

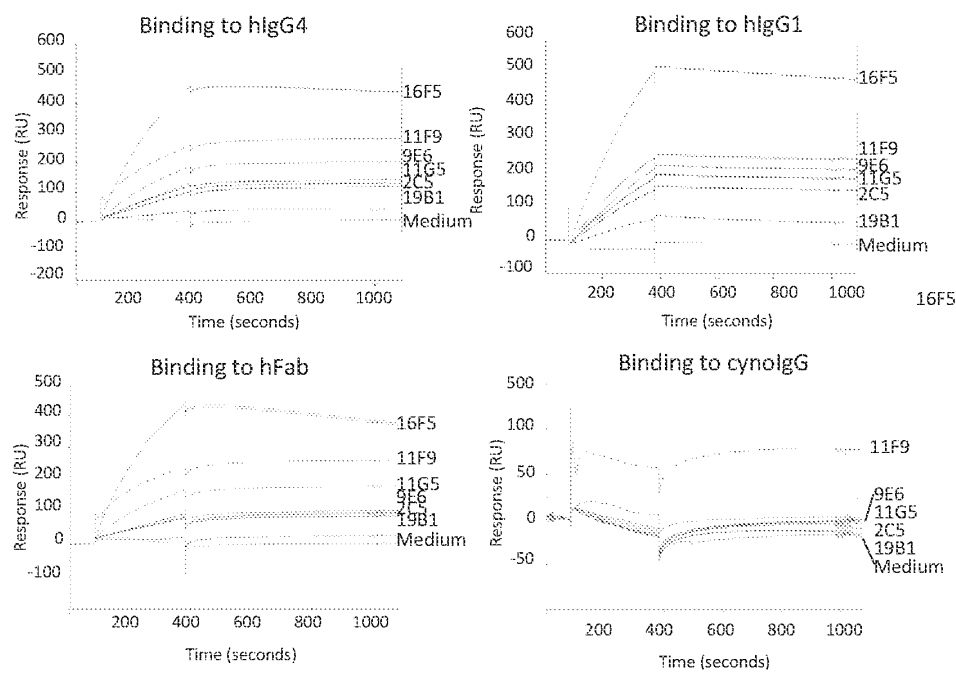


FIG. 1

hlgG_Fab_16F5_H	Leader 1-19 aa	Variable domain 20-141 aa	
hlgG_Fab_11F9_H	METGLRWLLLVAVLKGVCQQQLLEESGGGLVKGPGTILITCTASGFSFSSSYIMCWVRQA	60	
hlgG_Fab_9B6_H	METGLRWLLLVAVLKGVCQQQLLEESGGGLVKGPGTILITCTASGFSFSSSYIMCWVRQA	60	
hlgG_Fab_11G5_H	METGLRWLLLVAVLKGVCQQQLLEESGGGLVKGPGTILITCTASGFSFSSSYIMCWVRQA	59	
hlgG_Fab_2C5_H	METGLRWLLLVAVLKGVCQQQLLEESGGGLVKGPGTILITCTASGFSFSSSYIMCWVRQA	59	
hlgG_Fab_19B1_H	METGLRWLLLVAVLKGVCQQQLLEESGGGLVKGPGTILITCTASGFSFSSSYIMCWVRQA	60	

hlgG_Fab_16F5_H	PGKGLLELIACINTGSSGGSTWYATWAKGRETISKTSETVTVLQMTSLTAADTATYFCARDR	120	
hlgG_Fab_11F9_H	PGKGLLELIACINTGSSGGSTWYATWAKGRETISKTSETVTVLQMTSLTAADTATYFCARDR	118	
hlgG_Fab_9B6_H	PGKGLLELIACINTGSSGGSTWYATWAKGRETISKTSETVTVLQMTSLTAADTATYFCARDR	117	
hlgG_Fab_11G5_H	PGKGLLELIACINTGSSGGSTWYATWAKGRETISKTSETVTVLQMTSLTAADTATYFCARDR	118	
hlgG_Fab_2C5_H	PGKGLLELIACINTGSSGGSTWYATWAKGRETISKTSETVTVLQMTSLTAADTATYFCARDR	119	
hlgG_Fab_19B1_H	PGKGLLELIACINTGSSGGSTWYATWAKGRETISKTSETVTVLQMTSLTAADTATYFCARDR	119	

	Constant region 142 aa - end		
hlgG_Fab_16F5_H	DVGSLHDSLLGLWGQGLTVTVSPGPKAPSVFPLAPCCGDTSPSTVTILGLCLVKGYLPEPVT	180	
hlgG_Fab_11F9_H	DVGSLHDSLLGLWGQGLTVTVSPGPKAPSVFPLAPCCGDTSPSTVTILGLCLVKGYLPEPVT	177	
hlgG_Fab_9B6_H	DVGSLHDSLLGLWGQGLTVTVSPGPKAPSVFPLAPCCGDTSPSTVTILGLCLVKGYLPEPVT	176	
hlgG_Fab_11G5_H	DVGSLHDSLLGLWGQGLTVTVSPGPKAPSVFPLAPCCGDTSPSTVTILGLCLVKGYLPEPVT	177	
hlgG_Fab_2C5_H	DVGSLHDSLLGLWGQGLTVTVSPGPKAPSVFPLAPCCGDTSPSTVTILGLCLVKGYLPEPVT	178	
hlgG_Fab_19B1_H	DVGSLHDSLLGLWGQGLTVTVSPGPKAPSVFPLAPCCGDTSPSTVTILGLCLVKGYLPEPVT	178	

hlgG_Fab_16F5_H	VTWNSGTLINGVRTFFSVRQSSGLYSLSLVSVTSSSSQPVTCNVAHPATNTKVDKTVAPS	240	
hlgG_Fab_11F9_H	VTWNSGTLINGVRTFFSVRQSSGLYSLSLVSVTSSSSQPVTCNVAHPATNTKVDKTVAPS	237	
hlgG_Fab_9B6_H	VTWNSGTLINGVRTFFSVRQSSGLYSLSLVSVTSSSSQPVTCNVAHPATNTKVDKTVAPS	236	
hlgG_Fab_11G5_H	VTWNSGTLINGVRTFFSVRQSSGLYSLSLVSVTSSSSQPVTCNVAHPATNTKVDKTVAPS	237	
hlgG_Fab_2C5_H	VTWNSGTLINGVRTFFSVRQSSGLYSLSLVSVTSSSSQPVTCNVAHPATNTKVDKTVAPS	238	
hlgG_Fab_19B1_H	VTWNSGTLINGVRTFFSVRQSSGLYSLSLVSVTSSSSQPVTCNVAHPATNTKVDKTVAPS	238	

hlgG_Fab_16F5_H	TCSEKMPCEPPELPGGFSVPIFPEPKPDITLMISRTPEVTCVVDVSDQDPEVQFTWYINNE	300	
hlgG_Fab_11F9_H	TCSEKMPCEPPELPGGFSVPIFPEPKPDITLMISRTPEVTCVVDVSDQDPEVQFTWYINNE	297	
hlgG_Fab_9B6_H	TCSEKMPCEPPELPGGFSVPIFPEPKPDITLMISRTPEVTCVVDVSDQDPEVQFTWYINNE	296	
hlgG_Fab_11G5_H	TCSEKMPCEPPELPGGFSVPIFPEPKPDITLMISRTPEVTCVVDVSDQDPEVQFTWYINNE	297	
hlgG_Fab_2C5_H	TCSEKMPCEPPELPGGFSVPIFPEPKPDITLMISRTPEVTCVVDVSDQDPEVQFTWYINNE	298	
hlgG_Fab_19B1_H	TCSEKMPCEPPELPGGFSVPIFPEPKPDITLMISRTPEVTCVVDVSDQDPEVQFTWYINNE	298	

hlgG_Fab_16F5_H	QVKTARPELREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ	360	
hlgG_Fab_11F9_H	QVKTARPELREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ	357	
hlgG_Fab_9B6_H	QVKTARPELREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ	356	
hlgG_Fab_11G5_H	QVKTARPELREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ	357	
hlgG_Fab_2C5_H	QVKTARPELREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ	358	
hlgG_Fab_19B1_H	QVKTARPELREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ	358	

hlgG_Fab_16F5_H	PLEPKVYTMGPPEELSSRSVSLTCMINGFYPSDI SVEWEKNGKAEDNYKTTPTVLSDSG	420	
hlgG_Fab_11F9_H	PLEPKVYTMGPPEELSSRSVSLTCMINGFYPSDI SVEWEKNGKAEDNYKTTPTVLSDSG	417	
hlgG_Fab_9B6_H	PLEPKVYTMGPPEELSSRSVSLTCMINGFYPSDI SVEWEKNGKAEDNYKTTPTVLSDSG	416	
hlgG_Fab_11G5_H	PLEPKVYTMGPPEELSSRSVSLTCMINGFYPSDI SVEWEKNGKAEDNYKTTPTVLSDSG	417	
hlgG_Fab_2C5_H	PLEPKVYTMGPPEELSSRSVSLTCMINGFYPSDI SVEWEKNGKAEDNYKTTPTVLSDSG	418	
hlgG_Fab_19B1_H	PLEPKVYTMGPPEELSSRSVSLTCMINGFYPSDI SVEWEKNGKAEDNYKTTPTVLSDSG	418	

hlgG_Fab_16F5_H	SYFLYSKLSVPTSEWQRGQDVFTCSVMHEALNNHYTKQKISRSFGK*	465 (SEQ ID NO: 67)	
hlgG_Fab_11F9_H	SYFLYSKLSVPTSEWQRGQDVFTCSVMHEALNNHYTKQKISRSFGK*	462 (SEQ ID NO: 65)	
hlgG_Fab_9B6_H	SYFLYSKLSVPTSEWQRGQDVFTCSVMHEALNNHYTKQKISRSFGK*	461 (SEQ ID NO: 64)	
hlgG_Fab_11G5_H	SYFLYSKLSVPTSEWQRGQDVFTCSVMHEALNNHYTKQKISRSFGK*	462 (SEQ ID NO: 66)	
hlgG_Fab_2C5_H	SYFLYSKLSVPTSEWQRGQDVFTCSVMHEALNNHYTKQKISRSFGK*	462 (SEQ ID NO: 63)	
hlgG_Fab_19B1_H	SYFLYSKLSVPTSEWQRGQDVFTCSVMHEALNNHYTKQKISRSFGK*	463 (SEQ ID NO: 68)	

FIG. 2A

Leader: 1-22 aa Variable domain 23-132 aa

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hlgG_Fab_9E6_L  MDTRAPTQLLGLLLWLPGARCAVVMQTASPVSGAVGGTVTINCCQASQSISSSYLSWYQ  60
hlgG_Fab_11G5_L MDTRAPTQLLGLLLWLPGARCAVVMQTASPVSGAVGGTVTINCCQASQSISSSYLSWYQ  60
hlgG_Fab_2C5_L  MDTRAPTQLLGLLLWLPGARCAVVMQTASPVSGAVGGTVTINCCQASQSISSSYLSWYQ  59
hlgG_Fab_19B1_L MDTRAPTQLLGLLLWLPGARCAVVMQTASPVSGAVGGTVTINCCQASQSISSSYLSWYQ  59
hlgG_Fab_11F9_L MDTRAPTQLLGLLLWLPGARCAVVMQTASPVSGAVGGTVTINCCQASQSISSSYLSWYQ  59
hlgG_Fab_16F5_L MDTRAPTQLLGLLLWLPGARCAVVMQTASPVSGAVGGTVTINCCQASQSISSSYLSWYQ  59
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hlgG_Fab_9E6_L  QKPGQPPKLLIYGASTLASGVPSRFKGGSGGTQFTLTISGVQCDDAATYYCAYDAYRLSS  120
hlgG_Fab_11G5_L QKPGQPPKLLIYGASTLASGVPSRFKGGSGGTQFTLTISGVQCDDAATYYCAYDAYRLSS  120
hlgG_Fab_2C5_L  QKPGQPPKLLIYFDASDLASGVPSRFKGGSGGTQFTLTISGVQCDDAATYYCAYDAYRLSS  118
hlgG_Fab_19B1_L QKPGQPPKLLIYFDASDLASGVPSRFKGGSGGTQFTLTISGVQCDDAATYYCAYDAYRLSS  118
hlgG_Fab_11F9_L QKPGQPPKLLIYFDASDLASGVPSRFKGGSGGTQFTLTISGVQCDDAATYYCAYDAYRLSS  118
hlgG_Fab_16F5_L QKPGQPPKLLIYFDASDLASGVPSRFKGGSGGTQFTLTISGVQCDDAATYYCAYDAYRLSS  118
*****
Constant region 133 aa - end
hlgG_Fab_9E6_L  EKNIFGGGTEVVKGDVAPTVLIFFPAADQVATGTVTIICVANKYFPDVTVTWEVDGTT  180
hlgG_Fab_11G5_L EKNIFGGGTEVVKGDVAPTVLIFFPAADQVATGTVTIICVANKYFPDVTVTWEVDGTT  180
hlgG_Fab_2C5_L  EKNIFGGGTEVVKGDVAPTVLIFFPAADQVATGTVTIICVANKYFPDVTVTWEVDGTT  178
hlgG_Fab_19B1_L EKNIFGGGTEVVKGDVAPTVLIFFPAADQVATGTVTIICVANKYFPDVTVTWEVDGTT  178
hlgG_Fab_11F9_L EKNIFGGGTEVVKGDVAPTVLIFFPAADQVATGTVTIICVANKYFPDVTVTWEVDGTT  178
hlgG_Fab_16F5_L EKNIFGGGTEVVKGDVAPTVLIFFPAADQVATGTVTIICVANKYFPDVTVTWEVDGTT  178
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hlgG_Fab_9E6_L  QTTGIENSKTPQNSADCTYNLSSSTLTSTQYNSHKEYTCKVTQGTTSVVQSFNPGDC* 238 (SEQ ID NO:70)
hlgG_Fab_11G5_L QTTGIENSKTPQNSADCTYNLSSSTLTSTQYNSHKEYTCKVTQGTTSVVQSFNPGDC* 238 (SEQ ID NO:72)
hlgG_Fab_2C5_L  QTTGIENSKTPQNSADCTYNLSSSTLTSTQYNSHKEYTCKVTQGTTSVVQSFNPGDC* 236 (SEQ ID NO:69)
hlgG_Fab_19B1_L QTTGIENSKTPQNSADCTYNLSSSTLTSTQYNSHKEYTCKVTQGTTSVVQSFNPGDC* 236 (SEQ ID NO:74)
hlgG_Fab_11F9_L QTTGIENSKTPQNSADCTYNLSSSTLTSTQYNSHKEYTCKVTQGTTSVVQSFNPGDC* 236 (SEQ ID NO:71)
hlgG_Fab_16F5_L QTTGIENSKTPQNSADCTYNLSSSTLTSTQYNSHKEYTCKVTQGTTSVVQSFNPGDC* 236 (SEQ ID NO:73)
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FIG. 2B

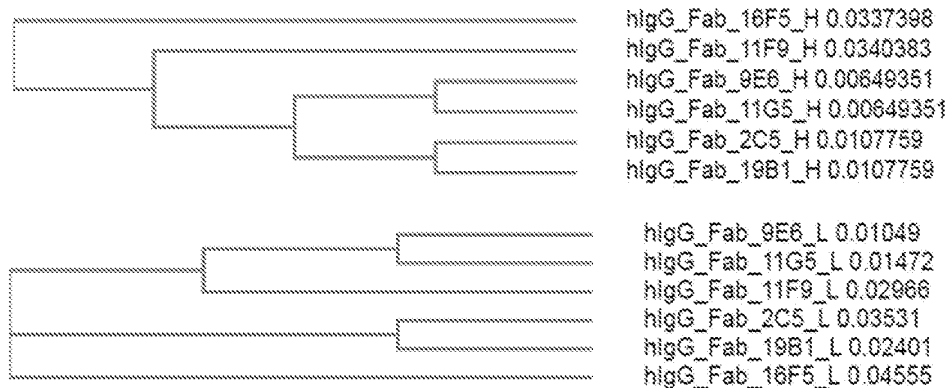


FIG. 2C

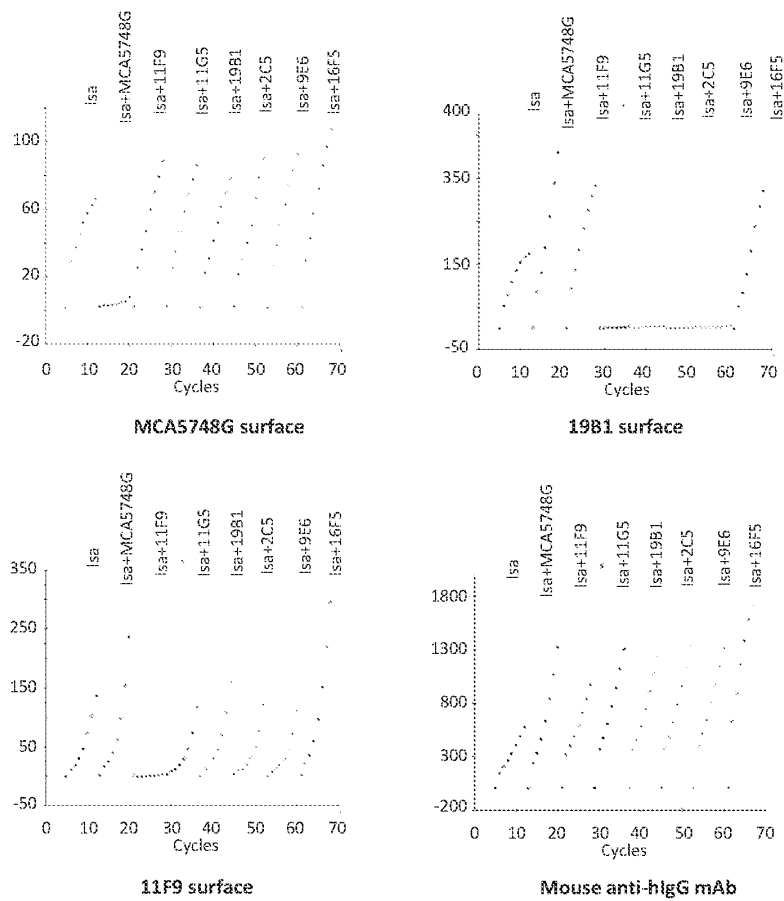
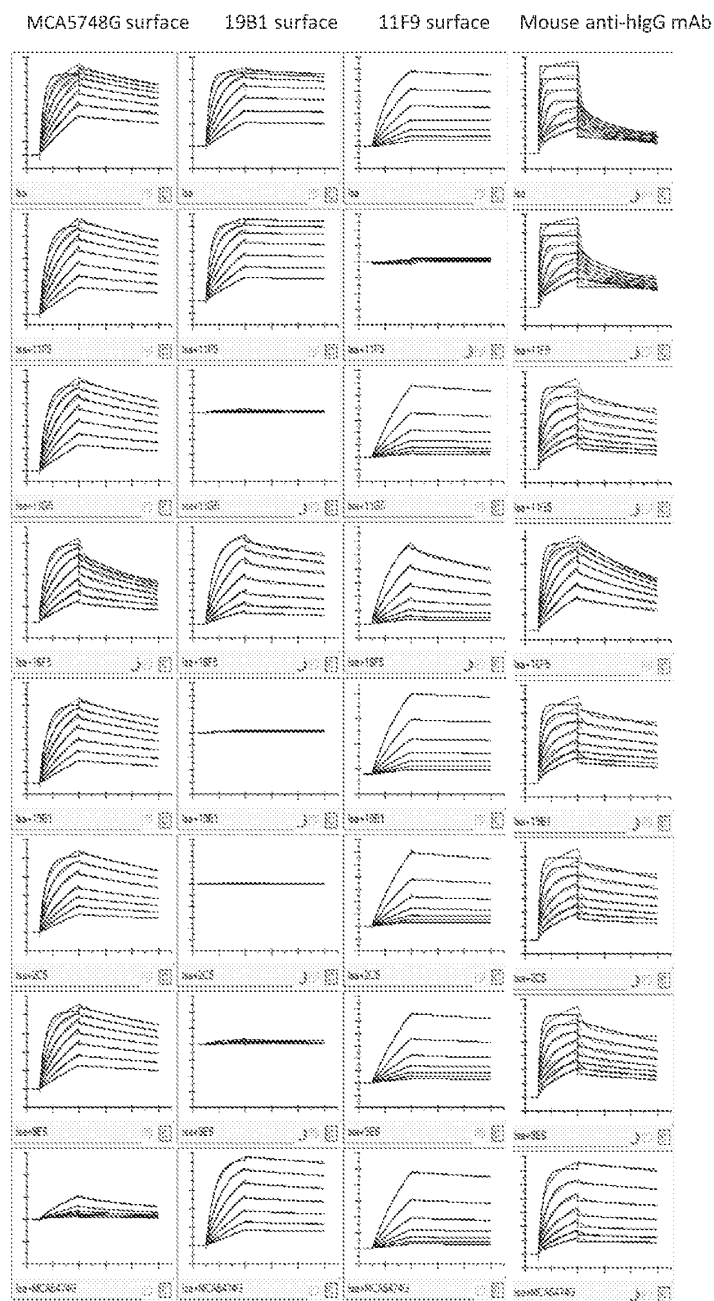


FIG. 3A



Overlay Graph

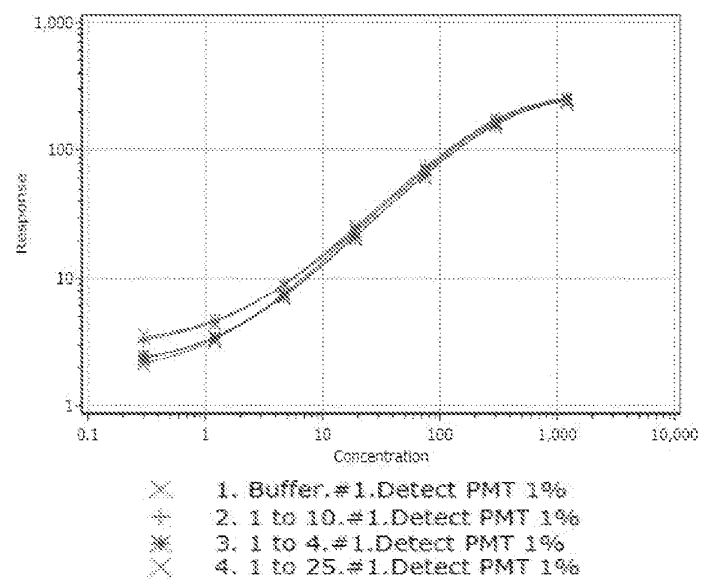


FIG. 4A

Standard Curve Graph

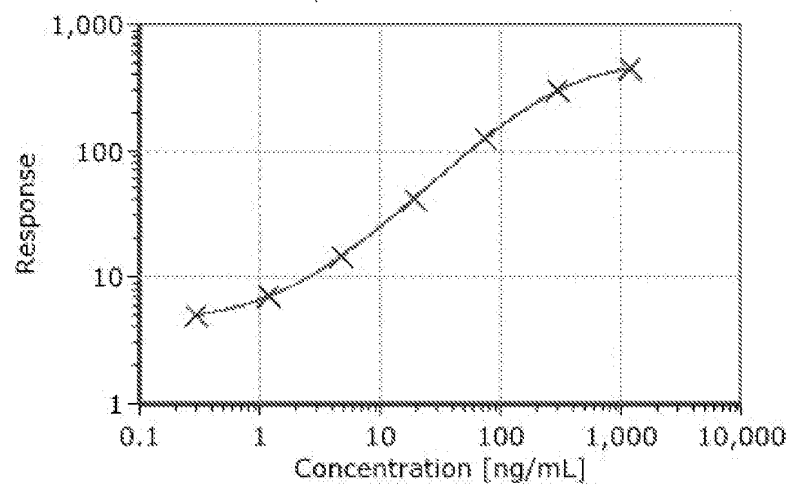


FIG. 4B

Quality Controls

Identity	Expected Conc [ng/ml]	Response	S/B	Calc Conc [ng/ml]	Average Conc [ng/ml]	CY Conc [%]	Bias [%]	Average Bias [%]	Average Response	CV Response [%]	Dilution	CD ID	CD Struct
WQC	0.500	5.86	1.29	0.657	0.647	2.27	9.55	7.82	5.86	0.566	1.00	0004321-183	C5
WQC	0.600	5.81	1.28	0.617	0.647	2.27	6.10	7.82	5.86	0.566	1.00	0004321-183	C6
LQC	40.0	68.6	15.0	34.8	36.9	4.30	-13.0	-10.2	70.3	3.48	1.00	0004321-183	C3
LQC	40.0	71.0	15.6	37.0	35.9	4.30	-7.62	-10.2	70.3	3.46	1.00	0004321-183	C4
HQC	750	400	87.7	650	796	30.9	-9.32	6.46	414	4.66	1.00	0004321-183	C1
HQC	750	427	93.6	917	796	30.9	22.2	8.46	414	4.66	1.00	0004321-183	C2

FIG. 4C

FIG. 5A Overlay Graph

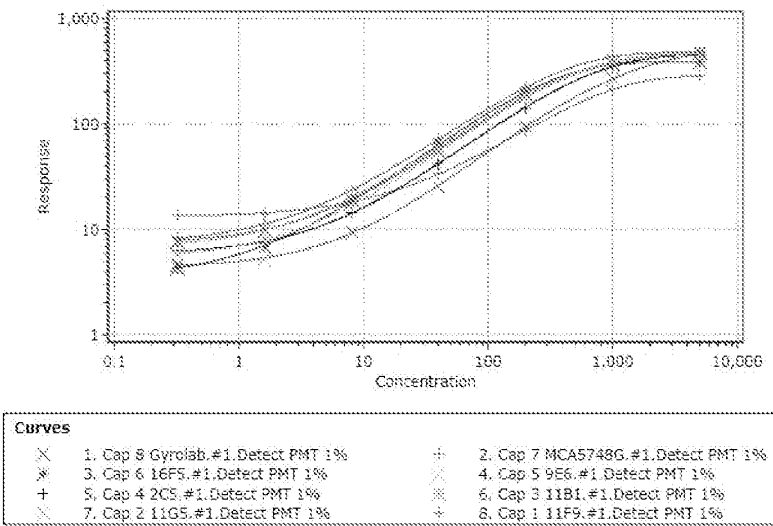
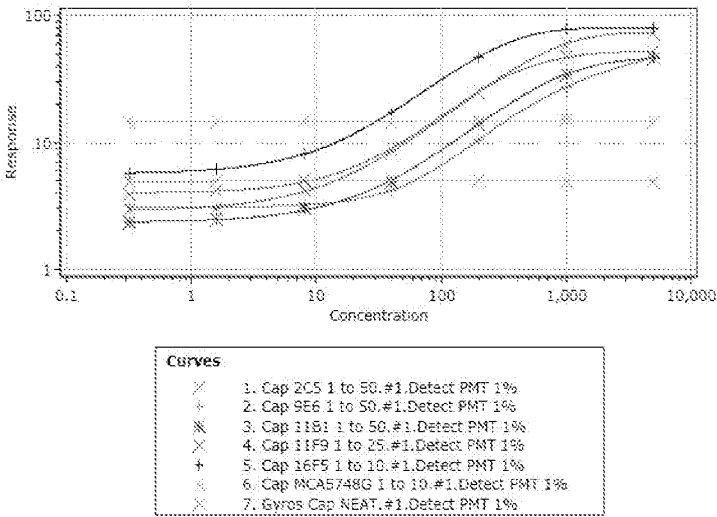


FIG. 5B Overlay Graph



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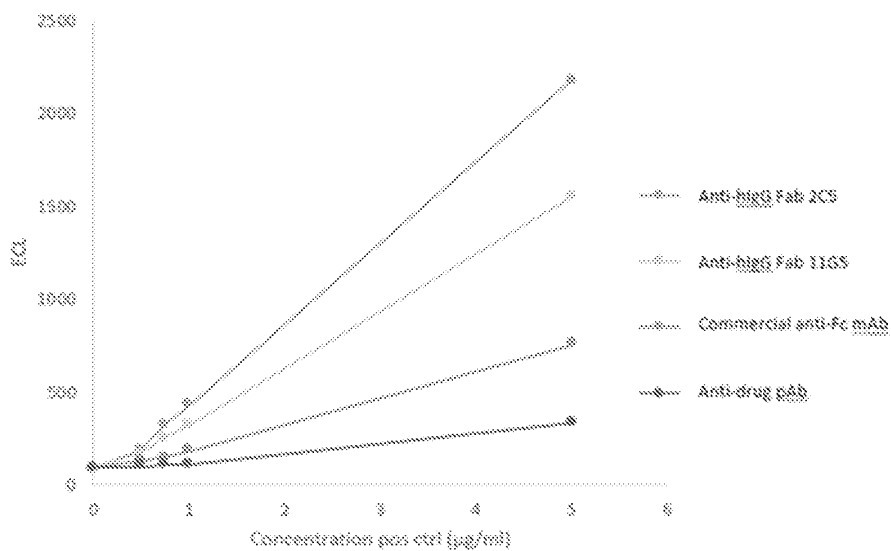


FIG. 6A

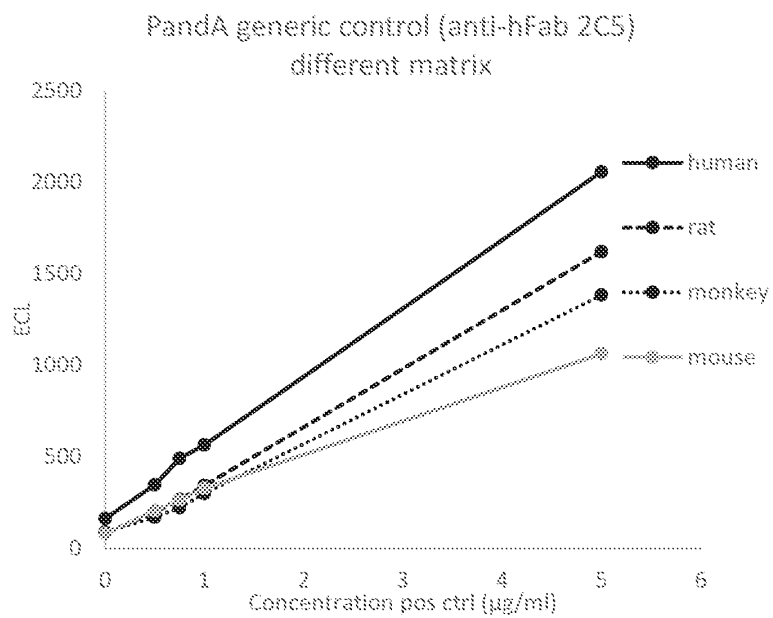


FIG. 6B

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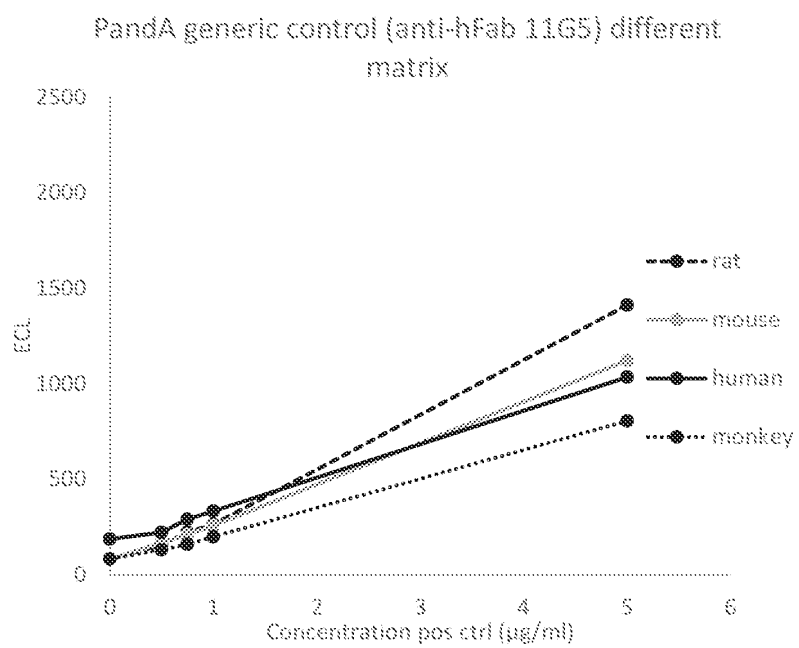


FIG. 6C