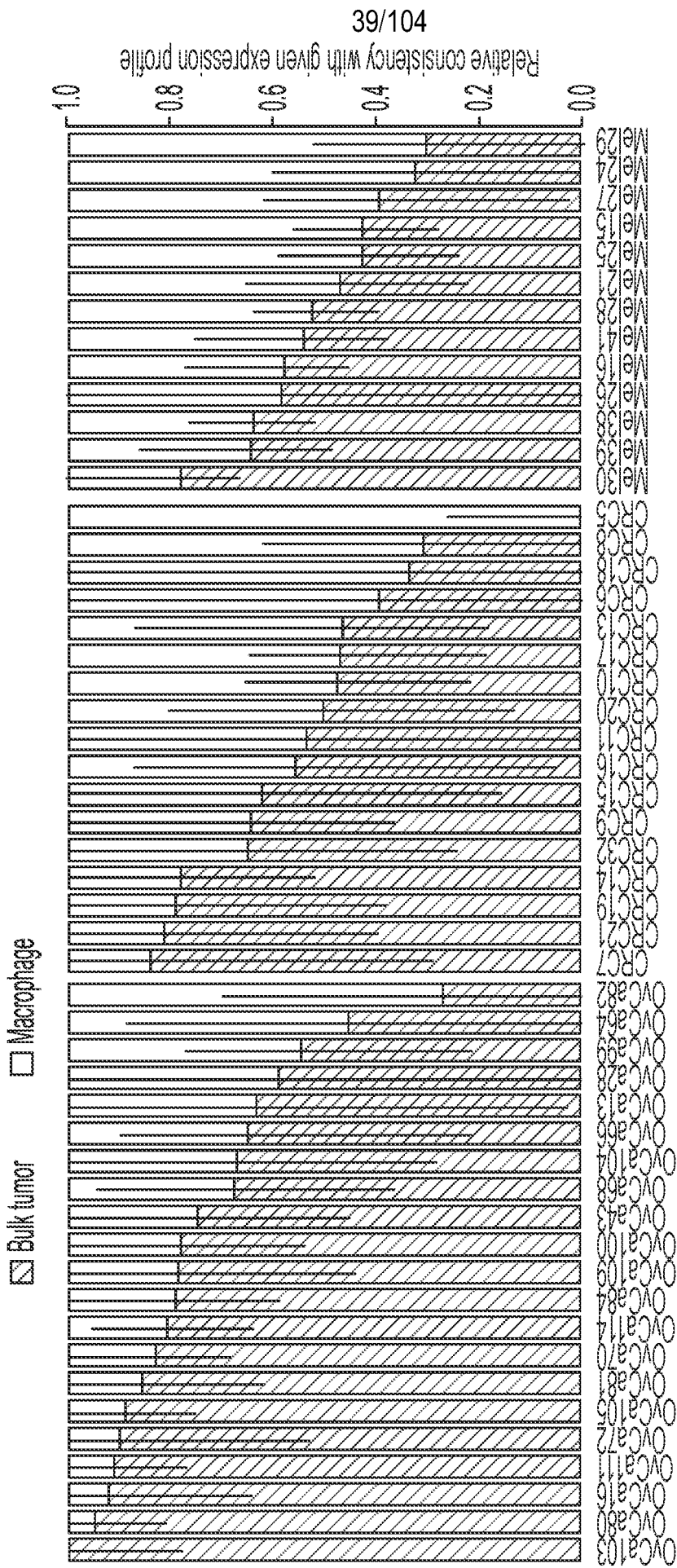
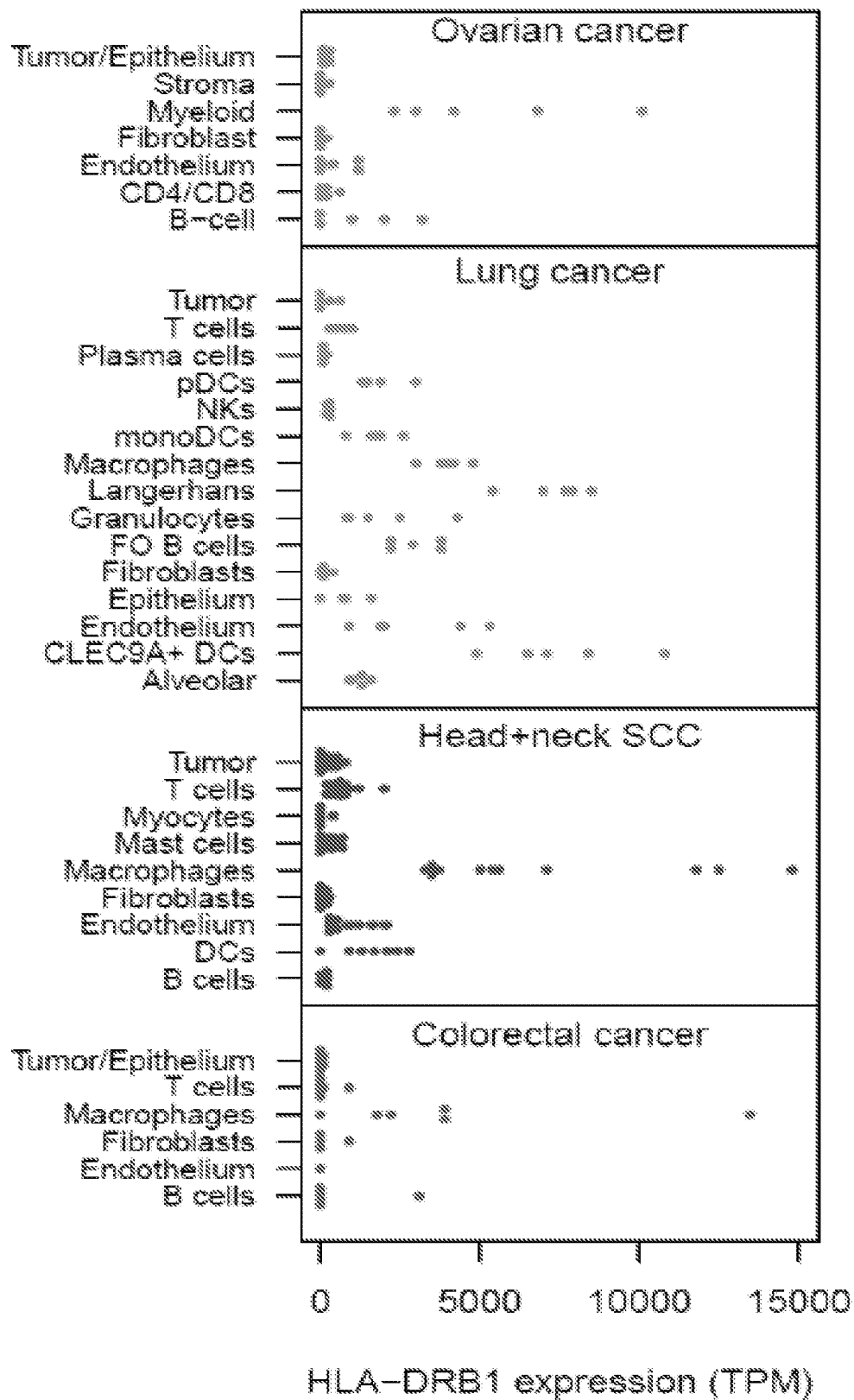
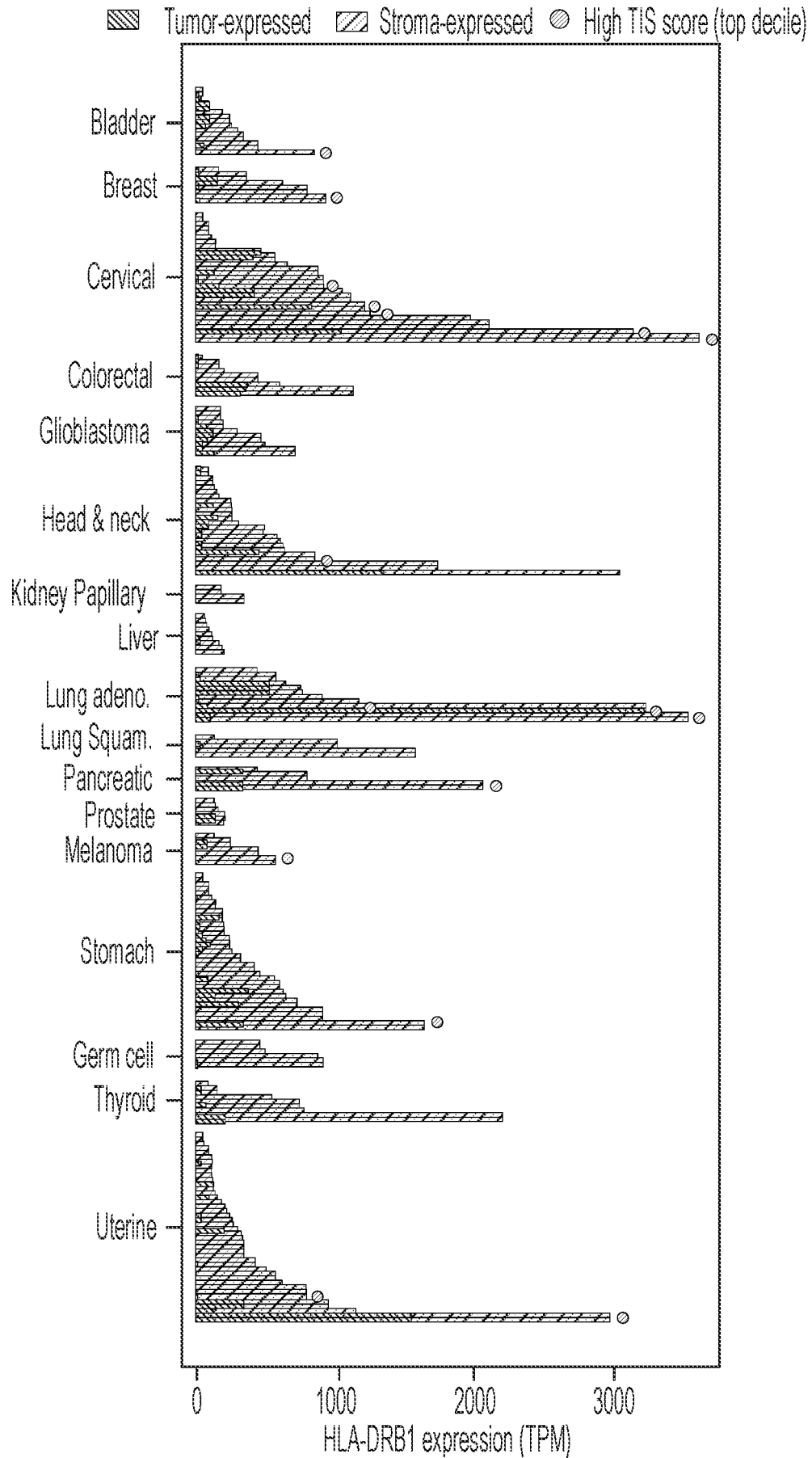


FIG. 18F

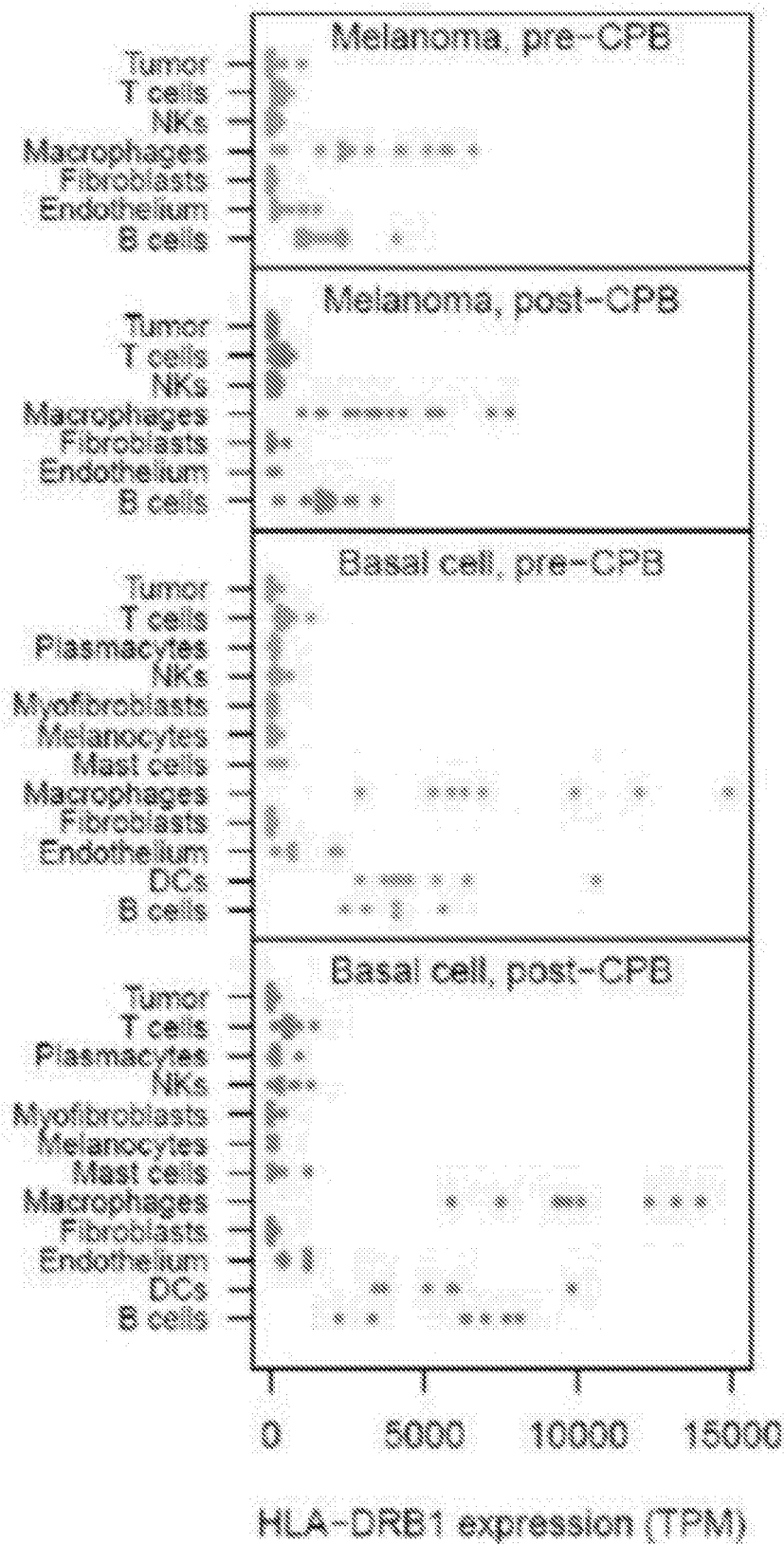
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**FIG. 19A**

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**FIG. 19B**

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**FIG. 19C**

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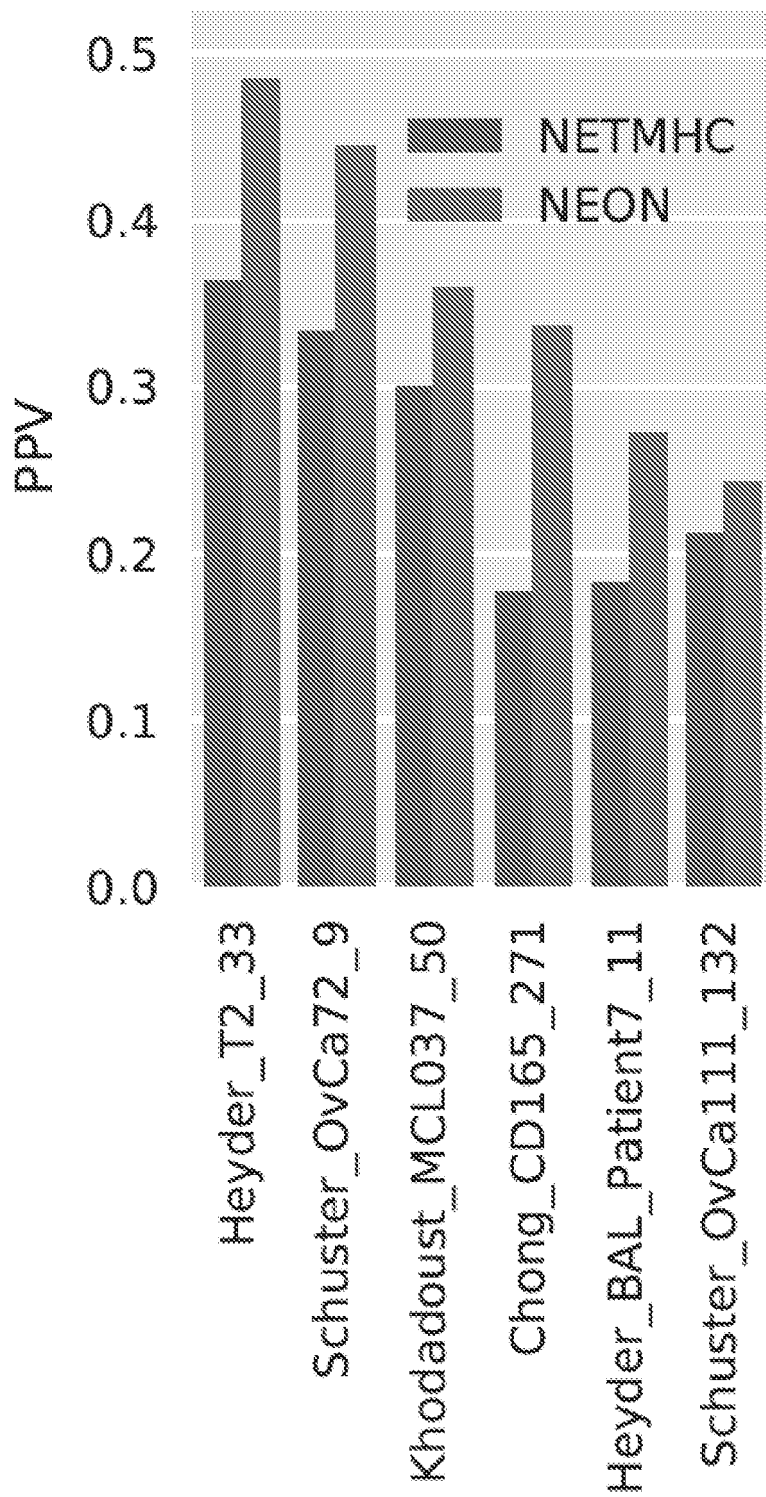
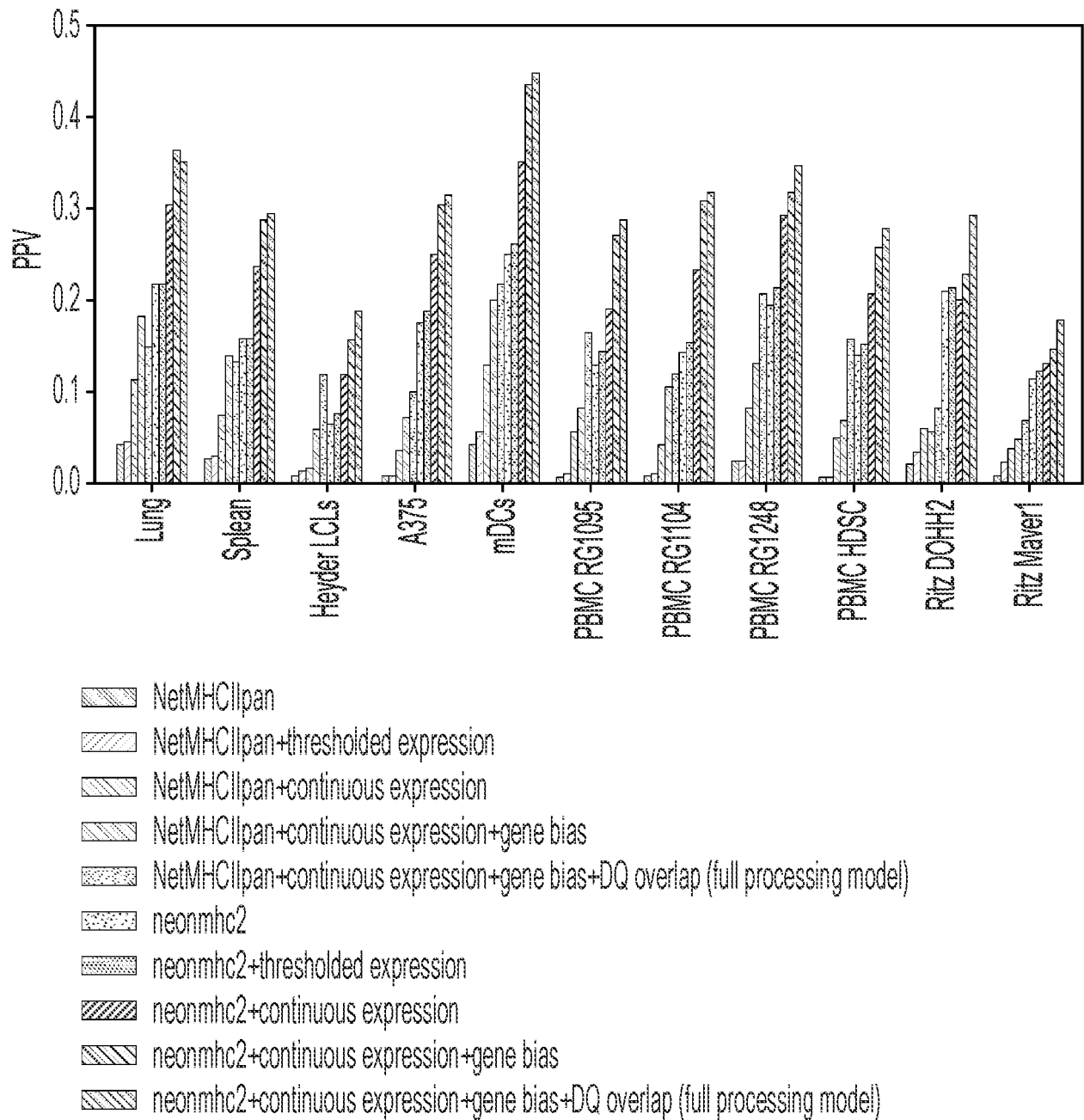
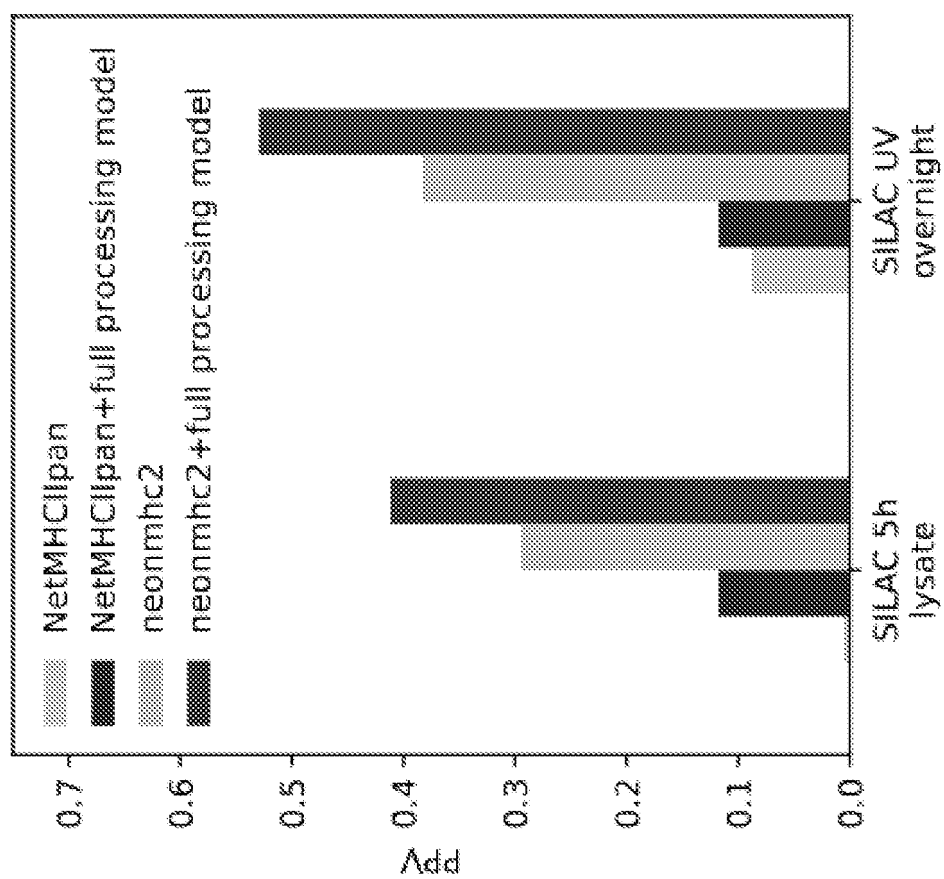


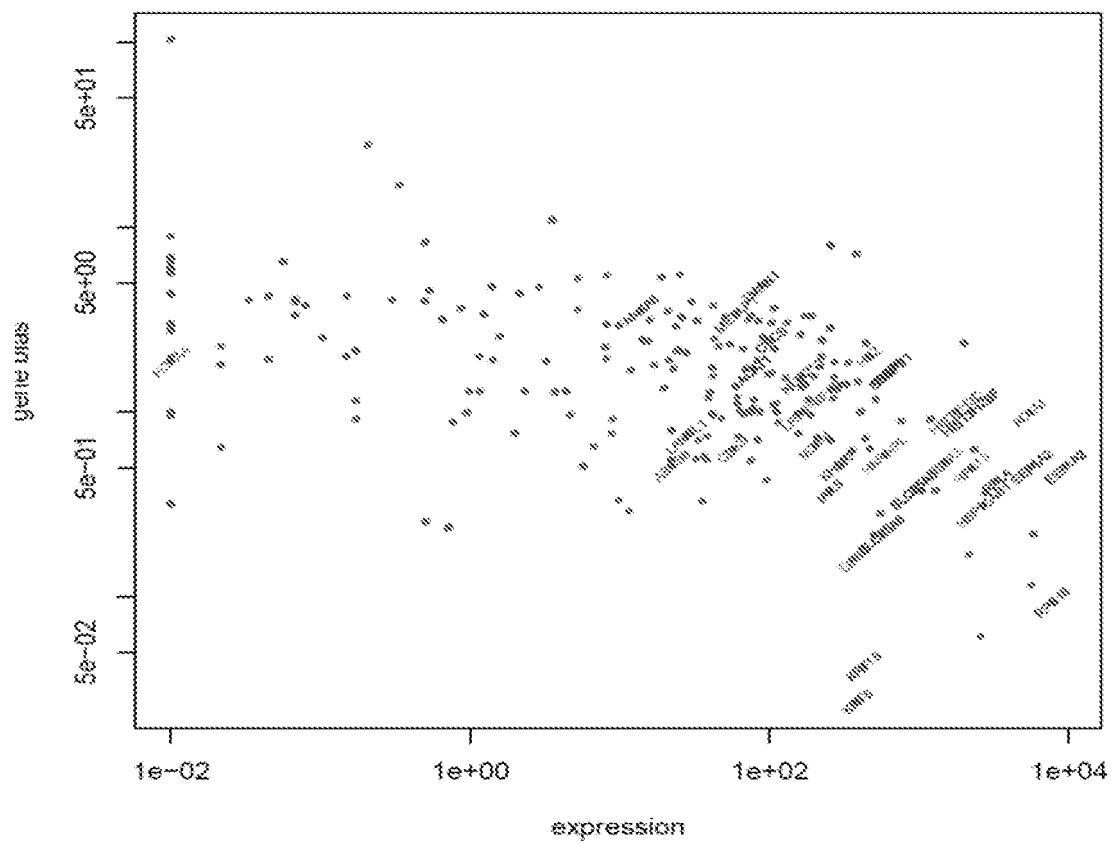
FIG. 20

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**FIG. 21A**

*FIG. 21B*

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**FIG. 21C**

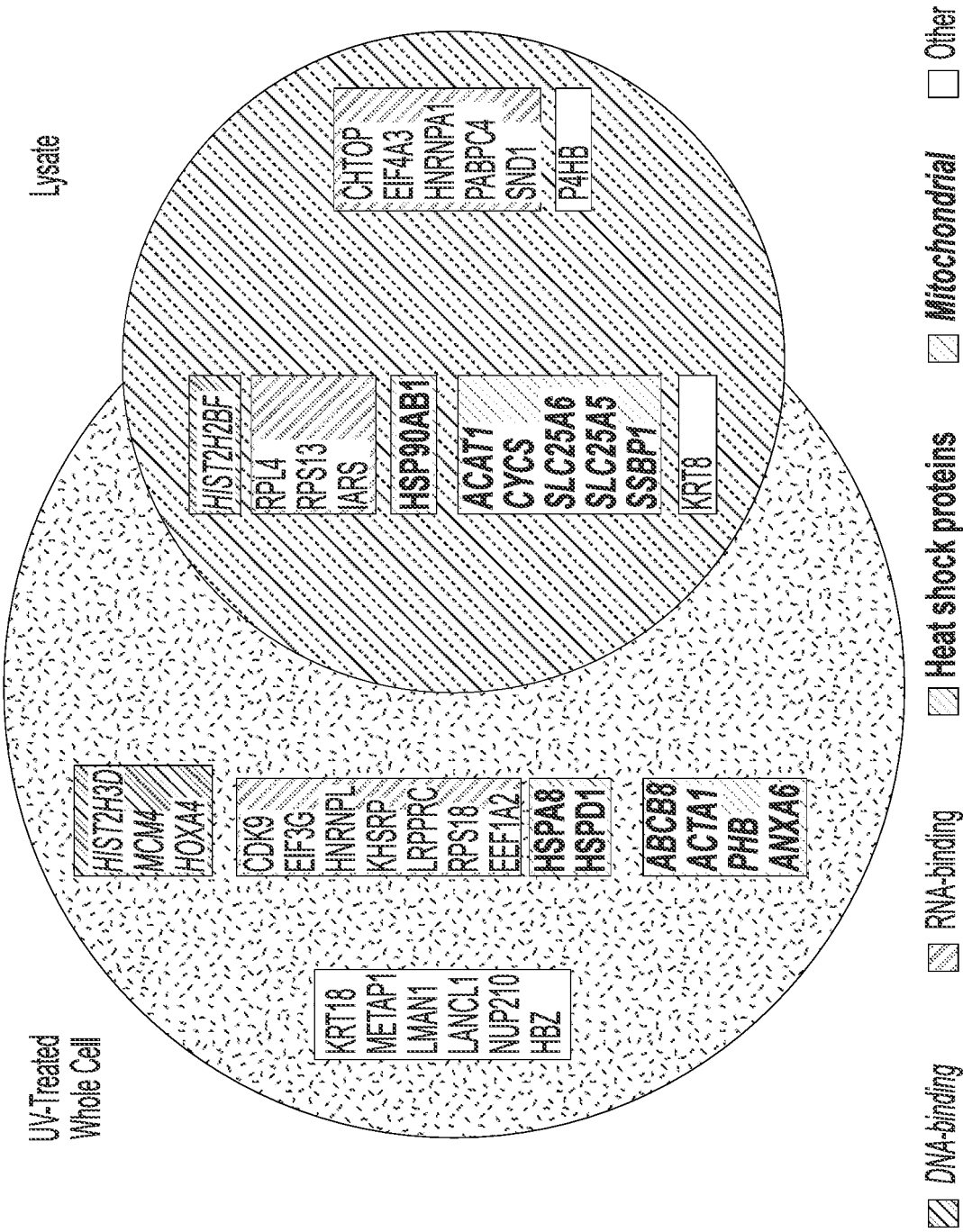


FIG. 21D

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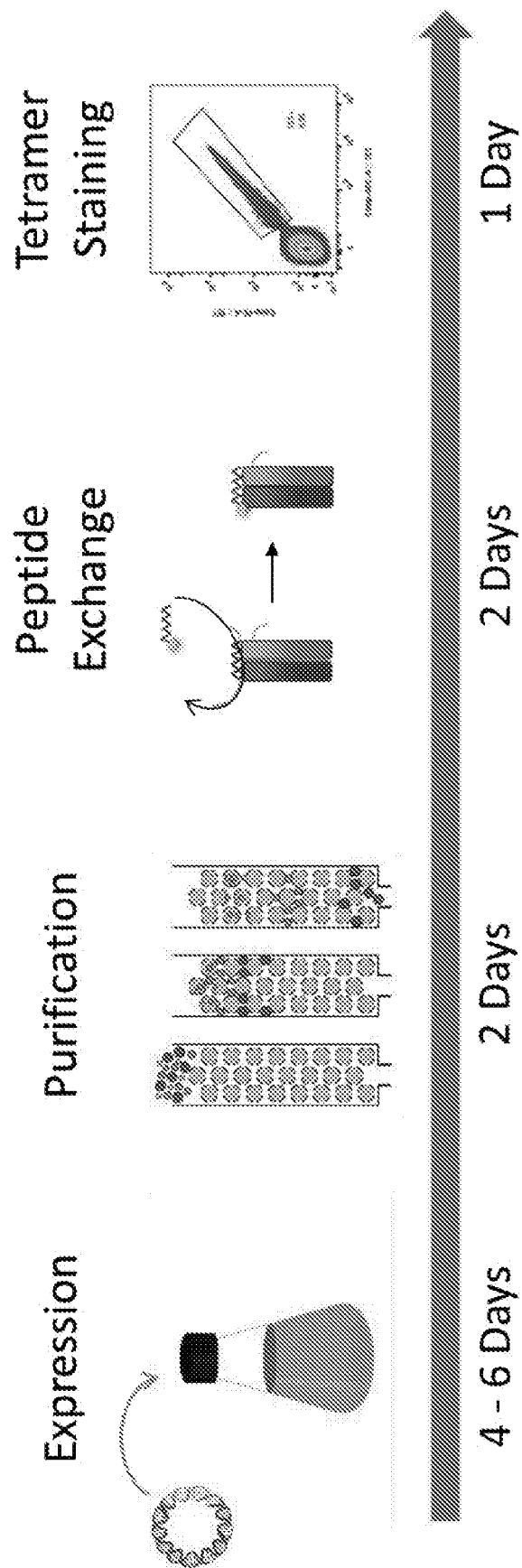


FIG. 22A

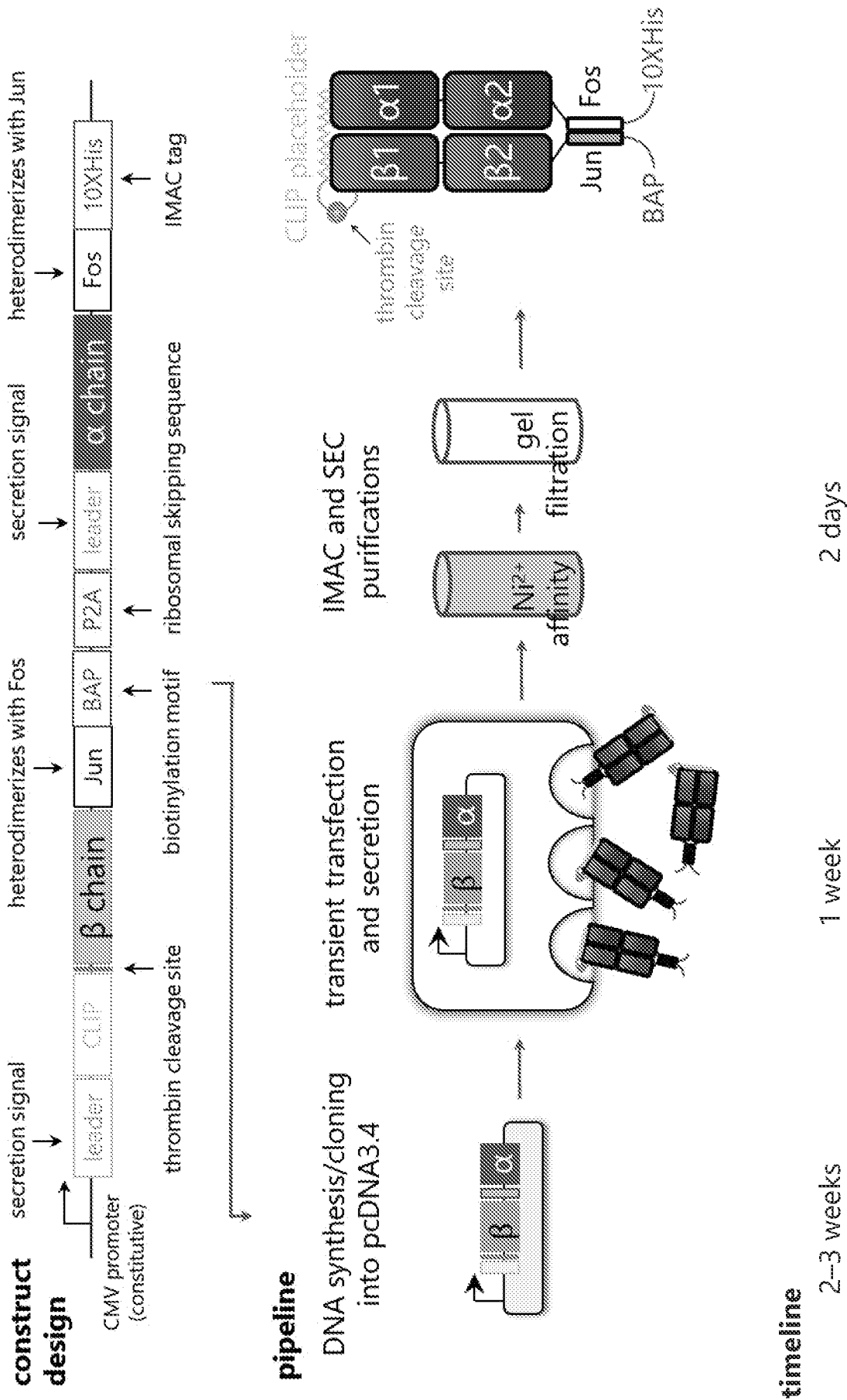


FIG. 22B

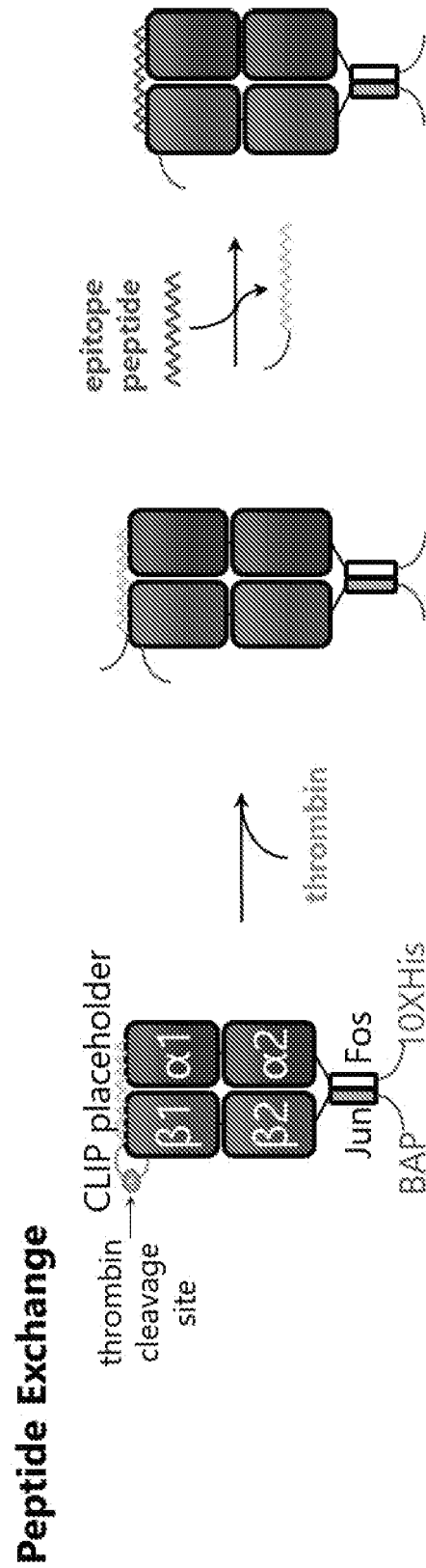
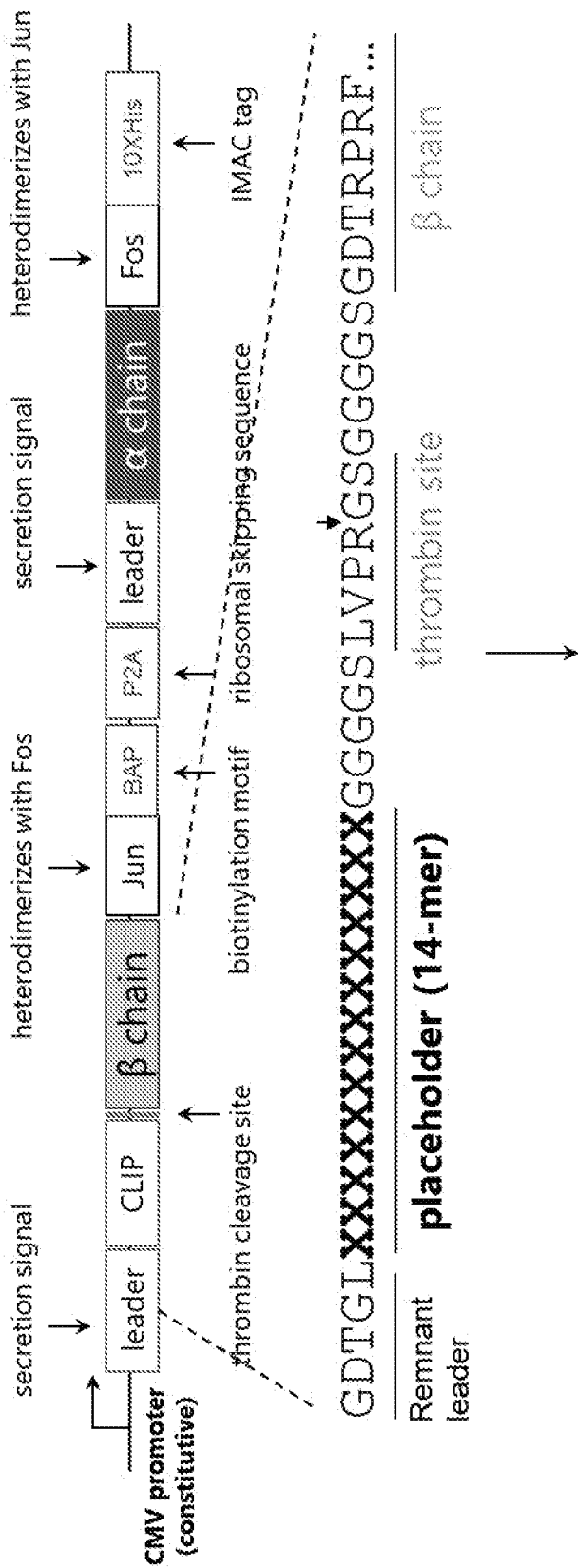


FIG. 23

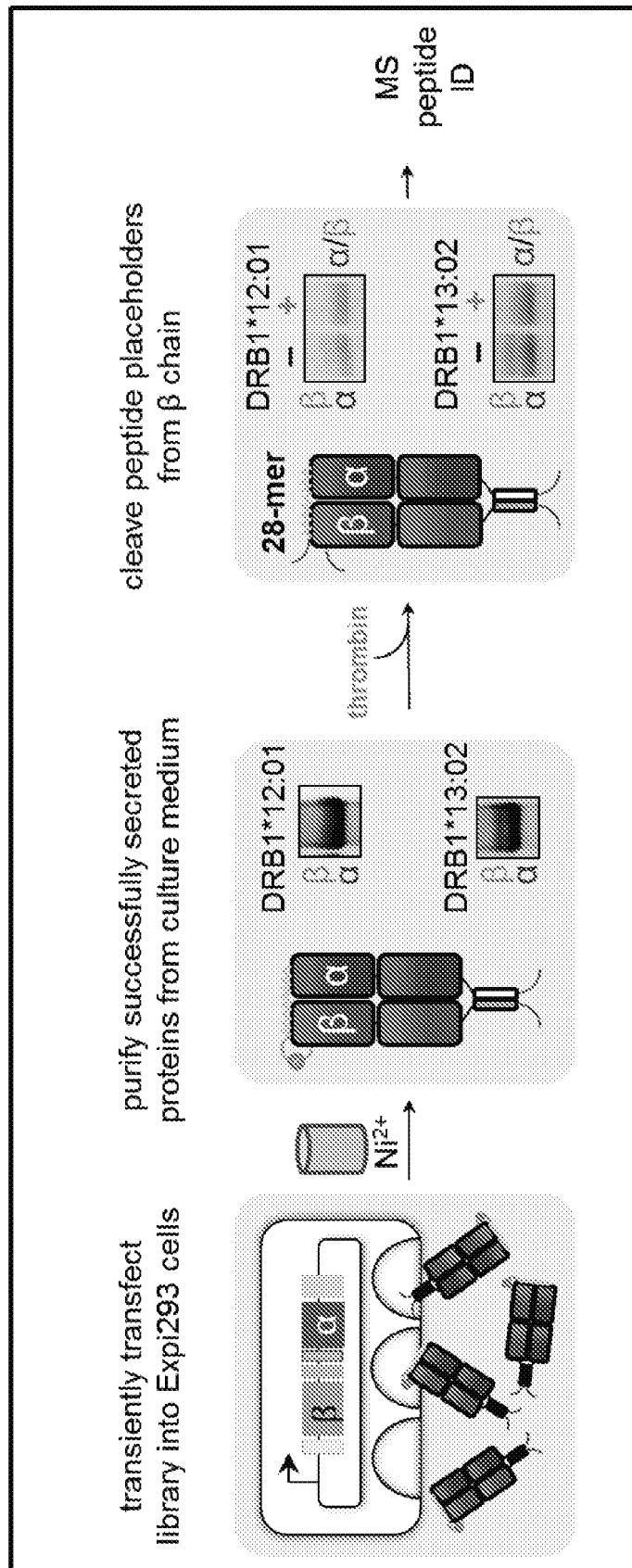


FIG. 24

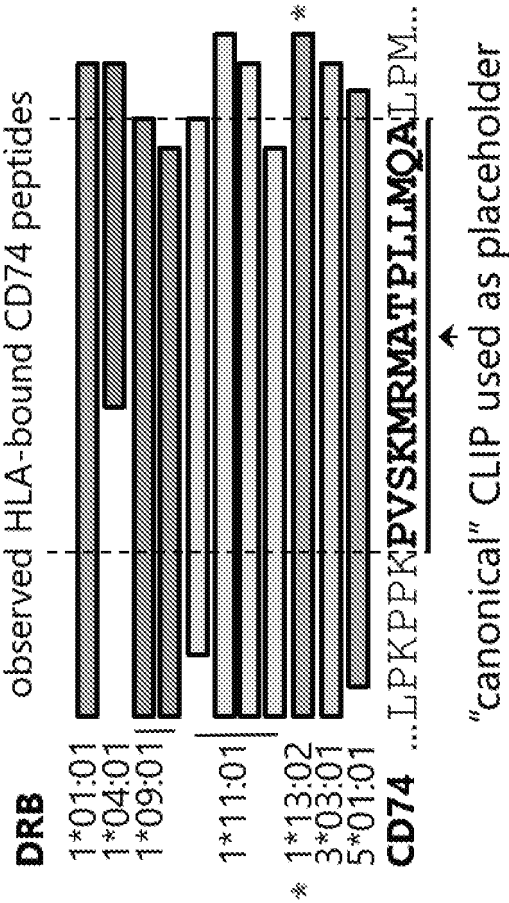


FIG. 25A

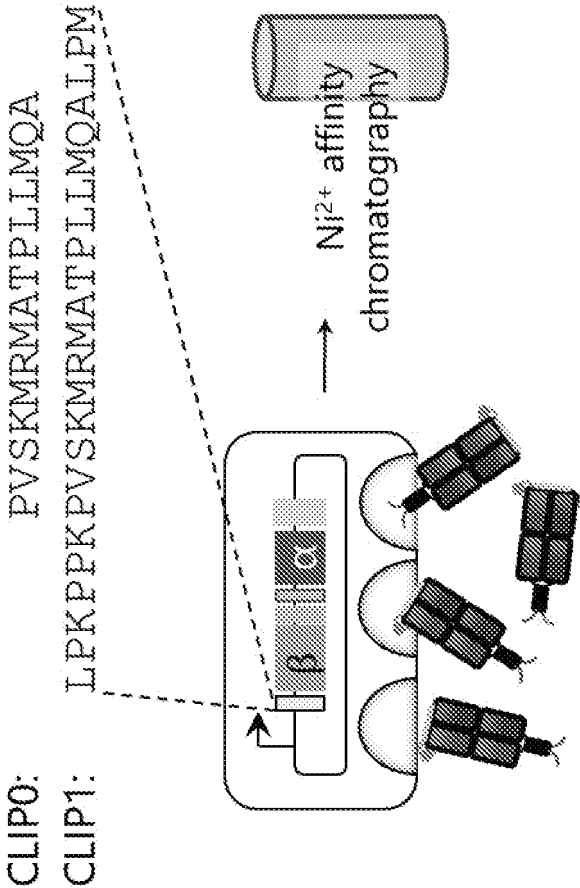


FIG. 25B



FIG. 25C

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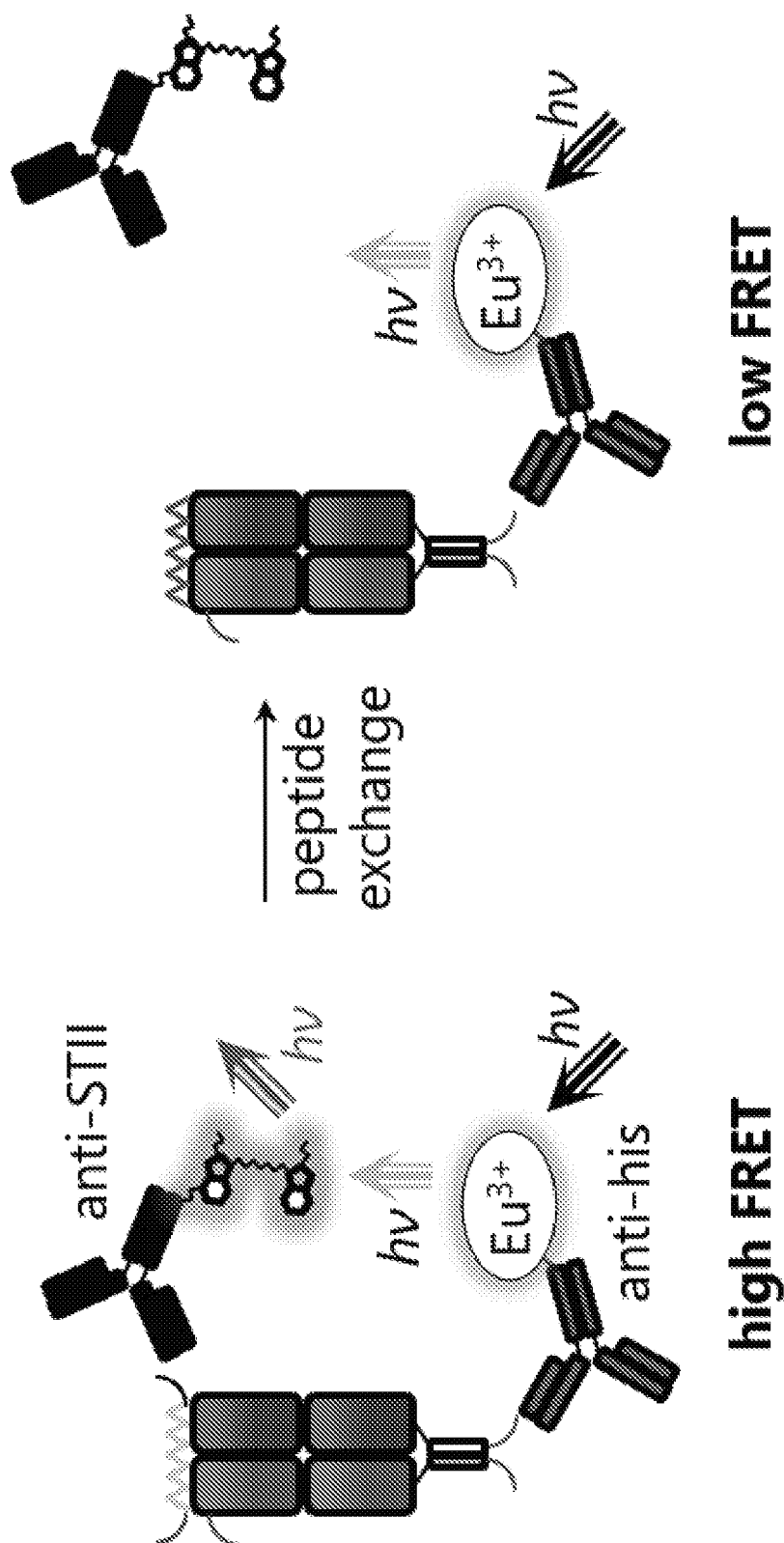
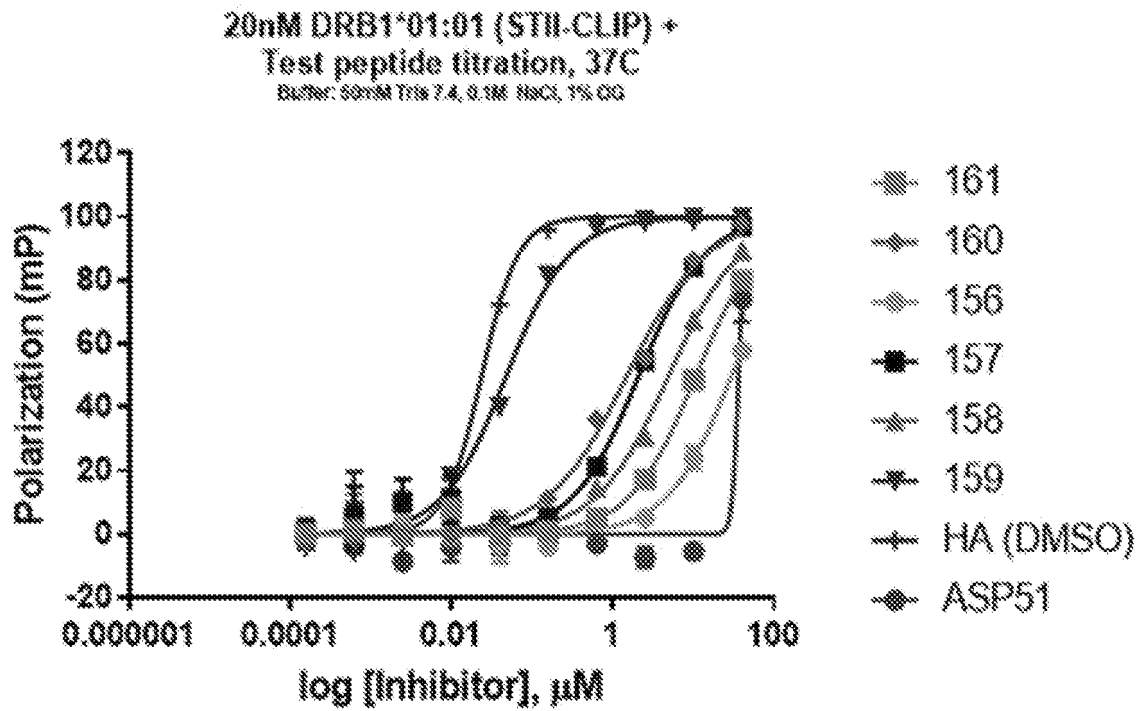
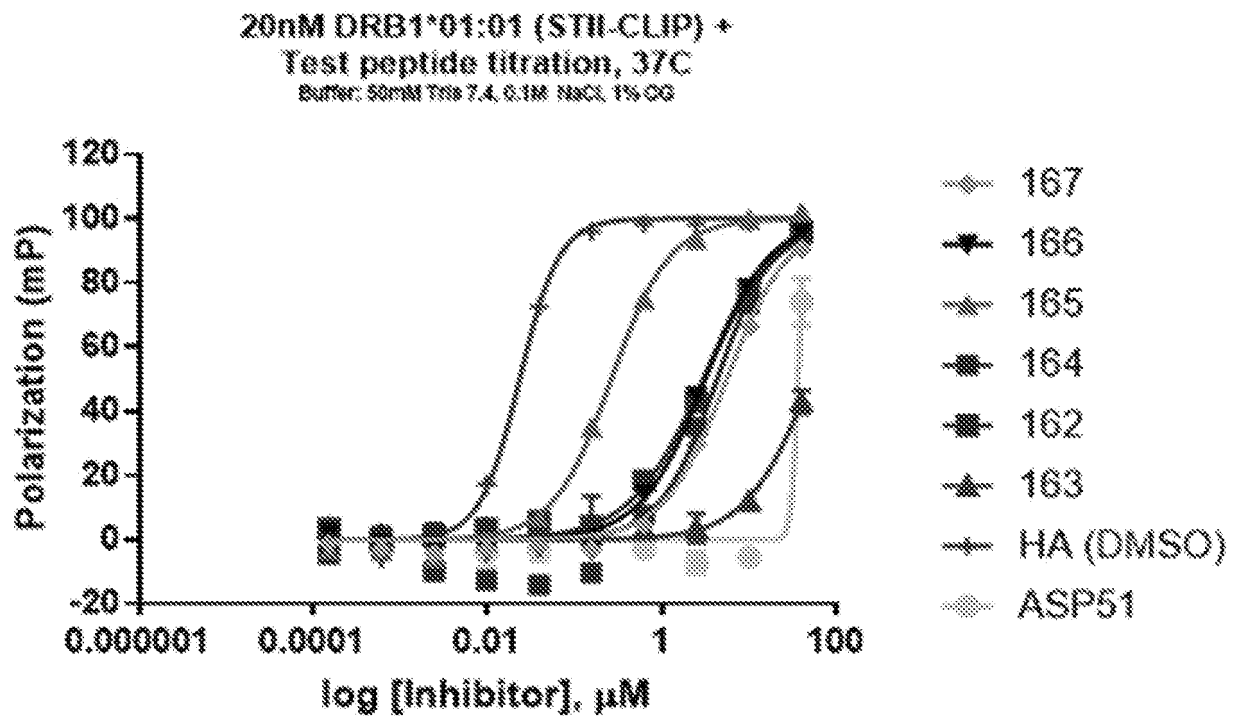


FIG. 26A

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*FIG. 26B**FIG. 26C*

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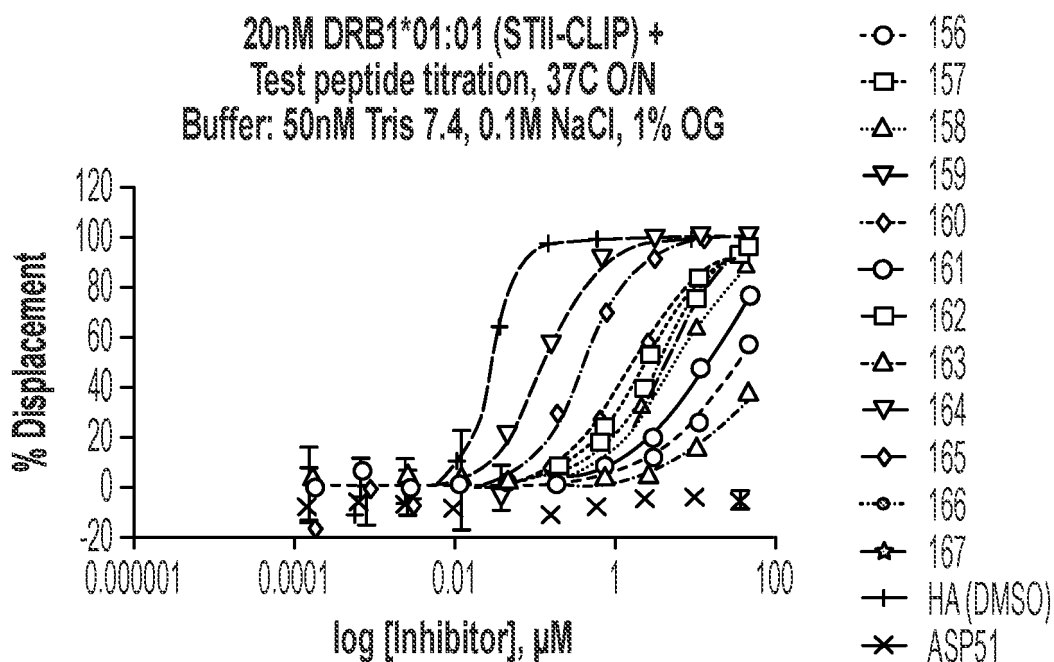


FIG. 26D

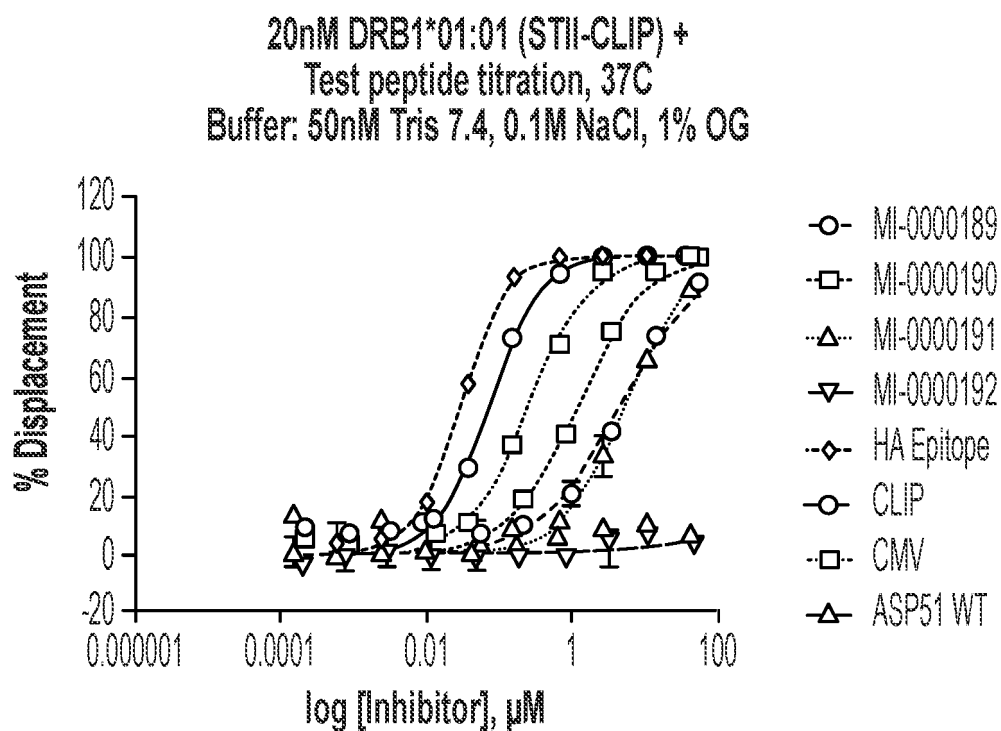


FIG. 26E

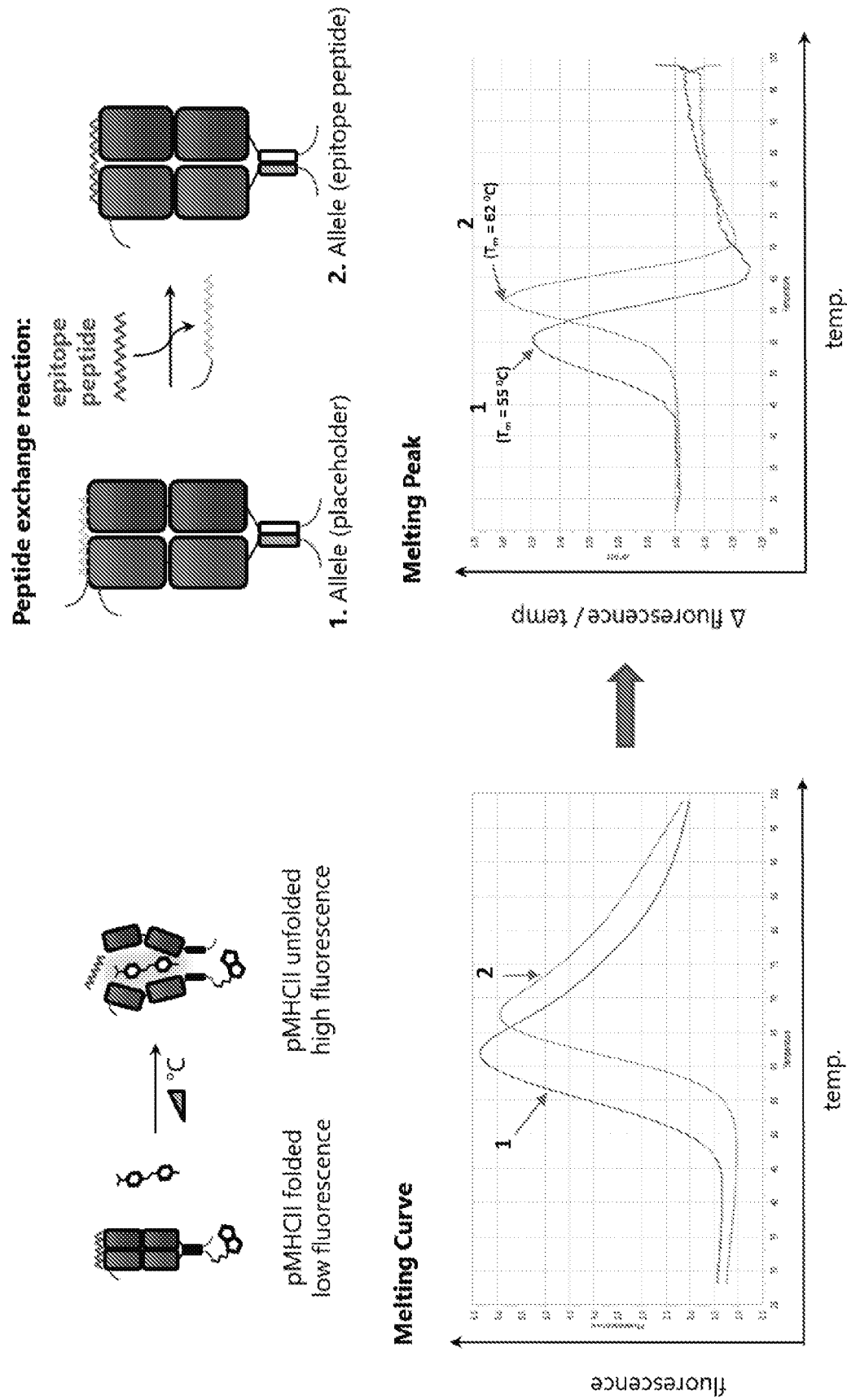


FIG. 26F

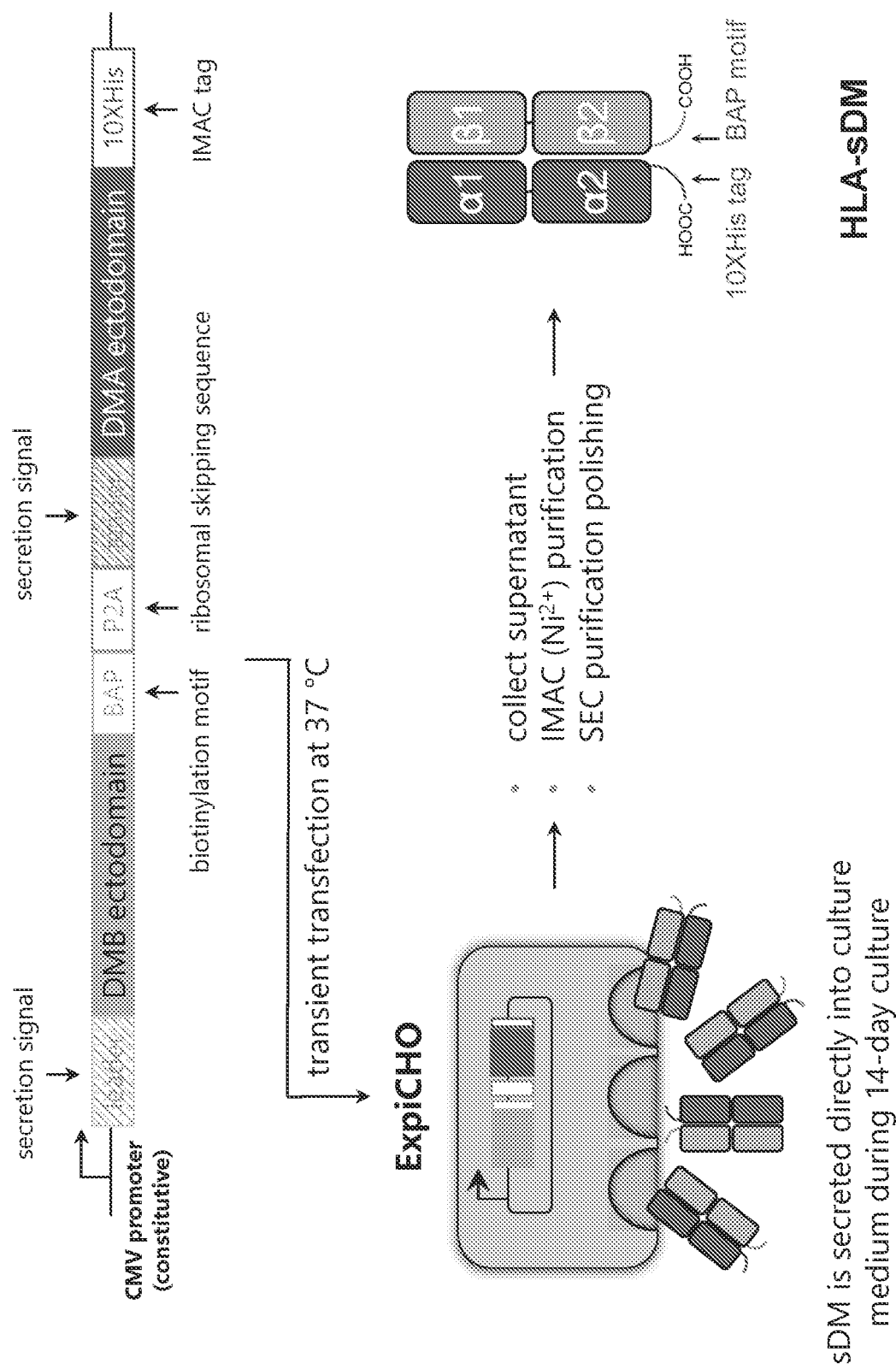


FIG. 26G

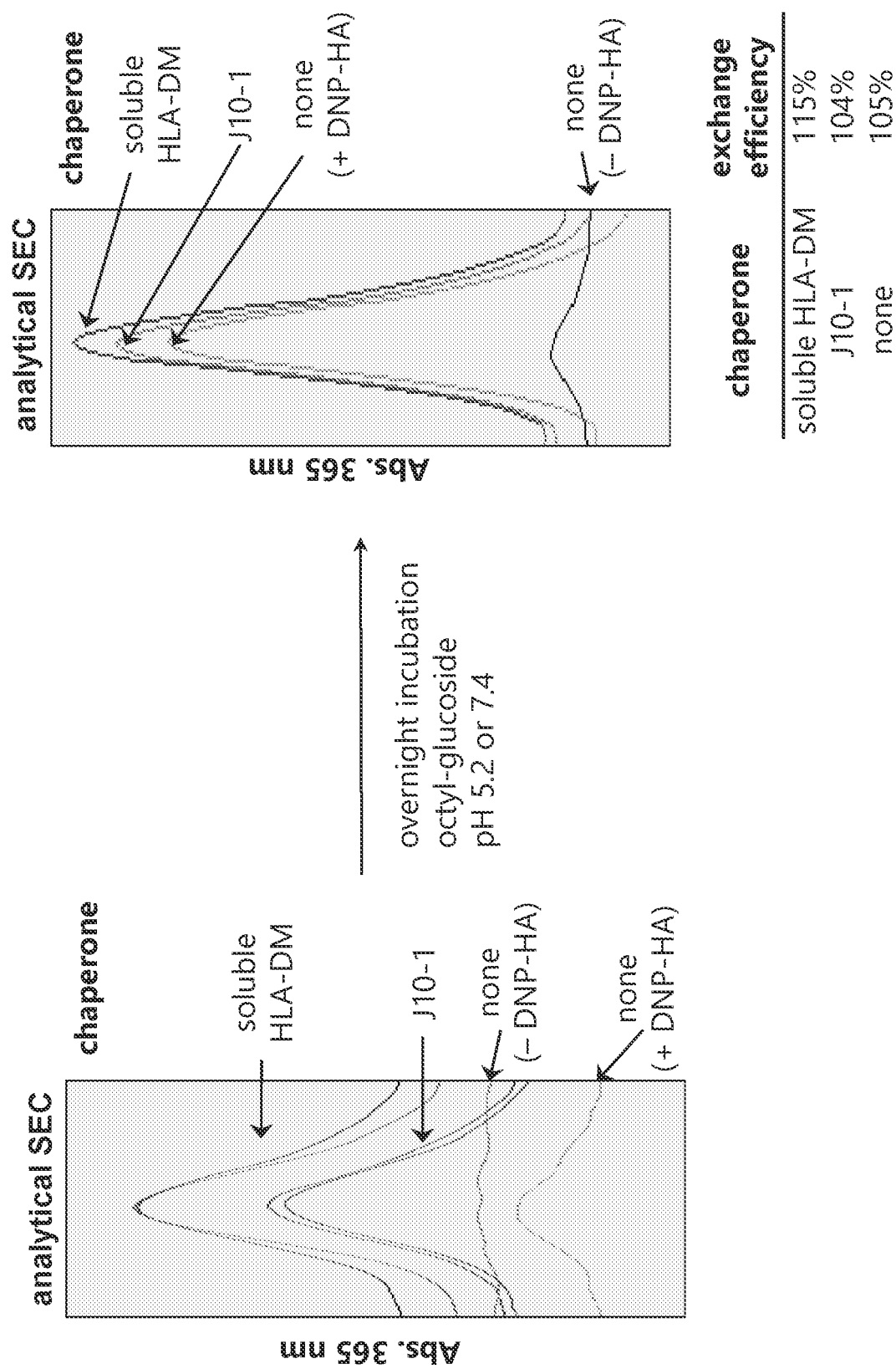
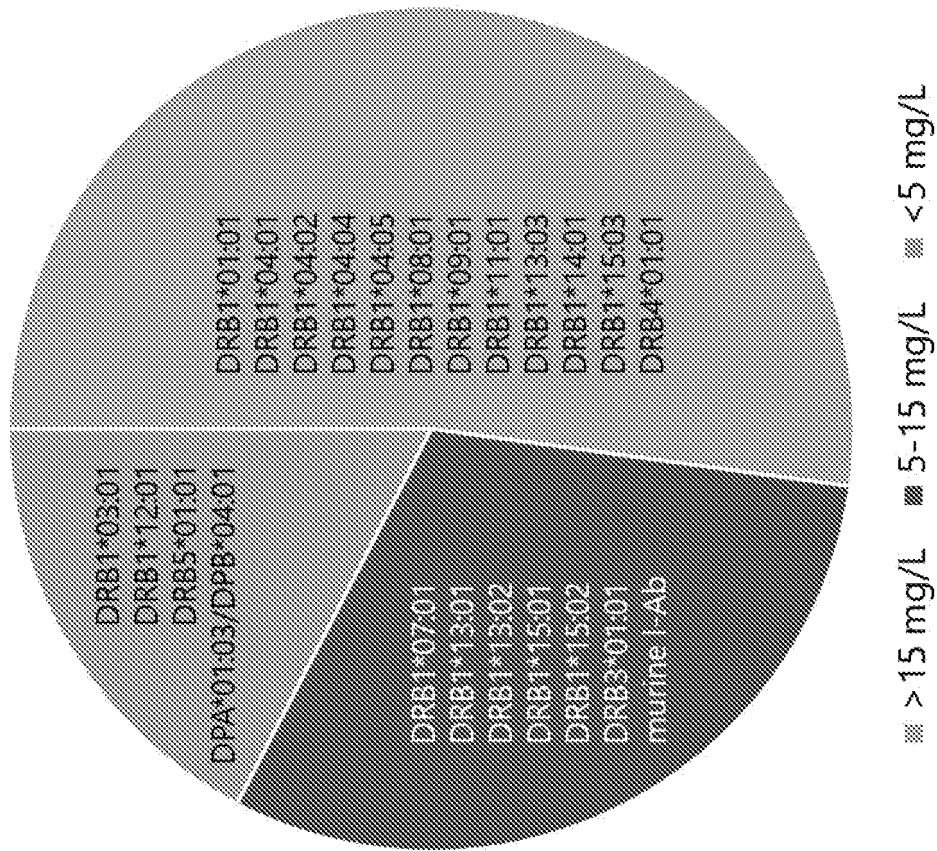


FIG. 26H

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**FIG. 27A**

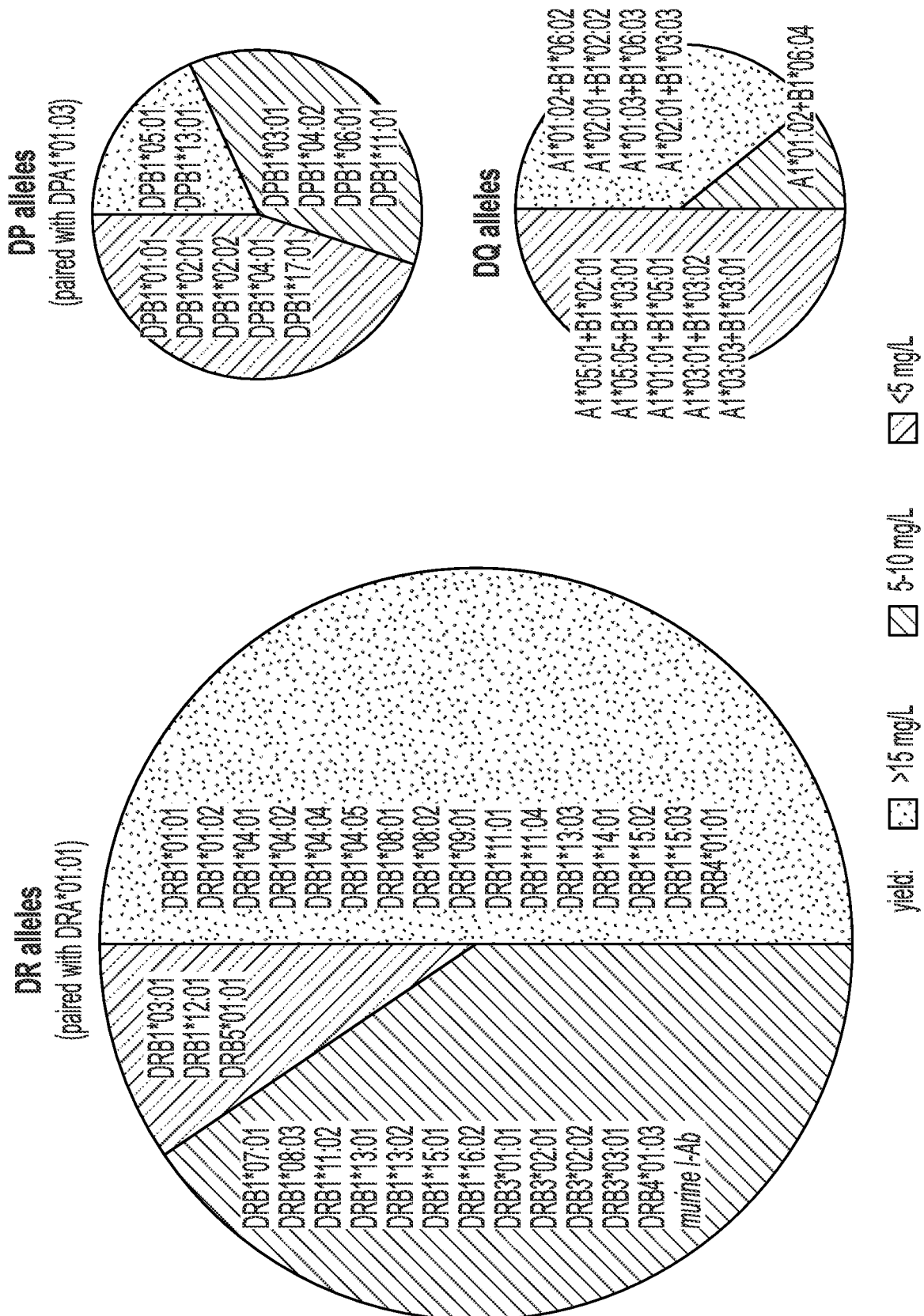


FIG. 27B

DRB1 alleles validated for peptide exchange

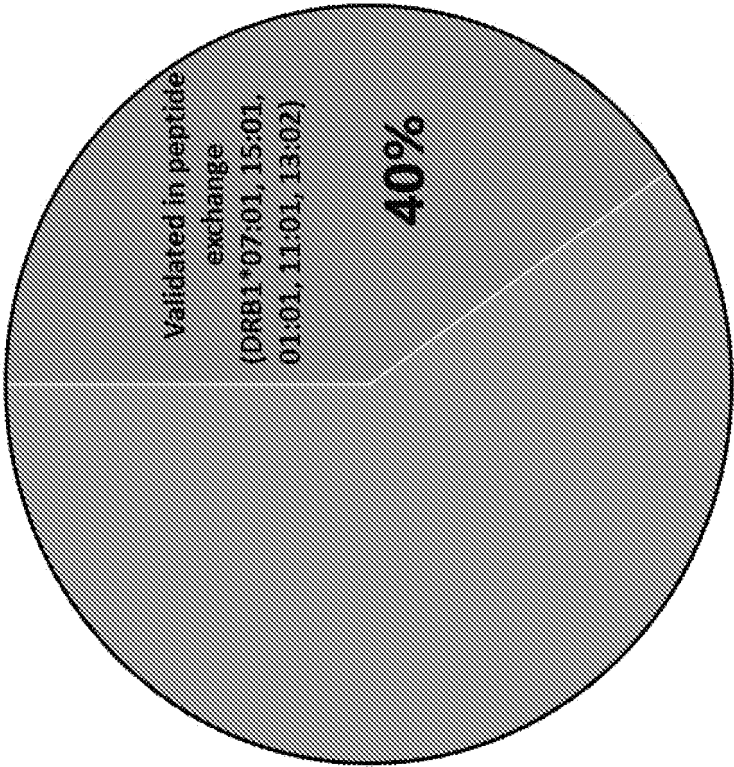


FIG. 27C

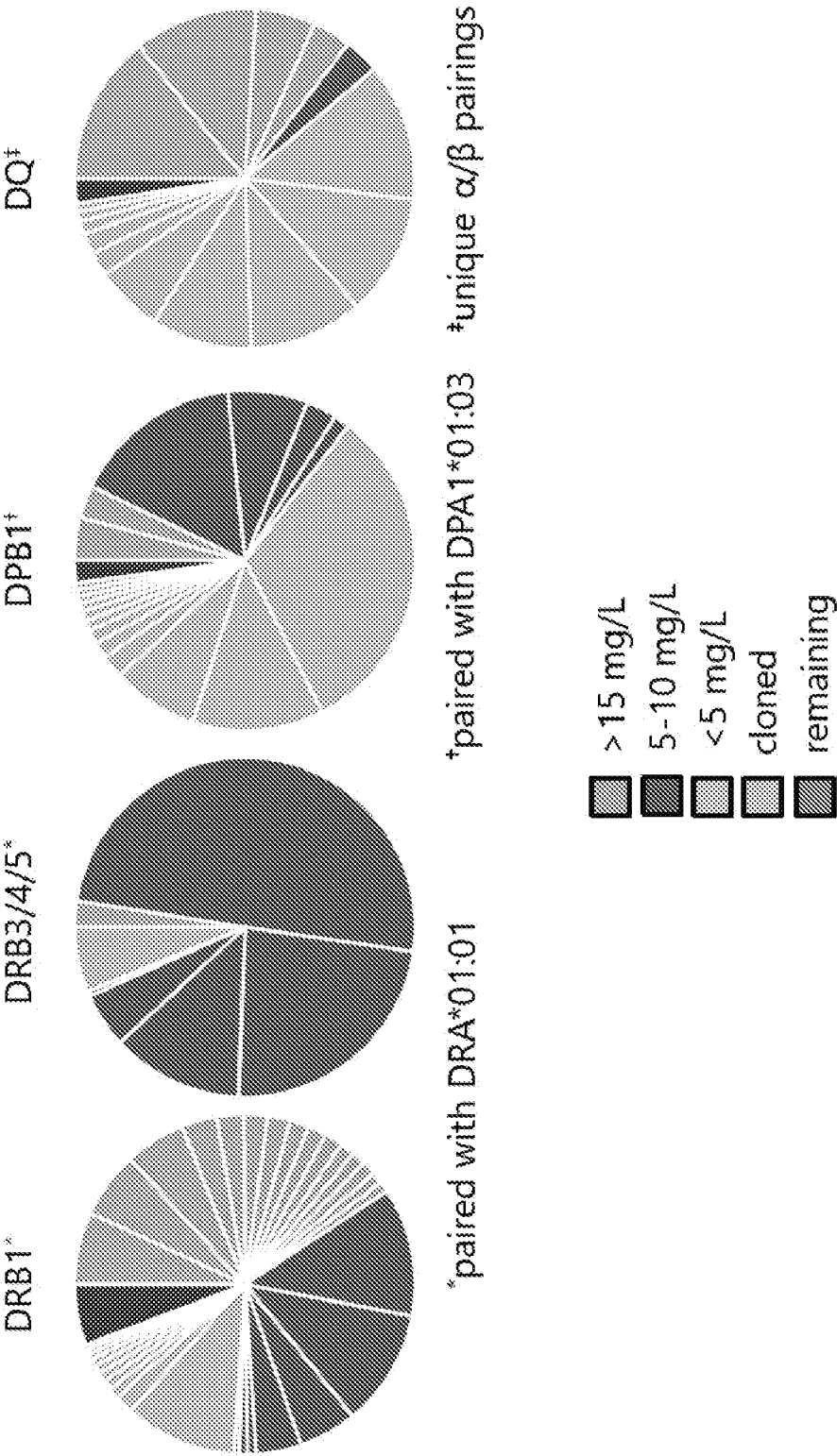


FIG. 27D

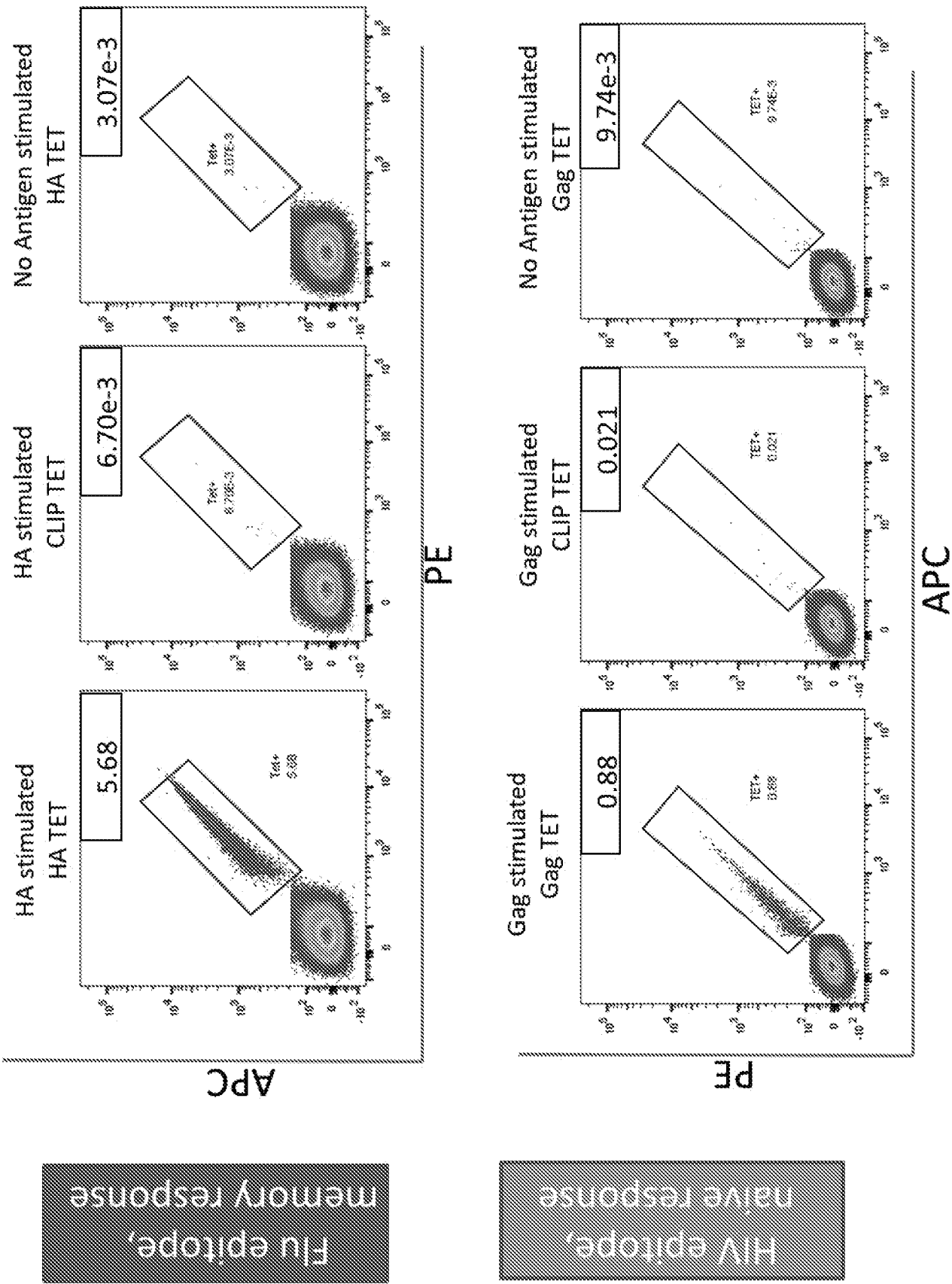


FIG. 27E

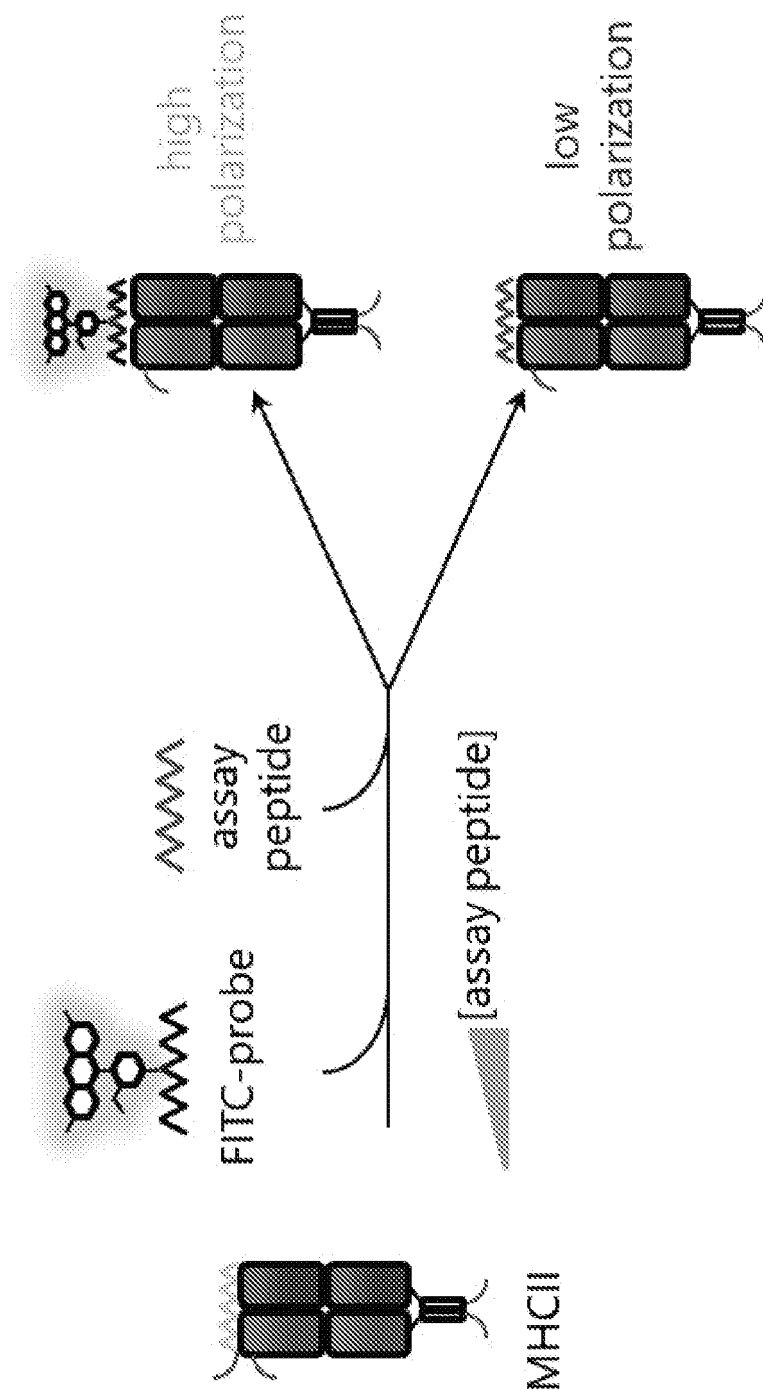


FIG. 28A

Variables	Conditions evaluated
pH	5.2 vs 7.4
Detergent	1% Octyl glucoside vs 1.6% NP40
Temperature	37C vs Room temp
Probe	FITC-CLIP0 vs FITC-HA (super binder)
Purification method	His tag vs Conformation specific antibody (L243)
Target format	Soluble vs Full length allele

Soluble MHC II allele

Full length MHC II allele

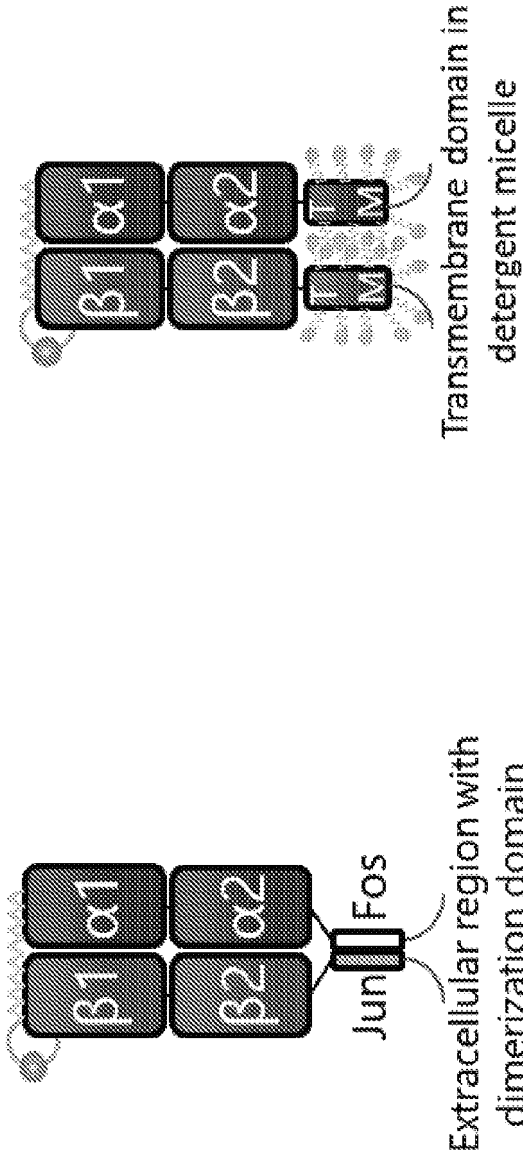


FIG. 28B

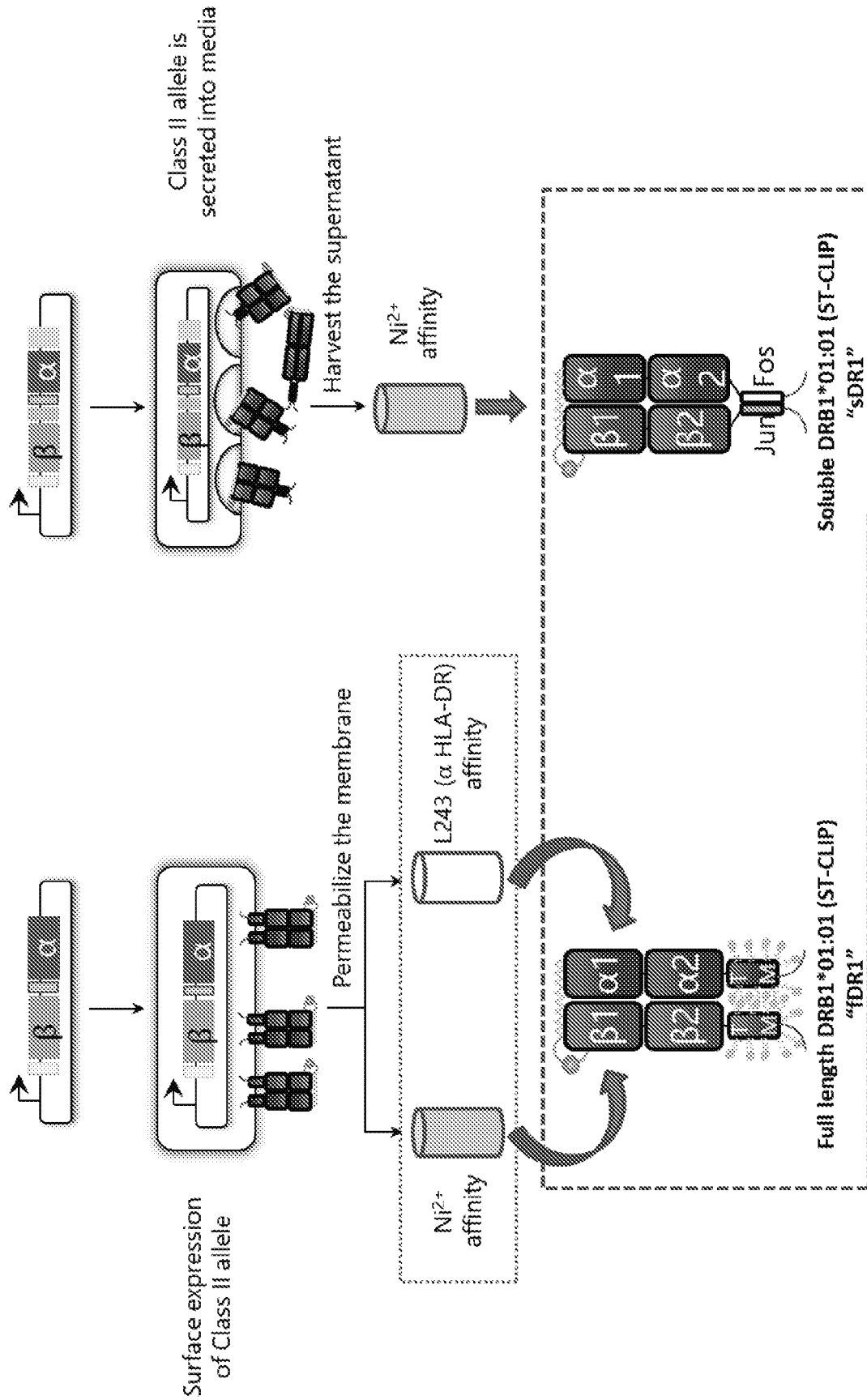
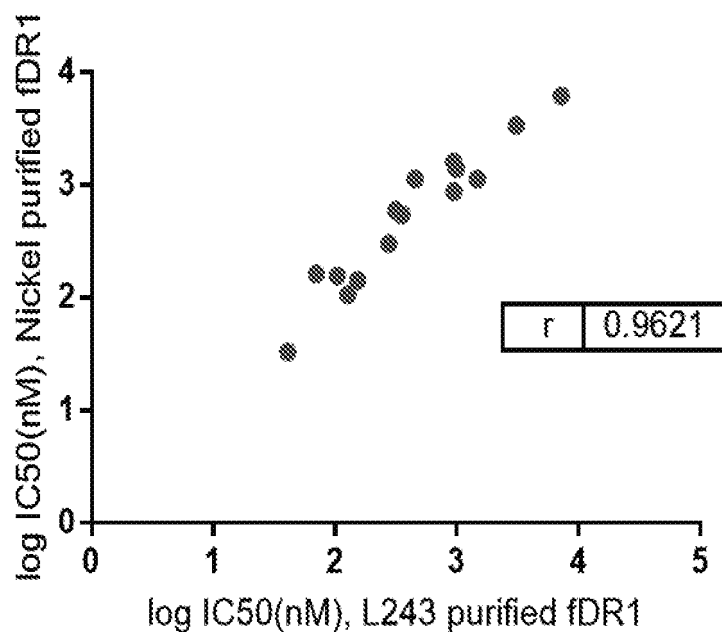


FIG. 28C

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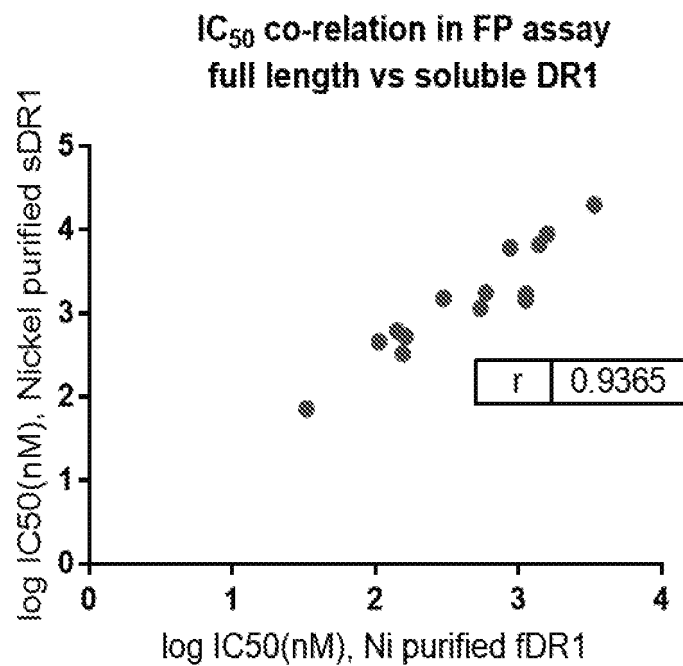
**IC₅₀ co-relation in FP assay
L243 vs. Nickel purified full length DR1**



Peptide	Average IC ₅₀ in nM (n=2)		IC ₅₀ fold change
	L243 purified fDR1	Ni purified fDR1	L243 fDR1 to Ni fDR1
Peptide 166	453	1128	2.5
Peptide 165	70	163	2.3
Peptide157	315	591	1.9
Peptide163	941	1585	1.7
Peptide158	357	542	1.5
Peptide159	104	156	1.5
Peptide190	992	1398	1.4
Peptide162	3073	3384	1.1
Peptide164	278	300	1.1
Peptide161	946	875	0.9
Peptide167	153	142	0.9
Peptide189	7173	6132	0.9
Peptide160	128	106	0.8
Peptide191	1470	1124	0.8
HA (Control)	41	33	0.8

FIG. 28D

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Peptide	Average IC ₅₀ in nM (n=2)		IC ₅₀ fold change
	Full length DR1 (fDR1)	Soluble DR1 (sDR1)	sDR1 to fDR1
Peptide 161	875	6076	6.9
Peptide 162	3384	20076	5.9
Peptide 163	1585	8915	5.6
Peptide 164	300	1517	5.1
Peptide 190	1398	6695	4.8
Peptide 160	106	457	4.3
Peptide 167	142	614	4.3
Peptide 165	163	529	3.2
Peptide 157	591	1773	3
HA (Control)	33	72	2.2
Peptide 158	542	1155	2.1
Peptide 159	156	331	2.1
Peptide 166	1128	1706	1.5
Peptide 191	1124	1444	1.3
Peptide 189	6132	>50,000	ND

FIG. 28E

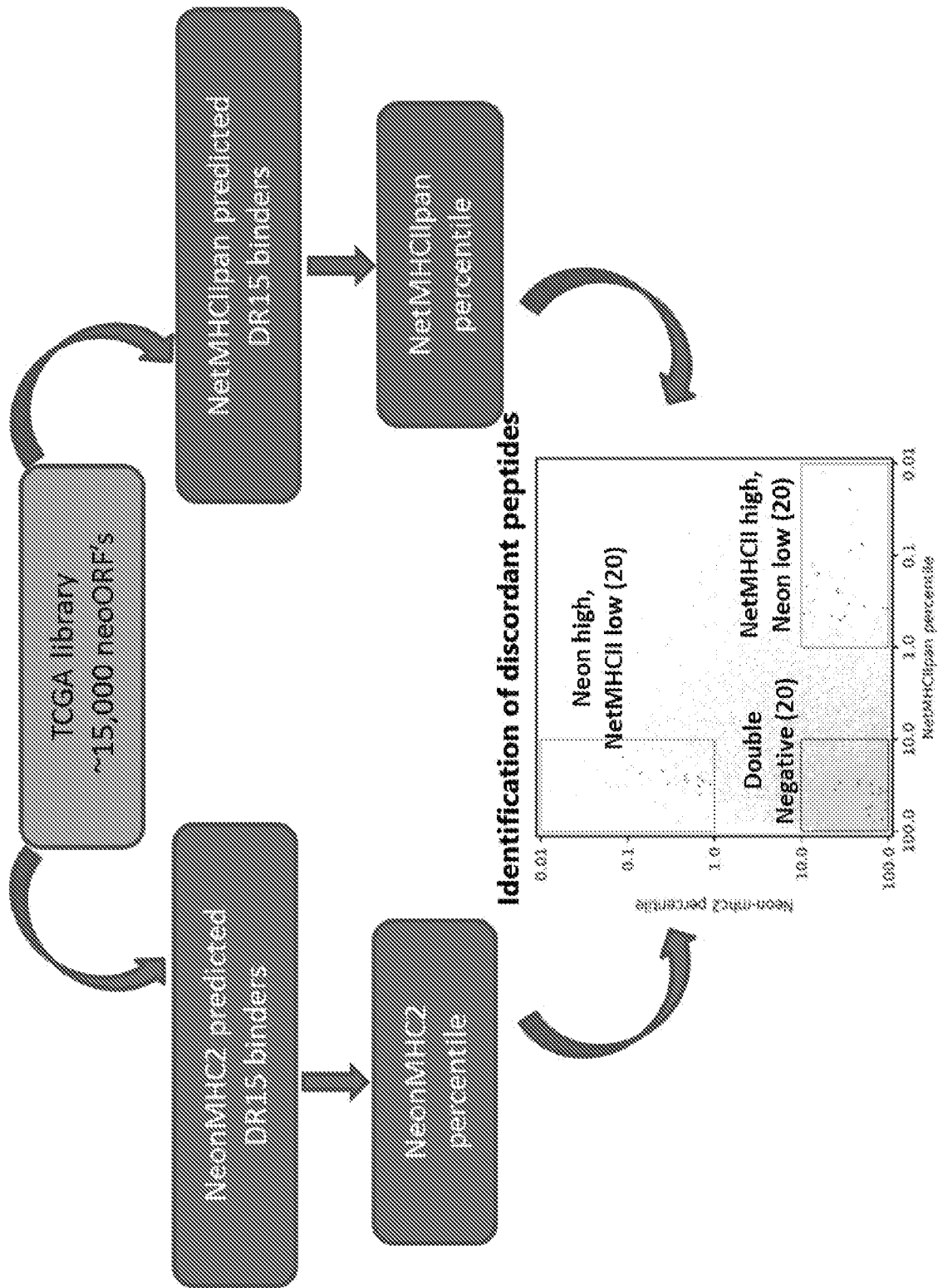


FIG. 28F

60nM Soluble DR15 +
10nM FITC-super binder +
assay peptide

5 hours at 37C in pH5.2
buffer

Read polarization & calculate
% probe displacement

% inhibition of probe binding				% inhibition of probe binding				% inhibition of probe binding						
External ID	Source	10uM	1uM	0.1uM	External ID	Source	10uM	1uM	0.1uM	External ID	Source	10uM	1uM	0.1uM
MI-0000236	nean_high	84%	58%	44%	MI-0000274	nmp_high	72%	28%	7%	MI-0000336	double_negative	47%	5%	0%
MI-0000230	nean_high	82%	79%	49%	MI-0000275	nmp_high	68%	62%	37%	MI-0000339	double_negative	12%	0%	1%
MI-0000242	nean_high	80%	82%	45%	MI-0000254	nmp_high	65%	39%	19%	MI-0000331	double_negative	11%	0%	0%
MI-0000371	nean_high	74%	58%	46%	MI-0000261	nmp_high	55%	13%	1%	MI-0000326	double_negative	11%	0%	0%
MI-0000229	nean_high	70%	54%	29%	MI-0000271	nmp_high	54%	9%	2%	MI-0000337	double_negative	10%	0%	0%
MI-0000240	nean_high	69%	68%	36%	MI-0000256	nmp_high	53%	17%	0%	MI-0000333	double_negative	7%	0%	3%
MI-0000372	nean_high	68%	49%	30%	MI-0000255	nmp_high	52%	52%	17%	MI-0000332	double_negative	5%	0%	0%
MI-0000243	nean_high	67%	58%	40%	MI-0000396	nmp_high	42%	28%	4%	MI-0000327	double_negative	4%	0%	0%
MI-0000231	nean_high	66%	50%	21%	MI-0000260	nmp_high	33%	0%	0%	MI-0000328	double_negative	2%	0%	0%
MI-0000251	nean_high	63%	50%	19%	MI-0000395	nmp_high	22%	17%	0%	MI-0000329	double_negative	1%	0%	0%
MI-0000252	nean_high	62%	31%	7%	MI-0000269	nmp_high	22%	0%	0%	MI-0000334	double_negative	1%	0%	0%
MI-0000248	nean_high	61%	6%	1%	MI-0000398	nmp_high	0%	0%	0%	MI-0000340	double_negative	0%	0%	0%
MI-0000232	nean_high	61%	43%	28%	MI-0000270	nmp_high	0%	0%	0%	MI-0000338	double_negative	0%	0%	5%
MI-0000250	nean_high	60%	24%	2%	MI-0000272	nmp_high	0%	0%	0%	MI-0000341	double_negative	0%	0%	0%
MI-0000247	nean_high	58%	50%	42%	MI-0000374	nmp_high	0%	5%	0%	MI-0000342	double_negative	0%	0%	0%
MI-0000238	nean_high	53%	43%	19%	MI-0000259	nmp_high	0%	0%	0%	MI-0000343	double_negative	0%	0%	2%
MI-0000246	nean_high	51%	47%	25%	MI-0000277	nmp_high	0%	0%	0%	MI-0000335	double_negative	0%	0%	10%
MI-0000241	nean_high	50%	42%	26%	MI-0000257	nmp_high	0%	0%	1%	MI-0000324	double_negative	0%	0%	0%
MI-0000244	nean_high	44%	47%	20%	MI-0000265	nmp_high	0%	0%	1%	MI-0000325	double_negative	0%	0%	4%
MI-0000237	nean_high	41%	4%	7%	MI-0000378	nmp_high	0%	24%	23%	MI-0000330	double_negative	0%	0%	0%

nmp- NetM-HCipan

FIG. 28G

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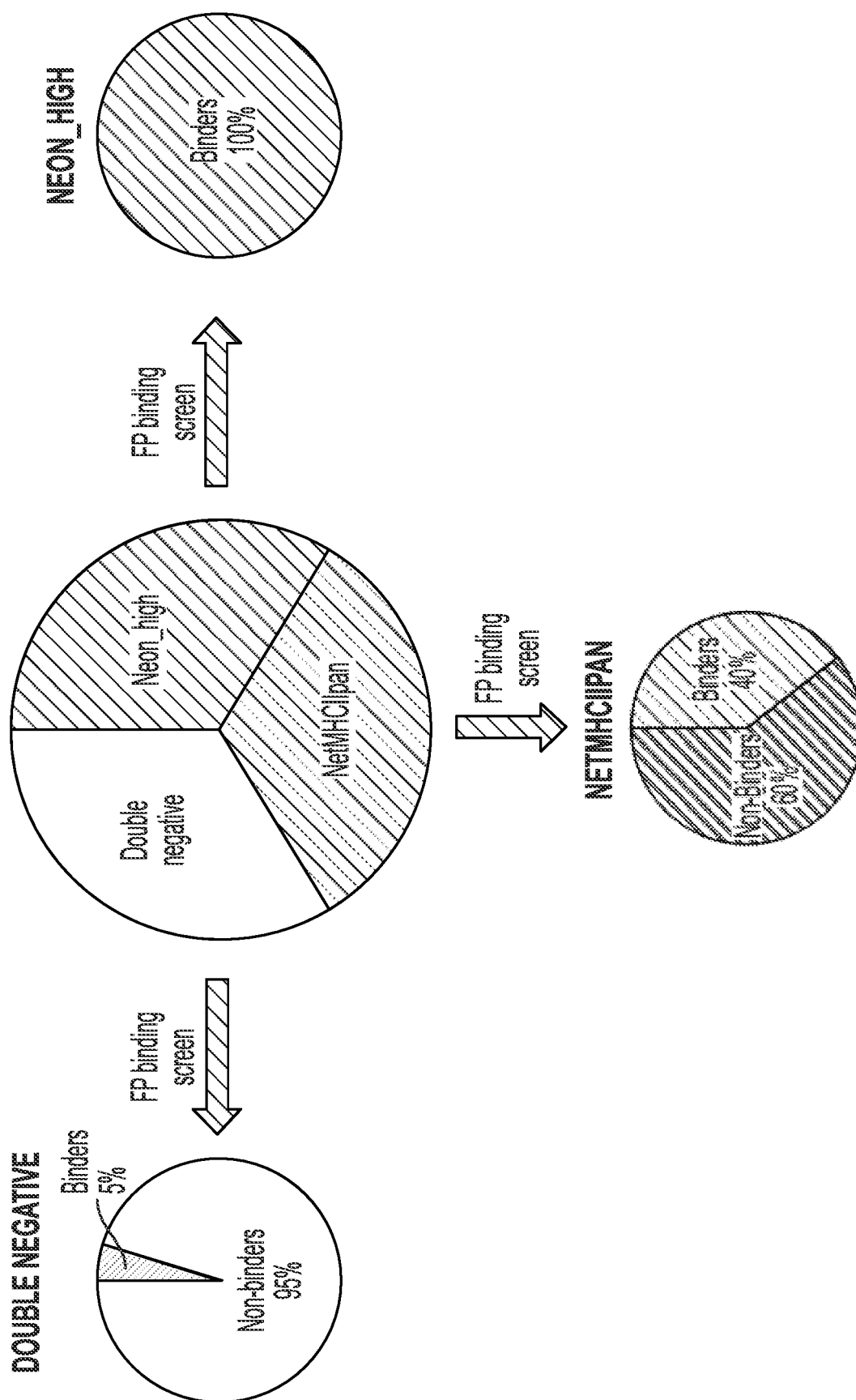


FIG. 28H



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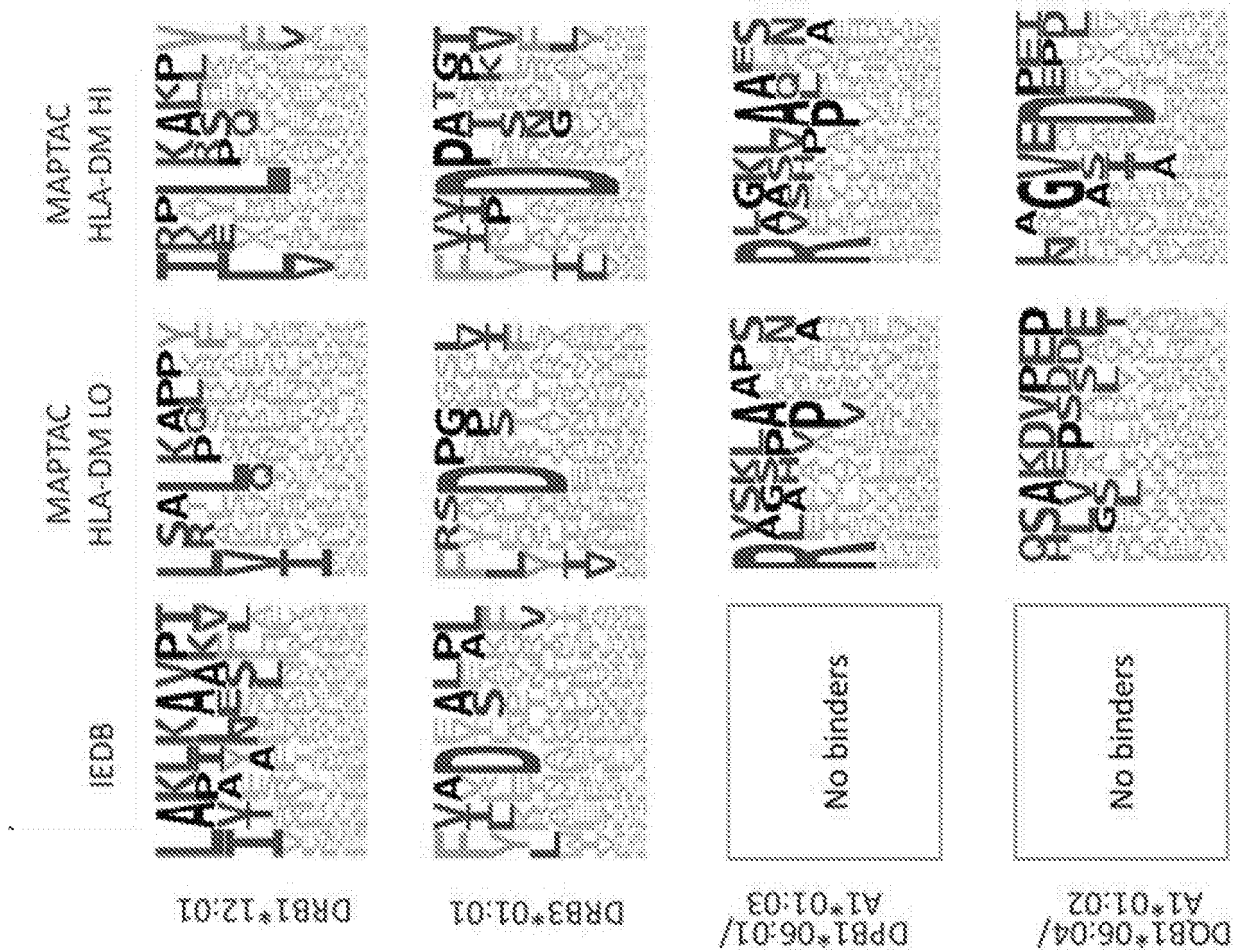


FIG. 30A

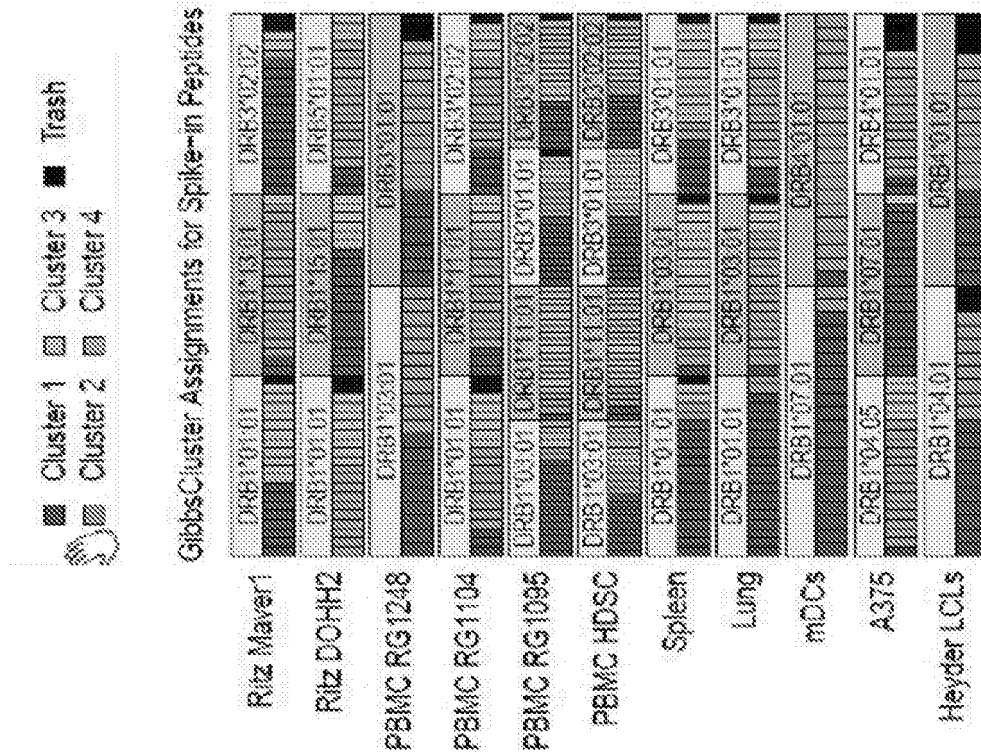
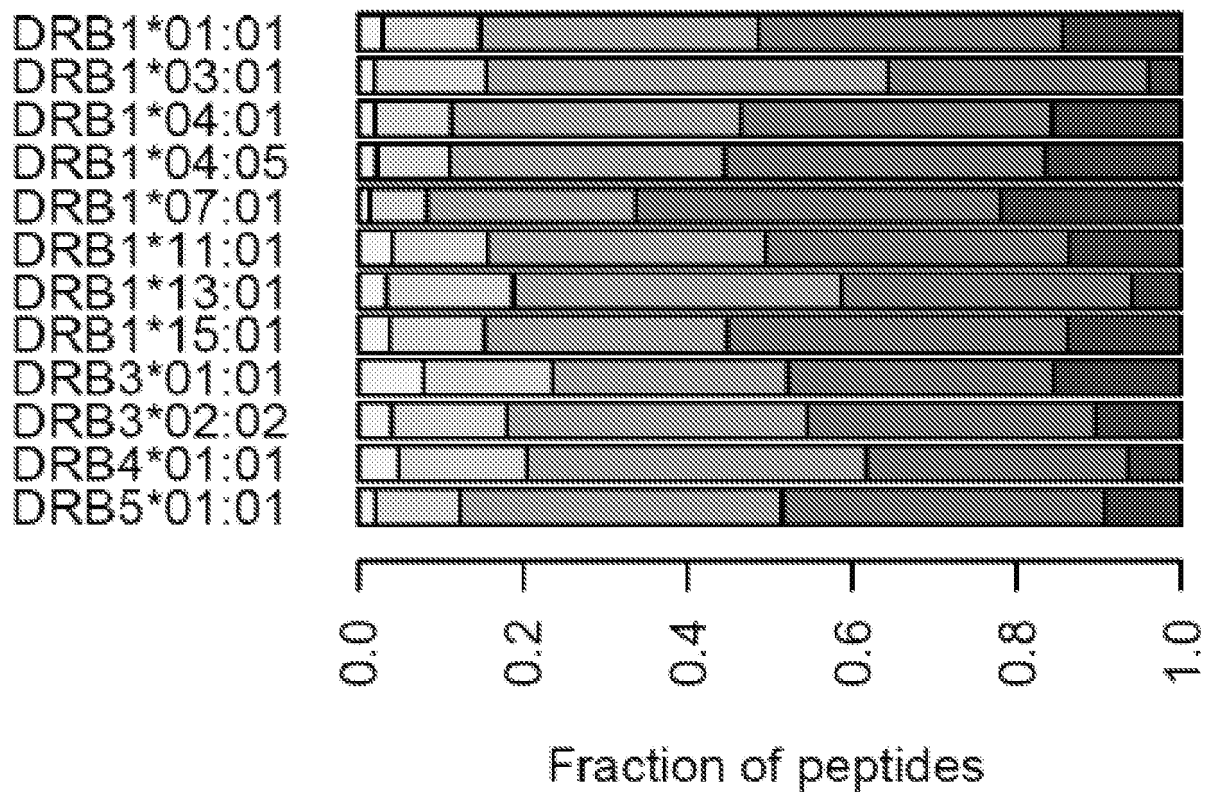
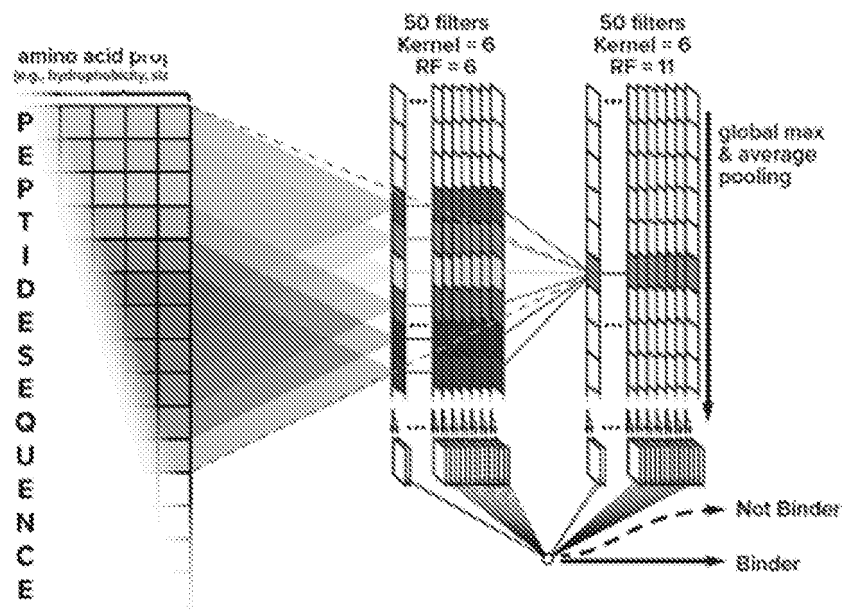


FIG. 30B

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*FIG. 30C*

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*FIG. 31A*

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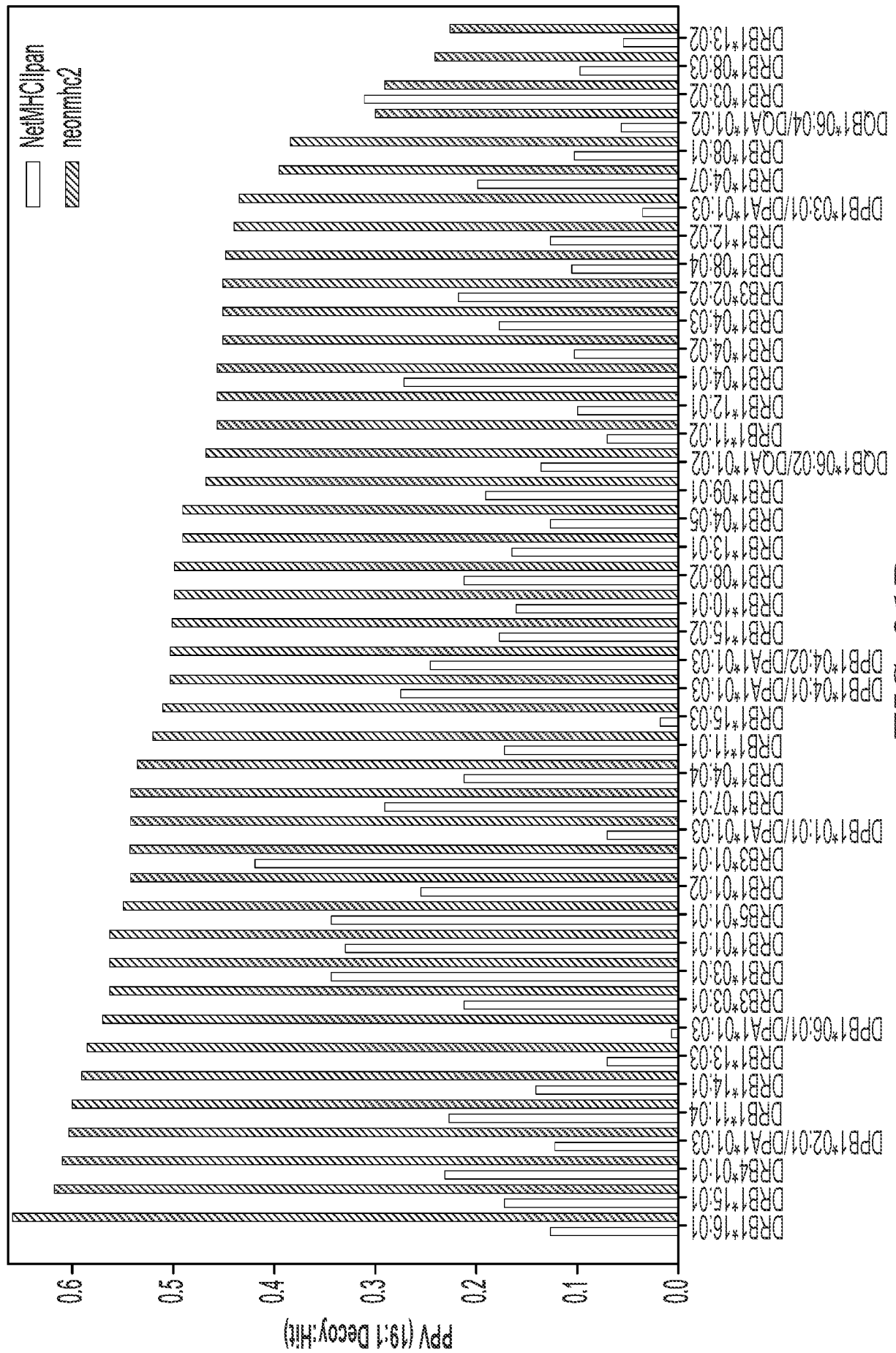
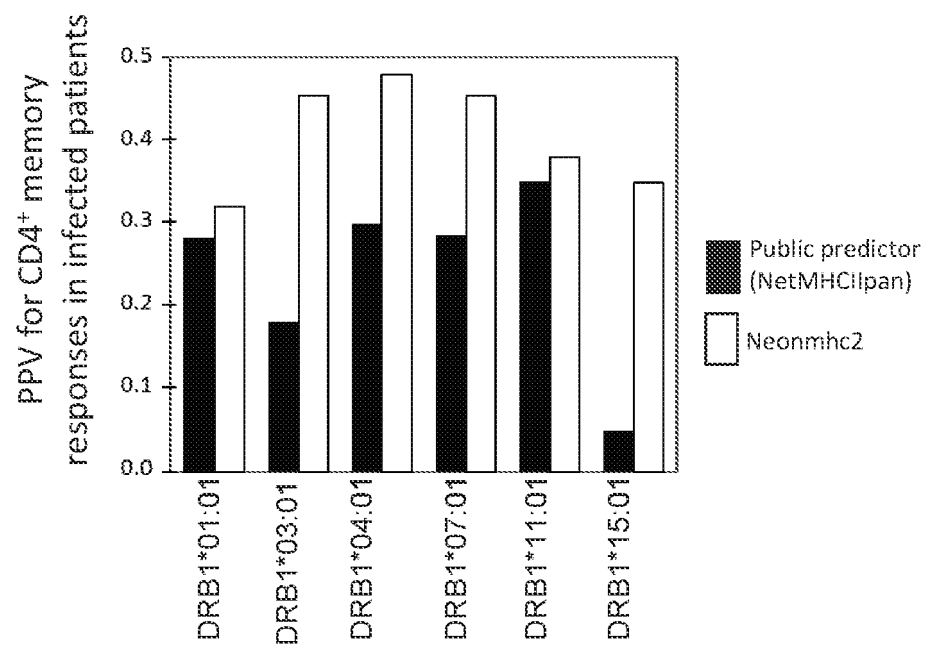


FIG. 31B

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*FIG. 31C*

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Neoantigen peptide	NetMHCipan affinity (nM)	NetMHCipan %Rank	neomhc2 %Rank	Status
GEGLFQPAHRYPDAG	744	39.00%	0.43%	hit
RNQWKCLGKPVGAEM	426	29.00%	0.10%	assayed
VPAWTRAWRNSSPKG	395	27.00%	0.51%	hit
DGGSYFSLWKIWTQV	354	26.00%	0.11%	hit
LHPELLPLWRLLPDG	367	26.00%	0.23%	hit
PEASLYGALSKGSGG	353	26.00%	0.24%	hit
HEGGFPPLRRAAED	325	24.00%	0.63%	hit
LSPVWCLQWKLSGTD	293	23.00%	0.31%	hit
KNTIVYTTKQVQSCQ	259	21.00%	0.57%	assayed
PATYILLKEFCLVG	246	20.00%	0.32%	assayed
NNEQFQWKIRHVGPE	222	19.00%	0.50%	hit
YKGGYELVKKSQTEL	200	17.00%	0.37%	assayed

FIG. 31D

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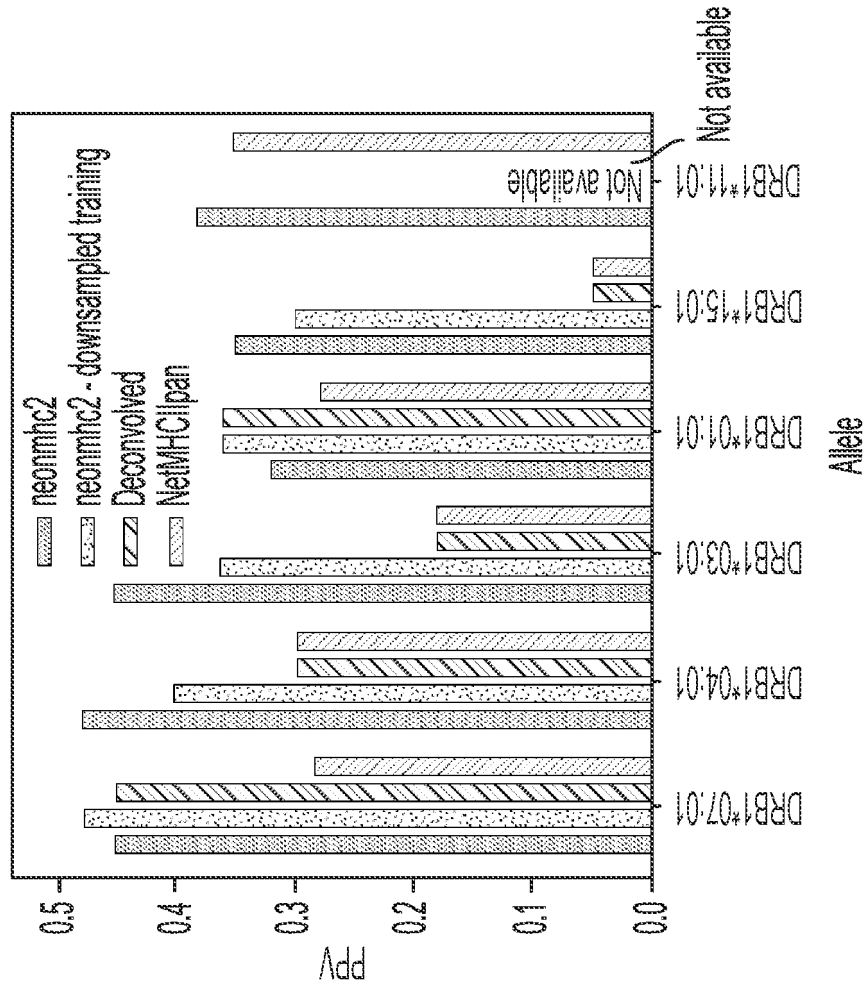


FIG. 31F

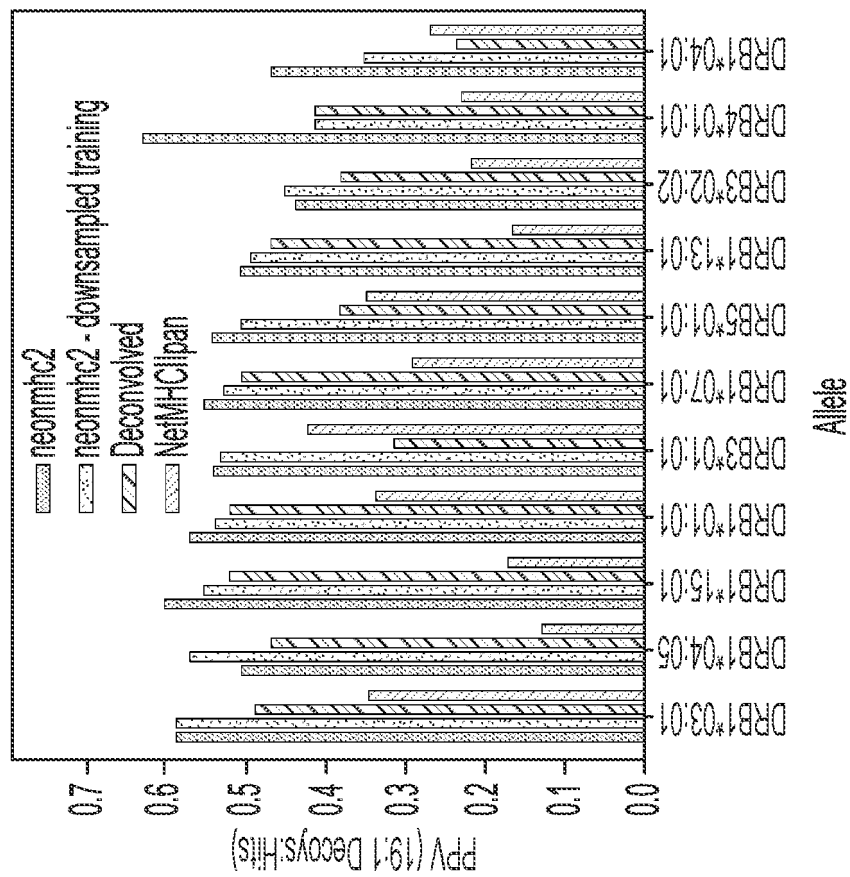


FIG. 31E

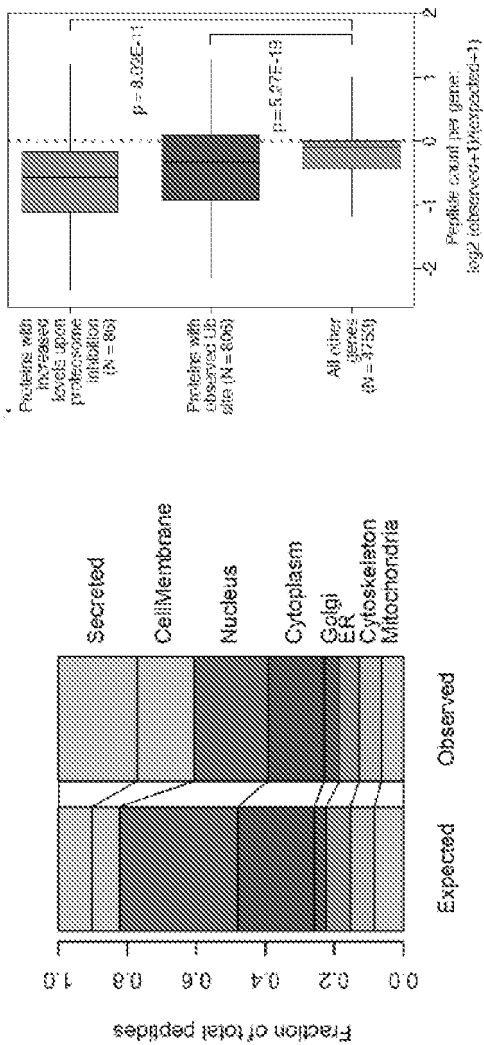


FIG. 32B

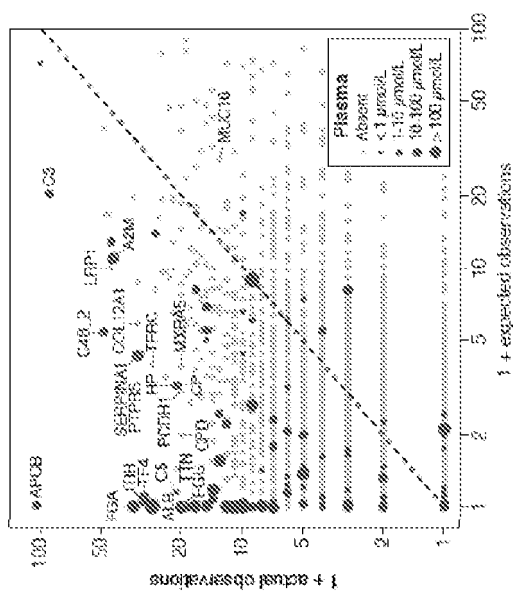


FIG. 32A

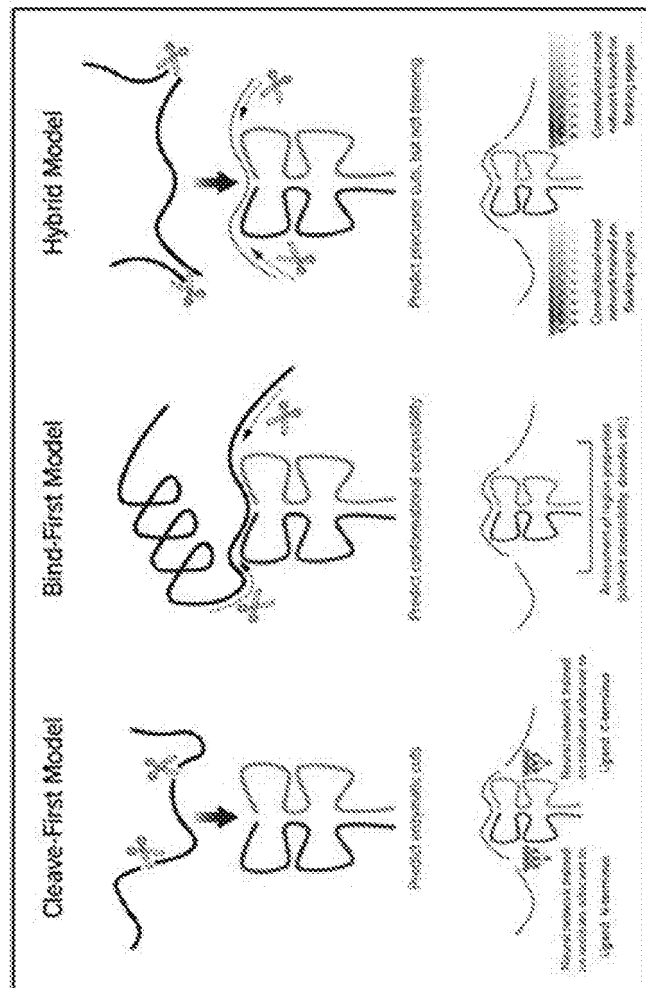


FIG. 32D

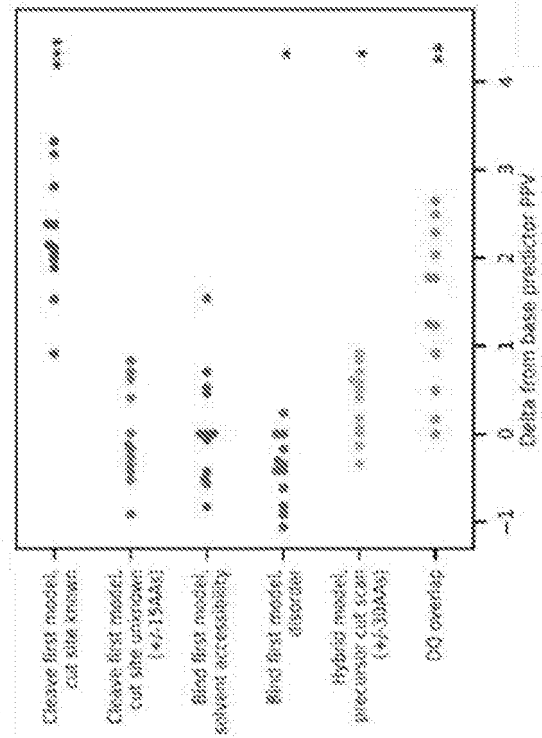


FIG. 32E

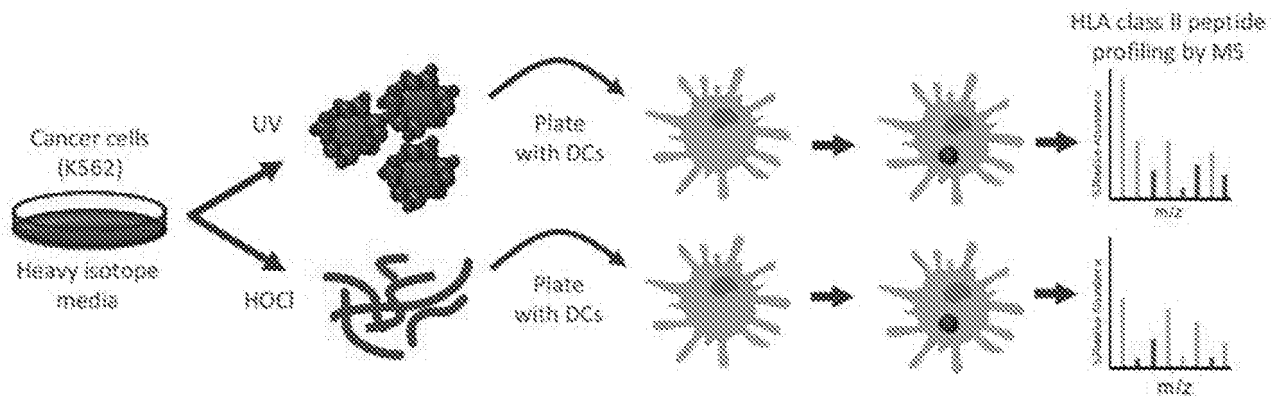


FIG. 33A

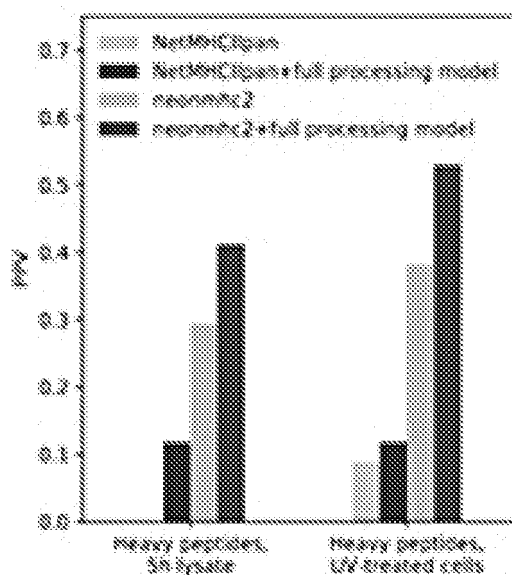


FIG. 33B

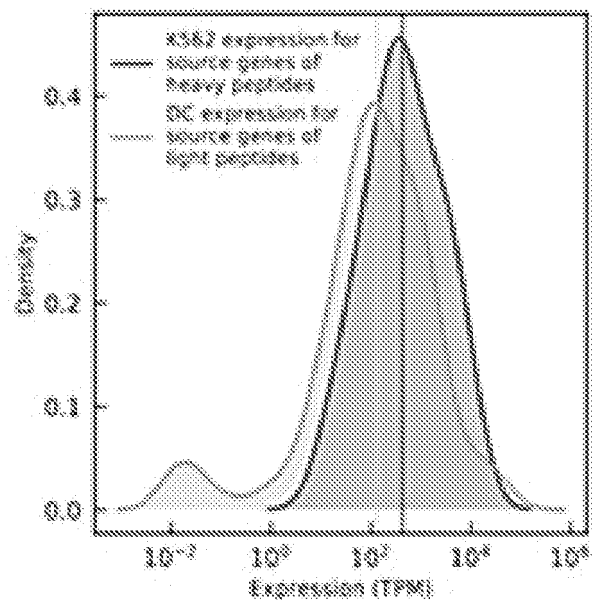


FIG. 33C

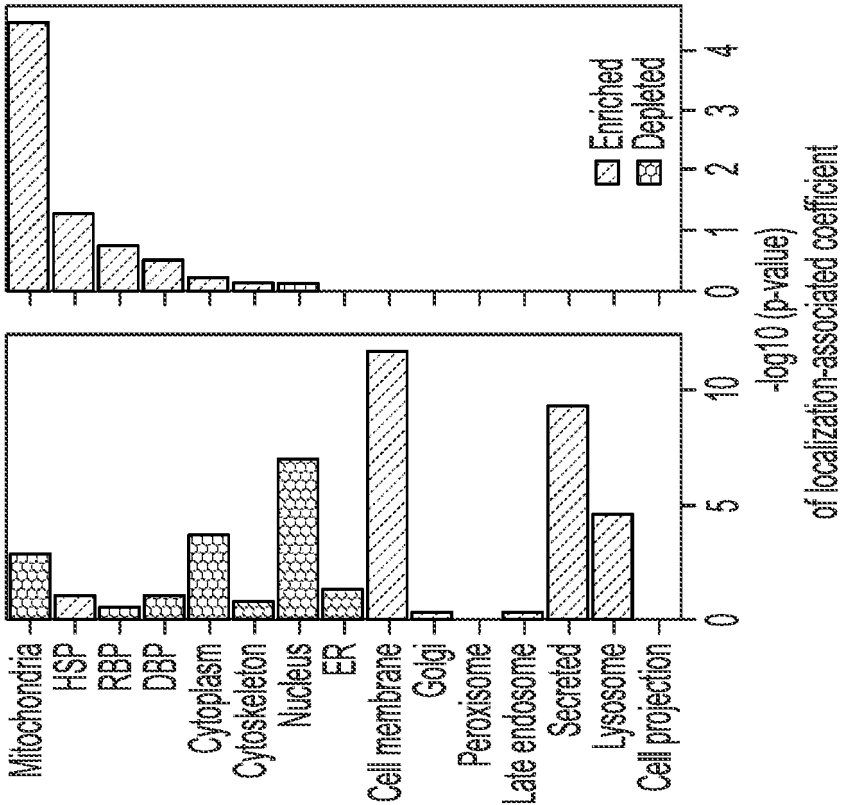


FIG. 33E

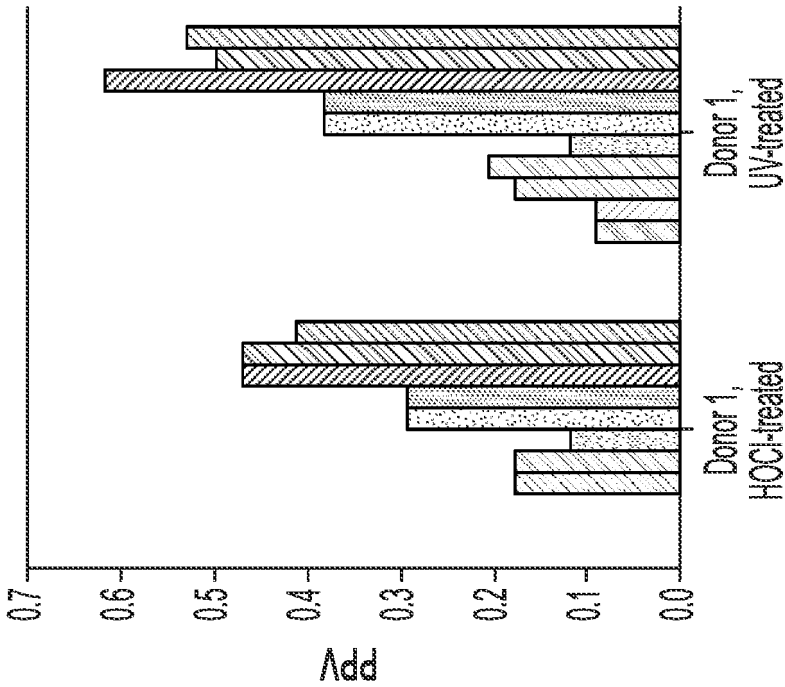
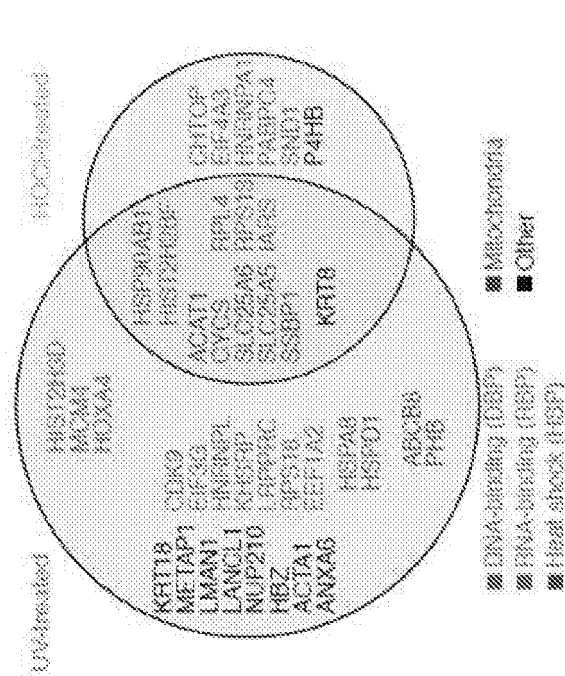
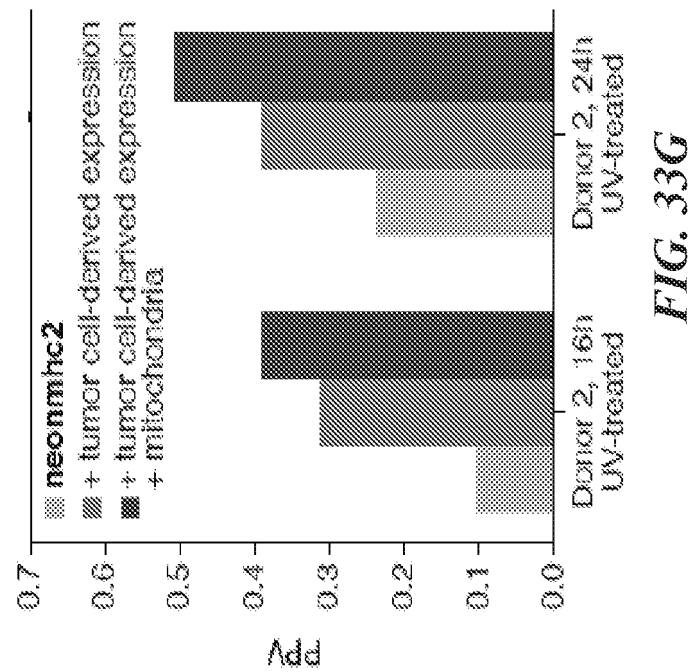


FIG. 33D



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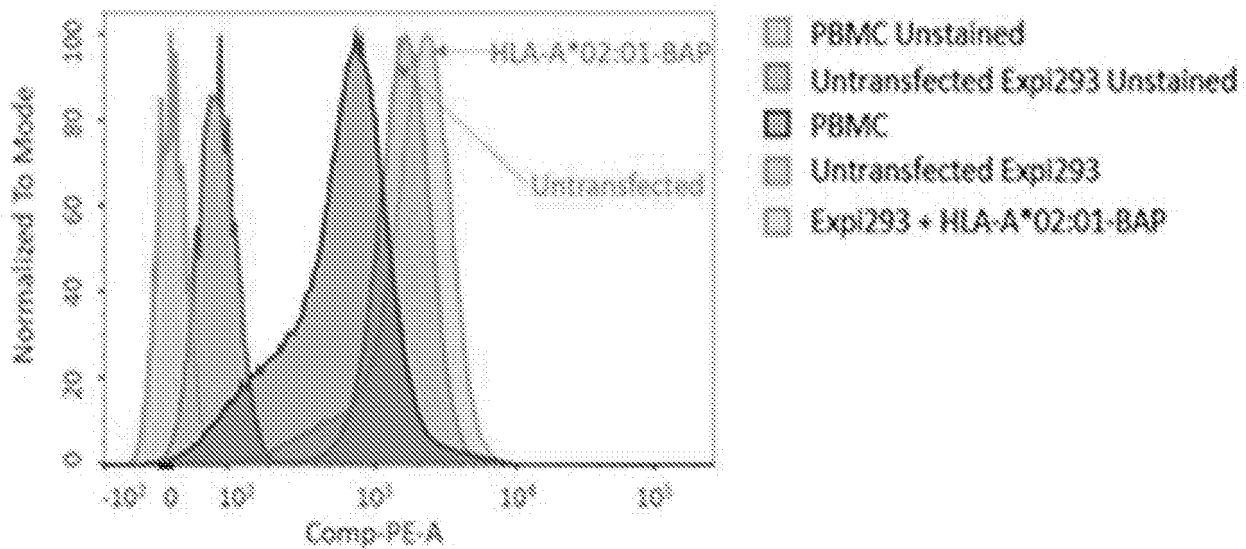
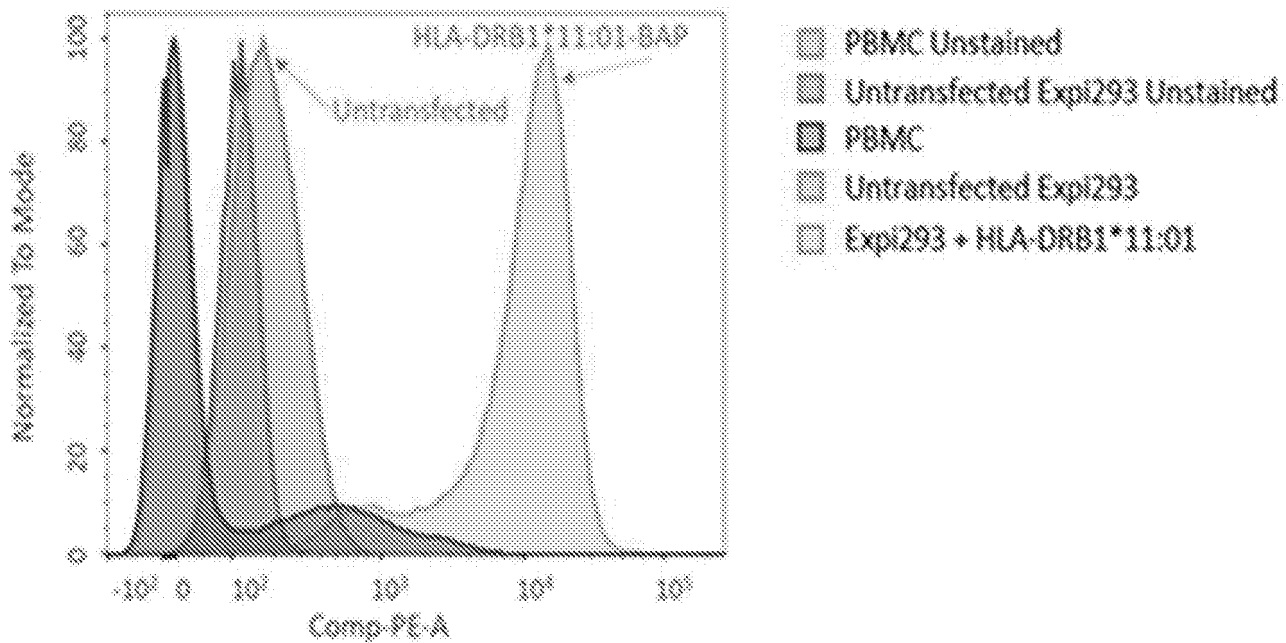
**FIG. 34A****FIG. 34B**



FIG. 35

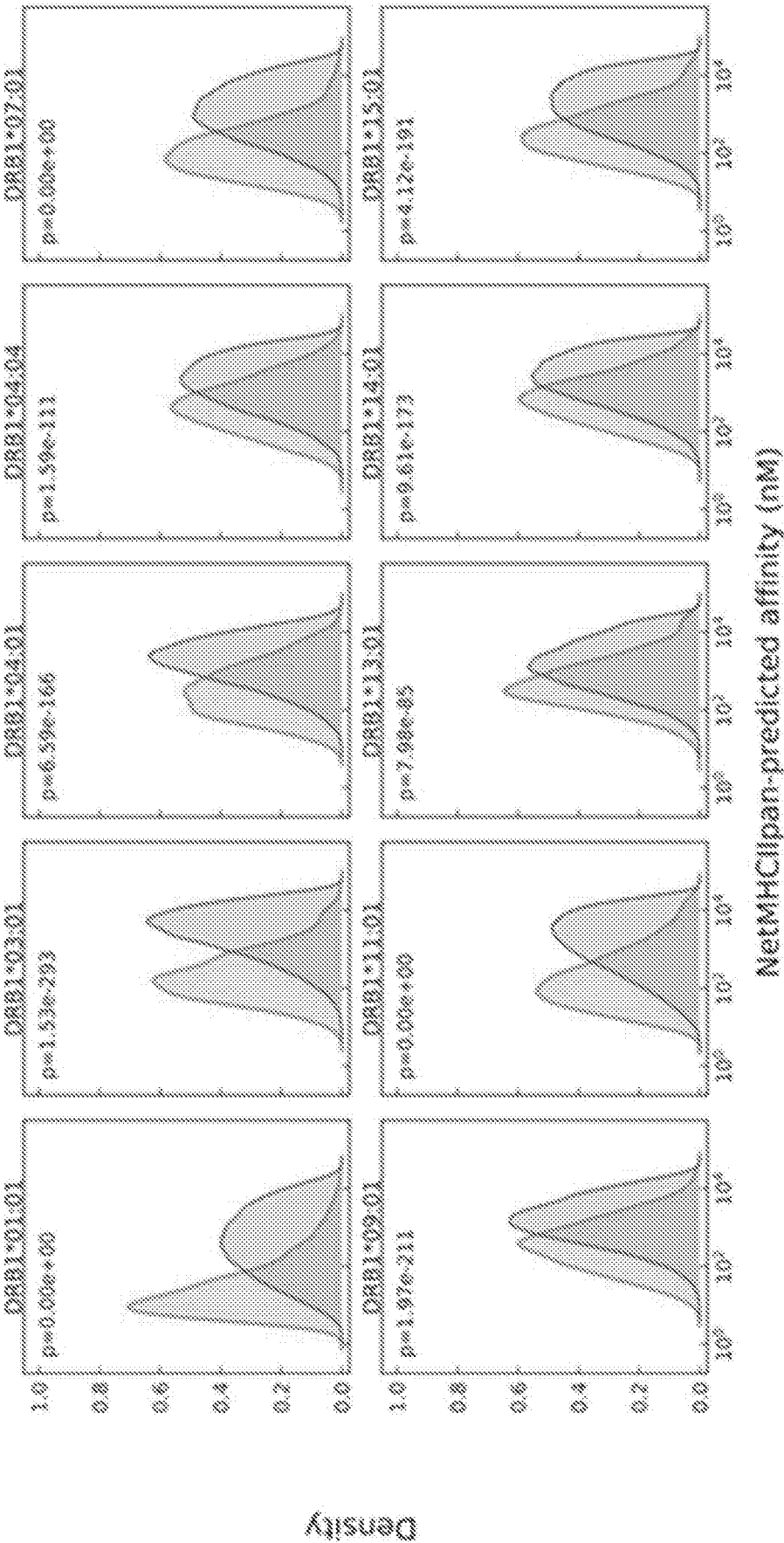


FIG. 36A

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HLA-DRB1*01:01					HLA-DRB1*09:01					HLA-DRB1*11:01				
Peptide and NetMHCpan-imputed binding core	NetMHCpan affinity	NetMHCpan percent rank	Measured affinity		Peptide and NetMHCpan-imputed binding core	NetMHCpan affinity	NetMHCpan percent rank	Measured affinity		Peptide and NetMHCpan-imputed binding core	NetMHCpan affinity	NetMHCpan percent rank	Measured affinity	
DRYEDGKVIER	218	31	54		NNLOPESGNTIGN	996	34	5		EGEYQGIPEESGG	1103	43	153	
GGMTLSGEEISYTG	239	48	17		ERFYTNMGQGVIN	1132	43	39		EPEDTEVERELIVGVE	1704	65	59	
KTFEQLTTEESKER	193	34	12		VGGTWPSGGDPYA	3415	80	40		IAGEWQVHEEGAIT	561	34	35	
APRYEALRGCEPPD	179	33	22		KEALEPSENVVQ	4856	85	23		EPAEFLIDGHDAGYG	1654	60	195	
DKRMILLGEGKEILVG	354	60	27		SGRRILGSDVDLER	886	41	12		GLELEVLIEHKPAAG	587	35	63	
KEAAVHFPEVAPQVR	352	48	17		IDRALMEACESVIO	2919	75	262		EMNLVEAMERFGSRNG	853	45	79	
DARFENDSQYEVHHQ	332	55	74		NENNLESGAGLIDDLR	758	43	64		GFNMNNINQGGKRG	611	36	12	
CHFDLGGQFAEEIFES	212	48	189		DSKSLRTALQKEIYTR	847	45	23		GFPGSGVIDAPFG	814	32	209	
LEKNPFGKSDRINSE	131	36	18		TGGDINAIEIRLL	937	30	21		EWELKPISGGHSS	977	40	67	
NPFGVPSGQGRAD	143	29	3		SLDNLKASVSGVEADL	619	35	17		GVNEYAPVPEERSYK	588	35	223	
GLAVKHLHDPKQWIT	189	40	30		DERRTYAADLNGGL	1025	45	127		LAPTWEELSHKEFPG	8213	95	174	
TIKTFEREAAMGKG	234	44	39		KPAPALRSKASAPEN	591	38	15		TRNEVITPMSEHFGAVD	1193	44	36	
GVSSGLVGEIILKR	120	20	8		KTSYVTSVEENTVD	1759	60	76		ENPYTATWELIRQ	421	18	128	
TRWQFARKIR	155	7	8		SAVEFQERQAYADDN	725	44	72		VEDKFRNNLEKGRILD	297	18	254	
EFKVFEMKATWERR	529	55	114		RDLAQYDAHHZEE	1127	58	237		ENGAYKVEETNKVDFY	308	19	12	
SPHAFETSGKEEDL	1100	75	333							EQQNTVEQRTIVE	685	20	145	

FIG. 36B



FIG. 36C

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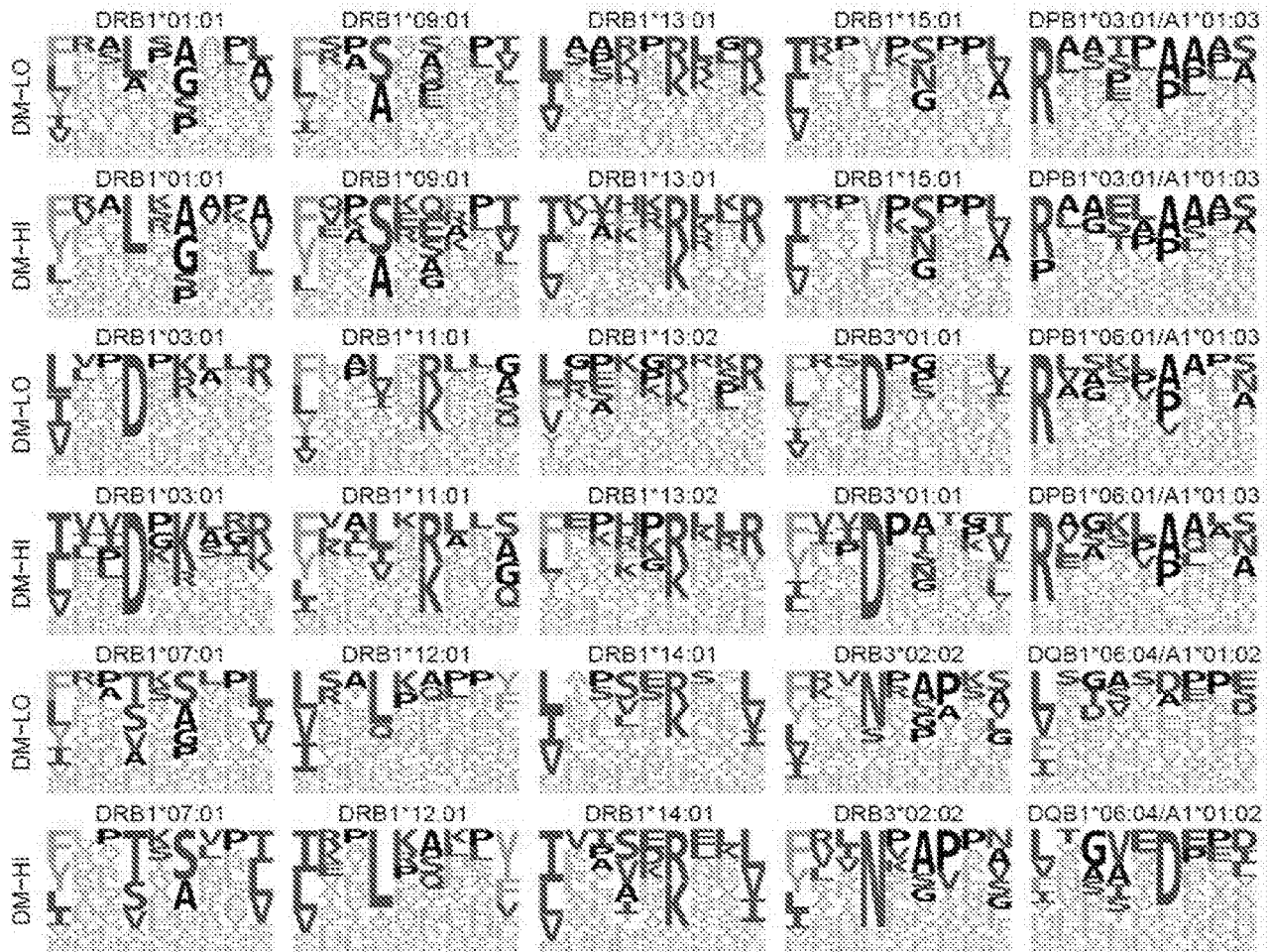


FIG. 37A

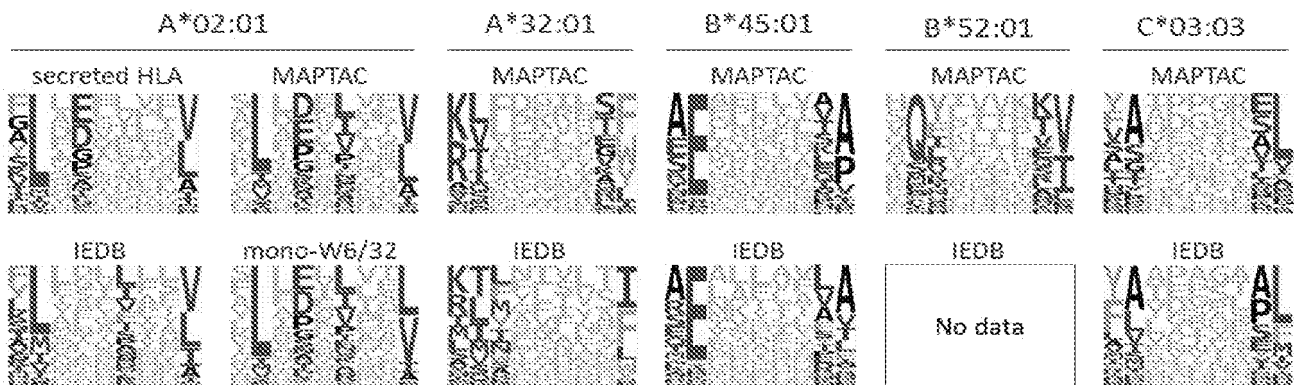


FIG. 37B

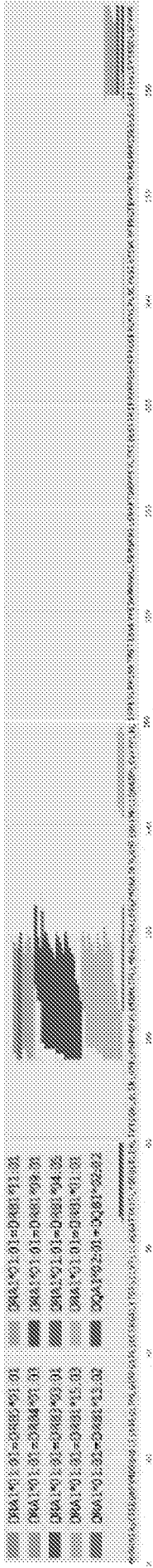


FIG. 37C

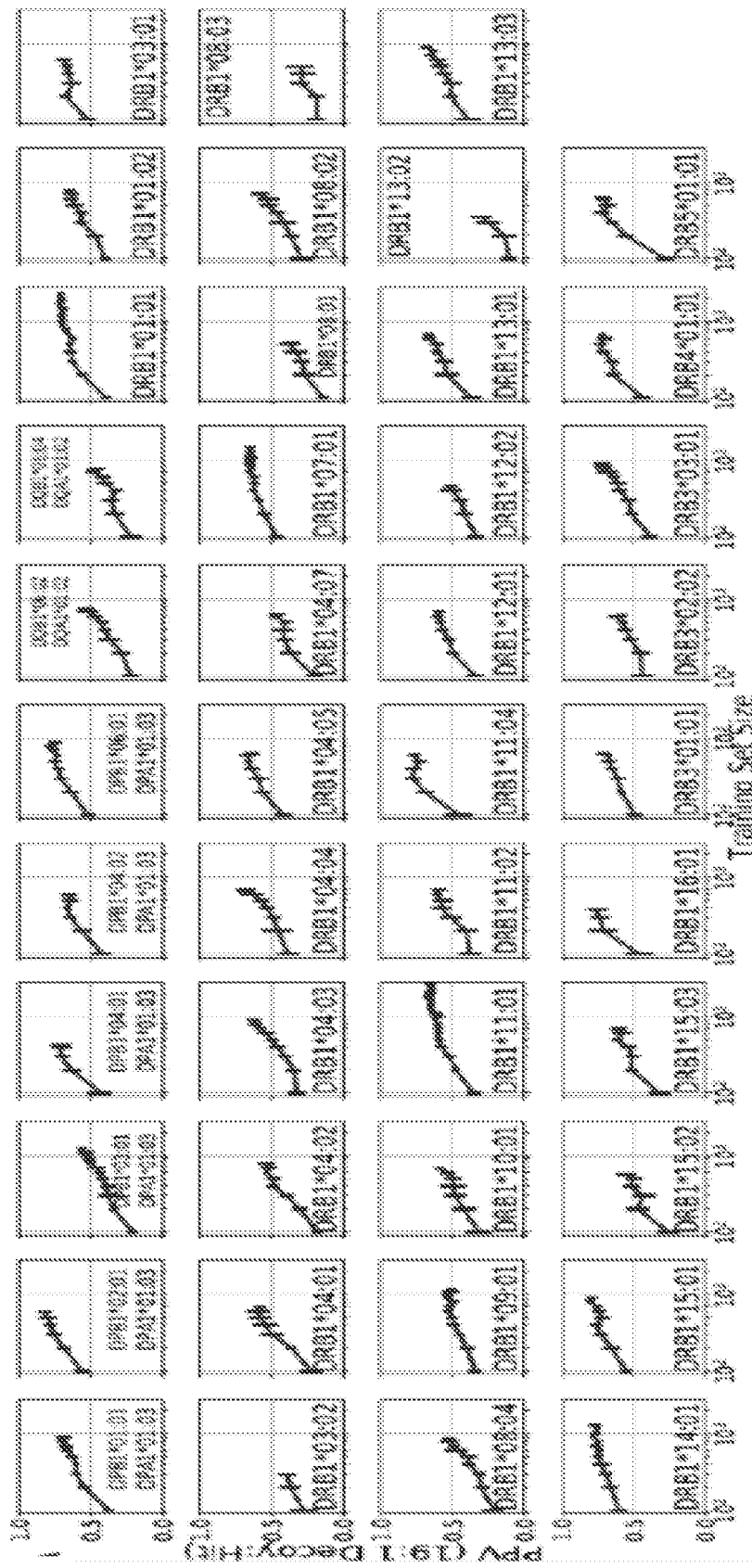
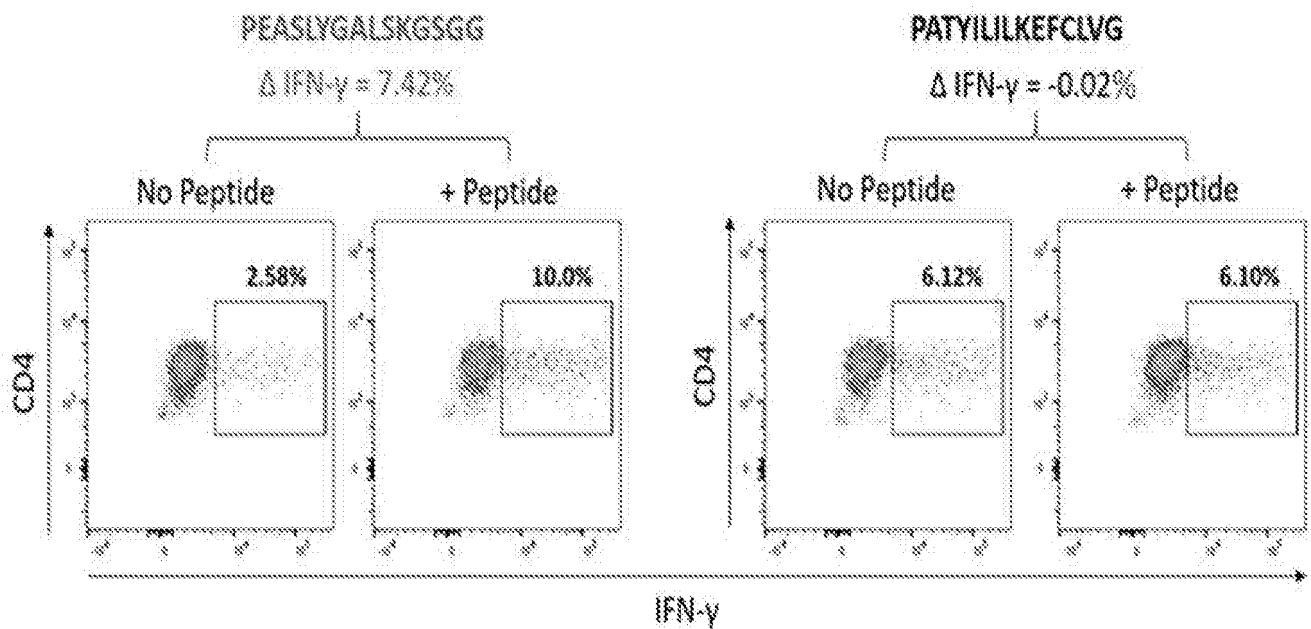


FIG. 38Ai

EBV B cells (Heyder)	DRB1*0401	Not assigned	DRB1*0405	A375 cell line	DRB1*0701	Not assigned	DRB1*0301	P8MC (Donor RG1095)	DRB1*1101	Not assigned	Not assigned
DCs	DRB1*0701	DRB4*0101	DRB1*0101	Lung Tissue (Donor DRLU082018A)	DRB1*0301	DRB3*0101	Not assigned	P8MC (Donor SC)	Not assigned	Not assigned	Not assigned
Spleen (Donor DRLU082018A)	DRB1*0101	DRB1*0301	Not assigned	Not assigned	Not assigned	Not assigned	Not assigned	DOHH2 cell line (Ritz)	DRB1*0101	DRB1*1501	DRB3*0101
P8MC (Donor RG1248)	DRB1*0301	Not assigned	Maver1 cell line (Ritz)	DRB1*0101	DRB1*1301	DRB3*0202	Not assigned				

FIG. 38Aii

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**FIG. 38B**

peptide	status	# Positive Wells	Well1	Well2	Well3	Well4	Well5	Well6	Well7	Well8
GEGLFQPAHRYPDAG	induction_hit	4	3.28	3.5	3.87	3.33	0.81			
RNQWKCLGKPVGAEM	assayed	0	1.88	-1.44	-1.27	-15.43	-10.18	-0.09		
VPAWTRAWRNSSPKG	induction_hit	2	3.53	0.4	-0.36	2.93	2.2	6.3		
LHPELLPLWRLLPDG	induction_hit	1	-1.25	0.46	-0.36	-1.74	0.75	3.92		
DGGSYFSLWKIWTQV	induction_hit	5	4.83	3.84	4.34	13.8	8.1			
PEASLYGALSKGSGG	induction_hit	5	1.96	7.42	1.09	5.24	6.03	1.72	12.93	9.74
HEGGFPPLRRAAED	induction_hit	5	-0.36	3.58	2.58	-22.75	6.59	3.5	8.44	10.39
LSPVWCLOWKLSGTD	induction_hit	2	-0.08	2.52	0.71	13.27	11.32			
KNTIVYTTKQVQSCQ	assayed	0	-1.19							
PATYILILKEFCLVG	assayed	0	-0.02	0.69	1.47	-0.17				
NNEQFQWKIRHVGPE	induction_hit	4	5.44	5.7	0.93	2.97	5.1	4.5		
YKGGYELVKKSQTEL	assayed	0	2.28	-2.01	-2.31					

FIG. 38C

EBV B cells (Heyder) DRB1*0401 Not assigned DRB1*0405	A375 cell line DRB1*0701 Not assigned DRB1*0405	DRB1*0301 Not assigned DRB1*0301	PEMC (Donor RG1095) DRB1*1101 Not assigned DRB1*1101	Not assigned Not assigned
DCs DRB1*0701 DRB4*0101 DRB1*0301 DRB4*0101	Lung Tissue (Donor DRLL082018A) DRB1*0101 DRB1*0301 DRB1*0101 DRB1*0301	DRB1*0101 DRB1*0301 DRB1*0101 DRB1*0301	PEMC (Donor SC) Not assigned Not assigned Not assigned Not assigned	Not assigned Not assigned Not assigned Not assigned
Spleen (Donor DRLL082018A) DRB1*0101 DRB1*0301 DRB1*0101 DRB1*0301	PEMC (Donor RG1104) Not assigned Not assigned Not assigned Not assigned	DRB1*0101 DRB1*0301 DRB1*0101 DRB1*0301	DOH42 cell line (Ritz) DRB1*0101 DRB1*1501 DRB1*0101 DRB1*1501	DRB1*0101 DRB1*1501 DRB1*0101 DRB1*1501
PEMC (Donor RG1248) DRB1*0301 Not assigned DRB1*0301 Not assigned	Maver1 cell line (Ritz) DRB1*0101 DRB1*1301 DRB1*0101 DRB1*1301	DRB1*0101 DRB1*1301 DRB1*0101 DRB1*1301	DRB1*0101 DRB1*1301 DRB1*0101 DRB1*1301	DRB1*0101 DRB1*1301 DRB1*0101 DRB1*1301

FIG. 38D

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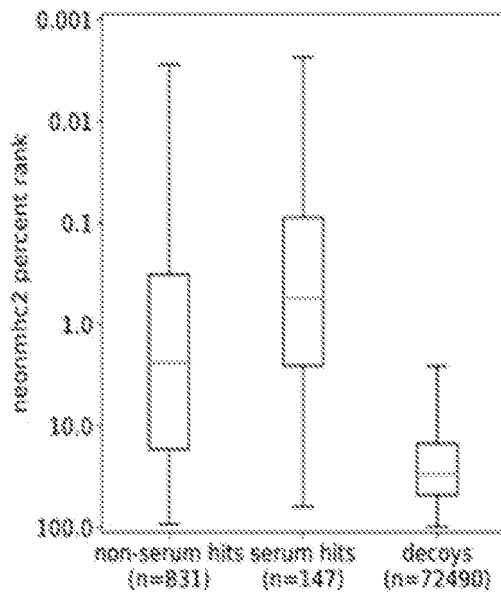


FIG. 39A

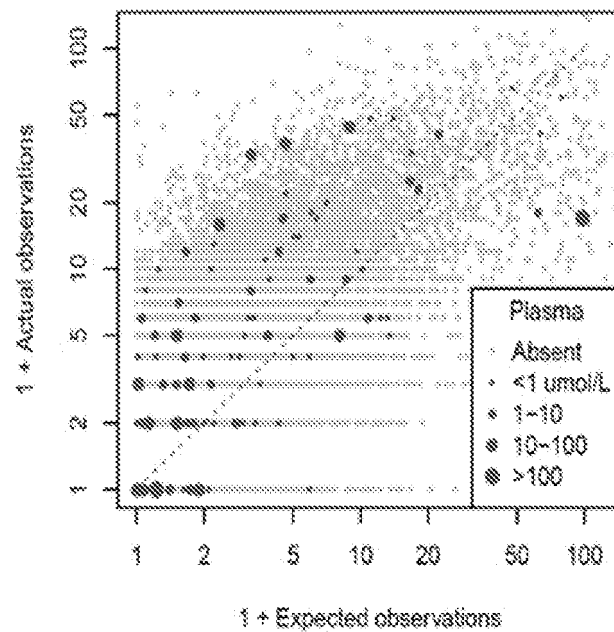


FIG. 39B

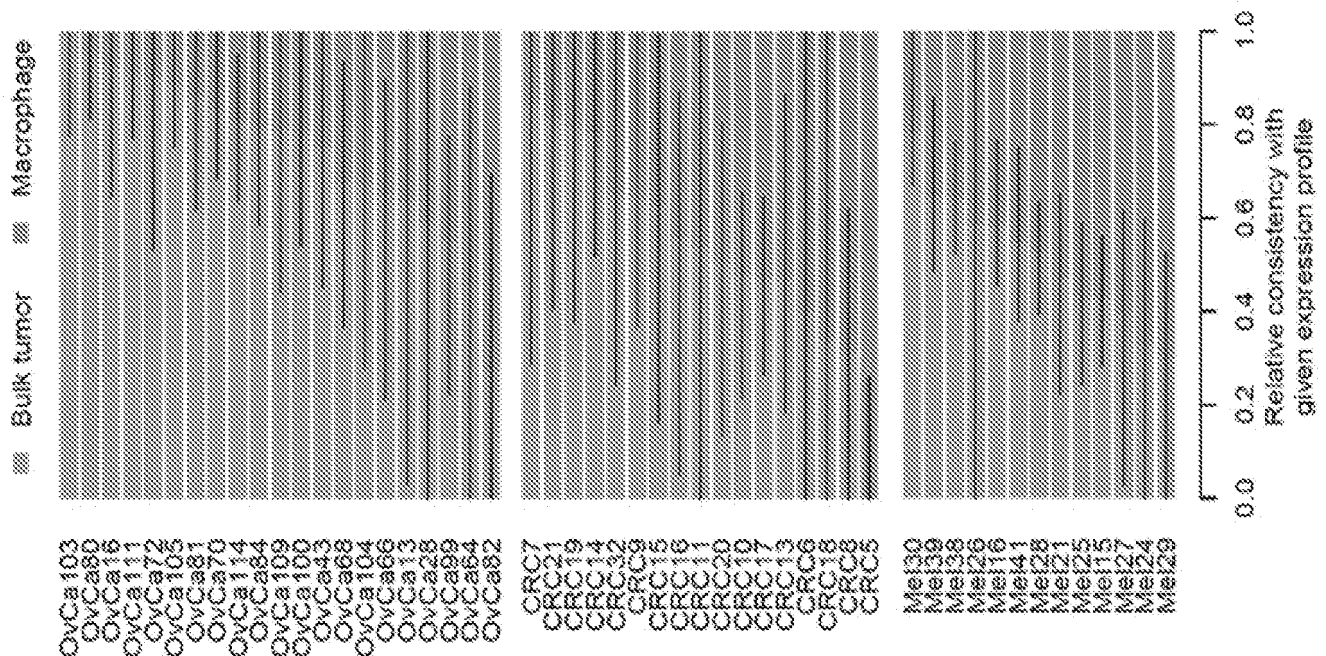


FIG. 39C

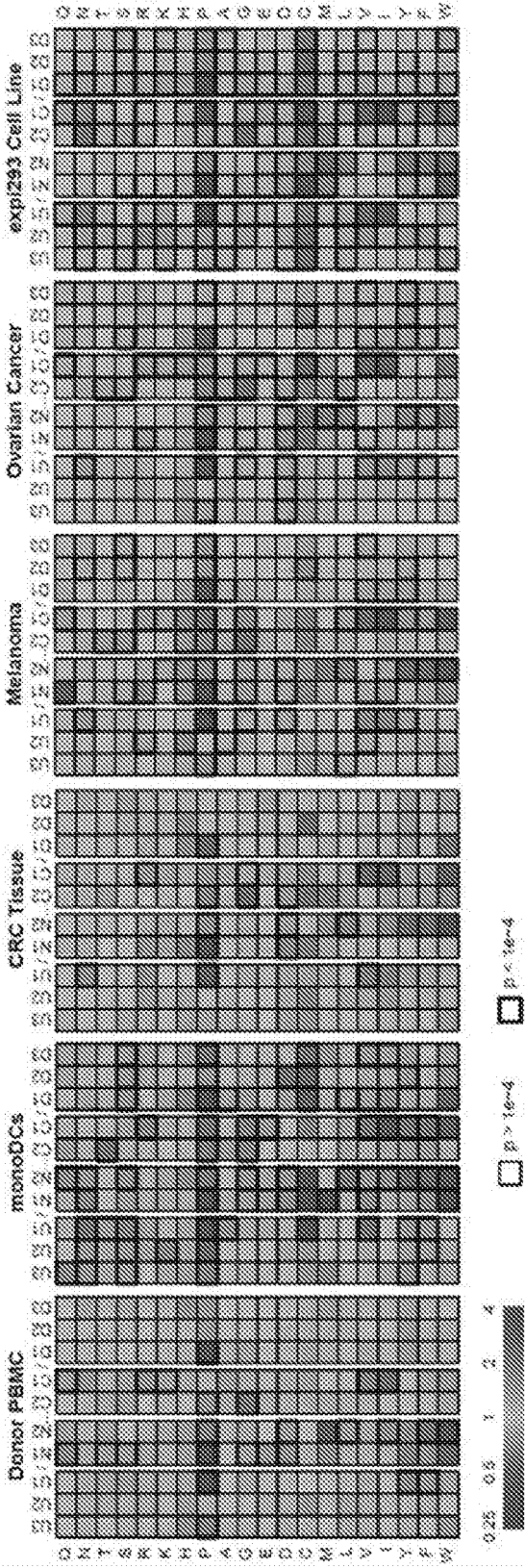


FIG. 40A

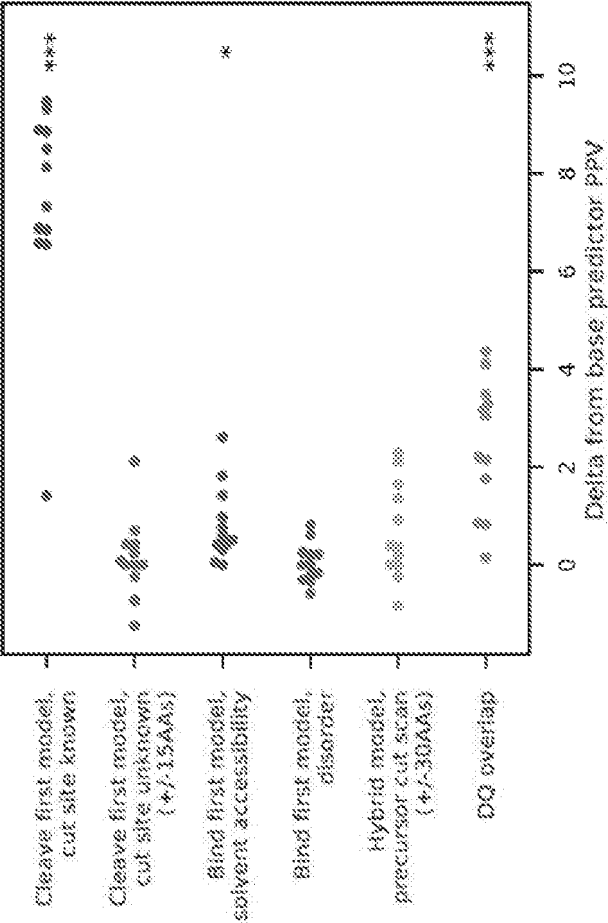


FIG. 40B

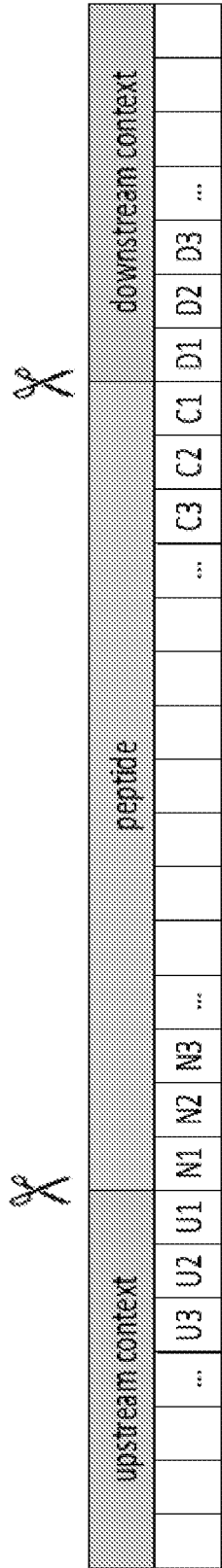


FIG. 41

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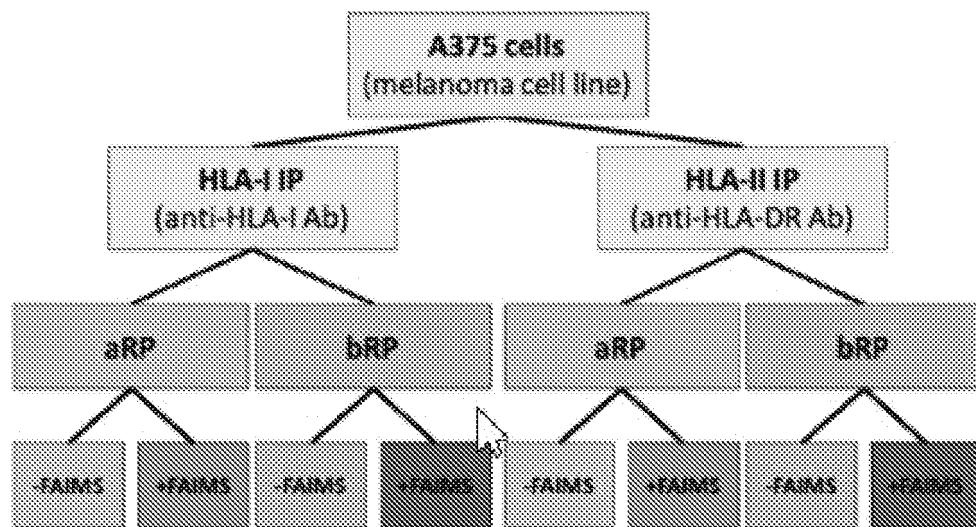


FIG. 42A

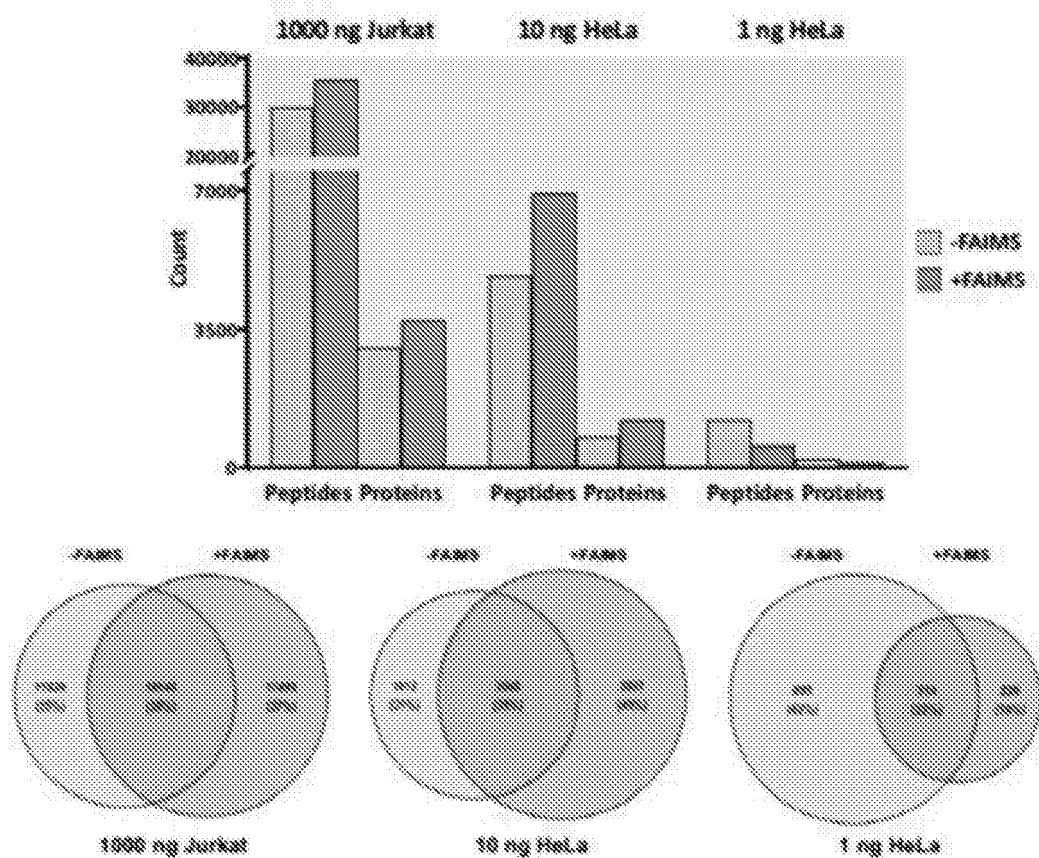
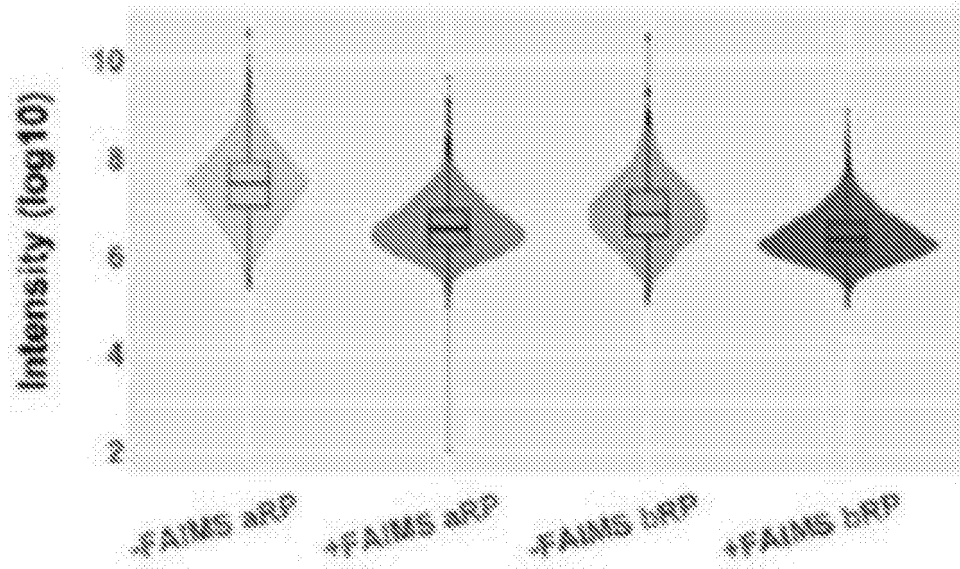
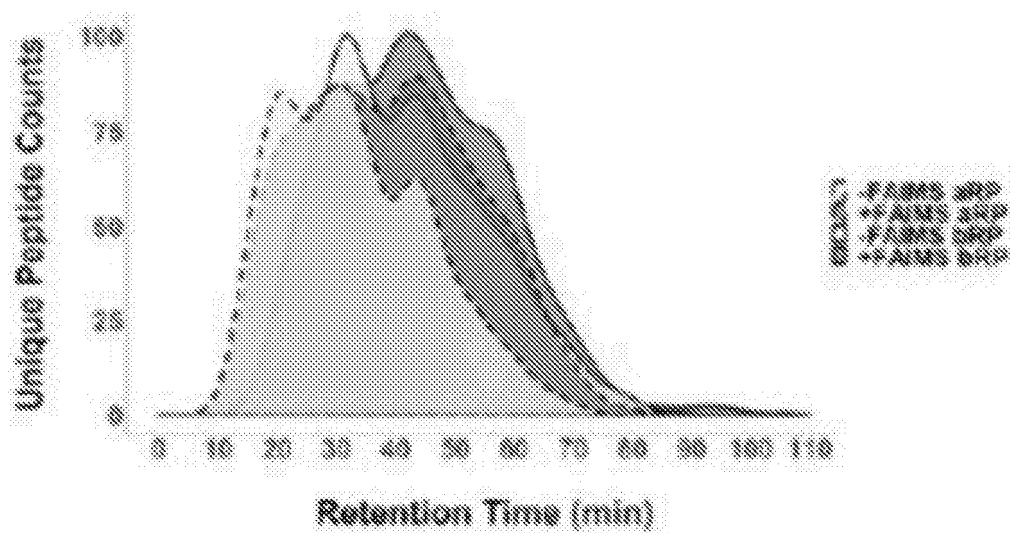
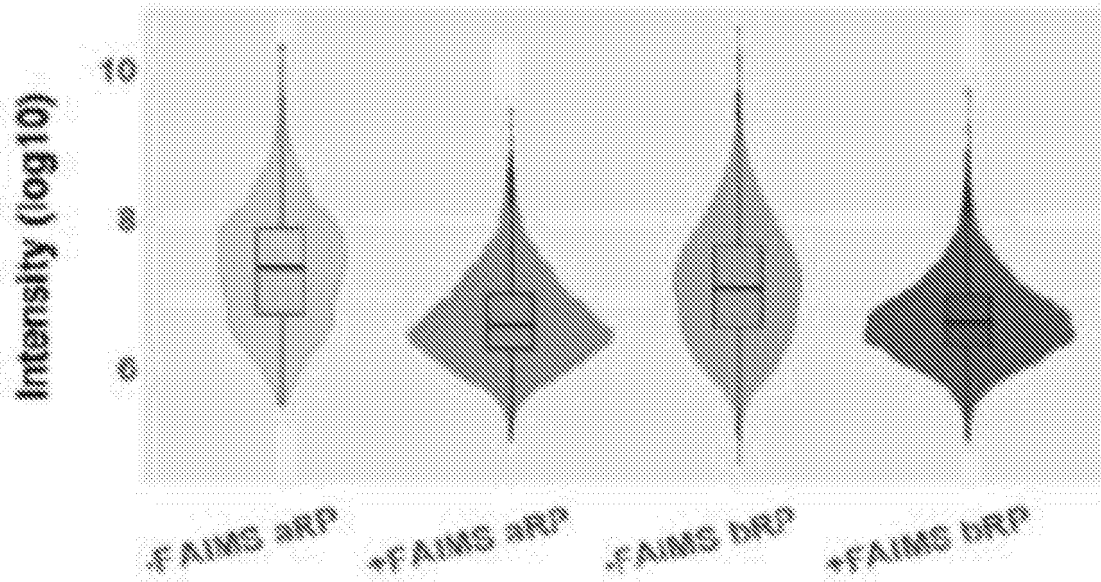
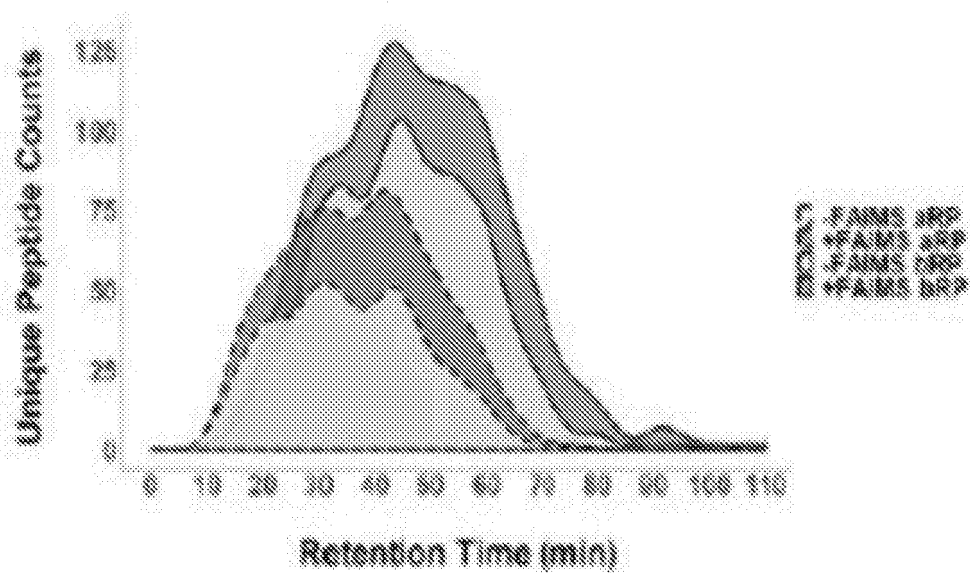


FIG. 42B

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*FIG. 43A**FIG. 43B*

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**FIG. 44A****FIG. 44B**

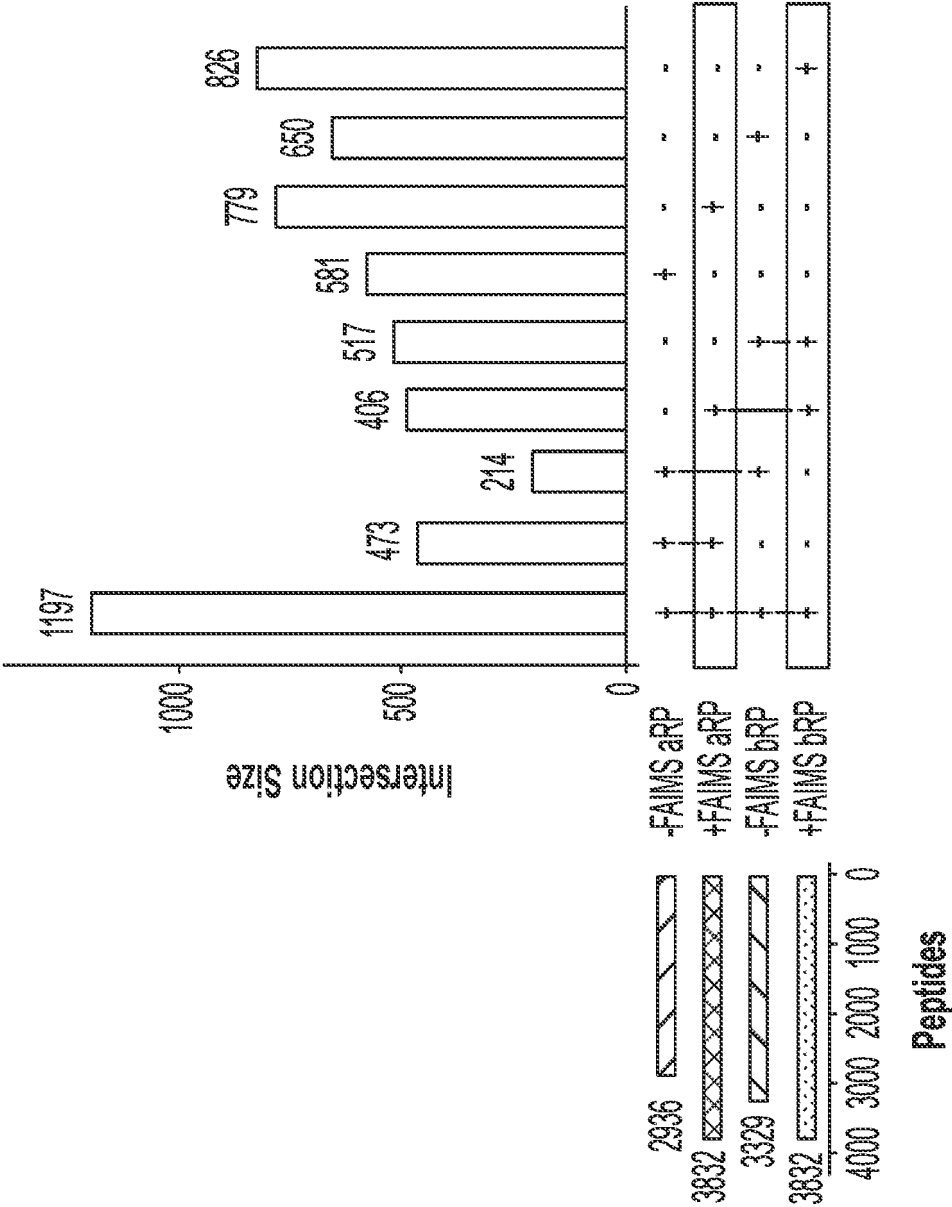
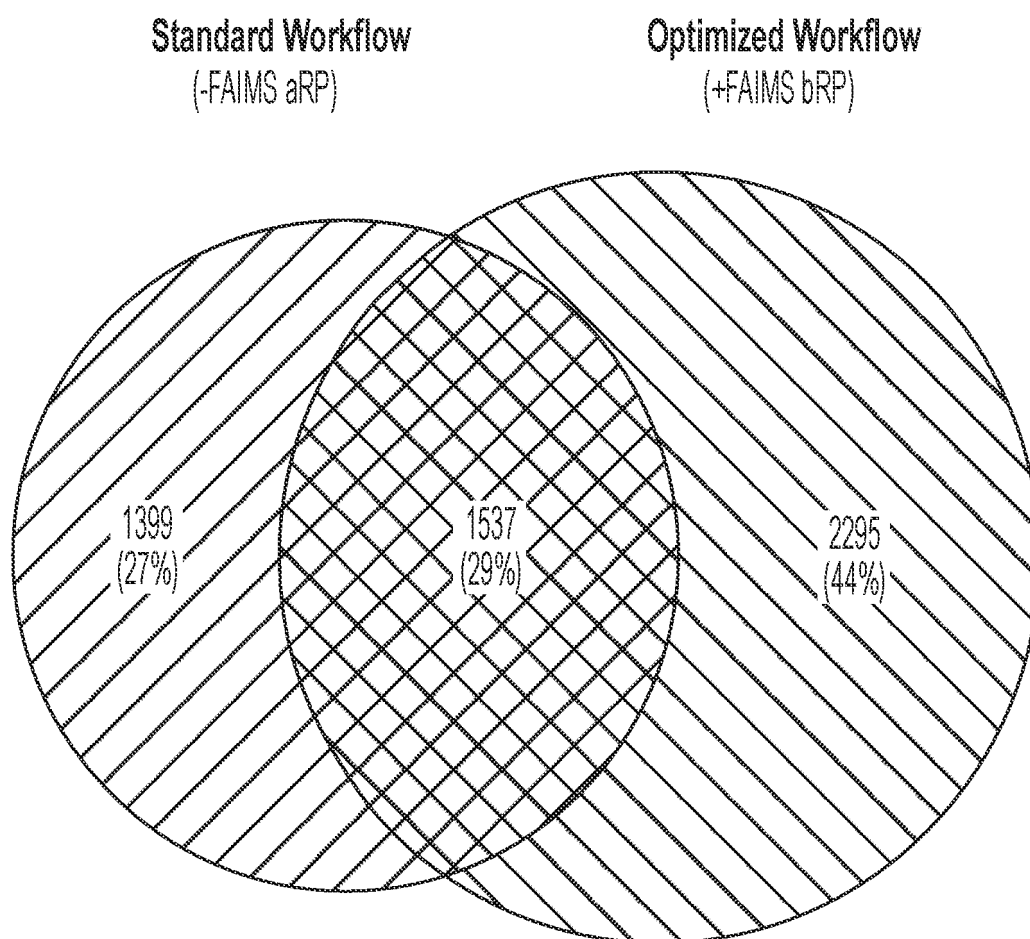


FIG. 45

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***FIG. 45(Continued)***

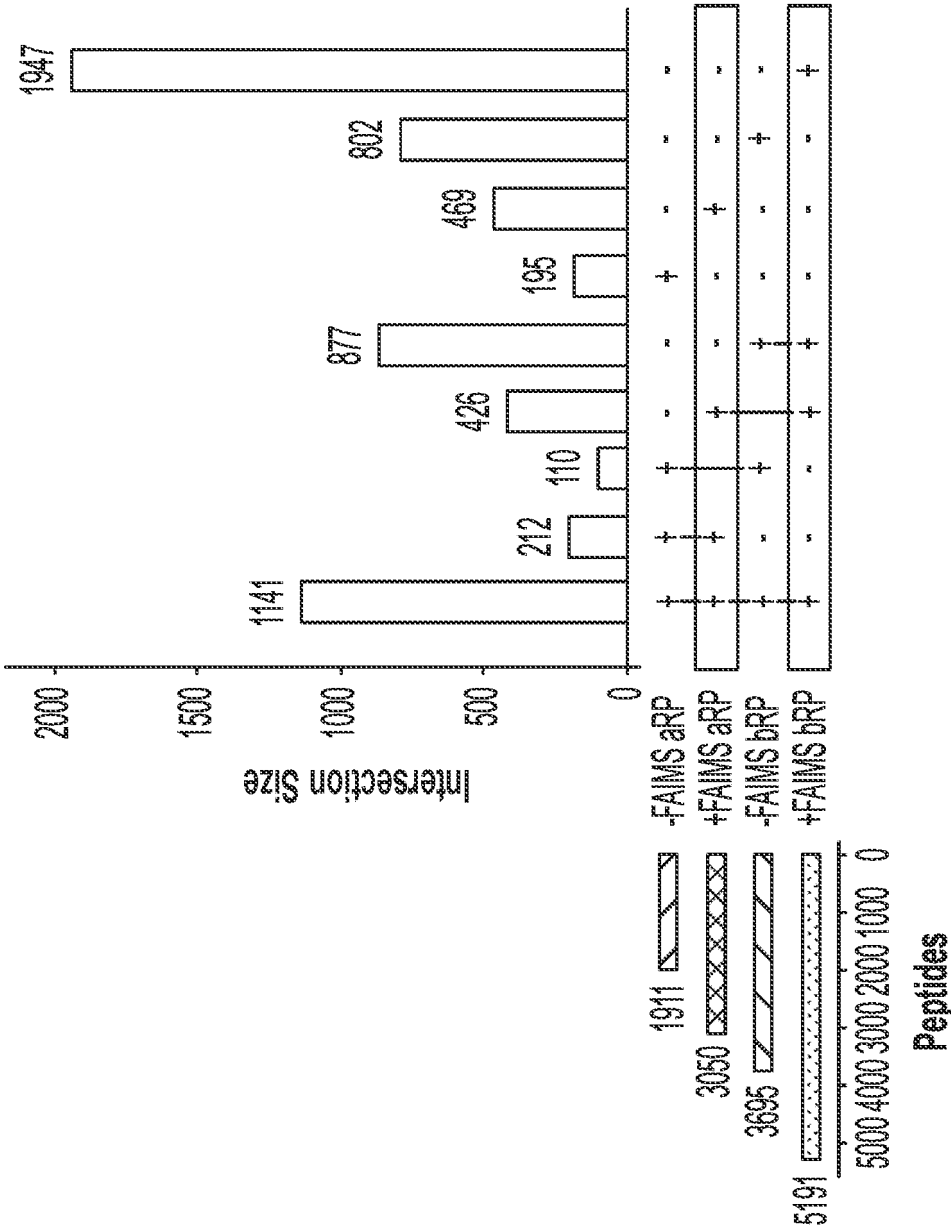
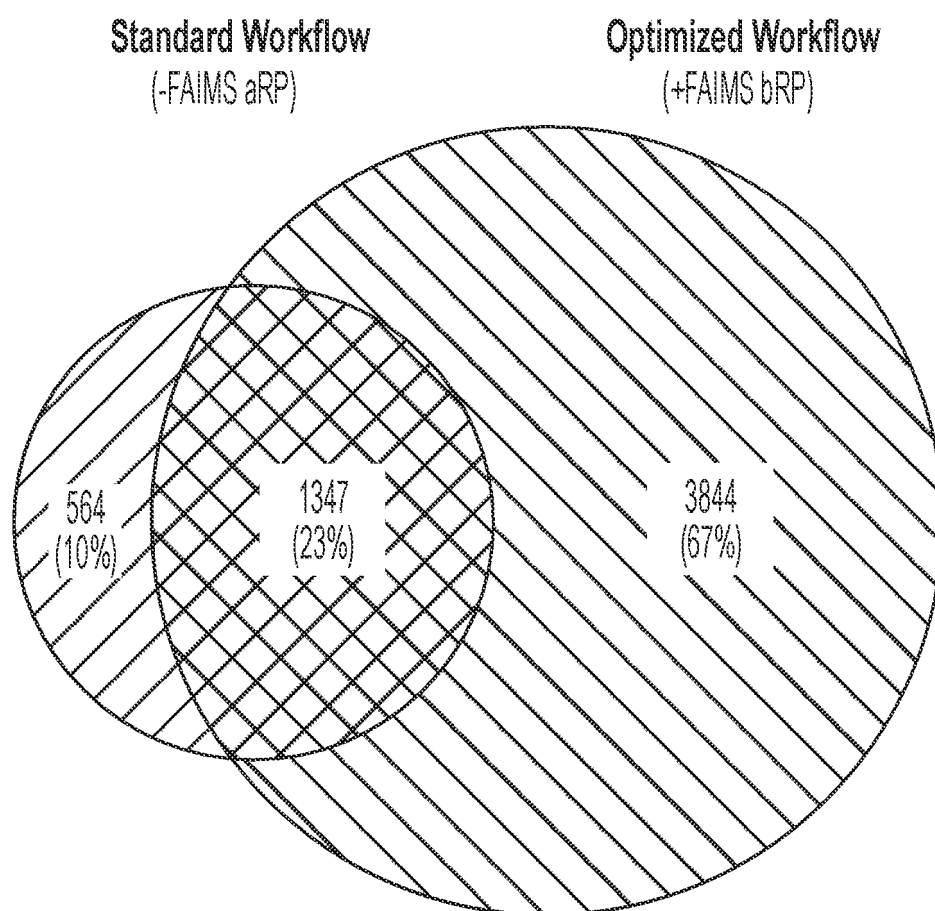


FIG. 46

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***FIG. 46(Continued)***