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IGKV1-39*01	FR1-IMGT----- CDR1 -----FR2-IMGT--- C -----	SEQ ID NO:1
A	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASLQSGVPS	
B	F...T H I...V...YT....	
C	A.....I...NF.....G.YN.....	
D	 HN .NN.....H.....N.....	
E	A...T...N.....	
F	N.....N...D.....	
G	A..L.....N.N.. H D..F.....	
H	A.....N.N.. H D..F.....	
I	A..L.....	
J	A.....	
K	A..L.....M.....	
IGKV1-39*01	-----FR3-IMGT----- CDR3-	
A	RFSGSGGTDFTLTISSLQPEDFATYYCQQSYST-P-----	
B	...A.....T.....NI...FTFGPGTKVDIKR	
C	I... H -----LTFGGGTKVEIKR	
D	Y.....T.H...GN.....SMYTFGQGTQLEIKR	
E	 H I...ITFGQGTGLEIKR	
F	T.H..... H ITFGQGTGLEIKR	
G	T..... H ITFGQGTGLEIKR	
H	P.ITFGQGTGLEIKR	
I	K..... IH .ITFGQGTGLEIKR	
J	 H .IP.ITFGQGTGLEIK.	
K	T.....R..... H .P.ITFGQGTGLEIKR	

FIG. 1

WT	105	106		108		111	
	Q	Q	S	Y	S	T	P
	CAG	CAG	AGC	TAC	AGC	ACC	CCC
							SEQ ID NO:3
							SEQ ID NO:2
H105/106/108/111	H	H	S	H	S	T	H
	CAC	CAT	AGC	CAC	AGC	ACC	CAC
							SEQ ID NO:5
							SEQ ID NO:4
H105	CAC	CAG	AGC	TAC	AGC	ACC	CCC
							SEQ ID NO:6
H106	CAG	CAT	AGC	TAC	AGC	ACC	CCC
							SEQ ID NO:8
H108	CAG	CAG	AGC	CAC	AGC	ACC	CCC
							SEQ ID NO:10
H111	CAG	CAG	AGC	TAC	AGC	ACC	CAC
							SEQ ID NO:12
H105/106	CAC	CAT	AGC	TAC	AGC	ACC	CCC
							SEQ ID NO:14
H105/108	CAC	CAG	AGC	CAC	AGC	ACC	CCC
							SEQ ID NO:16
H105/111	CAC	CAG	AGC	TAC	AGC	ACC	CAC
							SEQ ID NO:18
H106/108	CAG	CAT	AGC	CAC	AGC	ACC	CCC
							SEQ ID NO:20
H106/111	CAG	CAT	AGC	TAC	AGC	ACC	CAC
							SEQ ID NO:22
H108/111	CAG	CAG	AGC	CAC	AGC	ACC	CAC
							SEQ ID NO:24
H105/106/108	CAC	CAT	AGC	CAC	AGC	ACC	CCC
							SEQ ID NO:26
H105/106/111	CAC	CAT	AGC	TAC	AGC	ACC	CAC
							SEQ ID NO:28
H105/108/111	CAC	CAG	AGC	CAC	AGC	ACC	CAC
							SEQ ID NO:30
H106/108/111	CAG	CAT	AGC	CAC	AGC	ACC	CAC
							SEQ ID NO:32

FIG. 2

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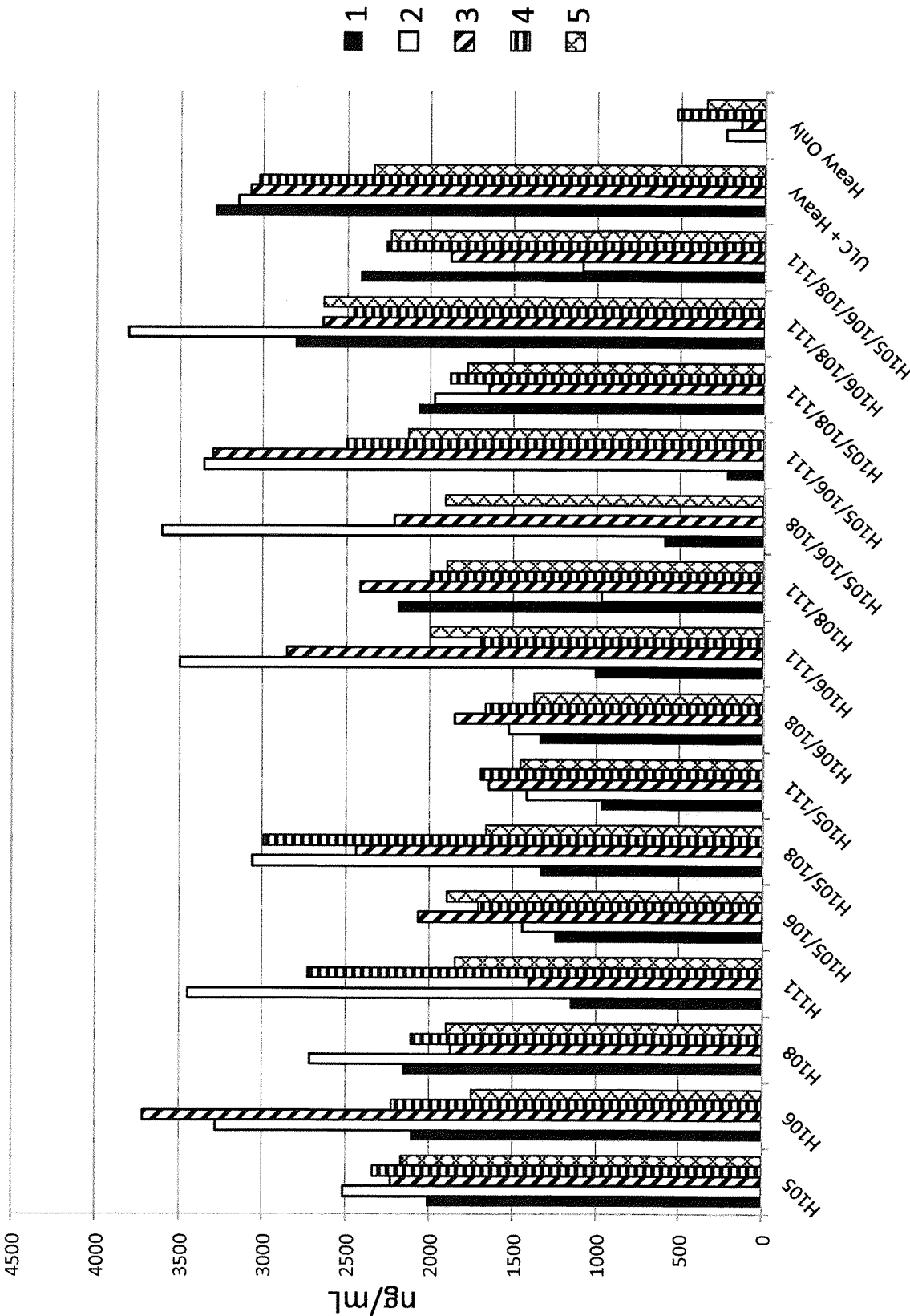


FIG. 3

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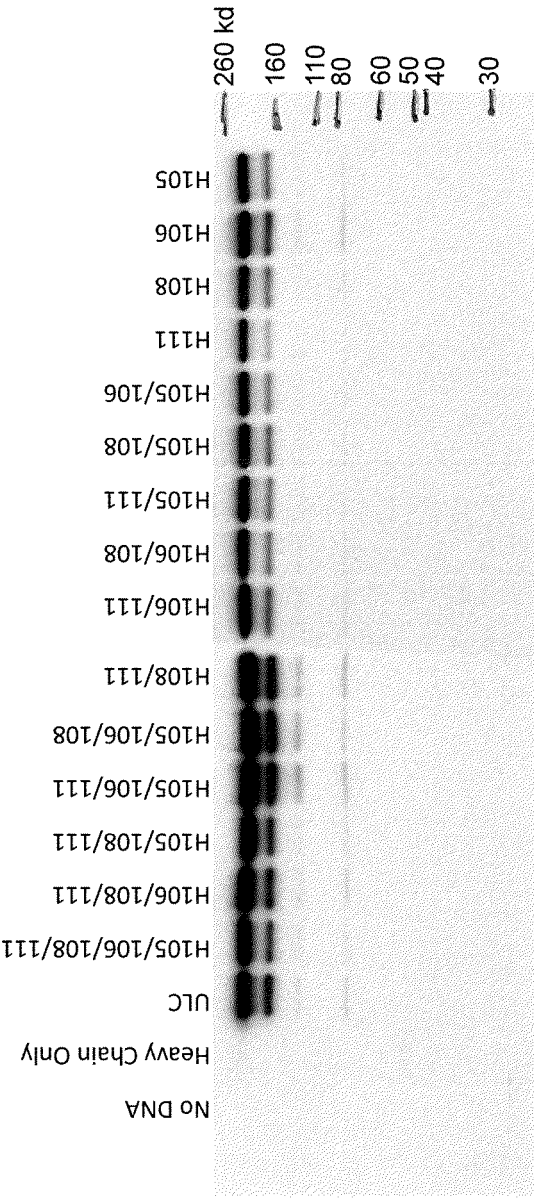


FIG. 4

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Heavy Chain	Light Chain Mutant	Kinetics at pH 7.4						Kinetics at pH 5.75						Ratio of low pH / neutral pH		
		mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	ka	kd	KD
1	H105	488	47.2	3.52E+05	9.30E-03	2.64E-08	1.2	378	37.8	4.24E+05	1.38E-02	3.24E-08	0.8	1.2	1.5	1.2
	H106	620	73.7	3.22E+05	3.67E-03	1.14E-08	3.1	505	65.4	3.66E+05	4.86E-03	1.33E-08	2.4	1.1	1.3	1.2
	H108	648	99.0	3.17E+05	2.07E-03	6.54E-09	5.6	496	80.7	3.59E+05	3.02E-03	8.41E-09	3.8	1.1	1.5	1.3
	H111	669	81.0	3.01E+05	3.81E-03	1.27E-08	3.0	536	62.8	3.32E+05	5.41E-03	1.63E-08	2.1	1.1	1.4	1.3
	H105/106	492	55.6	3.74E+05	6.44E-03	1.72E-08	1.8	404	45.7	4.30E+05	1.01E-02	2.34E-08	1.1	1.2	1.6	1.4
	H105/108	538	75.2	3.28E+05	4.17E-03	1.27E-08	2.8	416	56.3	3.87E+05	7.43E-03	1.92E-08	1.6	1.2	1.8	1.5
	H105/111	501	44.6	3.44E+05	9.77E-03	2.84E-08	1.2	402	31.9	4.06E+05	1.70E-02	4.19E-08	0.7	1.2	1.7	1.5
	H106/108	494	64.9	3.36E+05	4.14E-03	1.23E-08	2.8	407	43.0	4.07E+05	1.17E-02	2.86E-08	1.0	1.2	2.8	2.3
	H106/111	536	78.2	3.09E+05	3.10E-03	1.00E-08	3.7	423	61.4	3.62E+05	4.68E-03	1.29E-08	2.5	1.2	1.5	1.3
	H108/111	584	78.5	3.11E+05	3.80E-03	1.22E-08	3.0	473	59.0	3.50E+05	6.13E-03	1.75E-08	1.9	1.1	1.6	1.4
	H105/106/108	442	51.2	3.72E+05	6.38E-03	1.71E-08	1.8	370	28.4	4.26E+05	2.13E-02	5.00E-08	0.5	1.1	3.3	2.9
	H105/106/111	473	62.8	3.40E+05	4.55E-03	1.34E-08	2.5	378	47.6	4.07E+05	7.42E-03	1.82E-08	1.6	1.2	1.6	1.4
	H105/108/111	433	49.5	3.57E+05	7.42E-03	2.08E-08	1.6	354	31.3	4.09E+05	1.73E-02	4.23E-08	0.7	1.1	2.3	2.0
	H106/108/111	491	66.6	3.44E+05	3.82E-03	1.11E-08	3.0	415	43.3	3.91E+05	1.06E-02	2.72E-08	1.1	1.1	2.8	2.5
	H105/106/108/111	454	57.9	3.51E+05	5.77E-03	1.64E-08	2.0	368	36.8	4.06E+05	1.35E-02	3.32E-08	0.9	1.2	2.3	2.0
	ULC + Heavy	586	76.0	3.16E+05	3.85E-03	1.22E-08	3.0	483	66.5	3.45E+05	4.58E-03	1.33E-08	2.5	1.1	1.2	1.1
	Heavy only	141	-1.3	NB	NB	NB	NB	107	-6.7	NB	NB	NB	NB	Negative Control		
	No DNA	60	-1.5	NB	NB	NB	NB	26	-7.2	NB	NB	NB	NB			

FIG. 5A

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Heavy Chain	Light Chain Mutant	Kinetics at pH 7.4						Kinetics at pH 5.75						Ratio of low pH / neutral pH		
		mAb capture d (RU)	50nM Antigen Binding (RU)	ka (1/ Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	mAb capture d (RU)	50nM Antigen Binding (RU)	ka (1/ Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	ka	kd	KD
2	H105	720	33.7	1.02E+05	9.10E-04	8.89E-09	12.7	595	0.3	NB	NB	NB	NB	No binding at Low pH		
	H106	735	32.9	9.11E+04	4.47E-04	4.91E-09	25.8	623	4.3	2.27E+04	6.41E-03	2.82E-07	1.8	0.2	14.3	57.4
	H108	728	32.2	8.48E+04	2.67E-04	3.14E-09	43.3	598	3.6	1.16E+03	3.41E-03	2.93E-06	3.4	0.0	12.8	933.1
	H111	802	42.4	1.17E+05	1.15E-04	9.88E-10	100.3	670	14.1	3.01E+04	7.08E-04	2.35E-08	16.3	0.3	6.1	23.8
	H105/106	570	24.9	8.51E+04	2.92E-04	3.43E-09	39.5	484	2.4	1.14E+04	6.47E-03	5.69E-07	1.8	0.1	22.1	165.9
	H105/108	723	28.4	8.73E+04	1.30E-03	1.49E-08	8.9	603	-2.6	NB	NB	NB	NB	No binding at Low pH		
	H105/111	627	28.5	8.82E+04	3.60E-04	4.08E-09	32.1	519	2.3	1.02E+04	1.30E-02	1.27E-06	0.9	0.1	36.2	311.3
	H106/108	550	21.1	6.75E+04	9.12E-04	1.35E-08	12.7	470	-1.9	NB	NB	NB	NB	No binding at Low pH		
	H106/111	808	32.7	9.01E+04	6.78E-04	7.52E-09	17.0	678	0.9	NB	NB	NB	NB	No binding at Low pH		
	H108/111	801	40.5	1.17E+05	9.80E-05	8.40E-10	117.8	676	10.6	1.87E+04	5.84E-04	3.12E-08	19.8	0.2	6.0	37.1
	H105/106/108	409	13.0	8.21E+04	4.29E-04	5.22E-09	26.9	345	-4.4	NB	NB	NB	NB	No binding at Low pH		
	H105/106/111	767	9.3	4.84E+04	1.25E-03	2.58E-08	9.3	645	-6.1	NB	NB	NB	NB	No binding at Low pH		
	H105/108/111	578	24.5	8.99E+04	2.87E-04	3.19E-09	40.2	479	-0.7	NB	NB	NB	NB	No binding at Low pH		
	H106/108/111	765	15.1	5.04E+04	1.65E-03	3.27E-08	7.0	661	-5.9	NB	NB	NB	NB	No binding at Low pH		
	H105/106/108/111	723	0.3	NB	NB	NB	NB	611	-7.0	NB	NB	NB	NB	No binding at either pH tested		
	ULC + Heavy	781	39.8	1.13E+05	1.78E-04	1.57E-09	64.9	665	11.7	2.04E+04	1.22E-03	6.00E-08	9.4	0.2	6.9	38.2
	Heavy only	143	-1.8	NB	NB	NB	NB	115	-6.1	NB	NB	NB	NB	Negative Control		
	No DNA	63	-2.1	NB	NB	NB	NB	35	-6.4	NB	NB	NB	NB			

FIG. 5B

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Heavy Chain	Light Chain Mutant	Kinetics at pH 7.4						Kinetics at pH 5.75						Ratio of low pH / neutral pH		
		mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/MS)	kd (1/s)	KD (M)	t _{1/2} (min)	mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/MS)	kd (1/s)	KD (M)	t _{1/2} (min)	ka	kd	KD
3	H105	574	12.4	5.64E+04	1.21E-03	2.15E-08	9.5	496	0.1	NB	NB	NB	NB	No binding at Low pH		
	H106	662	16.1	7.37E+04	5.36E-04	7.27E-09	21.5	584	3.0	3.00E+04	4.79E-03	1.58E-07	2.4	0.4	8.9	21.7
	H108	518	12.3	4.82E+04	2.15E-04	4.46E-09	53.7	440	2.2	3.70E+04	1.25E-03	3.40E-08	9.3	0.8	5.8	7.6
	H111	480	9.1	1.82E+04	4.16E-04	2.28E-08	27.7	406	0.4	NB	NB	NB	NB	No binding at Low pH		
	H105/106	487	7.4	1.82E+04	7.45E-03	4.10E-07	1.6	423	-4.1	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/108	548	11.8	3.25E+04	5.25E-04	1.62E-08	22.0	468	0.0	NB	NB	NB	NB	No binding at Low pH		
	H105/111	504	7.9	1.06E+04	1.66E-03	1.57E-07	7.0	430	-1.6	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H106/108	487	10.7	6.64E+04	2.91E-04	4.38E-09	39.7	424	-4.2	NB	NB	NB	NB	No binding at Low pH		
	H106/111	563	10.5	2.75E+04	3.71E-04	1.35E-08	31.2	482	-1.9	NB	NB	NB	NB	No binding at Low pH		
	H108/111	528	10.1	1.10E+04	8.01E-05	7.27E-09	144.2	449	-0.5	NB	NB	NB	NB	No binding at Low pH		
	H105/106/108	470	6.4	2.64E+04	5.40E-03	2.04E-07	2.1	412	-5.3	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/106/111	539	0.8	NB	NB	NB	NB	462	-5.6	NB	NB	NB	NB	No binding at either pH tested		
	H105/108/111	419	6.5	1.76E+04	4.01E-04	2.27E-08	28.8	354	-3.8	NB	NB	NB	NB	No binding at Low pH		
	H106/108/111	509	3.3	5.47E+04	9.07E-04	1.66E-08	12.7	443	-5.9	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/106/108/111	450	-1.1	NB	NB	NB	NB	382	-6.4	NB	NB	NB	NB	No binding at either pH tested		
	ULC + Heavy	688	16.9	3.54E+04	3.57E-04	1.01E-08	32.3	598	5.0	1.16E+04	1.76E-03	1.52E-07	6.6	0.3	4.9	15.0
	Heavy only	152	-1.6	NB	NB	NB	NB	127	-5.4	NB	NB	NB	NB	Negative Control		
	No DNA	54	-1.7	NB	NB	NB	NB	30	-5.6	NB	NB	NB	NB			

FIG. 5C

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Heavy Chain	Light Chain Mutant	Kinetics at pH 7.4						Kinetics at pH 5.75						Ratio of low pH / neutral pH		
		mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	ka	kd	KD
4	H105	598	4.9	2.80E+04	1.38E-03	4.91E-08	8.4	512	-0.2	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H106	569	7.1	1.49E+04	9.67E-04	6.49E-08	11.9	494	1.2	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H108	587	6.3	2.25E+04	2.02E-03	8.96E-08	5.7	500	-0.9	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H111	606	5.6	3.46E+04	2.19E-03	6.33E-08	5.3	521	-0.9	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/106	517	3.1	2.00E+04	2.05E-03	1.03E-07	5.6	460	-1.1	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/108	581	2.5	1.61E+05	2.30E-03	1.43E-08	5.0	506	-2.7	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/111	575	3.8	1.01E+04	1.70E-03	1.68E-07	6.8	504	-2.0	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H106/108	498	2.5	4.01E+04	6.07E-04	1.51E-08	19.0	447	-3.9	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H106/111	587	3.0	7.85E+04	9.20E-04	1.17E-08	12.6	509	-2.6	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H108/111	599	4.0	9.68E+04	2.02E-03	2.09E-08	5.7	528	-2.6	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/106/108	64	-1.7	NB	NB	NB	NB	46	-5.4	NB	NB	NB	NB	No binding at either pH tested		
	H105/106/111	561	1.1	NB	NB	NB	NB	493	-2.8	NB	NB	NB	NB	No binding at either pH tested		
	H105/108/111	521	2.7	7.66E+04	1.29E-03	1.68E-08	9.0	461	-3.2	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H106/108/111	577	1.3	NB	NB	NB	NB	514	-4.2	NB	NB	NB	NB	No binding at either pH tested		
	H105/106/108/111	554	0.6	NB	NB	NB	NB	495	-4.8	NB	NB	NB	NB	No binding at either pH tested		
	ULC + Heavy	585	7.4	5.69E+04	2.01E-03	3.53E-08	5.7	527	1.9	NB	NB	NB	NB	No binding at Low pH		
	Heavy only	187	-2.4	NB	NB	NB	NB	161	-5.4	NB	NB	NB	NB	Negative Control		
	No DNA	49	-2.6	NB	NB	NB	NB	25	-5.6	NB	NB	NB	NB			

FIG. 5D

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Heavy Chain	Light Chain Mutant	Kinetics at pH 7.4						Kinetics at pH 5.75						Ratio of low pH / neutral pH		
		mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	mAb captured (RU)	50nM Antigen Binding (RU)	ka (1/Ms)	kd (1/s)	KD (M)	t _{1/2} (min)	ka	kd	KD
5	H105	522	3.2	5.05E+04	9.48E-03	1.88E-07	1.2	463	-4.3	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H106	496	0.3	NB	NB	NB	NB	437	-5.2	NB	NB	NB	NB	No binding at either pH tested		
	H108	475	-0.1	NB	NB	NB	NB	415	-5.7	NB	NB	NB	NB	No binding at either pH tested		
	H111	523	1.6	NB	NB	NB	NB	463	-4.7	NB	NB	NB	NB	No binding at either pH tested		
	H105/106	534	-0.6	NB	NB	NB	NB	472	-5.5	NB	NB	NB	NB	No binding at either pH tested		
	H105/108	499	2.0	5.80E+04	1.16E-02	1.99E-07	1.0	433	-5.5	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/111	489	0.1	NB	NB	NB	NB	426	-4.7	NB	NB	NB	NB	No binding at either pH tested		
	H106/108	441	-0.5	NB	NB	NB	NB	386	-4.2	NB	NB	NB	NB	No binding at either pH tested		
	H106/111	529	-0.8	NB	NB	NB	NB	461	-6.3	NB	NB	NB	NB	No binding at either pH tested		
	H108/111	495	4.1	1.73E+05	1.06E-02	6.11E-08	1.1	435	-4.0	NB	NB	NB	NB	Poor binding at Neutral, No binding at Low pH		
	H105/106/108	505	-1.1	NB	NB	NB	NB	444	-5.5	NB	NB	NB	NB	No binding at either pH tested		
	H105/106/111	499	-1.7	NB	NB	NB	NB	438	-5.8	NB	NB	NB	NB	No binding at either pH tested		
	H105/108/111	436	0.8	NB	NB	NB	NB	388	-3.7	NB	NB	NB	NB	No binding at either pH tested		
	H106/108/111	539	-1.4	NB	NB	NB	NB	477	-4.0	NB	NB	NB	NB	No binding at either pH tested		
	H105/106/108/111	556	-1.6	NB	NB	NB	NB	490	-4.4	NB	NB	NB	NB	No binding at either pH tested		
	ULC + Heavy	516	0.6	NB	NB	NB	NB	451	-5.0	NB	NB	NB	NB	No binding at either pH tested		
	Heavy only	144	-1.3	NB	NB	NB	NB	122	-5.7	NB	NB	NB	NB	Negative Control		
	No DNA	47	-1.4	NB	NB	NB	NB	25	-5.8	NB	NB	NB	NB			

FIG. 5E

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V_H	V_K	K_D at pH7.4 (nM)	K_D at pH5.75 (nM)	$T_{1/2}$ at pH7.4 (min)	$T_{1/2}$ at pH5.75 (min)
2	Parental ULC	1.6	60	65	9.4
2	ULC (His105,106)	3.4	570	39	1.8
2	ULC (His105,111)	4.1	1270	32	0.9
2	ULC (His105,108,111)	3.2	NB	40	NB
2	ULC (His105,106,108)	5.2	NB	27	NB
3	Parental ULC	10.1	152	32	6.6
3	ULC (His106,108)	4.4	NB	40	NB
3	ULC (His108,111)	7.3	NB	144	NB
6	Parental ULC	3.0	2.4	10	6
6	ULC (His105,111)	3.5	NB	9	NB
6	ULC (His106, 108,111)	2.0	NB	16	NB

FIG. 6

Site-directed mutagenesis primers for Histidine substitutions in CDR3 of Universal Light Chain of hVK1-39JK5

Primer name	Sequence	%GC	N	%mismatch	Tm
GERMLINE hVH1-39/JK5	CAACTTACTACTGTCAACAGAGT TACAGTACCCCTCCGATCACCTTCGGC				
1633-H106/108/111 F	CTTACTACTGTCAACA T AGT C ACAGTACCC A TCCGATCACCTTCG	47.0	45	6.7	79.0
1633-H105/106/108/111 F	CAACTTACTACTGTCA C CA T AGT C ACAGTACCC A TCCGATCACCTTCGGC	50.0	50	8.0	80.5
1633-H106/108/111 R	CGAAGGTGATCGGA T GGGTACTGT G ACT A TGTTGACAGTAGTAAG	47.0	45	6.7	79.0
1633-H105/106/108/111 R	GCCGAAGGTGATCGGA T GGGTACTGT G ACT A TGTTGACAGTAGTAAGTTG	50.0	50	8.0	80.5

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Primer	SEQ ID NO
GERMLINE hVK1-39/JK5	81
1633-H106/108/111 F	34
1633-H105/106/108/111 F	35
1633-H106/108/111 R	36
1633-H105/106/108/111 R	37

FIG. 7

Construction of VK1-39 HULC LTVECs

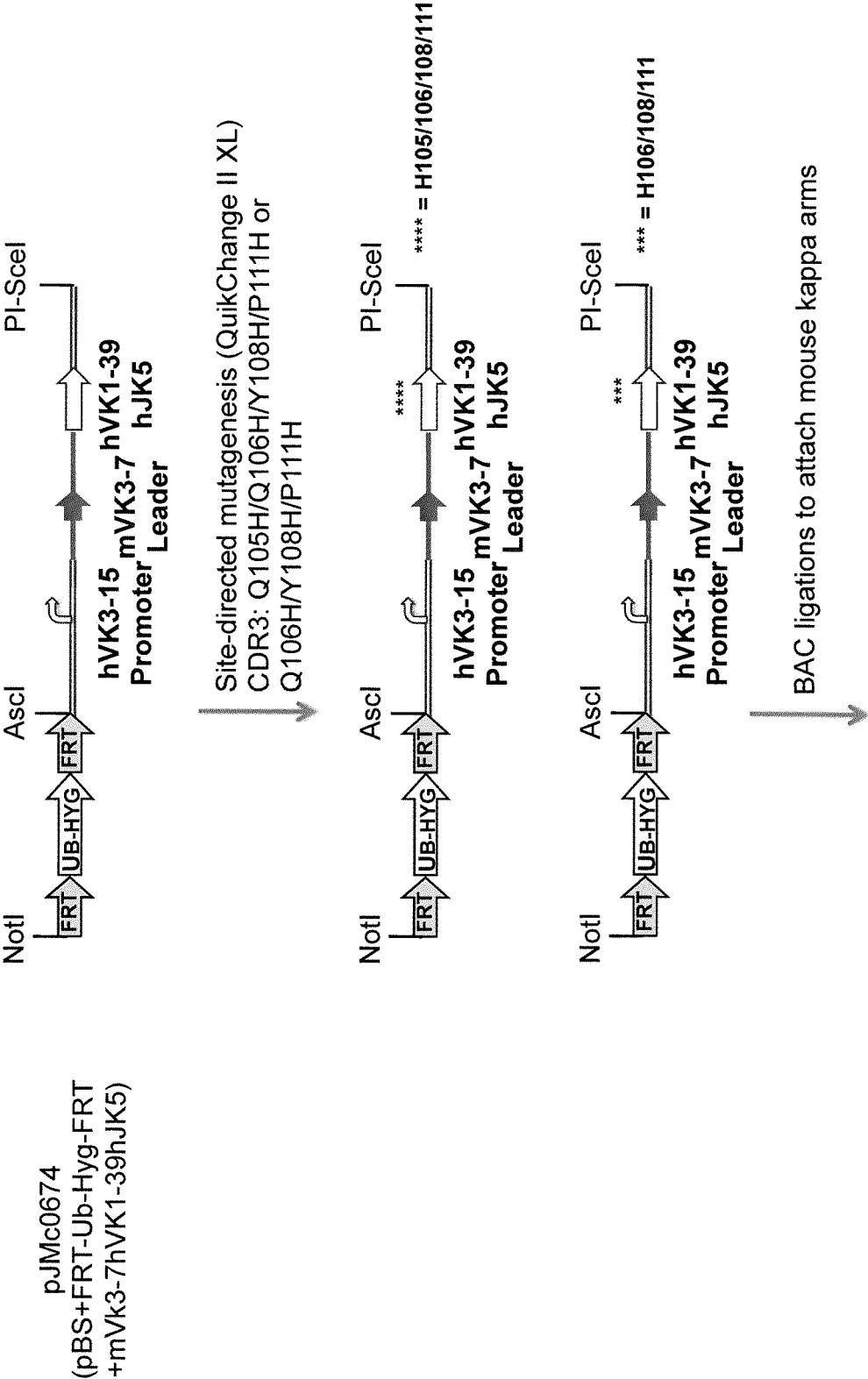


FIG. 8A

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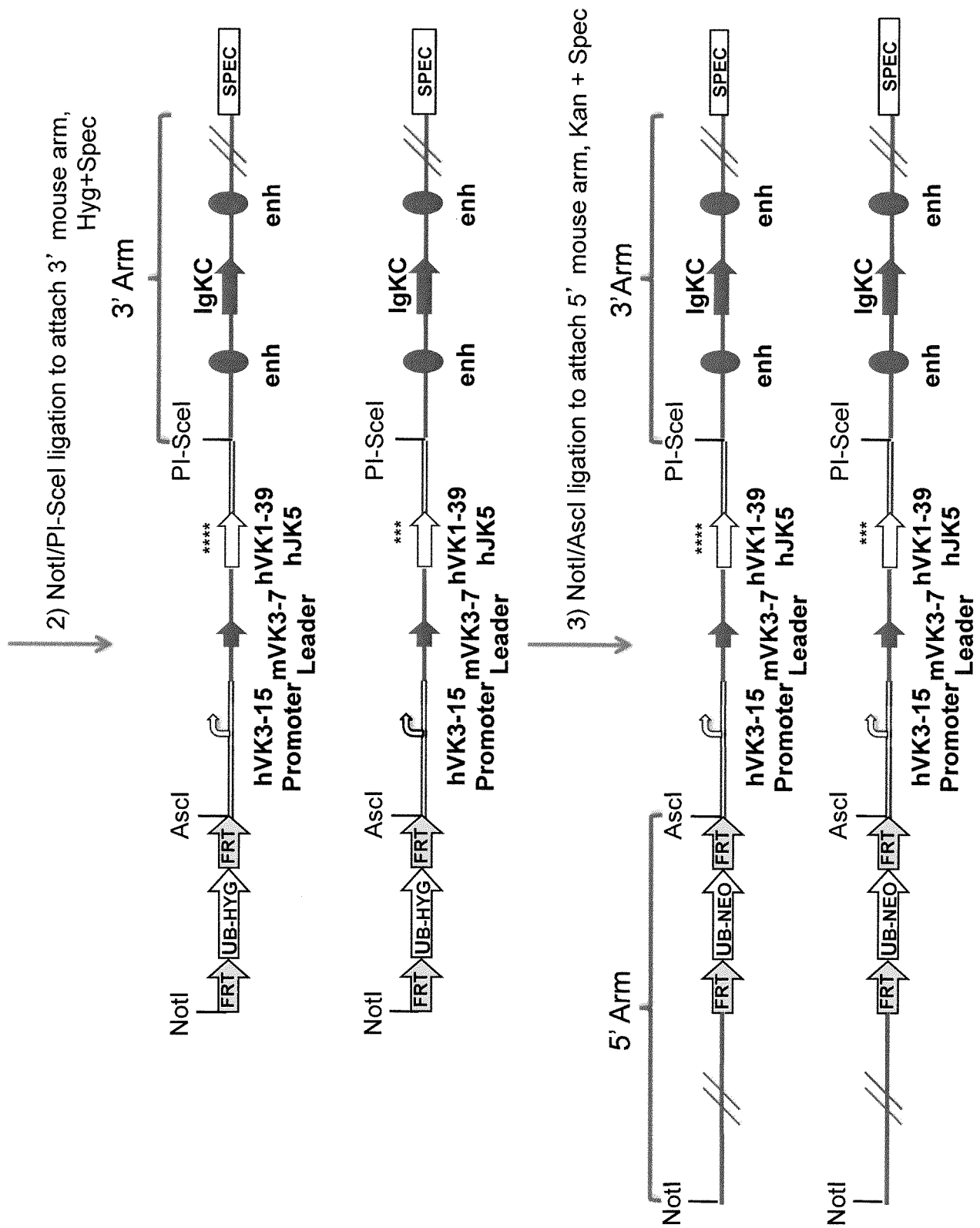


FIG. 8B

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(ULC-H105/106/108/111)

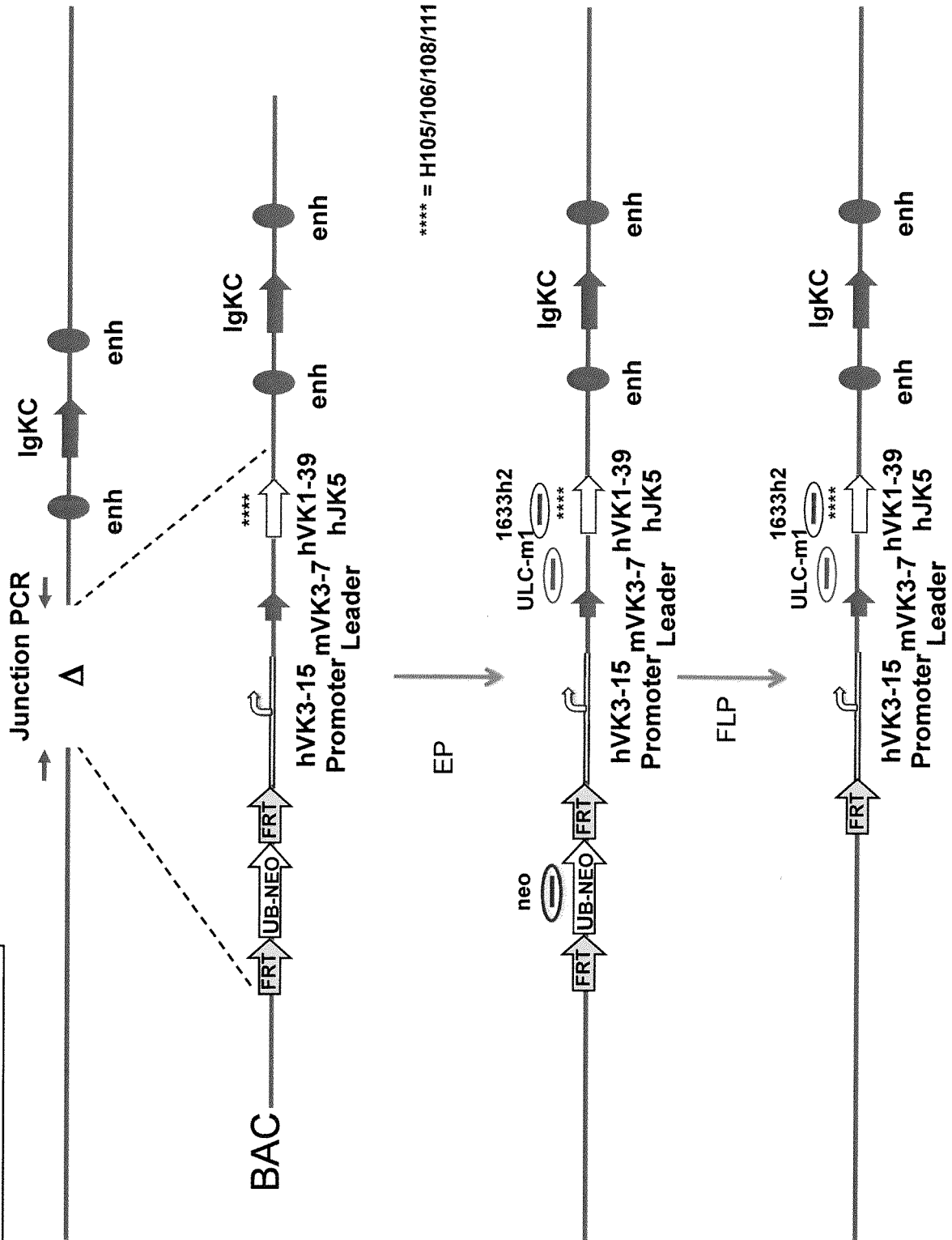
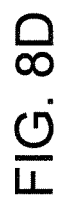


FIG. 8C



(ULC-H106/108/111)

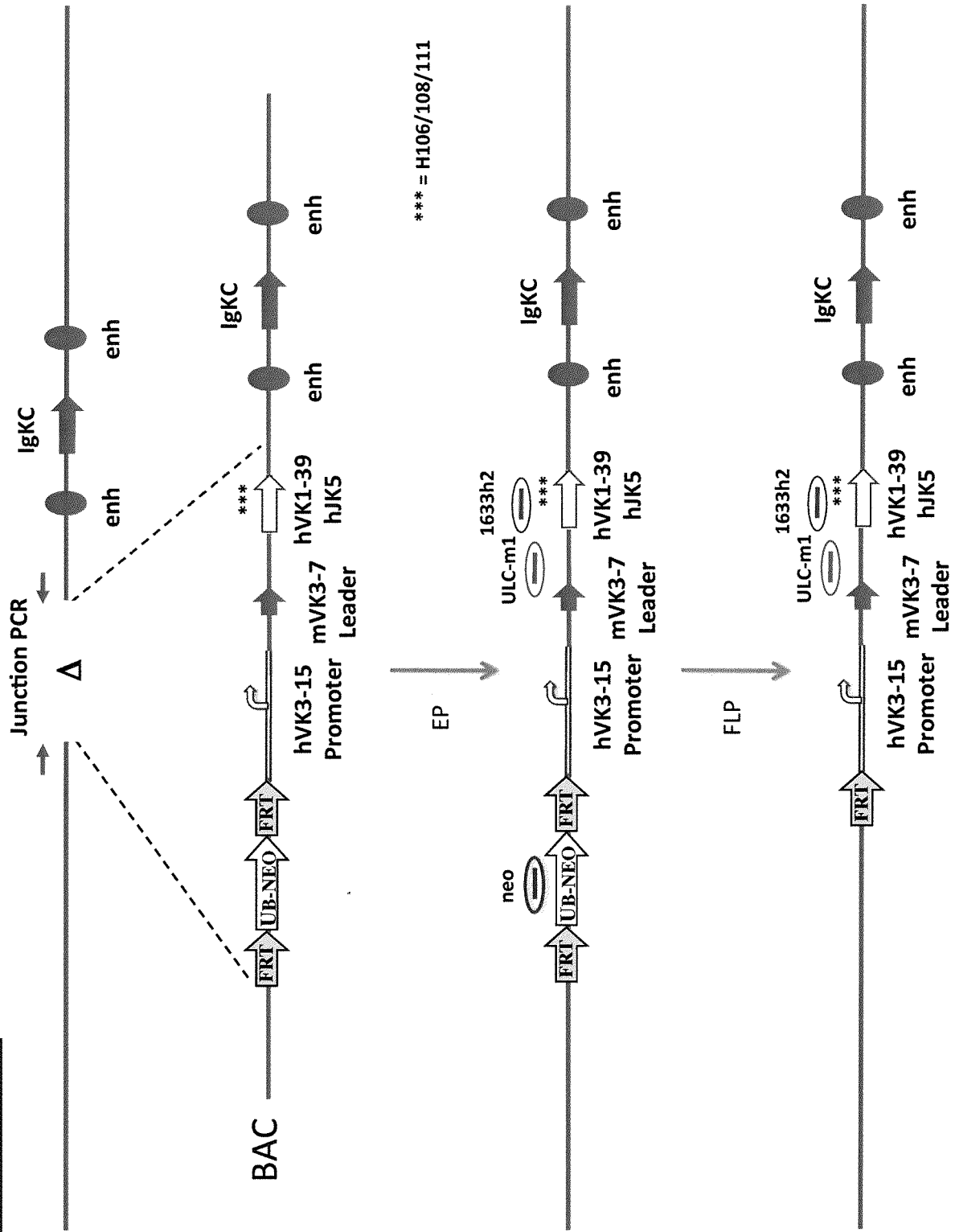


FIG. 8E

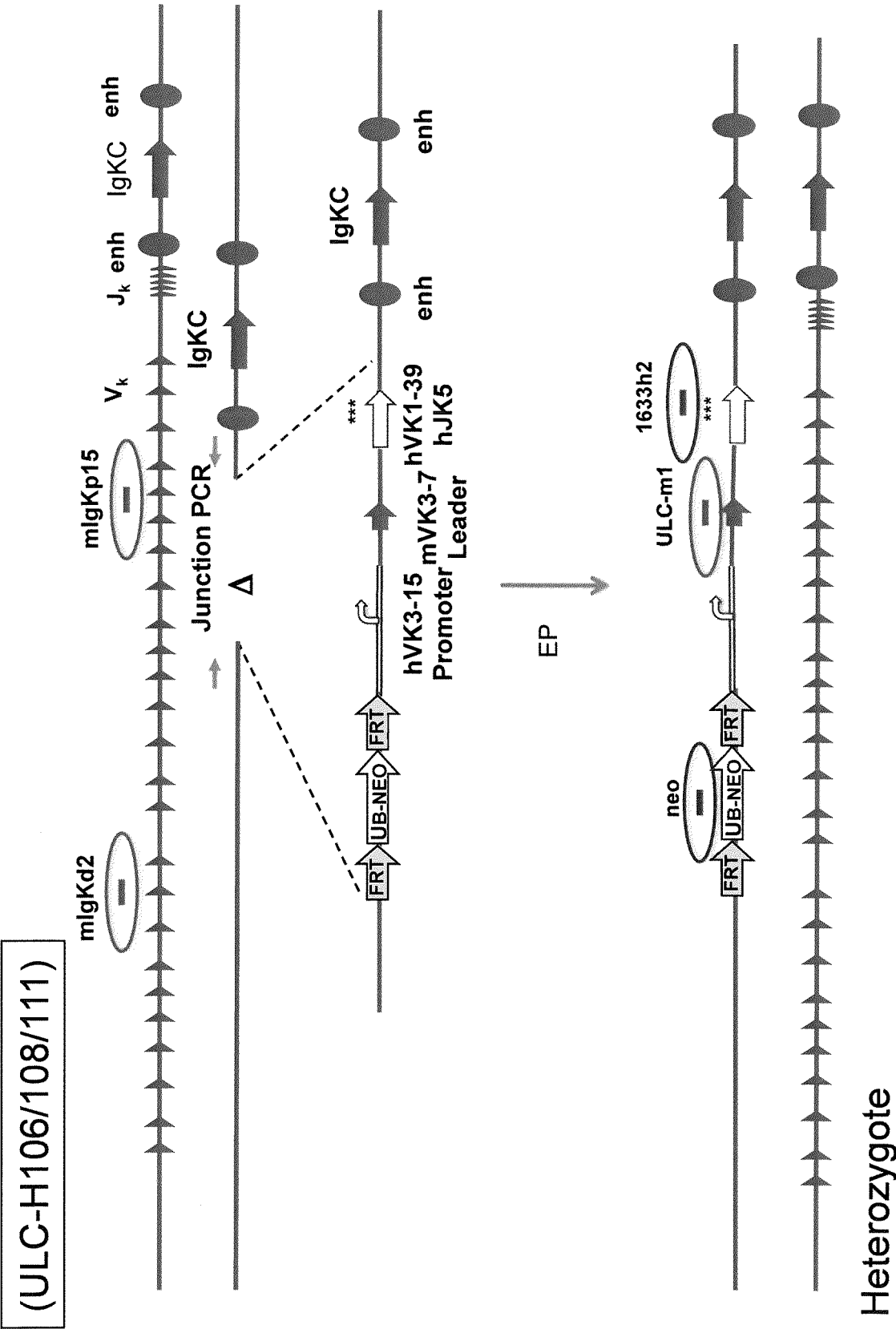


FIG. 8F

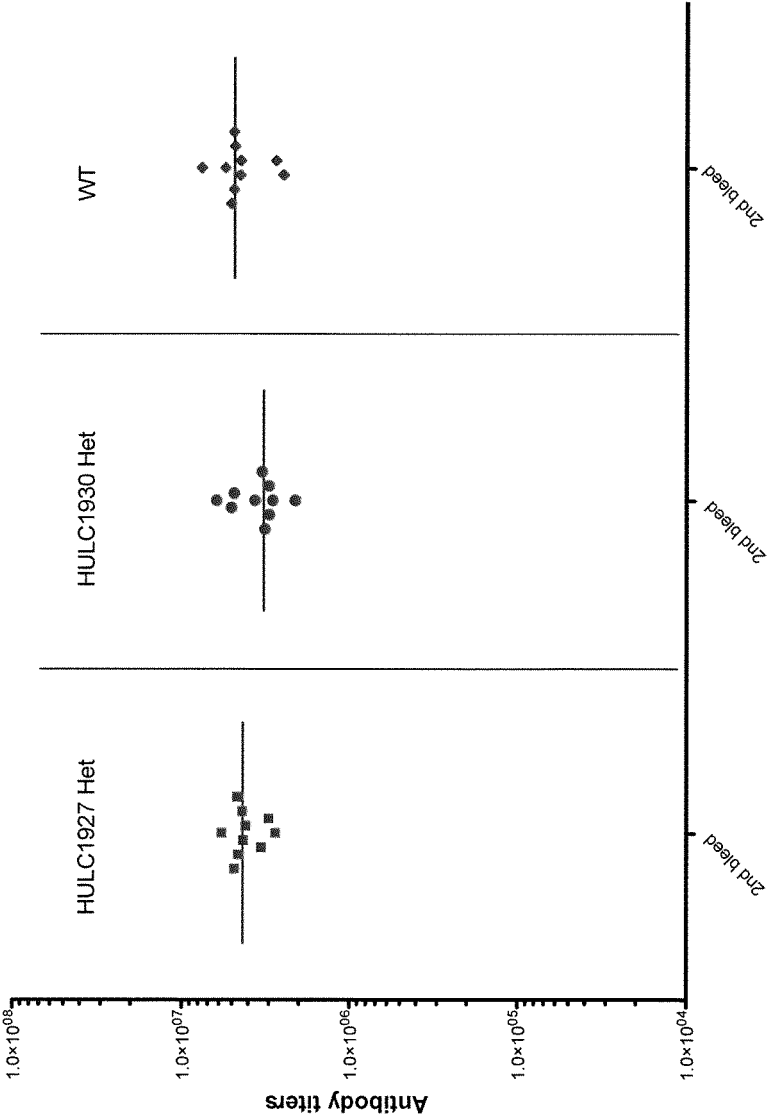


FIG. 9

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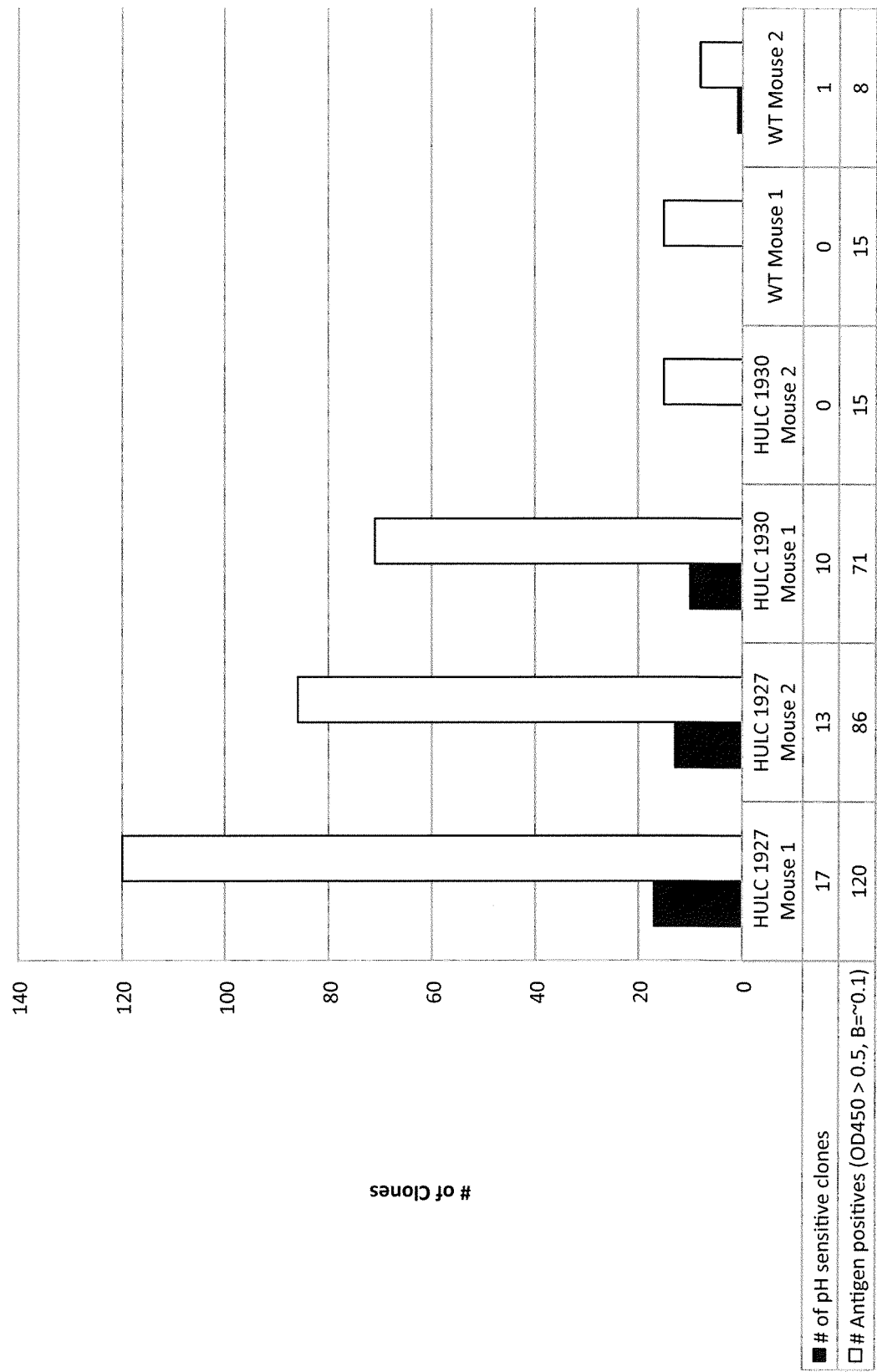


FIG. 10

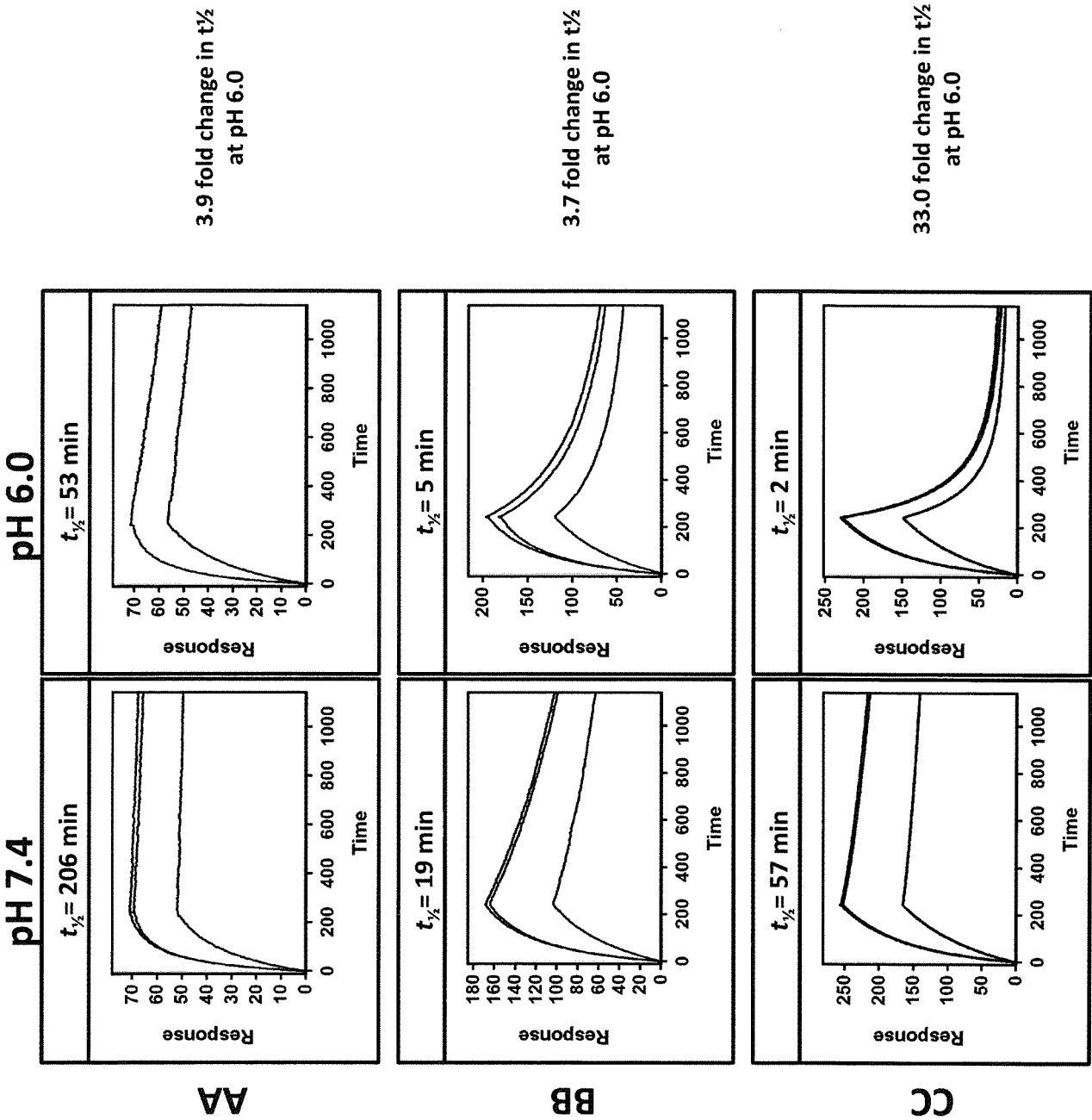


FIG. 11A

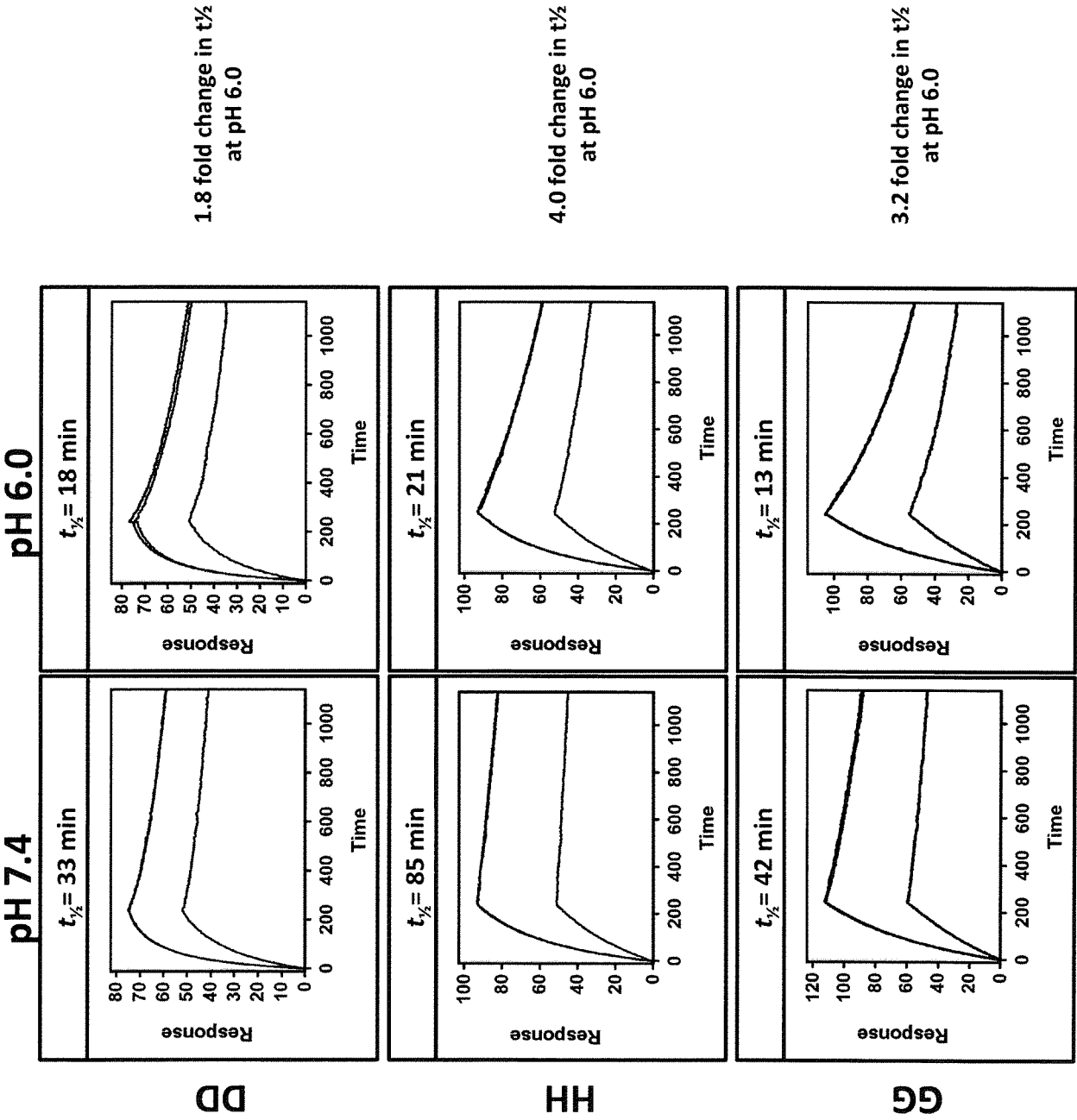


FIG. 11B

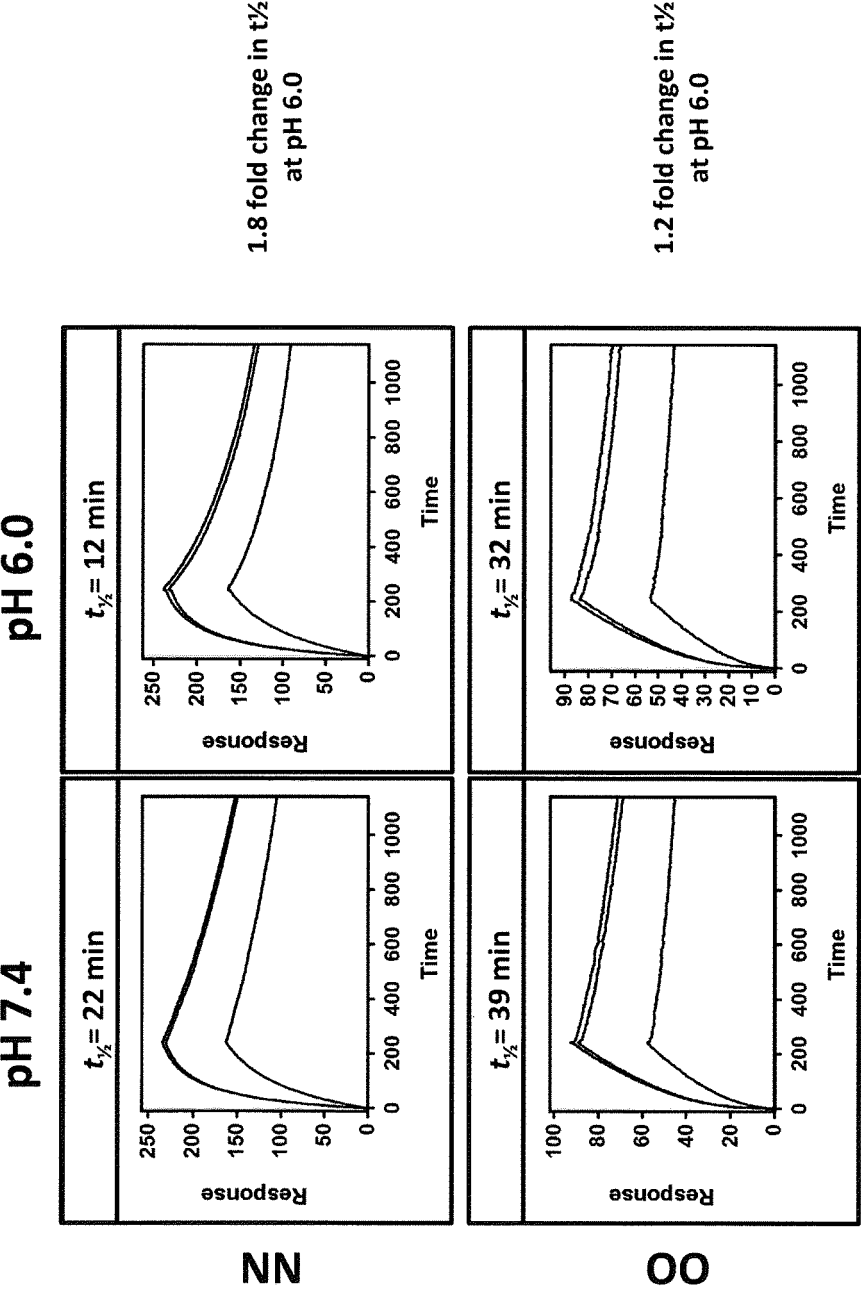


FIG. 11C

	105	106	107	108	109	110	111	
WT	Q	Q	Y	G	S	S	P	SEQ.ID NO:75
	CAG	CAG	TAT	GGT	AGC	TCA	CCT	SEQ.ID NO:74
H105/106/107/109	H	H	H	G	H	S	P	SEQ.ID NO:77
	CAT	CAC	CAT	GGT	CAC	TCA	CCT	SEQ.ID NO:76
H105/106/109	H	H	Y	G	H	S	P	SEQ.ID NO:79
	CAT	CAC	TAT	GGT	CAC	TCA	CCT	SEQ.ID NO:78

FIG. 12

Site-directed mutagenesis primers for Histidine substitutions in CDR3 of VK3-20JK1 ULC plasmid

Primer name	Sequence	%GC	N	mismatches	Tm
GERMLINE hVK3-20	GATTTTGCAGTGTATTACTGTCTCAGCAGTATGGTAGCTCACCTTGGACGTTTCGGC				
hVK3-20 (H105/106/107/109) F	GATTTTGCAGTGTATTACTGTCTC ATCA CC AT GGT CA CTCACCTTGGACGTTTCGGC	48	54	5	79.5
hVK3-20 (H105/106/107/109) R	GCCGAACGTCCAAGGTGAG TG ACCAT GGTGA TGACAGTAATACACTGCAAAATC	48	54	5	79.5
hVK3-20 (H105/106/109) F	GCAGTGTATTACTGTCTC ATCA CTATGGT CA CTCACCTTGGACGTTTCGG	49	47	4	78.7
hVK3-20 (H105/106/109) R	CCGAACGTCCAAGGTGAG TG ACCATA GTGA TGACAGTAATACACTGC	49	47	4	79.7

Primer	SEQ ID NO
GERMLINE hVK3-20/JK1	60
hVK3-20 H105/106/107/109 F	61
hVK3-20 H105/106/107/109 R	62
hVK3-20 H105/106/109 F	63
hVK3-20 H105/106/109 R	64

FIG. 13

Construction of VK3-20 HULC LTVECs

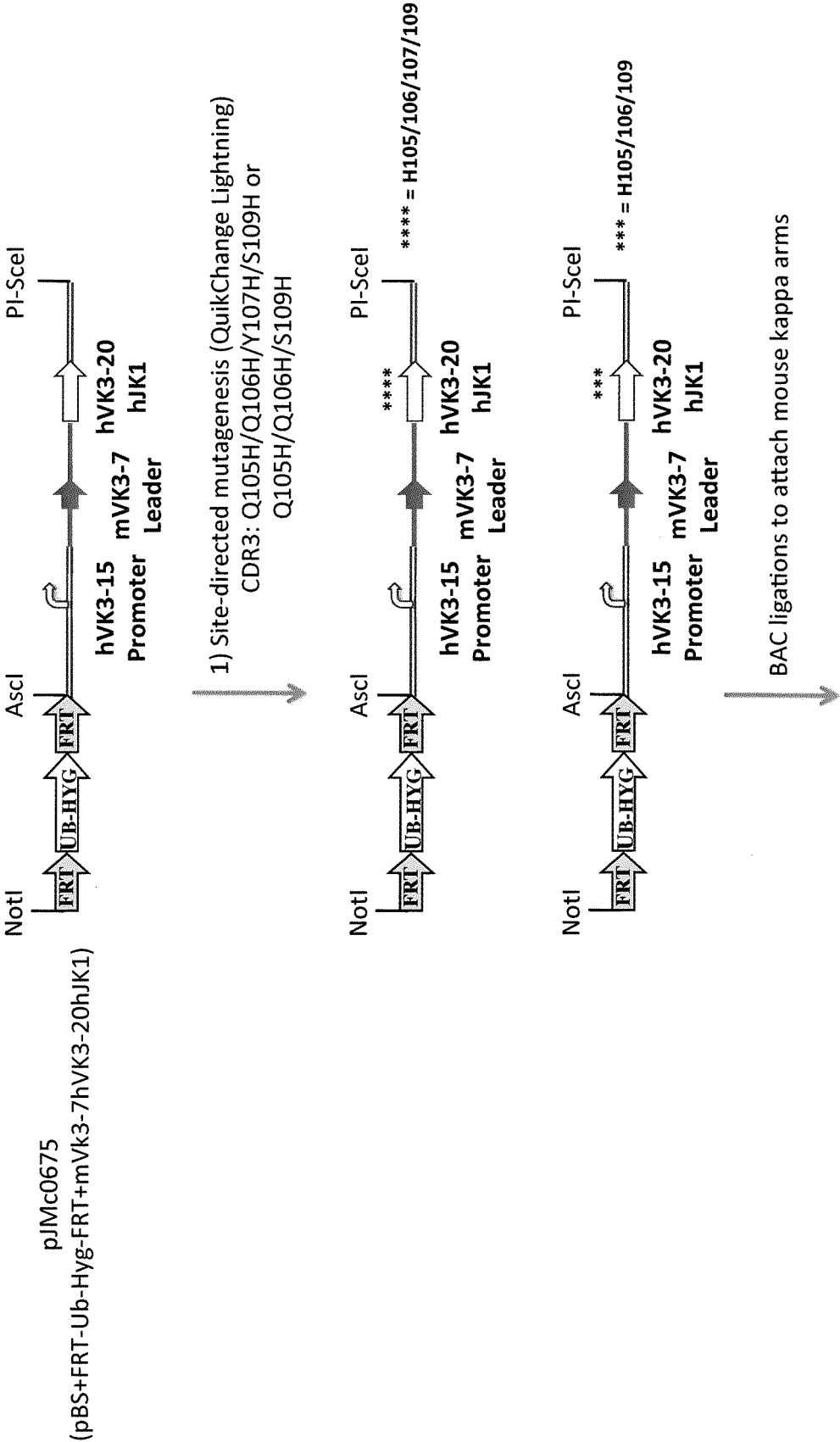


FIG. 14A

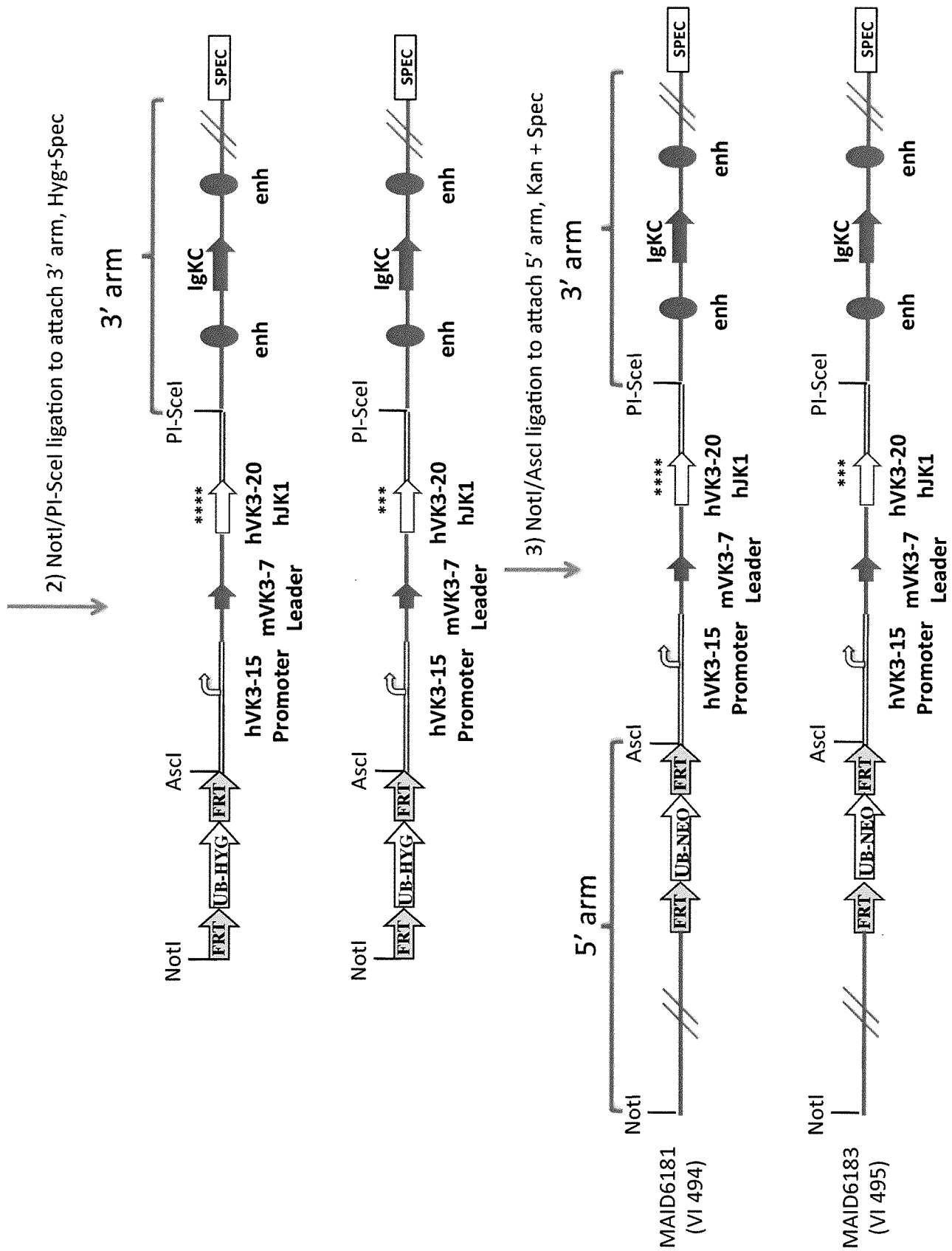


FIG. 14B

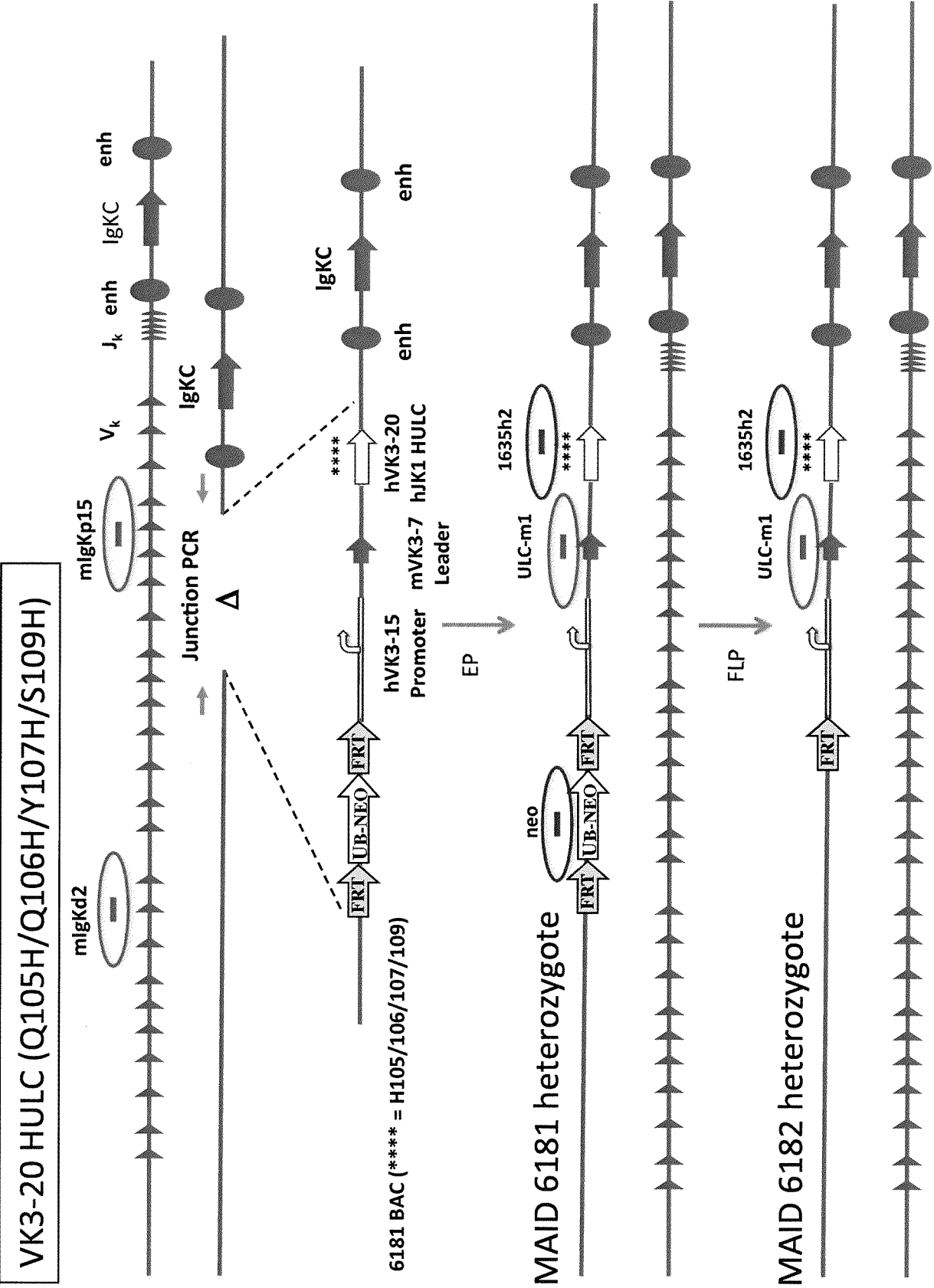


FIG. 14C

VK3-20 HULC (Q105H/Q106H/S109H)

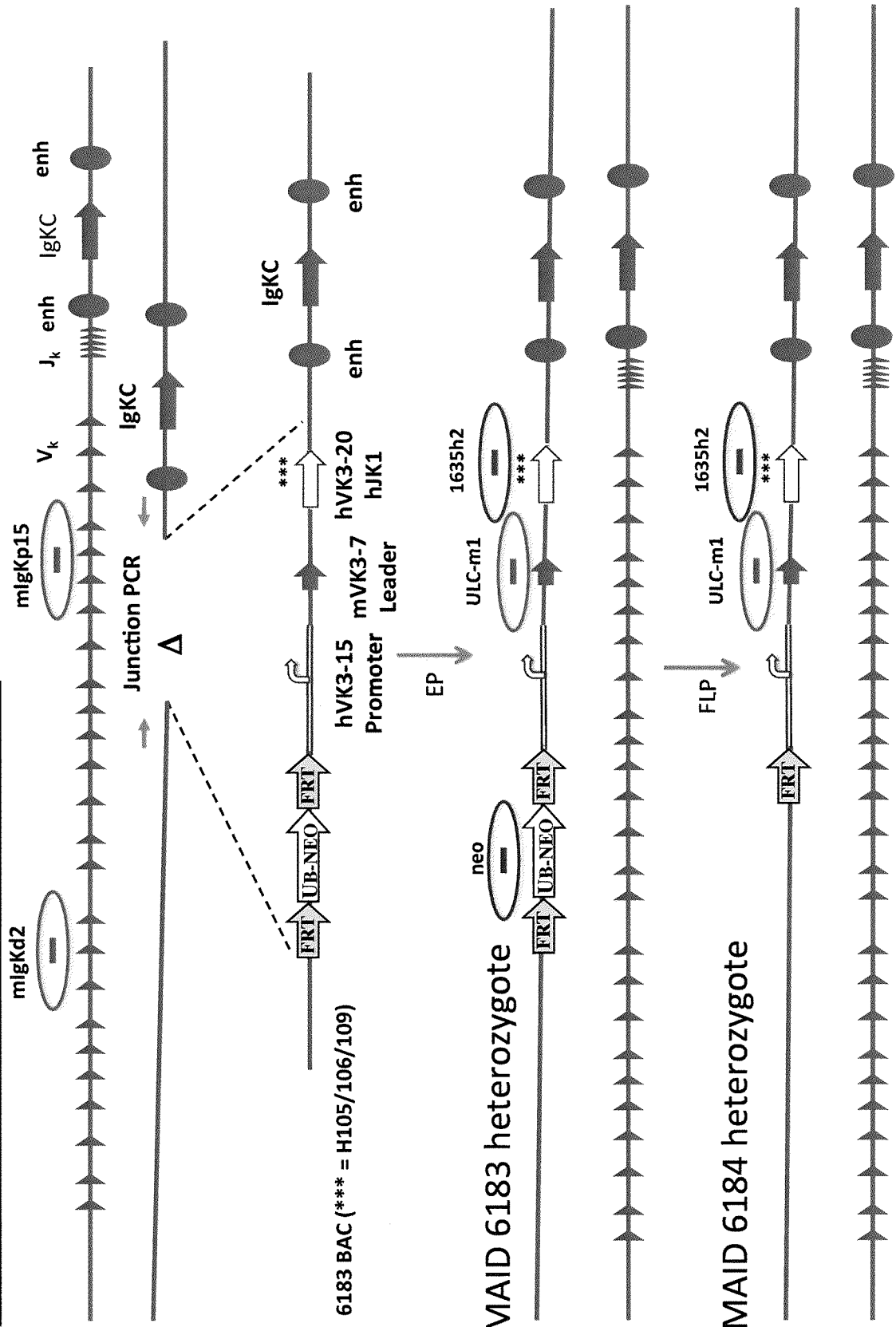


FIG. 14D