

FIG. 1

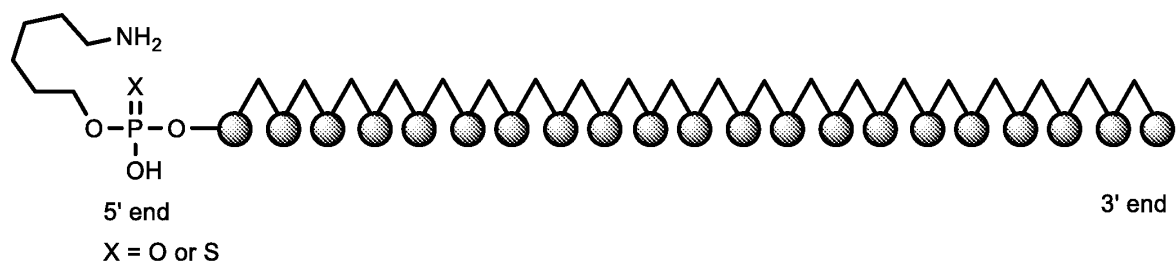


FIG. 2

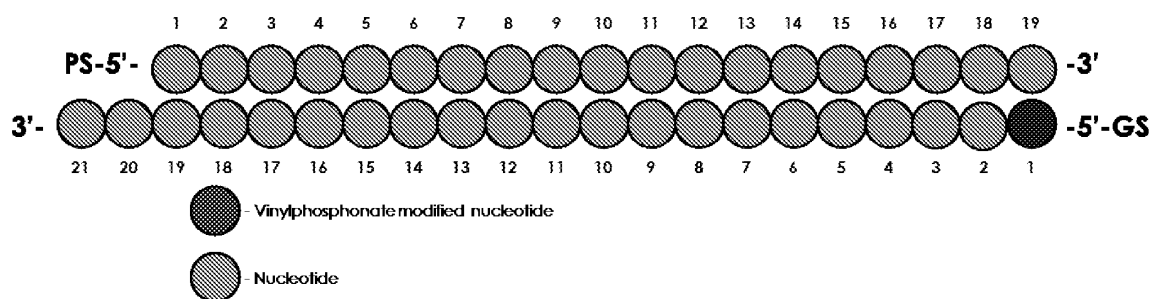
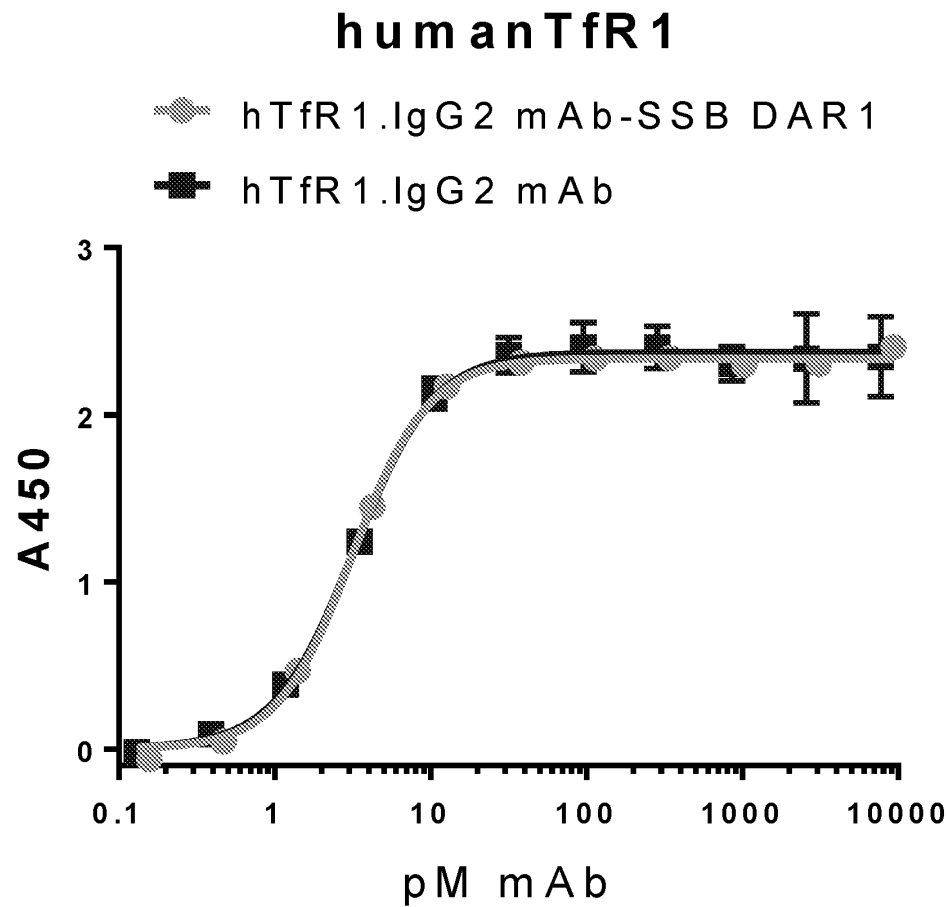
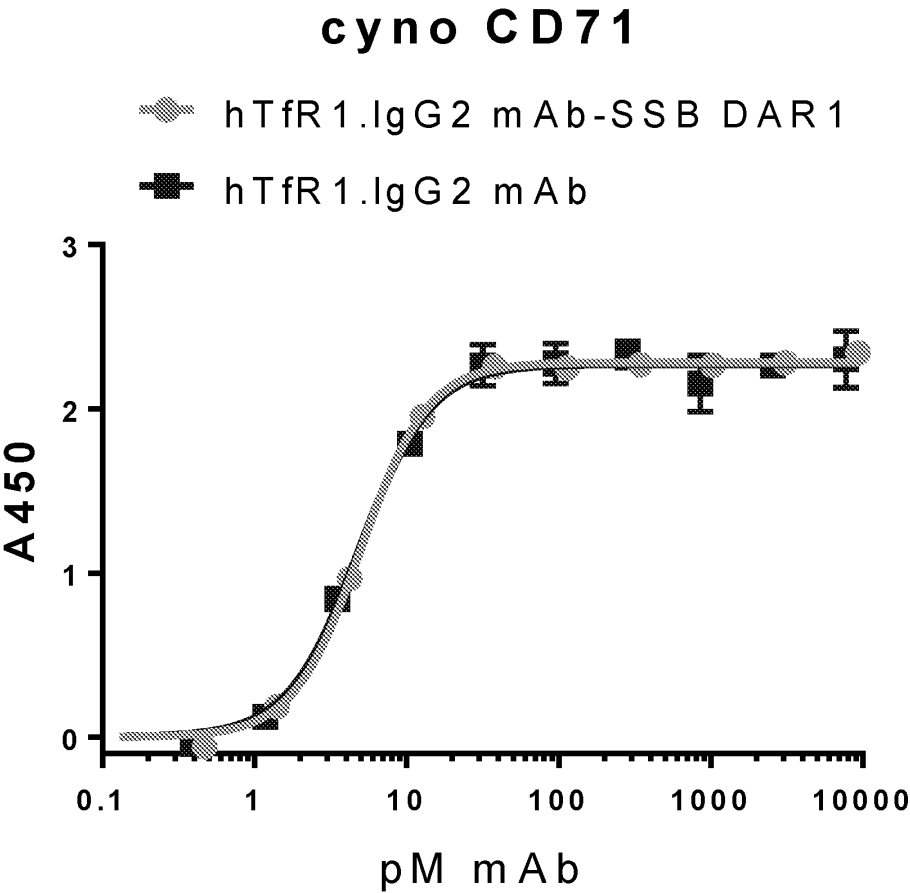


FIG. 3A



	hTfR1.IgG2 mAb-SSB DAR1	hTfR1.IgG2 mAb
Specific binding with Hill slope		
Best-fit values		
Bmax	2.339	2.371
h	1.794	1.717
Kd	3.179	3.224

FIG. 3B



	hTfR1.IgG2 mAb-SSB DAR1	hTfR1.IgG2 mAb
Specific binding with Hill slope		
Best-fit values		
Bmax	2.283	2.273
h	1.959	1.86
Kd	4.994	4.872

FIG. 4A

HeI92

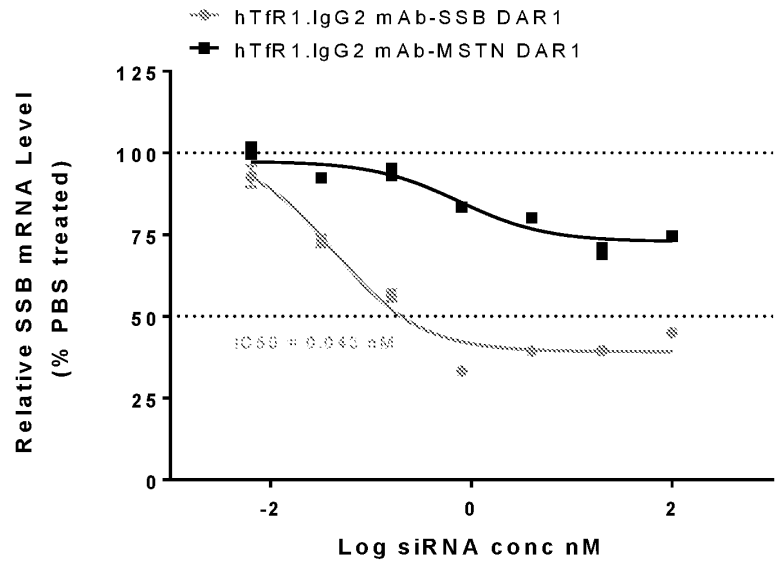


FIG. 4B

human Skeletal Muscle Cells

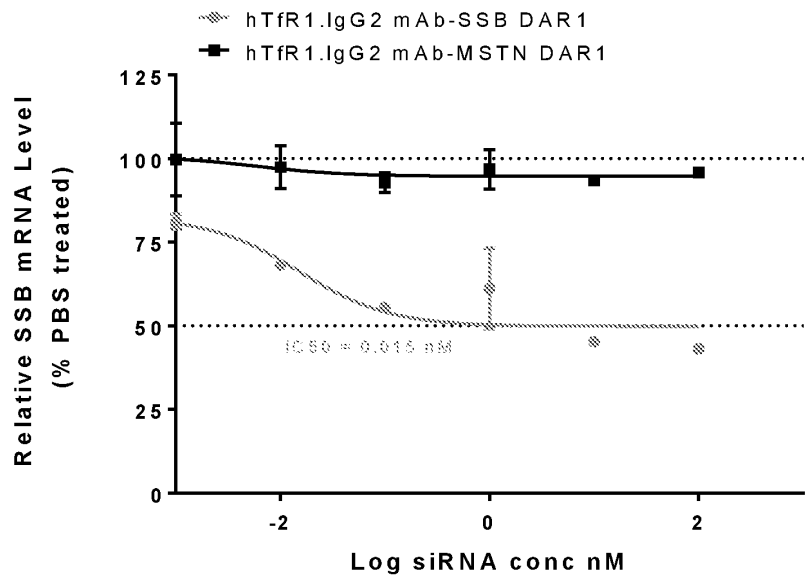


FIG. 5A

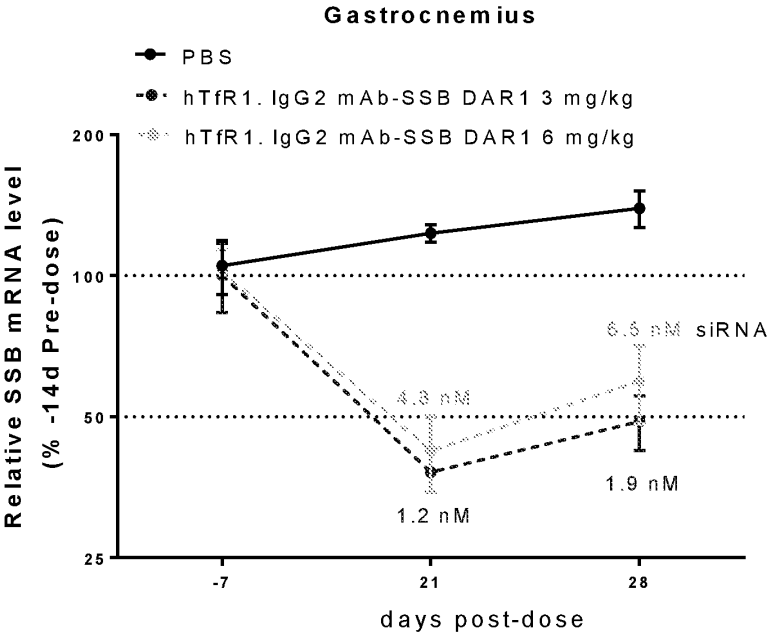


FIG. 5B

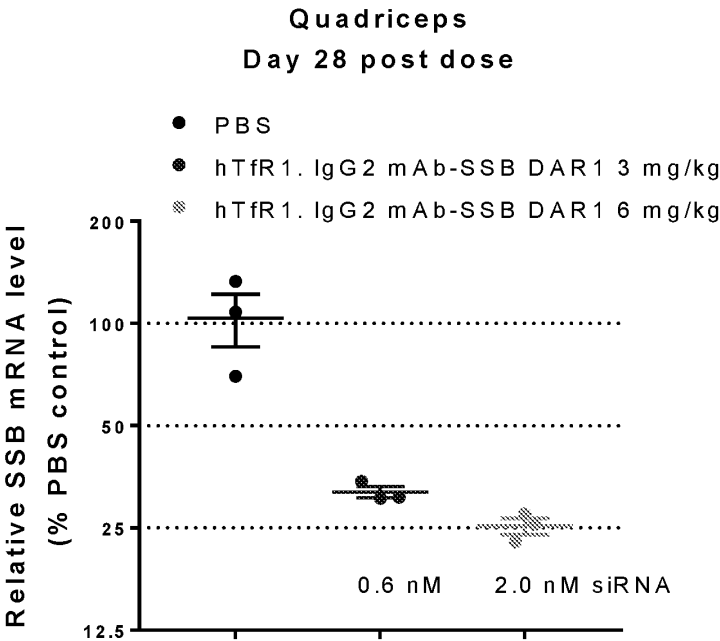


FIG. 6

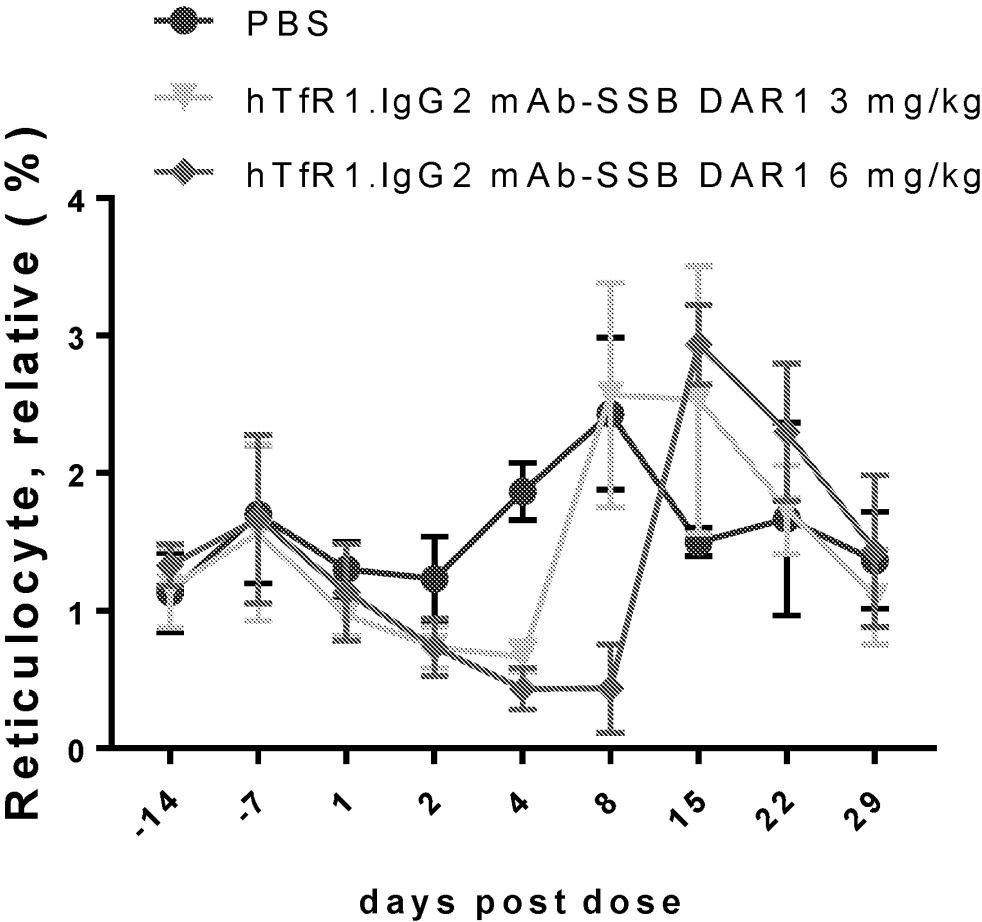
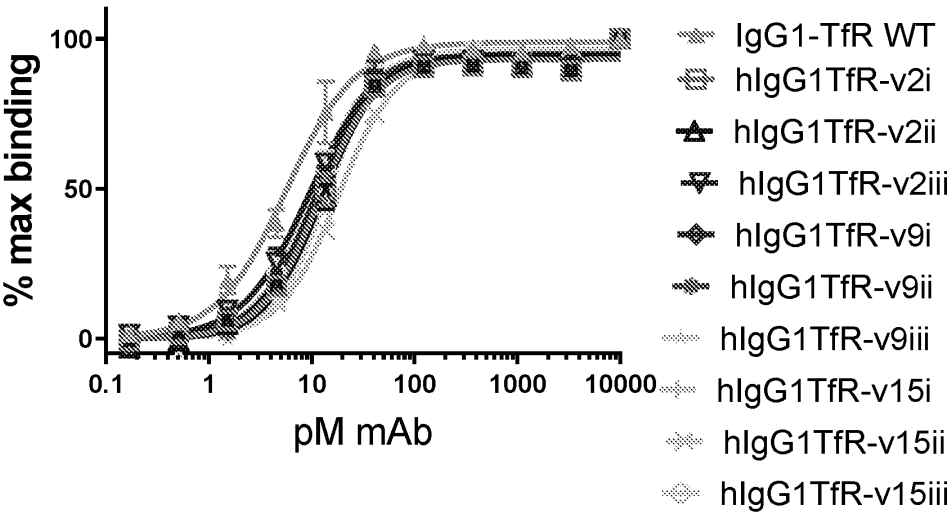


FIG. 7

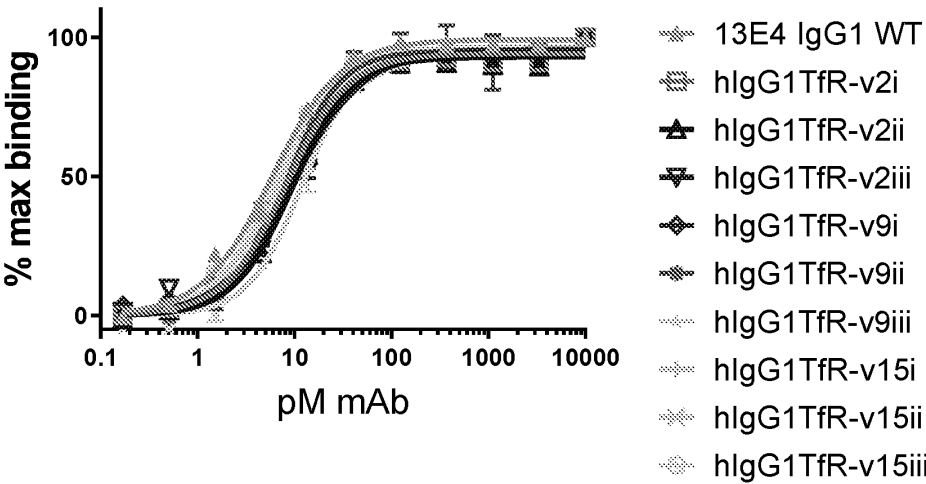
Binding to Cyno CD71



	IgG1-TfR WT	hlgG1TfR-v2i	hlgG1TfR-v2ii	hlgG1TfR-v2iii	hlgG1TfR-v9i
Bmax	99.11	93.14	94.21	94.32	94.96
h	1.339	1.559	1.58	1.349	1.513
Kd	5.819	11.95	12.72	9.2	11.01
	hlgG1TfR-v9ii	hlgG1TfR-v9iii	hlgG1TfR-v15i	hlgG1TfR-v15ii	hlgG1TfR-v15iii
Bmax	94.32	94.02	94.21	94.39	96.37
h	1.743	1.736	1.551	1.535	1.539
Kd	11.37	13.69	12.46	17.95	10.31

FIG. 8

Binding to Human CD71



	lgG1-TfR WT	hlgG1TfR-v2i	hlgG1TfR-v2ii	hlgG1TfR-v2iii	hlgG1TfR-v9i
Bmax	98.26	94.18	92.89	95.01	95.74
h	1.181	1.352	1.434	1.202	1.223
Kd	6.196	8.175	9.643	9.578	9.729
	hlgG1TfR-v9ii	hlgG1TfR-v9iii	hlgG1TfR-v15i	hlgG1TfR-v15ii	hlgG1TfR-v15iii
	95.16	93.76	95.31	93.7	96.48
	1.571	1.56	1.291	1.252	1.351
	8.235	11.97	7.127	9.874	6.295

FIG. 9A

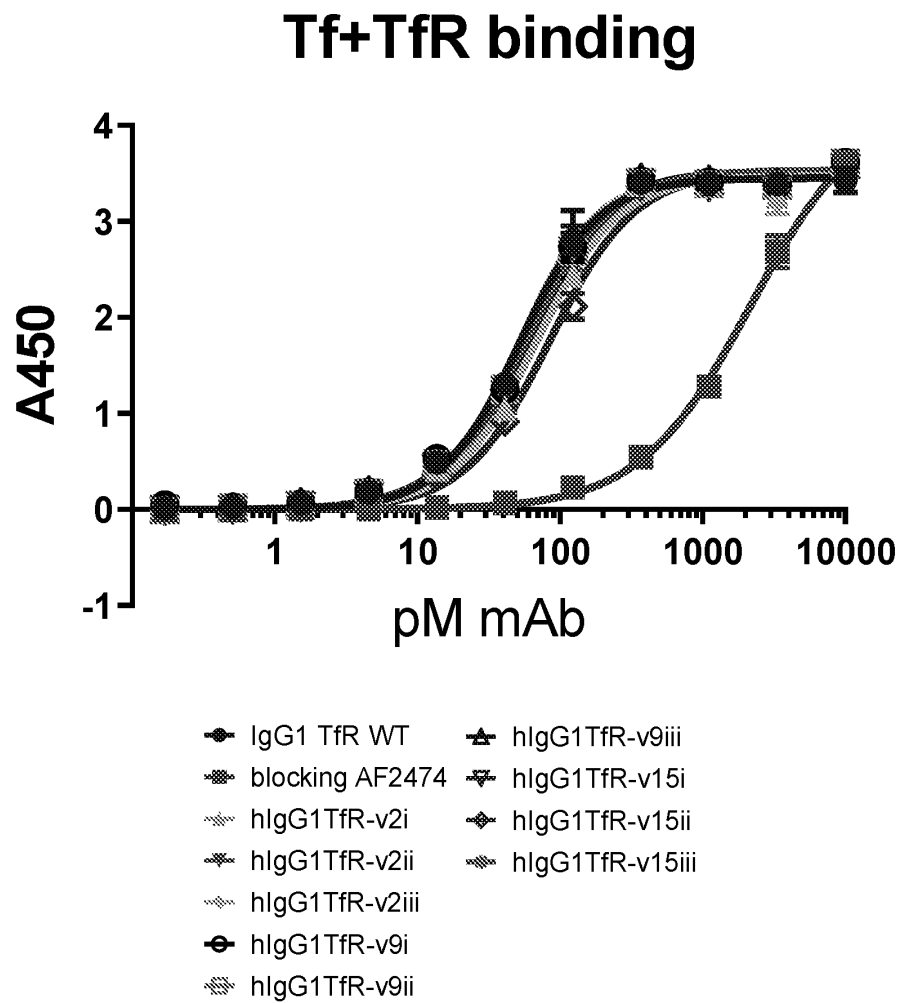


FIG. 9B

	IgG1 TfR WT	blocking AF2474	hlgG1TfR-v2i	hlgG1TfR-v2ii	hlgG1TfR-v2iii	hlgG1TfR-v9i
Bmax	3.452	4.258	3.477	3.533	3.474	3.528
h	1.575	1.117	1.487	1.447	1.614	1.451
Kd	51.79	2181	67.76	57.8	52.17	55.95
Kd(Tf+ TfR)/Kd(TfR)	3.1	51.8	2.8	2.5	2.1	2.2
	hlgG1TfR-v9ii	hlgG1TfR-v9iii	hlgG1TfR-v15i	hlgG1TfR-v15ii	hlgG1TfR-v15iii	
Bmax	3.509	3.527	3.473	3.523	3.5	
h	1.481	1.491	1.562	1.456	1.516	
Kd	56.99	54.62	61.87	84.94	60.39	
Kd(Tf+ TfR)/Kd(TfR)	2.6	2.5	2.9	2.5	2.4	

FIG. 10A

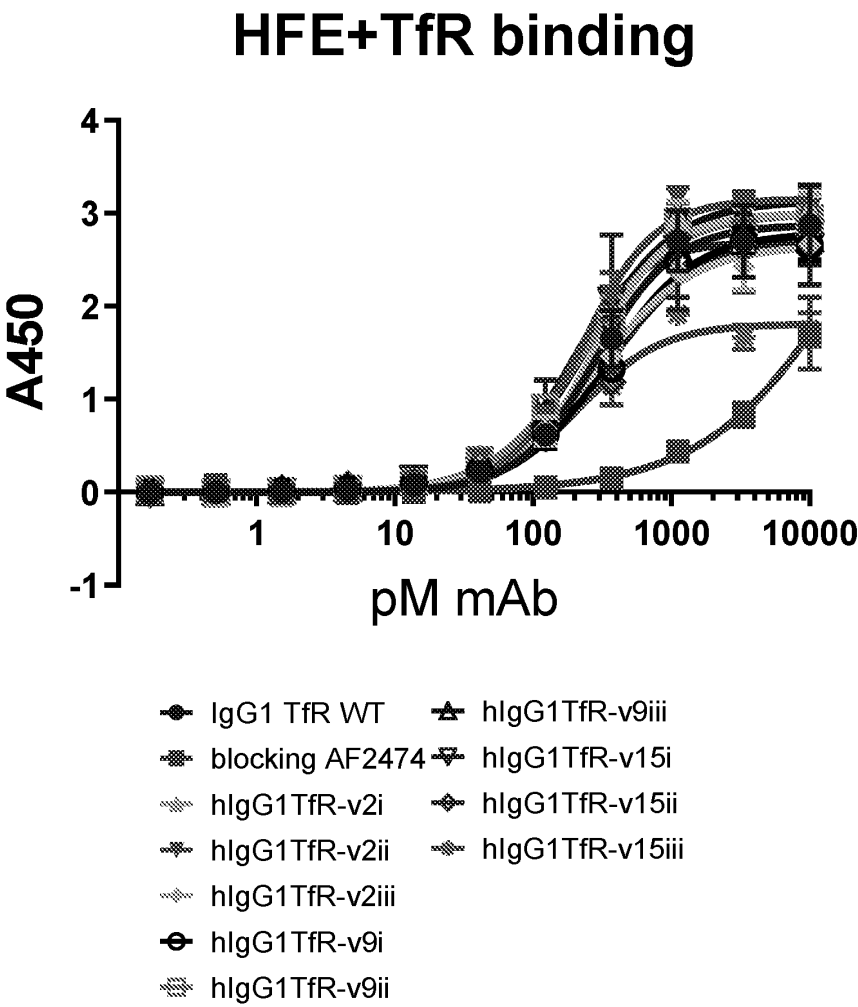


FIG. 10B

HFE+TfR	IgG1 TfR WT	blocking AF2474	hlgG1TfR-v2i	hlgG1TfR-v2ii	hlgG1TfR-v2iii	hlgG1TfR-v9i
Bmax	2.875	5.703	2.999	3.155	2.658	2.789
h	1.544	0.8004	1.627	1.642	1.261	1.368
Kd	286.4	28940	273.2	227	289.2	340.9
Kd(HFE+TfR)/Kd(TfR)	16.9	687.7	11.1	9.9	11.9	13.6
	hlgG1TfR-v9ii	hlgG1TfR-v9iii	hlgG1TfR-v15i	hlgG1TfR-v15ii	hlgG1TfR-v15iii	
Bmax	2.996	3.136	2.699	2.79	1.811	
h	1.357	1.38	1.653	1.285	1.452	
Kd	229.2	248.2	182.3	346.4	213.5	
Kd(HFE+TfR)/Kd(TfR)	10.4	11.4	8.5	10.2	8.5	

FIG. 11

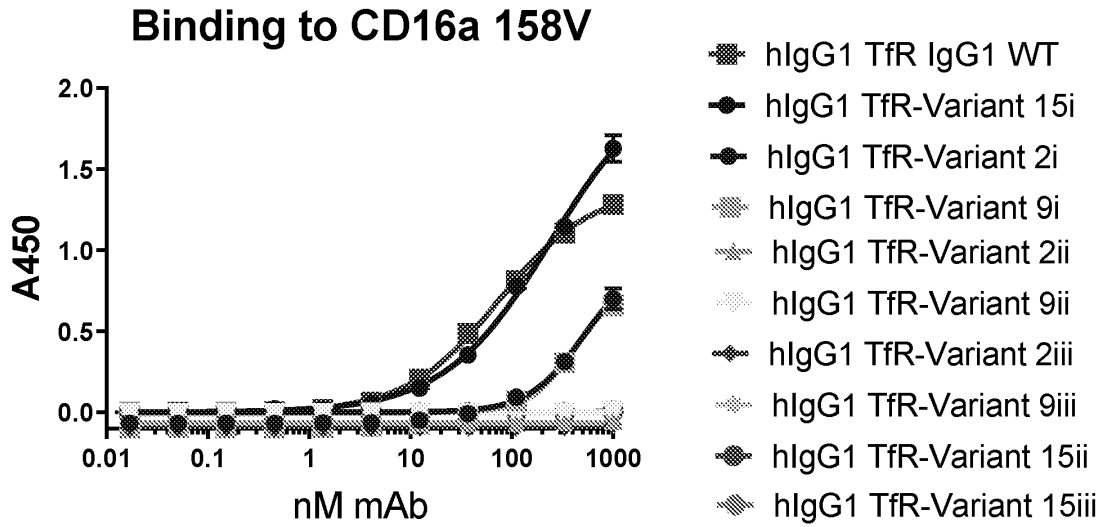


FIG. 12

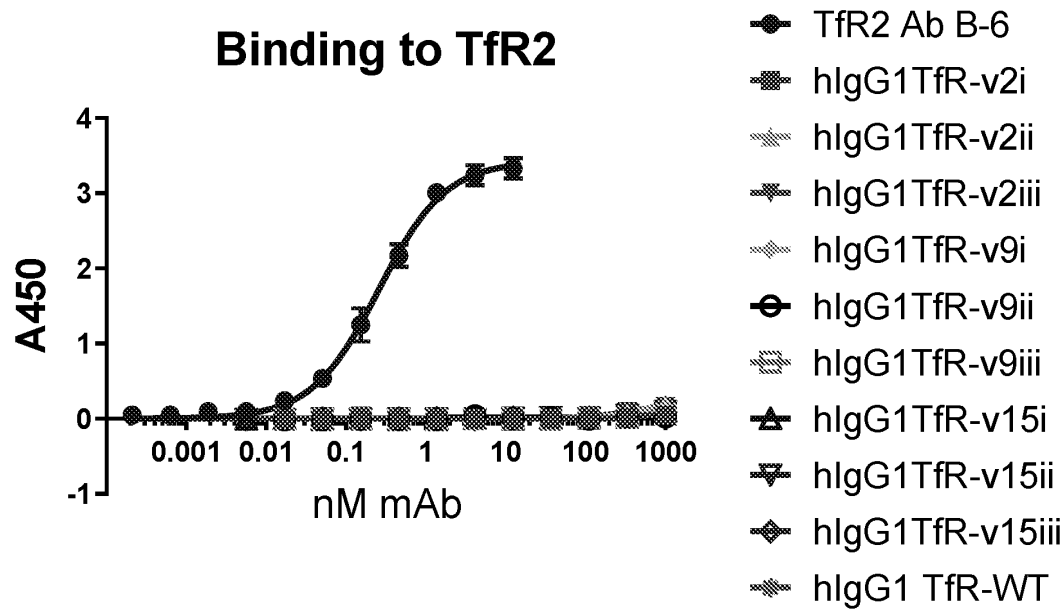


FIG. 13A

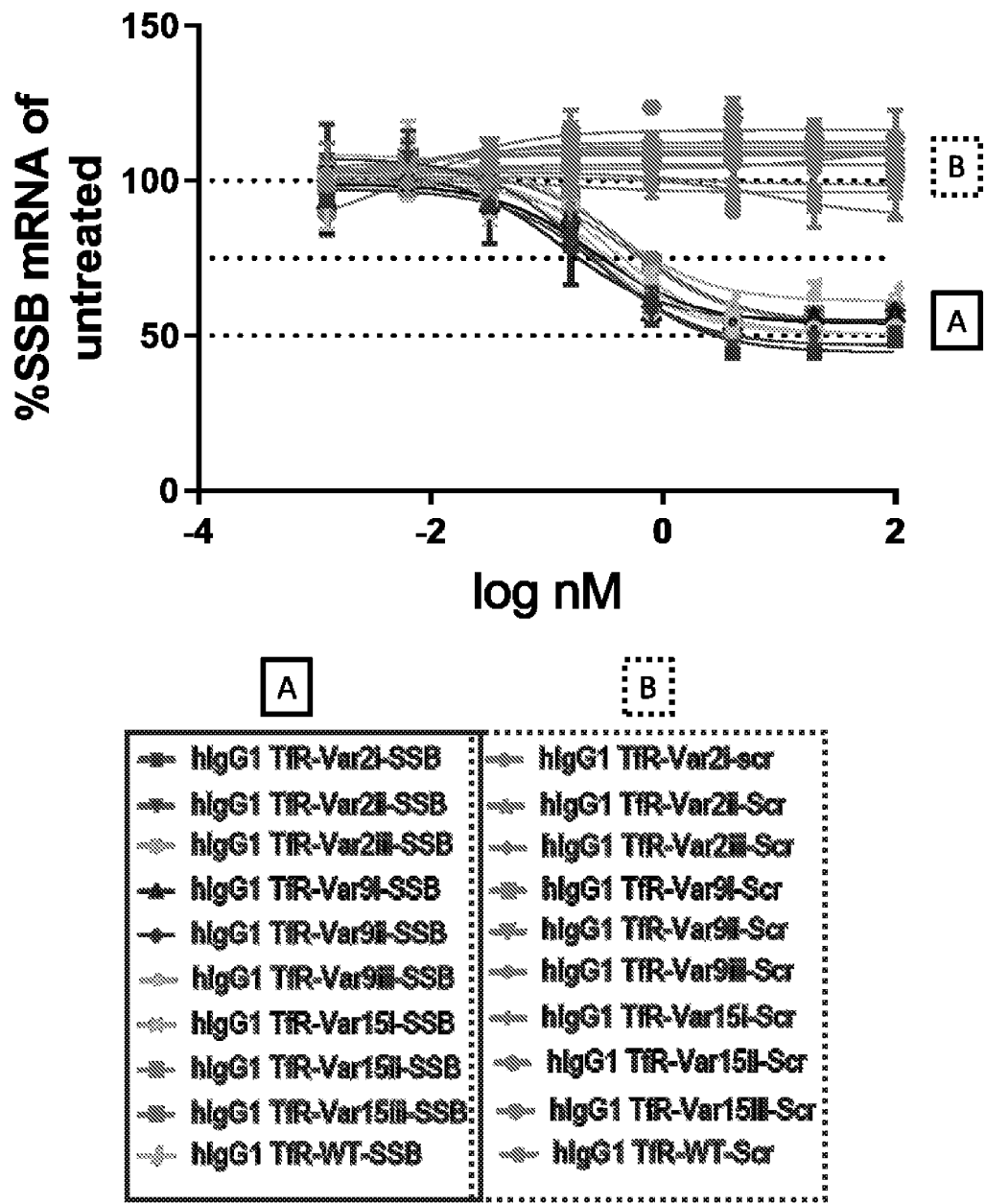


FIG. 13B

	hlgG1 TfR-Var2i-SSB	hlgG1 TfR-Var2ii-SSB	hlgG1 TfR-Var2iii-SSB	hlgG1 TfR-Var9i-SSB	hlgG1 TfR-Var9ii-SSB
Bottom	97.38	107.3	102.3	99.1	103.2
Top	44.58	46.89	50.43	53.83	54.82
LogEC50	-0.4851	-0.6479	-0.5046	-0.5777	-0.8734
EC50 (nM)	0.3273	0.225	0.3129	0.2644	0.1338
Span	-52.8	-60.46	-51.83	-45.26	-48.37
E _{max} (%KD)	55.42	53.11	49.57	46.17	45.18
	hlgG1 TfR-Var9iii-SSB	hlgG1 TfR-Var15i-SSB	hlgG1 TfR-Var15ii-SSB	hlgG1 TfR-Var15iii-SSB	hlgG1 TfR-WT Chim-SSB
Bottom	98.01	103	99.32	104	108.4
Top	50.34	50.4	53.94	54.36	61.06
LogEC50	-0.5671	-0.4047	-0.2551	-0.289	-0.4791
EC50 (nM)	0.2709	0.3938	0.5557	0.514	0.3318
Span	-47.67	-52.59	-45.37	-49.62	-47.38
E _{max} (%KD)	49.66	49.6	46.06	45.64	38.94

FIG. 14

HEL92:PBMC (1:20)

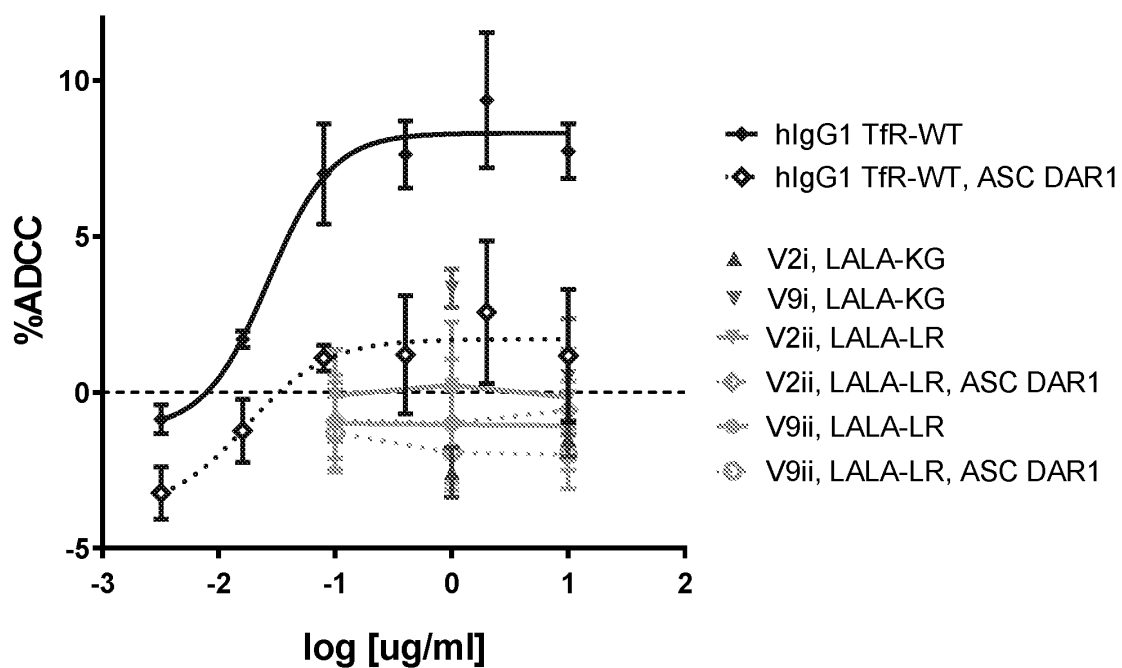


FIG. 15

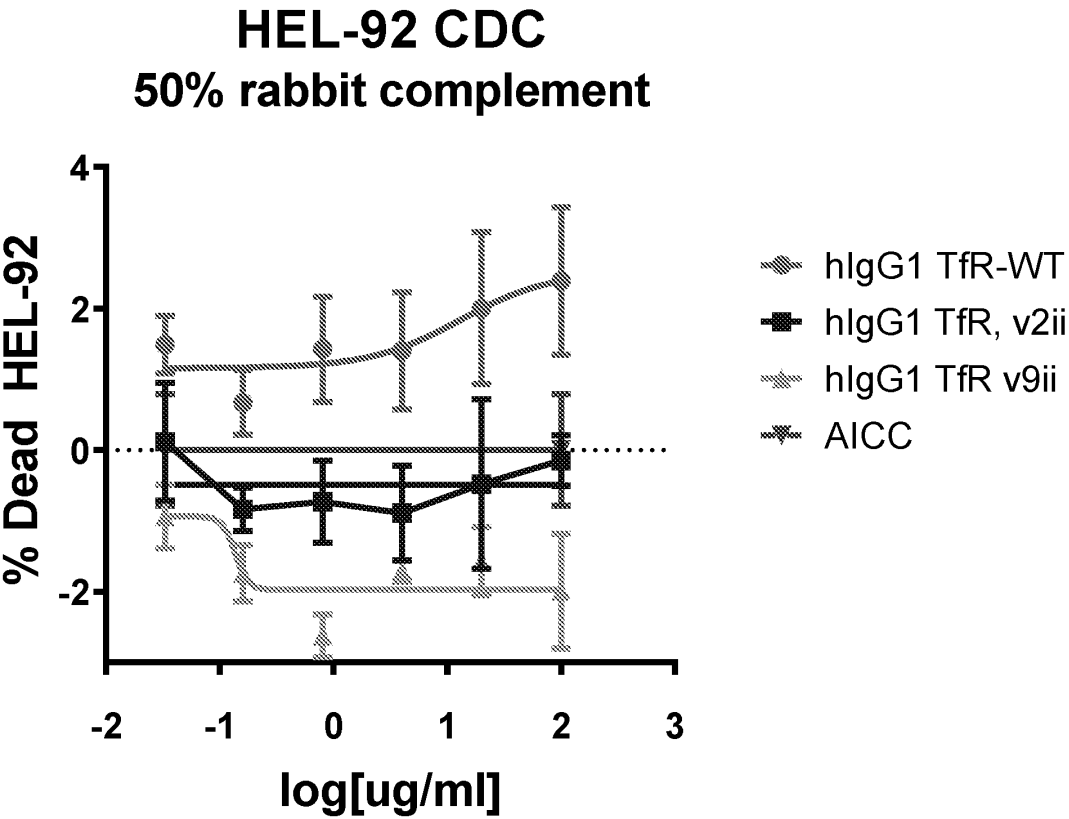
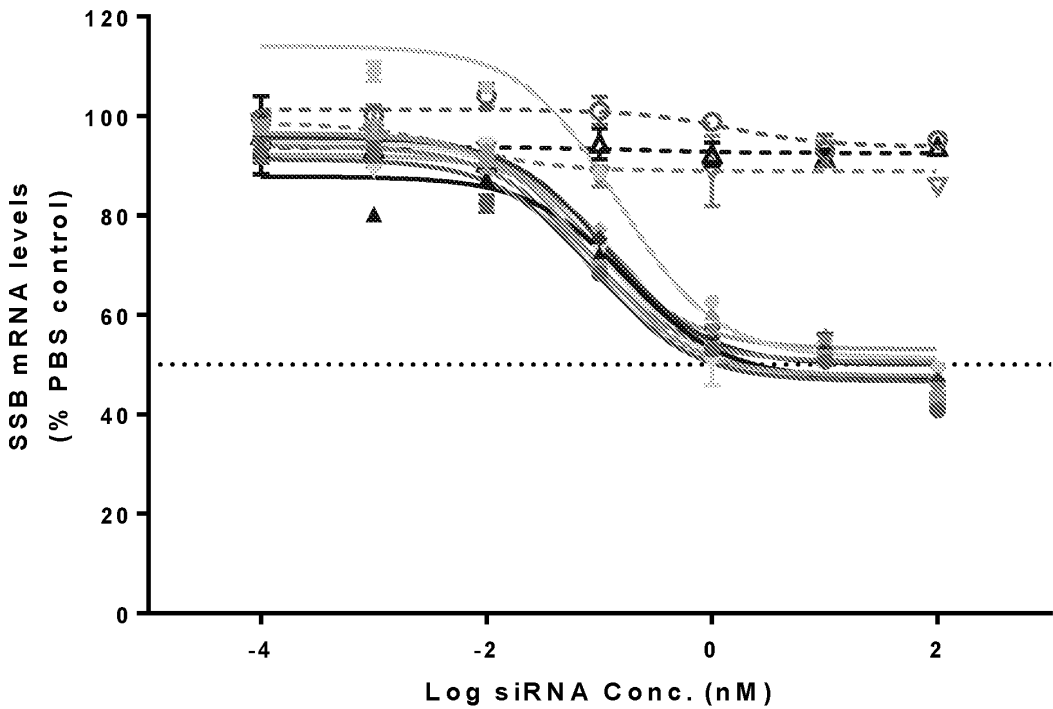


FIG. 17



- TfR1.hIgG2 mAb-SSB DAR 1
- TfR1.hIgG1mAb-Var(parent)ii-SSB DAR 1
- TfR1.hIgG1mAb-Var(parent)iii-SSB DAR 1
- TfR1.hIgG1mAb-Var2ii-SSB DAR 1
- TfR1.hIgG1mAb-Var2iii-SSB DAR 1
- TfR1.hIgG1mAb-Var9ii-SSB DAR 1
- TfR1.hIgG1mAb-Var9iii-SSB DAR 1
- TfR1.hIgG1mAb-Var15ii-SSB DAR 1
- TfR1.hIgG1mAb-Var15iii-SSB DAR 1
- TfR1.hIgG2 mAb-Scramble DAR 1
- TfR1.hIgG1mAb-Var2ii-Scramble DAR 1
- TfR1.hIgG1mAb-Var9ii-Scramble DAR 1

FIG. 18

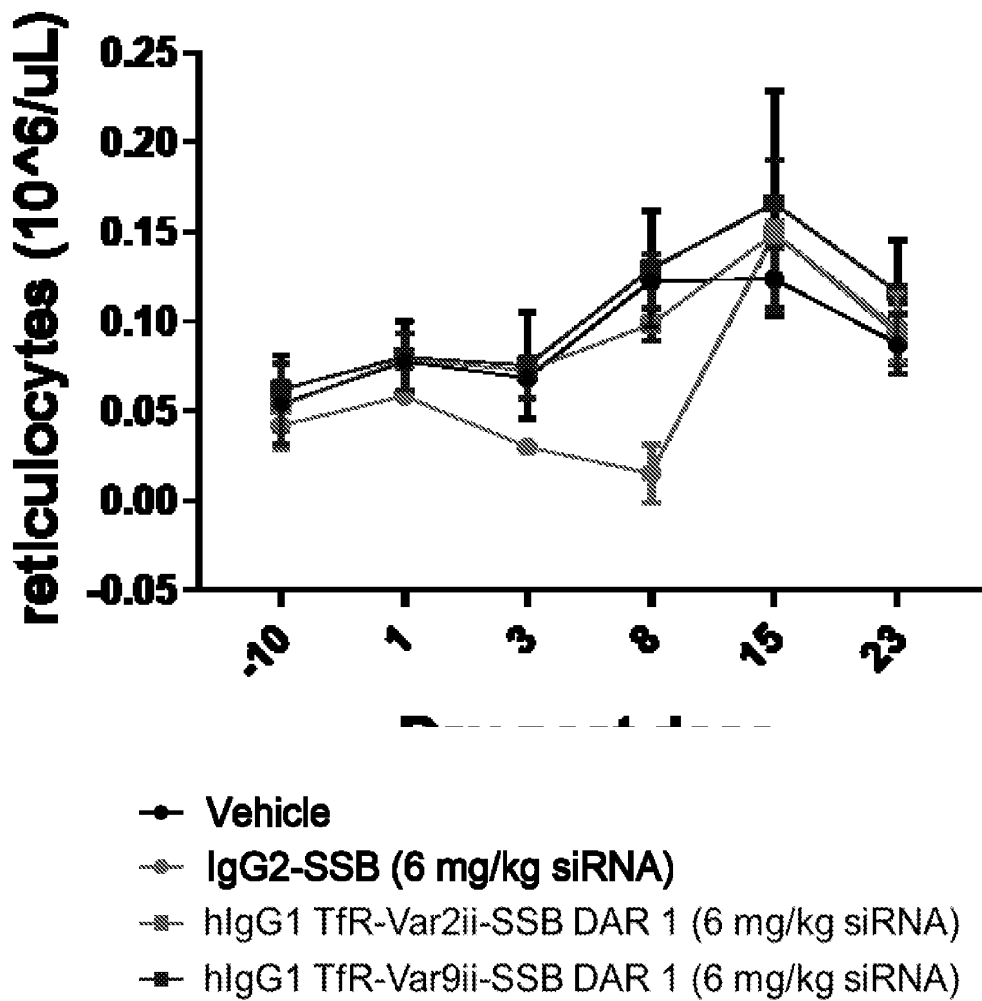


FIG. 19

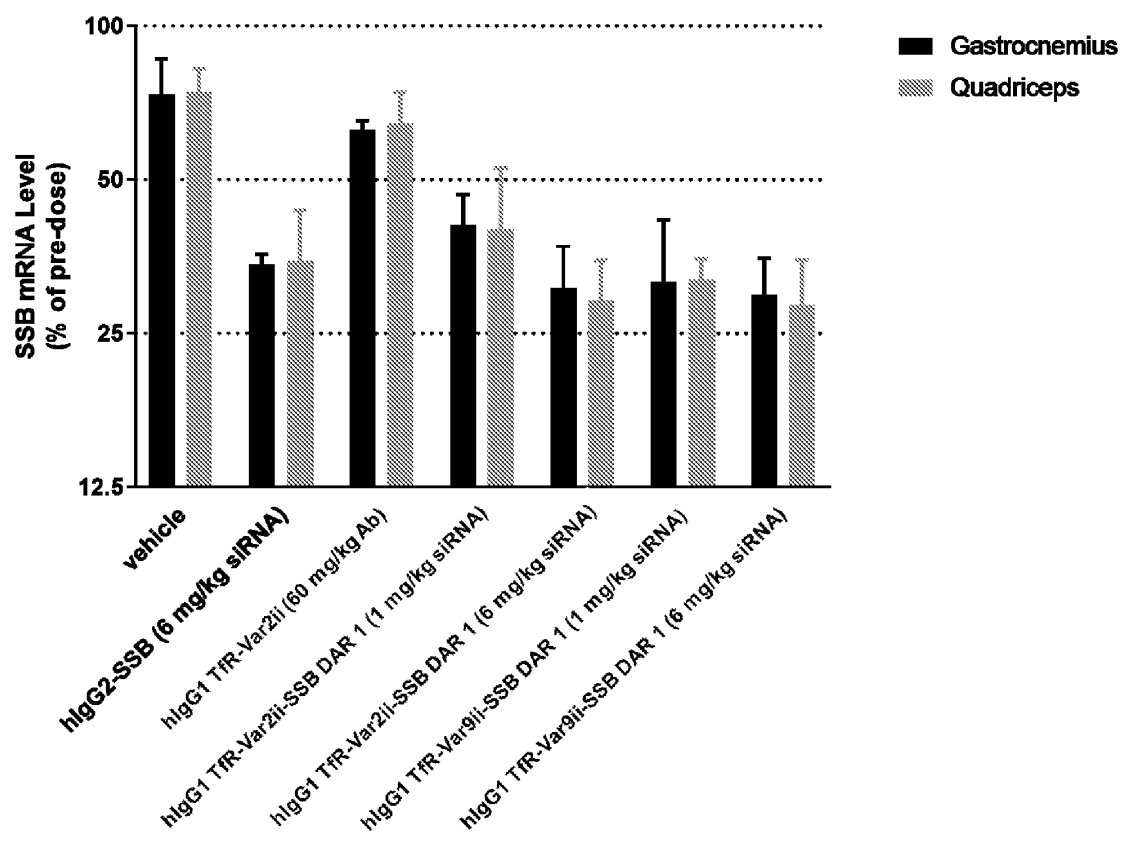


FIG. 20A

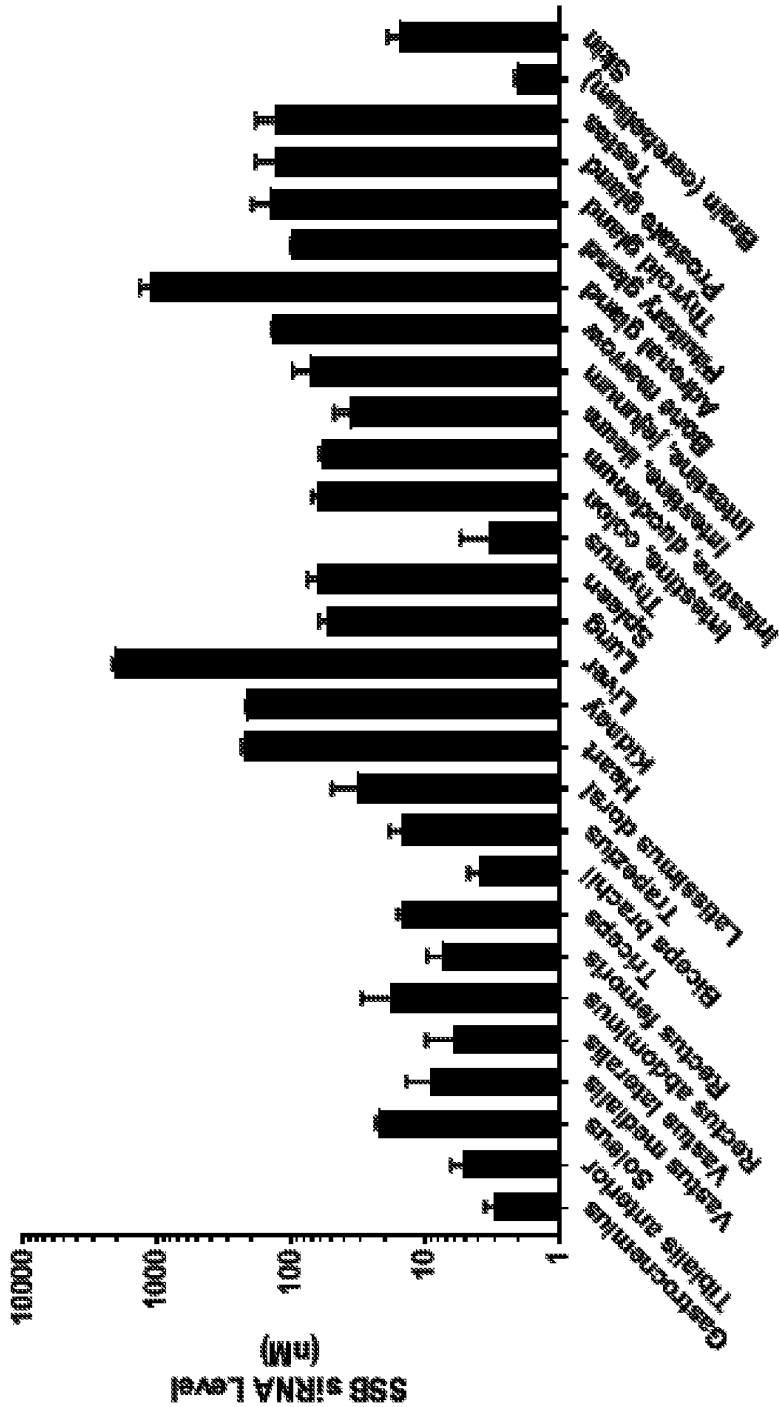


FIG. 20B

