



163163

Figure 1

Adenovirus Hexon Protein

CLUSTAL W (1.83) multiple sequence alignment



G00002

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PanAd1  MATPSMMPQWSYMHISGQDASEYLSPLGVQFARATDSYFSLSNKFRNPTVAPTHDVTDDR
PanAd2  MATPSMMPQWSYMHISGQDASEYLSPLGVQFARATDSYFSLSNKFRNPTVAPTHDVTDDR
PanAd3  MATPSMMPQWSYMHISGQDASEYLSPLGVQFARATDSYFSLSNKFRNPTVAPTHDVTDDR
ChAd55  MATPSMLPQWAYMHIAGQDASEYLSPLGVQFARATDTYFSLGNKFRNPTVAPTHDVTDDR
ChAd73  MATPSMLPQWAYMHIAGQDASEYLSPLGVQFARATDTYFSLGNKFRNPTVAPTHDVTDDR
ChAd83  MATPSMLPQWAYMHIAGQDASEYLSPLGVQFARATDTYFSLGNKFRNPTVAPTHDVTDDR
ChAd146 MATPSMLPQWAYMHIAGQDASEYLSPLGVQFARATDTYFSLGNKFRNPTVAPTHDVTDDR
ChAd147 MATPSMLPQWAYMHIAGQDASEYLSPLGVQFARATDTYFSLGNKFRNPTVAPTHDVTDDR
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PanAd1  SQRLTLRFIPVDREDTAYSYKARFTLAVGDNRLVDMASTYFDIRGVLDRGPTFKPYSGTA
PanAd2  SQRLTLRFIPVDREDTAYSYKARFTLAVGDNRLVDMASTYFDIRGVLDRGPTFKPYSGTA
PanAd3  SQRLTLRFIPVDREDTAYSYKARFTLAVGDNRLVDMASTYFDIRGVLDRGPTFKPYSGTA
ChAd55  SQRLTLRFVPVDREDNTYSYKVRYTLAVGDNRLVDMASTYFDIRGVLDRGPSFKPYSGTA
ChAd73  SQRLTLRFVPVDGEDNTYSYKVRYTLAVGDNRLVDMASTYFDIRGVLDRGPSFKPYSGTA
ChAd83  SQRLTLRFVPVDREDNTYSYKVRYTLAVGDNRLVDMASTYFDIRGVLDRGPSFKPYSGTA
ChAd146 SQRLTLRFVPVDREDNTYSYKVRYTLAVGDNRLVDMASTYFDIRGVLDRGPSFKPYSGTA
ChAd147 SQRLTLRFVPVDREDNTYSYKVRYTLAVGDNRLVDMASTYFDIRGVLDRGPSFKPYSGTA
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←----- HVR 1-6 -----

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PanAd1  YNSLAPKGAPNSCEWEQVEP--AEEAAENE-DEEEEDVVDPEQEPTTKTHVYAQAPLS
PanAd2  YNSLAPKGAPNPCEWDEAVT--AVDINLDELGEDEDDAEGEAEQQ---KSHVFGQAPYS
PanAd3  YNSLAPKGAPNSCEWEQEETQTAEAAQDEEEDEAEAEEMPQEEQAPVKKTHVYAQAPLS
ChAd55  YNSLAPKGAPNTSQWITKDN-----GTDKTYSGFNAPVR
ChAd73  YNALAPKGAPNTSQWITKDN-----GTDKTYSGFNAPVR
ChAd83  YNSLAPKGAPNTSQWITKDN-----GTDKTYSGFNAPVR
ChAd146 YNSLAPKGAPNTSQWITKDN-----GTDKTYSGFNAPVR
ChAd147 YNSLAPKGAPNTSQWVTKDN-----GTDKTYSGFNAPVR
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----- HVR 1-6 -----

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PanAd1  GEKITKDGLQIGTEATAAGGTKDLFADPTFQPEPQVGESQWNEAD--ATAAGGRVLKKT
PanAd2  GQNITKEGIQIGVDTTSQA-QTPLYADKTFQPEPQVGESQWNETE--INYAGRVLKKT
PanAd3  GEKITKDGLQIGTDATATE-QKPIYADPTFQPEPQIGESQWNEAD--ASVAGGRVLKKT
ChAd55  GLDITEEGLQIGPDESGGE-SKKIFADKTYQPEPQLGDEEWHDTIGAEDKYGGRALKPAT
ChAd73  GLDITEEGLQIRTDESGGE-SKKIFADKTYQPEPQLGDEEWHDTIGAEDKYGGRALKPAT
ChAd83  GLDITEEGLQIGTDESGGE-SKKIFADKTYQPEPQLGDEEWHDTIGAEDKYGGRALKPAT
ChAd146 GLDITEEGLQIGTDESGGK-SKKIFADKTYQPEPQLGDEEWHDTIGAEDKYGGRALKPAT
ChAd147 GLDITEEGLQIGTDDSSSTE-SKKIFADKTYQPEPQVGDEEWHDTIGAEDKYGGRALKPAT
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----- HVR 1-6 -----

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PanAd1  PMKPCYGSYARPTNANGGQGV LKANAQGVLESQVEMQFFSTSTNATN-EQNNIQPKLVLY

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PanAd2 LMKPCYGSYARPTNENGGQGILLEKEGGKPESQVEMQFFSTTQAAAAGNSDNLTPKVVLY
 PanAd3 PMKPCYGSYARPTNANGGQVLVEKDGGKMESQVDMQFFSTSENARN-EANNIQPKLVLY
 ChAd55 NMKPCYGSFAKPTNAKGGQAKSRTKDDGTTEPDIDMAFFDDRSQQAS-----FSPELVLY
 ChAd73 NMKPCYGSFAKPTNAKGGQAKSRTKDDGTTEPDIDMAFFDDRSQQAS-----FSPELVLY
 ChAd83 NMKPCYGSFAKPTNAKGGQAKSRTKDDGTTEPDIDMAFFDDRSQQAS-----FSPELVLY
 ChAd146 NMKPCYGSFAKPTNAKGGQAKSRTKDDGTTEPDIDMAFFDDRSQQAS-----FSPELVLY
 ChAd147 NMKPCYGSFAKPTNAKGGQAKTRTKDDGTTEPDIDMAFFDDRSQQAS-----FSPELVLY
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--- HVR 1-6 ----->

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PanAd1      SEDVHMETPDTHISYKPTKSDDNSKVMLGQQSMPNRPNYIAFRDNFIGLMYYNSTGNMGV
PanAd2      SEDVHLETPDTHISYMPTSNEANSRELLGQQAMPNRPNYIAFRDNFIGLMYYNSTGNMGV
PanAd3      SEDVHMETPDTHISYKPAKSDDNSKVMLGQQSMPNRPNYIGFRDNFIGLMYYNSTGNMGV
ChAd55      TENVDLDTPDTHIIYKPGTDETSSSFNLGQQSMPNRPNYIGFRDNFIGLMYYNSTGNMGV
ChAd73      TENVDLDTPDTHIIYKPGTDETSSSFNLGQQSMPNRPNYIGFRDNFIGLMYYNSTGNMGV
ChAd83      TENVDLDTPDTHIIYKPGTDETSSSFNLGQQSMPNRPNYIGFRDNFIGLMYYNSTGNMGV
ChAd146     TENVDLDTPDTHIIYKPGTDETSSSFNXGQQSMPNRPNYIGFRDNFIGLMYYNSTGNMGV
ChAd147     TENVDLETPDTHIIYKPGTDETSSSFNLGQQSMPNRPNYIGFRDNFIGLMYYNSTGNMGV
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PanAd1 LAGQASQLNAVVDLQDRNTELSYQLLLDSMGDRTRYFSMWNQAVDSYDPDVRI IENHGTE
 PanAd2 LAGQASQLNAVVDLQDRNTELSYQLLLDSMGDRTRYFSMWNQAVDSYDPDVRI IENHGTE
 PanAd3 LAGQASQLNAVVDLQDRNTELSYQLLLDSMGDRTRYFSMWNQAVDSYDPDVRI IENHGTE
 ChAd55 LAGQASQLNAVVDLQDRNTELSYQLLLDSLGDRTYFSMWNQAVDSYDPDVRI IENHGVE
 ChAd73 LAGQASQLNAVVDLQDRNTELSYQLLLDSLGDRTYFSMWNQAVDSYDPDVRI IENHGVE
 ChAd83 LAGQASQLNAVVDLQDRNTELSYQLLLDSLGDRTYFSMWNQAVDSYDPDVRI IENHGVE
 ChAd146 LAGQASQLNAVVDLQDRNTELSYQLLLDSLGDRTYFSMWNQAVDSYDPDVRI IENHGVE
 ChAd147 LAGQASQLNAVVDLQDRNTELSYQLLLDSLGDRTYFSMWNQAVDSYDPDVRI IENHGVE
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←----- HVR 7 -----→

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PanAd1      DELPNYCFPLGGIGITDTYQAIKTNG-NGAGDQATTWQKDSQFADRNEIGVGNNFAMEIN
PanAd2      DELPNYCFPLGGIINTETLTQVKP-----KTGDAQWEKDETFSEKNEIRVGNNFAMEIN
PanAd3      DELPNYCFPLGGIGVTDYQAIKTNG-NGNGGGNTTWTKDETFAADRNEIGVGNNFAMEIN
ChAd55      DELPNYCFPLNGVGFTDTFQGIKVKTTNNGTANATEWESDTSVNNANEIAKGNPFAMEIN
ChAd73      DELPNYCFPLNGVGFTDTFQGIKVKTTNNGTANATEWESDTSVNNANEIAKGNPFAMEIN
ChAd83      DELPNYCFPLNGVGFTDTFQGIKVKTTNNGTANATEWESDTSVNNANEIAKGNPFAMEIN
ChAd146     DELPNYCFPLNGVGFTDTFQGIKVKTTNNGTANATEWESDTSVNNANEIAKGNPFAMEIN
ChAd147     DELPNYCFPLNGVGFTDTFQGIKVKTTNNGTANATEWESDTSVNNANEIAKGNPFAMEIN
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PanAd1 L S A N L W R N F L Y S N V A L Y L P D K L K Y N P S N V E I S D N P N T Y D Y M N K R V V A P G L V D C Y I N L G A R
PanAd2 L N A N L W R N F L Y S N V A L Y L P D K L K Y T P A N V Q I S S N S N S Y D Y M N K R V V A P G L V D C Y I N L G A R
PanAd3 L S A N L W R N F L Y S N V A L Y L P D K L K Y N P S N V E I S D N P N T Y D Y M N K R V V A P G L V D C Y I N L G A R
ChAd55 I Q A N L W R N F L Y A N V A L Y L P D S Y K Y T P A N I T L P T N T N T Y D Y M N G R V V A P S L V D A Y I N I G A R
ChAd73 I Q A N L W R N F L Y A N V A L Y L P D S Y K Y T P A N I T L P T N T N T Y D Y M N G R V V A P S L V D A Y I N I G A R
ChAd83 I Q A N L W R N F L Y A N V A L Y L P D S Y K Y T P A N I T L P T N T N T Y D Y M N G R V V A P S L V D A Y I N I G A R
ChAd146 I Q A N L W R N F L Y A N V A L Y L P D S Y K Y T P A N I T L P T N T N T Y D Y M N G R V V A P S L V D A Y I N I G A R
ChAd147 I Q A N L W R N F L Y A N V A L Y L P D S Y K Y T P A N V T L P T N T N T Y E Y M N G R V V A P S L V D S Y I N I G A R
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PanAd1 WSLDYMDNVNPFNHHRNAGLRYRSMLLGNGRYVPFHIQVPQKFFAIKNLLLLPGSYTYEW
PanAd2 WSLDYMDNVNPFNHHRNAGLRYRSMLLGNGRYVPFHIQVPQKFFAIKNLLLLPGSYTYEW
PanAd3 WSLDYMDNVNPFNHHRNAGLRYRSMLLGNGRYVPFHIQVPQKFFAIKNLLLLPGSYTYEW

ChAd55 WSLDPMDNVNPFNHHRNAGLRYRSMLLGNGRYVPFHIQVPQKFFAIKSLLLLPGSYTYEW
 ChAd73 WSLDPMDNVNPFNHHRNAGLRYRSMLLGNGRYVPFHIQVPQKFFAIKSLLLLPGSYTYEW
 ChAd83 WSLDPMDNVNPFNHHRNAGLRYRSMLLGNGRYVPFHIQVPQKFFAIKSLLLLPGSYTYEW
 ChAd146 WSLDPMDNVNPFNHHRNAGLRYRSMLLGNGRYVPFHIQVPQKFFAIKSLLLLPGSYTYEW
 ChAd147 WSLDPMDNVNPFNHHRNAGLRYRSMLLGNGRFXRVPFHIQVPQKFFAIKSLLLLPGSYTYEW
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PanAd1 NFRKDVNMVLQSSLGNDLRVDGASIKFESICLYATFFPMAHNTASTLEAMLRNDTNDQSF
 PanAd2 NFRKDVNMVLQSSLGNDLRVDGASIKFESICLYATFFPMAHNTASTLEAMLRNDTNDQSF
 PanAd3 NFRKDVNMVLQSSLGNDLRVDGASIKFESICLYATFFPMAHNTASTLEAMLRNDTNDQSF
 ChAd55 NFRKDVNMILQSSLGNDLRVDGASIAFTSINLYATFFPMAHNTASTLEAMLRNDTNDQSF
 ChAd73 NFRKDVNMILQSSLGNDLRVDGASIAFTSINLYATFFPMAHNTASTLEAMLRNDTNDQSF
 ChAd83 NFRKDVNMILQSSLGNDLRVDGASIAFTSINLYATFFPMAHNTASTLEAMLRNDTNDQSF
 ChAd146 NFRKDVNMILQSSLGNDLRVDGASIAFTSINLYATFFPMAHNTASTLEAMLRNDTNDQSF
 ChAd147 NFRKDVNMILQSSLGNDLRVDGASISFTSINLYATFFPMAHNTASTLEAMLRNDTNDQSF
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PanAd1 NDYLSAANMLYPIPANATNVPISIPSRNWAAFRGWAFTRLKTKETPSLGSGFDPYYTYSG
 PanAd2 NDYLSAANMLYPIPANATNVPISIPSRNWAAFRGWAFTRLKTKETPSLGSGFDPYYTYSG
 PanAd3 NDYLSAANMLYPIPANATNVPISIPSRNWAAFRGWAFTRLKTKETPSLGSGFDPYYTYSG
 ChAd55 NDYLSAANMLYPIPANATNVPISIPSRNWAAFRGWSFTRLKTRETSLGSGFDPYFVYSG
 ChAd73 NDYLSAANMLYPIPANATNVPISIPSRNWAAFRGWSFTRLKTRETSLGSGFDPYFVYSG
 ChAd83 NDYLSAANMLYPIPANATNVPISIPSRNWAAFRGWSFTRLKTRETSLGSGFDPYFVYSG
 ChAd146 NDYLSAANMLYPIPANATNVPISIPSRNWAAFRGWSFTRLKTRETSLGSGFDPYFVYSG
 ChAd147 NDYLSAANMLYPIPANATNVPISIPSRNWAAFRGWSFTRLKTKETPSLGSGFDPYFVYSG
 *****:*****:*****:***

PanAd1 SIPYLDGTFYLNHTFKKVSITFDSSVSWPGNDRLLTPNEFEIKRSVDGEGYNVAQCNMTK
 PanAd2 SIPYLDGTFYLNHTFKKVSITFDSSVSWPGNDRLLTPNEFEIKRSVDGEGYNVAQCNMTK
 PanAd3 SIPYLDGTFYLNHTFKKVSITFDSSVSWPGNDRLLTPNEFEIKRSVDGEGYNVAQCNMTK
 ChAd55 SIPYLDGTFYLNHTFKKVSITFDSSVSWPGNDRLLTPNEFEIKRTVDGEGYNVAQCNMTK
 ChAd73 SIPYLDGTFYLNHTFKKVSITFDSSVSWPGNDRLLTPNEFEIKRTVDGEGYNVAQCNMTK
 ChAd83 SIPYLDGTFYLNHTFKKVSITFDSSVSWPGNDRLLTPNEFEIKRTVDGEGYNVAQCNMTK
 ChAd146 SIPYLDGTFYLNHTFKKVSITFDSSVSWPGNDRLLTPNEFEIKRTVDGEGYNVAQCNMTK
 ChAd147 SIPYLDGTFYLNHTFKKVSITFDSSVSWPGNDRLLTPNEFEIKRTVDGEGYNVAQCNMTK
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PanAd1 DWFLIQMLANYNIGYQGFYIPESYKDRMYSFFRNFPMSRQVVDETKYKDYQQVGIIHQH
 PanAd2 DWFLIQMLANYNIGYQGFYIPESYKDRMYSFFRNFPMSRQVVDETKYKDYQQVGIIHQH
 PanAd3 DWFLIQMLANYNIGYQGFYIPESYKDRMYSFFRNFPMSRQVVDETKYKDYQQVGIIHQH
 ChAd55 DWFLVQMLAHYNIGYQGFYVPEGYKDRMYSFFRNFPMSRQVVDEVNYKDYQAVTLAYQH
 ChAd73 DWFLVQMLAHYNIGYQGFYVPEGYKDRMYSFFRNFPMSRQVVDEVNYKDYQAVTLAYQH
 ChAd83 DWFLVQMLAHYNIGYQGFYVPEGYKDRMYSFFRNFPMSRQVVDEVNYKDYQAVTLAYQH
 ChAd146 DWFLVQMLAHYNIGYQGFYVPEGYKDRMYSFFRNFPMSRQVVDEVNYKDYQAVTLAYQH
 ChAd147 DWFLVQMLAHYNIGYQGFYVPEGYKDRMYSFFRNFPMSRQVVDEVNYKDYQAVTLAYQH
 ****:****:*****:*.*****:***** * : :**

PanAd1 NNSGFVGYLAPTMREGQAYPANFPYPLIGKTAVDSTQKKFLCDRTLWRIPFSSNFMSMG
 PanAd2 NNSGFVGYLAPTMREGQAYPANFPYPLIGKTAVDSTQKKFLCDRTLWRIPFSSNFMSMG
 PanAd3 NNSGFVGYLAPTMREGQAYPANFPYPLIGKTAVDSTQKKFLCDRTLWRIPFSSNFMSMG
 ChAd55 NNSGFVGYLAPTMREGQAYPANFPYPLIGKSAVASVTQKKFLCDRVMWRIPFSSNFMSMG
 ChAd73 NNSGFVGYLAPTMREGQAYPANFPYPLIGKSAVASVTQKKFLCDRVMWRIPFSSNFMSMG
 ChAd83 NNSGFVGYLAPTMREGQAYPANFPYPLIGKSAVASVTQKKFLCDRVMWRIPFSSNFMSMG
 ChAd146 NNSGFVGYLAPTMREGQAYPANFPYPLIGKSAVASVTQKKFLCDRVMWRIPFSSNFMSMG

ChAd147 NNSGFVGYLAPTMROGQPYPANYPYPLIGKSAVTSVTQKKFLCDRVMWRIPFSSNFMSMG
 *****:*.****:*****:*. *:*****.:*****

PanAd1 ALTDLGQNLLYANSAHALDMTFEVDPMDEPTLLYVLFVFDVVRVHQPHRGVIETVYLRT
 PanAd2 ALTDLGQNLLYANSAHALDMTFEVDPMDEPTLLYVLFVFDVVRVHQPHRGVIETVYLRT
 PanAd3 ALTDLGQNLLYANSAHALDMTFEVDPMDEPTLLYVLFVFDVVRVHQPHRGVIETVYLRT
 ChAd55 ALTDLGQNMLYANSAHALDMNFEVDPMDESTLLYVVFVFDVVRVHQPHRGVIEAVYLRT
 ChAd73 ALTDLGQNMLYANSAHALDMNFEVDPMDESTLLYVVFVFDVVRVHQPHRGVIKAVYLRT
 ChAd83 ALTDLGQNMLYANSAHALDMNFEVDPMDESTLLYVVFVFDVVRVHQPHRGVIEAVYLRT
 ChAd146 ALTDLGQNMLYANSAHALDMNFEVDPMDESTLLYVVFVFDVVRVHQPHRGVIEAVYLRT
 ChAd147 ALTDLGQNMLYANSAHALDMNFEVDPMDESTLLYVVFVFDVVRVHQPHRGVIEAVYLRT
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PanAd1 PFSAGNATT
 PanAd2 PFSAGNATT
 PanAd3 PFSAGNATT
 ChAd55 PFSAGNATT
 ChAd73 PFSAGNATT
 ChAd83 PFSAGNATT
 ChAd146 PFSAGNATT
 ChAd147 PFSAGNATT

CLUSTAL W (1.83) multiple sequence alignment

PanAd1 LAVAGTSLTMQSQAPLTVQDAKLGLATQGPLTVSEGKLTQLQTSAPLTAADSSTLTVSATP
 PanAd2 LAVAGTSLTMQSQAPLTVQDAKLGLATQGPLTVSEGKLTQLQTSAPLTAADSSTLTVSATP
 PanAd3 LAVAGTSLTMQSQAPLTVQDAKLGLATQGPLTVSEGKLTQLQTSAPLTAADSSTLTVGTTTP
 ChAd55 -----KATA
 ChAd73 -----KATA
 ChAd83 -----KAAA
 ChAd146 -----KAAA
 ChAd147 -----KANS

PanAd1 RVTGALSVDTEGNIQLQAGGG-----MRIDNNGQLILNVAYPFDAQNNL^{SL}R^{LG}QGP
PanAd2 RVTGALSVDTEGNIQLQAGGG-----MRIDNNGQLILNVAYPFDAQNNL^{SL}R^{LG}QGP

PanAd3 KVAGALGYDSSGNLELRAAGG-----MRINTGGQLILDVAYPFDAQNNLSRLGQGP
 ChAd55 QLVSPPLTFDNKGNVKINLGNGLPTVAANRLSVTCKRGLYVTTTG-DALESNISWAKG--I
 ChAd73 QLTHPLTFSS-NSITVKTD-----KGLYINSSGNRGLLEANISLKRK--L
 ChAd83 QLVSPPLTFDGDGNIKLTLD-----RGLHVTTG--DAIESNISWAKG--L
 ChAd146 QLVSPPLTFDGDGNIKLTLD-----RGLHVTTG--DAIESNISWAKG--L
 ChAd147 QVTSPLTFDN-SKVKINLGNGLPLMVSANKLSINCLRGLYVAPNN-TGLETNISWANA--M
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PanAd1 LIVNSAHNLDLNLNRGLYLFTSGNTKKLEVNITAKGLFYDGTAIAINAGDGLQFGSGSD
 PanAd2 LIVNSAHNLDLNLNRGLYLFTSGNTKKLEVNITAKGLFYDGTAIAINAGDGLQFGSGSD
 PanAd3 LYVNTNHNLDLNCNRGLTTTTSSNTTKLETKIDS-----
 ChAd55 RFEGNAIAANIG--KGLEFGTTSSSES-----
 ChAd73 IFDGNAIATYLG--SGLDYGSDYSDGKTRPIITK-----
 ChAd83 KFEDGAIATNIG--NGLEFGSSSTET-----
 ChAd146 KFEDGAIATNIG--NGLEFGSSSTET-----
 ChAd147 RFEGNAMAVYIDTNKGLQFGTTSTET-----
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PanAd1 TNPLQTKLGLGLEYSNKAIIITKLTGLSFDNTGAITVGNKNDDKLTLLWTTDPDPSNCRI
 PanAd2 TNPLQTKLGLGLEYSNKAIIITKLTGLSFDNTGAITVGNKNDDKLTLLWTTDPDPSNCRI
 PanAd3 -----GLDYNANGAIIAKLTGLTFDNTGAITVGNKGDDKLTLLWTTDPDPSNCRI
 ChAd55 -----DVSNAIPIQVKLTGLTFDSTGAIVAWNKEDDKLTLLWTTADPSNCHI
 ChAd73 -----IGAGLNFDSSNAMAVKLTGLSFDSTGAIMAGNKEDDKLTLLWTTDPDPSNCQI
 ChAd83 -----GVDDAYPIQVKLGSLGSLFDSTGAIMAGNKEDDKLTLLWTTDPDPSNCQI
 ChAd146 -----GVDDAYPIQVKLGSLGSLFDSTGAIMAGNKEDDKLTLLWTTDPDPSNCQI
 ChAd147 -----GVTNAYPIQVKLGAGLAFDSTGAIVAWNKENDSLTLWTTDPDPSNCKI
 :..

PanAd1 NSEKDAKLTLLVLTCKGSQVLASVSVLSVKG--SLAPISGTVTSAQIVLRFDENGVLSSNS
 PanAd2 NSEKDAKLTLLVLTCKGSQVLASVSVLSVKG--SLAPISGTVTSAQIVLRFDENGVLSSNS
 PanAd3 HADKDKCKFTLLVLTCKGSQILASVAALAVSG--NLSSMTGTVSSVTIFLRFDQNGVLMENS
 ChAd55 YSDKDAKLTLLVLTCKGSQILGTVSLIAVDG--GSLNPITGQVTTALVSLKFDANGVLQTS
 ChAd73 LSDRDAKFTLLVLTCKGSQILGTVAVAAVTSSALNPINDTVKSAIVFLRFDSDGVLMSSNS
 ChAd83 LAENDAKLTLLVLTCKGSQILATVSVLVVGS--GNLNPITGTVSSAQVFLRFDANGVLLTEH
 ChAd146 LAENDAKLTLLVLTCKGSQILATVSVLVVGS--GNLNPITGTVSSAQVFLRFDANGVLLTEH
 ChAd147 ASEKDAKLTLLVLTCKGSQILGTVSLLAVS--GSLAPITGAVSTALVSLKFNANGALLDKS
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PanAd1 SLDPQYWNRYRKGDSSTEGTAYTNAVGFMPNLTAAYPKTQSQTAKSNIVSQVYLNQDGTKPMT
 PanAd2 SLDPQYWNRYRKGDSSTEGTAYTNAVGFMPNLTAAYPKTQSQTAKSNIVSQVYLNQDGTKPMT
 PanAd3 SLDKEYWNFRNGNSTNATPYTNAVGFMPNLSAYPKTQSQTAKNNIVSEVYLHGDGSKPMI
 ChAd55 TLDKEYWNFRKGDVTPAEPYTNAIGFMPNIAKAYPKNTNSAAKSHIVGKVYLHGEVSKPLD
 ChAd73 SMVGDYWNFRGQTTQSVAYTNAVGFMPNLGAYPKTQSKTPKNSIVSQVYLNGETTMPMT
 ChAd83 STLKKYWGVRQGDSIDGTPYVNAVGFMPNLKAYPKSQSSTTKNNIVGQVYMNGDVSKPML
 ChAd146 STLKKYWGVRQGDSIDGTPYVNAVGFMPNLKAYPKSQSSTTKNNIVGQVYMNGDVSKPML
 ChAd147 TLNKEYWNRYRQGDLPITGYTHAVGFMPNKKAYPKNTTAASKSHIVGDVYLDGDADKPLS
 :..

PanAd1 LTITLNGTNETG-DATVSTYSMSFSWNWNGS-NYINDTFQTNSTFTSYIAQE
 PanAd2 LTITLNGTNETG-DATVSTYSMSFSWNWNGS-NYINDTFQTNSTFTSYIAQE

PanAd3 LTITLNGTNESSETSQVSHYSMSFTWSWDSG-KYATETFATNSFTFSYIAEQ
 ChAd55 LIITFNETSNE-----TCTYCINFQWQWGTG-KYKNETLAVSSFTFSYIAQE
 ChAd73 LTITFNGTDEKD-TTPVSTYSMTFTWQWTGDYKDKNITFATNSFTFSYMAQE
 ChAd83 LTITLNGTDDS-----NSTYSMSFSYTTWTNG-SYVGATFGANSYTFYSYIAQE
 ChAd146 LTITLNGTDDS-----NSTYSMSFSYTTWTNG-SYVGATFGANSYTFYSYIAQE
 ChAd147 LIITFNETDDE-----TCDYCINFQWKWGAD-QYKDKTLATSSFTFSYIAQE
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Figure 3

Adenovirus Penton Protein

CLUSTAL W (1.83) multiple sequence alignment

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PanAd1  -MRRAAMYHEGPPPSYESVVGA--AAASPFASQLEPPYVPPRYLRPTGGRNSIRYSELAP
PanAd2  -MRRAAMYHEGPPPSYESVVGA--AAASPFASQLEPPYVPPRYLRPTGGRNSIRYSELAP
PanAd3  -MRRAAMYHEGPPPSYESVVGA--AAASPFASQLEPPYVPPRYLRPTGGRNSIRYSELAP
ChAd55  MMRR--VYPEGPPPSYESVMQQ--AVAAAMQPPLEAPYVPPRYLAPTEGRNSIRYSELAP
ChAd73  MMRR--VYPEGPPPSYESVMQQ--AVAVAMQPPLEAPYVPPRYLAPTEGRNSIRYSELAP
ChAd83  MMRR--VYPEGPPPSYESVMQQ--AVAAAMQPPLEAPYVPPRYLAPTEGRNSIRYSELAP
ChAd146 MMRR--VYPEGPPPSYESVMQQ--AVAAAMQPPLEAPYVPPRYLAPTEGRNSIRYSELAP
ChAd147 MMRR--AYPEGPPPSYESVMQQAMAAAAAMQPPLEAPYVPPRYLAPTEGRNSIRYSELAP
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PanAd1  LYDTTRVYLVDNKSADVASLNYQNDHSNFLTTVIQNNDYTPSEASTQTINLDDRSWGGD
PanAd2  LYDTTRVYLVDNKSADVASLNYQNDHSNFLTTVIQNNDYTPSEASTQTINLDDRSWGGD
PanAd3  LYDTTRVYLVDNKSADVASLNYQNDHSNFLTTVIQNNDYTPSEASTQTINLDDRSWGGD
ChAd55  LYDTTRLYLVDNKSADIASLNYQNDHSNFLTTVVQNNDFTPTEASTQTINFDESRWGGQ
ChAd73  LYDTTRLYLVDNKSADIASLNYQNDHSNFLTTVVQNNDFTPTEASTQTINFDESRWGGQ
ChAd83  LYDTTRLYLVDNKSADIASLNYQNDHSNFLTTVVQNNDFTPTEASTQTINFDESRWGGQ
ChAd146 LYDTTRLYLVDNKSADIASLNYQNDHSNFLTTVVQNNDFTPTEASTQTINFDESRWGGQ
ChAd147 LYDTTRLYLVDNKSADIASLNYQNDHSNFLTTVVQNNDFTPTEASTQTINFDESRWGGQ
      *****:*****:*****:*****:*****:*****:*****:*****:*****:

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PanAd1  LKTILHTNMPNVNEFMFTNKFKARVMVSRSHK-----DDRVELKYEWVEFELPEG
PanAd2  LKTILHTNMPNVNEFMFTNKFKARVMVSRSHK-----DDRVELKYEWVEFELPEG
PanAd3  LKTILHTNMPNVNEFMFTNKFKARVMVSRSHK-----DDRVELKYEWVEFELPEG
ChAd55  LKTIMHTNMPNVNEFMYSNKFARVMVSRKTPNGVAVGDDYDGGQDELTYEWVEFELPEG
ChAd73  LKTIMHTNMPNVNEFMYSNKFARVMVSRKTPNGVTVGDDYDGSQDELTYEWVEFELPEG
ChAd83  LKTIMHTNMPNVNEFMYSNKFARVMVSRKTPNGVTVTD---GSQDELTYEWVEFELPEG
ChAd146 LKTIMHTNMPNVNEFLYSNKFARVMVSRKTPNGVTVTD---GSQDELTYEWVEFELPEG
ChAd147 LKTIMHTNMPNVNEFMYSNKFARVMVSRKTPNGVTVTEDYDGSQDELKYEWVEFELPEG
      ****:*****:..:*****. .:      ...: **.*****

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PanAd1  NYSETMTIDLMNNAIVEHYLKVGRQNGVLES DIGVKFDTRNFRLGLDPVTGLVMPGVYTN
PanAd2  NYSETMTIDLMNNAIVEHYLKVGRQNGVLES DIGVKFDTRNFRLGLDPVTGLVMPGVYTN
PanAd3  NYSETMTIDLMNNAIVEHYLKVGRQNGVLES DIGVKFDTRNFRLGLDPVTGLVMPGVYTN
ChAd55  NFSVTMTIDLMNNAIIDNYLAVGRQNGVLES DIGVKFDTRNFRLGWDPVTELVMMPGVYTN
ChAd73  NFSVTMTIDLMNNAIIDNYLAVGRQNGVLES DIGVKFDTRNFRLGWDPVTELVMMPGVYTN
ChAd83  NFSVTMTIDLMNNAIIDNYLAVGRQNGVLES DIGVKFDTRNFRLGWDPVTELVMMPGVYTN
ChAd146 NFSVTMTIDLMNNAIIDNYLAVGRQNGVLES DIGVKFDTRNFRLGWDPVTELVMMPGVYTN
ChAd147 NFSVTMTIDLMNNAIIDNYLAVGRQNGVLES DIGVKFDTRNFRLGWDPVTELVMMPGVYTN
      *: * *****:..: * *****

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PanAd1  EAFHPDIILLPGCGVDFTYSRLSNLLGIRKRQPFQEGFRITYEDLEGGNIPALLDVEAYQ
PanAd2  EAFHPDIILLPGCGVDFTYSRLSNLLGIRKRQPFQEGFRITYEDLEGGNIPALLDVEAYQ

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PanAd3      EAFHPDIILLPGCGVDFTYSRLSNLLGIRKRQPFQEGFRITYEDLEGGNI PALLDVEAYQ
ChAd55      EAFHPDIVLLPGCGVDFTESRLSNLLGIRKRQPFQEGFQILYEDLEGGNI PALLDVEAYE
ChAd73      EAFHPDIVLLPGCGVDFTESRLSNLLGIRKRQPFQEGFQILYEDLEGGNI PALLDVEAYE
ChAd83      EAFHPDIVLLPGCGVDFTESRLSNLLGIRKRQPFQEGFQILYEDLEGGNI PALLDVEAYE
ChAd146     EAFHPDIVLLPGCGVDFTESRLSNLLGIRKRQPFQEGFQIMYEDLEGGNI PALLDVEAYE
ChAd147     EAFHPDIVLLPGCGVDFTESRLSNLLGIRKRQPFQEGFQIMYEDLEGGNI PALLDVDAYE
*****:***** *****.*****

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PanAd1    DSLKEEEAGEGSGGG--AGQEEGGASSEASADPAAAAEAEAADPAMVVVEEEKDMNDEAVR
PanAd2    NSLKEEEAGEGSGGGG-AGQEEGGASSEASADAAAAEAEAAADPAMVVVEEEKDMNDEAVR
PanAd3    DSLKEEEAGEGSGGGGGAGQEEGGASSEASADAAAAEAEAAADPAMVVVEEEKDMNDEAVR
ChAd55    KSKEE-----SAAAATAAVA-----TASTEVR
ChAd73    KSKEDS-----AAATTAAVATAATTD-----ADATTTR
ChAd83    KSKED-----STAVATAATV-----ADATVTR
ChAd146   KSKED-----SAAAATAAVA-----TASTEVR
ChAd147   KSKEE-----SAAAATAAVA-----TASTEVR
          . * ::                : * * * . . . *

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PanAd1      GDTFATRGEKKAEAEAAAEAAAAAAAA-VEAAAAEAEKPPKEPVIKPLTEDSKKRSYNVL
PanAd2      GDTFATRGEKKAEAEAAAEAAAAAAAA-VEAAAAEAEKPPKEPVIKPLTEDSKKRSYNVL
PanAd3      GDTFATRGEKKAEAEAAAEAAAAAAAAVEAAAAEAEKPPKEPVIKALTEDSKKRSYNVL
ChAd55      GDNFASAAAVA---EAAETESKIVIQP-----VEKDSKDRSYNVL
ChAd73      GDTFATQAEAAALAATDDSESKIVIKP-----VEKDSKDRSYNVL
ChAd83      GDTFATQAEAAALAATDDSESKIVIKP-----VEKDSKDRSYNVL
ChAd146     GDNFASAAAVA---EAAETESKIVIQP-----VEKDSKDRSYNVL
ChAd147     GDNFASAAAVAA--AEAAETESKIVIQP-----VEKDSKDRSYNVL
**.**.*: .      :      *: . . .      : . ** *****

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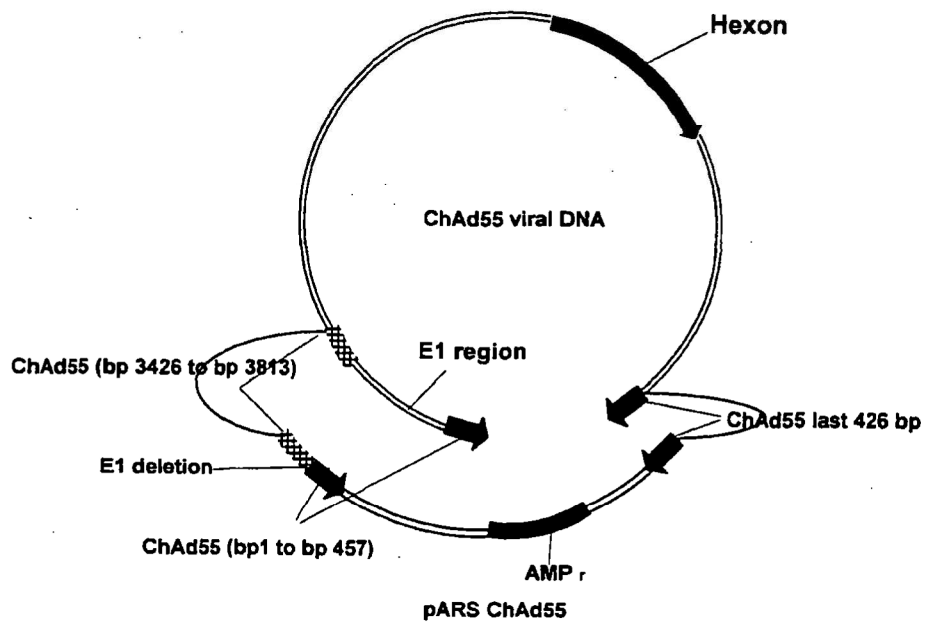
PanAd1      KDSTNTEYRSWYLAYNYGDPATGVRSWTLLCTPDVTCGSEQVYWSLPDMMQDPVTFRSTR
PanAd2      KDSTNTEYRSWYLAYNYGDPATGVRSWTLLCTPDVTCGSEQVYWSLPDMMQDPVTFRSTR
PanAd3      KDSTNTAYRSWYLAYNYGDPATGVRSWTLLCTPDVTCGSEQVYWSLPDMMQDPVTFRSTR
ChAd55      ADKKN TAYRSWYLAYNYGDPEKGVRSWTLLTTS DVT CGVEQVYWSLPDMMQDPVTFRSTR
ChAd73      ADKKN TAYRSWYLAYNYGDPEKGVRSWTLLTTS DVT CGVEQVYWSLPDMMQDPVTFRSTR
ChAd83      SDGKN TAYRSWYLAYNYGDPEKGVRSWTLLTTS DVT CGVEQVYWSLPDMMQDPVTFRSTR
ChAd146     ADKKN TAYRSWYLAYNYGDPEKGVRSWTLLTTS DVT CGVEQVYWSLPDMMQDPVTFRSTR
ChAd147     PDKIN TAYRSWYLAYNYGDPEKGVRSWTLLTTS DVT CGVEQVYWSLPDMMQDPVTFRSTR
            *  ** ***** , ***** * *****

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PanAd1 QVSNFPVVGAE LLPVHKS SFYNDQAVYSQLIRQFTSLTHVFNRFPENQILARPPAPTITT
 PanAd2 QVSNFPVVGAE LLPVHKS SFYNDQAVYSQLIRQFTSLTHVFNRFPENQILARPPAPTITT
 PanAd3 QVSNFPVVGAE LLPVHKS SFYNDQAVYSQLIRQFTSLTHVFNRFPENQILARPPAPTITT
 ChAd55 QVS NYPVVGAE LLPVYSK SFFNEQAVYSQQLRAFTSLTHVFNRFPENQILVRPPAPTITT
 ChAd73 QVS NYPVVGAE LLPVYSK SFFNEQAVYSQQLRAFTSLTHVFNRFPENQILVRPPAPTITT
 ChAd83 QVS NYPVVGAE LLPVYSK SFFNEQAVYSQQLRAFTSLTHVFNRFPENQILVRPPAPTITT
 ChAd146 QVS NYPVVGAE LLPVYSK SFFNEQAVYSQQLRAFTSLTHVFNRFPENQILVRPPAPTITT
 ChAd147 QVS NYPVVGAE LLPVYSK SFFNEQAVYSQQLRAFTSLTHVFNRFPENQILVRPPAPTITT
 ****:*****:****:*.*****:* *****

PanAd1	VSENVPALTDHGTLP L RNSIGGVQ RVTVT DARRRTC P YVYKALGIVSPRVLSSRTF
PanAd2	VSENVPALTDHGTLP L RNSIGGVQ RVTVT DARRRTC P YVYKALGIVSPRVLSSRTF
PanAd3	VSENVPALTDHGTLP L RNSIGGVQ RVTVT DARRRTC P YVYKALGIVSPRVLSSRTF
ChAd55	VSENVPALTDHGTLP L RSSIRGVQ RVTVT DARRRTC P YVYKALGVVAPRVLSSRTF

ChAd73 VSENVPALTDHGTLPLRSSIRGVQRTVTDARRRTPYVYKALGVVAPRVLSSRTF
ChAd83 VSENVPALTDHGTLPLRSSIRGVQRTVTDARRRTPYVYKALGVVAPRVLSSRTF
ChAd146 VSENVPALTDHGTLPLRSSIRGVQRTVTDARRRTPYVYKALGVVAPRVLSSRTF
ChAd147 VSENVPALTDHGTLPLRSSIRGVQRTVTDARRRTPYVYKALGIVAPRVLSSRTF
*****. ** *****:*.*****

Figure 4

**Homologous recombination
in BJ5183**

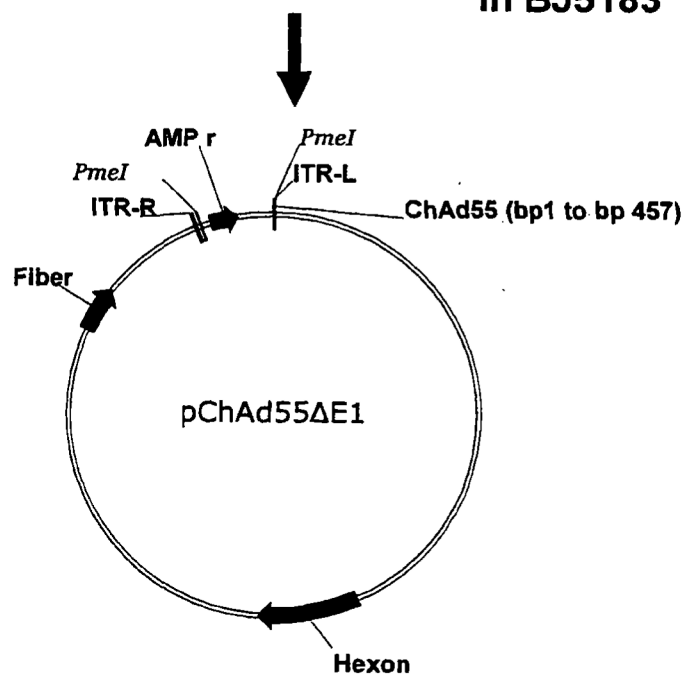


Figure 5A

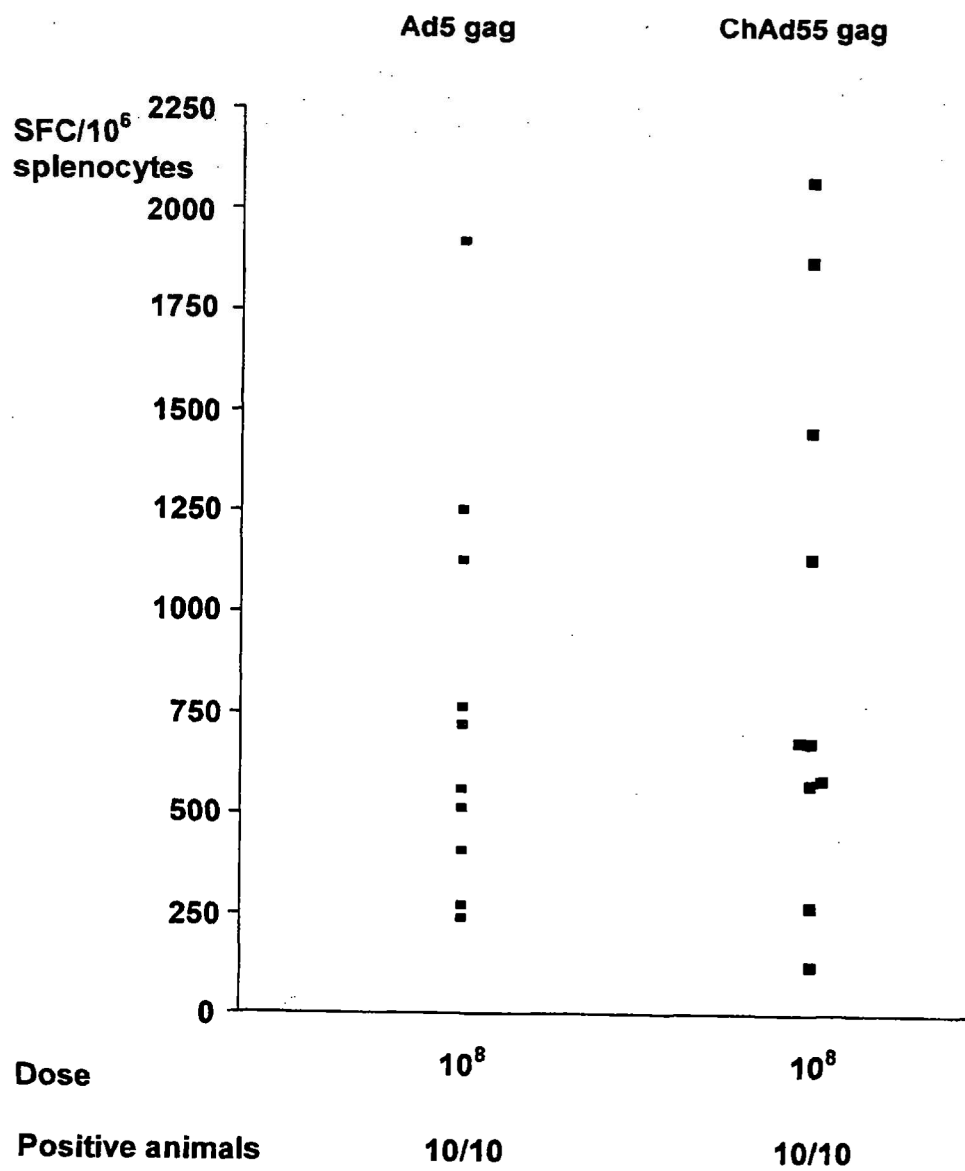


Figure 5B

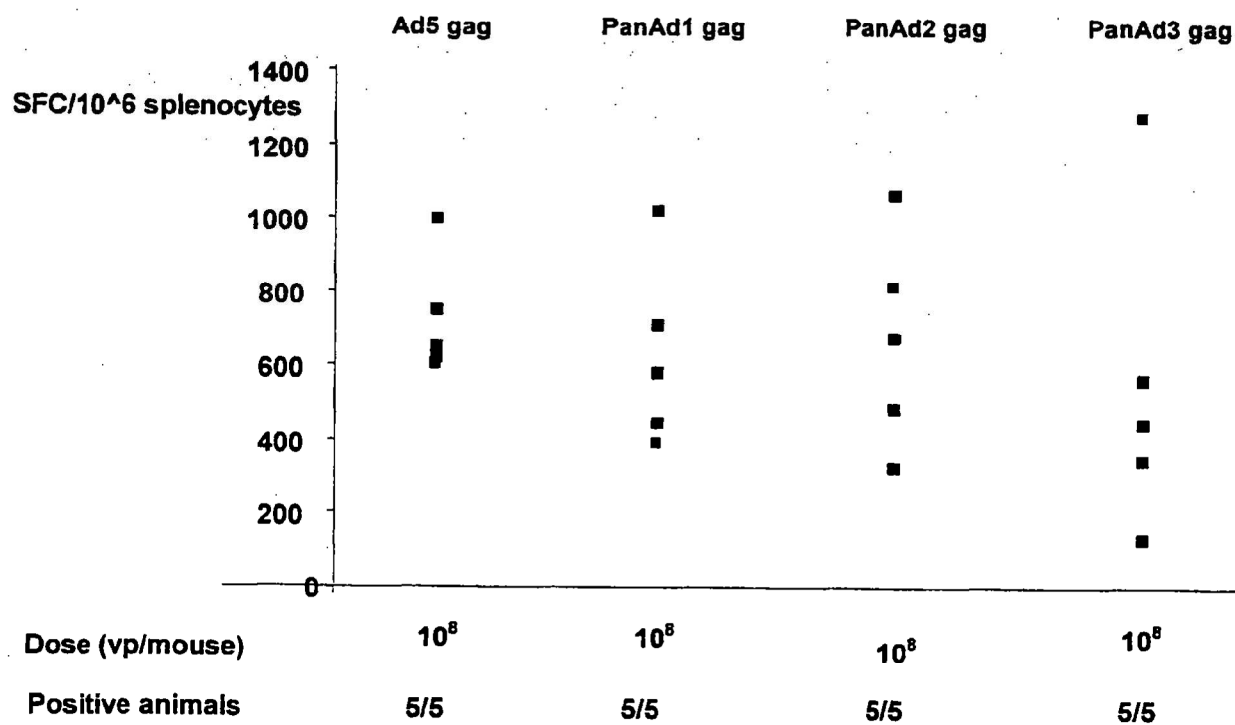


Figure 5C

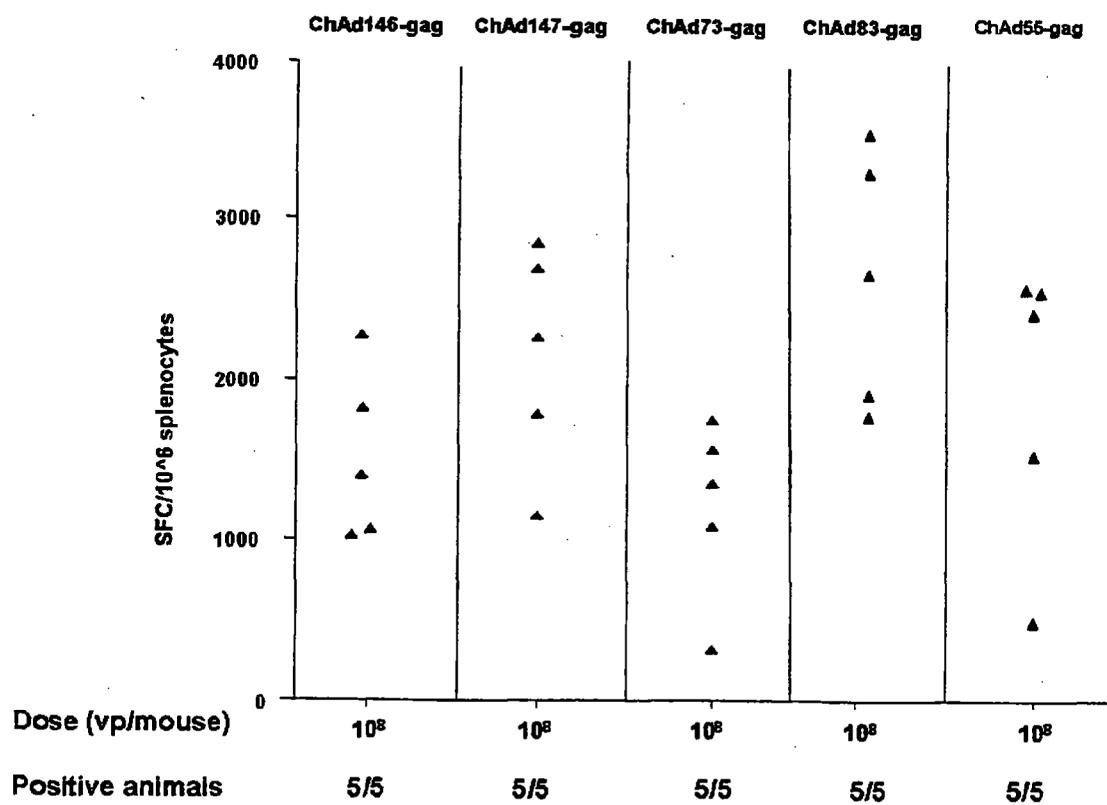


Figure 6

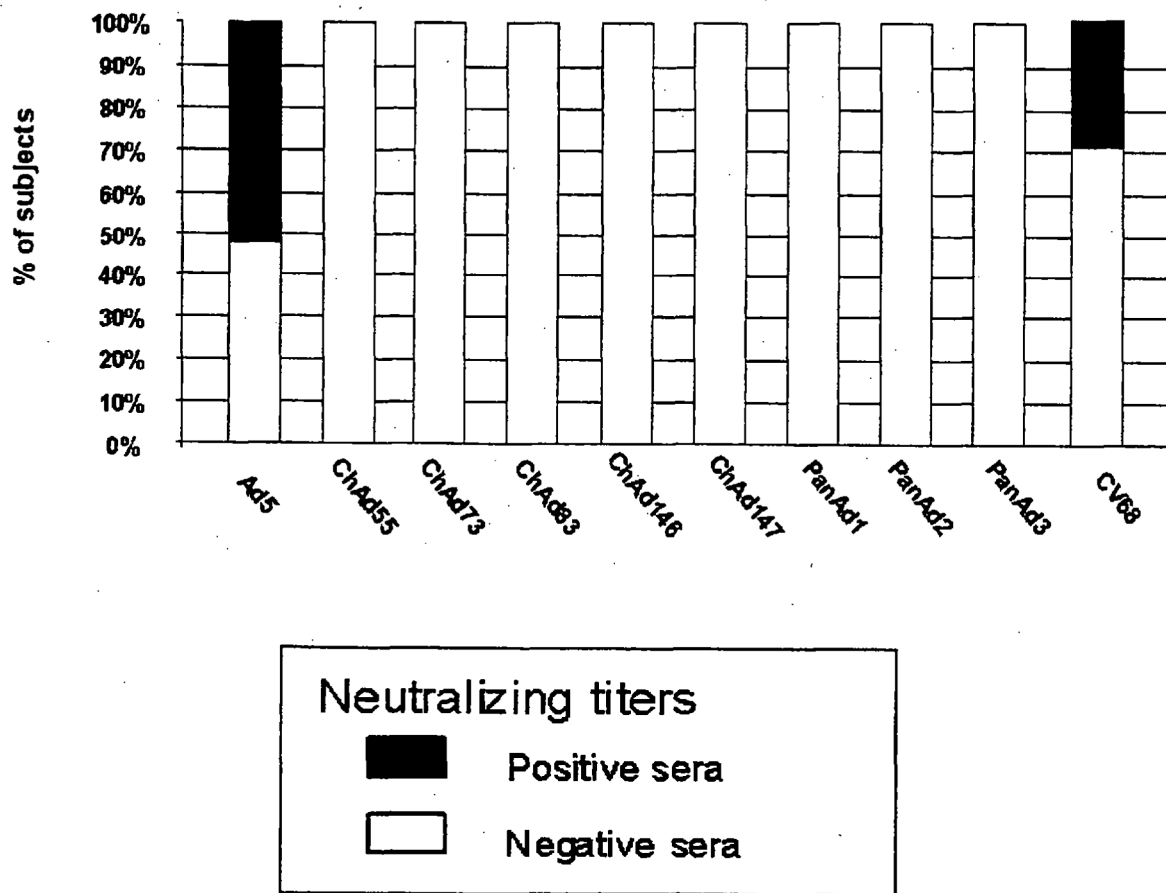
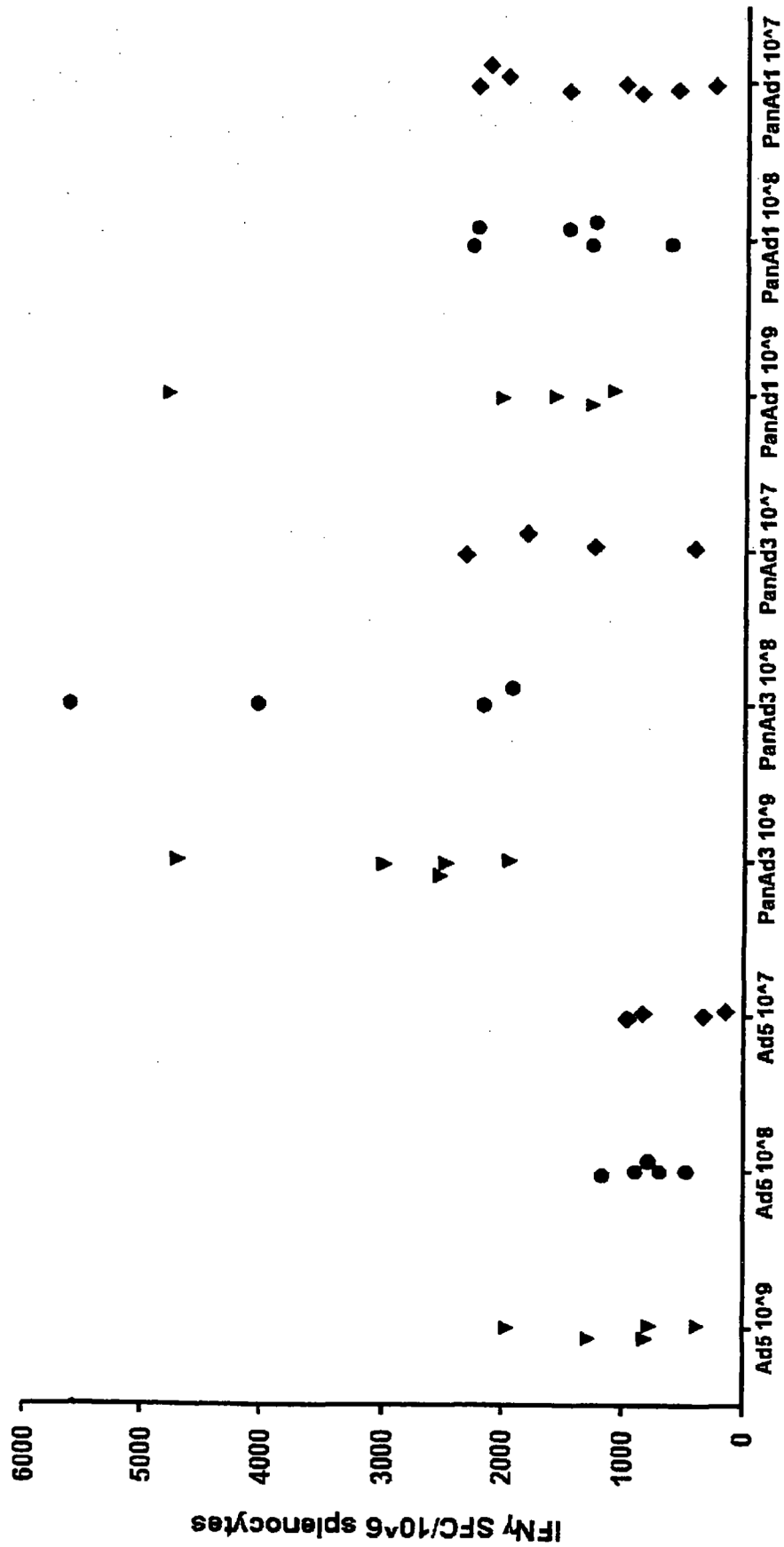


Figure 7A

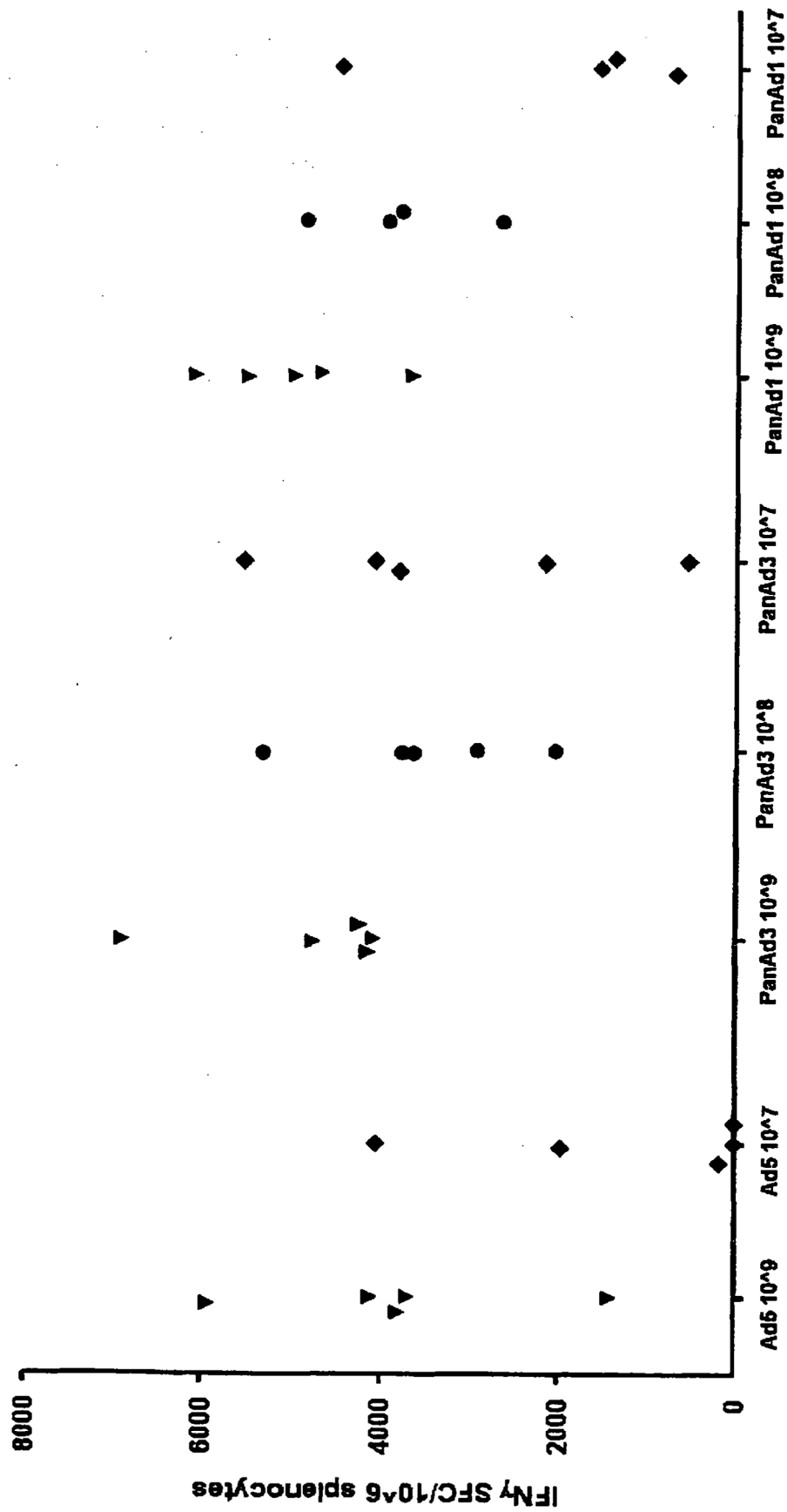
PanAd HSV immunization of BALB/c mice.
IFN γ ELISpot assay on splenocytes at week 3 post-vaccination.



Data are expressed as IFN γ Spot Forming Cells (SFC) per million splenocytes

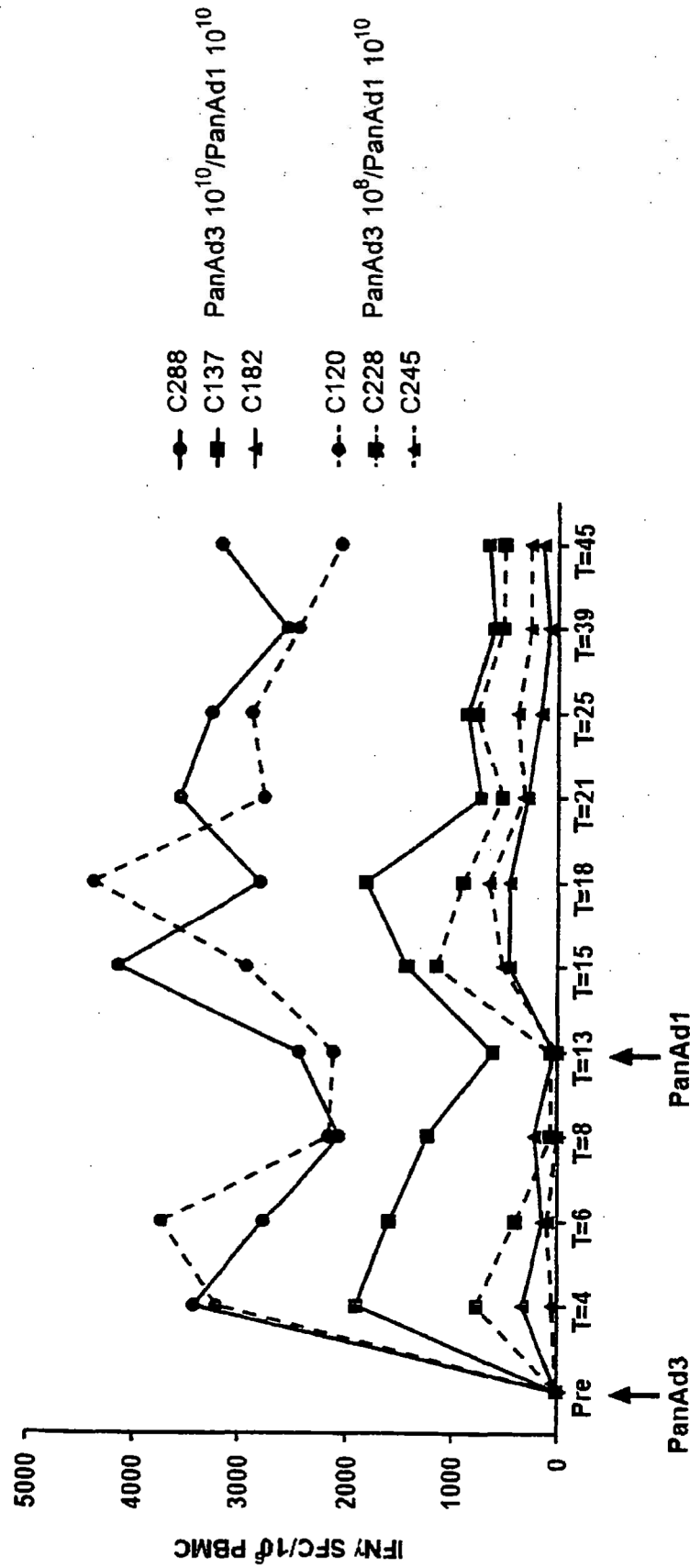
Figure 7B

PanAd cancer Ag immunization of BALB/c mice.
IFN γ ELISpot assay on splenocytes at week 3 post-vaccination.



Data are expressed as IFN γ Spot Forming Cells (SFC) per million splenocytes

Figure 8



PanAd Gag immunization of *Macaca fascicularis*.
 Heterologous immunization at week 0 and 13.
 IFN γ ELISpot assay on peripheral blood lymphocytes (PBMC) at different time points pre- and post-vaccination.

Data are expressed as IFN γ Spot Forming Cells (SFC) per million PBMC