

Figure 1A

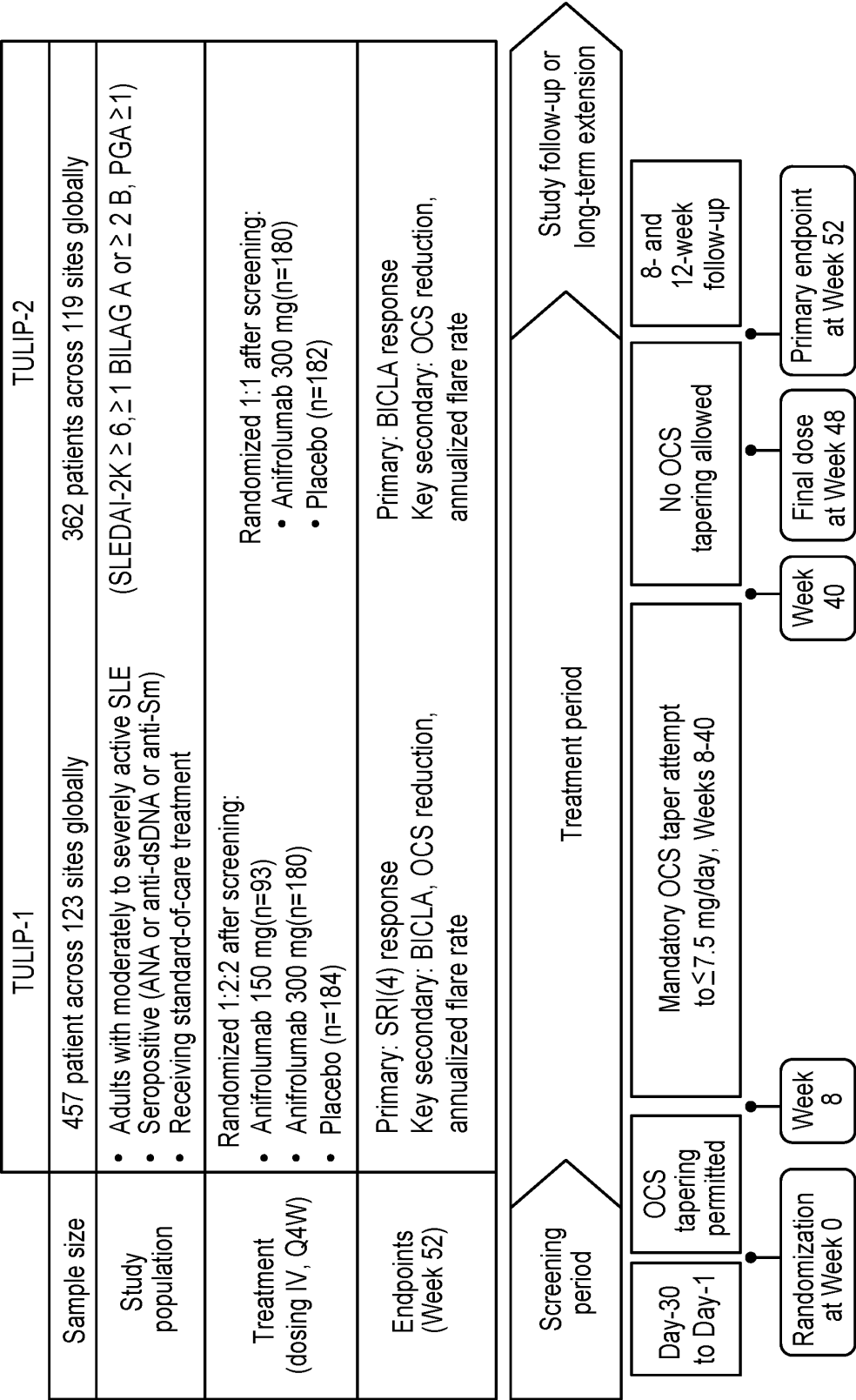


Figure 1B

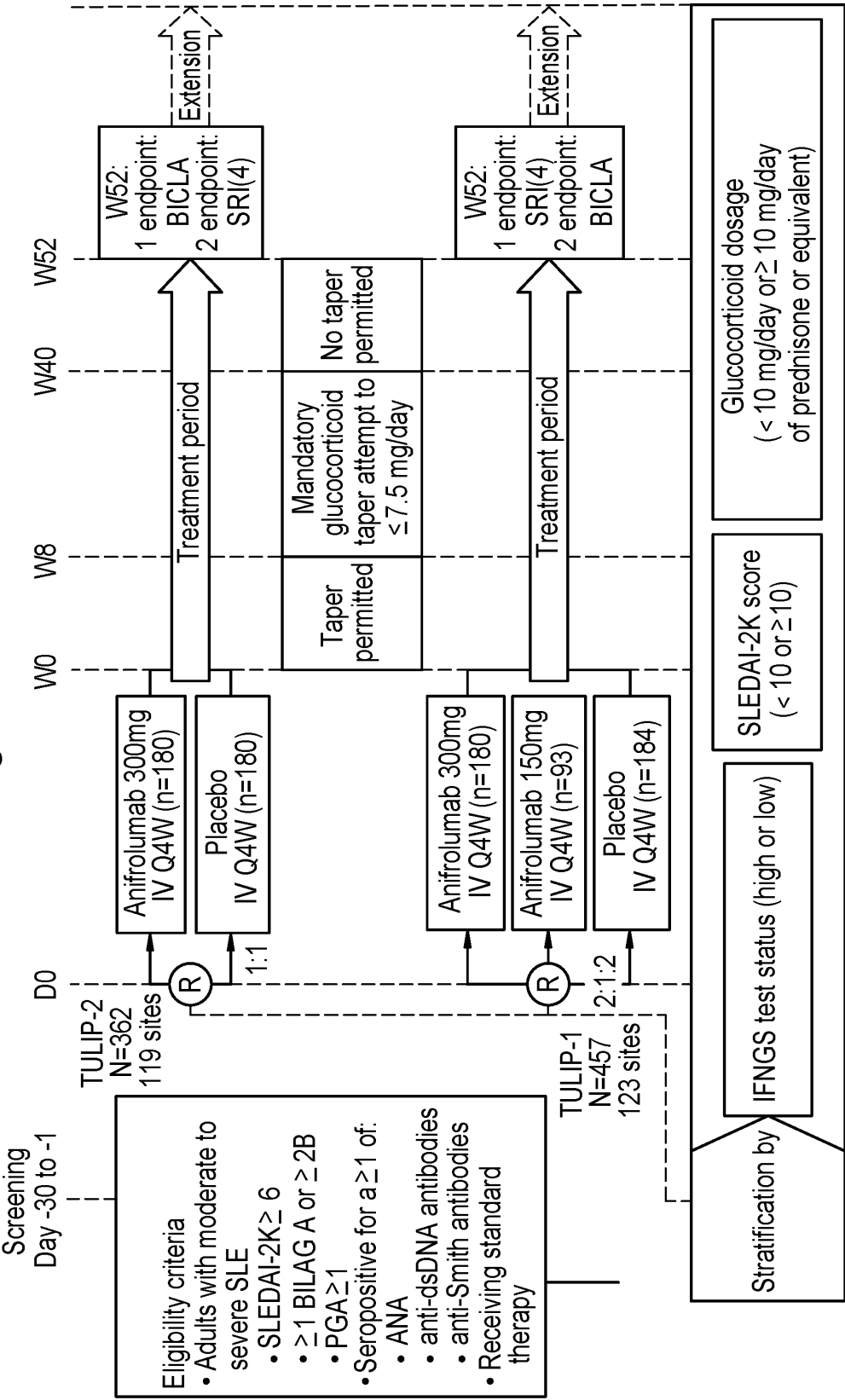


Figure 2

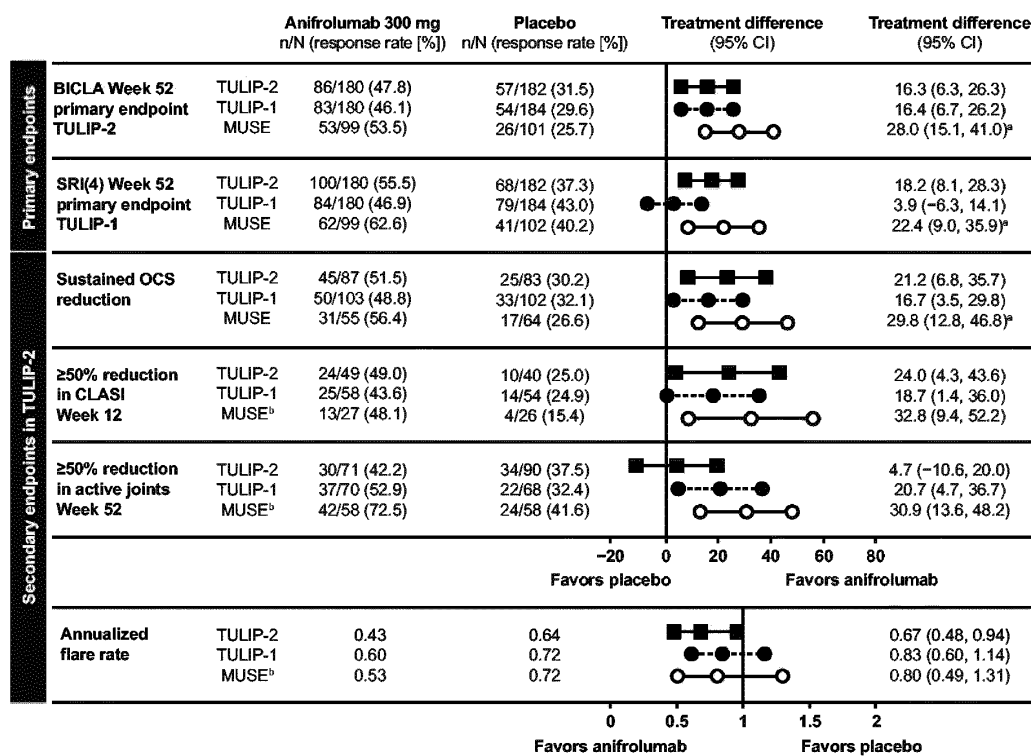


Figure 3A

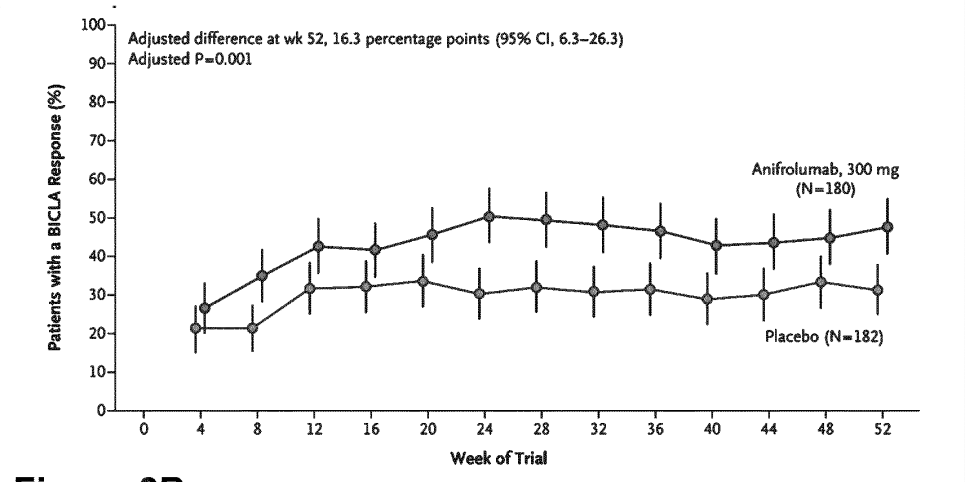


Figure 3B

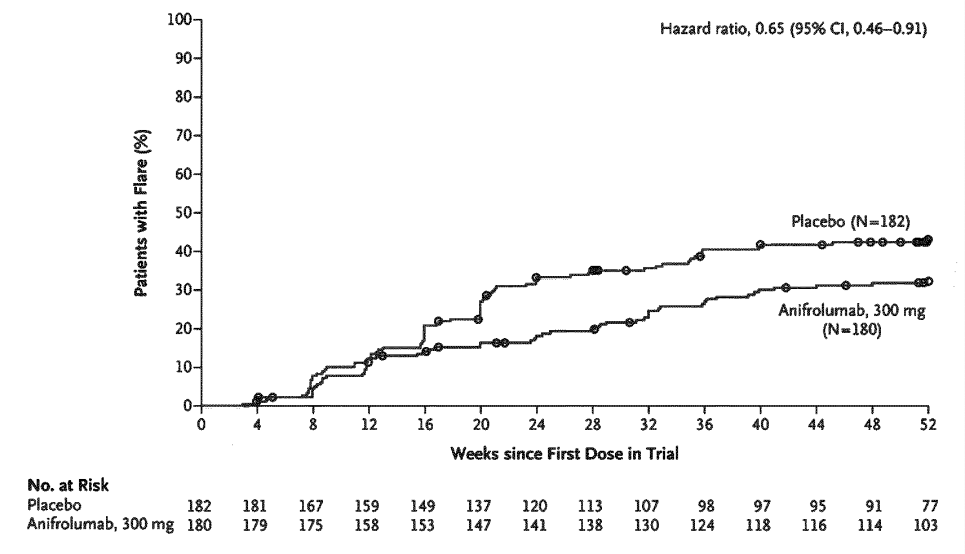


Figure 4

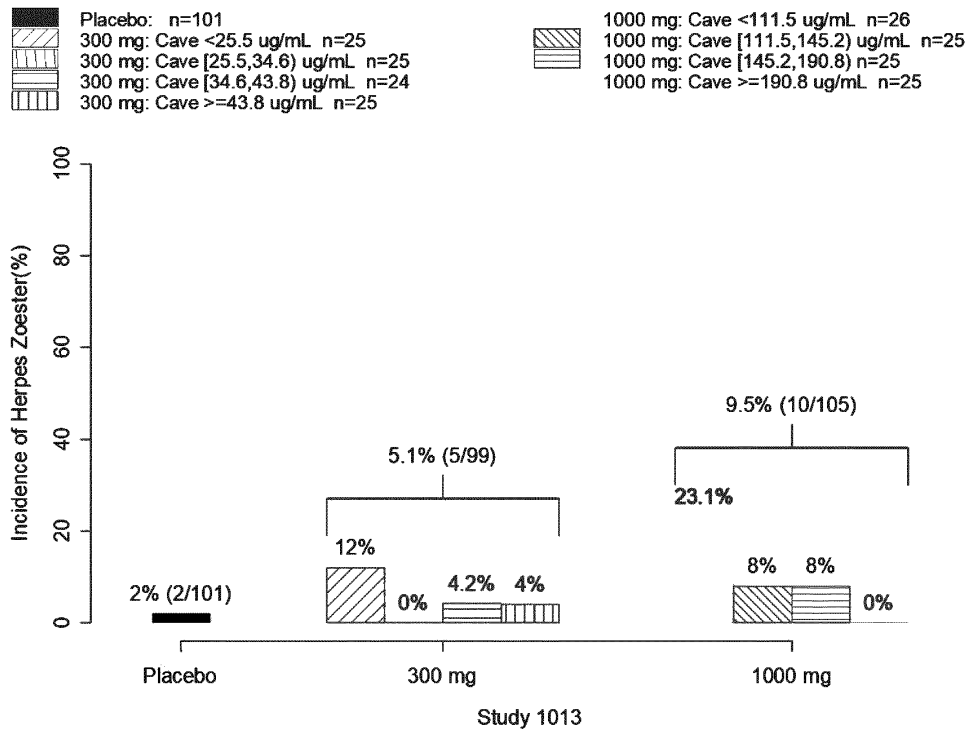


Figure 5A

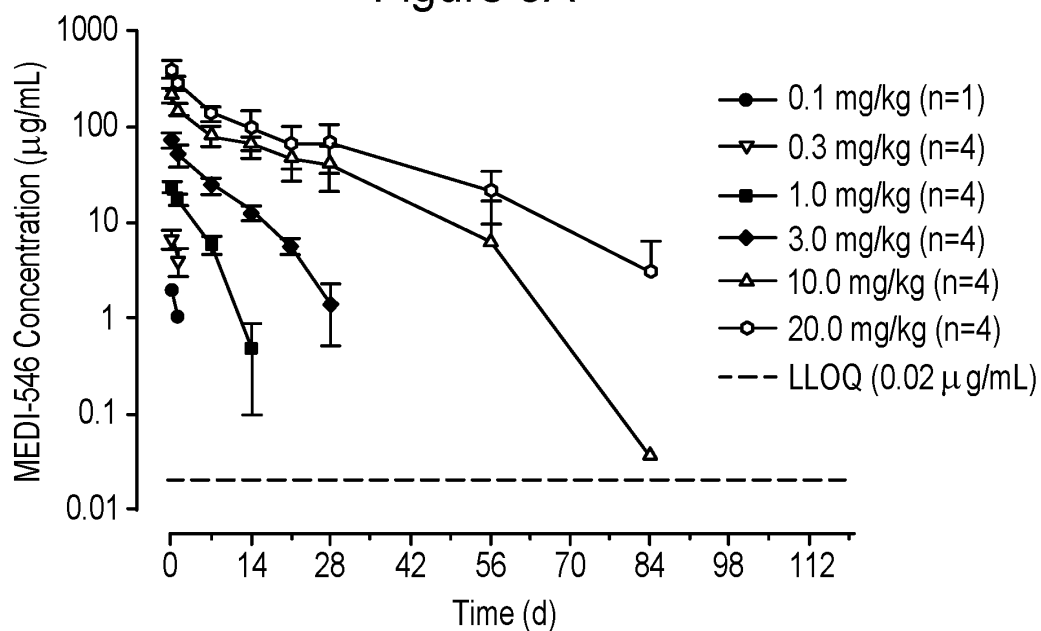


Figure 5B

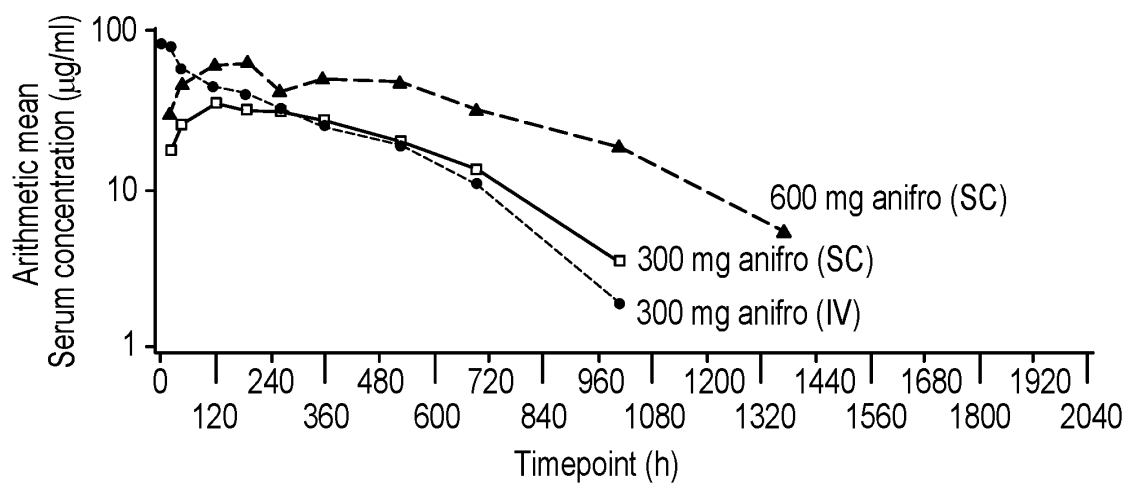
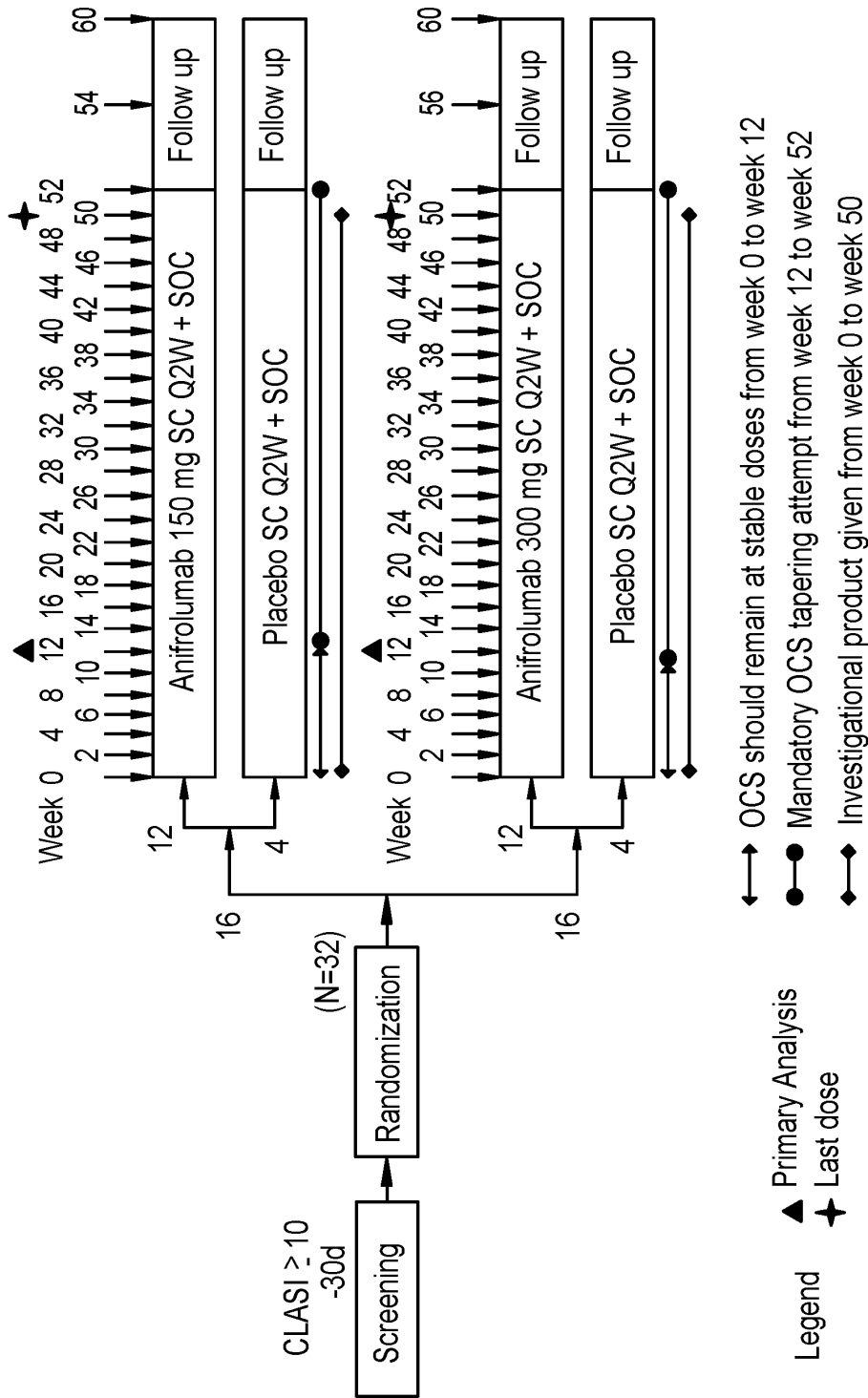
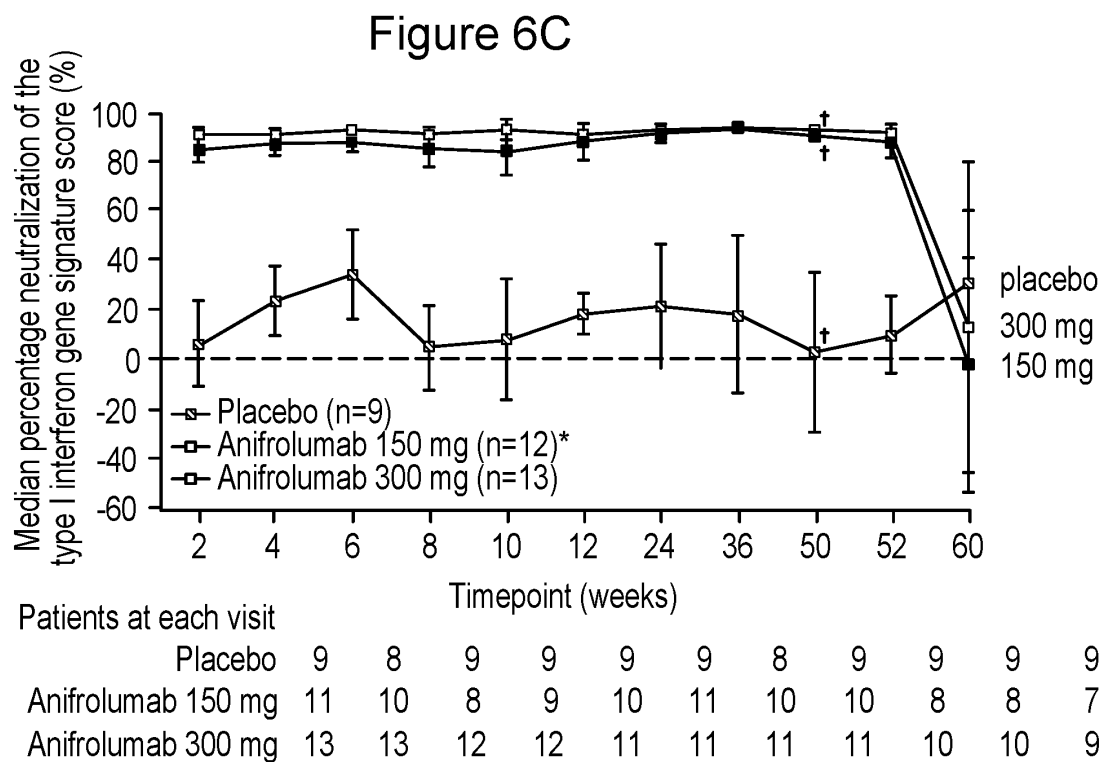
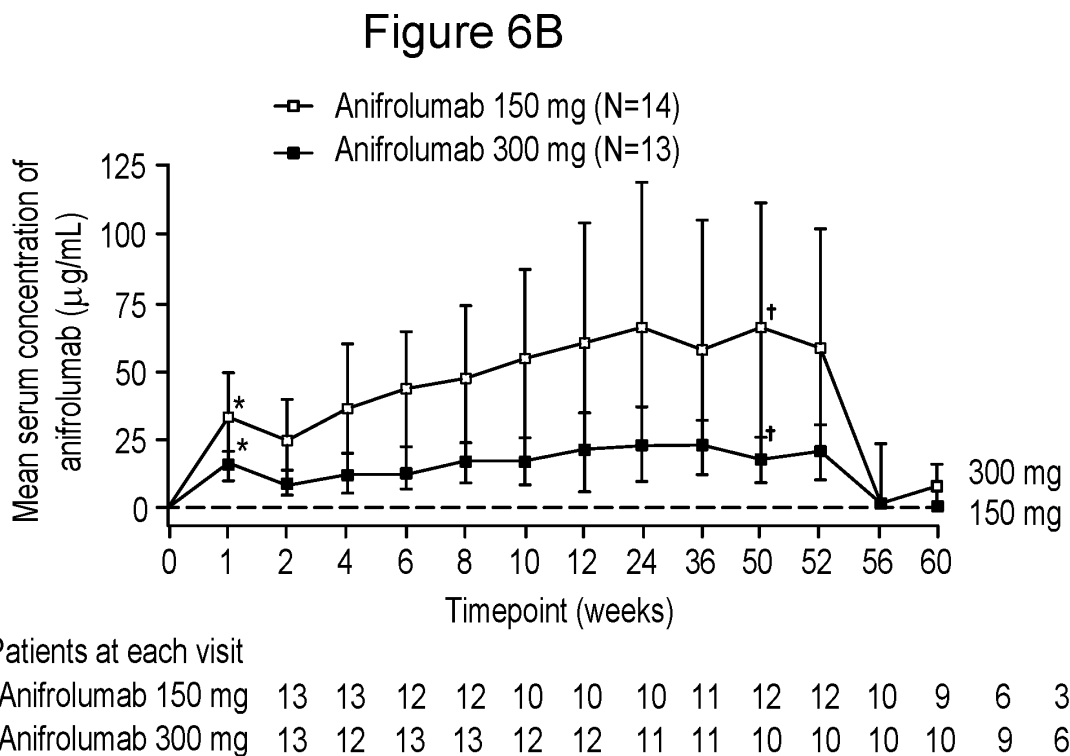


Figure 6A





SUBSTITUTE SHEET (RULE 26)

Figure 7A

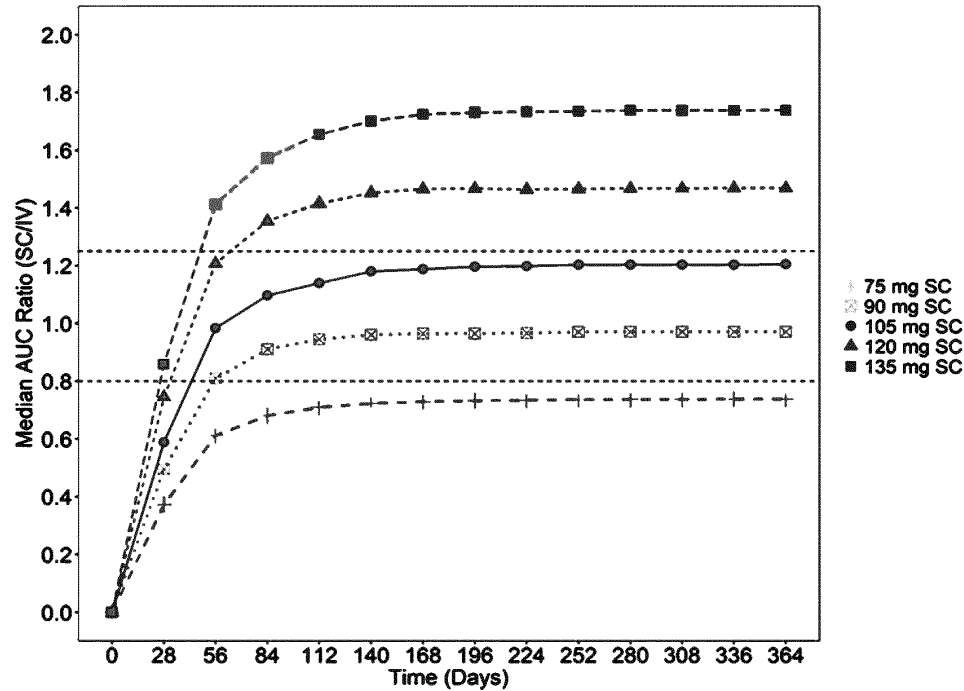


Figure 7B

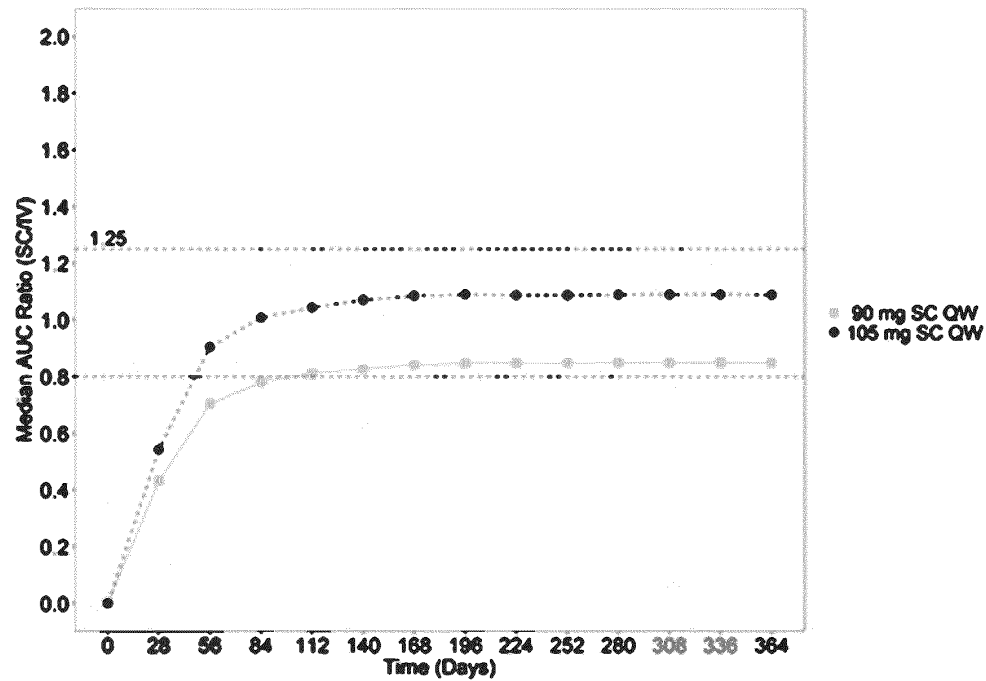


Figure 8A

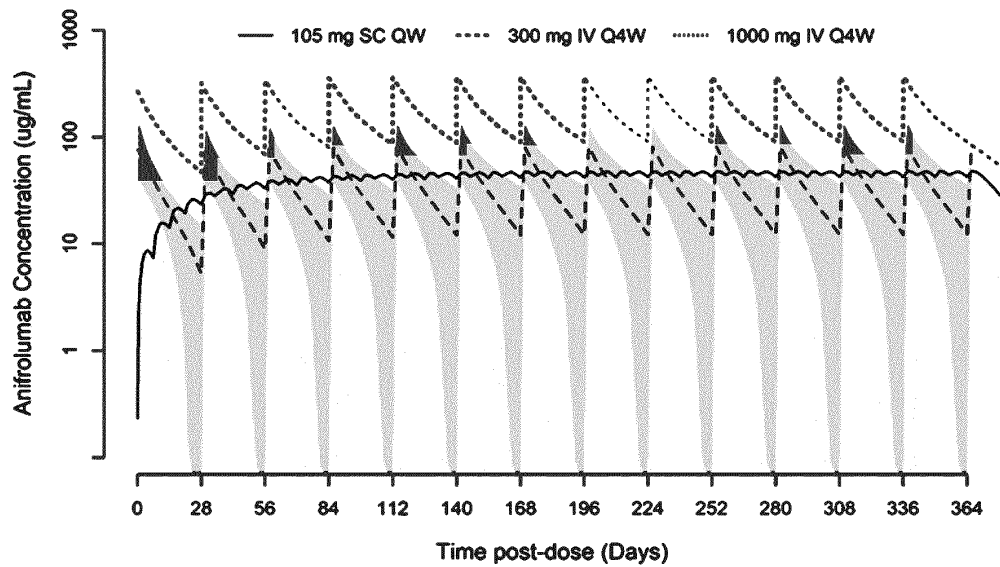


Figure 8B

IFNGS High SLE Subjects

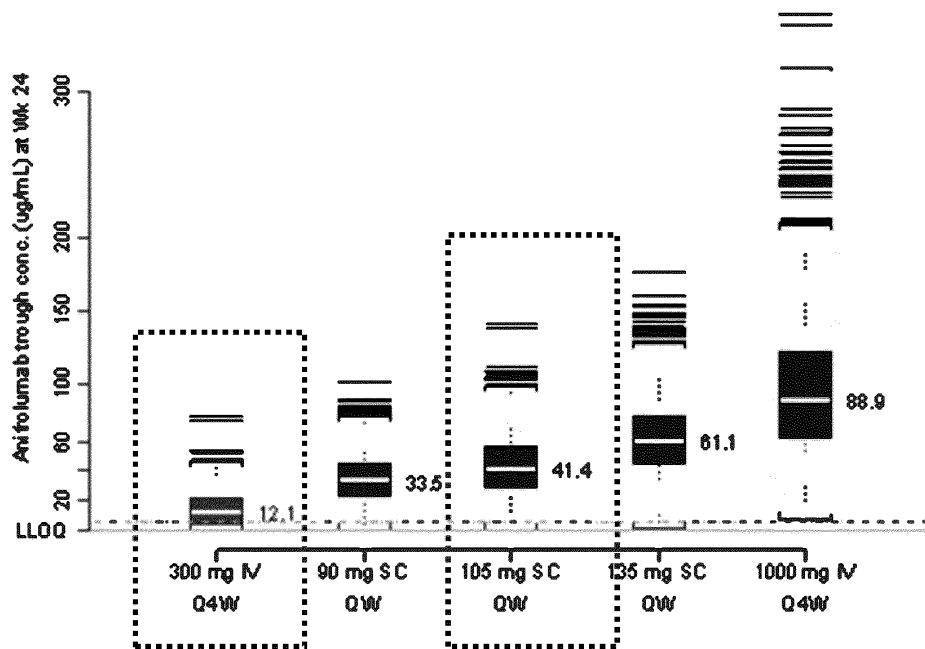


Figure 9A

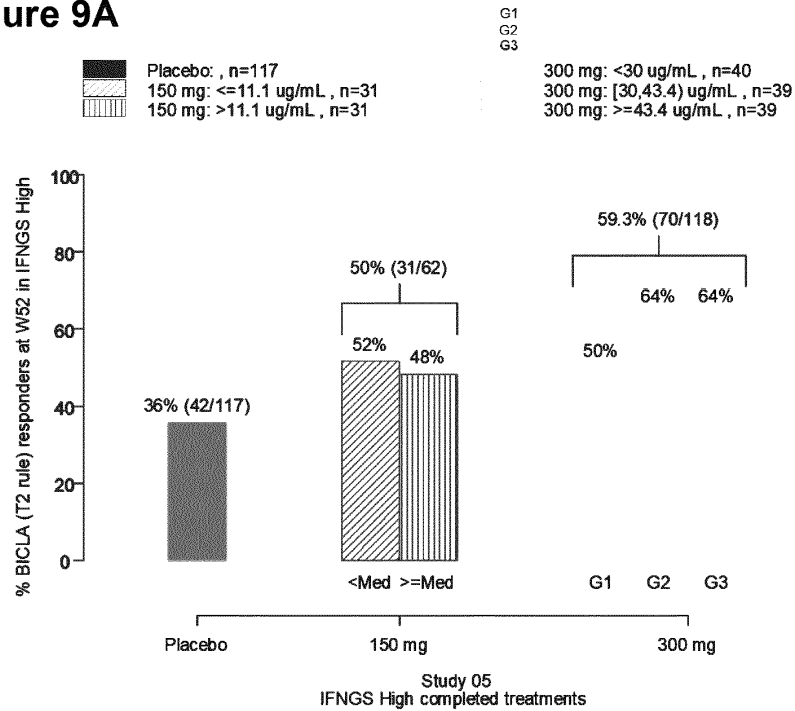


Figure 9B

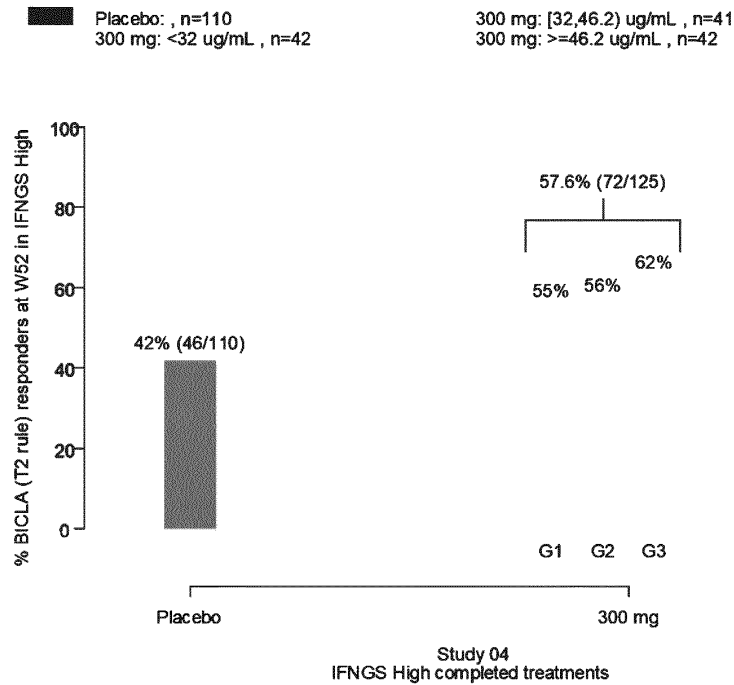


Figure 10A

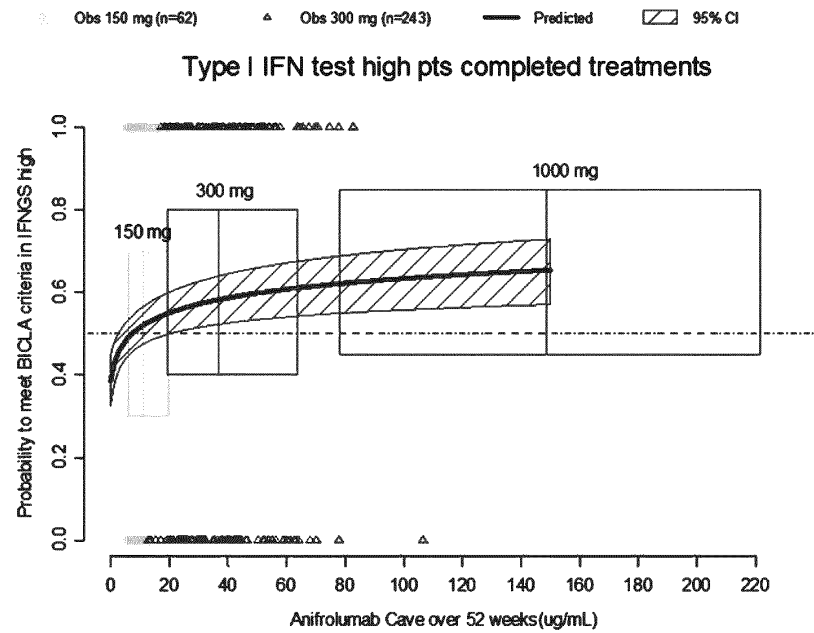


Figure 10B

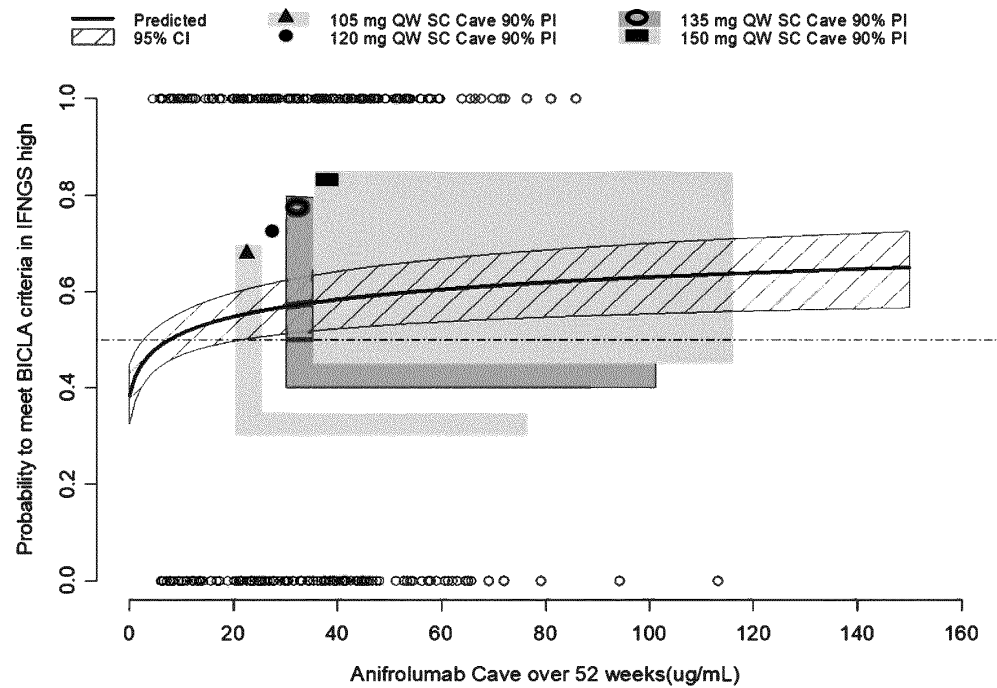


Figure 11A

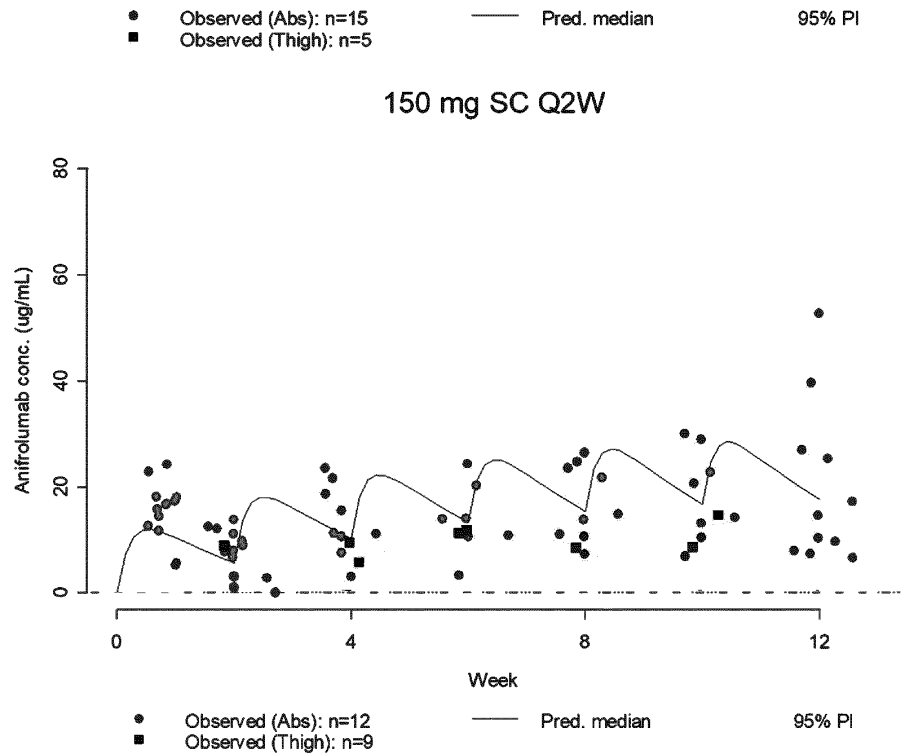


Figure 11B

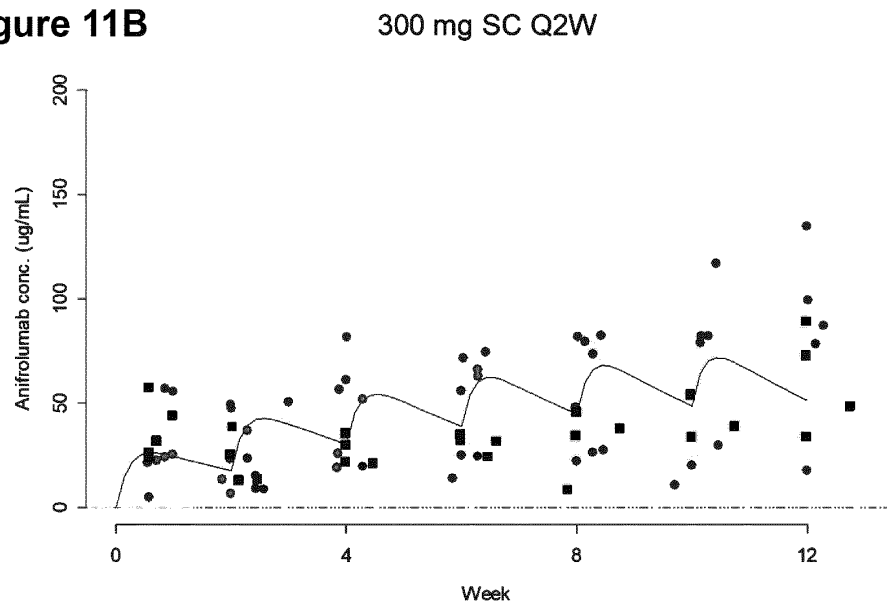


Figure 12

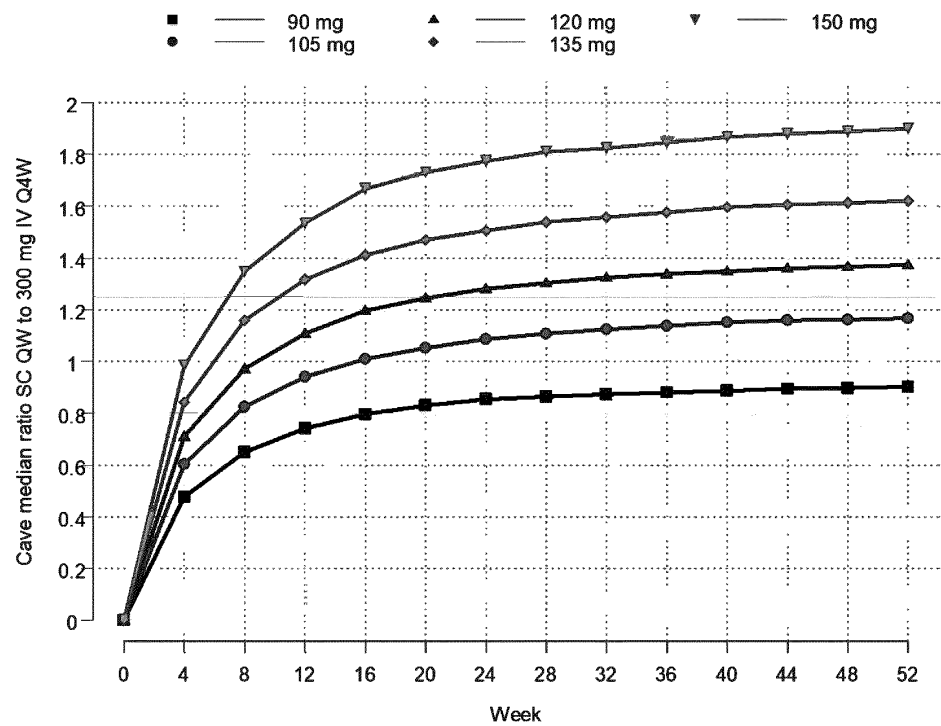


Figure 13A

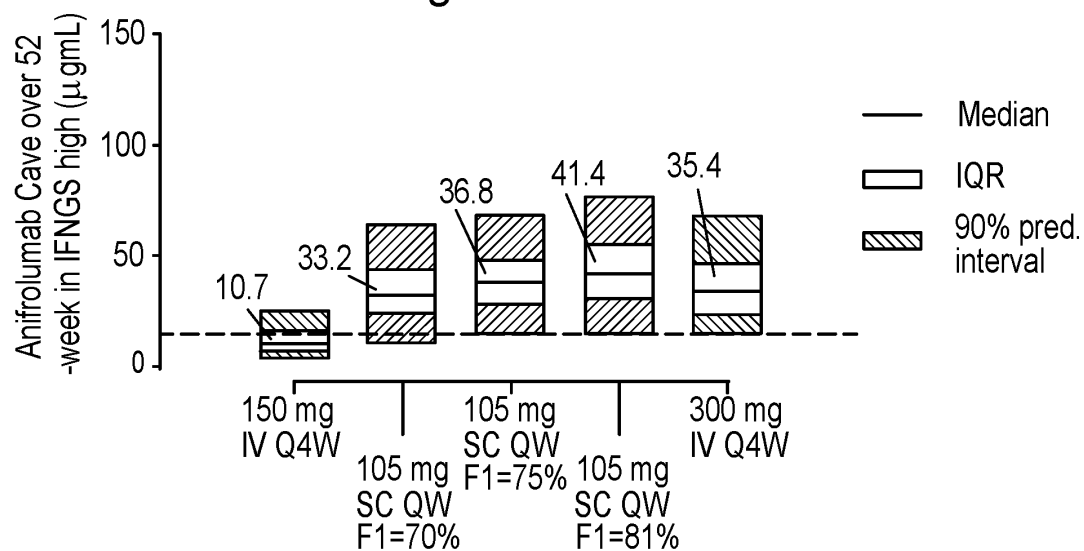


Figure 13B

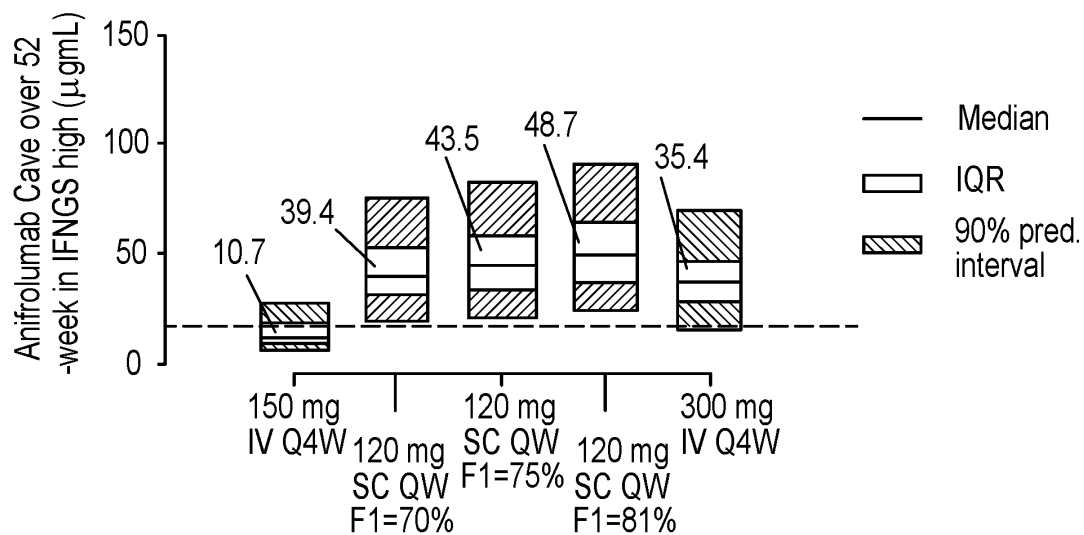


Figure 13C

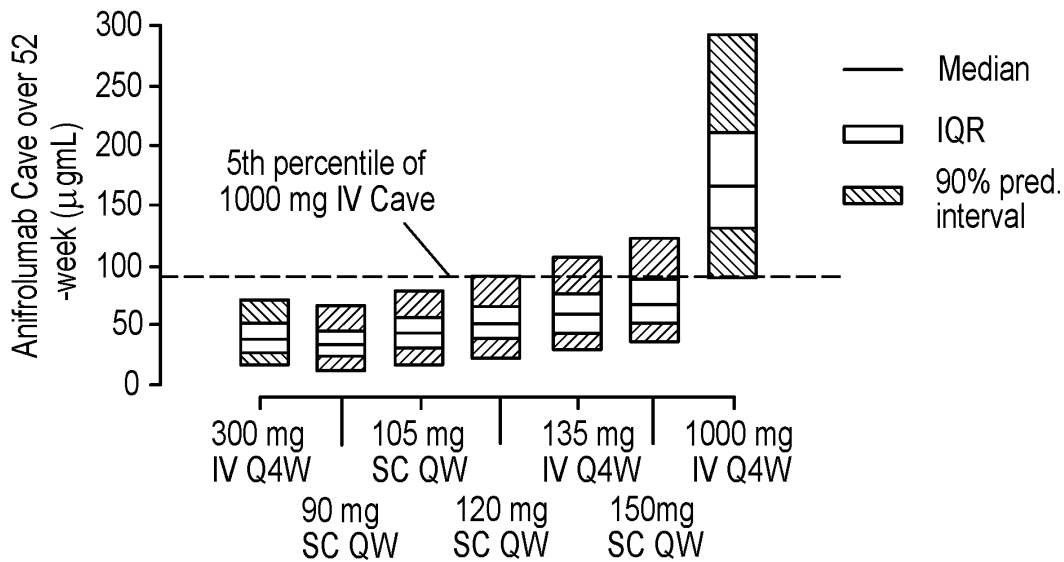


Figure 14A

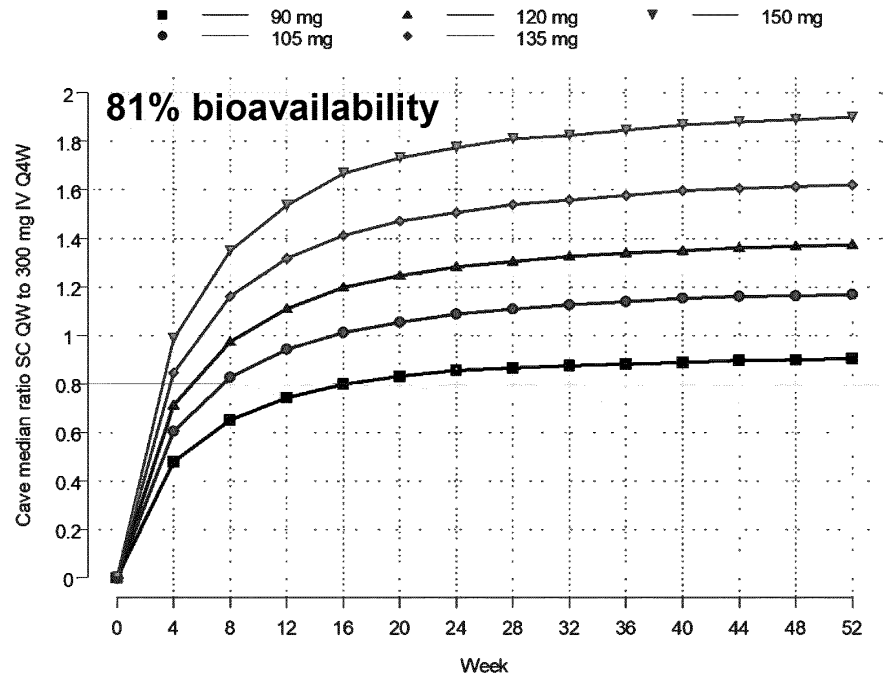


Figure 14B

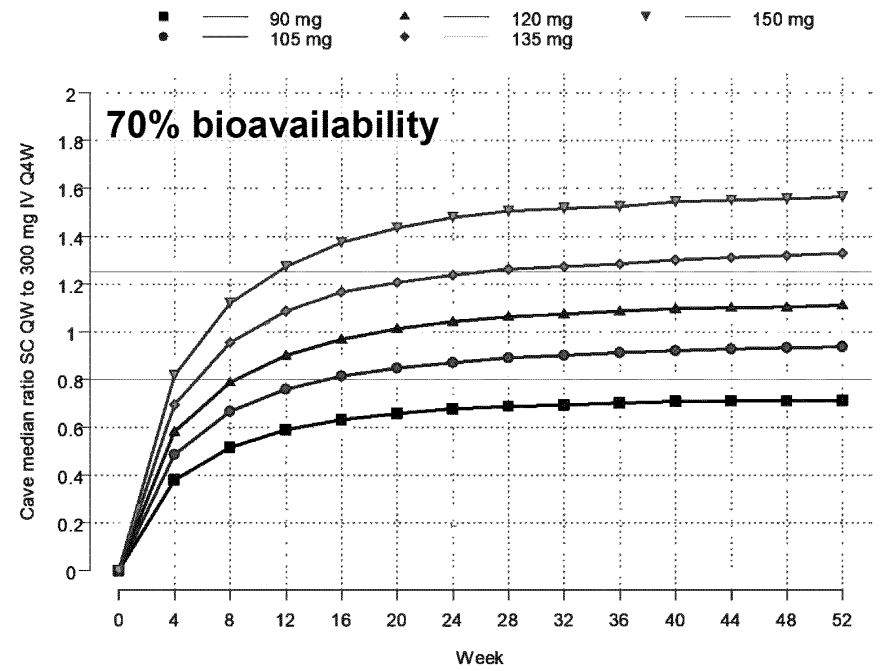


Figure 15

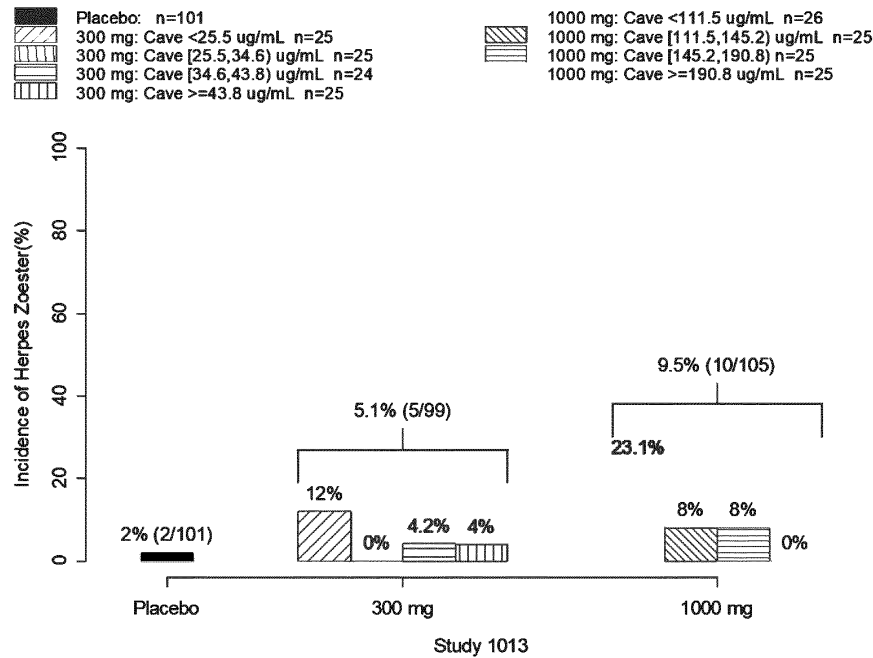


Figure 16

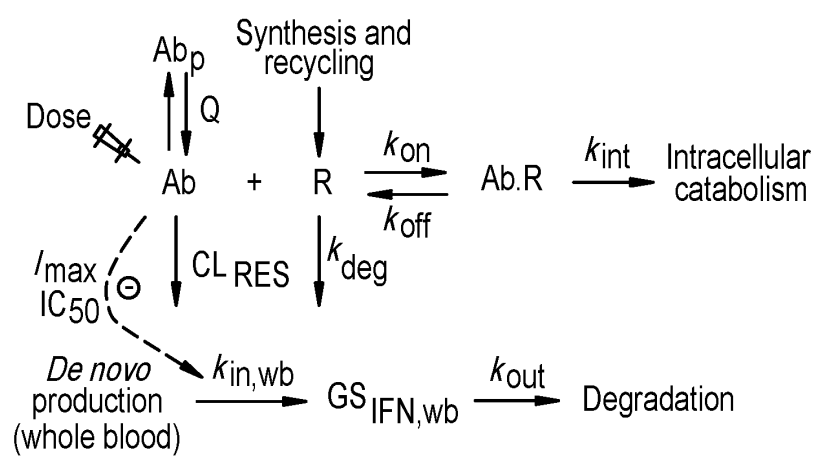


Figure 17

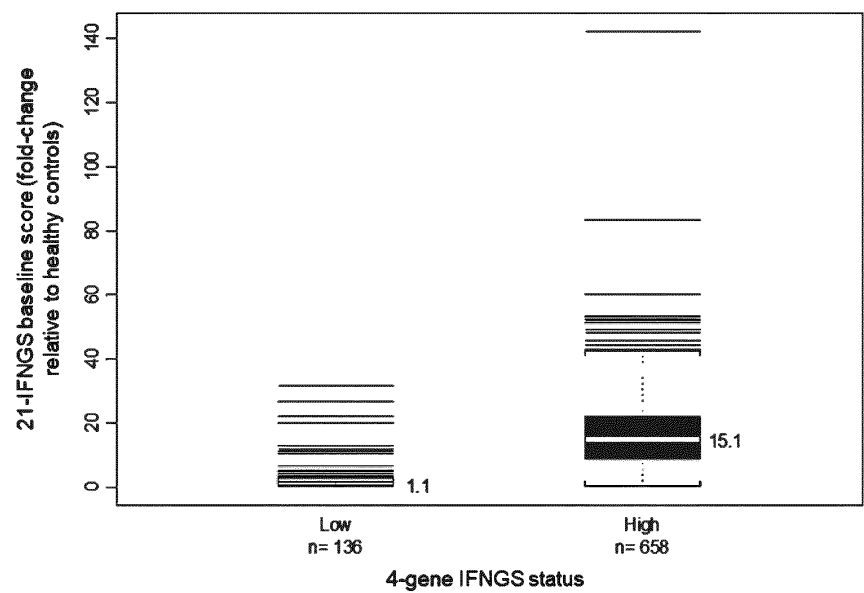


Figure 18

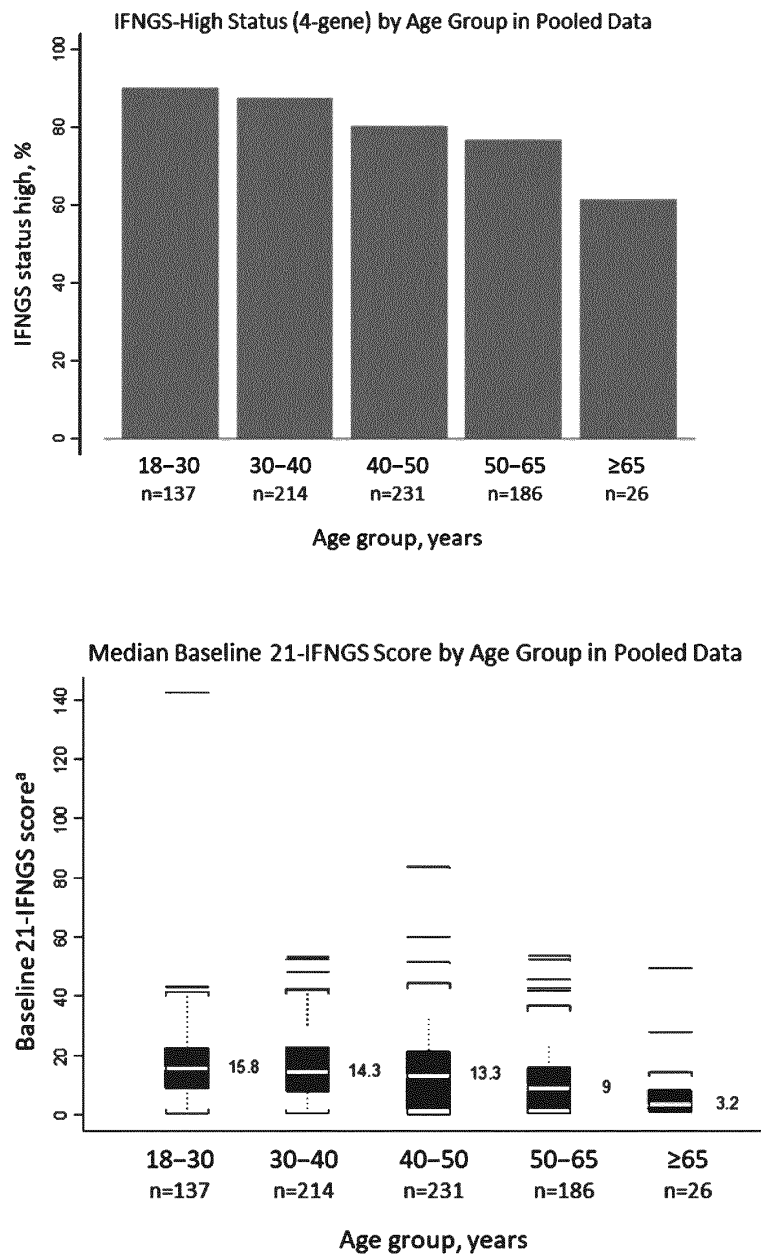


Figure 19

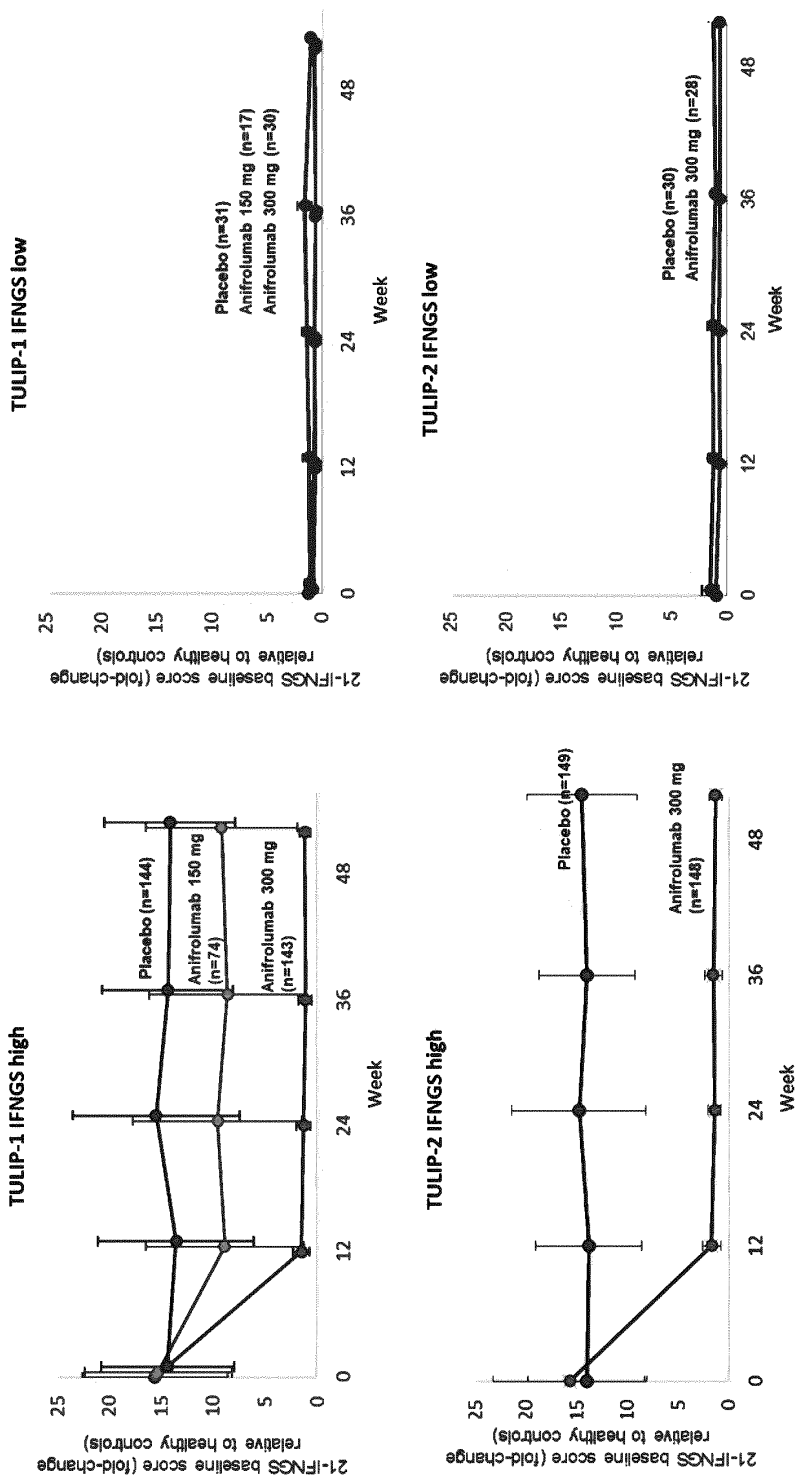


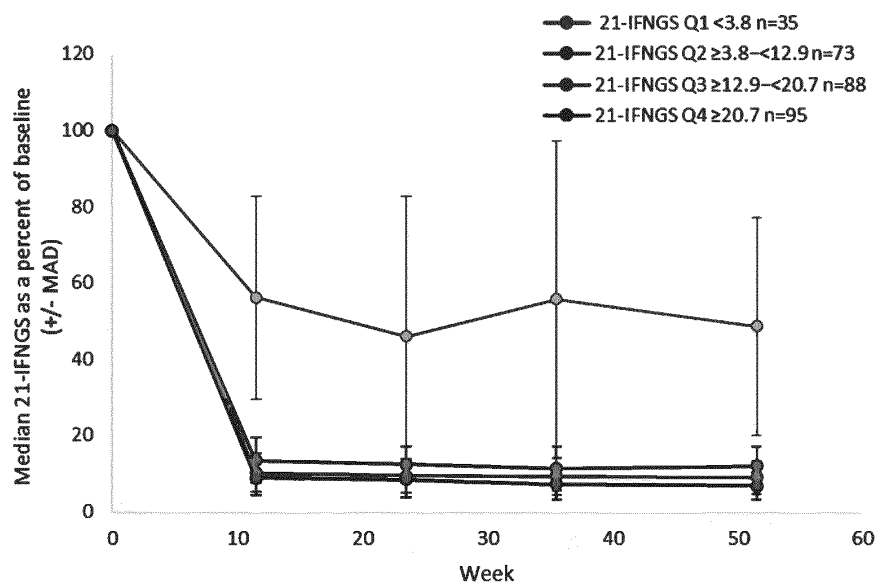
Figure 20

Figure 21A

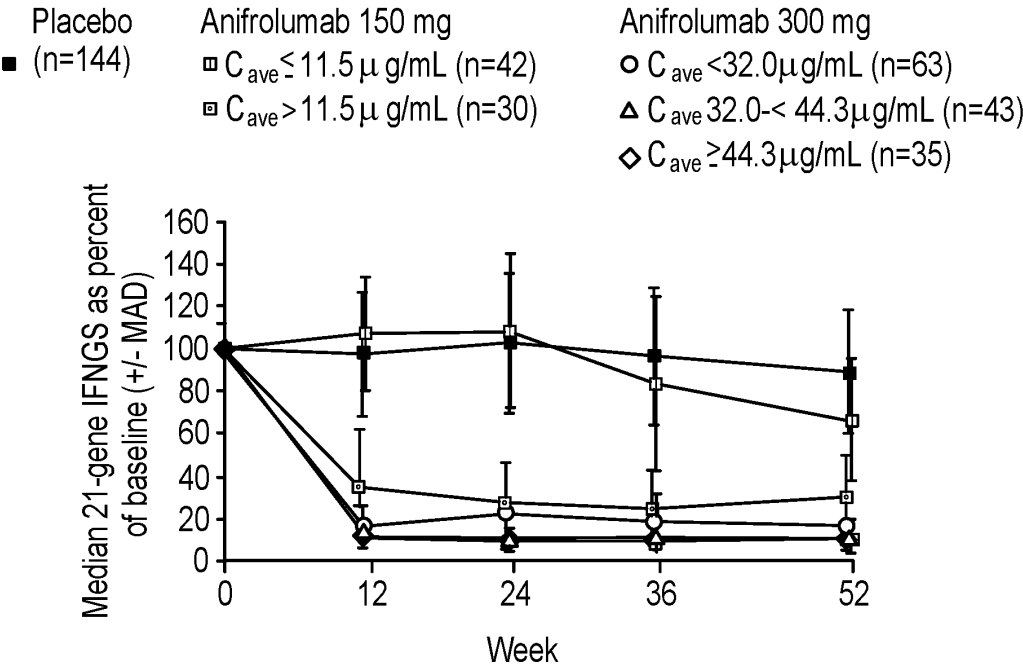


Figure 21B

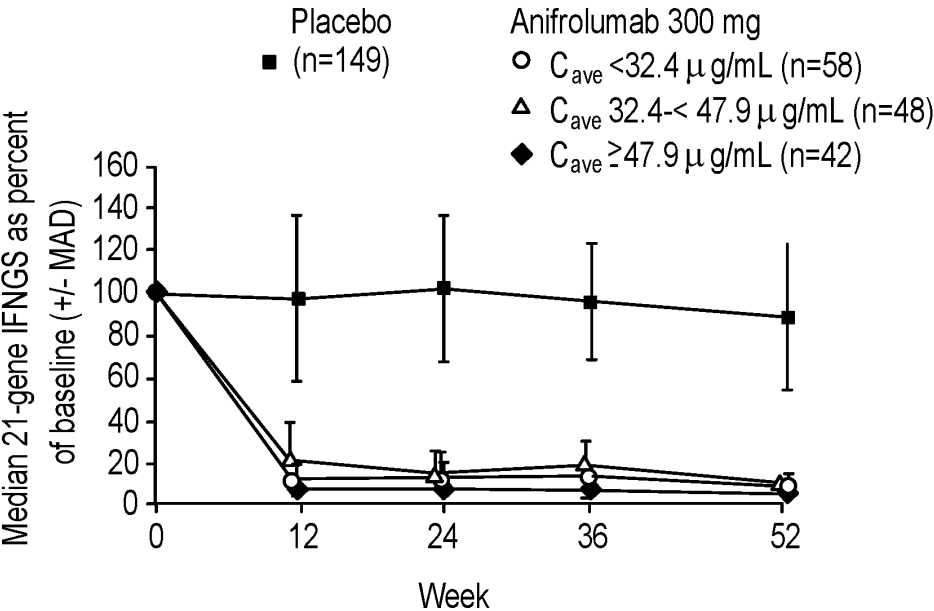


Figure 22

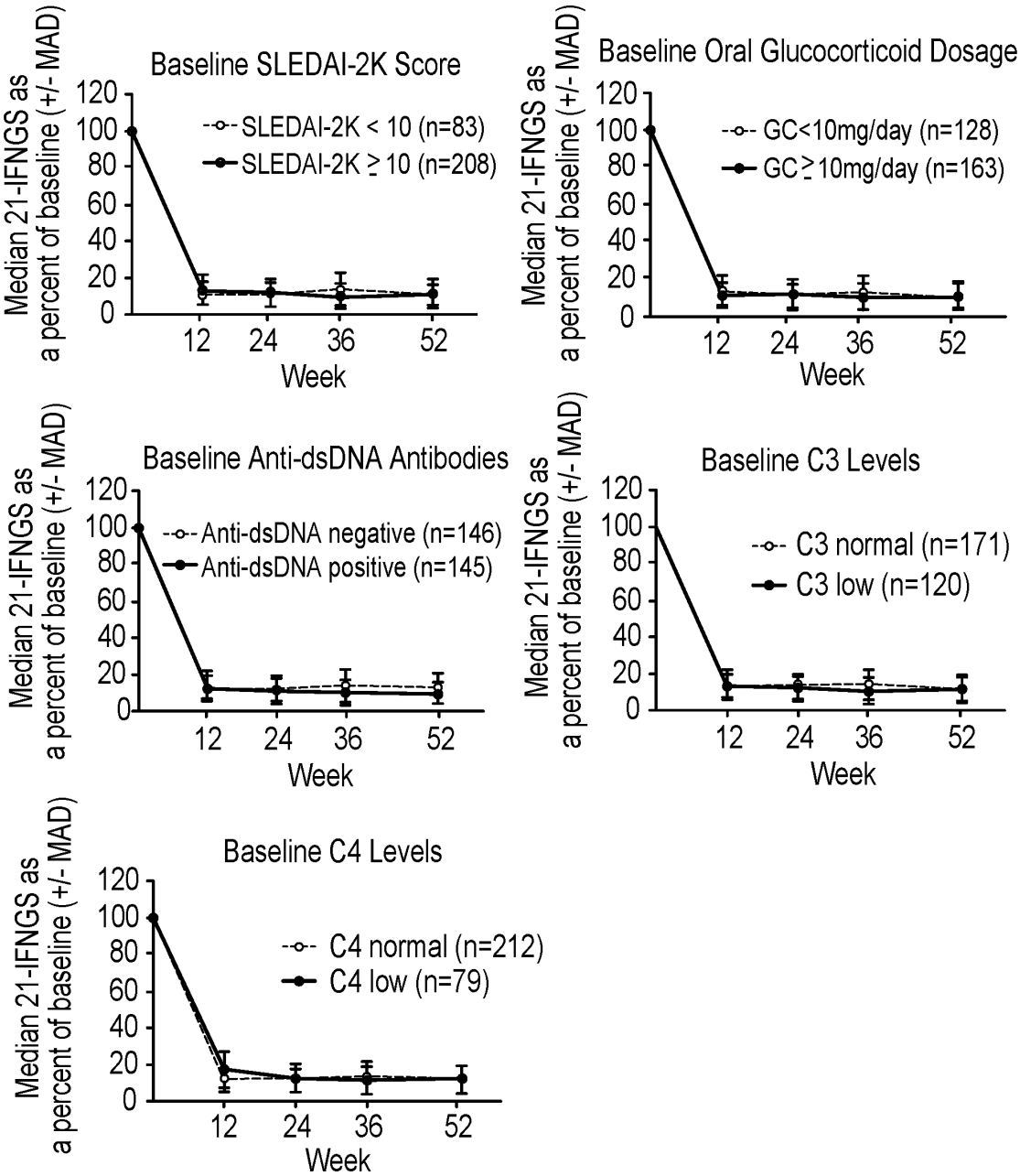


Figure 23

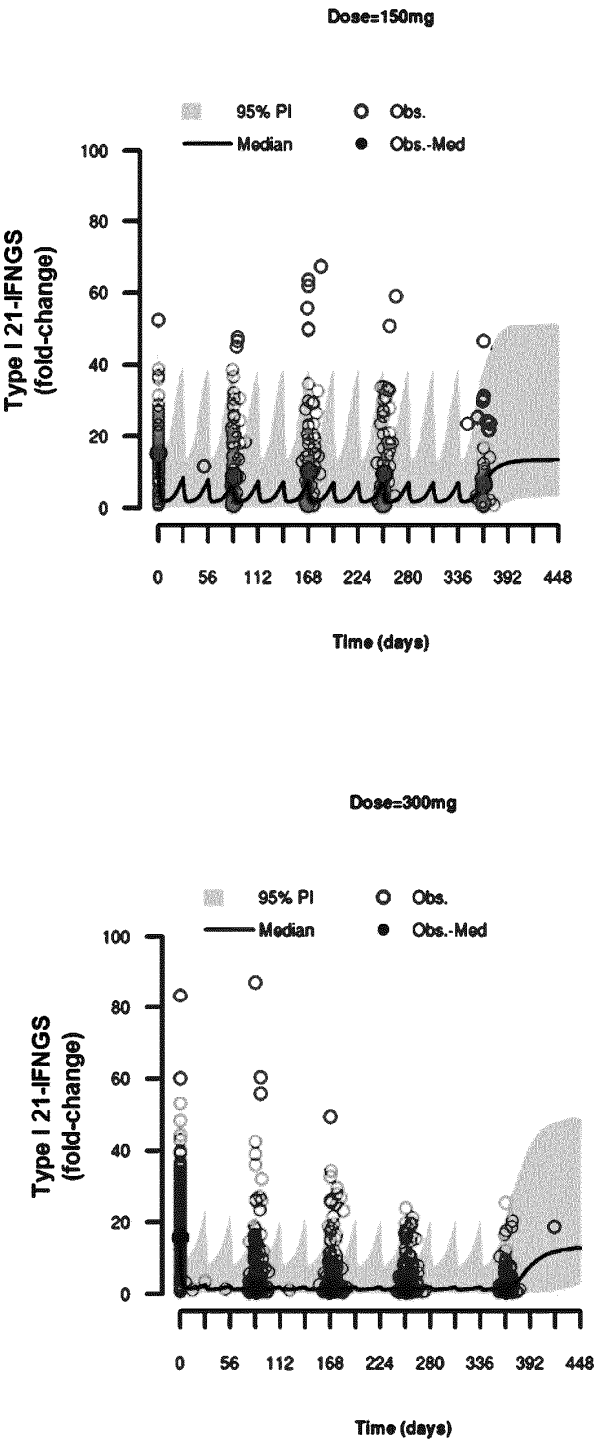


Figure 24

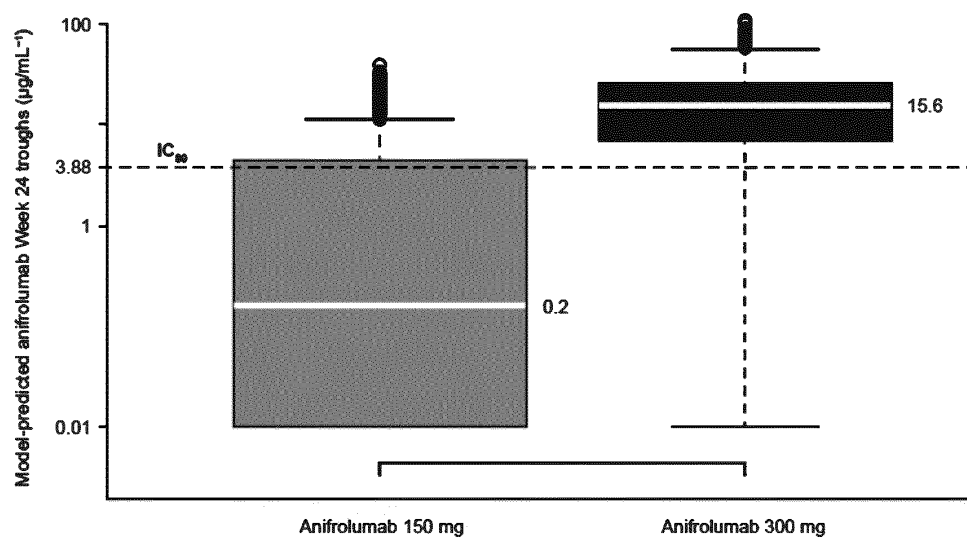


Figure 25A

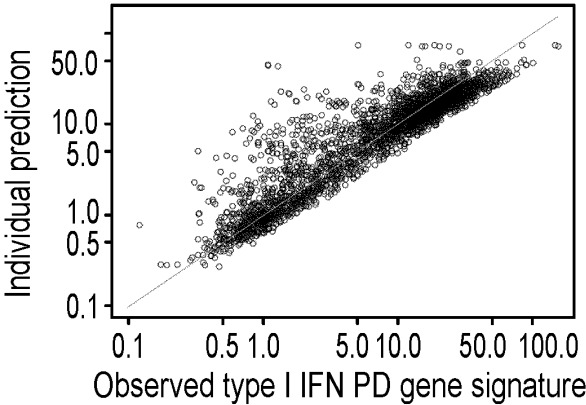


Figure 25B

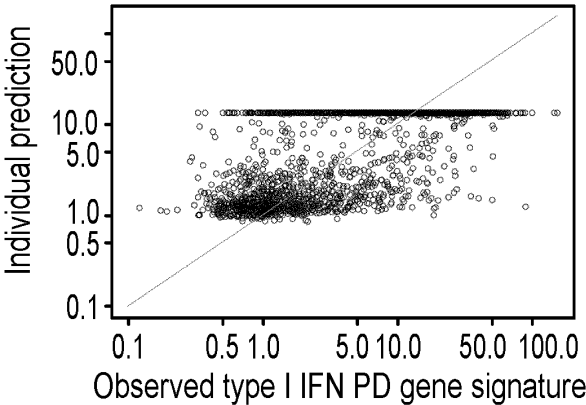


Figure 25C

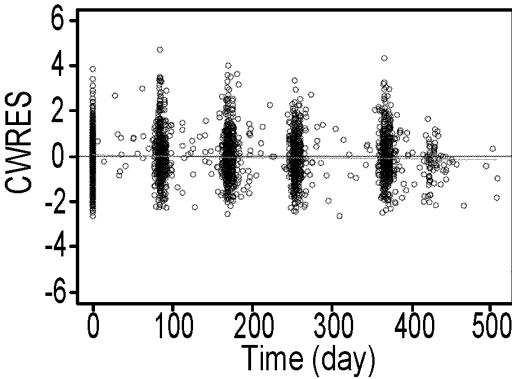


Figure 25D

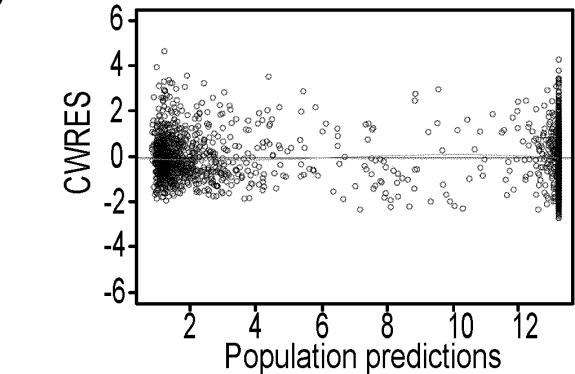


Figure 26A

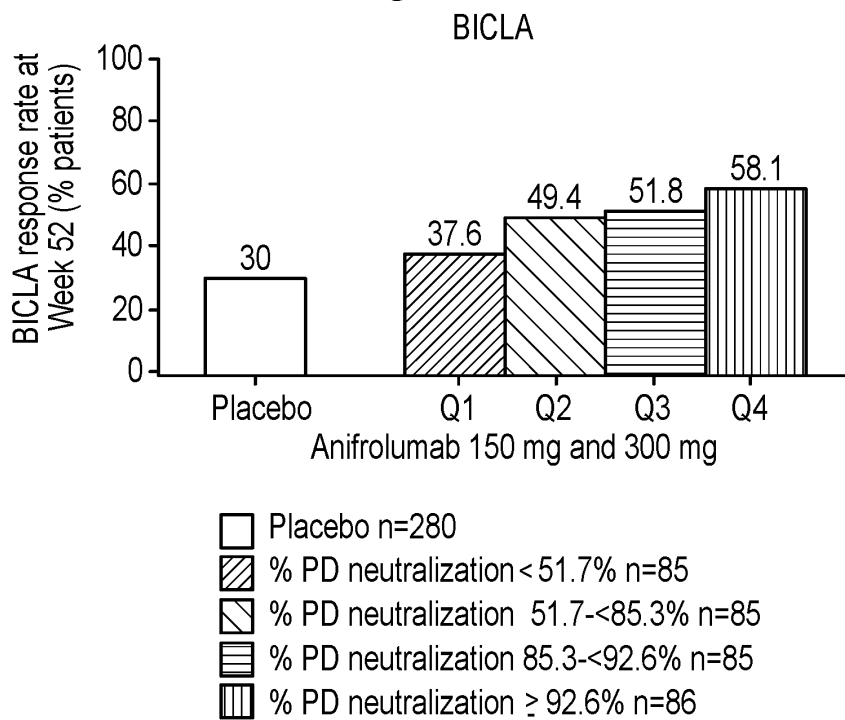
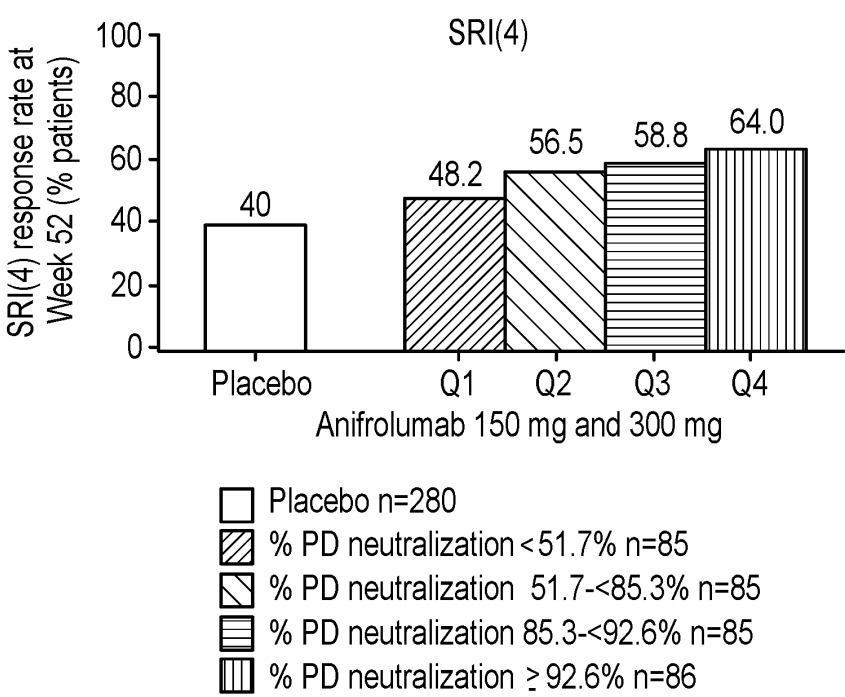


Figure 26B



SUBSTITUTE SHEET (RULE 26)

Figure 27

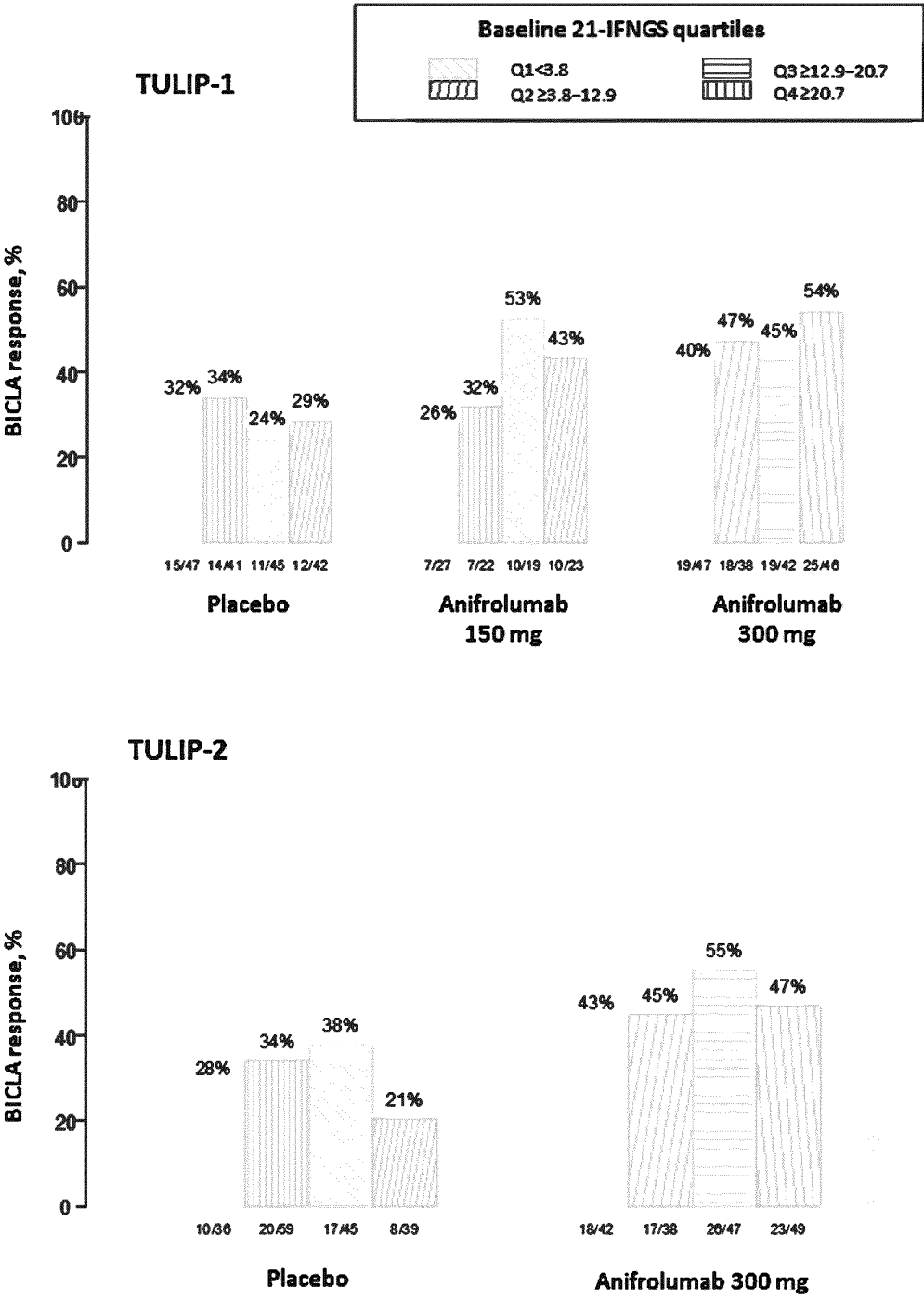


Figure 28

Gene title	Gene symbol	Gene Probe ID
Interferon, alpha-inducible protein 27	IFI27	202411
Interferon, alpha-inducible protein 6	IFI6	204415
Radical S-adenosyl methionine domain containing 2	RSAD2	213797
Interferon-induced protein 44	IFI44	214059
Interferon-induced protein 44-like	IFI44L	204439
Ubiquitin specific peptidase 18	USP18	219211
Lymphocyte antigen 6 complex, locus E	LY6E	202145
2,5-oligoadenylate synthetase 1, 40/46 kDa	OAS1	202869
Sialic acid binding Ig-like lectin 1, sialoadhesin	SIGLEC1	44673
ISG15 ubiquitin-like modifier	ISG15	205483
Interferon-induced protein with tetratricopeptide repeats 1	IFIT1	203153
2'-5'-oligoadenylate synthetase 3, 100 kDa	OAS3	218400
Hect domain and RLD 5	HERC5	219863
Myxovirus (influenza virus) resistance 1	MX1	202086
Lysosomal-associated membrane protein 3	LAMP3	205569
Epithelial stromal interaction 1 (breast)	EPSTI1	227609
Interferon-induced protein with tetratricopeptide repeats 3	IFIT3	204747
2'-5'-oligoadenylate synthetase 2, 69/71 kDa	OAS2	204972
Receptor (chemosensory) transporter protein 4	RTP4	219684
Phospholipid scramblase 1	PLSCR1	241916
DNA polymerase-transactivated protein 6	DNAPTP6	241812

Figure 29A

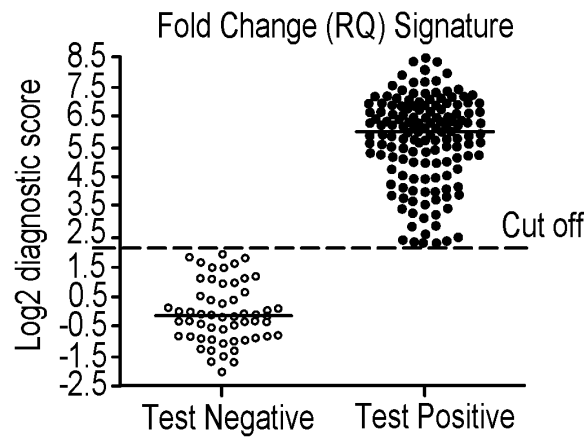


Figure 29B

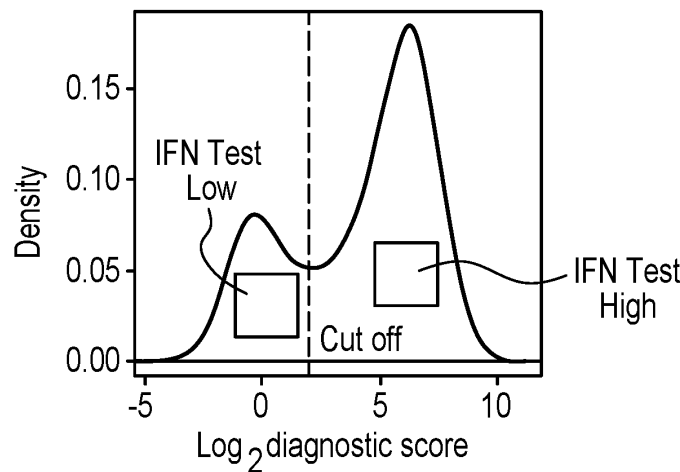
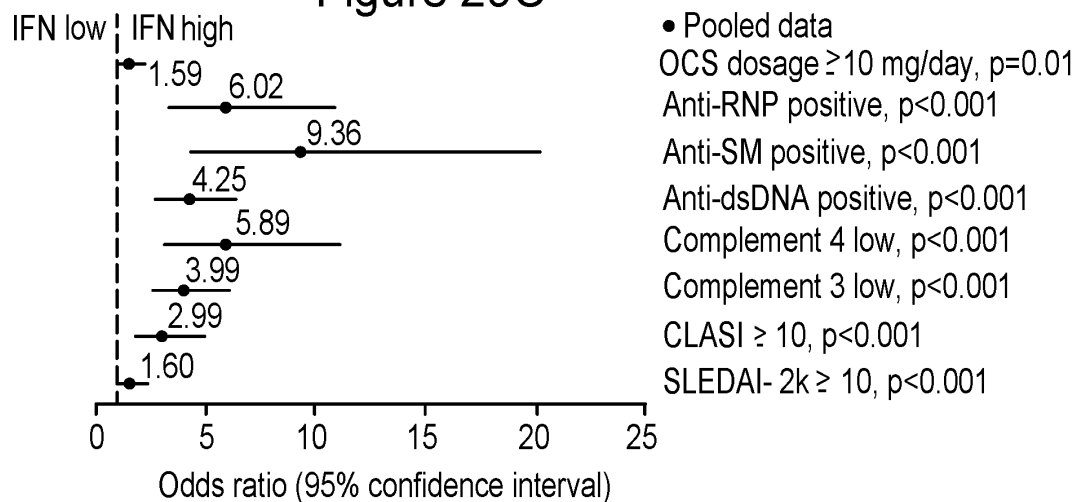


Figure 29C



SUBSTITUTE SHEET (RULE 26)

Figure 30A

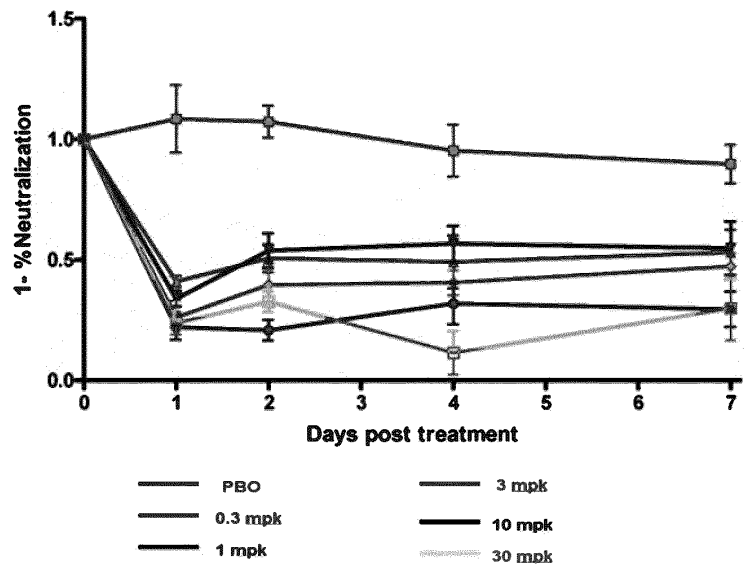


Figure 30B

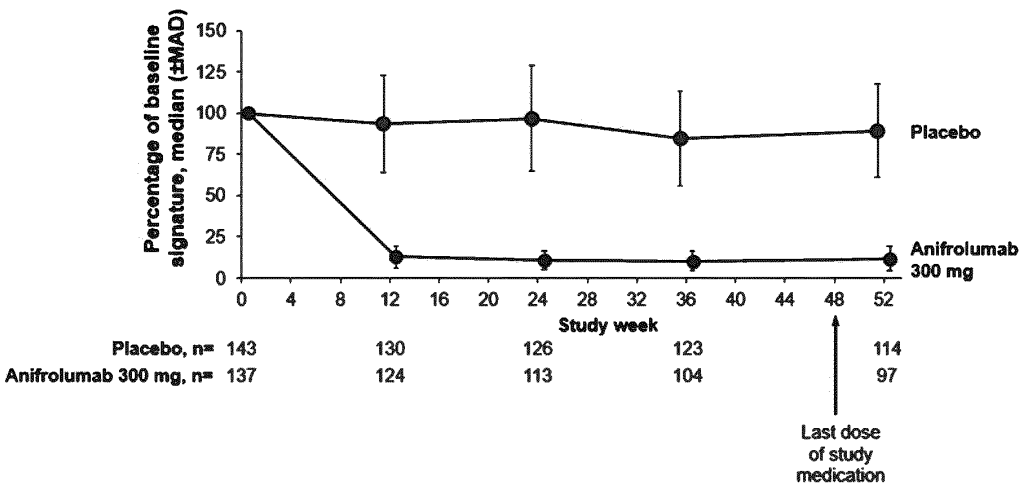


Figure 31A

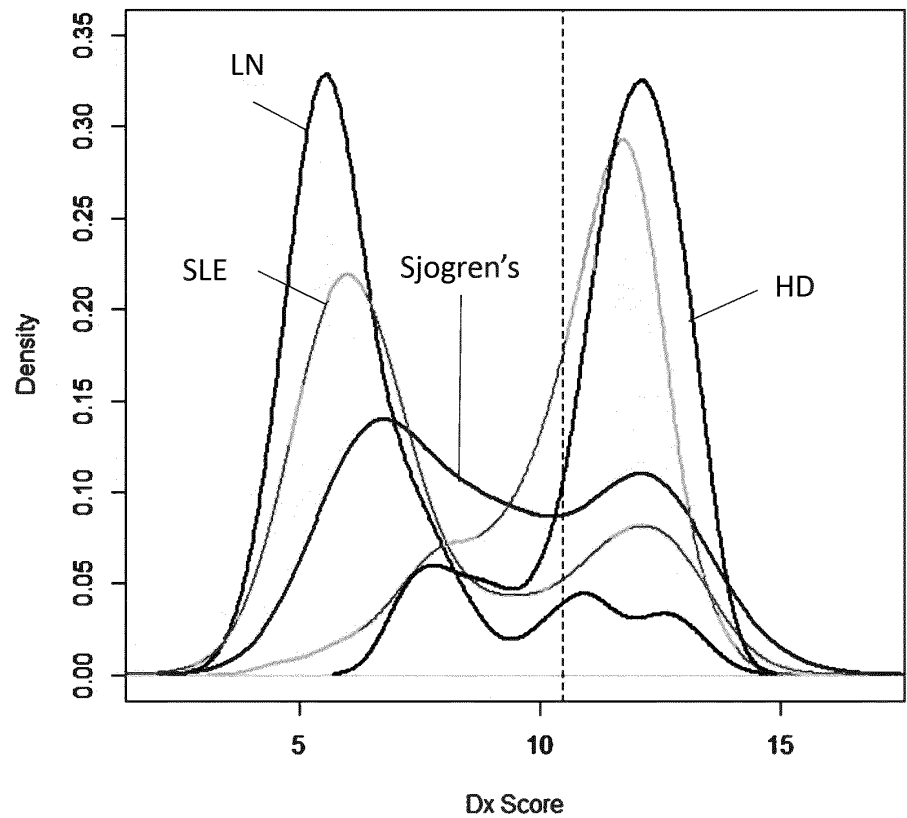


Figure 31B

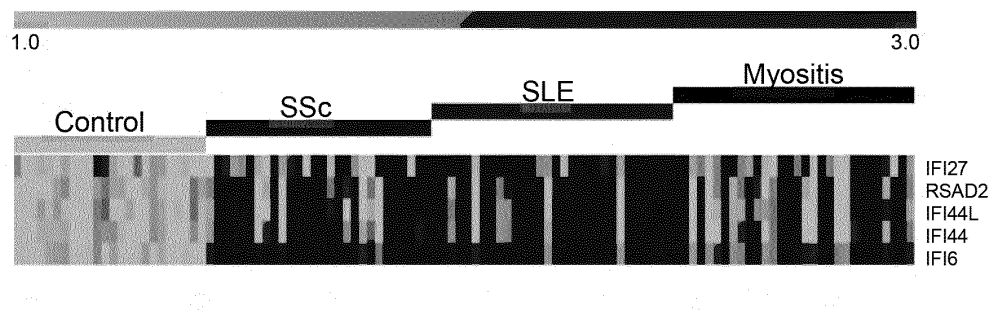


Figure 32B

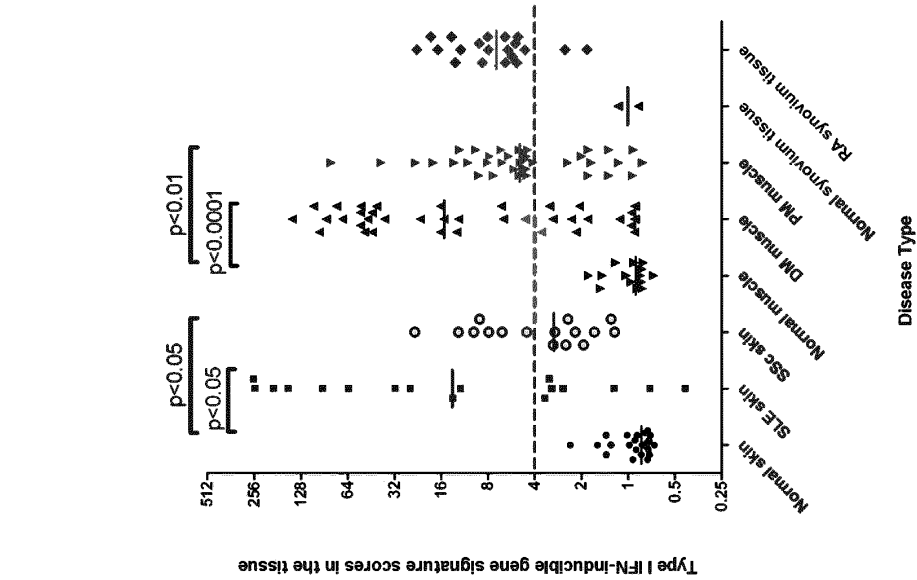


Figure 32A

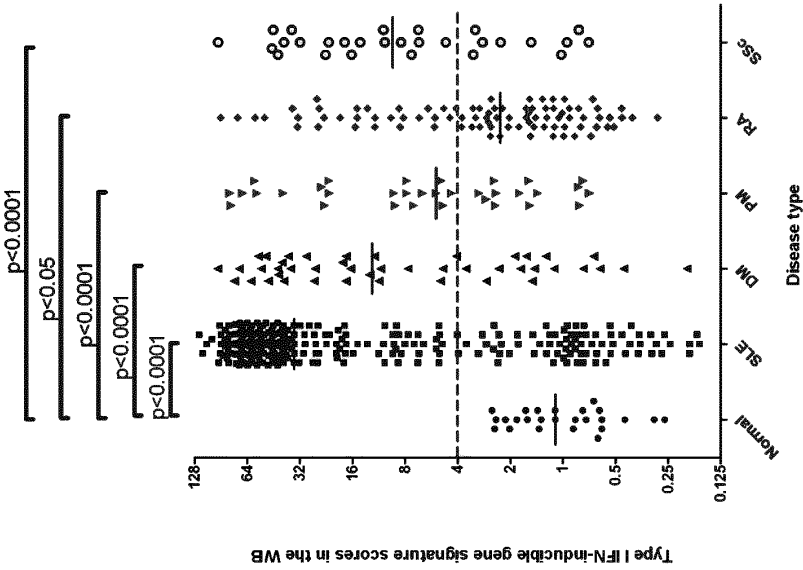


Figure 33

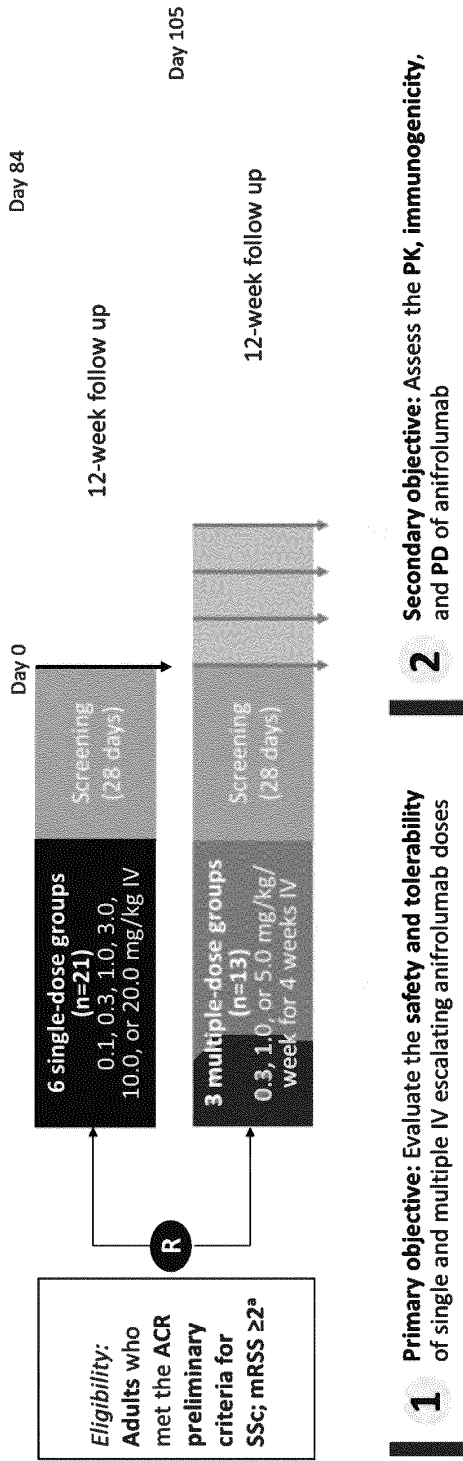


Figure 34A

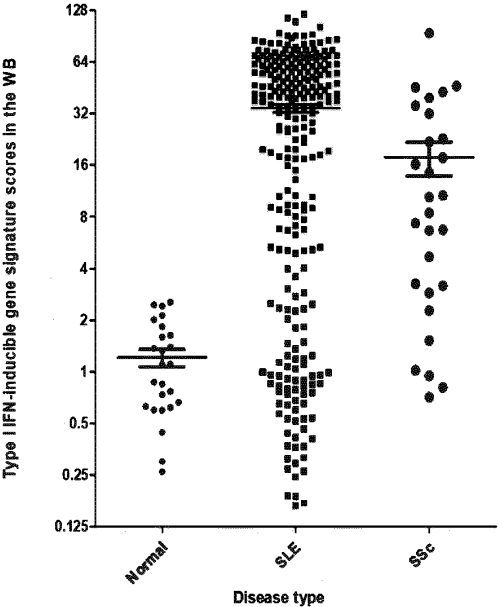


FIG. 34B

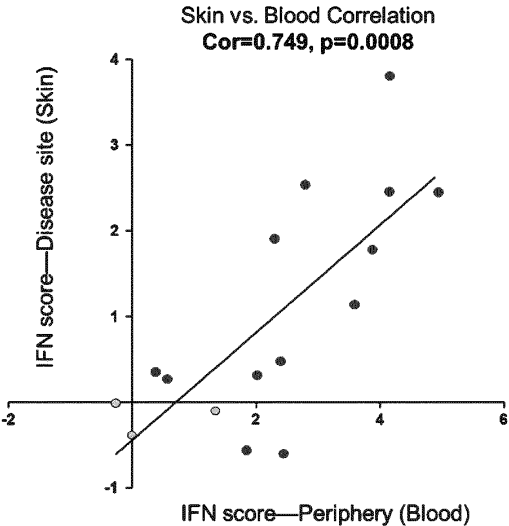


Figure 34C

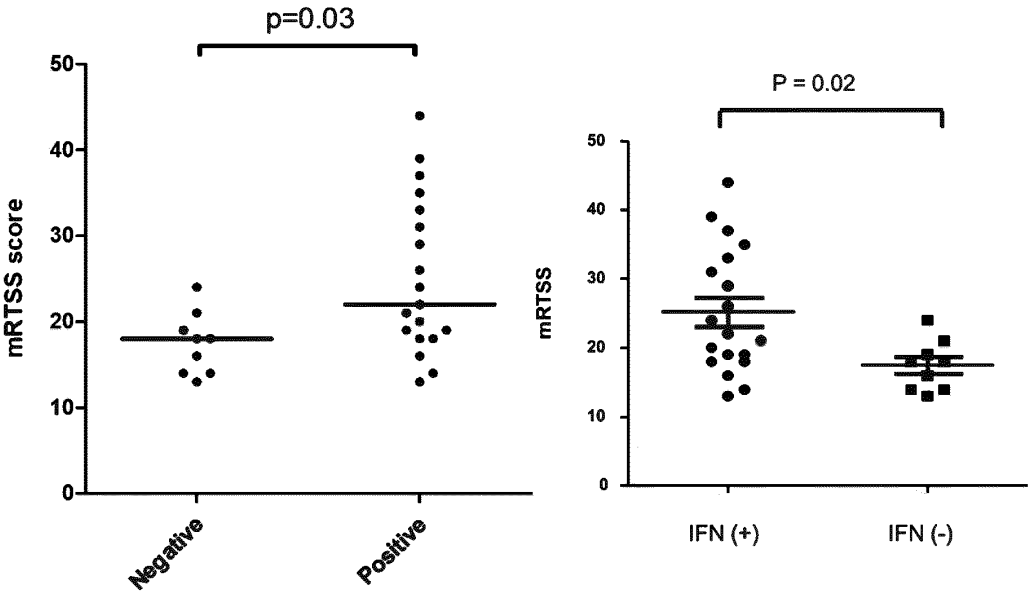


Figure 35

IFNGS Neutralization SD

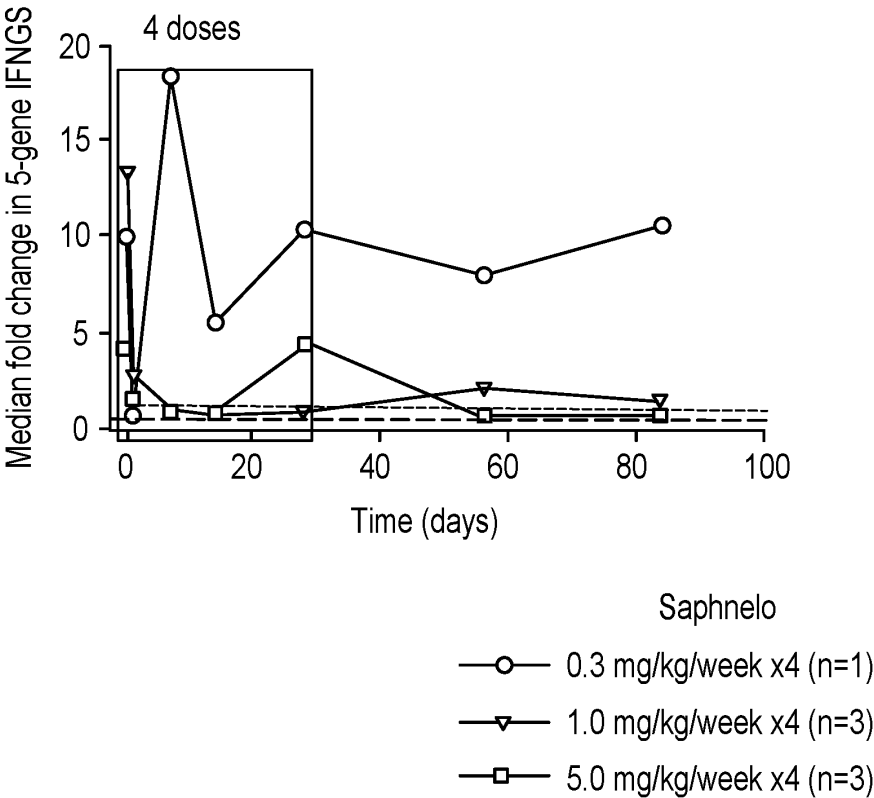


Figure 37

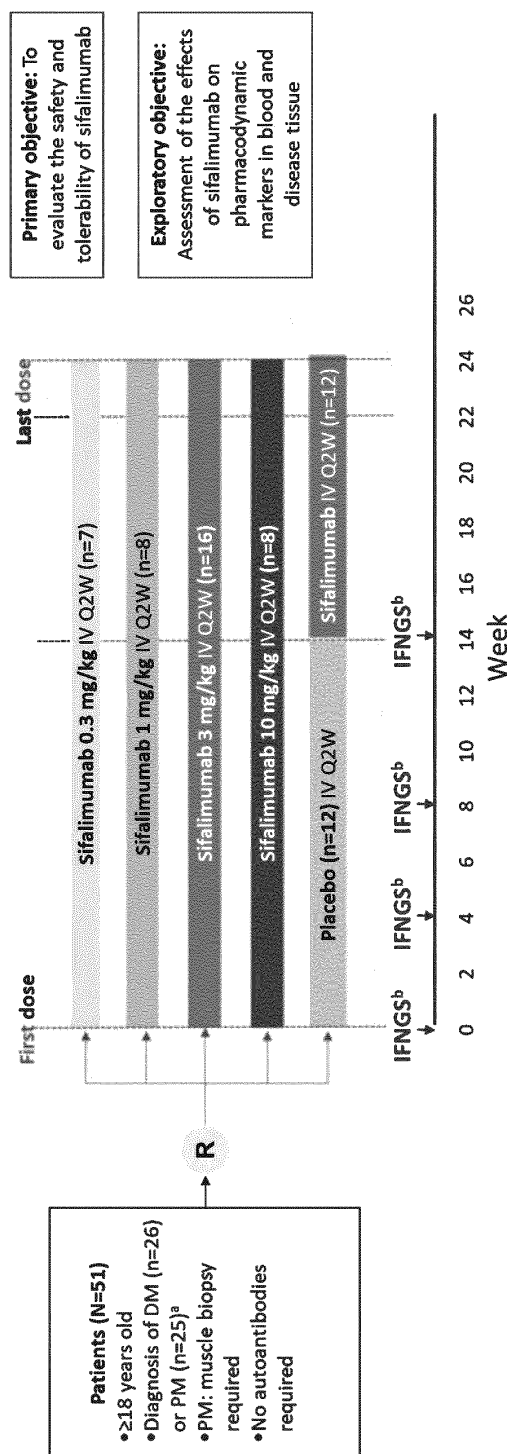


Figure 38

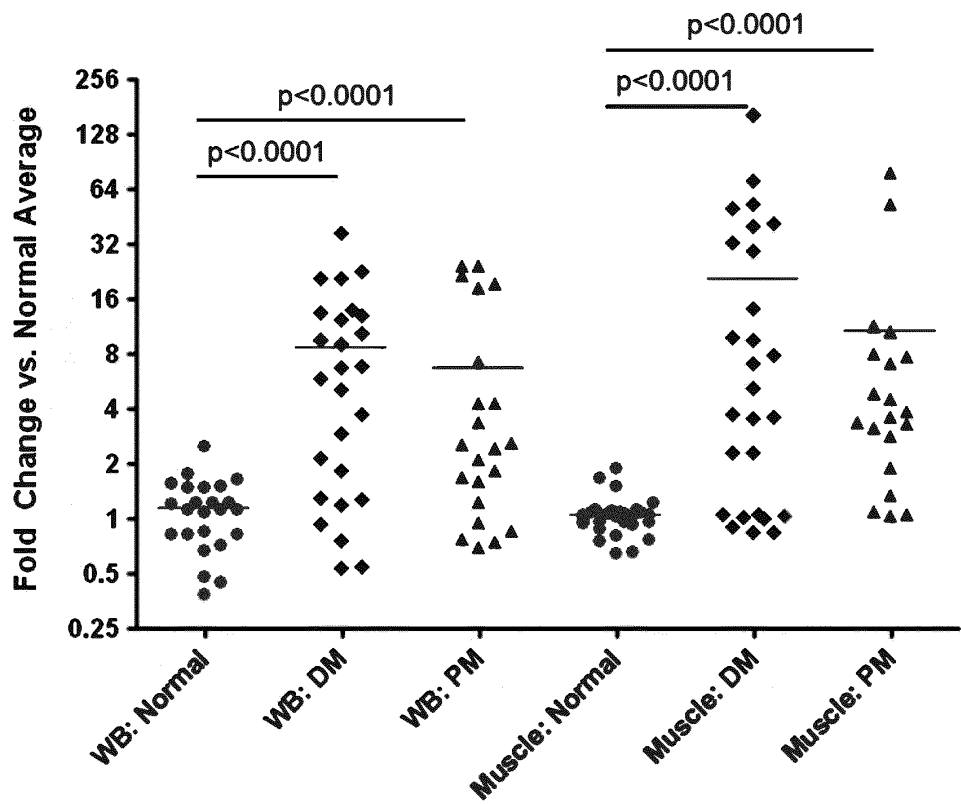


Figure 39

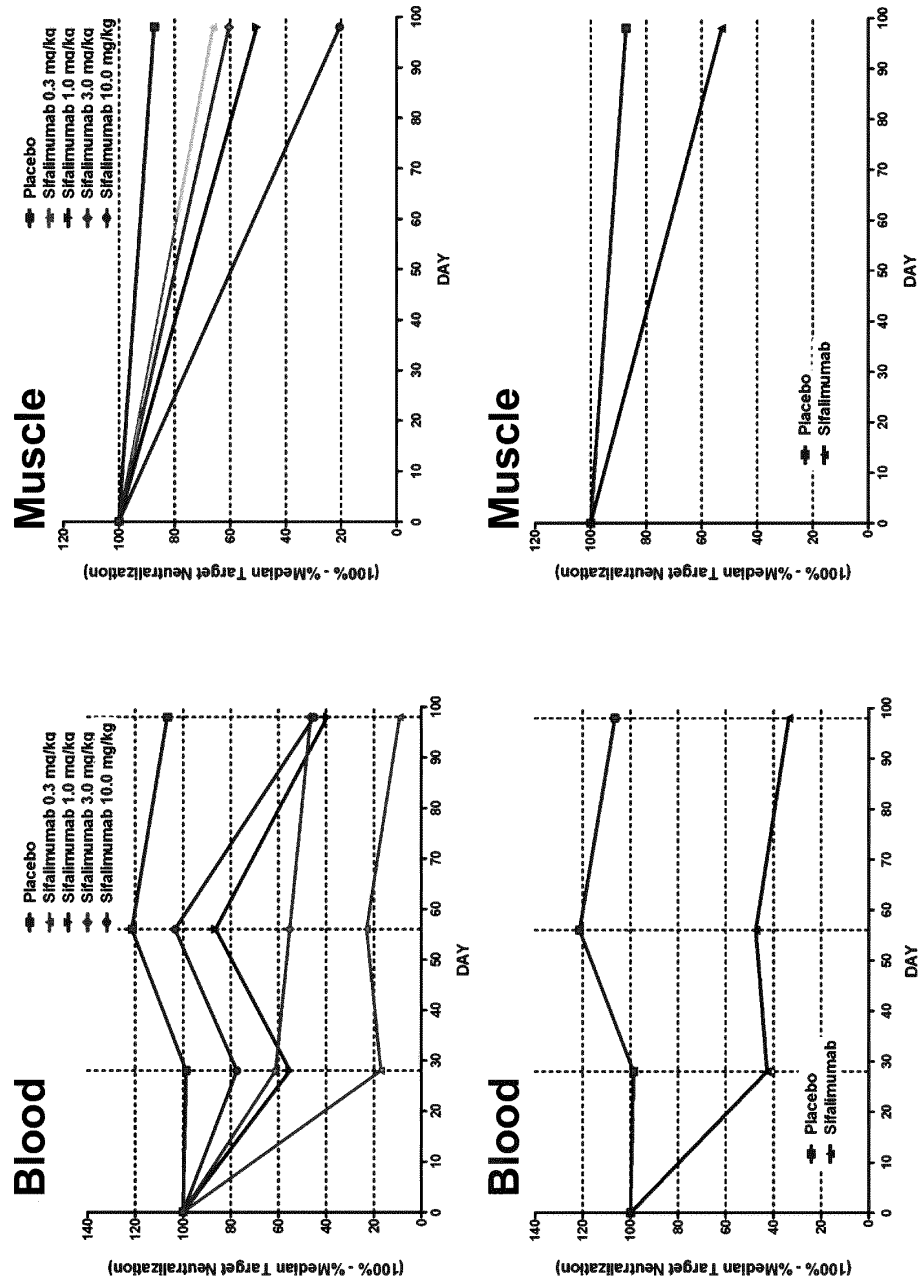


Figure 40A

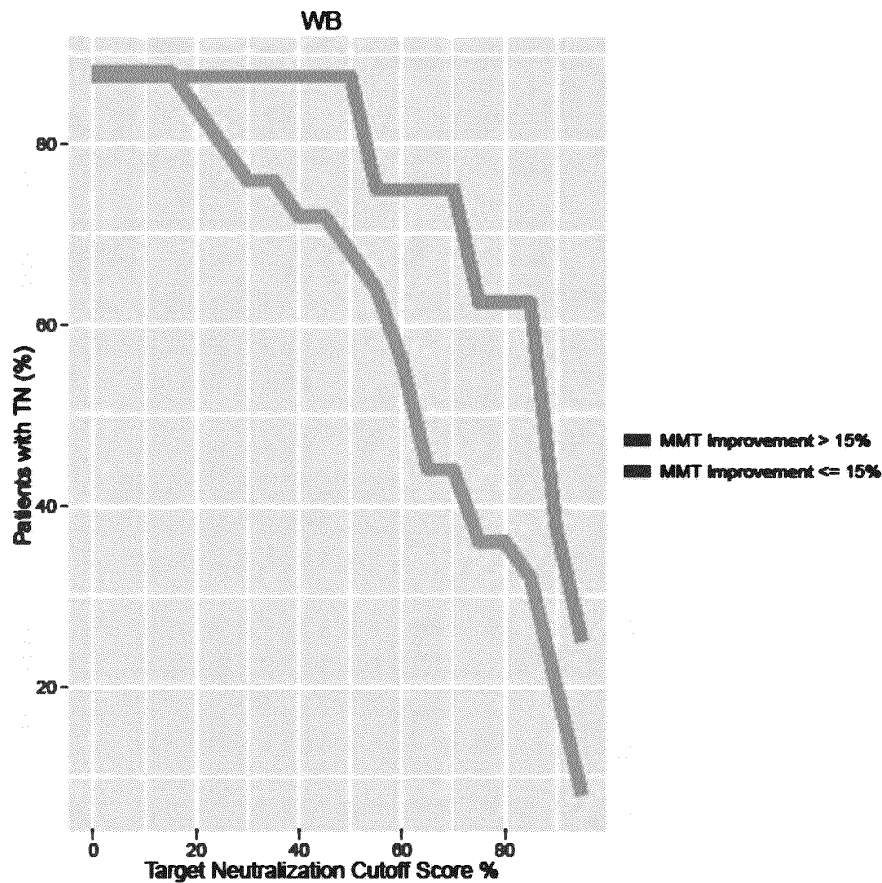


Figure 40B

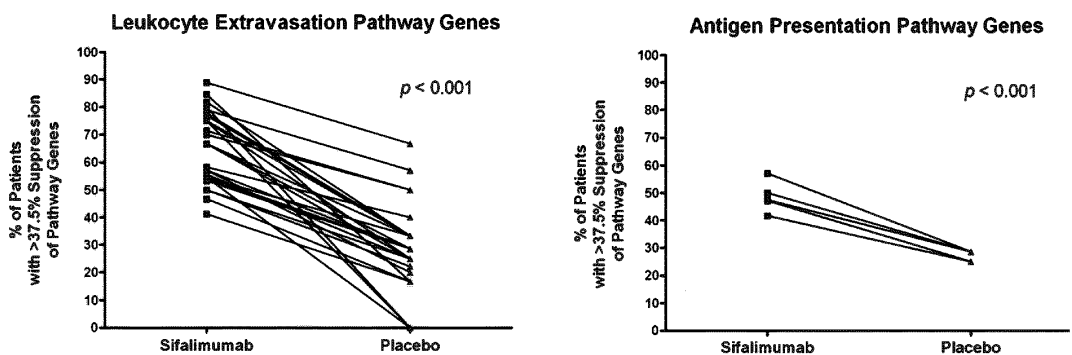


Figure 41

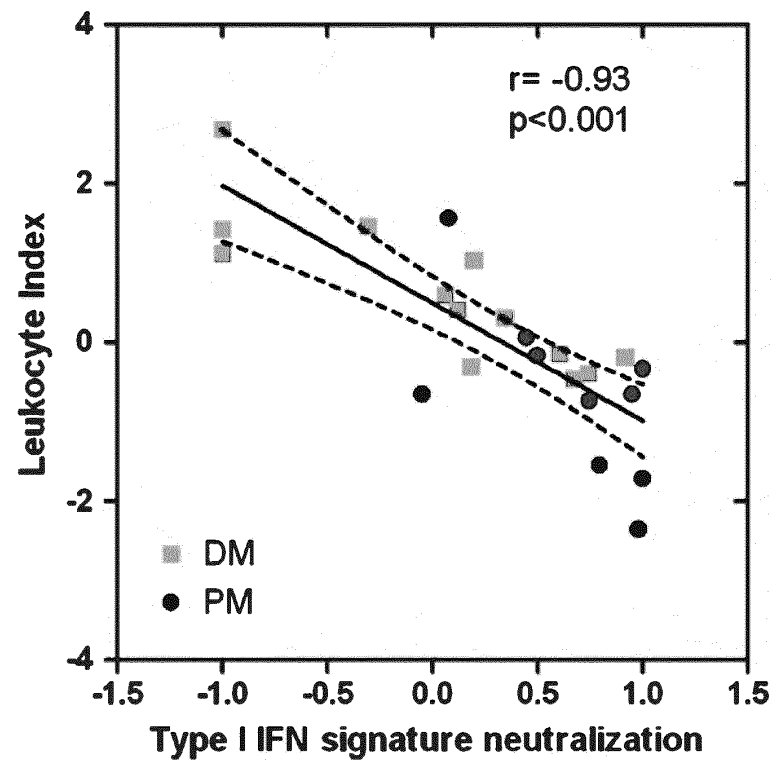


Figure 42A

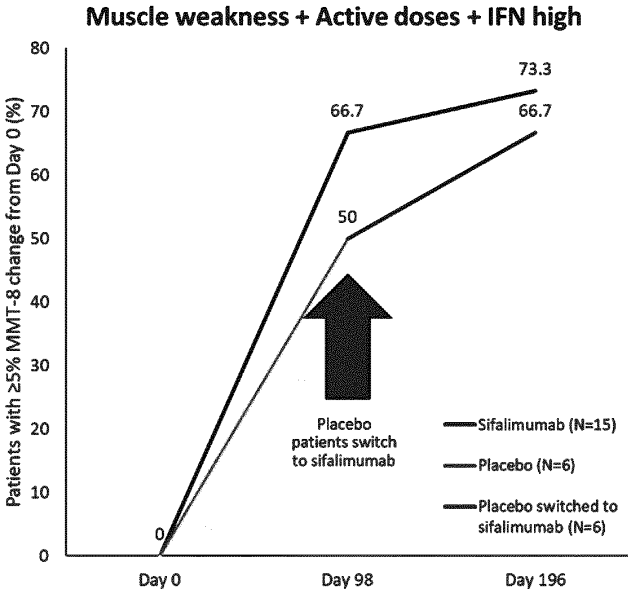


Figure 42B

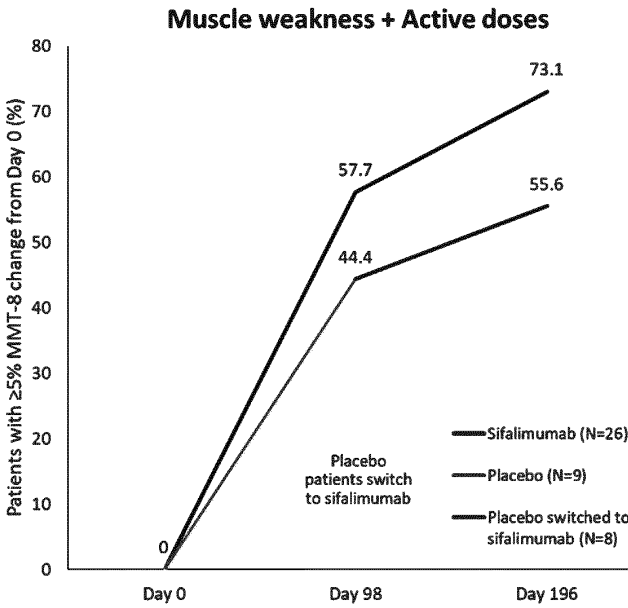
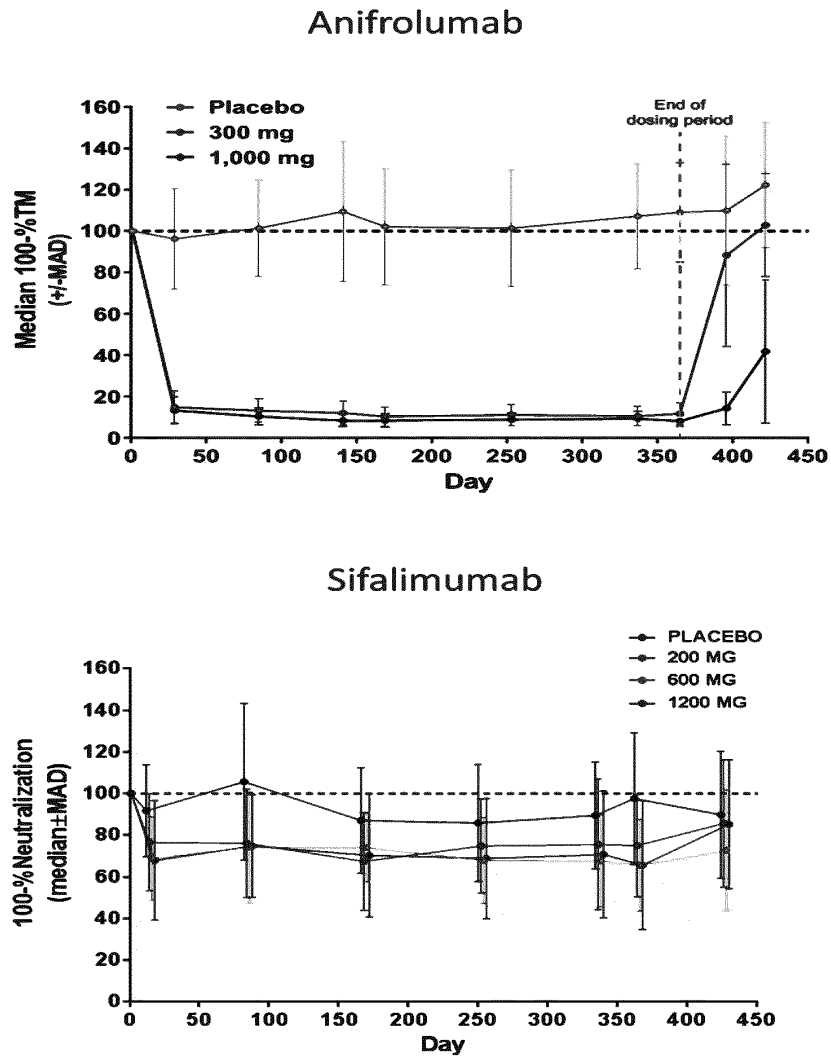


Figure 43



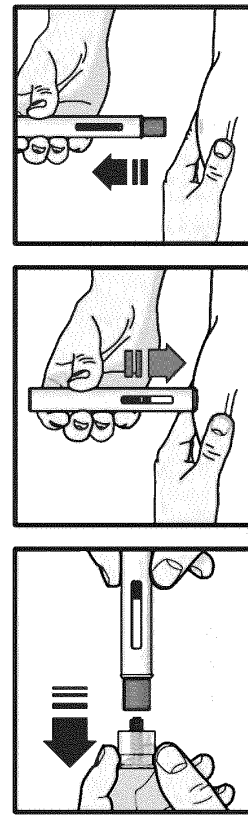
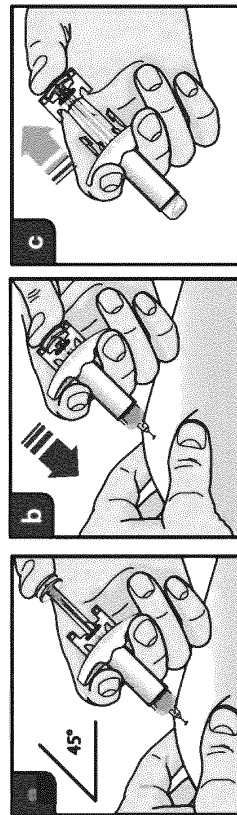
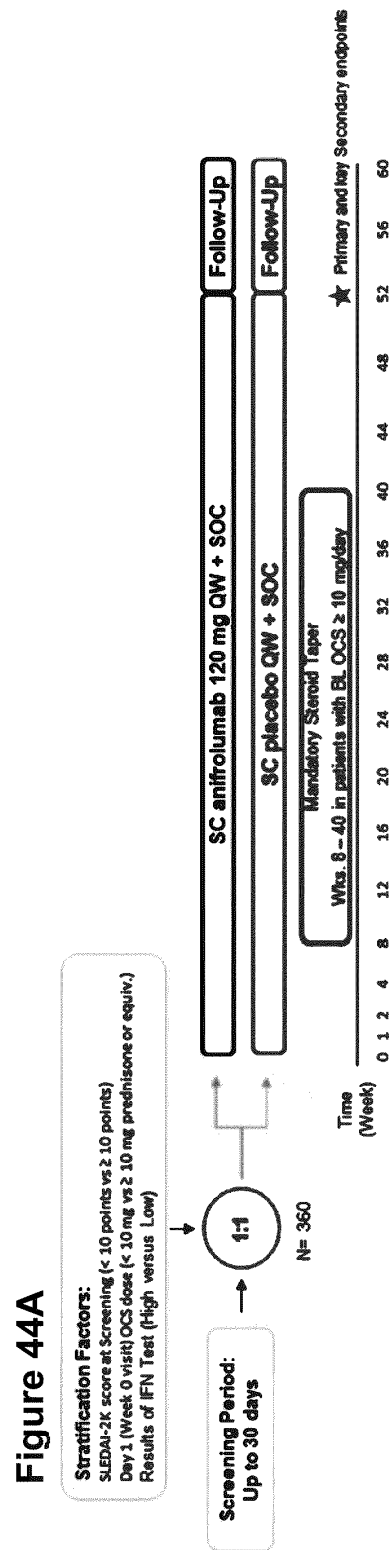


Figure 45A

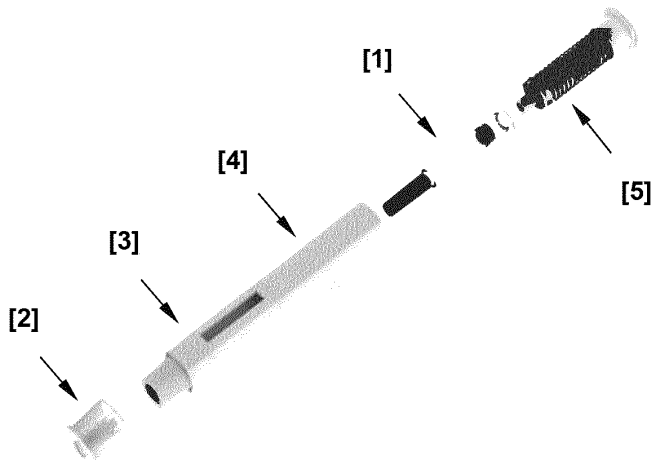


Figure 45B

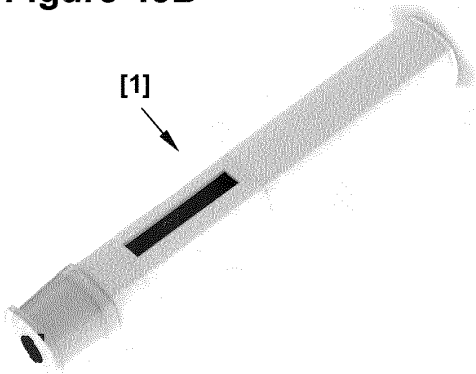


Figure 39C

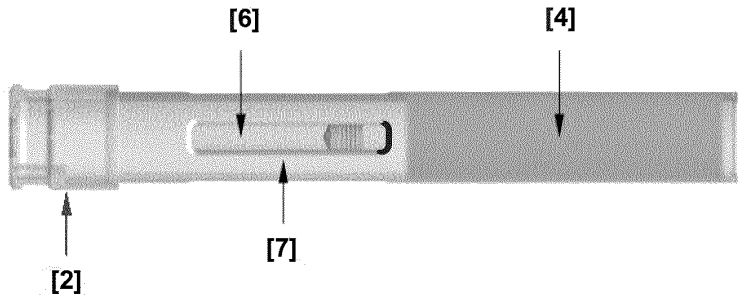


Figure 46A

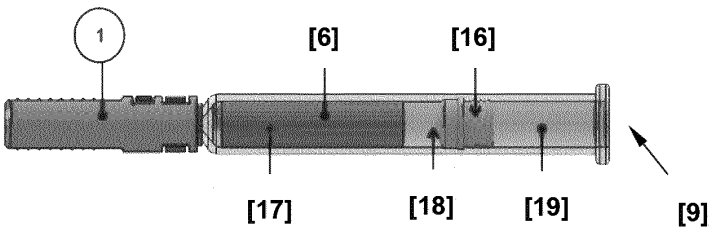


Figure 46B

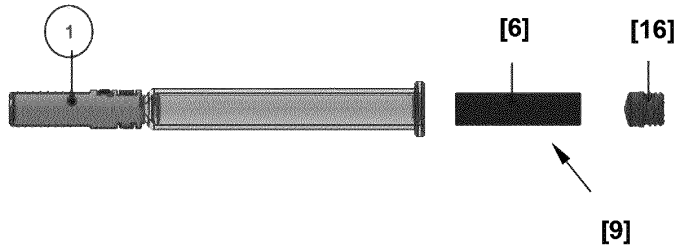


Figure 46C

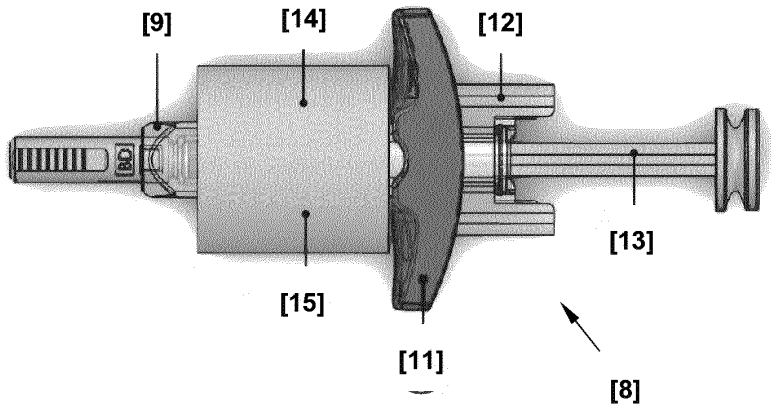


Figure 46D

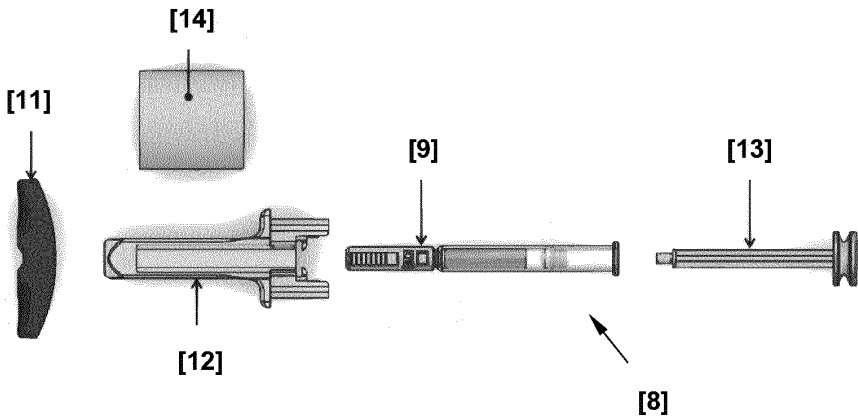


Figure 47

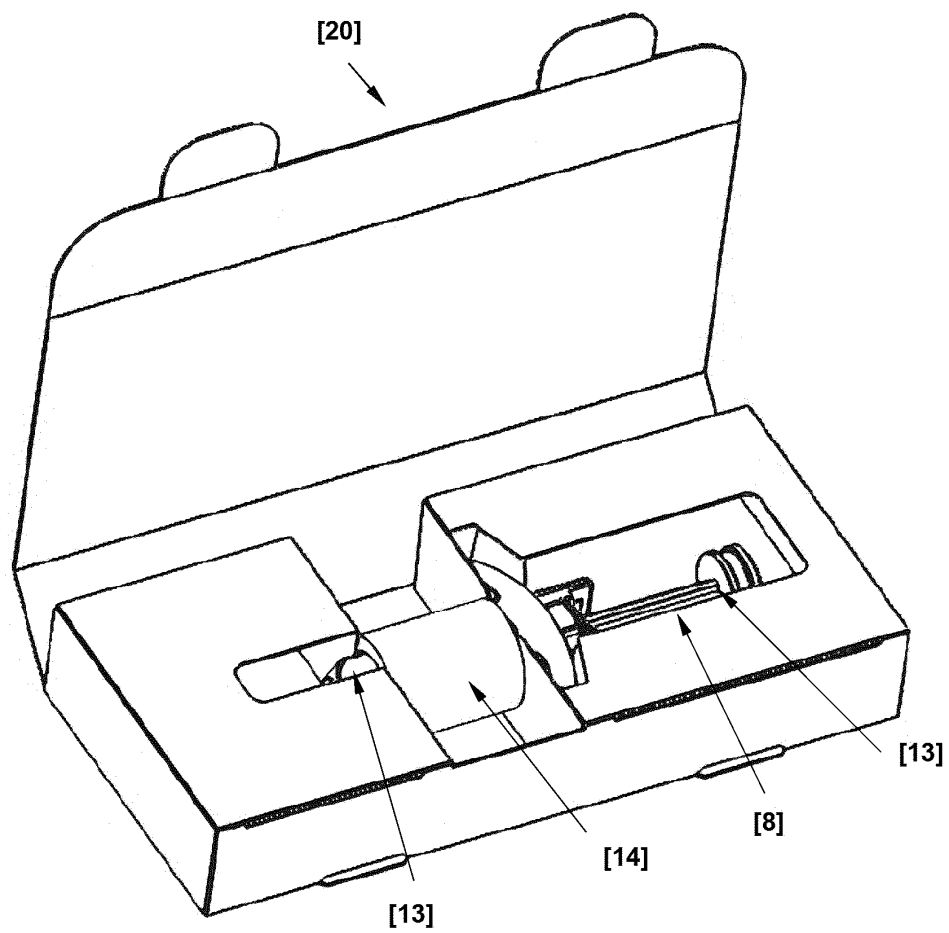


Figure 48

Consensus	EVQLVQSGAEVKKPGESLKISCKGSGYIFTNYWIAWVRQMPGKGLSEMGIIYPGDSDIRYSPSFQGGVTISADKSITTAY	80
SEQ ID NO: 1_anifro-VH	EVQLVQSGAEVKKPGESLKISCKGSGYIFTNYWIAWVRQMPGKGLSEMGIIYPGDSDIRYSPSFQGGVTISADKSITTAY	80
SEQ ID NO: 3_anifro-HCDR1	-----NYWIA-----	50
SEQ ID NO: 4_anifro-HCDR2	-----IITYPGDSDIRYSPSFQG-----	31
SEQ ID NO: 5_anifro-HCDR2	-----	
SEQ ID NO: 10_anifro-HFc	-----	
SEQ ID NO: 11_anifro-HC	EVQLVQSGAEVKKPGESLKISCKGSGYIFTNYWIAWVRQMPGKGLSEMGIIYPGDSDIRYSPSFQGGVTISADKSITTAY	80
INN - anifro-HC	EVQLVQSGAEVKKPGESLKISCKGSGYIFTNYWIAWVRQMPGKGLSEMGIIYPGDSDIRYSPSFQGGVTISADKSITTAY	80
Consensus	LQWSSSLKASDTAMYYCARHDIEGFDYWGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWSNS	160
SEQ ID NO: 1_anifro-VH	LQWSSSLKASDTAMYYCARHDIEGFDYWGRGTLVTVSS-----	160
SEQ ID NO: 3_anifro-HCDR1	-----	130
SEQ ID NO: 4_anifro-HCDR2	-----	111
SEQ ID NO: 5_anifro-HCDR2	-----HDIEGFDY-----	62
SEQ ID NO: 10_anifro-HFc	-----ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWSNS	43
SEQ ID NO: 11_anifro-HC	LQWSSSLKASDTAMYYCARHDIEGFDYWGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWSNS	160
INN - anifro-HC	LQWSSSLKASDTAMYYCARHDIEGFDYWGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWSNS	160
Consensus	GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEFEGGSPV	240
SEQ ID NO: 1_anifro-VH	-----	240
SEQ ID NO: 3_anifro-HCDR1	-----	210
SEQ ID NO: 4_anifro-HCDR2	-----	191
SEQ ID NO: 5_anifro-HCDR2	-----	142
SEQ ID NO: 10_anifro-HFc	GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEFEGGSPV	123
SEQ ID NO: 11_anifro-HC	GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEFEGGSPV	240
INN - anifro-HC	GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEFEGGSPV	240
Consensus	FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVVGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK	320
SEQ ID NO: 1_anifro-VH	-----	320
SEQ ID NO: 3_anifro-HCDR1	-----	290
SEQ ID NO: 4_anifro-HCDR2	-----	271
SEQ ID NO: 5_anifro-HCDR2	-----	222
SEQ ID NO: 10_anifro-HFc	FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVVGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK	203
SEQ ID NO: 11_anifro-HC	FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVVGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK	320
INN - anifro-HC	FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVVGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK	320
Consensus	CKVSNKALPASIIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDL	400
SEQ ID NO: 1_anifro-VH	-----	400
SEQ ID NO: 3_anifro-HCDR1	-----	370
SEQ ID NO: 4_anifro-HCDR2	-----	351
SEQ ID NO: 5_anifro-HCDR2	-----	302
SEQ ID NO: 10_anifro-HFc	CKVSNKALPASIIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDL	283
SEQ ID NO: 11_anifro-HC	CKVSNKALPASIIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDL	400
INN - anifro-HC	CKVSNKALPASIIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDL	400
Consensus	DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	447
SEQ ID NO: 1_anifro-VH	-----	117
SEQ ID NO: 3_anifro-HCDR1	-----	5
SEQ ID NO: 4_anifro-HCDR2	-----	17
SEQ ID NO: 5_anifro-HCDR2	-----	8
SEQ ID NO: 10_anifro-HFc	DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	330
SEQ ID NO: 11_anifro-HC	DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	447
INN - anifro-HC	DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	447

Figure 49

Consensus		EIVLTQSPGTLSLSPGERATLSCRASQSVSSSFFAMVYQKPGQAPRLLIYGASSRATGIPDRLSGSGGTDFTLTITRL	80
SEQ ID NO: 2_anifro-VK		EIVLTQSPGTLSLSPGERATLSCRASQSVSSSFFAMVYQKPGQAPRLLIYGASSRATGIPDRLSGSGGTDFTLTITRL	80
SEQ ID NO: 6_anifro-LCDR1		-----RASQSVSSSFFA-----	57
SEQ ID NO: 7_anifro-LCDR2		-----GASSRAT-----	30
SEQ ID NO: 8_anifro-LCDR3		-----	
SEQ ID NO: 09_anifro-LFc		-----	
SEQ ID NO: 12_anifro-LC		EIVLTQSPGTLSLSPGERATLSCRASQSVSSSFFAMVYQKPGQAPRLLIYGASSRATGIPDRLSGSGGTDFTLTITRL	80
Consensus		PEDFAVYCCQYDSSAITFGQGTIRLEIKRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS	160
SEQ ID NO: 2_anifro-VK		PEDFAVYCCQYDSSAITFGQGTIRLEIK-----	160
SEQ ID NO: 6_anifro-LCDR1		-----	137
SEQ ID NO: 7_anifro-LCDR2		-----	110
SEQ ID NO: 8_anifro-LCDR3		-----QQYDSSAIT-----	71
SEQ ID NO: 09_anifro-LFc		-----RTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS	52
SEQ ID NO: 12_anifro-LC		PEDFAVYCCQYDSSAITFGQGTIRLEIKRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS	160
Consensus		QESVTEQDSKDSITYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	215
SEQ ID NO: 2_anifro-VK		-----	108
SEQ ID NO: 6_anifro-LCDR1		-----	12
SEQ ID NO: 7_anifro-LCDR2		-----	7
SEQ ID NO: 8_anifro-LCDR3		-----	9
SEQ ID NO: 09_anifro-LFc		QESVTEQDSKDSITYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	107
SEQ ID NO: 12_anifro-LC		QESVTEQDSKDSITYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	215