

FIG. 1A

Constant Region 1

IGHG1 CHI .ASTGSGSVFPLPSSK .SSSGGTALGCVKDYEP .EPVYUNMSGALT .SGVHTPEA .VLOSGGLYSLSVVTPVSSSIG .TQ .TYICVNHKPSNKR .YDKV .
IGHG2 CHI .ASTGSGSVFPLAPCSR .SSSGGTALGCVKDYEP .EPVYUNMSGALT .SGVHTPEA .VLOSGGLYSLSVVTPVSSNFG .TQ .TYICVNHKPSNKR .YDKTV .
IGHG3 CHI .ASTGSGSVFPLAPCSR .SSSGGTALGCVKDYEP .EPVYUNMSGALT .SGVHTPEA .VLOSGGLYSLSVVTPVSSIG .TK .TYICVNHKPSNKR .YDKV .
IGHG4 CHI .ASTGSGSVFPLAPCSR .STSESTALGCVKDYEP .EPVYUNMSGALT .SGVHTPEA .VLOSGGLYSLSVVTPVSSIG .TQ .TYICVNHKPSNKR .YDKRV .
IGHA1 CHI .ASPTSPKVEPLBLST .QPDANVVIACLVGQHFPEPLSTWBSGQG .VYARNEPSPQASGDLYTSSQILLPACQCLAGK .SVTCHVKHXTNPSQDVAWPCP
IGHA2 CHI .ASPTSPKVEPLBLST .QPDANVVIACLVGQHFPEPLSTWBSGQG .VYARNEPSPQASGDLYTSSQILLPACQCPDQK .SVTCHVKHXTNPSQDVAWPCP
IGHD CHI .APTAPDVPEPLISGCH .KPDNSPVYVACLTIGTHP .TSVYVWTWNGTQS .QDPTPEP .IQDRSDYVNSQSILTPDQWQCP .EYKCVYGHAKSKR .KELF .
IGHI CHI .ASQSPSVFPLPCCNKI .PNALSTVIGLATGEP .EPVMTWIDGSLN .GEMTLPATLTLLISHYATISILTV .SAGWA .KQ .MFTCVAHKPS .SDVWVNEETES
IGHM CHI .GSAAPITLFLPVSGENS .PBDTSVAVGLADQFLP .DSITFSWKKNMADISTIRGEP .VLR .GGKYAATSYVLLPSKDAVAGTDDEHV .CAYGHENGNKE .KNVPLP

Hinge Region or equivalent

IGHG1 H EPKSCDKHTCP.....PCP.....
IGHG3 H ERKCC..VECP.....PCP.....
IGHG3 H ELKPLPLGDTHTCPCEPEPKSCDTPPCPEPKSCDTPPCPEPKSCDTPPCPCP
IGHG4 H ESKYG...PCP.....SCP.....
IGHA1 H VPSITPPTSPSTPTPS.....PS.....
.....VP..P.....P.....
IGHA2 H
IGHD CH2 RMDESPKAAQSVPAQPEGSIAK...ATTAPATRTYGRGGEKKKEKEKEOEERETKEPCP..
IGHD CH2
IGHE CH2 VCSNDFPTPTVKLIQSSCDGGGHFPTTILQLCLVSGYRPGTILNIMDEGVMDVDLSTASTQEGELAS...TQSELTLSQKHWLSDRYTTCQVYTGHTFEDSTKCA..
IGHM CH2 VIAELPRKVSFVPRPDGFGFNPRKSKILIQATGSPFQIÖVSWLREGQVSGVSTDDQVQAEASGPTTYKVTSTLIKSDWLGQSNMTCRDVHRRLTFOQNASMCVF

Constant Region 2/3

IGH1_CH2
APPELLGGVYELFPKKPKDTLMI.SRTEVEVTCVVVDVSHEDPEVKENWYVDYGVENVHNAKTK.PREEDQNSLTQVRRVSVLTGLHQLMNLGKREYKCKVSKKALPAPIEKTIISAKA
IGH2_CH2
APPVAG.PSVLEFPKKPKDTLMI.SRTEVEVTCVVVDVSHEDPEVFNWYVDYGVENVHNAKTK.PREEDFNSTQVRRVSVLTGLHQLMNLGKREYKCKVSKKGLPAPIEKTIISAKT
IGH3_CH2
APPELLGGSVYELFPKKPKDTLMI.SRTEVEVTCVVVDVSHEDPEVQKMYVDYGVENVHNAKTK.PREEDFNSTQVRRVSVLTGLHQLMNLGKREYKCKVSKKGLPAPIEKTIISAKT
IGH4_CH2
APPELLGGSVYELFPKKPKDTLMI.SRTEVEVTCVVVDVSDPEDEVFNWYVDYGVENVHNAKTK.PREEDFNSTQVRRVSVLTGLHQLMNLGKREYKCKVSKKGLPSIEKTIISAKK
IGH1_CH2
...CCHPRLSIHR.ALEDLLIGSEMTCTLTGLRDASG.VFTFTWTSSEK.SAVQG.PPERLDCGCVSVSVLPGCAEFEMNHGKFTCTGAAPDESKTPIPLTSLKS.
...CCHPRLSIHR.ALEDLLIGSEMTCTLTGLRDASG.AFTWTPSSGK.SAVQG.PPERLDCGCVSVSVLPGCAQPMNHGKFTCTGAAPDESKTPIPLTSLKS.
...CCHPRLSIHR.ALEDLLIGSEMTCTLTGLRDASG.AFTWTPSSGK.SAVQG.PPERLDCGCVSVSVLPGCAQPMNHGKFTCTGAAPDESKTPIPLTSLKS.
IGH2_CH2
...SHQPLGVLYLTP.AVQDLMLRDKRTCTCVVSGDLDKA.G.HITVEVYAGKPTGVTEGVEEGLRLERSNGGSOHSRLTPRLSLMAGTSVTCVLNDSLPPQRLMALREPA
IGH1_CH2
...SHQPLGVLYLTP.AVQDLMLRDKRTCTCVVSGDLDKA.G.HITVEVYAGKPTGVTEGVEEGLRLERSNGGSOHSRLTPRLSLMAGTSVTCVLNDSLPPQRLMALREPA
IGH3_CH2
..DSNRQSVAYLSASPPG.LFRKSPITCTLVADLPASGKGTVALTWLSASGKPVNHSR.KEEKQNLGTVTSSTLPVGRPMIEGGTQGRVTRPHILPALMNSTRTKS
IGH4_CH2
..DQDAIRVFAIDP.SRASIFLTKSRKLCIVTDLTITYS.VTISWTPONGEAVKHTHN.ISEHPNATFSAVGEASICEEDMNSGERFTCTVHTDLPSLKYOTISRPK

FIG. 1B

Constant Region 3/4

IGH1_CH3.GQPREPQVYTLPPSRDELTKNQ.VSLTCLVKGFPYSDIAVEMESNGQ..PENNYKTTPPVLDs...DGSFELYSKLTVDKSRMÖQGNVFS~~CS~~VMHEAL.HNHYTÖKSLSLSPGK.....
IGH2_CH3.GQPREPQVYTLPPSRREMTKNQ.VSLTCLVKGFPYSDIAVEMESNGQ..PENNYKTTPPMLDs...DGSFELYSKLTVDKSRMÖQGNVFS~~CS~~VMHEAL.HNHYTÖKSLSLSPGK.....
IGH3_CH3.GQPREPQVYTLPPSRREMTKNQ.VSLTCLVKGFPYSDIAVEMESNGQ..PENNYKTTPPMLDs...DGSFELYSKLTVDKSRMÖQGNVFS~~CS~~VMHEAL.HNHYTÖKSLSLSPGK.....
IGH4_CH3.GQPREPQVYTLPPSRREMTKNQ.VSLTCLVKGFPYSDIAVEMESNGQ..PENNYKTTPPVLDs...DGSFELYSRLTVDKSRMÖQGNVFS~~CS~~VMHEAL.HNHYTÖKSLSLSPGK.....
IGH1_CH3.GNTFRPEVHLPPPSBELALNELVTLTCLARGFSPKDVLVIRWLÖGSÖELPREKYLTMASRÖEPSÖGTTTFAVTSILRVAEDWKKGDTFSCNVGHEAL.PLAFTÖKTIIDRLAGK.....
IGH2_CH3.GNTFRPEVHLPPPSBELALNELVTLTCLARGFSPKDVLVIRWLÖGSÖELPREKYLTMASRÖEPSÖGTTTFAVTSILRVAEDWKKGDTFSCNVGHEAL.PLAFTÖKTIIDRWAGK.....
IGHD_CH3...AQAPVKLSINLLASSDPEEASWLLCEVSGFSPPNILLMWLEDORE~~VNT~~SGFAPARPPÖP..RSTTFWAMSVLRVPAPPSFÖPATYTCVVVSHEDSRITL~~NA~~SRSLSVSYTIDHGPMK
IGHE_CH4.GPRAPEVYAFATPEWPGSRDK.RTIA~~CL~~IONFMPEDISVO~~WL~~HNHEVÖLEDPARHSTTÖPRKTK...GSGFEVFSRLVETRAEWÖQKDEFICRAVHEAASPSÖTVÖRAVSYPGK.....
IGHM_CH4.GVALHRPDVYLLPPAREÖNLRESA~~IT~~CLVTGFSPADVFVÖWMÖRGÖPLSPKRYVTSAMPEP.ÖAPGRYFAHSILTVSEEMNTGELYTCVVAHEAL.PNRVTERTVDSSTGK.....

C-terminal "Tailpiece"

IGHA1_TP.PTHVN/SVVMAEVDGTCY
IGHA2_TP.PTHIN/SVMAEADGTCY
IGHM_TP.PTIYN/SIVMSDFAGTCY

↓

↓ = Intra-chain disulfide bond

↓ = Inter-chain disulfide bond

FIG. 2A

		N1	
Human	GSASAPTLFPLVSCENSPTSSTSSVAVGCLAQDFLPDSITFSWKYKNNSSDISS-TRGFPSV	59	
Mouse	ASQSFPNVFPLVSCESPLSDKNLVAMGCLARDFLPSTISFTWNYQNNTTEVIQGITFTPTL	60	
Cynomolgus	ESAGPFKEWPSVSSPNAPLDTNEVAVGCLAQDFLPDSITFSWKFKNNSSDISKGVWGFPSV	60	
Rhesus	GSASAPTLFPLVSCENAPLDTNEVAVGCLAQDFLPDSITFSWKFKNNSSDISKGVWGFPSV	60	
Chimpanzee	-SASAPTLFPLVSCENSPTSSTSSVAVGCLAQDFLPDSITFSWKYKNNSSDISS-TRGFPSV	59	
Orangutan	GSASAPTLFPLVSCENSLSSTSSVAVGCLAQDFLPDSITFSWKYKNNSSDISS-TRGFPSV	59	
Human	LRGGKYAATSQVLLPSKDVMOGTDEHVVCVKVQHPNGNKEKNVPLPVIAELPPKVSFVFP	119	
Mouse	RTGGKYLATSQVLLSPKSILEGSDVYLVCKIHYGGKNRDLHVPPIPAVAEMNPVNVFVFP	120	
Cynomolgus	LRGGKYAATSQVLLASKDVMOGTDEHVVCVKVQHPNGNKEQNVPLPVVAERPPNVSVFVFP	120	
Rhesus	LRGGKYAATSQVLLASKDVMOGTDEHVVCVKVQHPNGNKEQNVPLPVLAERPPNVSVFVFP	120	
Chimpanzee	LRGGKYAATSQVLLPSKEVMOGTDEHVVCVKVQHPNGNKEKNVPLPVTAELPPKVSIFVFP	119	
Orangutan	LTGSKYVATSQVLLPSKDVMOGTDEHVVCVKVQHPNGNKEKNVPLPVIAELPPKVSIFVFP	119	
Human	RDGFFGN-PRKSKLICQATGFSPRQIQVSWLREGKQVGSVTTDQVQAEAKESGPTTYKV	178	
Mouse	RDGFGPAPRKSCLICEATNFTPKPITVSWLKDGLVESGFTTDPVTIENKGSTPQTYKV	180	
Cynomolgus	RDGFVGN-PRESKLICQATGFSPRQIEVSWLREGKQVGSGITTDREAEAKESGPTTFKV	179	
Rhesus	RDGFVGN-PRESKLICQATGFSPRQIEVSWLREGKQVGSGITTDREAEAKESGPTTFKV	179	
Chimpanzee	RDGFFGN-PRSSKLICQATGFSPRQIQVSWLREGKQVGSVTTDQVQAEAKQSGPTTYKV	178	
Orangutan	RDGFFGS-PRKSKLICQATGFSPRQIQVSWLREGKQVASGITTDQVQAEAKESGPTTYKV	178	
Human	TSTLTIKESDWLQSMFTCRVDHRGLTFQKNASSMCVDPQDTAIRVFAIPPSFASIFLT	237	
Mouse	ISTLTISEIDWLNLVYTCRVDHRGLTFLEKNVSETCAASPSTDILNFTIPPSFADIFLS	239	
Cynomolgus	TSTLTVSERDWLSQSVFTCRVDHRGLTFQKNVSSVCGPNPDIAIRVFAIPPSFASIFLT	238	
Rhesus	TSTLTVSERDWLSQSVFTCRVDHRGLTFQKNVSSVCGPNPDIAIRVFAIPPSFASIFLT	238	
Chimpanzee	TSTLTIKESDWLSQSVFTCRVDHRGLTFQKNASSMCSPGPDIAIRVFAIPPSFASIFLT	238	
Orangutan	TSTLTINESDWLSQSMFTCRVDHRGLTFQKNASSMCSPNPNTAIRVFAIPPSFASIFLT	237	
Human	KSTKLTCLVTDLTFTYDSVTISWTRQNGEAVKTHNISESHENATFSAVGEASICEDDWN	297	
Mouse	KSANLTCLVSNLATYETLSISWASQSGEPLTKIKIMESHENGTFSAKGVASVCVEDWNN	299	
Cynomolgus	KSTKLTCLVTDLATYDSVTITWTRQNGEALKTHNISESHENGTFSAVGEASICEDDWN	298	
Rhesus	KSTKLTCLVTDLATYDSVTITWTRQNGEALKTHNISESHENGTFSAVGEASICEDDWN	298	
Chimpanzee	KSTKLACLVTDLTFTYDSLTSWTRQNGEAVKTHNISESHENATFSAVGEASICEDDWN	298	
Orangutan	KSTKLTCLVTDLASYSMTISWTRQNGEAVKTHNISESHENATFSAVGEASICEDDWN	297	
Human	GERFTCTVTHDLPSPKQTI SRPKGVAMHRPDVYLLPPAREQLNLRESATITCLVTGFS	357	
Mouse	RKEFVCTVTHRDLPSPQKKFISKPNVHKHPPAVYLLPPAREQLNLRESATITCLVKGFS	359	
Cynomolgus	GERFRCTVTHDLPSPKQTI SRPKGVAMHRPDVYLLPPAREQLNLRESATITCLVTGFS	358	
Rhesus	GERFRCTVTHDLPSPKQTI SRPKGVAMHRPDVYLLPPAREQLNLRESATITCLVTGFS	358	
Chimpanzee	GERFTCTVTHDLPSPKQTI SRPKGVAMHRPDVYLLPPAREQLNLRELATITCLVTGFS	358	
Orangutan	GERFTCTVTHADLPSPKQTI SRPKGVAMHRPDVYLLPPAREQLNLRESATITCLVTGFS	357	

FIG. 2B

Human	PADVQVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTGETYTCVVAH	416
Mouse	PADISVQWKQRGQLLPQEKYVTSAPMPEPGAPGEYFTHSILTVTEEEWNSGETYTCVVGH	419
Cynomolgus	PADIFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEDWNTGETYTCVVAH	418
Rhesus	PADIFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEDWNTGETYTCVVAH	418
Chimpanzee	PADVQVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEEWNTGETYTCVVAH	418
Orangutan	PADVQVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEDWNTGETYTCVVAH	417

	N5	
Human	EALPNRVTERTVDKSTGKPTLYNVSLV-----MSDTAGTCY-----	452
Mouse	EALPHLVTERTVDKSTGKPTLYNVSLI-----MSDTGGTCY-----	455
Cynomolgus	EALPNRVTERTVDKSTGKPTLYNVSLVILWTLSTFVALFVLTLLYSGIVTFIKVR----	474
Rhesus	EALPNRVTERTVDKSTGKPTLYNVSLV-----MSDTAGTCY-----	454
Chimpanzee	EALPNRVTERTVDKSTGKPTLYNVSLV-----MSDTAGTCY-----	452
Orangutan	EALPNRVTERTVDKSTGKPTLYNVSLV-----MSDTAGTCY-----	453

FIG. 3

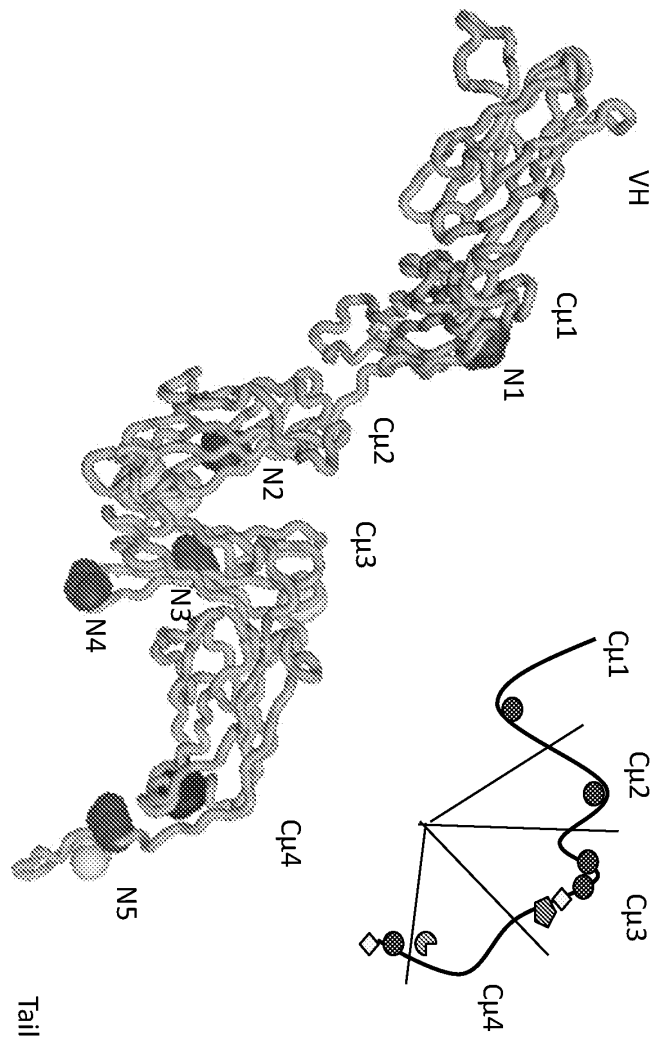


FIG. 4

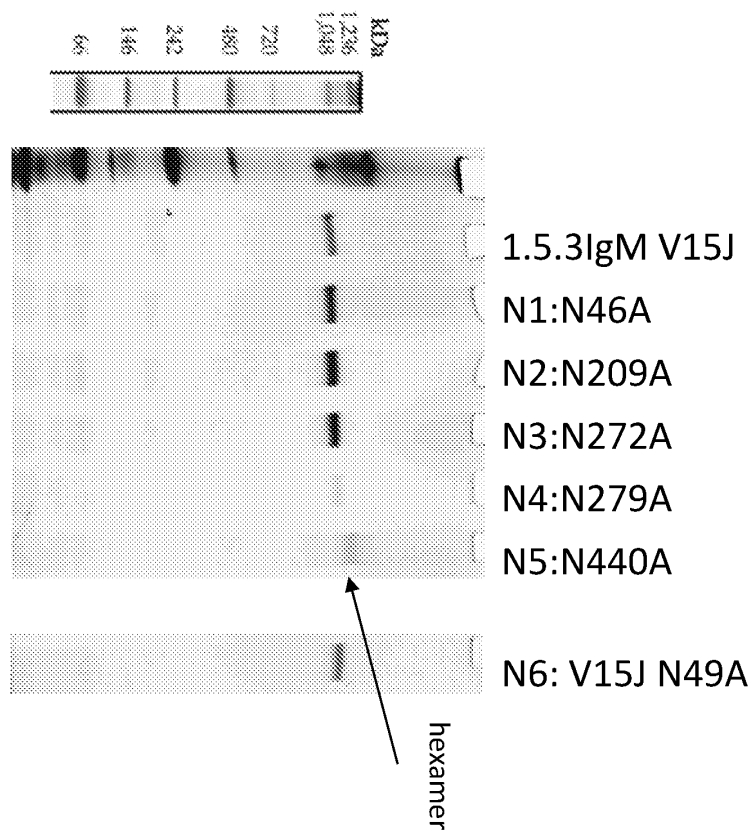


FIG. 5

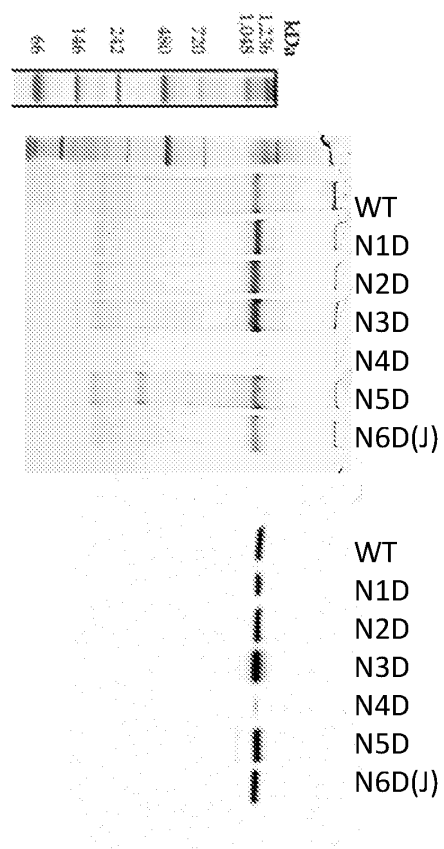
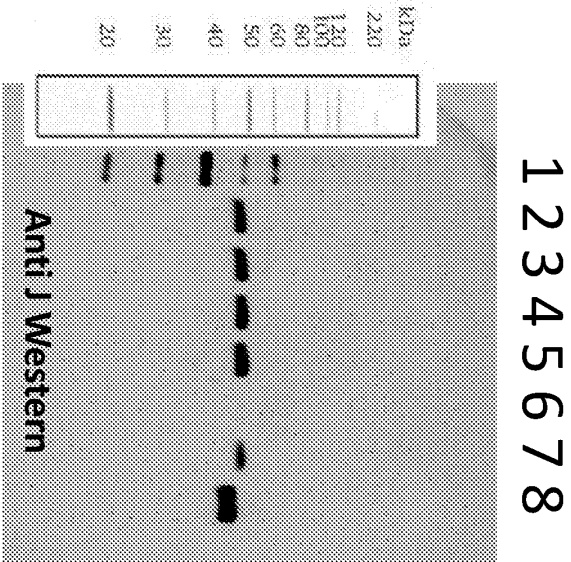


FIG. 6



- 1. MagicMark
- 2. 153IgM VJ WT
- 3. N1D, N2D
- 4. N2D, N3D
- 5. N1D, N3D
- 6. N1D, N5D
- 7. 153VJ WT
- 8. 153VJ N6D(j)

FIG. 7

