

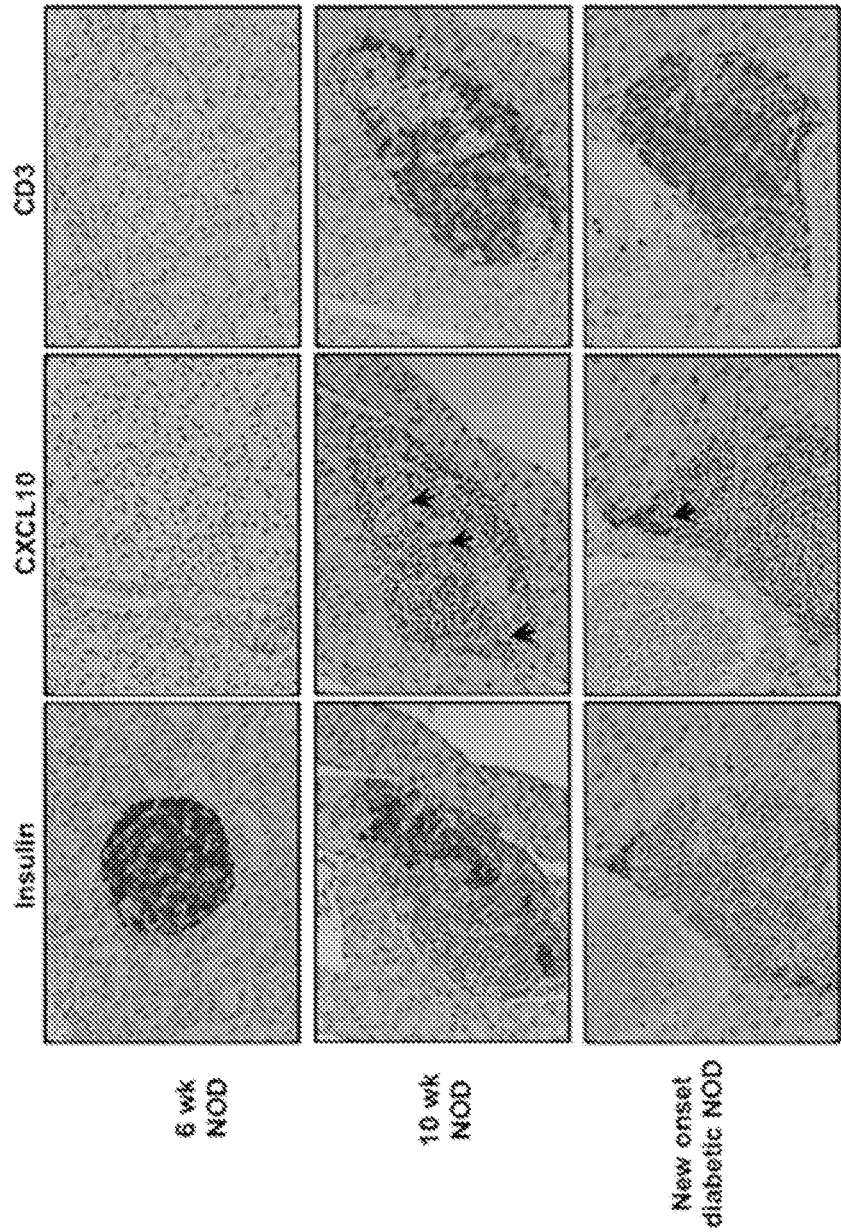


Fig. 1

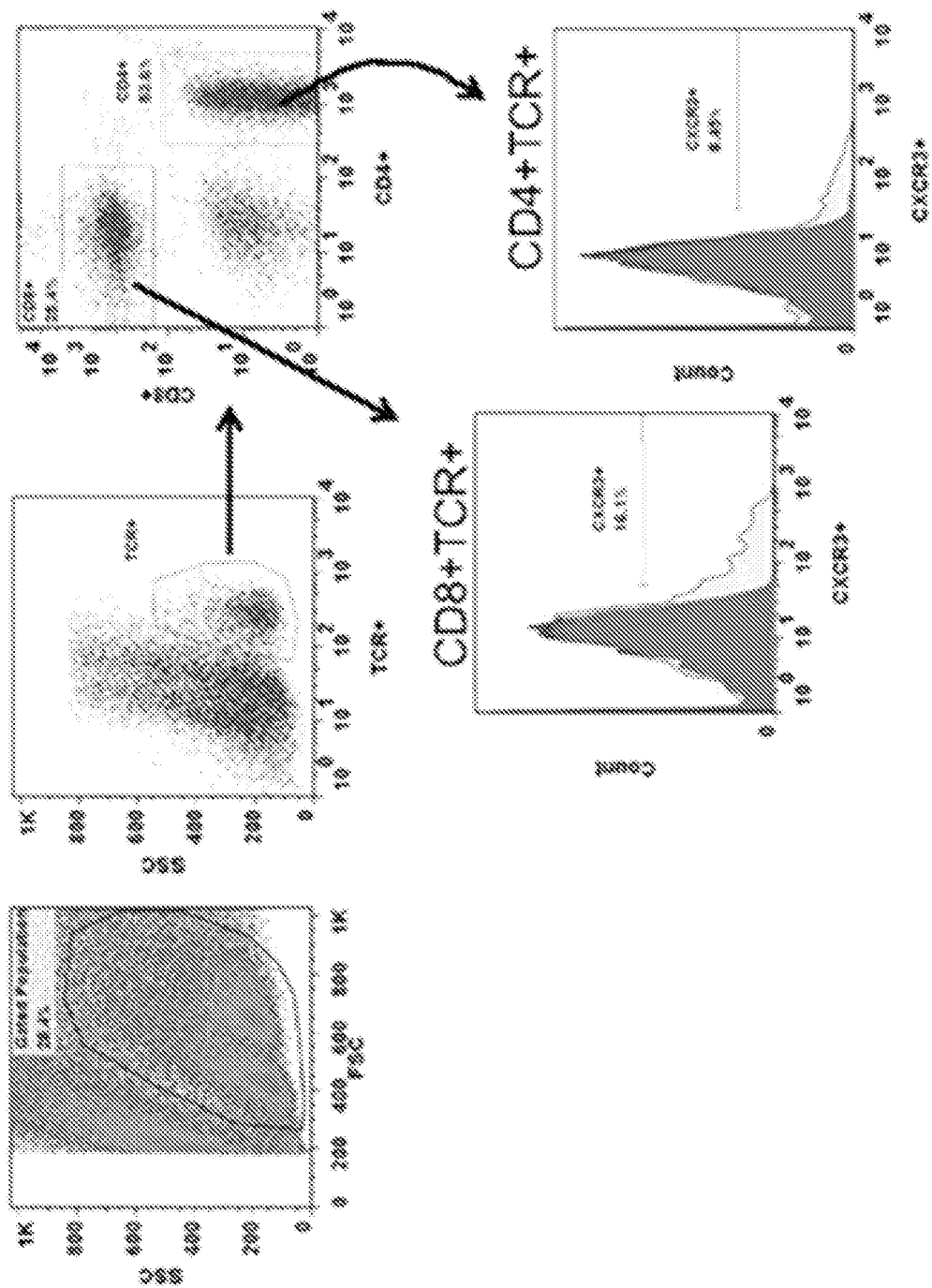


Fig. 2

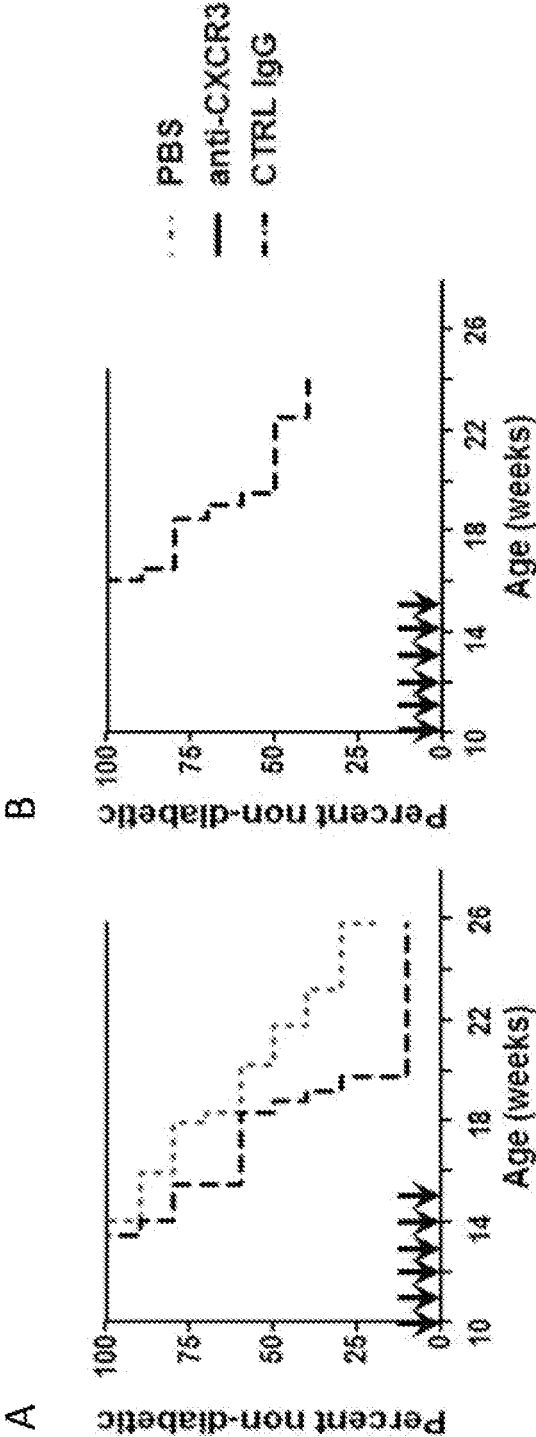


Fig. 3

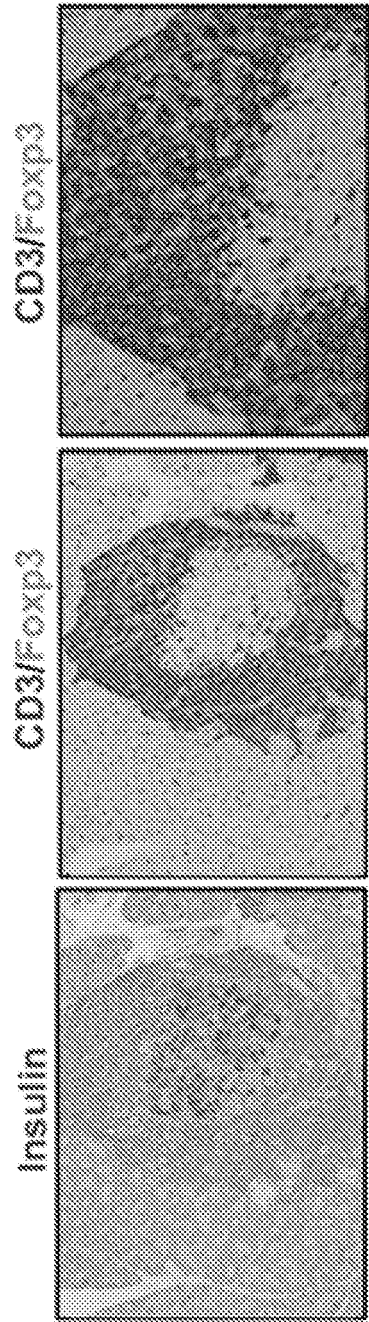


Fig. 4

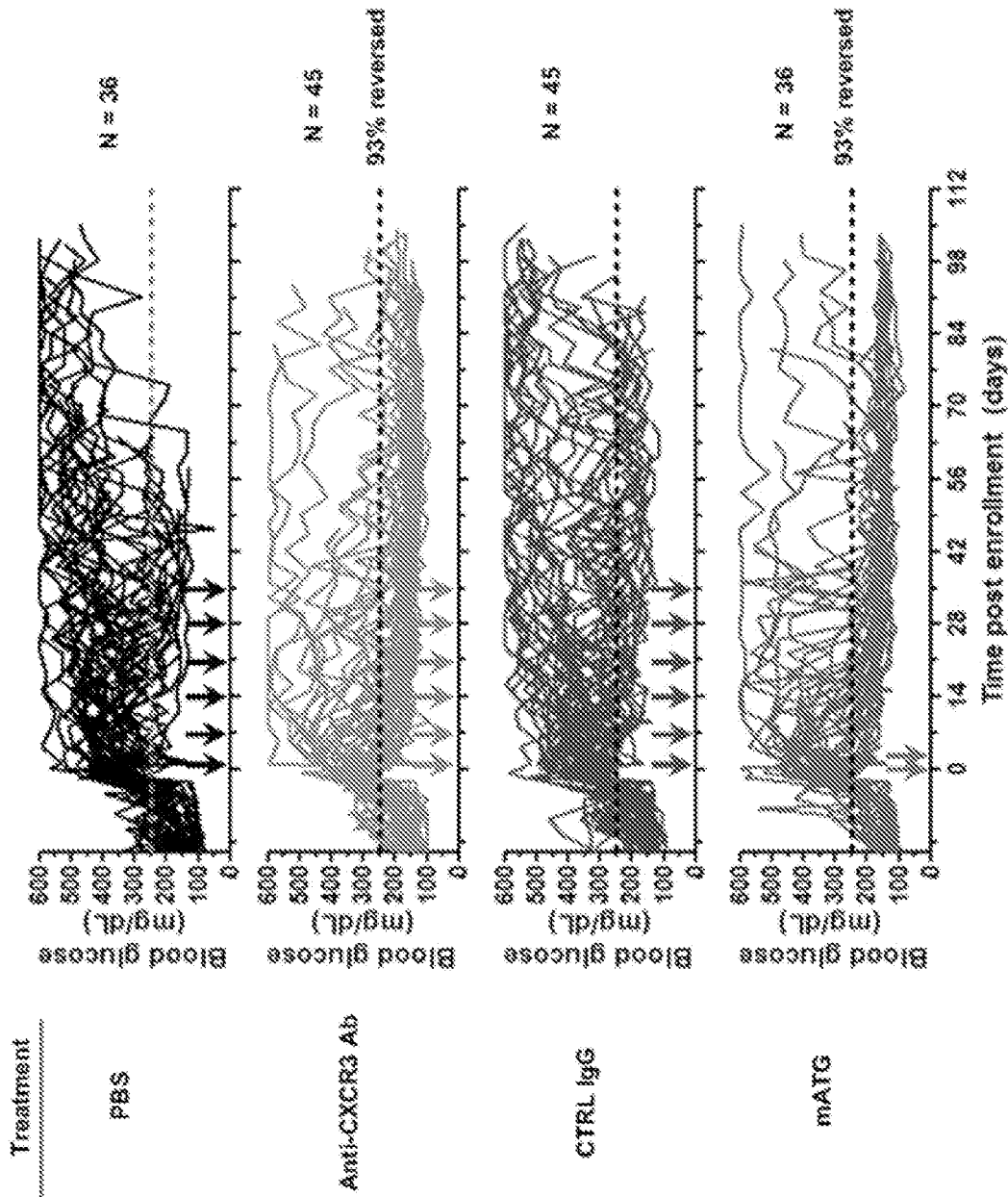


Fig. 5

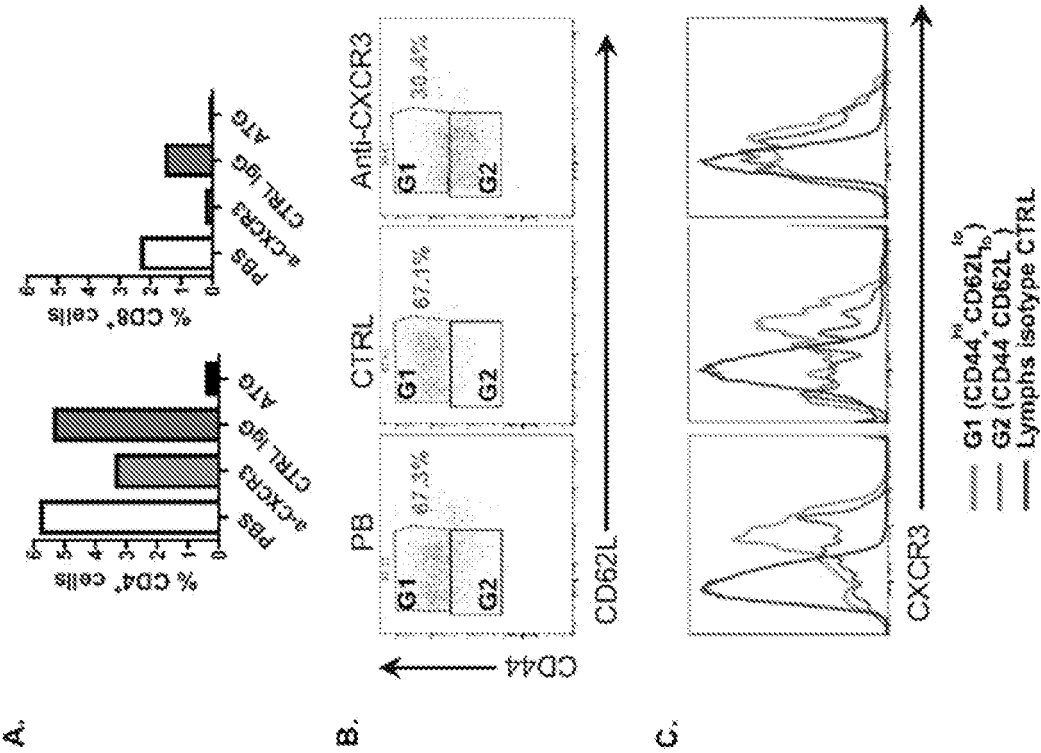


Fig. 6

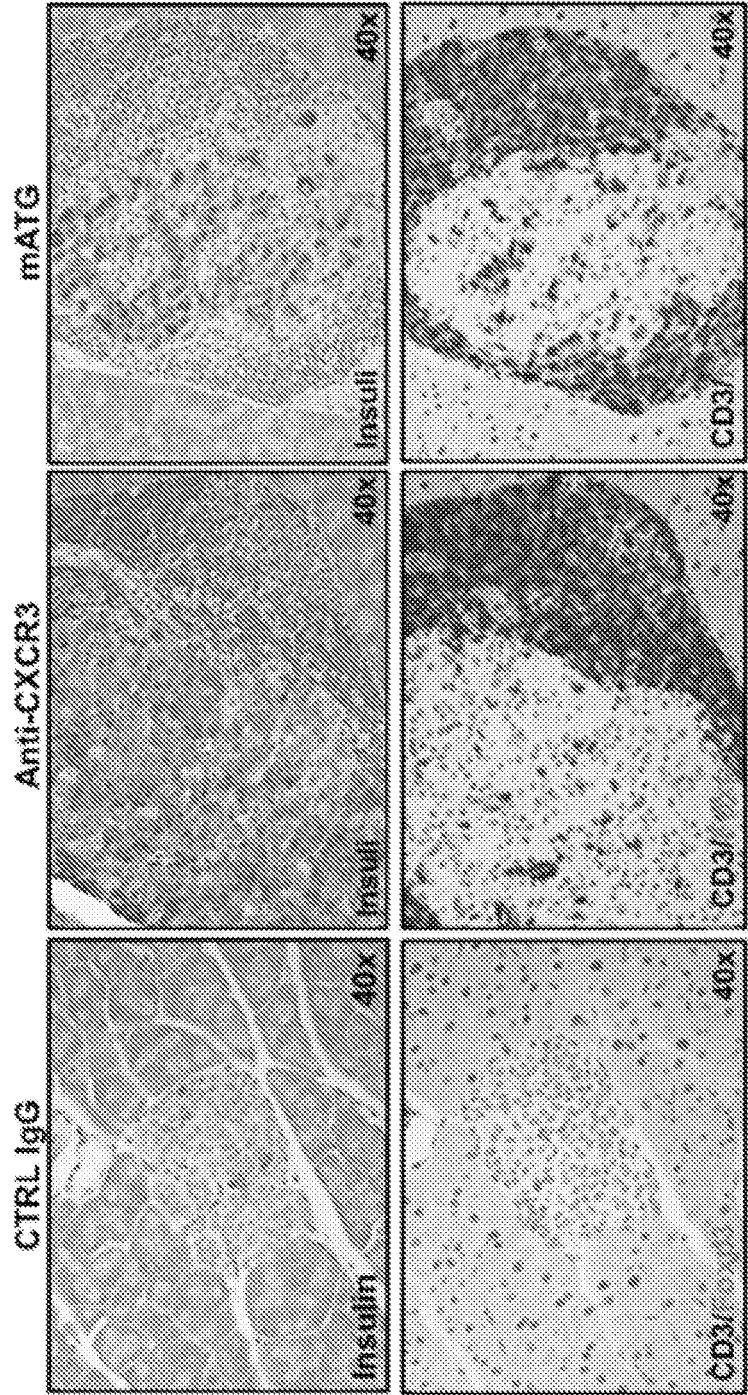


Fig. 7

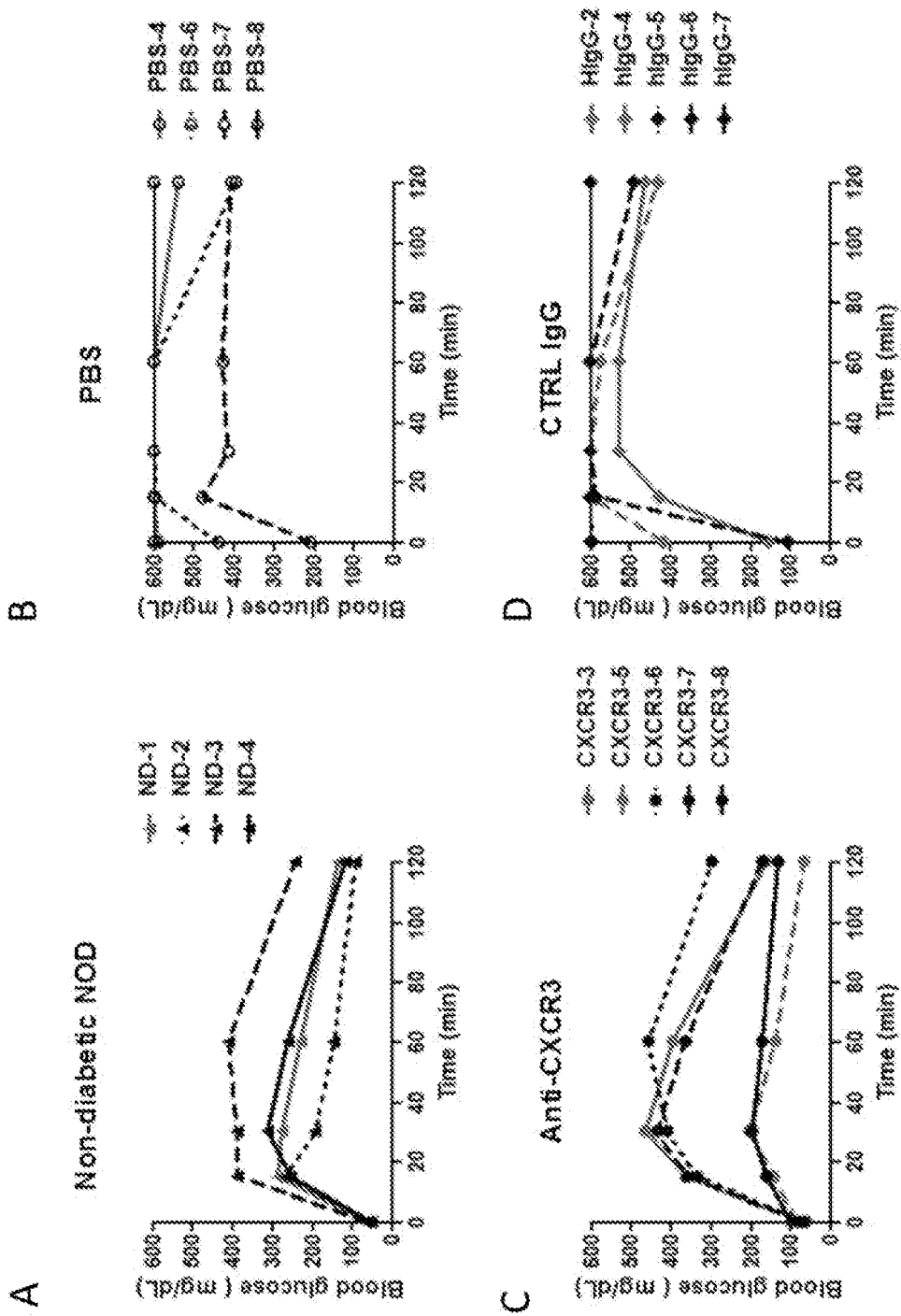


Fig. 8

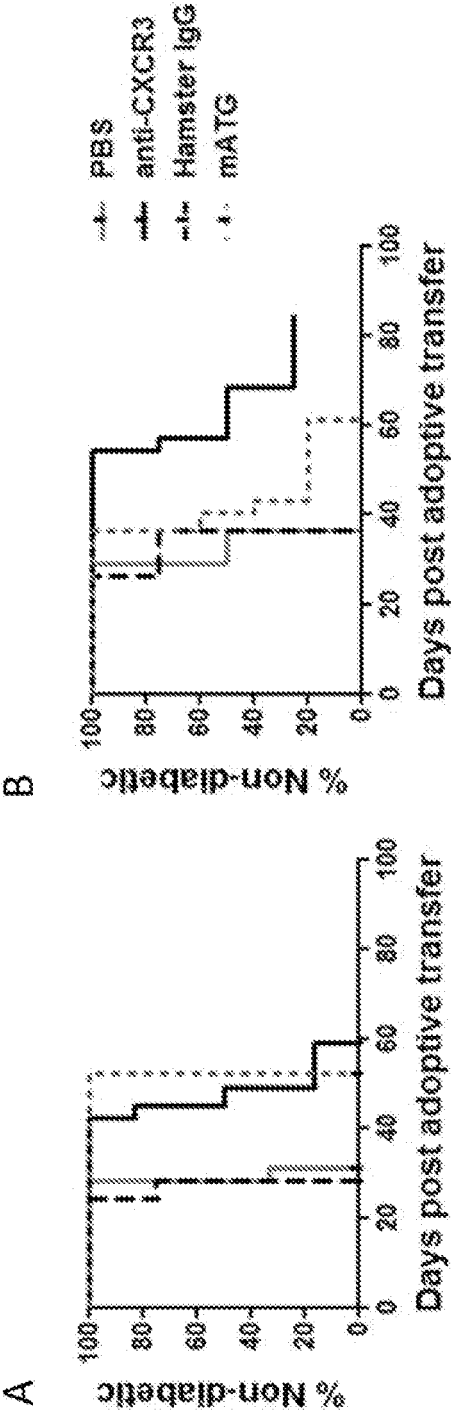


Fig. 9

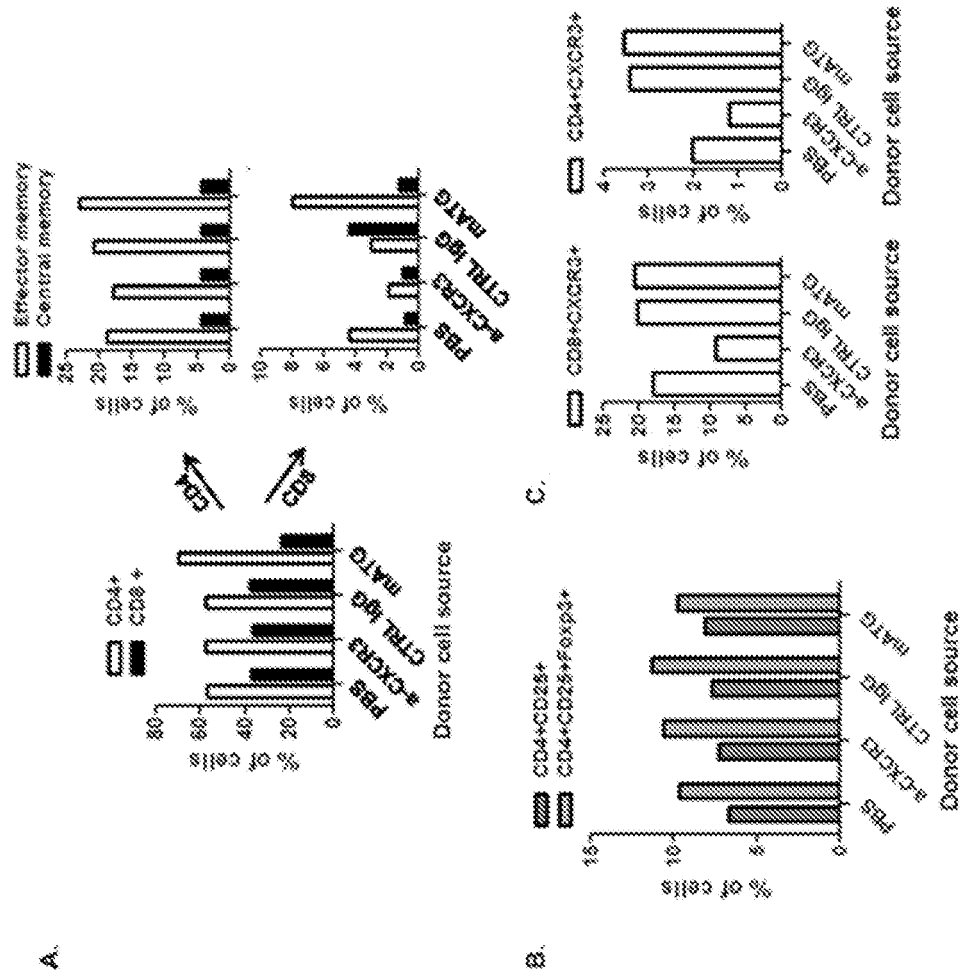


Fig. 10

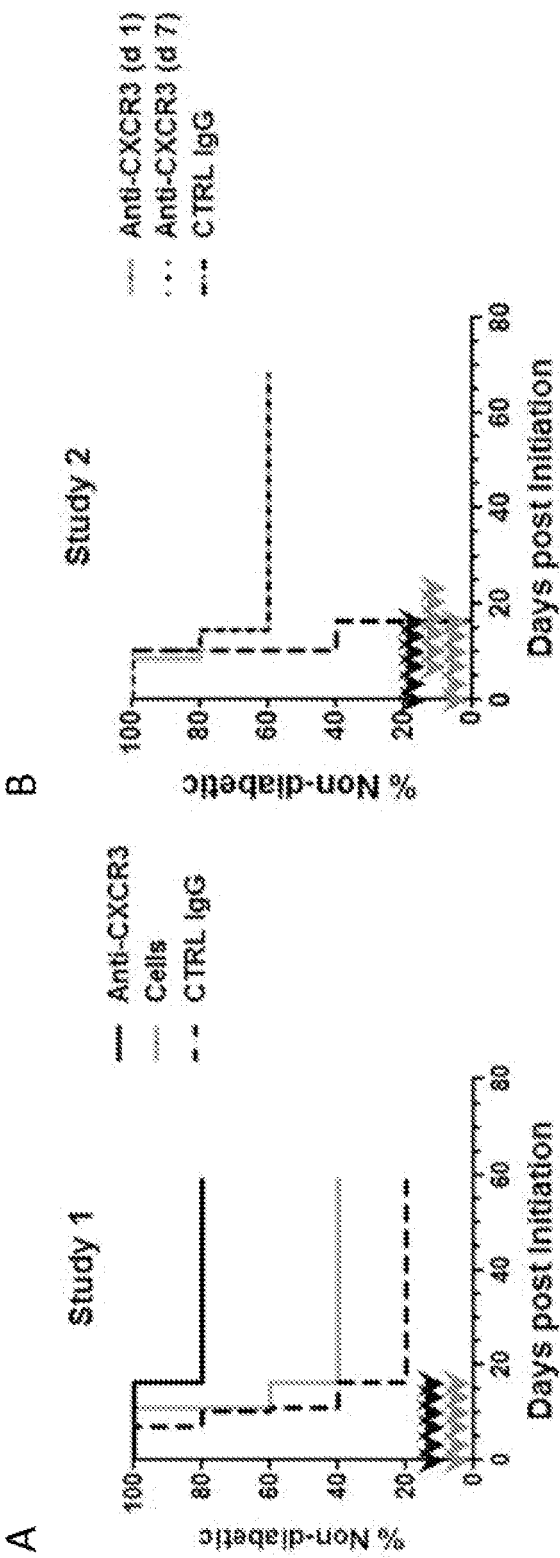


Fig. 11

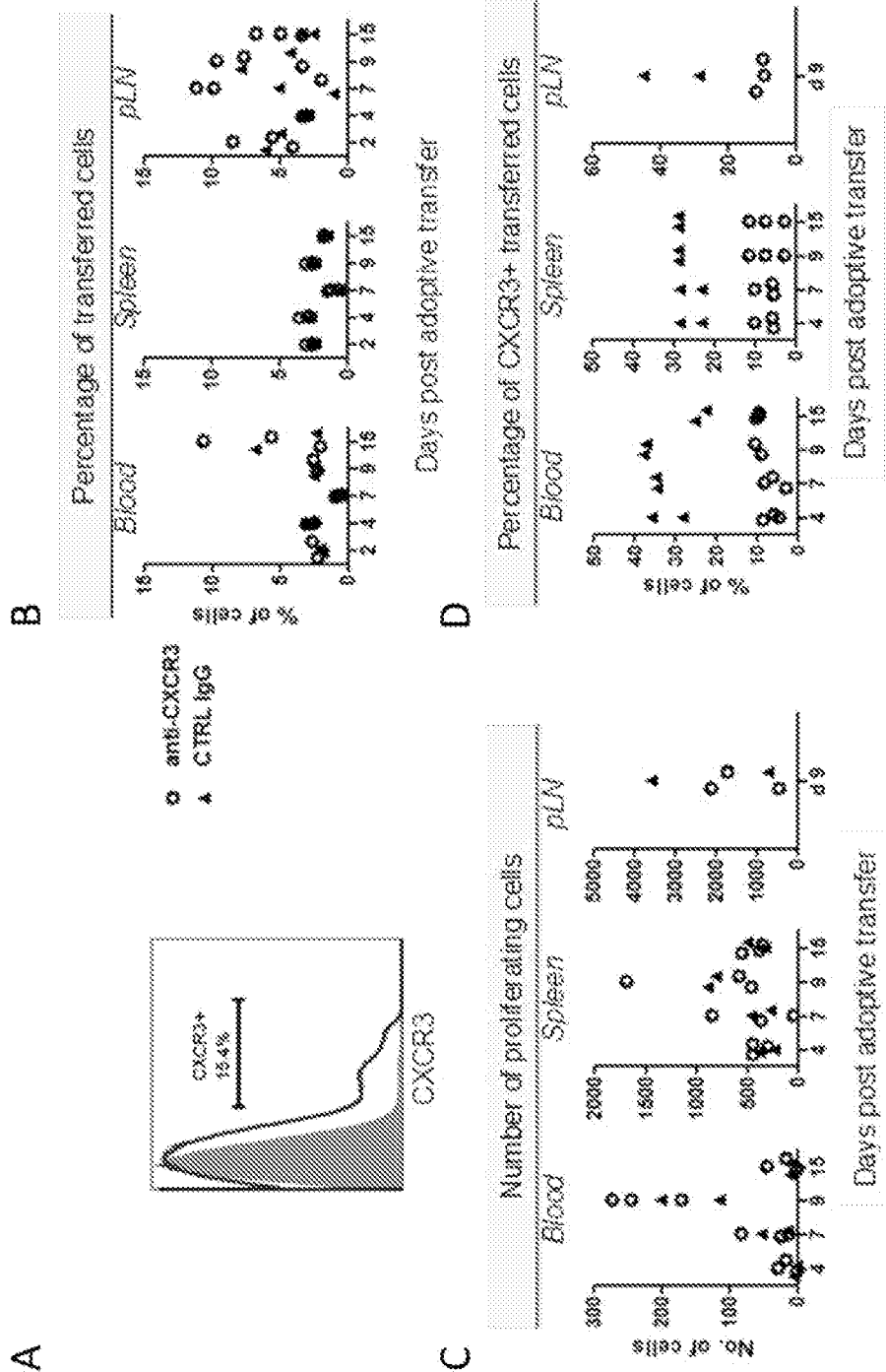


Fig. 12

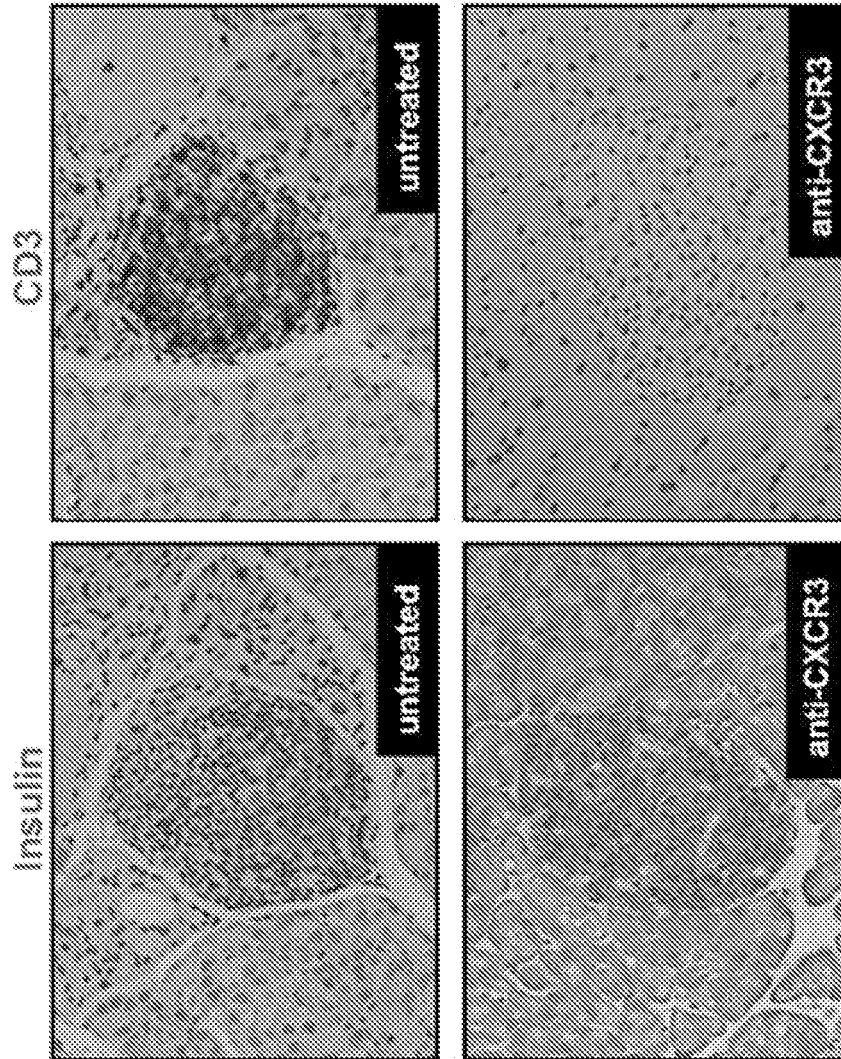


Fig. 13

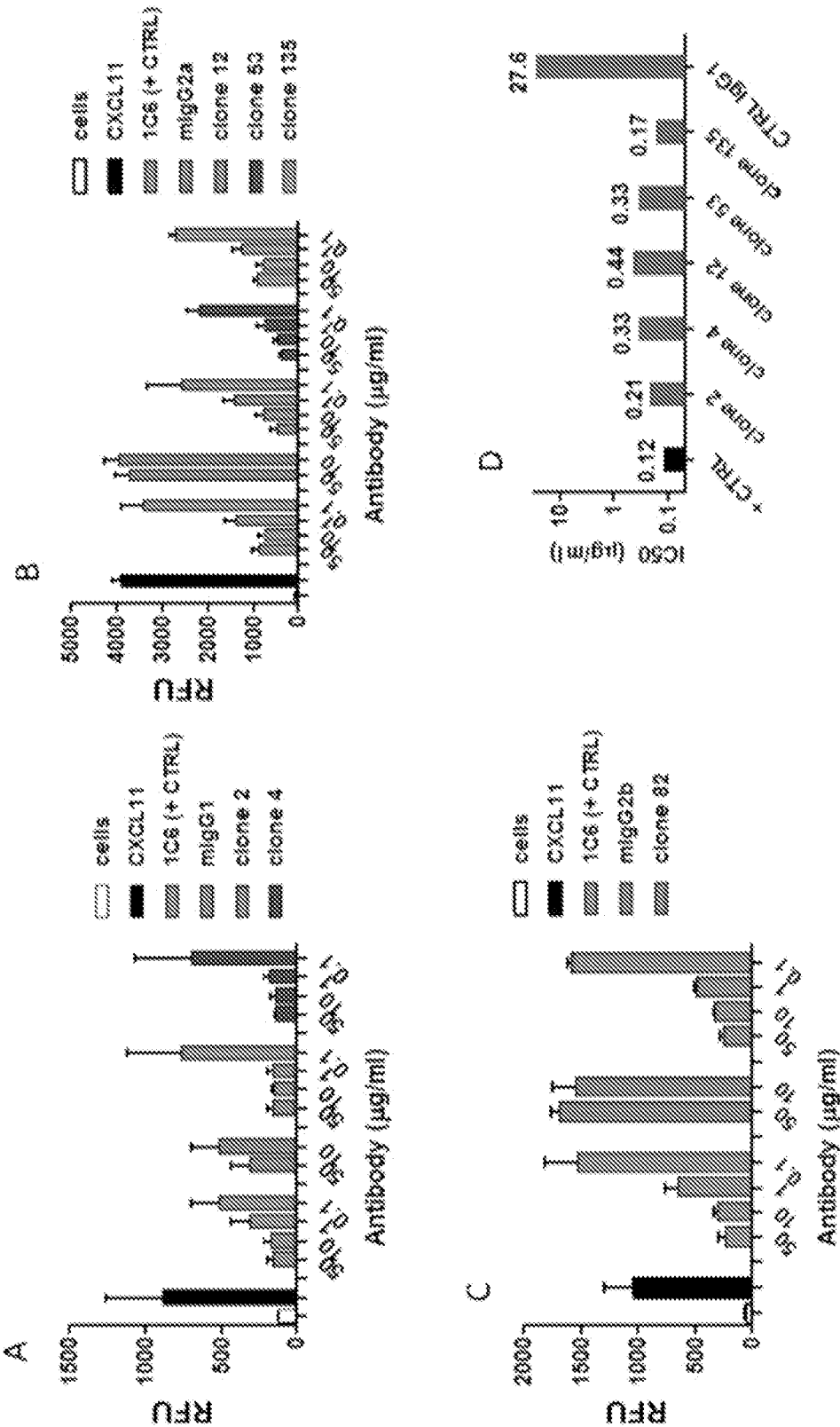


Fig. 14

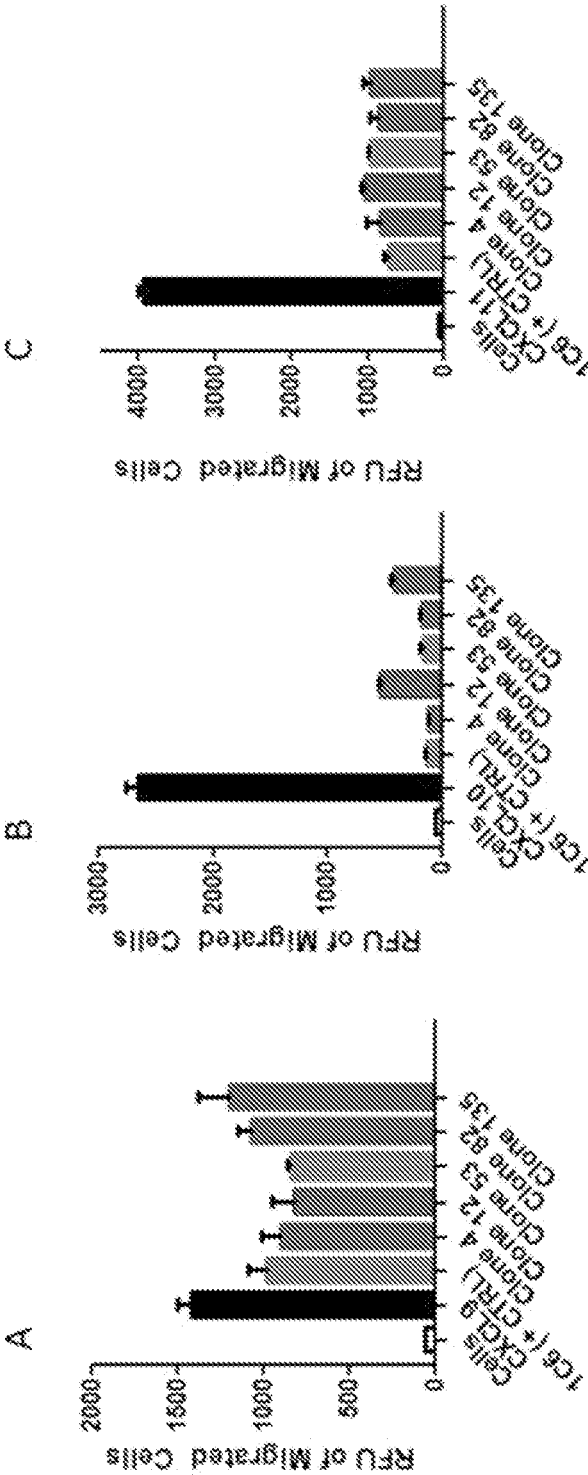


Fig. 15

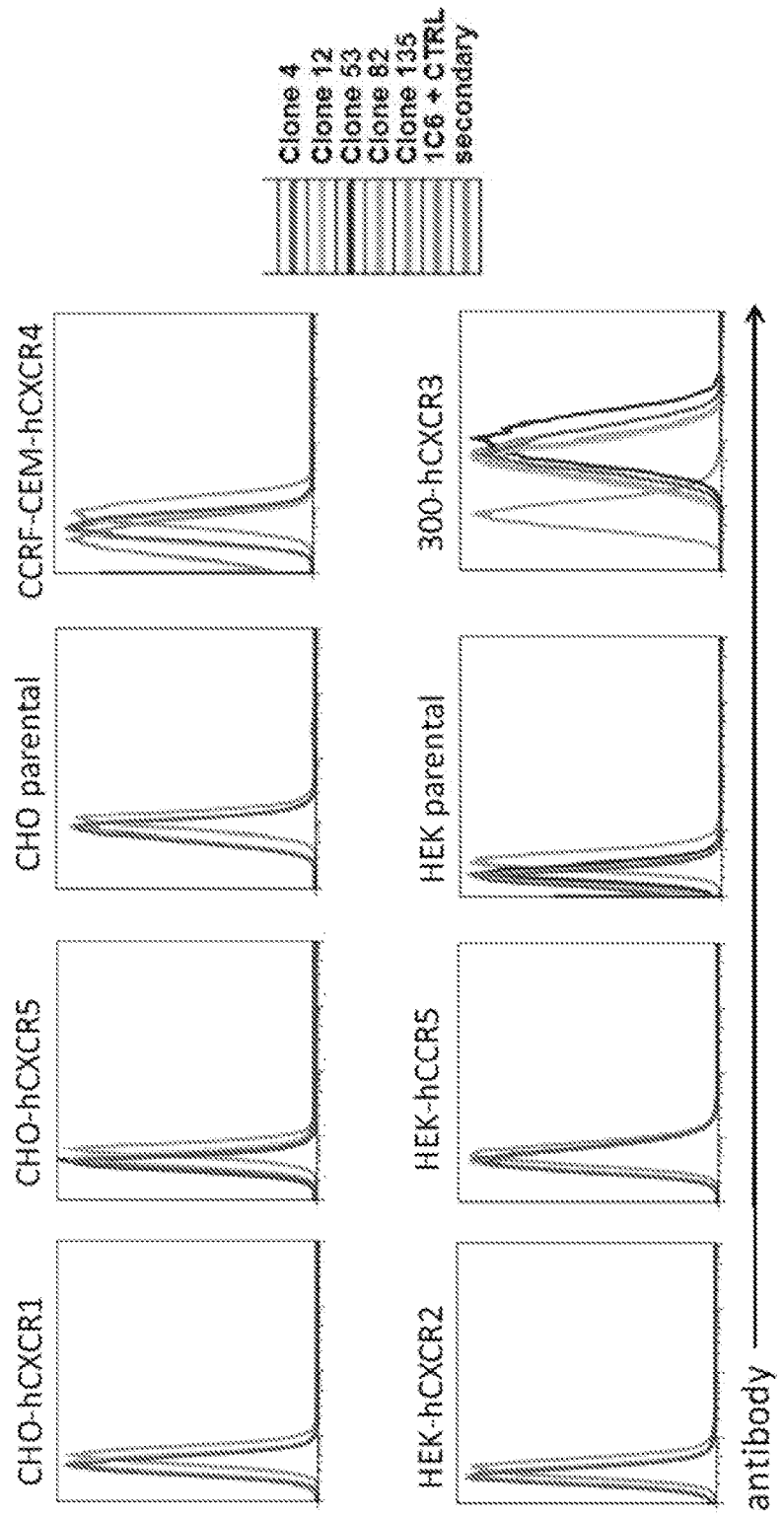
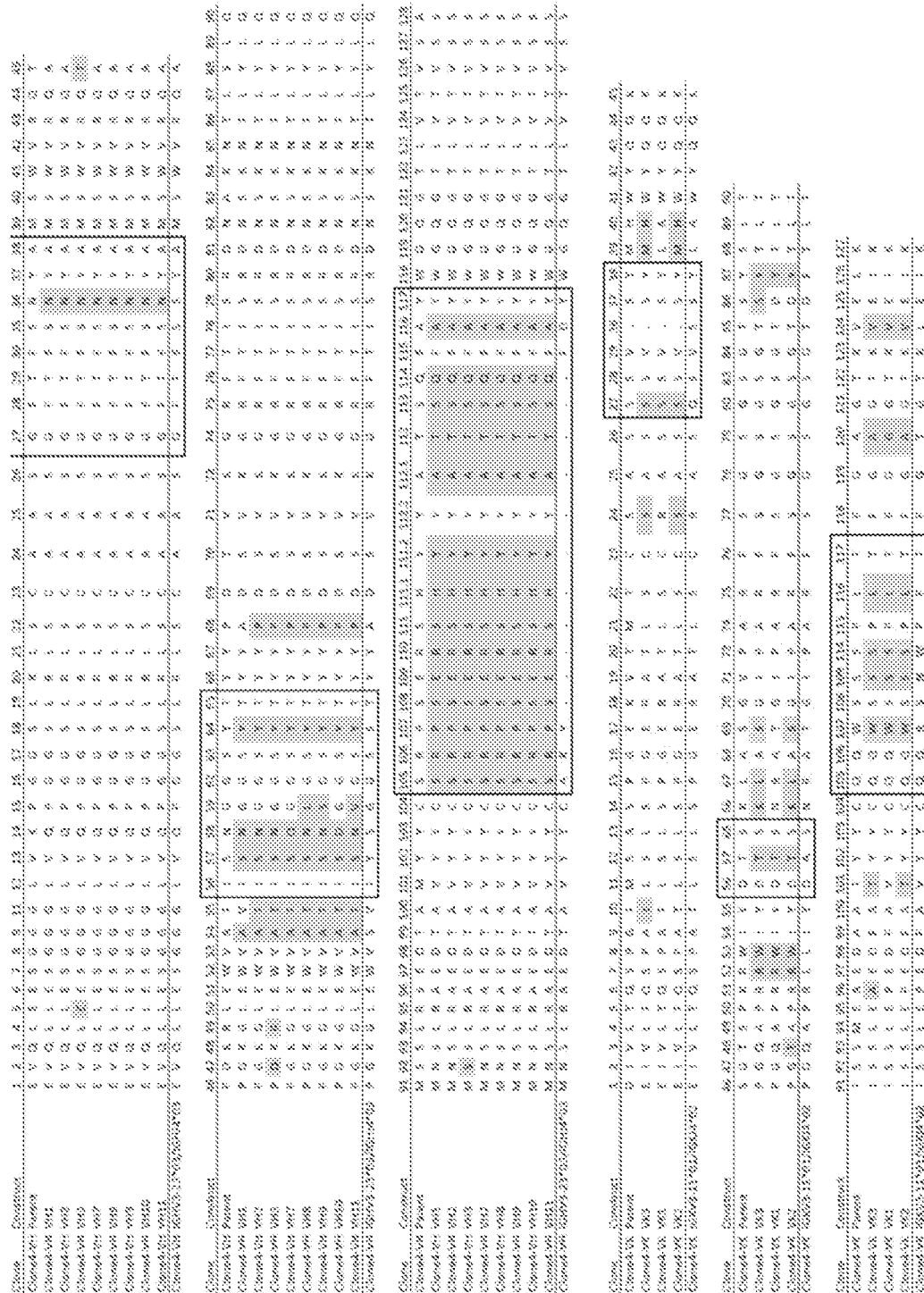


Fig. 16



Chromosome	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45			
Chromosome	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90			
Chromosome	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136		
Chromosome	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182		
Chromosome	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228		
Chromosome	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274		
Chromosome	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320		
Chromosome	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366		
Chromosome	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412		
Chromosome	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458		
Chromosome	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504		
Chromosome	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550		
Chromosome	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596		
Chromosome	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642		
Chromosome	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688		
Chromosome	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734		
Chromosome	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780		
Chromosome	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826		
Chromosome	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872		
Chromosome	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920
Chromosome	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	
Chromosome	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000	1001	1002	1003	1004	1005	1006	1007	1008	1009	1010	1011	1012	1013	1014	
Chromosome	1015	1016	1017	1018	1019	1020	1021	1022	1023	1024	1025	1026	1027	1028	1029	1030	1031	1032	1033	1034	1035	1036	1037	1038	1039	1040	1041	1042	1043	1044	1045	1046	1047	1048	1049	1050	1051	1052	1053	1054	1055	1056	1057	1058	1059	1060		
Chromosome	1061	1062	1063	1064	1065	1066	1067	1068	1069	1070	1071	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090	1091	1092	1093	1094	1095	1096	1097	1098	1099	1100	1101	1102	1103	1104	1105	1106	1107	
Chromosome	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154	
Chromosome	1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196	1197	1198	1199	1200	1201	1202
Chromosome	1203	1204	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247	1248	1249	1250
Chromosome	1251	1252	1253	1254	1255	1256	1257	1258	1259	1260	1261	1262	1263	1264	1265	1266	1267	1268	1269	1270	1271	1272	1273	1274	1275	1276	1277	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291	1292	1293	1294	1295	1296	1297	1298
Chromosome	1299	1300	1301	1302	1303	1304	1305	1306	1307	1308	1309	1310	1311	1312	1313	1314	1315	1316	1317	1318	1319	1320	1321	1322	1323	1324	1325	1326	1327	1328	1329	1330	1331	1332	1333	1334	1335	1336	1337	1338	1339	1340	1341	1342	1343	1344	1345	1346
Chromosome	1347	1348	1349	1350	1351	1352	1353	1354	1355	1356	1357	1358	1359	1360	1361	1362	1363	1364	1365	1366	1367	1368	1369	1370	1371	1372	1373	1374	1375	1376	1377	1378	1379	1380	1381	1382	1383	1384	1385	1386	1387	1388	1389	1390	1391	1392	1393	
Chromosome	1394	1395	1396	1397	1398	1399	1400	1401	1402	1403	1404	1405	1406	1407	1408	1409	1410	1411	1412	1413	1414	1415	1416	1417	1418	1419	1420	1421	1422	1423	1424	1425	1426	1427	1428	1429	1430	1431	1432	1433	1434	1435	1436	1437	143			

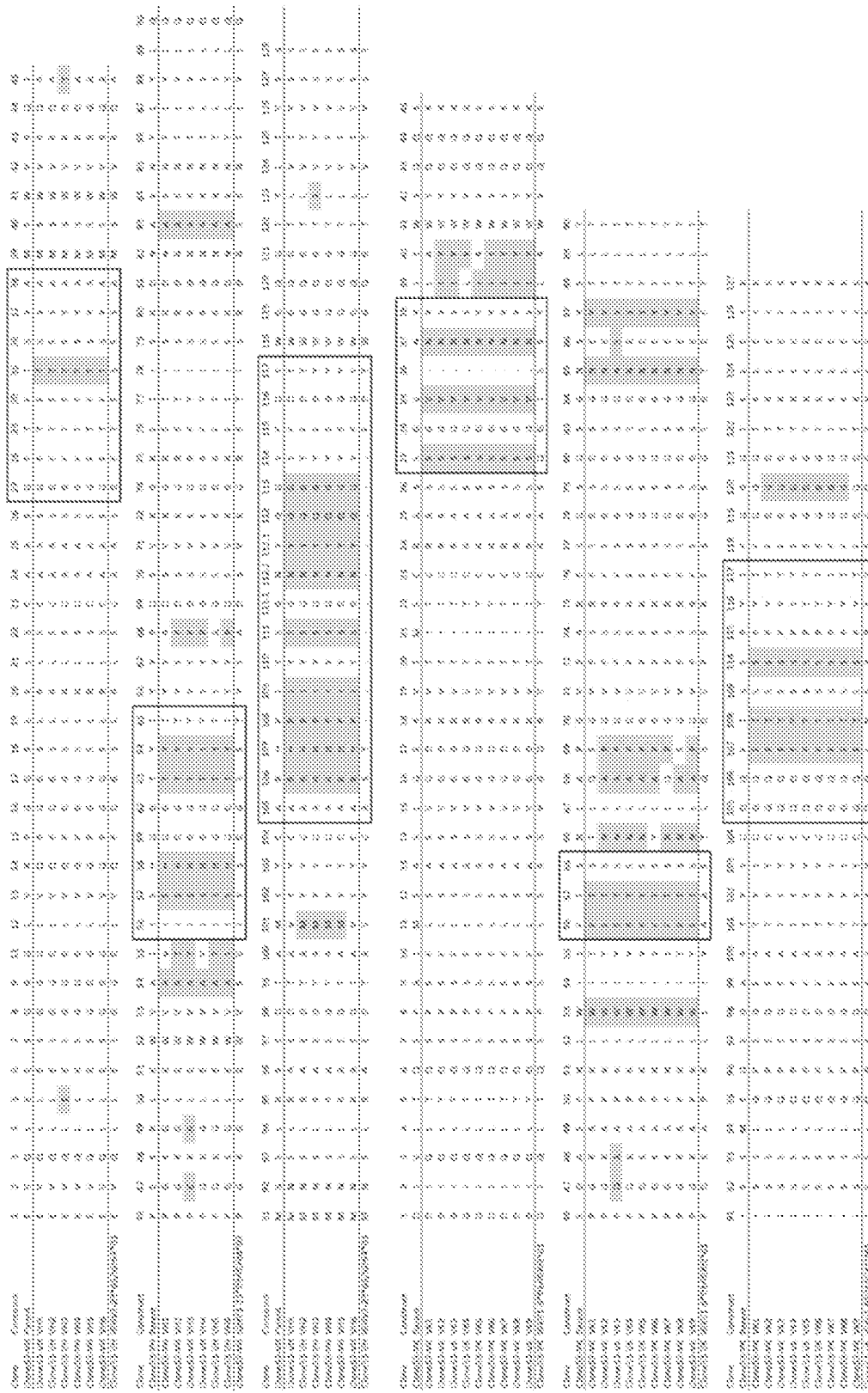


Fig. 17C

[illegible]

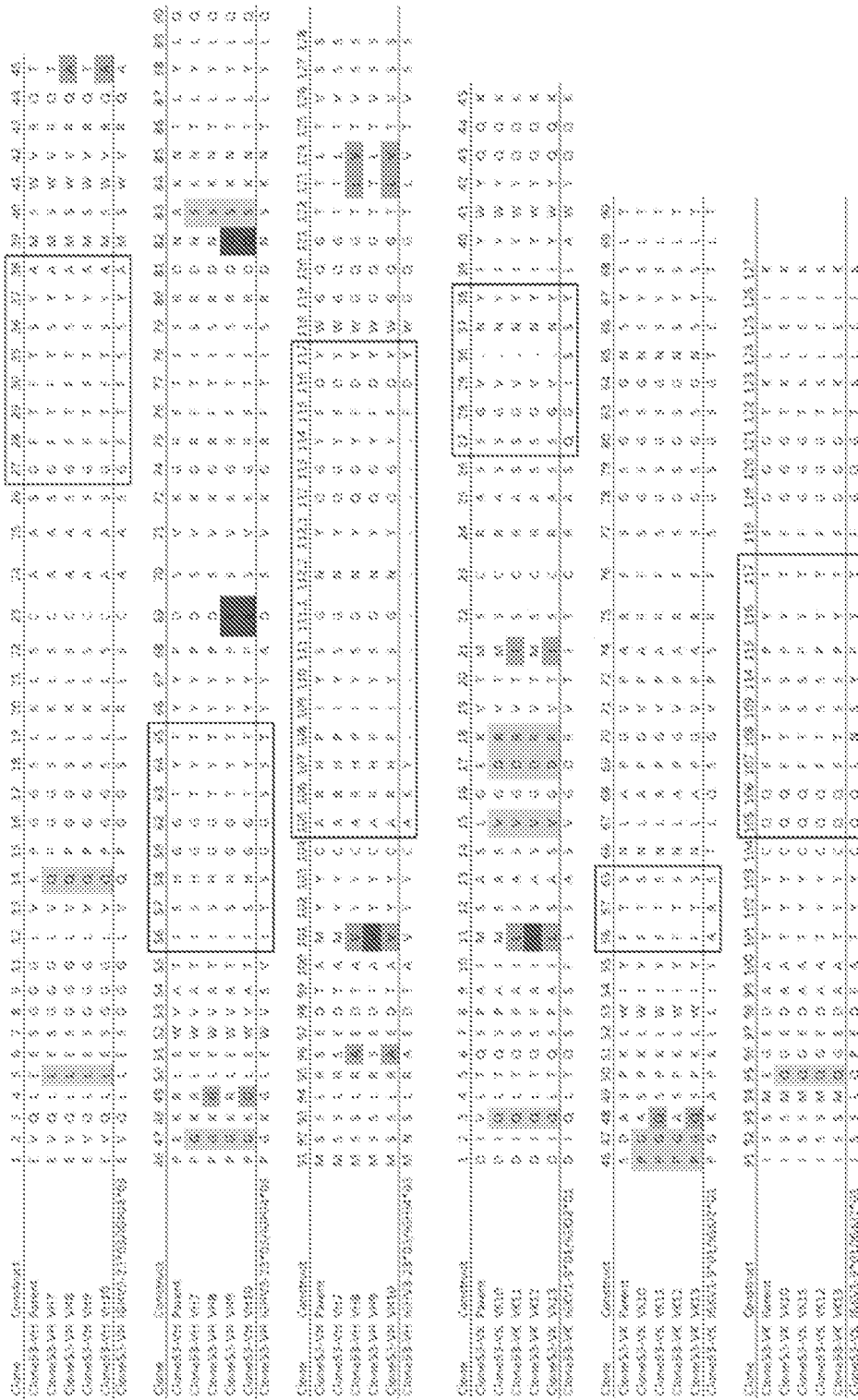
Fig. 17D

Clone	Construct	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
Clone135-VH	Parent	E	V	K	L	E	E	S	G	G	L	V	K	P	G	G	S	L	K	L	E	C	A	A	A	A	A	S	G	F	T	T	S	V	A	L	S	W	V	R	Q	A					
Clone135-VH	VH1	E	V	K	L	E	E	S	G	G	L	V	K	P	G	G	S	L	K	L	E	C	A	A	A	A	A	S	G	F	T	T	S	V	A	L	S	W	V	R	Q	A					
Clone135-VH	VH2	E	V	K	L	E	E	S	G	G	L	V	K	P	G	G	S	L	K	L	E	C	A	A	A	A	A	S	G	F	T	T	S	V	A	L	S	W	V	R	Q	A					
Clone135-VH	VH3	E	V	K	L	E	E	S	G	G	L	V	K	P	G	G	S	L	K	L	E	C	A	A	A	A	A	S	G	F	T	T	S	V	A	L	S	W	V	R	Q	A					
Clone135-VH	IGRPV3-23*03/IGRPV3	E	V	K	L	E	E	S	G	G	L	V	K	P	G	G	S	L	K	L	E	C	A	A	A	A	A	S	G	F	T	T	S	V	A	L	S	W	V	R	Q	A					
Clone	Construct	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	
Clone135-VH	Parent	P	E	K	R	L	E	W	V	A	T	L	S	M	G	G	S	V	T																												
Clone135-VH	VH1	P	E	K	R	L	E	W	V	A	T	L	S	M	G	G	S	V	T																												
Clone135-VH	VH2	P	E	K	R	L	E	W	V	A	T	L	S	M	G	G	S	V	T																												
Clone135-VH	VH3	P	E	K	R	L	E	W	V	A	T	L	S	M	G	G	S	V	T																												
Clone135-VH	IGRPV3-23*03/IGRPV3	P	E	K	R	L	E	W	V	A	T	L	S	M	G	G	S	V	T																												
Clone	Construct	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128								
Clone135-VH	Parent	M	S	L	R	A	E	D	T	A	M	V	Y	C	A	R	M	P	F	Y	S	G	N	Y	G	G	Y	D	V	W	G	G	G	T	L	I	T	V	S								
Clone135-VH	VH1	M	S	L	R	A	E	D	T	A	M	V	Y	C	A	R	M	P	F	Y	S	G	N	Y	G	G	Y	D	V	W	G	G	G	T	L	I	T	V	S								
Clone135-VH	VH2	M	S	L	R	A	E	D	T	A	M	V	Y	C	A	R	M	P	F	Y	S	G	N	Y	G	G	Y	D	V	W	G	G	G	T	L	I	T	V	S								
Clone135-VH	VH3	M	S	L	R	A	E	D	T	A	M	V	Y	C	A	R	M	P	F	Y	S	G	N	Y	G	G	Y	D	V	W	G	G	G	T	L	I	T	V	S								
Clone135-VH	IGRPV3-23*03/IGRPV3	M	S	L	R	A	E	D	T	A	M	V	Y	C	A	R	M	P	F	Y	S	G	N	Y	G	G	Y	D	V	W	G	G	G	T	L	I	T	V	S								
Clone	Construct	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	
Clone135-VH	Parent	S	D	A	S	P	K	L	W	L	Y	F	T	S	M	L	A	P	G	V	P	S	R	F	S	G	S	G	S	G	N	S	Y	S	L	T											
Clone135-VH	VH1	P	G	K	A	P	K	L	W	L	Y	F	T	S	M	L	A	P	G	V	P	S	R	F	S	G	S	G	S	G	N	S	Y	S	L	T											
Clone135-VH	VH2	P	G	K	A	P	K	L	W	L	Y	F	T	S	M	L	A	P	G	V	P	S	R	F	S	G	S	G	S	G	N	S	Y	S	L	T											
Clone135-VH	VH3	P	G	K	A	P	K	L	W	L	Y	F	T	S	M	L	A	P	G	V	P	S	R	F	S	G	S	G	S	G	N	S	Y	S	L	T											
Clone135-VH	IGRPV3-23*03/IGRPV3	P	G	K	A	P	K	L	W	L	Y	F	T	S	M	L	A	P	G	V	P	S	R	F	S	G	S	G	S	G	N	S	Y	S	L	T											
Clone	Construct	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	
Clone135-VH	Parent	D	L	V	L	T	Q	S	P	A	L	M	S	A	S	L	G	E	K	V	T	M	N	C	R	A	N	S	G	V	N	Y	M	Y	M	Y	M	Y	M	Y	M	Y	M	Y	M		
Clone135-VH	VH1	D	L	V	L	T	Q	S	P	A	L	M	S	A	S	L	G	E	K	V	T	M	N	C	R	A	N	S	G	V	N	Y	M	Y	M	Y	M	Y	M	Y	M	Y	M	Y	M		
Clone135-VH	VH2	D	L	V	L	T	Q	S	P	A	L	M	S	A	S	L	G	E	K	V	T	M	N	C	R	A	N	S	G	V	N	Y	M	Y	M	Y	M	Y	M	Y	M	Y	M	Y	M		
Clone135-VH	VH3	D	L	V	L	T	Q	S	P	A	L	M	S	A	S	L	G	E	K	V	T	M	N	C	R	A	N	S	G	V	N	Y	M	Y	M	Y	M	Y	M	Y	M	Y	M	Y	M		
Clone135-VH	IGRPV3-23*03/IGRPV3	D	L	V	L	T	Q	S	P	A	L	M	S	A	S	L	G	E	K	V	T	M	N	C	R	A	N	S	G	V	N	Y	M	Y	M	Y	M	Y	M	Y	M	Y	M	Y	M		
Clone	Construct	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	
Clone135-VH	Parent	S	D	A	S	P	K	L	W	L	Y	F	T	S	M	L	A	P	G	V	P	S	R	F	S	G	S	G	S	G	N	S	Y	S	L	T											
Clone135-VH	VH1	P	G	K	A	P	K	L	W	L	Y	F	T	S	M	L	A	P	G	V	P	S	R	F	S	G	S	G	S	G	N	S	Y	S	L	T											
Clone135-VH	VH2	P	G	K	A	P	K	L	W	L	Y	F	T	S	M	L	A	P	G	V	P	S	R	F	S	G	S	G	S	G	N	S	Y	S	L	T											
Clone135-VH	VH3	P	G	K	A	P	K	L	W	L	Y	F	T	S	M	L	A	P	G	V	P	S	R	F	S	G	S	G	S	G	N	S	Y	S	L	T											
Clone135-VH	IGRPV3-23*03/IGRPV3	P	G	K	A	P	K	L	W	L	Y	F	T	S	M	L	A	P	G	V	P	S	R	F	S	G	S	G	S	G	N	S	Y	S	L	T											
Clone	Construct	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354		
Clone135-VH	Parent	I	S	S	S	G	S	D	A	A	T	Y	Y	C	Q	Q	F	Y	S	S	P	Y	T	F	G	G	G	T	K	L	E	I	K														
Clone135-VH	VH1	I	S	S	S	G	S	D	A	A	T	Y	Y	C	Q	Q	F	Y	S	S	P	Y	T	F	G	G	G	T	K	L	E	I	K														
Clone135-VH	VH2	I	S	S	S	G	S	D	A	A	T	Y	Y	C	Q	Q	F	Y	S	S	P	Y	T	F	G	G	G	T	K	L	E	I	K														
Clone135-VH	VH3	I	S	S	S	G	S	D	A	A	T	Y	Y	C	Q	Q	F	Y	S	S	P	Y	T	F	G	G	G	T	K	L	E	I	K														
Clone135-VH	IGRPV3-23*03/IGRPV3	I	S	S	S	G	S	D	A	A	T	Y	Y	C	Q	Q	F	Y	S	S	P	Y	T	F	G	G	G	T	K	L	E	I	K														

Fig. 17E

[illegible]

Fig. 17F



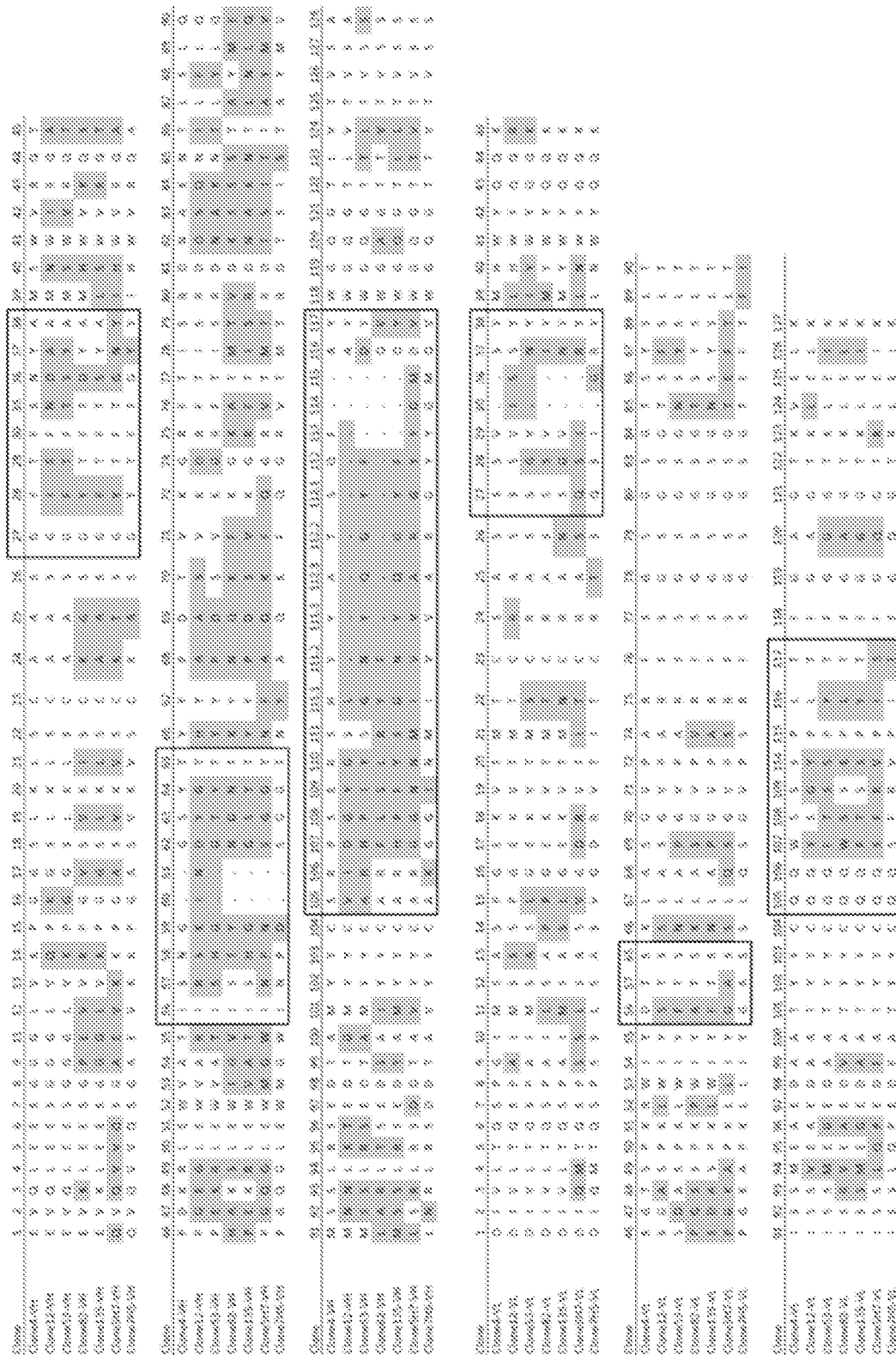




Fig. 18

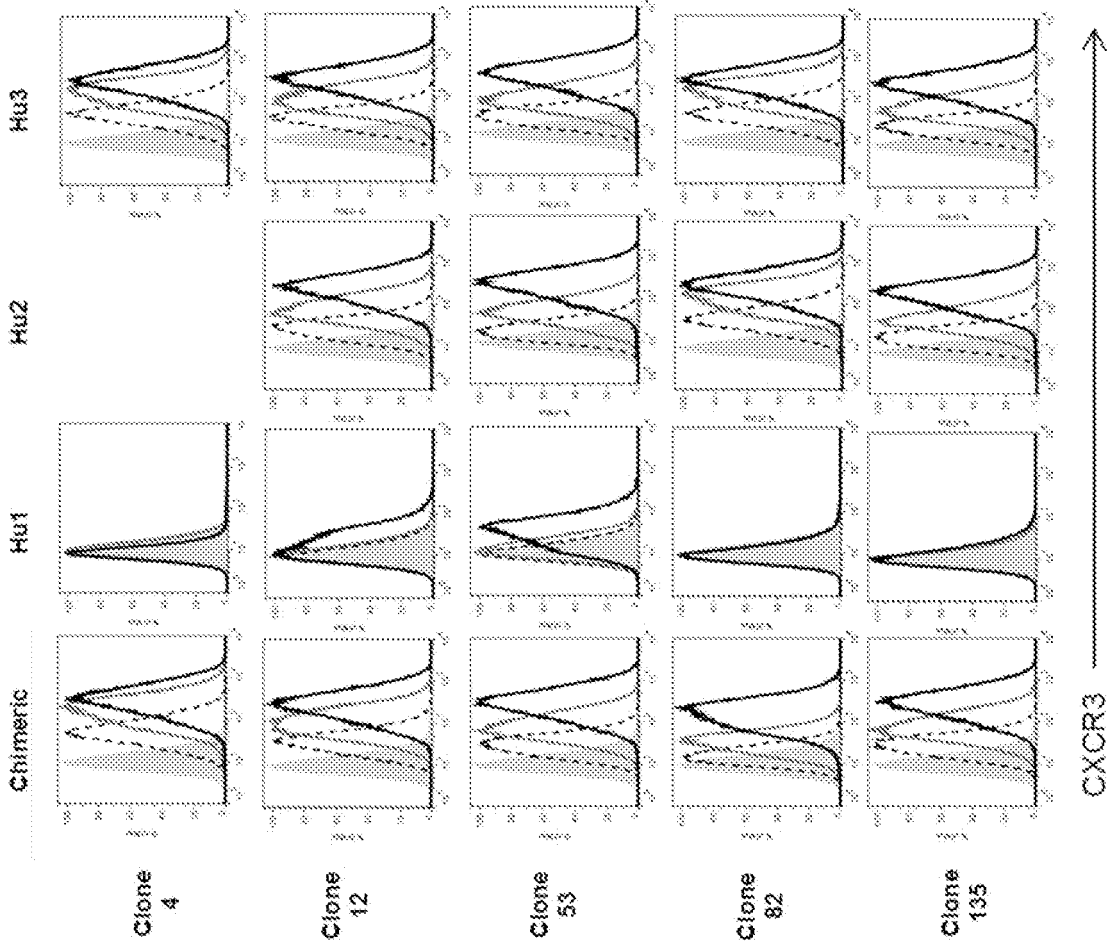


Fig. 19

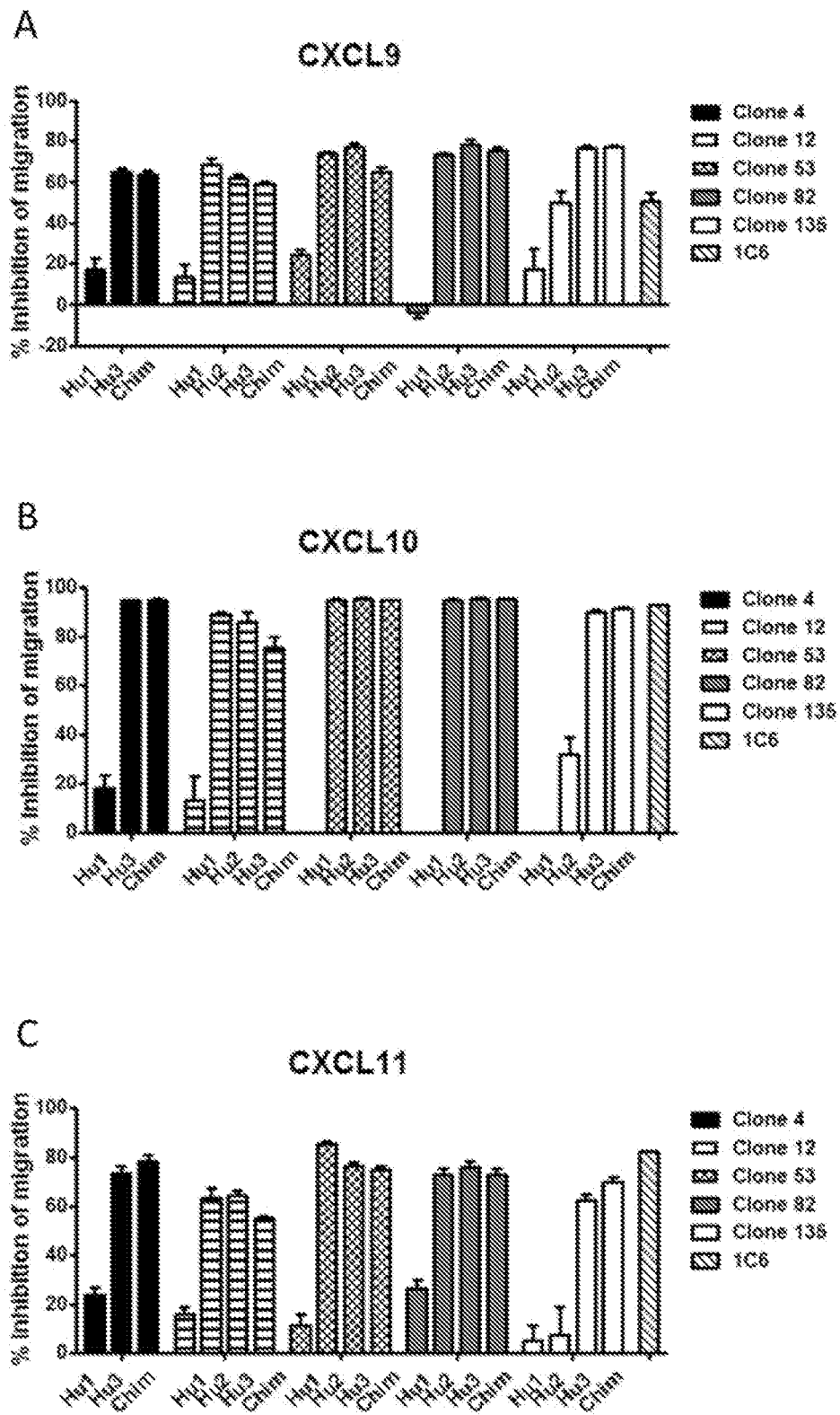


Fig. 20

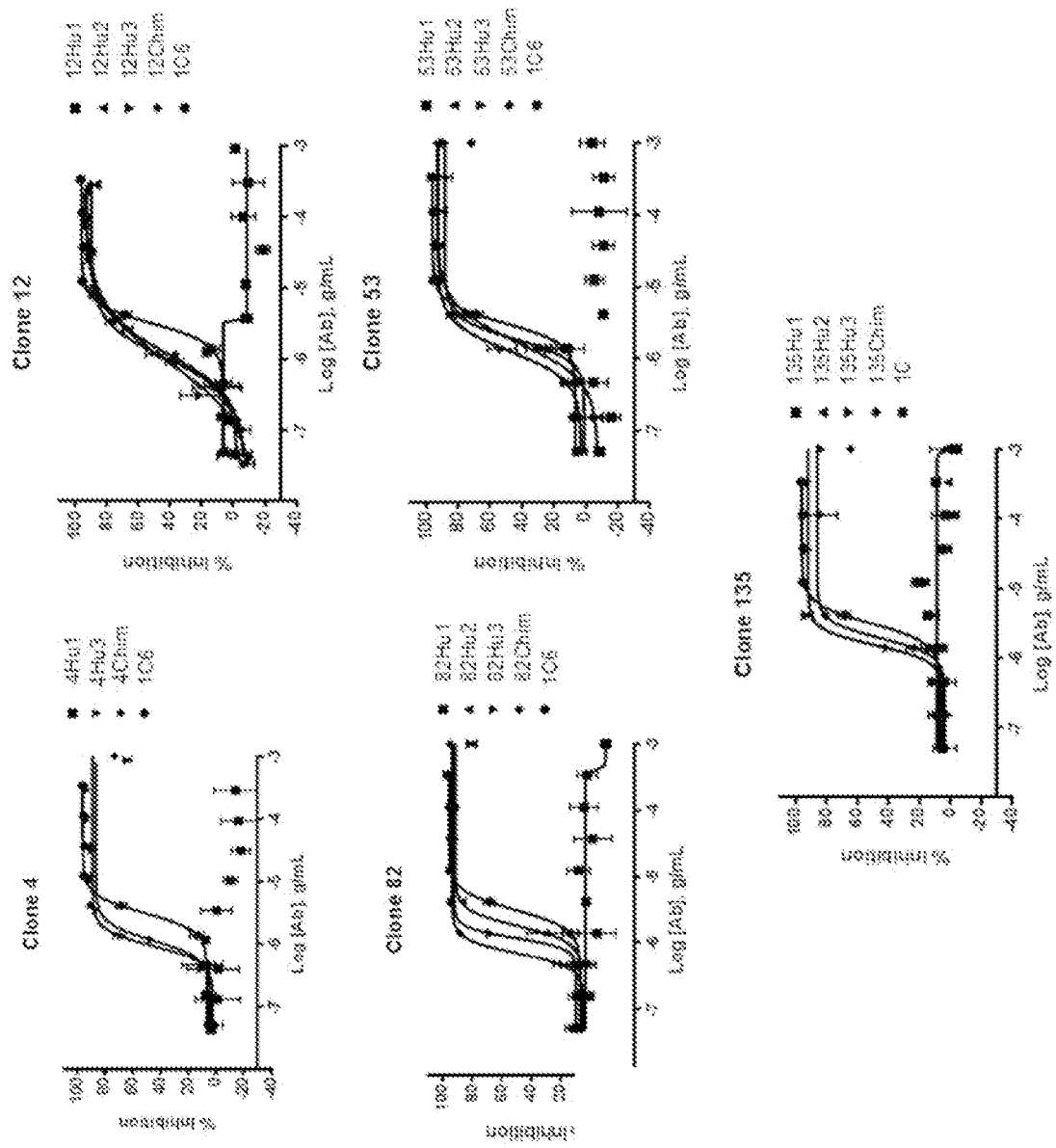
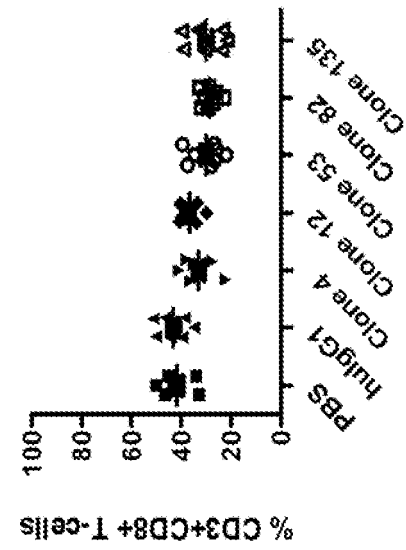
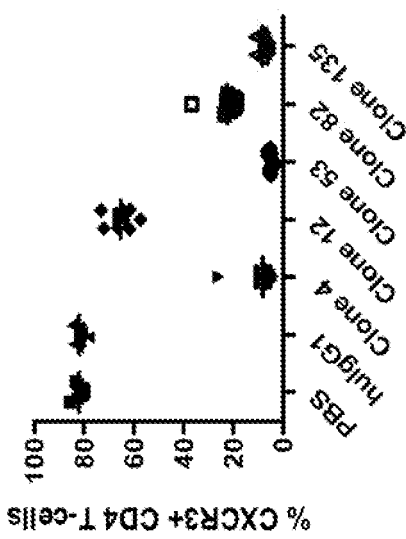


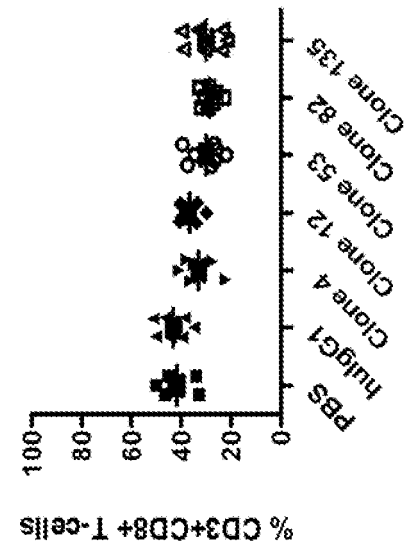
Fig. 21



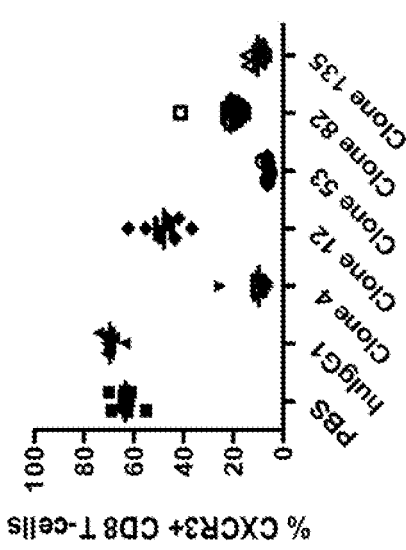
A.



B.



C.



D.

Fig. 22

Clone 12.0 - VH amino acid sequence
- CDRs in bold and underlined

1 10 20 30 40 50
EVQLEESGGGLVQPKGSLKLSCAAS**GISFNDAAM**NWIRQAPGEGLEWVAR

 60 70 80 90 100
IRSKINDYGTHYAASVKDRFTISRDDSQNILFLQMNNLKTEDTGMYYC**VI**

 110
DGYGSLAYWGQGTSLVTVSA (SEQ ID NO: 2)

Clone 12.0 - VL amino acid sequence
- CDRs in bold and underlined

1 10 20 30 40 50
DIVLTQSF AIMSSSFGEKVTMTCRAS**SSVISSY**LHWYQQRSGASPKLWIY

 60 70 80 90 100
STSSSLASGVPARFSGSGSGTSFSLTISSVEAEDAATYYC**QQYSGYPLT**FG

AGTKLELK (SEQ ID NO: 3)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLEESGGGLVQPKGSLKLSCAAS
	CDR1	<u>GISFNDAAM</u>
	FR2	MNWIRQAPGEGLEWVAR
	CDR2	<u>IRSKINDYGT</u>
	FR3	HYAASVKDRFTISRDDSQNILFLQMNNLKTEDTGMYYC
	CDR3	<u>VIDGYGSLAY</u>
	FR4	WGQGTSLVTVSA
Light Chain		
	FR1	DIVLTQSF AIMSSSFGEKVTMTCRAS
	CDR1	<u>SSVISSY</u>
	FR2	LHWYQQRSGASPKLWIY
	CDR2	<u>STS</u>
	FR3	SLASGVPARFSGSGSGTSFSLTISSVEAEDAATYYC
	CDR3	<u>QQYSGYPLT</u>
	FR4	FGAGTKLELK

Fig. 23A

Clone 12.1 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLVESGGGLVQPGGSLKLSCAAS**GISFNDAAM**HWVRQASGKGLEWVAR
 60 70 80 90 100
IRSKINDYGTAYAASVKGRFTISRDDSQNTLYLQMNSLKTEDTAVYYC**VI**
 110
DGYGSLAYWGQGTLLTVSS (SEQ ID NO: 4)

Clone 12.1 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EIVLTQSPATLSLSPGERATLSCRAS**SSVISSY**LAWYQQKPGQAPRLWIY
 60 70 80 90 100
STSNRATGIPARFSGSGSGTDFTLTISSELPEDFATYYC**QQYSGYPLT**FG
 GGTKVEIK (SEQ ID NO: 5)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLVESGGGLVQPGGSLKLSCAAS
	CDR1	<u>GISFNDAAM</u>
	FR2	MHWVRQASGKGLEWVAR
	CDR2	<u>IRSKINDYGT</u>
	FR3	AYAASVKGRFTISRDDSQNTLYLQMNSLKTEDTAVYYC
	CDR3	<u>VIDGYGSLAY</u>
	FR4	WGQGTLLTVSS
Light Chain		
	FR1	EIVLTQSPATLSLSPGERATLSCRAS
	CDR1	<u>SSVISSY</u>
	FR2	LAWYQQKPGQAPRLWIY
	CDR2	<u>STS</u>
	FR3	NRATGIPARFSGSGSGTDFTLTISSELPEDFATYYC
	CDR3	<u>QQYSGYPLT</u>
	FR4	FGGGTKVEIK

Fig. 23B

Clone 12.2 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLVESGGGLVQPGGSLKLSCAAS**GISFNDAAM**NWIRQASGKGLEWVAR
 60 70 80 90 100
IRSKINDYGTHYAASVKGRFTISRDDSQNTLYLQMNSLKTEDTAMY**YCVI**
 110
DGYGSLAYWGQGTTLVTVSS (SEQ ID NO: 6)

Clone 12.2 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EIVLTQSPATLSLSPGERATLSCRAS**SSVISSYL**HWYQQKPGQAPRLWIY
 60 70 80 90 100
STSSSLASGIPARFSGSGSGTDFTLTIS**SSLEPEDFATYYC****QQYSGYPLT**FG
 AGTKVEIK (SEQ ID NO: 7)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLVESGGGLVQPGGSLKLSCAAS
	CDR1	<u>GISFNDAAM</u>
	FR2	MNWIRQASGKGLEWVAR
	CDR2	<u>IRSKINDYGT</u>
	FR3	HYAASVKGRFTISRDDSQNTLYLQMNSLKTEDTAMY <u>YCVI</u>
	CDR3	<u>VIDGYGSLAY</u>
	FR4	WGQGTTLVTVSS
Light Chain		
	FR1	EIVLTQSPATLSLSPGERATLSCRAS
	CDR1	<u>SSVISSYL</u>
	FR2	LHWYQQKPGQAPRLWIY
	CDR2	<u>STS</u>
	FR3	SLASGIPARFSGSGSGTDFTLTIS <u>SSLEPEDFATYYC</u>
	CDR3	<u>QQYSGYPLT</u>
	FR4	FGAGTKVEIK

Fig. 23C

Clone 12.3 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLVESGGGLVQPKGSLKLSCAASGISFNDAAMNWIRQASGKGLEWVAR

           60           70           80           90          100
IRSKINDYGTHYAASVKDRFTISRDDSQNILYLQMNNLKTEDTAMYYCVI

           110
DGYGSLAYWGQGTTLVTVSS (SEQ ID NO: 8)

```

Clone 12.3 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EIVLTQSPAILSSSPGERATLSCRASSSVISSYLHWYQQKPGAAPRLWIY

           60           70           80           90          100
STSSSLASGIPARFSGSGSGTSFTLTISSSLEAEDFATYYCQQYSGYPLTFG

AGTKVEIK (SEQ ID NO: 9)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLVESGGGLVQPKGSLKLSCAAS
	CDR1	<u>GISFNDAAM</u>
	FR2	MNWIRQASGKGLEWVAR
	CDR2	<u>IRSKINDYGT</u>
	FR3	HYAASVKDRFTISRDDSQNILYLQMNNLKTEDTAMY <u>YCVI</u>
	CDR3	<u>VIDGYGSLAY</u>
	FR4	WGQGTTLVTVSS
Light Chain		
	FR1	EIVLTQSPAILSSSPGERATLSCRAS
	CDR1	<u>SSVISSYL</u>
	FR2	LHWYQQKPGAAPRLWIY
	CDR2	<u>STS</u>
	FR3	SLASGIPARFSGSGSGTSFTLTIS <u>SSLEAEDFATYYC</u>
	CDR3	<u>QQYSGYPLT</u>
	FR4	FGAGTKVEIK

Fig. 23D

Clone 135.0 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVKLEESGGGLVKPGGSLKLSCAAS**GFTFTSYA**LSWVRQTPEKRLEWVAT
 60 70 80 90 100
ISHGGSYTYYPDSVKGRFTISRDNKNTLNLQMSSLRSEDTAMYYC**ARHP**
 110 120
FYSGNYQGYFDYWGQGTLLTVSS (SEQ ID NO: 10)

Clone 135.0 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIVLTQSPAIMASLGEKVTMNCRAN**SGVNY**MYWYQQKSDASPRLWIY**FT**
 60 70 80 90 100
SNLAPGVPARFSGSGSGNSYSLTISSMEGEDAATYYC**QQFTSSPYT**FGGG
 TKLEIK (SEQ ID NO: 11)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVKLEESGGGLVKPGGSLKLSCAAS
	CDR1	<u>GFTFTSYA</u>
	FR2	LSWVRQTPEKRLEWVAT
	CDR2	<u>ISHGGSYT</u>
	FR3	YYPDSVKGRFTISRDNKNTLNLQMSSLRSEDTAMYYC
	CDR3	<u>ARHPFYSGNYQGYFDY</u>
	FR4	WGQGTLLTVSS
Light Chain		
	FR1	DIVLTQSPAIMASLGEKVTMNCRAN
	CDR1	<u>SGVNY</u>
	FR2	MYWYQQKSDASPRLWIY
	CDR2	<u>FTS</u>
	FR3	NLAPGVPARFSGSGSGNSYSLTISSMEGEDAATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	FGGGTKLEIK

Fig. 24A

Clone 135.1 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLEESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVAV

           60           70           80           90          100
ISHGGSYTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHP

           110          120
FYSGNYQGYFDYWGQGTTLVTVSS (SEQ ID NO: 12)

```

Clone 135.1 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIQLTQSPSFSLASVGDRTITCRASSGVNYLAWYQQKPGKAPKLWIYFT

           60           70           80           90          100
STLQSGVPSRFSGSGSGNEYTLTISSLQFEDFATYYCQQFTSSPYTFGQG

TKLEIK (SEQ ID NO: 13)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLEESGGGLVQPGGSLRLSCAAS
	CDR1	<u>GFTFTSYA</u>
	FR2	MSWVRQAPGKGLEWVAV
	CDR2	<u>ISHGGSYT</u>
	FR3	YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC
	CDR3	<u>ARHPFYSGNYQGYFDY</u>
	FR4	WGQGTTLVTVSS
Light Chain		
	FR1	DIQLTQSPSFSLASVGDRTITCRAS
	CDR1	<u>SGVNY</u>
	FR2	LAWYQQKPGKAPKLWIY
	CDR2	<u>FTS</u>
	FR3	TLQSGVPSRFSGSGSGNEYTLT
	CDR3	<u>ISSLQFEDFATYYCQQFTSSPYT</u>
	FR4	FGQGTKLEIK

Fig. 24B

Clone 135.2 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLEESGGGLVQPGGSLRLSCAASGFTFTSYALSWVRQAPGKGLEWVAT

           60           70           80           90          100
ISHGGSYTYYPDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHP

           110          120
FYSGNYQGYFDYWGQGTTLVTVSS (SEQ ID NO: 14)

```

Clone 135.2 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIQLTQSPSFSLASVGDRTITCRANSGVNYMYWYQQKPGKAPKLWIYFT

           60           70           80           90          100
SNLAPGVPSRFSGSGSGNEYTLTISSLQFEDFATYYCQQFTSSPYTFGGG

TKLEIK (SEQ ID NO: 15)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLEESGGGLVQPGGSLRLSCAAS
	CDR1	<u>GFTFTSYA</u>
	FR2	LSWVRQAPGKGLEWVAT
	CDR2	<u>ISHGGSYT</u>
	FR3	YYPDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC
	CDR3	<u>ARHPFYSGNYQGYFDY</u>
	FR4	WGQGTTLVTVSS
Light Chain		
	FR1	DIQLTQSPSFSLASVGDRTITCRAN
	CDR1	<u>SGVNY</u>
	FR2	MYWYQQKPGKAPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLAPGVPSRFSGSGSGNEYTLT <u>ISSLQFEDFATYYC</u>
	CDR3	<u>QQFTSSPYT</u>
	FR4	EGGGTKLEIK

Fig. 24C

Clone 135.3 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLLES GGGGLVQPGGSLRLS CAAS GFTFTSYALSWVRQTPEKRLEWVAT

           60           70           80           90          100
ISHGGSYTYYPDSVKGRFTISRDN SKNTLNLQMSSLRAEDTAVYYCARHP

           110          120
FYSGNYQGYFDYWGQGT LVTVSS (SEQ ID NO: 16)

```

Clone 135.3 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIQLTQSPSFSL SASVGDRVTITCRAN SGVNYMYWYQQKPD AAPKLWIYFT

           60           70           80           90          100
SNLAPGVPSRFSGSGSGNSYTLTISSLQFEDFATYYCQQFTSSPYTFGGG

TKLEIK (SEQ ID NO: 17)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLLES GGGGLVQPGGSLRLS CAAS
	CDR1	<u>GFTFTSYA</u>
	FR2	LSWVRQTPEKRLEWVAT
	CDR2	<u>ISHGGSYT</u>
	FR3	YYPDSVKGRFTISRDN SKNTLNLQMSSLRAEDTAVYYC
	CDR3	<u>ARHPFYSGNYQGYFDY</u>
	FR4	WGQGT LVTVSS
Light Chain		
	FR1	DIQLTQSPSFSL SASVGDRVTITCRAN
	CDR1	<u>SGVNY</u>
	FR2	MYWYQQKPD AAPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLAPGVPSRFSGSGSGNSYTLT ISSLQFEDFATYYC
	CDR3	<u>QQFTSSPYTF</u>
	FR4	EGGGTKLEIK

Fig. 24D

Clone 4.0 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLEESGGGLVKGPGGSLKLSCAASGFTFSNYAMSWVRQTPDKRLEWVAT

           60           70           80           90          100
ISNGGSYTYYPDTVKGRFTISRDNKNTLSLQMSSLRSEDTAMYYCSRPS

           110          120
ERSHYATSQFAYWGQGTTLVTVSA (SEQ ID NO: 18)

```

Clone 4.0 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIVLTQSPFGIMASPGGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDT

           60           70           80           90          100
SKLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSSPLTFGAG

TKVELK (SEQ ID NO: 19)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLEESGGGLVKGPGGSLKLSCAAS
	CDR1	<u>GFTFSNYA</u>
	FR2	MSWVRQTPDKRLEWVAT
	CDR2	<u>ISNGGSYT</u>
	FR3	YYPDTVKGRFTISRDNKNTLSLQMSSLRSEDTAMYYC
	CDR3	<u>SRPSERSHYATSQFAY</u>
	FR4	WGQGTTLVTVSA
Light Chain		
	FR1	DIVLTQSPFGIMASPGGEKVTMTCSAS
	CDR1	<u>SSVSY</u>
	FR2	MHWYQQKSGTSPKRWIY
	CDR2	<u>DTS</u>
	FR3	KLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYC
	CDR3	<u>QQWSSSPLT</u>
	FR4	FGAGTKVELK

Fig. 25A

Clone 4.1 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLLES GGGGLVQPGGSLRLS CAAS GFTFSNYAMSWVRQAPGKGLEWVAV

           60           70           80           90          100
ISNGGSYTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC SRPS

           110          120
ERSHYATSQFAYWGQGT LVTVSS (SEQ ID NO: 20)

```

Clone 4.1 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EIVLTQSPATLSLSPGERATLSCRAS SSVSYLAWYQQKPGQAPRRWIY DT

           60           70           80           90          100
SNRATGIPARFSGSGSGTDYTLTISSLEPEDFAVYYC QQWSSSPLTFGGG

TKVEIK (SEQ ID NO: 21)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLLES GGGGLVQPGGSLRLS CAAS
	CDR1	<u>GFTFSNYA</u>
	FR2	MSWVRQAPGKGLEWVAV
	CDR2	<u>ISNGGSYT</u>
	FR3	YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC
	CDR3	<u>SRPSERSHYATSQFAY</u>
	FR4	WGQGT LVTVSS
Light Chain		
	FR1	EIVLTQSPATLSLSPGERATLSCRAS
	CDR1	<u>SSVSY</u>
	FR2	LAWYQQKPGQAPRRWIY
	CDR2	<u>DTS</u>
	FR3	NRATGIPARFSGSGSGTDYTLT ISSLEPEDFAVYYC
	CDR3	<u>QQWSSSPLT</u>
	FR4	FGGGTKVEIK

Fig. 25B

Clone 4.2 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLLES GGGGLVQPGGSLRLS CAAS GFTFSNYAMSWVRQAPGKGLEWVAT

           60           70           80           90          100
ISNGGSYTYYPDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC SRPS

           110          120
ERSHYATSQFAYWGQGT LVTVSS (SEQ ID NO: 22)

```

Clone 4.2 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EIVLTQSPATLSLSPGERATLSCSAS SSVSYMHWYQQKPGTAPRRWIY DT

           60           70           80           90          100
SKLASGIPARFSGSGSGTDYTLTISSLEPEDFATYYC QQWSSSPLTFGAG

TKVEIK (SEQ ID NO: 23)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLLES GGGGLVQPGGSLRLS CAAS
	CDR1	<u>GFTFSNYA</u>
	FR2	MSWVRQAPGKGLEWVAT
	CDR2	<u>ISNGGSYT</u>
	FR3	YYPDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC
	CDR3	<u>SRPSERSHYATSQFAY</u>
	FR4	WGQGT LVTVSS
Light Chain		
	FR1	EIVLTQSPATLSLSPGERATLSCSAS
	CDR1	<u>SSVSY</u>
	FR2	MHWYQQKPGTAPRRWIY
	CDR2	<u>DTS</u>
	FR3	KLASGIPARFSGSGSGTDYTLT ISSLEPEDFATYYC
	CDR3	<u>QQWSSSPLT</u>
	FR4	FGAGTKVEIK

Fig. 25C

Clone 4.3 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLEESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQTPDKRLEWVAT

           60           70           80           90          100
ISNGGSYTYYPDSVKGRFTISRDN SKNTLYLQMSSLRAEDTAVYYCSRPS

           110          120
ERSHYATSQFAYWGQGT LVTVSS (SEQ ID NO: 24)

```

Clone 4.3 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EIVLTQSPAILS LSPGERATLSCSASSSVSYMHWYQQKPGQAPRRWIYDT

           60           70           80           90          100
SKLASGIPARFSGSGSGTSYTLTISSLEAEDFATYYCQQWSSSPLTFGAG

TKVEIK (SEQ ID NO: 25)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLEESGGGLVQPGGSLRLSCAAS
	CDR1	<u>GFTFSNYA</u>
	FR2	MSWVRQTPDKRLEWVAT
	CDR2	<u>ISNGGSYT</u>
	FR3	YYPDSVKGRFTISRDN SKNTLYLQMSSLRAEDTAVYYC
	CDR3	<u>SRPSERSHYATSQFAY</u>
	FR4	WGQGT LVTVSS
Light Chain		
	FR1	EIVLTQSPAILS LSPGERATLSCSAS
	CDR1	<u>SSVSY</u>
	FR2	MHWYQQKPGQAPRRWIY
	CDR2	<u>DTS</u>
	FR3	KLASGIPARFSGSGSGTSYTLT ISSLEAEDFATYYC
	CDR3	<u>QQWSSSPLT</u>
	FR4	FGAGTKVEIK

Fig. 25D

Clone 4.4 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLVESGGGVKKPGGSLKLSCAAS**GFTFSNYA**MSWVRQTPGKGLEWVAT
 60 70 80 90 100
ISNGGSYTYYPDSFQGRFTISRDNASTLSLQMSLSEDTAMYYC**SRPS**
 110 120
ERSHYATSQFAYWGQGTLVTVSA (SEQ ID NO: 26)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FP1	EVQLVESGGGVKKPGGSLKLSCAAS
	CDR1	<u>GFTFSNYA</u>
	FR2	MSWVRQTPGKGLEWVAT
	CDR2	<u>ISNGGSYT</u>
	FR3	YYPDSFQGRFTISRDNASTLSLQMSLSEDTAMYYC
	CDR3	<u>SRPSERSHYATSQFAY</u>
	FR4	WGQGTLVTVSA

Fig. 25E

Clone 4.5 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLVESGGGVKKPGGSLKLSCAAS**GFTFSNYA**MSWVRQTPGKGLEWVAT
 60 70 80 90 100
ISNGGSYTYYPDSFQGRFTISRDNASTLSLQMSLKAEDTAMYYC**SRPS**
 110 120
ERSHYATSQFAYWGQGTLLTVSS (SEQ ID NO: 27)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FP1	EVQLVESGGGVKKPGGSLKLSCAAS
	CDR1	<u>GFTFSNYA</u>
	FR2	MSWVRQTPGKGLEWVAT
	CDR2	<u>ISNGGSYT</u>
	FR3	YYPDSFQGRFTISRDNASTLSLQMSLKAEDTAMYYC
	CDR3	<u>SRPSERSHYATSQFAY</u>
	FR4	WGQGTLLTVSS

Fig. 25F

Clone 4.6 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLVESGGGVKKPGGSLKLSCAAS**GFTFSNYA**MSWVRQTPGKGLEWVAT
 60 70 80 90 100
ISQGGSYTYYPESFQGRFTISRDAQSTLSLQMSLKSSEDAMYYC**SRPS**
 110 120
ERSHYATSQFAYWGQGTLLVTVSA (SEQ ID NO: 28)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FP1	EVQLVESGGGVKKPGGSLKLSCAAS
	CDR1	<u>GFTFSNYA</u>
	FR2	MSWVRQTPGKGLEWVAT
	CDR2	<u>ISQGGSYT</u>
	FR3	YYPESFQGRFTISRDAQSTLSLQMSLKSSEDAMYYC
	CDR3	<u>SRPSERSHYATSQFAY</u>
	FR4	WGQGTLLVTVSA

Fig. 25G

Clone 4.7 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFSNYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISQGGSYTYYFDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC**SRPS**
 110 120
ERSHYATSQFAYWGQGTLLTVSS (SEQ ID NO: 29)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FP1	EVQLLESGGGLVQPGGSLRLSCAAS
	CDR1	<u>GFTFSNYA</u>
	FR2	MSWVRQAPGKGLEWVAT
	CDR2	<u>ISQGGSYT</u>
	FR3	YYFDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC
	CDR3	<u>SRPSERSHYATSQFAY</u>
	FR4	WGQGTLLTVSS

Fig. 25H

Clone 4.8 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLES~~GGGLVQPGGSLRL~~SCAAS**GFTFSNYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISNLGSYTYYFDSVKGRFTISRDN~~SKNTLYLQMN~~SLRAEDTAVYYC**SRPS**
 110 120
ERSHYATSQFAYWGQGT~~LVTVSS~~ (SEQ ID NO: 30)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FP1	EVQLLES GGGLVQPGGSLRL SCAAS
	CDR1	<u>GFTFSNYA</u>
	FR2	MSWVRQAPGKGLEWVAT
	CDR2	<u>ISNLGSYT</u>
	FR3	YYFDSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYC
	CDR3	<u>SRPSERSHYATSQFAY</u>
	FR4	WGQGT LVTVSS

Fig. 25I

Clone 4.9 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFSNYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISNSGSYTYYFDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC**SRPS**
 110 120
ERSHYATSQFAYWGQGTLVTVSS (SEQ ID NO: 31)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FP1	EVQLLESGGGLVQPGGSLRLSCAAS
	CDR1	<u>GFTFSNYA</u>
	FR2	MSWVRQAPGKGLEWVAT
	CDR2	<u>ISNSGSYT</u>
	FR3	YYFDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC
	CDR3	<u>SRPSERSHYATSQFAY</u>
	FR4	WGQGTLVTVSS

Fig. 25J

Clone 4.10 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLES~~GGGLVQPGGSLRL~~SCAAS**GFTFSNYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISDGGSYTYYFDSVKGRFTISRDN**SKNTLYLQ**MNSLRAEDTAVYYC**SRPS**
 110 120
ERSHYATSQFAYWGQGT**LVTVSS** (SEQ ID NO: 32)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FP1	EVQLLES GGGLVQPGGSLRL SCAAS
	CDR1	<u>GFTFSNYA</u>
	FR2	MSWVRQAPGKGLEWVAT
	CDR2	<u>ISDGGSYT</u>
	FR3	YYFDSVKGRFTISRDN SKNTLYLQ MNSLRAEDTAVYYC
	CDR3	<u>SRPS</u> ERSHYATSQFAY
	FR4	WGQGT LVTVSS

Fig. 25K

Clone 4.11 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLES~~GGGLVQPGGSLRL~~SCAAS**GFTFSNYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISNVGSYTYYFDSVKGRFTISRDN**SKNTLYLQMN**SLRAEDTAVYYC**SRPS**
 110 120
ERSHYYATSQFAYWGQGT**LVTVSS** (SEQ ID NO: 33)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FP1	EVQLLES GGGLVQPGGSLRL SCAAS
	CDR1	<u>GFTFSNYA</u>
	FR2	MSWVRQAPGKGLEWVAT
	CDR2	<u>ISNVGSYT</u>
	FR3	YYFDSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYC
	CDR3	<u>SRPS</u> ERSHYAT SQFAY
	FR4	WGQGT LVTVSS

Fig. 25L

Clone 4.4 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIVLTQSPGSLASVGDRTMTCSAS**SSVS**YMHWYQQKPGTSPKRWIY**DT**
 60 70 80 90 100
SKLASGVPARFSGSGSGTSYSLTISSLQPEDAATYYC**QQWSSSPLT**FGAG

TKVELK (SEQ ID NO: 34)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIVLTQSPGSLASVGDRTMTCSAS
	CDR1	<u>SSVS</u> Y
	FR2	MHWYQQKPGTSPKRWIY
	CDR2	<u>DT</u>
	FR3	KLASGVPARFSGSGSGTSYSLTISSLQPEDAATYYC
	CDR3	<u>QQWSSSPLT</u>
	FR4	FGAGTKVELK

Fig. 25M

Clone 4.5 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIVLTQSPSSLSASVGDRVITITCSAS**SSVS**YMHWYQQKPGTSPKRWIY**DT**
 60 70 80 90 100
SKLASGVPARFSGSGSGTSYSLTISSLQPEDAATYYC**QQWSSSPLT**FGAG

TKVEIK (SEQ ID NO: 35)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIVLTQSPSSLSASVGDRVITITCSAS
	CDR1	<u>SSVS</u> Y
	FR2	MHWYQQKPGTSPKRWIY
	CDR2	<u>DT</u>
	FR3	KLASGVPARFSGSGSGTSYSLTISSLQPEDAATYYC
	CDR3	<u>QQWSSSPLT</u>
	FR4	FGAGTKVEIK

Fig. 25N

Clone 4.6 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIVLTQSPSSLSASVGDRVITITCSAS**SSVSY**MHWYQQKPGQSPKRWIY**DT**
 60 70 80 90 100
SKLASGVPARFSGSGSGTSSYSLTISSLQPEDAATYYC**QQWSSSPLT**FGAG

TKVEIK (SEQ ID NO: 36)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIVLTQSPSSLSASVGDRVITITCSAS
	CDR1	<u>SSVSY</u>
	FR2	MHWYQQKPGQSPKRWIY
	CDR2	<u>DTS</u>
	FR3	KLASGVPARFSGSGSGTSSYSLTISSLQPEDAATYYC
	CDR3	<u>QQWSSSPLT</u>
	FR4	FGAGTKVEIK

Fig. 250

Clone 4.7 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPGSLASVGDRTMTCSAS**SSVS**YMHWYQQKPGTSPKRWIY**DT**
 60 70 80 90 100
SKLASGVPARFSGSGSGTSYSLTISSLQPEDAATYYC**QQWSSSPLT**FGAG

TKVELK (SEQ ID NO: 37)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIQLTQSPGSLASVGDRTMTCSAS
	CDR1	<u>SSVS</u> Y
	FR2	MHWYQQKPGTSPKRWIY
	CDR2	<u>DT</u> S
	FR3	KLASGVPARFSGSGSGTSYSLTISSLQPEDAATYYC
	CDR3	<u>QQWSSSPLT</u>
	FR4	FGAGTKVELK

Fig. 25P

Clone 53.0 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLEESGGGLVKGPGSLKLSCAASGFTFTSYAMSWVRQTPEKRLEWVAT

           60           70           80           90          100
ISHGGTYTYYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDAMYYCARHP

           110          120
IYSGNYQGYFDYWGQGTTLTVSS (SEQ ID NO: 38)

```

Clone 53.0 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIVLTQSPAIMASASLGEKVTMSCRASSGVNYIYWYQQKSDASPCLWIYFT

           60           70           80           90          100
SNLAPGVPARFSGSGSGNSYSLTISMEGEDAATYYCQQFTSSPYTFGGG

TKLEIK (SEQ ID NO: 39)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLEESGGGLVKGPGSLKLSCAAS
	CDR1	<u>GFTFTSYA</u>
	FR2	MSWVRQTPEKRLEWVAT
	CDR2	<u>ISHGGTYT</u>
	FR3	YYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDAMYYC
	CDR3	<u>ARHP</u> IYSGNYQGYFDY
	FR4	WGQGTTLTVSS
Light Chain		
	FR1	DIVLTQSPAIMASASLGEKVTMSCRAS
	CDR1	<u>SGVNY</u>
	FR2	IYWYQQKSDASPCLWIY
	CDR2	<u>FTS</u>
	FR3	SNLAPGVPARFSGSGSGNSYSLTISMEGEDAATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	FGGGTKLEIK

Fig. 26A

Clone 53.1 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLLES GGGGLVQPGGSLRLS CAAS GFTFTSYAMSWVRQAPGKGLEWVAV

           60           70           80           90          100
ISHGGTYTYYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCARHP

           110          120
IYSGNYQGYFDYWGQGTTLVTVSS (SEQ ID NO: 40)

```

Clone 53.1 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIQLTQSPSFSLASVGDRTITCRAS SGVNYLAWYQQKPGKAPKLWIYFT

           60           70           80           90          100
STLQSGVPSRFSGSGSGNEYTLTISSLPEDFATYYCQQFTSSPYTFGQG

TKLEIK (SEQ ID NO: 41)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLLES GGGGLVQPGGSLRLS CAAS
	CDR1	<u>GFTFTSY</u>
	FR2	MSWVRQAPGKGLEWVAV
	CDR2	<u>ISHGGTYT</u>
	FR3	YYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYC
	CDR3	<u>ARHP</u> IYSGNYQGYFDY
	FR4	WGQGTTLVTVSS
Light Chain		
	FR1	DIQLTQSPSFSLASVGDRTITCRAS
	CDR1	<u>SGVNY</u>
	FR2	LAWYQQKPGKAPKLWIY
	CDR2	<u>FTS</u>
	FR3	TLQSGVPSRFSGSGSGNEYTLTISSLPEDFATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	FGQGTKLEIK

Fig. 26B

Clone 53.2 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLLES GGGGLVQP GGS LRLSCAAS GFTFTSYAMSWVRQAPGKGLEWVAT

           60           70           80           90          100
ISHGGTYTYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYCARHP

           110          120
IYSGNYQGYFDYWGQGT LVT VSS   (SEQ ID NO: 42)

```

Clone 53.2 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIQLTQSPSFSL SASV GDRV TITCRAS SGVNYIYWYQQKPGKAPKLWIYFT

           60           70           80           90          100
SNLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYCQQFTSSPYTFGGG

TKLEIK   (SEQ ID NO: 43)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLLES GGGGLVQP GGS LRLSCAAS
	CDR1	<u>GFTFTSY</u>
	FR2	MSWVRQAPGKGLEWVAT
	CDR2	<u>ISHGGTYT</u>
	FR3	YYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYC
	CDR3	<u>ARHP</u> IYSGNYQGYFDY
	FR4	WGQGT LVT VSS
Light Chain		
	FR1	DIQLTQSPSFSL SASV GDRV TITCRAS
	CDR1	<u>SGVNY</u>
	FR2	IYWYQQKPGKAPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLAPGVPSRFSGSGSGNE YTLTISSLQPEDFATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	FGGGTKLEIK

Fig. 26C

Clone 53.3 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVQLEESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQTP EKRL EWVAT

           60           70           80           90          100
ISHGGTYTYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYCARHP

           110          120
IYSGNYQGYFDYWGQGTITVTVSS (SEQ ID NO: 44)

```

Clone 53.3 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIQLTQSPSFSLASVGDRTITCRASSGVNYIYWYQQKPD AAPKLWIYFT

           60           70           80           90          100
SNLAPGVPSRFSGSGSGNSYTLTISSLQPEDFATYYCQQFTSSPYTFGGG

TKLEIK (SEQ ID NO: 45)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLEESGGGLVQPGGSLRLSCAAS
	CDR1	<u>GFTFTSY</u>
	FR2	MSWVRQTP EKRL EWVAT
	CDR2	<u>ISHGGTYT</u>
	FR3	YYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYC
	CDR3	<u>ARHP</u> IYSGNYQGYFDY
	FR4	WGQGTITVTVSS
Light Chain		
	FR1	DIQLTQSPSFSLASVGDRTITCRAS
	CDR1	<u>SGVNY</u>
	FR2	IYWYQQKPD AAPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLAPGVPSRFSGSGSGNSYTLTISSLQPEDFATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	EGGGTKLEIK

Fig. 26D

Clone 53.4 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFTSYA**MSWVRQAPGKGLEWVAV
 60 70 80 90 100
ISHGGTYTYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYC**ARHP**
 110 120
IYSGNYQGYFDYWGQGTLTVSS (SEQ ID NO: 46)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLLES GGGLVQPGGSLRLS CAAS
	CDR1	GFTFTSYA
	FR2	MSWVRQAPGKGLEWVAV
	CDR2	ISHGGTYT
	FR3	YYPDSVKGRFTISRDNAKNTLYLQMN SLRAEDTAMYYC
	CDR3	ARHP IYSGNYQGYFDY
	FR4	WGQGT LTV SS

Fig. 26E

Clone 53.5 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFTSYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISHGGTYTYYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYC**ARHP**
 110 120
IYSGNYQGYFDYWGQGTLLTVSS (SEQ ID NO: 47)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLLESGGGLVQPGGSLRLSCAAS
	CDR1	<u>GFTFTSYA</u>
	FR2	MSWVRQAPGKGLEWVAT
	CDR2	<u>ISHGGTYT</u>
	FR3	YYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAMYYC
	CDR3	<u>ARHP</u> IYSGNYQGYFDY
	FR4	WGQGTLLTVSS

Fig. 26F

Clone 53.6 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLRLSCAAS**GFTFTSYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISHGGTYTYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYC**ARHP**
 110 120
IYSGNYQGYFDYWGQGTTLVTVSS (SEQ ID NO: 48)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLLES GGGLVQPGGSLRLS CAAS
	CDR1	<u>GFTFTSYA</u>
	FR2	MSWVRQAPGKGLEWVAT
	CDR2	<u>ISHGGTYT</u>
	FR3	YYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYC
	CDR3	<u>ARHP</u> IYSGNYQGYFDY
	FR4	WGQGTTLVTVSS

Fig. 26G

Clone 53.4 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFSLASVGDRVITITCRAS**SGVNY**LYWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC**QQFTSSPYT**FGGG

TKLEIK (SEQ ID NO: 49)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIQLTQSPSFSLASVGDRVITITCRAS
	CDR1	<u>SGVNY</u>
	FR2	LYWYQQKPGKAPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	EGGGTKLEIK

Fig. 26H

Clone 53.5 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFSLASVGDRTITCRAS**SGVNY**IAWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC**QQFTSSPYT**FGGG

TKLEIK (SEQ ID NO: 50)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIQLTQSPSFSLASVGDRTITCRAS
	CDR1	<u>SGVNY</u>
	FR2	IAWYQQKPGKAPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	EGGGTKLEIK

Fig. 26I

Clone 53.6 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFSLASVGDRVITITCRAS**SGVNY**IYWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
STLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC**QQFTSSPYT**FGGG

TKLEIK (SEQ ID NO: 51)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIQLTQSPSFSLASVGDRVITITCRAS
	CDR1	<u>SGVNY</u>
	FR2	IYWYQQKPGKAPKLWIY
	CDR2	<u>FTS</u>
	FR3	TLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	EGGGTKLEIK

Fig. 26J

Clone 53.7 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFSLASVGDRTITCRAS**SGVNY**IYWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
SNLQPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC**QQFTSSPYT**FGGG

TKLEIK (SEQ ID NO: 52)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIQLTQSPSFSLASVGDRTITCRAS
	CDR1	<u>SGVNY</u>
	FR2	IYWYQQKPGKAPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLQPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	FGGGTKLEIK

Fig. 26K

Clone 53.8 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFSLASVGDRVITITCRAS**SGVNY**IYWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
SNLASGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC**QQFTSSPYT**FGGG

TKLEIK (SEQ ID NO: 53)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIQLTQSPSFSLASVGDRVITITCRAS
	CDR1	<u>SGVNY</u>
	FR2	IYWYQQKPGKAPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLASGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	EGGGTKLEIK

Fig. 26L

Clone 53.9 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFLSASVGDRVITITCRAS**SGVNY**IYWYQQKPGKAPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC**QQFTSSPYT**FGQG

TKLEIK (SEQ ID NO: 54)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIQLTQSPSFLSASVGDRVITITCRAS
	CDR1	<u>SGVNY</u>
	FR2	IYWYQQKPGKAPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLAPGVPSRFSGSGSGNEYTLTISSLQPEDFATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	FGQGTKLEIK

Fig. 26M

Clone 53.7 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLES^{GGGLVQPGGSLKLS}CAAS**GFTFTSYA**MSWVRQTPGKRLEWVAT
 60 70 80 90 100
ISHGGTYTYYPDSVKGRFTISRDN SKNTLYLQMS^{SLR}SEDTAMYYC**ARHP**
 110 120
IYSGNYQGYFDYWGQGTTLTVSS (SEQ ID NO: 63)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLLES ^{GGGLVQPGGSLKLS} CAAS
	CDR1	<u>GFTFTSYA</u>
	FR2	MSWVRQTPGKRLEWVAT
	CDR2	<u>ISHGGTYT</u>
	FR3	YYPDSVKGRFTISRDN SKNTLYLQMS ^{SLR} SEDTAMYYC
	CDR3	<u>ARHP</u> IYSGNYQGYFDY
	FR4	WGQGTTLTVSS

Fig. 26N

Clone 53.8 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLES GGGGLVQPGGSLKLS CAAS **GFTFTSYA**MSWVRQAPGKGLEWVAT

60 70 80 90 100
ISHGGTYTYYPDSVKGRFTISRDN SKNTLYLQMSSLRAEDTAVYYC **ARHP**

110 120
IYSGNYQGYFDYWGQGT LVTVSS (SEQ ID NO: 64)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLLES GGGGLVQPGGSLKLS CAAS
	CDR1	<u>GFTFTSYA</u>
	FR2	MSWVRQAPGKGLEWVAT
	CDR2	<u>ISHGGTYT</u>
	FR3	YYPDSVKGRFTISRDN SKNTLYLQMSSLRAEDTAVYYC
	CDR3	<u>ARHP</u> IYSGNYQGYFDY
	FR4	WGQGT LVTVSS

Fig. 26O

Clone 53.9 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLESGGGLVQPGGSLKLSCAAS**GFTFTSYA**MSWVRQTPGKRLEWVAT
 60 70 80 90 100
ISHGGTYTYYPESVKGRFTISRDSKNTLYLQMSSLRSEDTAVYYC**ARHP**
 110 120
IYSGNYQGYFDYWGQGTTLTVSS (SEQ ID NO: 65)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLLESGGGLVQPGGSLKLSCAAS
	CDR1	<u>GFTFTSYA</u>
	FR2	MSWVRQTPGKRLEWVAT
	CDR2	<u>ISHGGTYT</u>
	FR3	YYPESVKGRFTISRDSKNTLYLQMSSLRSEDTAVYYC
	CDR3	<u>ARHP</u> IYSGNYQGYFDY
	FR4	WGQGTTLTVSS

Fig. 26P

Clone 53.10 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 EVQLLES~~GGGLVQPGGSLKLS~~CAAS**GFTFTSYA**MSWVRQAPGKGLEWVAT
 60 70 80 90 100
ISHGGTYTYYPESVKGRFTISR~~DQSKNTLYLQ~~MSSSLRAEDTAVYYC**ARHP**
 110 120
IYSGNYQGYFDYWGQGT~~LVTVSS~~ (SEQ ID NO: 66)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVQLLES GGGLVQPGGSLKLS CAAS
	CDR1	<u>GFTFTSYA</u>
	FR2	MSWVRQAPGKGLEWVAT
	CDR2	<u>ISHGGTYT</u>
	FR3	YYPESVKGRFTISR DQSKNTLYLQ MSSSLRAEDTAVYYC
	CDR3	<u>ARHP</u> IYSGNYQGYFDY
	FR4	WGQGT LVTVSS

Fig. 26Q

Clone 53.10 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPAIMASASVGDRVTMSCRAS**SGVNY**IYWYQQKPGASPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC**QQFTSSPYT**FGGG

TKLEIK (SEQ ID NO: 67)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIQLTQSPAIMASASVGDRVTMSCRAS
	CDR1	<u>SGVNY</u>
	FR2	IYWYQQKPGASPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	FGGGTKLEIK

Fig. 26R

Clone 53.11 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPAILSASVGDRVTISCRAS**SGVNY**IYWYQQKPGQSPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC**QQFTSSPYT**FGGG

TKLEIK (SEQ ID NO: 68)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIQLTQSPAILSASVGDRVTISCRAS
	CDR1	<u>SGVNY</u>
	FR2	IYWYQQKPGQSPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	FGGGTKLEIK

Fig. 26S

Clone 53.12 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPAILSASVGDRVTMSCRAS**SGVNY**IYWYQQKPGASPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC**QQFTSSPYT**FGGG

TKLEIK (SEQ ID NO: 69)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIQLTQSPAILSASVGDRVTMSCRAS
	CDR1	<u>SGVNY</u>
	FR2	IYWYQQKPGASPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	EGGGTKLEIK

Fig. 26T

Clone 53.13 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPAILSASVGDRVTISCRAS**SGVNY**IYWYQQKPGQSPKLWIY**FT**
 60 70 80 90 100
SNLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC**QQFTSSPYT**FGGG

TKLEIK (SEQ ID NO: 70)

SEQ ID NO	Region	Sequence
Light Chain		
	FR1	DIQLTQSPAILSASVGDRVTISCRAS
	CDR1	<u>SGVNY</u>
	FR2	IYWYQQKPGQSPKLWIY
	CDR2	<u>FTS</u>
	FR3	NLAPGVPARFSGSGSGNSYSLTISSMQGEDAATYYC
	CDR3	<u>QQFTSSPYT</u>
	FR4	EGGGTKLEIK

Fig. 26U

Clone 82.0 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
EVKLEESGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGV

           60           70           80           90          100
ISTYNGNTKYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARFL

110
SLRYFDVWGAGTTVTVSS    (SEQ ID NO: 55)

```

Clone 82.0 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIVLTQSPAILSAPPGEKVTMTCRASSSVIYMYWYQQKPGSSPKPWIYAT

           60           70           80           90          100
SKLASGVPVRFSGSGSGTSYSLTISRVEAEDVATYYCQQWSSEPLTFGAG

TKLELK    (SEQ ID NO: 56)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	EVKLEESGPEVVRPGVSVKISCKGS
	CDR1	<u>GYTFTDY</u> A
	FR2	MHWVKQSHAKSLEWIGV
	CDR2	<u>ISTYNGNT</u>
	FR3	KYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYC
	CDR3	A <u>RFLSLRYFDV</u>
	FR4	WGAGTTVTVSS
Light Chain		
	FR1	DIVLTQSPAILSAPPGEKVTMTCRAS
	CDR1	<u>SSVIY</u>
	FR2	MYWYQQKPGSSPKPWIY
	CDR2	<u>ATS</u>
	FR3	KLASGVPVRFSGSGSGTSYS <u>LTISRVEAEDVATYYC</u>
	CDR3	<u>QQWSSEPLT</u>
	FR4	FGAGTKLELK

Fig. 27A

Clone 82.1 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 QVKLVQSGAEVKKPGASVKVSCKAS**GYTFTDYA**MHWVRQAPGQRLEWIGW
 60 70 80 90 100
ISTYNGNTKYSQKFQGRATMTVDKSASTAYMELSSLRSEDTAVYYC**ARFL**
 110
SLRYFDVWGKGTITVTVSS (SEQ ID NO: 57)

Clone 82.1 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFSLASVGDRTITCRAS**SSVIY**LAWYQQKPGKAPKRWIY**AT**
 60 70 80 90 100
STLQSGVPSRFSGSGSGTEYTLTISSLQPEDFATYYC**QQWSSEPLT**FGGG
 TKVEIK (SEQ ID NO: 58)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	QVKLVQSGAEVKKPGASVKVSCKAS
	CDR1	<u>GYTFTDYA</u>
	FR2	MHWVRQAPGQRLEWIGW
	CDR2	<u>ISTYNGNT</u>
	FR3	KYSQKFQGRATMTVDKSASTAYMELSSLRSEDTAVYYC
	CDR3	<u>ARFLSLRYFDV</u>
	FR4	WGKGTITVTVSS
Light Chain		
	FR1	DIQLTQSPSFSLASVGDRTITCRAS
	CDR1	<u>SSVIY</u>
	FR2	LAWYQQKPGKAPKRWIY
	CDR2	<u>ATS</u>
	FR3	TLQSGVPSRFSGSGSGTEYTLTISSLQPEDFATYYC
	CDR3	<u>QQWSSEPLT</u>
	FR4	EGGGTKVEIK

Fig. 27B

Clone 82.2 - VH amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 QVKLVQSGAEVKKPGASVKVSCCKGS **GYTFTDY**AMHWVRQAPGQRLEWIGV
 60 70 80 90 100
ISTYNGNTKYNQKFQGRATMTVDKSASTAYMELSSLRSEDTAIYYC**ARFL**
 110
SLRYFDVWGAGTTVTVSS (SEQ ID NO: 59)

Clone 82.2 - VL amino acid sequence - CDRs in bold and underlined

1 10 20 30 40 50
 DIQLTQSPSFSLASVGDRTTITCRAS **SSVIY**MYWYQQKPGKAPKRWIY**AT**
 60 70 80 90 100
SKLASGVPSRFSGSGSGTEYTLTISSLQPEDFATYYC**QQWSSEPLT**FGAG
 TKVEIK (SEQ ID NO: 60)

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	QVKLVQSGAEVKKPGASVKVSCCKGS
	CDR1	<u>GYTFTDY</u>
	FR2	AMHWVRQAPGQRLEWIGV
	CDR2	<u>ISTYNGNT</u>
	FR3	KYNQKFQGRATMTVDKSASTAYMELSSLRSEDTAIYYC
	CDR3	<u>ARFLSLRYFDV</u>
	FR4	WGAGTTVTVSS
Light Chain		
	FR1	DIQLTQSPSFSLASVGDRTTITCRAS
	CDR1	<u>SSVIY</u>
	FR2	MYWYQQKPGKAPKRWIY
	CDR2	<u>AT</u>
	FR3	SKLASGVPSRFSGSGSGTEYTLTISSLQPEDFATYYC
	CDR3	<u>QQWSSEPLT</u>
	FR4	FGAGTKVEIK

Fig. 27C

Clone 82.3 - VH amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
QVKLVQSGPEVKVPGASVKVSCCKGSGYTFTDYAMHWVRQAPGQSLEWIGV

           60           70           80           90          100
ISTYNGNTKYNQKFQGRATMTVDKSASTAYMELSRRLRSEDTAIYYCARFL

           110
SLRYFDVWGAGTTVTVSS    (SEQ ID NO: 61)

```

Clone 82.3 - VL amino acid sequence - CDRs in bold and underlined

```

1           10           20           30           40           50
DIQLTQSPSFSLASPGDRVITITCRASSSVIYMYWYQQKPGSAPKRWIYAT

           60           70           80           90          100
SKLASGVPVRFSGSGSGTSYTLTISRLQAEDFATYYCQQWSSEPLTFGAG

TKVEIK    (SEQ ID NO: 62)

```

SEQ ID NO	Region	Sequence
Heavy Chain		
	FR1	QVKLVQSGPEVKVPGASVKVSCCKGS
	CDR1	<u>GYTFTDYA</u>
	FR2	MHWVRQAPGQSLEWIGV
	CDR2	<u>ISTYNGNT</u>
	FR3	KYNQKFQGRATMTVDKSASTAYMELSRRLRSEDTAIYYC
	CDR3	<u>ARFLSLRYFDV</u>
	FR4	WGAGTTVTVSS
Light Chain		
	FR1	DIQLTQSPSFSLASPGDRVITITCRAS
	CDR1	<u>SSVIY</u>
	FR2	MYWYQQKPGSAPKRWIY
	CDR2	<u>ATS</u>
	FR3	KLASGVPVRFSGSGSGTSYTLTISRLQAEDFATYYC
	CDR3	<u>QQWSSEPLT</u>
	FR4	FGAGTKVEIK

Fig. 27D

SEQ ID NO	Antibody	Sequence
	12.0 VH	5'GAGGTGCAGCTGGAAGAGTCCGGCGGAGGCCTGGTGCAGCCCAAG GGCAGCCTGAAGCTGAGCTGTGCGGCCAGCGGCATCAGCTTCAACGA CGCCGCCATGAACTGGATCCGGCAGGCCCCCTGGCGAGGGCCTGGAAT GGGTGGCCCGGATCAGAAGCAAGATCAACGACTACGGCACCCACTAC GCCGCCAGCGTGAAGGACCGGTTCAACATCAGCCGGGACGACAGCCA GAATATCCTGTTCTGTCAGATGAACAACCTGAAAACCGAGGACACCG GCATGTACTACTGCGTGATCGACGGCTACGGCAGCCTGGCCTACTGG GGCCAGGGAACCCCTGGTGACAGTGTCCGCC3'
	12.0 VL	5'GACATCGTGCTGACCCAGAGCCCCGCCATCATGAGCAGCAGCCCT GGCGAGAAAGTGACCATGACCTGCCGGGCCAGCAGCAGCGTGATCAG CAGCTACCTGCACTGGTATCAGCAGCGGAGCGGCCAGCCCCAAGC TGTGGATCTACAGCACCAGCAGCCTGGCCAGCGGCGTGCCAGCCAGA TTTTCTGGCAGCGGCAGCGGCACCTCCTTCAGCCTGACCATCAGCAG CGTGGAAGCCGAGGACGCCGCCACCTACTACTGCCAGCAGTACAGCG GCTACCCCCTGACCTTCGGAGCCGGCACCAAGCTGGAAGTGAAG3'
	12.1 VH	5'GAGGTGCAGCTGGTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGC GGCAGCCTGAAGCTGTCTTGTGCGGCCAGCGGCATCAGCTTCAACGA CGCCGCCATGCACTGGGTGCGCCAGGCCTCTGGCAAGGGCCTGGAAT GGGTGGCCCGGATCAGAAGCAAGATCAACGACTACGGCACCGCCTAC GCCGCCAGCGTGAAGGCGAGATTCAACATCAGCCGGGACGACAGCCA GAACACCCCTGTACCTGCAGATGAACAGCCTGAAAACCGAGGACACCG CCGTGTACTACTGCGTGATCGACGGCTACGGCAGCCTGGCCTACTGG GGCCAGGGAACCCCTGGTGACAGTGTCCAGC3'
	12.1 VL	5'GAGATCGTGCTGACCCAGAGCCCCGCCACCCTGTCTCTGAGCCCT GGCGAGAGAGCCACCCTGAGCTGCAGAGCCAGCAGCAGCGTGATCAG CAGCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCCAGAC TGTGGATCTACAGCACCAGCAACCGGGCCACCGGCATCCCCGCCAGA TTTTCTGGCAGCGGCAGCGGCACCGACTTCACCCCTGACCATCAGCAG CCTGGAACCCGAGGACTTCGCCACCTACTACTGCCAGCAGTACAGCG GCTACCCCCTGACCTTCGGCGGAGGACCAAGGTGGAATCAAG3'

Fig. 28A

SEQ ID NO	Antibody	Sequence
	12.2 VH	5'GAGGTGCAGCTGGTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGC GGCAGCCTGAAGCTGTCTTGTGCCGCCAGCGGCATCAGCTTCAACGA CGCCGCCATGAACTGGATCCGGCAGGCCAGCGGCAAGGGCCTGGAAT GGGTGGCCCGGATCAGAAGCAAGATCAACGACTACGGCACCCACTAC GCCGCCAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCCA GAACACCCTGTACCTGCAGATGAACAGCCTGAAAACCGAGGACACCG CCATGTACTACTGCGTGATCGACGGCTACGGCAGCCTGGCCTACTGG GGCCAGGGAACCCTGGTGACAGTGTCCAGC3'
	12.2 VL	5'GAGATCGTGCTGACCCAGAGCCCCGCCACCCCTGTCTCTGAGCCCT GGCGAGAGAGCCACCCCTGAGCTGCAGAGCCAGCAGCAGCGTGATCAG CAGCTACCTGCACTGGTATCAGCAGAAGCCCGGCCAGGCCCCCAGAC TGTGGATCTACAGCACCCAGCAGCCTGGCCAGCGGCATCCCCGCCAGA TTTTCTGGCAGCGGCAGCGGCACCGACTTCACCCCTGACCATCAGCTC CCTGGAACCCGAGGACTTCGCCACCTACTACTGCCAGCAGTACAGCG GCTACCCCCTGACCTTCGGAGCCGGCACCAAGGTGGAAATCAAG3'
	12.3 VH	5'GAGGTGCAGCTGGTGGAAAGCGGCGGAGGCCTGGTGCAGCCCCAAG GGCAGCCTGAAGCTGAGCTGTGCCGCCAGCGGCATCAGCTTCAACGA CGCCGCCATGAACTGGATCCGGCAGGCCAGCGGCAAGGGCCTGGAAT GGGTGGCCCGGATCAGAAGCAAGATCAACGACTACGGCACCCACTAC GCCGCCAGCGTGAAGGACCGGTTACCATCAGCCGGGACGACAGCCA GAACATCCTGTACCTGCAGATGAACAACCTGAAAACCGAGGACACCG CCATGTACTACTGCGTGATCGACGGCTACGGCAGCCTGGCCTACTGG GGCCAGGGAACCCTGGTGACAGTGTCCAGC3'
	12.3 VL	5'GAGATCGTGCTGACCCAGAGCCCCGCCATCCTGAGCAGCTCTCCA GGCGAGAGAGCCACCCCTGAGCTGCAGAGCCAGCAGCAGCGTGATCAG CAGCTACCTGCACTGGTATCAGCAGAAGCCTGGCGCCGCTCCCCGGC TGTGGATCTACAGCACCAAGCAGCCTGGCCAGCGGCATCCCCGCCAGA TTTTCTGGCAGCGGCAGCGGCACCGACTTCACCCCTGACCATCAGCAG CCTGGAAGCCGAGGACTTCGCCACCTACTACTGCCAGCAGTACAGCG GCTACCCCCTGACCTTCGGAGCCGGCACCAAGGTGGAAATCAAG3'

Fig. 28B

SEQ ID NO	Antibody	Sequence
	135.0 VH	5'GAAGTGAAGCTGGAAGAGTCCGGCGGAGGCCTGGTGAACCTGGCGGCA GCCTGAAGCTGAGCTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCC TGAGCTGGGTGCGCCAGACCCCCGAGAAGAGACTGGAATGGGTGGCCACCA TCAGCCACGGCGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCAGAGACAACGCCAAGAACACCCTGAACCTGCAGATGAGCA GCCTGCGGAGCGAGGACACCGCCATGTACTACTGCGCCAGGCACCCCTTCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGC TGACCGTGTCTCT3'
	135.0 VL	5'GACATCGTGCTGACCCAGAGCCCCGCCATCATGAGCGCCAGCCTGGGGCG AGAAAGTGACCATGAACTGCCGGGCCAACAGCGGCGTGAACCTACATGTACT GGTATCAGCAGAAGTCCGACGCCAGCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA ACAGCTACAGCCTGACCATCAGCAGCATGGAAGGCGAGGACGCCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'
	135.1 VH	5'GAGGTGCAGCTGGAAGAGTCCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGGCCCTGGCAAGGGACTGGAATGGGTGGCCGTGA TCAGCCACGGCGGCAGCTACACCTACTACGCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGACACCCCTTCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
	135.1 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGGCG ACAGAGTGACCATCACCTGTGCGGGCCAGCAGCGGCGTGAACCTACCTGGCCT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGCAGAGCGGCGTGCCCGCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCTGACCATCAGCAGCCTGCAGTTCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCCAGGGCACCA AGCTGGAAATCAAG3'

Fig. 28C

SEQ ID NO	Antibody	Sequence
	135.2 VH	5'GAGGTGCAGCTGGAAGAGTCCGCGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCC TGAGCTGGGTGCGCCAGGCCCTCGCAAAGGACTGGAATGGGTGGCCACCA TCAGCCACGGCGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCAGAGACAACAGCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGACACCCCTTCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
	135.2 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTGCGGCCAACAGCGGCGTGAACCTACATGTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGTTCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'
	135.3 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCC TGAGCTGGGTGCGCCAGACCCCGAGAAGAGACTGGAATGGGTGGCCACCA TCAGCCACGGCGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCAGAGACAACAGCAAGAACACCCTGAACCTGCAGATGAGCA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGGCACCCCTTCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
	135.3 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTGCGGCCAACAGCGGCGTGAACCTACATGTACT GGTATCAGCAGAAGCCCGACGCGGCTCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACAGCTACACCCTGACCATCAGCAGCCTGCAGTTCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'

Fig. 28D

SEQ ID NO	Antibody	Sequence
	4.0 VH	5'GAAAGTGCAGCTGGAGGAGTCAGGGGGAGGCTTAGTGAAGCCTGGAGGGT CCCTAAAACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAATTATGCCA TGTCTTGGGTTCCGCCAGACTCCGGATAAGCGGCTGGAGTGGGTCCGAACCA TTAGTAATGGTGGTAGTTACACCTACTATCCAGACACTGTGAAGGSTCGCT TCACCATCTCCAGAGACAATGCCAAGAACACCCTGTCTCTGCAAATGAGCA GTCTGAGGTCTGAGGACACGGCCATGTATTACTGTTCAAGACCCTCTGAGA GATCCCATTTACTACGCTACTAGCCAGTTTGCTTACTG GGGCCAAGGGACTCTGGTCACTGTCTCTGCA3'
	4.0 VL	5'GACATTGTGCTGACCCAGTCTCCAGGAATCATGTCTGCATCTCCAGGGG AGAAAGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGCATT GGTACCAGCAGAAGTCAGGCACCTCCCCCAAAGATGGATTATGACACAT CCAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGA CCTCTTACTCTCTCACAATCAGCAGCATGGAGGCTGAAGATGCTGCCACTT ATTACTGCCAGCAGTGGAGTAGTAGCCCGCTCACGTTCCGGTCTGGGACCA AGGTGGAGCTGAAA3'
	4.1 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGGCGCCGCGAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCTGGCAAGGGACTGGAATGGGTGGCCGTGA TCAGCAACGGCGGCAGCTACACCTACTACGCCGACAGCGTGAAGGGCCGCT TCACCATCAGCCGGGACAACAGCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGGCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTCGCCTACTGGGGCCAGGSCACCC TGGTGACAGTGTCCAGC3'
	4.1 VL	5'GAGATCGTGCTGACCCAGAGCCCCGCCACCCTGTCTCTGAGCCCTGGCG AGAGAGCCACCCTGAGCTGCAGAGCCAGCAGCAGCGTGTCTTACCTGGCCT GGTATCAGCAGAAGCCCGGCCAGGCCCCCAGACGGTGGATCTACGACACCA GCAACCGGGCCACCGGCATCCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCGACTACACCCTGACCATCAGCAGCCTGGAACCCGAGGACTTCGCCGTGT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTCGGCGGAGGCACCA AGGTGGAAATCAAG3'

Fig. 28E

SEQ ID NO	Antibody	Sequence
	4.2 VH	5'GAGGTGCAGCTGCTGGAAAGCGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCTGGCAAGGGACTGGAATGGGTGGCCACCA TCAGCAACGGCGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGGCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'
	4.2 VL	5'GAGATCGTGCTGACCCAGAGCCCCGCCACCCCTGTCTCTGAGCCCTGGCG AGAGAGCCACCCTGAGCTGTAGCGCCAGCAGCAGCGTGTCTACATGCACT GGTATCAGCAGAAGCCCGGCCACCGCCCCAGACGGTGGATCTACGATACCA GCAAGCTGGCCAGCGGCATCCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCGACTACACCCTGACCATCAGCAGCCTGGAACCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTCGGAGCCGGCACCA AGGTGGAAATCAAG3'
	4.3 VH	5'GAGGTGCAGCTGGAAGAGTCCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGACCCCGACAAGCGGCTGGAATGGGTGGCCACCA TCAGCAACGGCGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCCTGTACCTGCAGATGAGCA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGGCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'
	4.3 VL	5'GAGATCGTGCTGACCCAGAGCCCCGCCATCCTGAGCCTGTCTCCAGGCG AGAGAGCCACCCTGAGCTGCAGCGCCAGCAGCAGCGTGTCTACATGCACT GGTATCAGCAGAAGCCCGGCCAGGCCCCCAGACGGTGGATCTACGATACCA GCAAGCTGGCCAGCGGCATCCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCAGCTACACCCTGACCATCAGCAGCCTGGAAGCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTCGGAGCCGGCACCA AGGTGGAAATCAAG3'

Fig. 28F

SEQ ID NO	Antibody	Sequence
	4.4 VH	5'GAGGTGCAGCTGGTGGAAAGCGGCGGAGGCGTGAAGAAGCCTGGCGGCA GCCTGAAGCTGAGCTGTGCGCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTCCGACAGACCCCCCGCAAGGGCCTGGAATGGGTGGCCACCA TCAGCAACGGCGGCAGCTACACCTACTACCCCGACAGCTTCCAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAGCACCCCTGAGCCTGCAGATGTCCA GCCTGAAGTCCGAGGACACCGCCATGTACTACTGCAGCCGGGCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTCACCGTGTCTGCT3'
	4.5 VH	5'GAGGTGCAGCTGGTGGAAAGCGGCGGAGGCGTGAAGAAGCCTGGCGGCA GCCTGAAGCTGAGCTGTGCGCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTCCGACAGACCCCCCGCAAGGGCCTGGAATGGGTGGCCACCA TCAGCAACGGCGGCAGCTACACCTACTACCCCGACAGCTTCCAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAGCACCCCTGAGCCTGCAGATGTCCA GCCTGAAGGCCGAGGACACCGCCATGTACTACTGCAGCCGGGCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTCACCGTGTCTGCT3'
	4.6 VH	5'GAGGTGCAGCTGGTGGAAAGCGGCGGAGGCGTGAAGAAGCCTGGCGGCA GCCTGAAGCTGAGCTGTGCGCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTCCGACAGACCCCCCGCAAGGGCCTGGAATGGGTGGCCACAA TCAGCCAGGGCGGCAGCTACACCTACTACCCCGAGAGCTTCCAGGGCCGGT TCACCATCAGCCGGGACCAGGCCAAGAGCACCCCTGAGCCTGCAGATGTCCA GCCTGAAGTCCGAGGACACCGCCATGTACTACTGCAGCCGGGCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTCACCGTGTCTGCT3'
	4.7 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCTGGCAAGGGACTGGAATGGGTGGCCACCA TCAGCCAGGGTGGCAGCTACACCTACTACCCCGACAGCTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGGCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'

Fig. 28G

SEQ ID NO	Antibody	Sequence
	4.9 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCTGGCAAGGGACTGGAATGGGTGGCCACCA TCAGCAATCTGGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGGCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'
	4.9 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCTGGCAAGGGACTGGAATGGGTGGCCACCA TCAGCAATTCAGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGGCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'
	4.10 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCTGGCAAGGGACTGGAATGGGTGGCCACCA TCAGCGACGGTGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGGCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'
	4.11 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCAGCAACTACGCCA TGAGCTGGGTGCGCCAGGCCCTGGCAAGGGACTGGAATGGGTGGCCACCA TCAGCAATGTCGGCAGCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACAGCAAGAACACCCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCAGCCGGGCCAGCGAGC GGAGCCACTACTACGCCACCAGCCAGTTTCGCCTACTGGGGCCAGGGCACCC TGGTGACAGTGTCCAGC3'

Fig. 28H

SEQ ID NO	Antibody	Sequence
	4.4 VL	5'GACATCGTGCTGACCCAGAGCCCCGGCAGCCTGTCTGCCAGCGTGGGCG ACAGAGTGACCATGACCTGCAGCGCCAGCAGCAGCGTGTCTTACATGCACT GGTATCAGCAGAAGCCCGGCCAGCCCCAAGCGGTGGATCTACGACACCA GCAAGCTGGCCAGCGGCGTGTCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCAGCTACAGCCTGACCATCAGCAGCCTGCAGCCCGAGGACGCCGCCACCT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTTGGAGCCGGCACCA AGGTGGAACTGAAG3'
	4.5 VL	5'GACATCGTGCTGACCCAGAGCCCCAGCAGCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTAGCGCCAGCAGCAGCGTGTCTTACATGCACT GGTATCAGCAGAAGCCCGGCCAGCCCCAAGCGGTGGATCTACGACACCA GCAAGCTGGCCAGCGGCGTGTCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCAGCTACAGCCTGACCATCAGCAGCCTGCAGCCCGAGGACGCCGCCACCT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTTGGAGCCGGCACCA AGGTGGAAATCAAG3'
	4.6 VL	5'GACATCGTGCTGACCCAGAGCCCCAGCAGCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTAGCGCCAGCAGCAGCGTGTCTTACATGCACT GGTATCAGCAGAAGCCCGGCCAGTCCCCAAGCGGTGGATCTACGACACCA GCAAGCTGGCCAGCGGCGTGTCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCAGCTACAGCCTGACCATCAGCAGCCTGCAGCCCGAGGACGCCGCCACCT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTTGGAGCCGGCACCA AGGTGGAAATCAAG3'
	4.7 VL	5'GACATCCAGCTGACCCAGAGCCCCGGCAGCCTGTCTGCCAGCGTGGGCG ACAGAGTGACCATGACCTGCAGCGCCAGCAGCAGCGTGTCTTACATGCACT GGTATCAGCAGAAGCCCGGCCAGCCCCAAGCGGTGGATCTACGACACCA GCAAGCTGGCCAGCGGCGTGTCCCGCCAGATTTTCTGGCAGCGGCAGCGGCA CCAGCTACAGCCTGACCATCAGCAGCCTGCAGCCCGAGGACGCCGCCACCT ACTACTGCCAGCAGTGGTCCAGCAGCCCCCTGACCTTTGGAGCCGGCACCA AGGTGGAACTGAAG3'

Fig. 28I

SEQ ID NO	Antibody	Sequence
	53.0 VH	5'GAGGTTTCAGCTGGAGGAGTCAGGGGGAGGCTTAGTGAAGCCTGGAGGGT CCCTGAAACTCTCCTGTGCAGCCTCTGGATTCACTTTCACTAGCTATGCCA TGTCTTGGGTTCCGCCAGACTCCGGAGAAGAGGCTGGAGTGGGTCCGAACCA TTAGTCATGGTGGTACTTTACACCTACTATCCAGACAGTGTGAAGGGACGAT TCACCATCTCCAGAGACAATGCCAAGAACACCCTGTACCTGCCAAATGAGCA GTCTGAGGTCTGAGGACACGGCCATGTATTACTGTGCAAGACATCCTATCT ACTCTGGTAACTACCAGGGATACTTTGACTACTGG GGCCAAGGCACCACTCTCACAGTCTCCTCA3'
	53.0 VL	5'GACATTGTGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCTAGGGG AGAAGGTCACCATGAGCTGCAGGGCCAGCTCAGGTGTAAATTACATATACT GGTACCAGCAGAAGTCAGATGCCTCCCCCAAACATATGGATTATTTTCACAT CCAACCTGGCTCCTGGAGTCCAGCTCGCTTCAGTGGCAGTGGGTCTGGGA ACTCTTATTTCTCTCACAATCAGCAGCATGGAGGGTGAAGATGCTGCCACTT ATTACTGCCAGCAGTTTACTAGTTCCCCGTACACGTTCCGAGGGGGGACCA AGCTGGAAATAAAA3'
	53.1 VH	5'GAGGTGCAGCTGCTGGAAAGCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGGCCCTGGCAAGGGACTGGAATGGGTGGCCGTGA TCAGCCACGGCGGCACCTACACCTACTACGCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAACACCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGACACCCCATCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
	53.1 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTGCGGGCCAGCAGCGGCGTGAACCTACCTGGCCT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCACCCCTGCAGAGCGGCGTGGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTTACCAGCAGCCCCCTACACCTTCGGCCAGGGCACCA AGCTGGAAATCAAG3'

Fig. 28J

SEQ ID NO	Antibody	Sequence
	53.2 VH	5'GAGGTGCAGCTGCTGGAAAGCGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGGCCCTCGCAAGGGACTGGAATGGGTGGCCACAA TCAGCCACGGCGGCACCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAACACCCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCATGTACTACTGCGCCAGACACCCCATCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
	53.2 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTGCGGCCAGCAGCGGCGTGAACCTACATCTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'
	53.3 VH	5'GAGGTGCAGCTGGAAGAGTCCGGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGACCCCGAGAAGCGGCTGGAATGGGTGGCCACAA TCAGCCACGGCGGCACCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAACACCCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCATGTACTACTGCGCCAGGCACCCCATCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCG TGACCGTGTCTCT3'
	53.3 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTGCGGCCAGCAGCGGCGTGAACCTACATCTACT GGTATCAGCAGAAGCCCGACGCGGCTCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCGTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACAGCTACACCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'

Fig. 28K

SEQ ID NO	Antibody	Sequence
	53.4 VH	5'GAGGTGCAGCTGCTGGAAAGCGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGGCCCTGGCAAGGGACTGGAATGGGTGGCCGTAA TCAGCCACGGCGGCACCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAACACCCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCATGTACTACTGCGCCAGACACCCCATCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
	53.5 VH	5'GAGGTGCAGCTGCTGGAAAGCGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGGCCCTGGCAAGGGACTGGAATGGGTGGCCACAA TCAGCCACGGCGGCACCTACACCTACTACGCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAACACCCCTGTACCTGCAGATGAACA GCCTGCGGGCCGAGGACACCGCCATGTACTACTGCGCCAGACACCCCATCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'
	53.6 VH	5'GAGGTGCAGCTGCTGGAAAGCGCGGAGGACTGGTGCAGCCTGGCGGCA GCCTGAGACTGTCTTGCGCCGCCAGCGGCTTCACCTTCACCAGCTACGCCA TGAGCTGGGTGCGCCAGGCCCTGGCAAGGGACTGGAATGGGTGGCCACAA TCAGCCACGGCGGCACCTACACCTACTACCCCGACAGCGTGAAGGGCCGGT TCACCATCAGCCGGGACAACGCCAAGAACACCCCTGTACCTGCAGGTGAACA GCCTGCGGGCCGAGGACACCGCCATGTACTACTGCGCCAGACACCCCATCT ACAGCGGCAACTACCAGGGCTACTTCGACTACTGGGGCCAGGGCACCCCTGG TGACAGTGTCCAGC3'

Fig. 28L

SEQ ID NO	Antibody	Sequence
	53.4 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCTGGGCCAGCAGCGGCGTGAACTACCTCTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCCTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'
	53.5 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCTGGGCCAGCAGCGGCGTGAACTACATCGCCT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCCCTGGCCTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'
	53.6 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCTGGGCCAGCAGCGGCGTGAACTACATCTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCACCCCTGGCCCCCTGGCCTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'
	53.7 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCTGGGCCAGCAGCGGCGTGAACTACATCTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGCAACCTGGCCTGCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3'

Fig. 28M

SEQ ID NO	Antibody	Sequence
	53.8 VL	5 'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCTGGGGCCAGCAGCGGCGTGAACTACATCTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCTCTGGCCTGCCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCGGAGGCACCA AGCTGGAAATCAAG3 '
	53.9 VL	5 'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTCTGGGGCCAGCAGCGGCGTGAACTACATCTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGTGGATCTACTTCACCA GCAACCTGGCCCTCTGGCCTGCCCAGCAGATTTTCTGGCAGCGGCAGCGGCA ACGAGTACACCCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCCAGCAGTTCACCAGCAGCCCCCTACACCTTCGGCCAAGGCACCA AGCTGGAAATCAAG3 '

Fig. 28N

SEQ ID NO	Antibody	Sequence
	82.0 VH	5'GAAGTGAAGCTGGAAGAGTCCGGCCCTGAGGTGGTGGCCCTGGCGTGT CCGTGAAGATCAGCTGCAAGGGCAGCGGCTACACCTTCACCGACTACGCCA TGCACTGGGTGAAACAGAGCCACGCCAAGAGCCTGGAATGGATCGGCGTGA TCAGCACCTACAACGGCAACACCAAGTACAACCAGAAGTTCAAGGGCAAGG CCACCATGACCGTGGACAAGAGCAGCAGCACCGCCTACATGGAAGTGGCCC GGCTGACCAGCGAGGACAGCGCCATCTACTACTGCGCCCGGTTCCCTGAGCC TGCGGTACTTCGATGTGTGGGGAGCCGGCACCACCGTGACCGTGTCTAGC3 ,
	82.0 VL	5'GACATCGTGCTGACCCAGAGCCCCGCCATCCTGTCTGCCCCCCTGGCG AGAAAGTGACCATGACCTGCCGGCCAGCAGCAGCGTGATCTACATGTACT GGTATCAGCAGAAGCCCGGCAGCAGCCCCAAGCCCTGGATCTACGCCACCA GCAAGCTGGCCAGCGGCGTGCCAGTGCAGTTTAGCGGCAGCGGCTCTGGCA CCAGCTACAGCCTGACCATCAGCCGGGTGGAAGCCGAGGACGTGGCCACCT ACTACTGCCAGCAGTGGTCCAGCGAGCCCCTGACCTTCGGAGCCGGCACCA AGCTGGAACTGAAG3'
	82.1 VH	5'CAGGTGAAACTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCA GCGTGAAGGTGTCTTGCAAGGCCAGCGGCTACACCTTCACCGACTACGCCA TGCACTGGGTGCGCCAGGCCCTGGCCAGAGACTGGAATGGATCGGCTGGA TCAGCACCTACAACGGCAACACCAAGTACAGCCAGAAGTTCCAGGGCAGAG CCACCATGACCGTGGACAAGAGCGCCAGCACCGCCTACATGGAAGTGAACA GCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCCGGTTCCCTGAGCC TGCGGTACTTCGACGTGTGGGGCAAGGGCACCAACCGTGACCGTGTCCAGC3 ,
	82.1 VL	5'GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTGCGGGCCAGCAGCAGCGTGATCTACCTGGCCT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCCCTGGATCTACGCCACCA GCACACTGCAGAGCGGCGTGCCAGCAGATTAGCGGCAGCGGCTCTGGCA CCGAGTACACCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTGGTCCAGCGAGCCCCTGACCTTCGGCGGAGGCACCA AGGTGGAAATCAAG3'

Fig. 280

SEQ ID NO	Antibody	Sequence
	82.2 VH	5' CAGGTGAAACTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCA GCGTGAAGGTGTCTTGCAAGGGCAGCGGCTACACCTTCACCGACTACGCCA TGCACTGGGTGCGCCAGGCCCTGGCCAGAGACTGGAATGGATCGGCGTGA TCAGCACCTACAACGGCAACACCAAGTACAACCAGAAGTTCCAGGGCAGAG CCACCATGACCGTGGACAAGAGCGCCAGCACCGCCTACATGGAAC TGAGCA GCCTGCGGAGCGAGGACACCGCCATCTACTACTGCGCCCGGTTCTTGAGCC TGCGGTACTTCGATGTGTGGGGAGCCGGCACCAACCGTGACCGTGTCTAGC3 ,
	82.2 VL	5' GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCGTGGGCG ACAGAGTGACCATCACCTGTGCGGGCCAGCAGCAGCGTGATCTACATGTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCCCTGGATCTACGCCACCA GCAAGCTGGCCAGCGGCGTGCCCGCAGAGATTTTCTGGCAGCGGCAGCGGCA CCAGGTACACCTGACCATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTGGTCCAGCGAGCCCCTGACCTTCGGAGCCGGCACCA AGGTGGAAATCAAG3'
	82.3 VH	5' CAGGTGAAACTGGTGCAGAGCGGCCCTGAAGTGAAGGTGCCAGGCGCCA GCGTGAAGGTGTCTTGCAAGGGCAGCGGCTACACCTTCACCGACTACGCCA TGCACTGGGTGCGCCAGGCCCTGGCCAGAGCCTGGAATGGATCGGCGTGA TCAGCACCTACAACGGCAACACCAAGTACAACCAGAAGTTCCAGGGCAGAG CCACCATGACCGTGGACAAGAGCGCCAGCACCGCCTACATGGAAC TGAGCC GGCTGCGGAGCGAGGACACCGCCATCTACTACTGCGCCCGGTTCTTGAGCC TGCGGTACTTCGATGTGTGGGGAGCCGGCACCAACCGTGACCGTGTCTAGC3 ,
	82.3 VL	5' GACATCCAGCTGACCCAGAGCCCCAGCTTCCTGAGCGCCAGCCCTGGCG ACAGAGTGACCATCACCTGTGCGGGCCAGCAGCAGCGTGATCTACATGTACT GGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCCCTGGATCTACGCCACAA GCAAGCTGGCCAGCGGCGTGCCCGTGCGGTTTAGCGGCTCTGGCAGCGGCA CCAGGTACACCTGACCATCAGCCGGCTGCAGGCCGAGGACTTCGCCACCT ACTACTGCCAGCAGTGGTCCAGCGAGCCCCTGACCTTCGGAGCCGGCACCA AGGTGGAAATCAAG3'

Fig. 28P