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Canadian Intellectual Property Office

CA 3055204 A1 2018/09/07

(21) 3 055 204

(12) DEMANDE DE BREVET CANADIEN
CANADIAN PATENT APPLICATION

(13) A1

(86) Date de dépôt PCT/PCT Filing Date: 2018/03/02
(87) Date publication PCT/PCT Publication Date: 2018/09/07
(85) Entrée phase nationale/National Entry: 2019/08/30
(86) N° demande PCT/PCT Application No.: US 2018/020788
(87) N° publication PCT/PCT Publication No.: 2018/161049
(30) Priorités/Priorities: 2017/03/03 (USPCT/US2017/020823); 2018/01/31 (US62/624,620)

(51) Cl.Int./Int.Cl. *C07K 14/16* (2006.01), *A61K 39/21* (2006.01), *A61P 31/18* (2006.01), *A61P 37/04* (2006.01), *C12N 15/49* (2006.01), *C12N 7/04* (2006.01)

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(54) Titre : COMPOSITIONS ET PROCEDES POUR INDUIRE DES ANTICORPS ANTI-VIH-1
(54) Title: COMPOSITIONS AND METHODS FOR INDUCING HIV-1 ANTIBODIES

Figure 1A

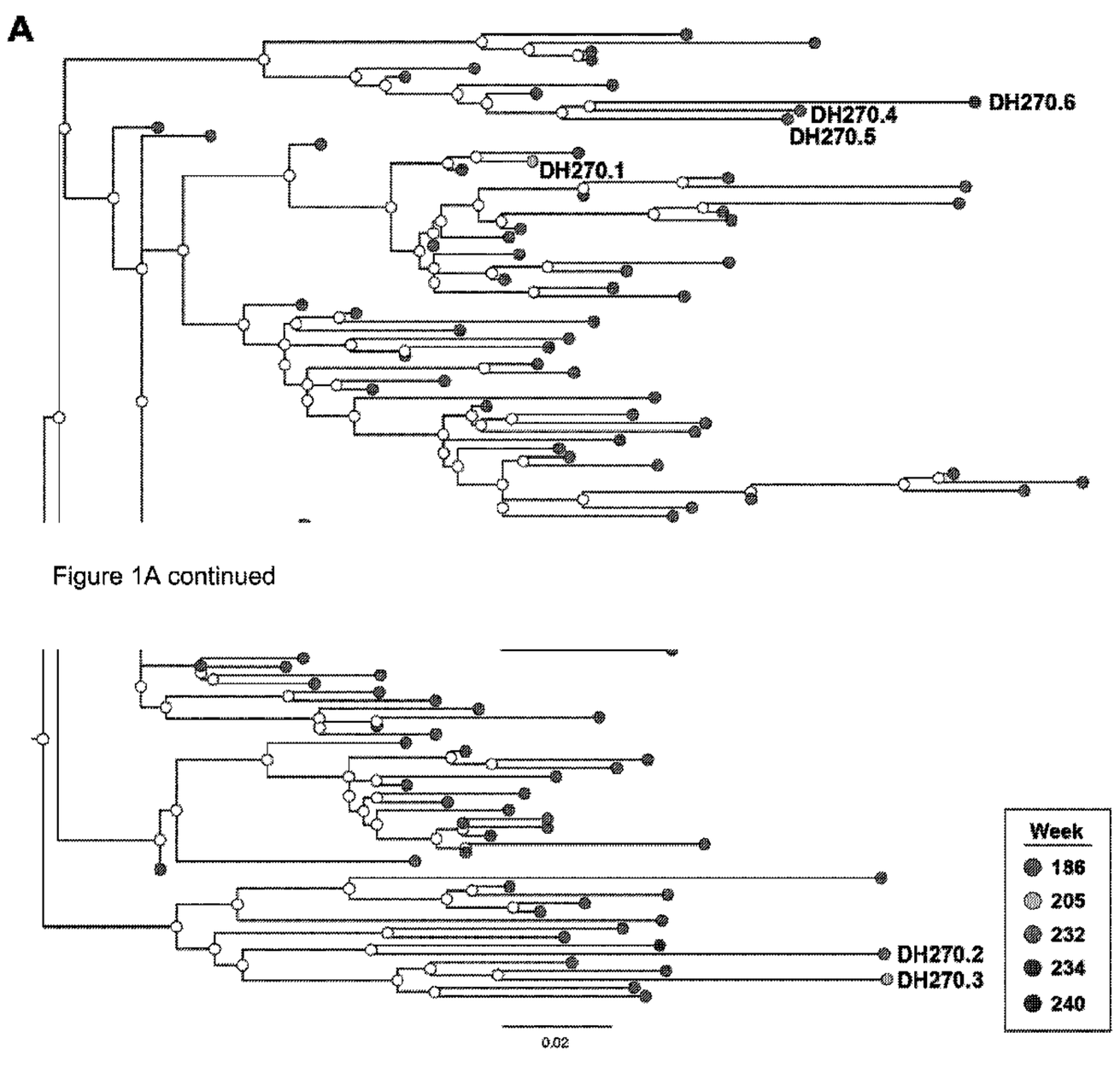


Figure 1A continued

(57) Abrégé/Abstract:
In certain aspects the invention provides HIV-1 immunogens, including envelopes (CH0848) and selections therefrom, and methods for swarm immunizations using combinations of HIV- 1 envelopes.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

CORRECTED VERSION

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
07 September 2018 (07.09.2018)

WIPO | PCT

(10) International Publication Number
WO 2018/161049 A8

(51) International Patent Classification:
A61K 39/21 (2006.01) *C12N 15/09* (2006.01)
A61K 39/39 (2006.01) *C12N 15/10* (2006.01)
A61K 38/16 (2006.01) *C07K 14/16* (2006.01)
C12N 7/04 (2006.01)

(21) International Application Number:
PCT/US2018/020788

(22) International Filing Date:
02 March 2018 (02.03.2018)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
PCT/US2017/020823 03 March 2017 (03.03.2017) US
62/624,620 31 January 2018 (31.01.2018) US

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK,

(54) Title: COMPOSITIONS AND METHODS FOR INDUCING HIV-1 ANTIBODIES

Figure 1A

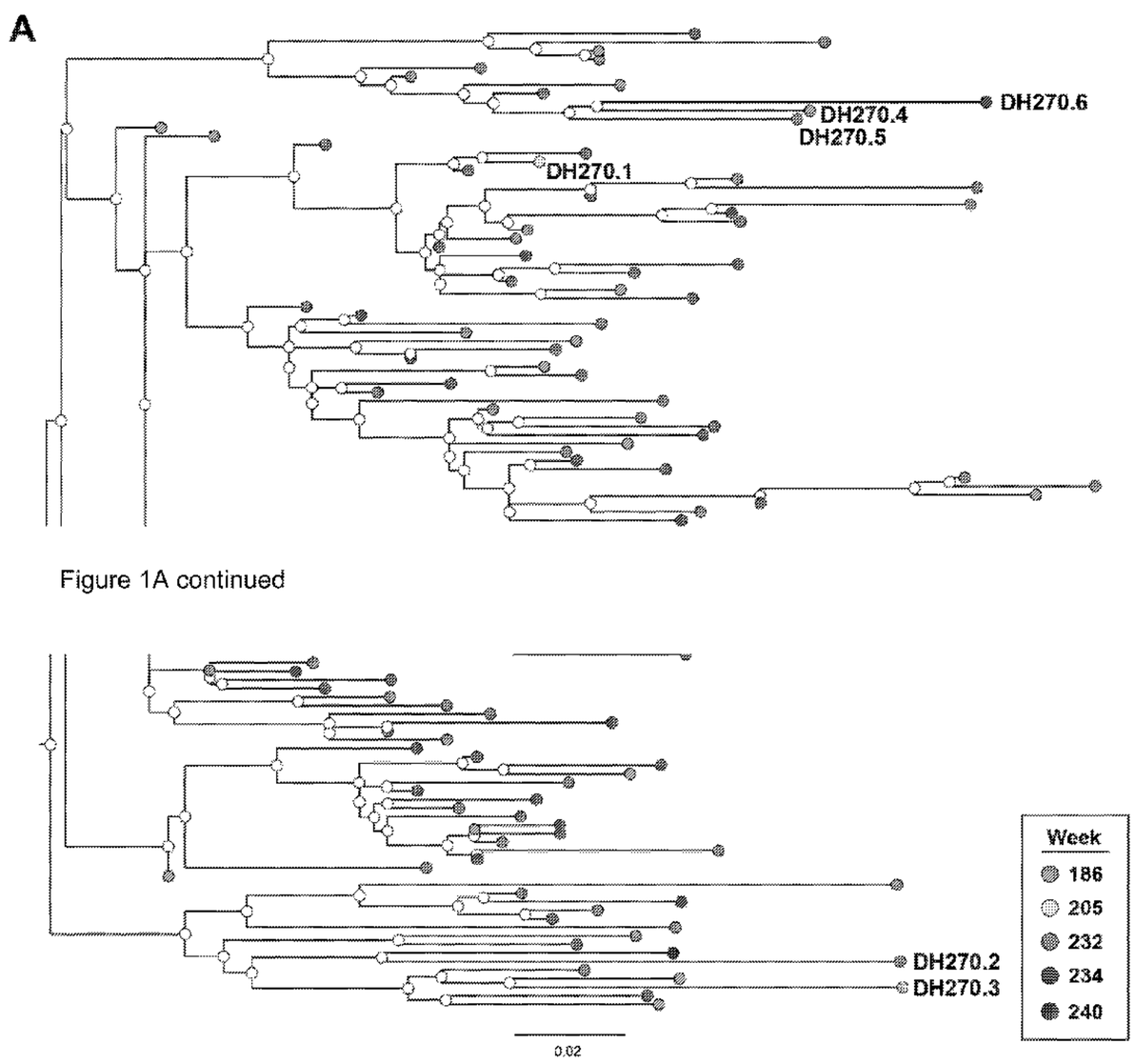


Figure 1A continued

(57) Abstract: In certain aspects the invention provides HIV-1 immunogens, including envelopes (CH0848) and selections therefrom, and methods for swarm immunizations using combinations of HIV- 1 envelopes.

[Continued on next page]

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EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

— *with international search report (Art. 21(3))*

— *with sequence listing part of description (Rule 5.2(a))*

(48) Date of publication of this corrected version:

04 October 2018 (04.10.2018)

(15) Information about Correction:

see Notice of 04 October 2018 (04.10.2018)

COMPOSITIONS AND METHODS FOR INDUCING HIV-1 ANTIBODIES

[0001] This application claims the benefit of and priority to U.S. Provisional Application No. 62/624,620 filed January 31, 2018 and International Application PCT/US2017/020823 filed March 3, 2017, the contents of each of which are hereby incorporated by reference in their entireties.

[0002] This invention was made with government support under Grant No. UM1-AI1006445 awarded by the National Institutes of Health, Division of AIDS, Bethesda, Maryland. The government has certain rights in this invention.

SEQUENCE LISTING

[0003] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety and forms part of the specification. Said ASCII copy, created on February 28, 2018, is named 1234300_00293WO1_SL.txt and is 985,914 bytes in size. The Sequence Listing contains sequences depicted in Figures 1-48, inclusive.

TECHNICAL FIELD

[0004] The present invention relates, in general, to human immunodeficiency virus (HIV), and, in particular, to HIV-1 immunogenic compositions their methods of making and their use in vaccination regimens.

BACKGROUND

[0005] Development of an effective vaccine for prevention of HIV-1 infection is a global priority. To provide protection, an HIV-1 vaccine should induce broadly neutralizing antibodies (bnAbs). One class of bnAbs among antibodies isolated from infected individuals targets the glycan-polypeptide at the base of the envelope third variable loop (V3). However, BnAbs have not been successfully induced by vaccine constructs thus far.

SUMMARY

[0006] In certain aspects the invention provides an HIV-1 envelope sequence comprising non-glycosylatable amino acids in the V1 loop, at positions corresponding to N133 and/or

N138 in the CH848.3.D0949.10.17 envelope sequence, wherein the envelope protomer sequence is based on the amino acid, comprises amino acids from the CH848.3.D0949.10.17 envelope sequence, and wherein the protomer is deglycosylated in the V1 loop (partially or completely in the V1 loop). In certain embodiments the envelope comprises amino acids substitutions within the CH848.3.D0949.10.17 sequence such that the envelope promoter forms a trimer. Any suitable envelope design or form is contemplated, so long as the envelope is based on CH848.3.D0949.10.17 sequence and the V1 loop is deglycosylated. In some embodiments short V1 loops of various length could be incorporated.

[0007] The invention provides amino acid or nucleic acids sequences encoding such deglycosylated proteins. Provided are also nucleic acids, including modified mRNAs which are stable and could be used as immunogens. Provided also are nucleic acids optionally designed as vectors, for example for recombinant expression and/or stable integration, e.g. but not limited, gp160 DNA encoding trimer for stable expression, or VLP incorporation.

[0008] In certain embodiments, the deglycosylated envelope is designed as a chimeric trimer chimeric (e.g incorporates amino acids and/or portions of envelope BG505). In certain embodiments, the deglycosylated envelopes are not chimeric, i.e. based on the sequence of envelope CH848.3.D0949.10.17 and comprising amino acids which help trimer formation. In certain embodiments, the envelope is designed as any suitable trimer, such as but not limited to various SOSIP desings, UFO trimers, or any other trimers. In certain embodiments, the envelopes of the invention comprising deglycosylated V1 positions binds and/or neutralizes DH270UCA3 and/or DH270UCA4. The envelope protomer, wherein the envelope is gp120, gp140, gp145, gp150 or gp160.In another aspect the invention provides a method of inducing an immune response in a subject comprising administering a combination of immunognes comprising V3-peptide and/or glycopeptide, wherein the peptide binds to a UCA of a V3 glycan antibody, HIV-1 envelope CH848.0949.10.17; CH848.0836.10.31; CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02 in any suitable form or any combination thereof as a prime and/or boost in an amount sufficient to induce an immune response, wherein the envelope is administered as a polypeptide or a nucleic acid encoding the same.

[0009] In certain embodiments, the compositions contemplate nucleic acid, as DNA and/or RNA, or proteins immunogens either alone or in any combination. In certain embodiments, the methods contemplate genetic, as DNA and/or RNA, immunization either alone or in combination with envelope protein(s).

[0010] In certain embodiments the nucleic acid encoding an envelope is operably linked to a promoter inserted an expression vector. In certain aspects the compositions comprise a suitable carrier. In certain aspects the compositions comprise a suitable adjuvant.

[0011] In certain embodiments the induced immune response includes induction of antibodies, including but not limited to autologous and/or cross-reactive (broadly) neutralizing antibodies against HIV-1 envelope. Various assays that analyze whether an immunogenic composition induces an immune response, and the type of antibodies induced are known in the art and are also described herein.

[0012] In certain aspects the invention provides an expression vector comprising any of the nucleic acid sequences of the invention, wherein the nucleic acid is operably linked to a promoter. In certain aspects the invention provides an expression vector comprising a nucleic acid sequence encoding any of the polypeptides of the invention, wherein the nucleic acid is operably linked to a promoter. In certain embodiments, the nucleic acids are codon optimized for expression in a mammalian cell, in vivo or in vitro. In certain aspects the invention provides nucleic acids comprising any one of the nucleic acid sequences of invention. In certain aspects the invention provides nucleic acids consisting essentially of any one of the nucleic acid sequences of invention. In certain aspects the invention provides nucleic acids consisting of any one of the nucleic acid sequences of invention. In certain embodiments the nucleic acid of the invention, is operably linked to a promoter and is inserted in an expression vector. In certain aspects the invention provides an immunogenic composition comprising the expression vector.

[0013] In certain aspects the invention provides a composition comprising at least one of the nucleic acid sequences of the invention. In certain aspects the invention provides a composition comprising any one of the nucleic acid sequences of invention. In certain aspects the invention provides a composition comprising at least one nucleic acid sequence encoding any one of the polypeptides of the invention.

[0014] The envelope used in the compositions and methods of the invention can be in any suitable form: a gp160, gp150, gp145, any suitable form of a trimer, for example but not limited to SOSIP trimers, gp140 (including but not limited to gp140C, gp140CF, gp140CFI), gp120, gp41, N-terminal deletion variants (e.g. delta 11 deletions) as described herein, cleavage resistant variants, or codon optimized sequences thereof.

[0015] The polypeptide contemplated by the invention can be a polypeptide comprising any one of the polypeptides described herein. The polypeptide contemplated by the invention can

be a polypeptide consisting essentially of any one of the polypeptides described herein. The polypeptide contemplated by the invention can be a polypeptide consisting of any one of the polypeptides described herein. In certain embodiments, the polypeptide is recombinantly produced. In certain embodiments, the polypeptides and nucleic acids of the invention are suitable for use as an immunogen, for example to be administered in a human subject.

[0016] In certain embodiments the envelope is any of the forms of HIV-1 envelope. In certain embodiments the envelope is gp120, gp140, gp145 (i.e. with a transmembrane), gp150, optionally as a trimer. In certain embodiments the trimer is a chimeric SOSIP trimer. See WO2016/037154 incorporated by reference in its entirety. In certain embodiments, envelope trimers are purified from cellular recombinant fractions by antibody binding and reconstituted in lipid comprising formulations. See for example WO2015/127108 titled "Trimeric HIV-1 envelopes and uses thereof" which content is herein incorporated by reference in its entirety. In certain embodiments, the envelope is in a liposome and transmembrane with a cytoplasmic tail in a liposome. In certain embodiments, the nucleic acid comprises a nucleic acid sequence which encode a gp120, gp140 (including but not limited to gp140C, gp140CF, gp140CFI), gp145, gp150 or gp160.

[0017] The envelope used in the compositions and methods of the invention can be a gp160, gp150, gp145, gp140, gp120, gp41, N-terminal deletion variants as described herein, cleavage resistant variants as described herein, or codon optimized sequences thereof. In certain embodiments the composition comprises envelopes as trimers. In certain embodiments, envelope proteins are multimerized, for example trimers are attached to a particle such that multiple copies of the trimer are attached and the multimerized envelope is prepared and formulated for immunization in a human. In certain embodiments, the compositions comprise envelopes, including but not limited to trimers as particulate, high-density array on liposomes or other particles, for example but not limited to nanoparticles. In some embodiments, the trimers are in a well ordered, near native like or closed conformation. In some embodiments the trimer compositions comprise a homogenous mix of native like trimers. In some embodiments the trimer compositions comprise at least 85%, 90%, 95% native like trimers.

[0018] In certain embodiments, where the nucleic acids are operably linked to a promoter and inserted in a vector, the vectors is any suitable vector. Non-limiting examples, include, the VSV, replicating rAdenovirus type 4, MVA, Chimp adenovirus vectors, pox vectors, and the like. In certain embodiments, the nucleic acids are administered in NanoTaxi block polymer

nanospheres. In certain embodiments, the composition and methods comprise an adjuvant. Non-limiting examples include, AS01 B, AS01 E, Gla/SE, alum, Poly I poly C (in any form, including but not limited to PolyIC/long chain (LC)), TLR agonists, TLR7/8 and 9 agonists, or a combination of TLR7/8 and TLR9 agonists (see Moody et al. (2014) J. Virol. March 2014 vol. 88 no. 6 3329-3339) , or any other adjuvant. Non-limiting examples of TLR7/8 agonist include TLR7/8 ligands, Gardiquimod, Imiquimod and R848 (resiquimod). A non-limiting embodiment of a combination of TLR7/8 and TLR9 agonist comprises R848 and oCpG in STS (see Moody et al. (2014) J. Virol. March 2014 vol. 88 no. 6 3329-3339).

[0019] In certain aspects, the invention provides a kit comprising a combination/selection of immunogens, for example but not limited to immunogens in Figure 37A-D, and Example 3. In some embodiments the selection of immunogens is selection F, selection G, or selection H. In some embodiments the kit comprises instructions on how to carry out the immunization regimen. In some embodiments the kit comprises instructions on administration of the selection of immunogens as a prime or boost as part of a prime/boost immunization regimen.

[0020] In certain aspects the invention provides a recombinant HIV-1 envelope polypeptide, wherein the polypeptide comprises the amino acid sequence of any one of the envelopes designs in Table 1, Table 3, Example 3, Example 5. In certain embodiments the envelope is engineered with modifications so as to improve its binding to the DH270UCA antibody. In certain embodiments, the engineered envelope is based on the sequence of HIV-1 envelope CH848.0949.10.17. In certain embodiments, the protein does not include the signal peptide. In certain aspects the invention provides a recombinant HIV-1 envelope polypeptide from Table 1, Table 3, Example 3, Example 5 wherein the polypeptide is non-naturally occurring and designed to form a soluble trimer. In certain embodiments, the protein does not include the signal peptide. In certain aspects the invention provides a nucleic acid encoding any one of the polypeptides of the invention. In certain embodiments, the nucleic acids could be formulated in any suitable way for immunogenic delivery of nucleic acids.

[0021] In certain aspects the invention provides an immunogenic composition comprising the recombinant HIV-1 envelope polypeptides of the invention and a carrier. In certain aspects the invention provides an immunogenic composition comprising the nucleic acid of the invention and a carrier. The compositions could comprise an adjuvant.

[0022] A method of inducing an immune response in a subject comprising administering a composition comprising an HIV-1 envelope polypeptide(s) in an amount sufficient to induce an immune response from one or more of the following groups:

deglycosylated envelope polypeptide form(s) of CH848.0949.10.17 designed to bind DH270UCA (Table 1, Table 3, Table 4, Ex. 3, Ex. 5), or any combination thereof as a prime;

and wherein the administration step can alternatively, or in addition, comprise administering any suitable form of a nucleic acid(s) encoding an HIV-1 envelope polypeptide(s) in an amount sufficient to induce an immune response from one or more of the following groups:

deglycosylated envelope polypeptide form(s) of CH848.0949.10.17 designed to bind DH270UCA (Table 1, Table 3, Table 4, Ex. 3, Ex. 5), or any combination thereof as a prime.

[0023] In certain aspects the invention provides methods of inducing an immune response in a subject comprising administering a composition comprising an HIV-1 envelope polypeptide(s) in an amount sufficient to induce an immune response from one or more of the following groups:

[0024] (a) deglycosylated envelope polypeptide form(s) of CH848.0949.10.17 designed to bind DH270UCA (Table 1, Table 3, Table 4, Ex. 3, Ex. 5), or any combination thereof as a prime;

[0025] (b) envelope polypeptide(s) CH848.0949.10.17, CH848.0836.10.31, CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02 (Figure 37A), or any combination thereof;

[0026] (c) envelope polypeptide CH0848.3.d1651.10.07;

[0027] and wherein the administration step can alternatively, or in addition, comprise administering any suitable form of a nucleic acid(s) encoding an HIV-1 envelope polypeptide(s) in an amount sufficient to induce an immune response from one or more of the following groups:

[0028] (a) deglycosylated envelope polypeptide form(s) of CH848.0949.10.17 designed to bind DH270UCA (Table 1, Table 3, Table 4, Ex. 3, Ex. 5), or any combination thereof as a prime;

[0029] (b) envelope polypeptide(s) CH848.0949.10.17, CH848.0836.10.31, CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02 (Figure 37A), or any combination thereof;

[0030] (c) envelope polypeptide CH0848.3.d1651.10.07.

[0031] In certain embodiments, the first boost administered after the prime comprises HIV-1 envelope polypeptide CH848.0949.10.17 in any suitable form. In certain embodiments the

boos could comprise any of the envelopes of the invention. In certain embodiments the boost is any of the envelopes of Table 1, Table 3 or Table 4. Non-limiting embodiment include any of the envelopes in Figure 50.

[0032] In certain embodiments, the nucleic acid encodes a gp120 envelope, gp120D11 envelope, a gp140 envelope (gp140C, gp140CF, gp140CFI) as soluble or stabilized protomer of a SOSIP trimer, a gp145 envelope, a gp150 envelope, or a transmembrane bound envelope. In certain embodiments, the polypeptide is gp120 envelope, gp120D11 envelope, a gp140 envelope (gp140C, gp140CF, gp140CFI) as soluble or stabilized protomer of a SOSIP trimer, a gp145 envelope, a gp150 envelope, or a transmembrane bound envelope. In certain embodiments, the methods further comprise administering an agent which modulates host immune tolerance. In certain embodiments, the immunogen of the invention is multimerized in a liposome or nanoparticle. In certain embodiment, the methods further comprise administering one or more additional HIV-1 immunogens to induce a T cell response.

[0033] In certain aspects the invention provides a kit comprising a combination/selection of immunogens of **Selection I** (V3 peptide in any suitable form such aglycone, glycosylated, multimerized, carrying T cell epitopes, etc.); recombinant HIV-1 envelopes CH848.0949.10.17; CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02), and optionally envelope polypeptide CH0848.3.d1651.10.0, and/or a nucleic acid encoding the same in any suitable form. A kit comprising a combination/selection of immunogens comprising any suitable envelope design which binds to the DH270UCA; recombinant HIV-1 envelopes CH848.0949.10.17; CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02), and optionally envelope polypeptide CH0848.3.d1651.10.0, and/or a nucleic acid encoding the same in any suitable form. The envelope and/or nucleic acid in the kits of the invention could be in any suitable form. The V3 peptide in the kits of the invention could be of SEQ ID NO: 1. In some embodiments the peptide is glycosylated. In some embodiments, the peptide is not glycosylated. In some embodiments the kit comprises an adjuvant. In some embodiment the kit comprises instructions on how to carry out the immunization regiment: the immunogen could be administered sequentially or additively.

[0034] In certain aspects the invention provides a recombinant CH848 envelope protein designed to form a soluble trimer, wherein the CH848 envelope protein comprises the sequence of any one of the envelopes or designs in Tables 1, 3, 4 and Ex, 3. Ex. 5, Figures 39A, 40A or 41A, Figs. 49, et seq. In certain embodiments, the protein does not include the signal peptide.

[0035] In certain aspects the invention provides an immunogenic composition comprising the recombinant HIV-1 envelope CH848.0949.10.17, CH848.0836.10.31, CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02 in any suitable form or a nucleic acid encoding the same. In certain embodiments the recombinant envelope comprises the sequence of the CHIM.6R.SOSIP.664V4.1 design, or any other suitable trimer design, or multimerized timer. In certain embodiments the recombinant envelope comprises the sequence any other envelope form (See e.g. Figures 39-41, 49-78; other forms such as gp140C, gp140CF, gp140CFI). The invention also provides compositions comprising suitable form of an HIV-1 envelope polypeptide or any suitable form of a nucleic acid encoding HIV-1 envelope from the selections of envelopes listed in Tables 1, 3 and Ex, 3, Ex. 5 Figures 39A, 40A or 41A, 49, or any combination thereof.

[0036] In certain aspects the invention provides a kit comprising a combination/selection of immunogens described in Tables 1, 3 and Ex, 3, and instructions for which immunogen are administered as a prime and which immunogens are administered as a boost. In some embodiments the kit of **Selection I** (V3 peptide in any suitable form such aglycone, glycosylated, multimerized, carrying T cell epitopes, etc.; recombinant HIV-1 envelopes CH848.0949.10.17; CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02) and/or a nucleic acid encoding the same. The envelope and/or nucleic acid in the kits of the invention could be in any suitable form. The V3 peptide in the kits of the invention could be of SEQ ID NO: 1. In some embodiments the peptide is glycosylated. In some embodiments, the peptide is not glycosylated. In some embodiments the kit comprises an adjuvant. In some embodiment the kit comprises instructions on how to carry out the immunization regiment: the immunogen could be administered sequentially or additively.

[0037] In some aspects the invention provides a recombinant cell, a clonal population of cells, or a pool of cells comprising a nucleic acid encoding any one of the envelope proteins or immunogens of the invention.

[0038] A recombinant HIV-1 Envelope ectodomain trimer, comprising three gpl20-gp41 protomers comprising a gpl20 polypeptide and a gp41 ectodomain, wherein each protomer is the same and comprises portions from envelope BG505 HIV-1 strain and gp120 polypeptide portions from a CH0848 HIV-1 strain and stabilizing mutations A316W and E64K, wherein the trimer is stabilized in a prefusion mature closed conformation, and wherein the trimer does not comprise non-natural disulfide bond between cysteine substitutions at positions 201 and 433 of the HXB2 reference sequence. In some embodiments, the amino acid sequence of

one monomer of trimer. In some embodiments, the trimer is immunogenic. In some embodiments the trimer binds to any one of the antibodies PGT145, PGT151, CH103UCA, CH103, VRC01, PGT128, or any combination thereof. In some embodiments the trimer does not bind to antibody 19B and/or 17B.

[0039] In certain embodiments the compositions comprising trimers are immunogenic. In certain aspects, the invention provides a pharmaceutical composition comprising any one of the recombinant trimers of the invention. In certain embodiments the compositions comprising trimers are immunogenic. The percent trimer in such immunogenic compositions could vary. In some embodiments the composition comprises 70%, 71%, 72%, 73%, 74%,75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% stabilized trimer.

[0040] In certain aspects the invention is directed to recombinant HIV-1 envelope which comprises changes in the amino acid sequence such that the envelope is partially deglycosylated. In certain embodiments, the partially deglycosylated envelopes binds to specific UCA antibodies, including but not limited to the DH270 UCA. The contemplated changes are with respect to a reference envelope sequence, which may or may not be naturally occurring. In certain embodiments deglycosylation is in the V1 loop of the HIV-1 envelope. In certain embodiments these changes are at positions N133, N138, N156, N301, N332, or any combination thereof. In certain non-limiting embodiments where the envelope is deglycosylated at positions N133 and/or N138, the envelope is glycosylated at positions N301 and N332 (See Example 5, Figures 49-78). Position given with respect to V1 loop sequence shown in Figure 75.

[0041] Any suitable amino acid change is contemplated so long as glycosylation at that position is abolished. Non-limiting embodiments include amino acids which are naturally occurring at the respective position in other envelopes such that the modified envelopes are deglycosylated. Non-limiting amino acid changes include change to alanine, or any of the following: N133D, N138T, N301A, N301S, N332A, N332T. Any envelope form, e.g. but not limited to stabilized SOSIP trimer designs, gp140s, etc. could be designed to comprise deglycosylation mutations. In some embodiments, the envelope is CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_N133DN138T. In other embodiments, the envelope is CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_N133DN138T and further comprises N301mut.

[0042] In certain aspects, he invention provides compositions comprising these deglycosylated envelopes. In certain embodiments, these deglycosylated envelopes are used as immunogens. In certain embodiments, these deglycosylated envelopes are comprised in immunogenic compositions with suitable carriers and/or adjuvants.

[0043] The invention also contemplates multimerized forms of any of the recombinant envelopes of the invention. In certain aspects the invention provides immunogenic compositions and their use to induce immune responses, wherein the envelope immunogen structure is stabilized by the addition of small molecules. A non-limiting example of such compound is BMS- 626529.

[0044] In certain aspects, the invention provides methods of inducing immune response in a subject comprising administering compositions comprising deglycosylated envelopes. In some embodiments these deglycosylated envelopes are administered as a prime. In some embodiments, the prime could be a nucleic acid encoding a deglycosylaed The glycosylated envelopes could also be administered as a boost.

[0045] The invention provides compositions comprising V3 antibody immunogens and methods for inducing antibodies to the V3 HIV-1 envelope region. In one aspect the invention provides selection of immunogens which are used to induce V3 antibodies. In some embodiments, the immunogens include a homogeneous minimal immunogen with high mannose glycans reflective of a native Env V3-glycan bnAb epitope, (Man_9-V3). In some embodiments, the immunogens include a homogeneous minimal immunogen without glycans.

[0046] V3-glycan bnAbs bound to Man_9-V3 glycopeptide and native-like gp140 trimers with similar affinities. Both fluorophore-labeled Man_9-V3 or native-like trimers similarly bound to bnAb memory B cells, and by flow sorting isolated members of a bnAb clonal lineage from an HIV-1-infected individual. The glycopeptide of Figure 38A-E bound the germline of a V3-glycan bnAb lineage. Thus, a Man_9-V3 glycopeptide mimics a HIV-1 V3-glycan bnAb epitope and is a candidate immunogen to initiate V3-glycan bnAb lineage maturation.

[0047] In some embodiments the compositions comprise immunologically and pharmaceutically acceptable carriers and/or excipients.

BRIEF DESCRIPTION OF THE DRAWINGS

[0048] To conform to the requirements for PCT patent applications, many of the figures presented herein are black and white representations of images originally created in color.

[0049] Figures 1A-B. DH270 lineage with time of appearance and neutralization by selected members. (A) Phylogenetic relationship of 6 mAbs and 93 NGS V_HDJ_H sequence reads in the DH270 clonal lineage. External nodes (filled circles) represent V_HDJ_H nucleotide sequences of either antibodies retrieved from cultured and sorted memory B cells (labeled) or a curated dataset of NGS V_HDJ_H rearrangement reads (unlabeled). Coloring is by time of isolation. Samples from week 11, 19, 64, 111, 160, 186 and 240 were tested and time-points from which no NGS reads within the lineage were retrieved are reported in Figures 30A-C. Internal nodes (open circles) represent inferred ancestral intermediate sequences. Units for branch-length estimates are nucleotide substitution per site. (B) Neutralization dendrograms display single mAb neutralization of a genetically diverse panel of 207 HIV-1 isolates. Coloring is by IC_{50}. See also Fig. 33.

[0050] Figures 2A-D. Heterologous breadth in the DH270 lineage. (A) Neutralizing activity of DH270.1, DH270.5 and DH270.6 bnAbs (columns) for 207 tier 2 heterologous viruses (rows). Coloring is by neutralization IC_{50} (μg/ml). The first column displays presence of a PNG site at position 332 (blue), N334 (orange) or at neither one (black). The second column indicates the clade of each individual HIV-1 strain and is color coded as indicated: clade A: green; clade B: blue; clade C: yellow; clade D: purple; CRF01: pink; clade G: cyan; others: gray. See Fig. 33. (B). Heterologous neutralization of all DH270 lineage antibodies for a 24-virus panel. Color coding for presence of PNG sites, clade and IC_{50} is the same of panel A. See Figures 7A-D and Figures 34-35. (C) Co-variation between V_H mutation frequencies (*x*-axis), neutralization breadth (*y*-axis, top panels) and potency (*y*-axis, bottom panels) of individual antibodies against viruses with a PNG site at position N332 from the larger (left) and smaller (right) pseudovirus panels. (D) Correlation between viral V1 loop length and DH270 lineage antibody neutralization. Top panel: neutralization of 17 viruses (with N332 and sensitive to at least one DH270 lineage antibody) by selected DH270 lineage antibodies from UCA to mature bnAbs (*x*-axis). Viruses are identified by their respective V1 loop lengths (*y*-axis); for each virus, neutralization sensitivity is indicated by an open circle and resistance by a solid circle. The *p*-value is a Wilcoxon rank sum comparison of V1 length distributions between sensitive and resistant viruses. Bottom panel: regression lines (IC_{50} for neutralization vs. V1 loop length) for DH270.1 and DH270.6, with a p-value based on Kendall's tau.

[0051] Figures 3A-E. A single disfavored mutation early during DH270 clonal development conferred neutralizing activity to the V3 glycan bnAb DH270 precursor antibodies. (A)

Nucleotide (nt) alignment of DH270.IA4 and DH272 to V_H1-2*02 sequence at the four V_H positions that mutated from DH270.UCA to DH270.IA4. The mutated codons are highlighted in yellow. AID hotspots are indicated by red lines (solid: canonical; dashed: non-canonical); AID cold spots by blue lines (solid: canonical; dashed: non-canonical) (*20*). At position 169, DH270.IA4 retained positional conformity with DH272 but not identity conformity (red boxes). (B) Sequence logo plot of aa mutated from germline (top) in NGS reads of the DH270 (middle) and DH272 (bottom) lineages at weeks 186 and 111 post-transmission, respectively. Red asterisks indicate aa mutated in DH270.IA4. The black arrow indicates lack of identity conformity between the two lineages at aa position 57. (C) Sequence logo plot of nucleotide mutations (position 165-173) in the DH270 and DH272 lineages at weeks 186 and 111 post-transmission, respectively. The arrow indicates position 169. (D) Effect of reversion mutations on DH270.IA4 neutralization. Coloring is by IC_{50}. (E) Effect of G57R mutation on DH270.UCA autologous (top) and heterologous (bottom) neutralizing activity.

[0052] Figures 4A-C. Cooperation among DH270, DH272 and DH475 N332 dependent V3 glycan nAb lineages. (A) Neutralizing activity of DH272, DH475 and DH270 lineage antibodies (columns) against 90 autologous viruses isolated from CH848 over time (rows). Neutralization potency (IC_{50}) is shown as indicated in the bar. For each pseudovirus, presence of an N332 PNG site and V1 loop length are indicated on the right. Also see Figs. 34-35. (B, C) Susceptibility to DH270.1 and to (B) DH475 or (C) DH272 of autologous viruses bearing selected immunotype-specific mutations.

[0053] Figures 5A-H. Fab/scFv crystal structures and 3D-reconstruction of DH270.1 bound with the 92BR SOSIP.664 trimer. Superposition of backbone ribbon diagrams for DH270 lineage members: UCA1 (gray), DH270.1 (green), and DH270.6 (blue) (A) alone, (B) with the DH272 cooperating antibody (red), (C) with PGT 128 (magenta), and (D) with PGT124 (orange). Arrows indicate major differences in CDR regions. (E) Top and (F) side views of a fit of the DH270.1 Fab (green) and the BG505 SOSIP trimer (gray) into a map obtained from negative-stain EM. (G) Top and (H) side views of the BG505 trimer (PDB ID: 5ACO) (*28*) (gray, with V1/V2 and V3 loops highlighted in red and blue, respectively) bound with PGT124 (PDB ID: 4R2G) (*27*) (orange), PGT128 (PDB ID: 3TYG) (*17*) (magenta), PGT135 (PDB ID: 4JM2) (*22*) (cyan) and DH270.1 (green), superposed. The arrows indicate the direction of the principal axis of each of the bnAb Fabs; the color of each arrow matches that of the corresponding bnAb. See also Fig. 24.

[0054] Figures 6A-B. DH270 lineage antibody binding to autologous CH848 Env components. (A) Binding of DH270 lineage antibodies (column) to 120 CH848 autologous gp120 Env glycoproteins (rows) grouped based on time of isolation (w: week; d: day; black and white blocks). The last three rows show the neutralization profile of the three autologous viruses that lost the PNG at position N332 (blue blocks). V1 aa length of each virus is color-coded as indicated. Antibody binding is measured in ELISA and expressed as log area under the curve (LogAUC) and color-coded based on the categories shown in the histogram. The histogram shows the distribution of the measured values in each category. The black arrow indicated Env 10.17. Viruses isolated at and after week 186, which is the time of first evidence of DH270 lineage presence, are highlighted in different colors according to week of isolation. (B) Left: Binding to CH848.TF mutants with disrupted N301 and/or N332 glycan sites. Results are expressed as LogAUC. V_H mutation frequency is shown in parenthesis for each antibody (see also Fig. 7A). Middle: Binding to CH848 Env trimer expressed on the cell surface of CHO cells. Results are expressed as maximum percentage of binding and are representative of duplicate experiments. DH270 antibodies are shown in red. Palivizumab is the negative control (gray area). The curves indicate binding to the surface antigen on a 0 to 100 scale (y-axis), the highest peak between the test antibody and the negative control sets the value of 100. Right: Binding to free glycans measured on a microarray. Results are the average of background-subtracted triplicate measurements and are expressed in RU. Figures 2A-D.

[0055] Figures 7A-D. Characteristics of DH270 lineage monoclonal antibodies. (A) Immunogenetics of DH270 lineage monoclonal antibodies. (B) Phylogenetic relationship of VHDJH rearrangements of the unmutated common ancestor (DH270.UCA) and maturation intermediates DH270.IA1 through DH270.IA4 inferred from mature antibodies DH270.1 through DH270.5. DH270.6 was not included and clusters close to DH270.4 and DH270.5 as shown in Fig. 1. (C) Amino acid alignment of the VHDJH rearrangements of the inferred UCA and intermediate antibodies and DH270.1 through DH270.6 mature antibodies (SEQ ID NOS 62-72, respectively, in order of appearance). (D) Amino acid alignment of VLJL rearrangements of the inferred UCA and intermediate antibodies and DH270.1 through DH270.6 mature antibodies (SEQ ID NOS 73-83, respectively, in order of appearance). For DH270.6, all experimental data presented in this manuscript were obtained using the light chain sequence reported here. The light chain sequence of DH270.6 was subsequently revised

to amino acids Q and A in positions 1 and 3 (instead of T and L). This difference did not affect neutralization and binding of DH270.6.

[0056] Figures 8A-C. DH270 lineage displays a N332-dependent V3 glycan bnAb functional profile. (A) DH270 antibody lineage neutralization of five HIV-1 pseudoviruses and respective N332A mutants. Data are expressed as IC50 μg/ml. Positivity <10 μg/ml is shown in bold. (B, C) DH270.1 ability to compete gp120 Env binding of V3 glycan bnAbs PGT125 and PGT128. Inhibition by cold PGT125 or PGT128 (grey line) was used as control (see Methods).

[0057] Figures 9A-D. DH475 and DH272 are strain-specific, N332-glycan dependent antibodies. (A) Phylogenetic trees of DH475 (top) and DH272 (bottom) clonal lineages. External nodes (filled circles) representing VHDJH observed sequences retrieved from cultured and sorted memory B cells (labeled) or NGS antibody sequences (unlabeled) are colored according to time point of isolation. Internal nodes (open circles) represent inferred ancestral intermediate sequences. Branch length estimates units are nucleotide substitution per site. (B) Immunogenetics of DH475 and DH272 monoclonal antibodies; (C) Binding of DH475 (top) and DH272 (bottom) monoclonal antibodies to wild-type CH848TF gp120 Env (wild-type (wt), on the x-axis, and mutants with disrupted the 301 and/or 332 N-linked glycosylation sites. Results are expressed as LogAUC. (D) Heterologous neutralization profile of DH475 and DH272 monoclonal antibodies expressed as IC50 μg/ml on a multiclade panel of 24 viruses. White square indicates IC50 > 50 μg/ml, the highest antibody concentration tested. Clades are reported on the left and virus identifiers on the right. DH475 neutralized no heterologous viruses and DH272 neutralized one Tier 1 heterologous virus.

[0058] Figure 10. CH848 was infected by a single transmitted founder virus. 79 HIV-1 3' half single genome sequences were generated from screening timepoint plasma. Depicted is a nucleotide Highlighter plot (www.hiv.lanl.gov/content/sequence/HIGHLIGHT/HIGHLIGHT_XYPLOT/highlighter.html). Horizontal lines represent single genome sequences and tic marks denote nucleotide changes relative to the inferred TF sequence (key at top, nucleotide position relative to HXB2).

[0059] Figures 11A-B. CH848 was infected by a subtype C virus. (A) PhyML was used to construct a maximum likelihood phylogenetic tree comparing the CH848 transmitted founder virus to representative sequences from subtypes A1, A2, B, C, D, F1, F2, G, H, and K (substitution model: GTR+I+G, scale bar bottom right). The CH848 TF sequence in the subtype C virus cluster is shown in red. (B) Similarity to each subtype reference sequence is

plotted on the y-axis and nucleotide position is plotted the x-axis (window size = 400 nt, significance threshold = 0.95, key to right). The two bars below the x-axis indicate which reference sequence is most similar to the CH848 TF sequence ("Best Match") and whether this similarity is statistically significant relative to the second best match ("Significant").

[0060] Figure 12. Co-evolution of CH848 autologous virus and N332-dependent V3 glycan antibody lineages DH272, DH475 and DH270. Mutations relative to the CH848 TF virus in the alignment of CH848 sequences with accompanying neutralization data (Insertion/deletions = black. Substitutions: red = negative charge; blue = positive charge; cyan = PNG sites) (43). The green line indicates the transition between DH272/DH475 sensitive and DH270 lineage sensitive virus immunotypes at day 356 (week 51). Viruses isolated after week 186, time of first evidence of DH270 lineage presence, are highlighted in different colors according to week of isolation.

[0061] Figures 13A-B. Mutations in CH848 Env over time. (A) Variable positions that are close to the PGT128 epitope in a trimer structure (PDB ID: 4TVP) (13) are represented by spheres color-coded by the time post-infection when they first mutate away from the CH848 TF sequence. The PGT128 antibody structure (PDB ID: 5C7K) (29) was used as a surrogate for DH270, as a high resolution structure is not yet available for DH270. Env positions with either main chain, side chain or glycans within 8.5Å of any PGT128 heavy atom are shown in yellow surface and brown ribbon representations. Time of appearance of mutations are color coded as indicated. (B) Same as (A) for mutating Env sites that were autologous antibody signatures of antibody sensitivity and resistance.

[0062] Figure 14. Accumulation of amino acid mutations in CH848 virus over time. This figure shows all of the readily aligned positions near the contact site of V3 glycan antibodies in Figures 13A-B, (excluding amino acids that are embedded in the V1 hypervariable regions). The magenta O is a PNG site, whereas an N is an Asn that is not embedded in a glycosylation site. The logo plots represent the frequency of amino acids at each position, and the TF amino acid is left blank to highlight the differences over time.

[0063] Figure 15. CH848 virus lineage maximum likelihood phylogenetic tree rooted on the transmitted founder sequence. The phylogenetic tree shows 1,223 Env protein sequences translated from single genome sequences. Sequences sampled prior to the development of Tier 2 heterologous breadth (week 186) are shaded in grey and sequences from after week 186 are highlighted using the color scheme from Figure 12. Four viral clades with distinct DH270 lineage phenotypes are indicated with a circle, triangle, cross and "X", respectively.

[0064] Figures 16A-F. Inverse-correlation between the potency of V3 glycan broadly neutralizing antibodies and V1 length shown for the full panel of 207 viruses. Correlation between neutralization potency (y-axis) and V1 length of the respective viruses (x-axis, n = 207) of DH270 lineage bnAbs DH270.1 (A), DH270.5 (B), DH270.6 (C) and V3 glycan bnAbs 10-1074 (D), PGT121 (E) and PGT128 (F) isolated from other individuals. Correlation p-values are non-parametric two sided, Kendall's tau. Slopes show linear regression.

[0065] Figures 17A-B. Role of V_H1-2*02 intrinsic mutability in determining DH270 lineage antibody somatic hypermutation. (A) The sequence logo plot shows the frequency of VH1-2*02 amino acid (aa) mutations from germline at each position, calculated from an alignment of 10,995 VH1-2*02 reads obtained from 8 HIV-1 negative individuals by NGS that replicated across two independent Illumina experiments (35). The logo plot shows the frequency of mutated aa at each position. The red line indicates the threshold of mutation frequency (20%) used to define frequently mutated aa. The VH aa sequences of DH270 lineage antibodies, DH272 and VRC01 are aligned on the top. The 12 red vertical stripes indicate frequently mutated aa that were also frequently mutated (>25% of the VH sequences of isolated antibodies) in the DH270 lineage. Figure discloses SEQ ID NOS 84-96, respectively, in order of appearance. (B) VH aa encoded by VH1-2 sequences from genomic DNA aligned to DH270 lineage antibodies aa sequences (see "Sequencing of germline variable region from genomic DNA" in Methods). Figure discloses SEQ ID NOS 97-109, respectively, in order of appearance.

[0066] Figures 18A-B. Effect of the G57R mutation on DH270.IA4 and DH270.UCA binding to Env 10.17 gp120. (A) Binding to Env 10.17 gp120 by wild-type DH270.IA4 (black) and DH270.IA4 variants in which each mutated aa was reverted to germline (D31G, blue; I34M, orange; T55S, green, R57G, red). Mean and standard deviation from duplicate observations are indicated for each datapoint and curve fitting (non-linear, 4-parameters) is shown for each dataset. Binding is quantified as background subtracted OD450 values. (B) Binding to Env 10.17 by wild-type DH270.UCA (black) and the DH270.UCA with the G57R mutation (red).

[0067] Figure 19. Virus signature analysis. Logo plots represent the frequency of amino acids mutations in CH848 virus quasispecies from transmitted founder at indicated positions over time. Red indicates a negatively charged amino acid, blue positive, black neutral; the light blue O is a PNG site. The signatures outlined in detail in Figure 36 are summarized in the

bottom right column where a red amino acid is associated with resistance to the antibody on the right, a blue amino acid is associated with sensitivity.

[0068] Figures 20A-F. Autologous Env V1 length associations with DH270 lineage neutralization and gp120 binding. Eighty-two virus Envs - the subset from Figures 34-35 that were assayed for both neutralization (A-C) and binding (D-F) to DH270.1, DH270.4 and DH270.5 - were evaluated. The 3 Envs that had lost the PNG site at N332 were not included, as they were negative for all antibodies tested independently of V1 length. Only points from positive results are plotted: IC50 <50 μg/ml for neutralization in panels A-C, and AUC >1 for binding in panels D-F. N is the number of positive sample.

[0069] Figures 21A-C. Sequence and structural comparison of DH270.UCA1 and DH270.UCA3. Sequence alignments of UCA3 and UCA1. (A) Heavy chains (SEQ ID NOS 110-112, respectively, in order of appearance) and (B) light chains (SEQ ID NOS 113-114, respectively, in order of appearance), whose structures were obtained in this study, are aligned with UCA4, the germline antibody for the DH270 lineage (DH270.UCA). The UCA3 and UCA4 light chains are identical. Asterisks indicate positions in which the amino acids are the same. Colon ":", period "." and blanks " " correspond to strictly conserved, conserved and major differences, respectively. (C) Superposition of UCA3 (cyan) and UCA1 (gray). Structural differences in CDR regions are indicated with an arrow.

[0070] Figure 22. Accumulation of mutation in DH270 lineage antibodies. Mutations are highlighted as spheres on the Fv region of each antibody, where the CDR regions, labeled on the backbone of the UCA, face outward. The G57R mutation is shown in red; the other mutations incurred between the UCA and IA4 are shown in orange. Mutations between intermediates are colored as follows: between IA2 and IA4, yellow; between IA1 and IA2, green; between IA3 and IA4, magenta. Mutations between the late intermediates and DH270.1, DH270.2, DH270.3, DH270.4, and DH270.5 are in brown, light purple, dark purple, blue, and dark blue, respectively.

[0071] Figures 23A-B. Negative stain EM of DH270 Fab in complex with the 92BR SOSIP.664 trimer. (A) 2D class-averages of the complex. Fabs are indicated with a red arrow. (B) Fourier shell correlation curve for the complex along with the resolution determined using FSC = 0.5.

[0072] Figure 24. DH270.1 and other N332 bnAbs bound to the 92BR SOSIP.664 trimer. Top and side views of the BG505 trimer (PDB ID: 5ACO) (28) (gray, with V1/V2 and V3 loops highlighted in red and blue, respectively) bound with DH270.1 (green), PGT135 (PDB

ID: 4JM2) (22) (cyan), PGT124 (PDB ID: 4R2G) (27) (orange) and PGT128 (PDB ID: 3TYG) (17) (magenta) illustrate the different positions of the several Fabs on gp140. The arrows indicate the direction of the principal axis of each of the bnAb Fabs; the color of each arrow matches that of the corresponding bnAb.

[0073] Figures 25A-B. DH270.1 binding kinetics to 92BR SOSIP.664 trimers with mutated PNG sites. (A) Glycans forming a "funnel" are shown on the surface of the trimer. V1-V2 and V3 loops are colored red and blue, respectively. (B) Association and dissociation curves, using biolayer interferometry, against different 92BR SOSIP.664 glycan mutants.

[0074] Figures 26A-C. DH270.1 binding kinetics to 92BR SOSIP.664 trimer with additional mutations. (A) Sequence Logo of the V3 region of CH848 autologous viruses are shown. (B) Binding kinetics, using biolayer interferometry, against different 92BR SOSIP.664 V3 loop region mutants. (C) DH270.1 heavy chain mutants and 92BR SOSIP.664. Biolayer interferometry association and dissociation curves for the indicated Fab mutants for binding to 92BR SOSIP.664 (600nM curves are shown) Not shown are curves for DH270.1 heavy chain mutants K32A, R72A, D73A, S25D, S54D, S60D and double mutant S75/77A for which there was little or no reduction in affinity.

[0075] Figures 27A-B. Man_9-V3 glycopeptide binding of DH270 lineage antibodies. DH270 lineage tree (A, top left) is shown with VH mutations of intermediates and mature antibodies. DH270.6 mAb, which clusters close to DH270.4 and DH270.5, is not shown in the phylogenetic tree. Binding of Man9-V3 glycopeptide and its aglycone form to DH270 lineage antibodies was measured by BLI assay using either biotinylated Man9-V3 (A) or biotinylated aglycone V3 (B) as described in Methods. DH270 lineage antibodies were each used at concentrations of 5, 10, 25, 50, 100, 150 μg/mL. Insets in (A) for UCA (150 μg/mL), IA4 (100, 50, 25 μg/mL), IA3 and IA2 (100, 50, 25, 10 μg/mL) show rescaled binding curves following subtraction of non-specific signal on a control antibody (Palivizumab). Rate (ka, kd) and dissociation constants (Kd) were measured for intermediate IA1 and mature mAbs with glycan-dependent binding to Man9-V3. Kinetics analyses were performed by global curve fitting using bivalent avidity model and as described in methods ("Affinity measurements" section). Inset in (B) show overlay of binding of each mAbs to Man9-V3 (blue) and aglycone V3 (red) at the highest concentration used in each of the dose titrations.

[0076] Figure 28. Example of an immunization regimen derived from studies of virus-bnAb coevolution in CH848. An immunization strategy composed of the following steps: first, prime with an immunogen that binds the UCA and the boost with immunogens with the

following characteristics: i. engagement of DH270.IA4-like antibodies and selection for the G57R mutation; ii. Selection of antibodies that favor recognition of trimeric Env and expand the variation in the autologous signature residue to potentially expand recognition of diversity in population; iii. Exposing maturing antibodies to viruses with longer loops, even though these viruses are not bound or neutralized as well as viruses with shorter V1 loops, as this is the main constrain on antibody heterologous population neutralization breadth.

[0077] Figure 29. N332-dependent CH848 plasma neutralization. Fold difference in CH848 plasma neutralization IC50 of selected wild-type and N332 mutant HIV-1 strains

[0078] Figures 30A-C. NGS longitudinal sampling of V_HDJ_H rearrangements assigned to the DH270, DH272 and DH475 lineages from memory B cell mRNA.

[0079] Figure 31. CH848 plasma neutralization breadth over time.

[0080] Figure 32. Data collection and refinement statistics.

[0081] Figure 33. DH270 lineage heterologous neutralization (207-virus panel). Figure discloses SEQ ID NOS 115-322, respectively, in order of appearance.

[0082] Figures 34-35. Autologous binding and neutralization of DH270 lineage, DH272 and DH475 and heterologous neutralization on 24 virus panel.

[0083] Figure 36. Virus signatures.

[0084] Figures 37A-D. Figures 37A-37D show non-limiting embodiments of selection of immunogens to induce V3 antibodies. The figures show binding of gp120 envelopes listed (and/or neutralization) in the figure to various antibodies from the V3 glycan antibody lineage DH270. Figure 37A: Prime with Man9 V3 glycopeptide or aglycone. Boost (i) – expected to activate IA4, select for rare mutation; Boost (ii) -- select for antibodies that favor the trimer with, expand the variation in the autologous signature residue to potentially expand recognition of diversity in the population. Boost (ii) in Figure 37A is optional. Boost (iii) – expected to expose the virus to longer loops, even though these viruses don't bind or neutralize as well as viruses with shooter loops, as this is the main constrain on heterologous population breadth and that is what we need. One embodiment of a V3 peptide is SEQ ID NO: 1. Figure 37D shows one non-limiting embodiment of a selection of immunogens. These immunogens in any suitable form are expected to be used as boost(s) in the induction of V3 glycan antibodies such as but not limited to antibodies with the specificity of DH270 lineage antibodies. For priming: Man9 V3 glycopeptide or aglycone engages UCA and allows G57R to occur (i.e. UCA to IA4). Boost with CH848.d949.10.17 (V1 loop length = 17) selects IA4 with G57R. (1) CH848.d794.05.41 (V1 loop length = 17) engages IA3 and

IA2-like antibodies and further increase chances to induce DH270.1-like antibodies. The matching virus of this envelope is still neutralized by IA3 and IA2. (optional step). (2) CH848.d358.80.06 (V1 loop length = 24) engages DH270.1-like antibodies and bring them to DH270.4, .5 and .6-like gradually increasing exposure to longer V1 loops. The matching virus is neutralized by DH270.1 and more mature bnAbs antibodies. At this point, we may or may not already have induced bnAbs, according to the importance of exposing antibodies to longer V1 loops. (3) CH848.d526.25.09 (V1 loop length = 27) exposes bnAbs DH270.4 - DH270.6 to longer V1 loop. Binding to DH270.3 is disfavored . (4) CH848.d0526.25.02 (V1 loop length = 34) further exposes to even longer V1 loop. There is a cost in neutralization IC50, yet if increasing V1 length is correlated with breadth, then it should bring breadth. Figures 37B and 37C disclose SEQ ID NO: 1.

[0085] Figures 38A-E. Figure 38A shows synthesis of Man9 derivatized V3 glycopeptide. Chemical synthesis of oligomannose (Man_9) derivatized V3 glycopeptide. (A) Chemical structure of $Man_9GlcNAc_2–NH_2$. (B) Synthesis of Man_9–V3–biotin Glycopeptide 1 – reagents and conditions: (a) $Man_9GlcNAc_2–NH_2$ (2), PyAOP, DIEA, DMSO; (b) Cocktail R = 90:5:3:2 TFA/thioanisole/ethanedithiol/anisole, 32% (2 steps); (c) $Man_9GlcNAc_2–NH_2$ (2), PyAOP, DIEA, DMSO; (d) Cocktail R = 90:5:3:2 TFA/thioanisole/ethanedithiol/anisole, 35% (2 steps); (e) 6 M Gnd·HCl, 200 mM Na_2HPO_4, 200 mM MPAA, 20 mM TCEP·HCl, pH 7.2; (e) 0.1 M Gnd·HCl, pH 7, 40% (2 steps). (C) Chemical structure of Aglycone V3–biotin. PyAOP = (7-Azabenzotriazol-1-yloxy)tripyrrolidinophosphonium hexafluorophosphate; DIEA = N,N-Diisopropylethylamine; DMSO = dimethyl sulfoxide; TFA = trifluoroacetic acid; Gnd·HCl = guanidine hydrochloride; MPAA = 4-Mercaptophenylacetic Acid; TCEP·HCl = tris(2-carboxyethyl)phosphine hydrochloride. The aglycone V3 peptide has SEQ ID NO: 1. Figure 38A discloses SEQ ID NOS 514-517, 1, and 1, respectively, in order of appearance. Figure 38B discloses SEQ ID NOS 1, 1, 1, and 1, respectively, in order of appearance. Figure 38E discloses SEQ ID NOS 1, 518, 1, 519, 1, and 519, respectively, in order of appearance.

[0086] Figure 38B shows Synthetic lipid based V3 peptides for multivalent lipid nanoparticle constructs. Schematic of lipid nanoparticles with multimers of synthetic aglycone V3 (2C) and Man9V3 glycopeptide (D). In Figure 38C and 38D both Aglycone V3 and Man9V3 peptides were synthesized with a cholesterol moiety attached via PEG linker as outlined in Figure 38B. The length of PEG linker is variable and can be short with $[PEG]_3$ or longer with $[PEG]_9$ or more units. In addition to the cholesterol unit linked to the V3 peptides, the lipid

composition of the lipid nanoparticle constructs include the following phospholipid combinations- POPC:POPE:DMPA:cholesterol-V3 /POPC:POPG:cholesterol-V3 /DMPC:DOPG:cholesterol-V3 / POPC:sphingomyelin:cholesterol-V3, each with varying %molar of cholesterol-V3 peptide (5-28molar%). The V3 peptide to lipid ratio will be used to provide 50-200 mer V3 peptide units per 100nm lipid nanoparticle. The multimeric V3 peptide lipid nanoparticles will be produced by methods previously described (Alam et al., 2007; 2009; Dennison et al., 2009, 2011. Figure 38E shows synthetic V3 peptides for multivalent lipid nanoparticle constructs with T_h peptide. The schematics shown in 2 and 3 both include the T_h peptide GTH1 of the sequence shown above and will be covalently attached to the V3 aglycone or Man9 V3 glycopeptide (as shown in 2 and 3) via a [PEG]n linker of varying units. Other T_h peptide sequence can be substituted and synthesized as in constructs 2 and 3. The amphipathic GTH1 sequence is also utilized for anchoring to lipid nanoparticles (Alam et al., 2007). The lipid compositions, and peptide:lipid molar ratios used will be as described in Figures 38C and 38D.

[0087] Figures 39A-B. Figure 39A shows amino acids sequences of CH848.0949.10.17 in various forms (SEQ ID NOS 323-328 of Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety and forms part of the specification). Various other forms can readily be obtained from the gp160 amino acid sequence. A skilled artisan appreciates that recombinantly produced envelope of any form do not include the signal peptide. The endogenous signal peptide of CH0848.3.D0949.10.17 gp160 is provided in the figure. A heterologous signal peptide of CH0848.3.D0949.10.17 chim.6R.DS.SOSIP.664 is provided in the figure. Figure 39B shows one embodiment of nucleic acid sequences of the designs in Figure 39A (SEQ ID NOS 329-334 of Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety and forms part of the specification).

[0088] Figures 40A-C. Figure 40A shows amino acid sequences of various forms of CH848 envelopes CH848.0836.10.31; CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02. A skilled artisan appreciates that recombinantly produced envelope of any form do not include the signal peptide. Figure discloses SEQ ID NOS 335-370 of Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety and forms part of the specification. Figure 40B shows one embodiment of nucleic acid sequences of the designs in Figure 40A. Figure 40B shows one embodiment of codon optimized nucleic acid sequences of the designs in Figure 40A. Figure 40B discloses SEQ ID

NOS 371-406 of Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety and forms part of the specification. Figure 40C shows the amino acids sequence as gp160 of CH848 T/F envelope (SEQ ID NO: 407 of Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety and forms part of the specification). Using the description of the various envelopes, including but not limited to SOSIP designs, the CH848 T/F envelope can also be designed in any suitable form.

[0089] Figures 41A-C. Figure 41A shows amino acid sequences of various forms of CH0848 envelopes (SEQ ID NOS 408-427 of Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety and forms part of the specification). A heterologous signal peptide of CH0848.3.D0949.10.17 chim.6R.DS.SOSIP.664V4.1 is provided in the figure (MPMGSLQPLATLYLLGMLVASVLA). A skilled artisan appreciates that recombinantly produced envelope of any form do not include the signal peptide. Figure 41B shows one embodiment of nucleic acid sequences of the designs in Figure 41A (SEQ ID NOS 428-447 of Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety and forms part of the specification). Figure 41C shows annotated amino acid sequence of a chimeric trimer design of CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1. Figure discloses SEQ ID NOS 448-449, respectively, in order of appearance.

[0090] Figures 42 and 43 show the contacts, emphasizes position D325N, and that envelope CH848 1305.10.13 retains some binding and neutralization sensitivity. CH8481305.10.13 has a proline after the N, GDIR -> GNPR (SEQ ID NOS 34 and 35, respectively). The proline at that position is really rare. Thus envelope CH0848.3.d1651.10.07, which has GNIR (SEQ ID NO: 36), and residual binding to DH270.4 and DH270.6 is a better vaccine choice.

[0091] Figures 44A-44D show amino acid and nucleic acid sequences of envelopes: >CH848 703010848.3.d0949.10.17_signature_opt_b gp160 (Fig. 44A) (SEQ ID NOS 450-455, respectively, in order of appearance), >CH848 703010848.3.d0949.10.17_signature_opt_filled_rare_holes_a gp160 (Figure 44B) (SEQ ID NOS 456-461, respectively, in order of appearance), CH0848.3.d1651.10.07 (Figure 44C) (SEQ ID NOS 462-467, respectively, in order of appearance), CH848 703010848.3.d0949.10.17_signature_opt_b_T250.4_V1V2 (Fig. 44D) (SEQ ID NOS 468-

473, respectively, in order of appearance). Signal peptide, furin site and delta N deletion are indicated in Fig. 44C.

[0092] Figure 45 shows amino acid sequences listed in Table 3 of Example 3A (SEQ ID NOS 474-502, respectively, in order of appearance).

[0093] Figure 46 shows amino acid sequences of engineered V1 loop variants of CH848 3.d0949.10.17 envelope (Table 3 lines 23-25) (SEQ ID NOS 503-505, respectively, in order of appearance).

[0094] Figures 47A-47C shows SORTASE-C designs and sequences. Figure 47A discloses SEQ ID NOS 506-509, respectively, in order of appearance. Figure 47B discloses SEQ ID NOS 520-522, respectively, in order of appearance. Figure 47C discloses SEQ ID NOS 523, 61, and 524, respectively, in order of appearance.

[0095] Figures 48A-48B show screening of various envelope constructs for binding to DH270UCA4 by SPR (SPR—S200). Figure 48A shows DH270 UCA (unmutated common ancestor) binding to CH848 SOSIP gp140 trimers. CH848.3.D0949.10.17 SOSIP trimers (100mg/mL) were injected over DH270_UCA captured on an anti-human Ig-Fc immobilized mAb sensor surface and binding monitored by SPR analysis on BIAcore S200 (GE Healthcare). DH270_UCA bound to SOSIP gp140 trimers but not to gp120 of CH848 Env. Among the CH848 trimers, more stable binding was observed with N301A mutation, indicating that the removal of the glycan at N301 facilitate the formation of more stable complex with DH270_UCA. Figure 48B shows screening of various envelopes for binding to PGT121tkUCA_v2 and DH270UCA4_Protein Panel Screening by SPR (SPR—S200). Only J, K and O samples show binding to DH270UCA4. Figure 48C lists the names of different envelopes tested in Figure 48B. Figure 48B listing of tested envelopes is as follows:

[0096] B.JRFL gp120core_mini_V3_v2/Kif/293F EndoH treated/Denatured 01.31.2017 = "A"

[0097] B.JRFL gp120core_mini_V3_v2/Kif/293F EndoH treated/Native 01.31.2017 = "B"

[0098] CH0848.3.D0949.10.17 gp140c/5uM-Kif/293F Lot: 170131D = "C"

[0099] CH0848.3.D0836.10.31 gp140c/293F Lot: 170131B = "D"

[0100] CH0848.3.D0949.10.17 gp140c/25uM-Kif/293F Lot: 170131A = "E"

[0101] CH0848.3.D0949.10.17 gp140c/293F Lot: 170131C = "F"

[0102] BG5015_MUT11B D11 gp120_avi/293F/Mon Lot: 170130B = "G"

[0103] CON-S gp140 CFI_avi V1_4Q/293F Lot: 160809C = "H"

[0104] JRFL mini V3 gp120 Core GNTI-/- Lot: 539HC = "I"

[0105] CH848.3.D0949.10.17chim.6R.DS.SOSIP.664.avi_N301A/293F Lot: 20JAJ = "J"

[0106] CH848.3.D0949.10.17 CHIM.6R.SOSIP.664V4.1/293F Lot: 225ESD = "K"

[0107] CH848.3.D0949.10.17 GT1 D11gp120_avi/293F/MON Lot: 170130C = "L"

[0108] BG505_MUT11B D11 gp120_avi/Kif/293F/Mon Lot: 170130A = "M"

[0109] B.JRFL gp120 Core_mini-V3_v2/Kif/293F/Mon Lot: 170130D = "N"

[0110] CH848.3.D0949.10.17chim.6R.DS.SOSIP.664/293F Lot: 226ESD = "O"

[0111] CH0848.3.D0358.80.06CHIM.6R.SOSIP.664v4.1/293F Lot: 558HC = "P"

[0112] B.JRFLgp140CF_aviV1 3Q/293F Lot: 160908B = "Q"

[0113] Figure 49A shows an alignment of amino acid sequences of envelope CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 and CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_N133DN138T. Positions N133 and N138 could be mutated to any other suitable amino acid, such that glycosylation of the amino acid position is prevented.

[0114] Figure 49B shows the sequence of HIV envelope CH0848.3.d1305.10.19gp160 (amino acid and nucleic acid sequence).

[0115] Figures 50A-D shows sequences of various envelopes.

[0116] Figure 51 shows sequences of various envelopes.

[0117] Figure 52A shows sequence of CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160 (Amino acid). Figure 52B shows an alignment of CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160 and CH848d949.10.17_N133DN138T_SOSIPv5.2.8.

[0118] Figure 53A shows sequence of CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T. Figure 53B shows schematic diagram with various positions and mutations to make SOSIP, SOSIP v4.1, SOSIP v5.2, TD8 mutations. Figure 53C lists mutations to make SOSIP v.5.2.8.. Figure 53D shows an alignment of various envelopes. Figure 53E shows signal peptide prediction from a signal peptide prediction server Signal P-4.1.

[0119] Figure 54A-C show various amino acid sequences. Figure 54D depicts a schematic diagram of CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP. Figure 54E shows an annotated amino acid sequence of CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP. Figure 54F displays an alignment of amino acid sequences in Figures 54A, B and C

[0120] Figure 55A-D shows binding data for a trimer comprising **CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N133D_N138T produced in 293F cells.** BLI sensor tips were coated with different bnAb precursors. Two DH270 UCA precursors were inferred (See e.g. Figure 21) and binding to CH0848 Envelope in solution was examined with BLI. Both DH270 UCAs bound to the Env. DH270 UCA3 bound at a higher magnitude and had a low dissociation rate so once it is bound it remains engaged with Env. V3 glycan bnAb precursors PGT121 and PGT128 did not bind. BnAb precursors to bnAb epitopes with the CD4bs, V1V2 glycan did not bind to this trimer.

[0121] Figure 56A-D shows binding for a trimer comprising **CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_N133DN138T produced in 293F cells.** BLI sensor tips were coated with different bnAb precursors. Two DH270 UCA precursors were inferred (See e.g. Figure 21) and binding to CH0848 Envelope in solution was examined with BLI. Both DH270 UCAs bound to the Env. DH270 UCA3 bound at a higher magnitude and had a low dissociation rate so once it is bound it remains engaged with Env. V3 glycan bnAb precursors PGT121 and PGT128 did not bind. BnAb precursors to bnAb epitopes with the CD4bs, V1V2 glycan did not bind to this trimer.

[0122] Figure 57 A-D shows binding data for a trimer comprising **CH848.3.D0949.10.17SOFA.DS.chSOSIP_N133N138A produced in 293F cells.** BLI sensor tips were coated with different bnAb precursors. Two DH270 UCA precursors were inferred (See e.g. Figure 21) and binding to CH0848 Envelope in solution was examined with BLI. Both DH270 UCAs bound to the Env. DH270 UCA3 bound at a higher magnitude and had a low dissociation rate so once it is bound it remains engaged with Env. V3 glycan bnAb precursors PGT121 and PGT128 did not bind. BnAb precursors to bnAb epitopes with the CD4bs, V1V2 glycan did not bind to this trimer.

[0123] Figure 58 shows CH0848.D0949.10.17 SOSIP trimer formation. Deglycosylated trimer in Figures 58-69 is CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_N133DN138T.

[0124] Figure 59 shows that CH0848 trimers are antigenic for cleaved trimer specific bnAb PGT151, but not coreceptor Ab 17B. "WT" refers to trimer design without N133 and N138 changes.

[0125] Figure 60 shows that DH270 UCA binds SOSIP trimers, but not uncleaved gp140 oligomers or monomeric gp120.

[0126] Figure 61A and 61B show that CH0848 10.17 N133D N138T SOSIP engages the DH270 UCA Fab with 29 nM affinity.

[0127] Figure 62 shows effect of V1 glycans on virus neutralization. Figure 62A shows that V1 glycans inhibit DH270 UCA recognition of native Env trimers: Autologous Env CH0848.3.D949.10.17 possessed a short V1 loop (17aa); N133D and N138T mutations removed potential N-linked glycosylation sites within the V1 loop. Figure 62B shows DH270UCA does not neutralize all viruses lacking V1 glycans. JR-FL N135Q N137Q N141Q SOSIPs also showed no binding to the DH270 UCA. Negative control virus MuLV titers were >50 μg/mL.

[0128] Figure 63 is a model of DH270.6 binding to SOSIP trimer and shows potential N137 glycan interference. DH270 structure in complex with Man9-V3 glycopeptide (Fera D. et al., Nature Communication in press) is modeled onto BG505 SOSIP gp120 from Stewart-Jones et al. Cell 2016 (PDB: 5FYL).

[0129] Figure 64 shows that CH0848 N133D N138T SOSIP induces Ca2+ flux in DH270 UCA and DH270 Ramos cell lines.

[0130] Figure 65 shows DH270 UCA knock-in (DH270 UCA3 $VH^{+/-}$, DH270 UCA $VL^{+/-}$) mice SOSIP immunization regimen-- Heterozygous pre-rearranged DH270 UCA knock-in mice. Protein dose: 25 μg; Route: Intramuscular; Adjuvant: GLA-SE. Group 1: CH848 N133D/N138T SOSIP; Group 2: Adjuvant only.

[0131] Figure 66 shows immunization with N133D/N138T SOSIP induced SOSIP-binding antibodies in DH270 UCA knock in mice. Figure shows serum IgG binding to CH0848.D494.10.17 N133D N138T SOSIP.

[0132] Figure 67 shows that DH270 UCA knock-in mouse serum antibodies can bind to CH0848.D949.10.17 in the presence of N133 and N138 glycans. Figure shows serum IgG binding to CH0848.D494.10.17 SOSIP.

[0133] Figure 68 show shows that DH270 UCA knock-in mouse sera neutralize CH0848.D0949.10.17 lacking the N133/N138 glycans.

[0134] Figure 69 shows DH270 UCA knock-in mouse sera neutralize tier 2 virus CH0848.D0949.10.17 with N133/N138 glycan.

[0135] Figure 70 shows JRFL, CH0848.D1305.10.19, and CH0848.D949.10.17 V3 loop alignment.

[0136] Figure 71 shows that DH270 UCA does not bind CH0848 natural Env (CH0848.D1305.10.19) that has a 17 aa V1 loop and lacks N133 and N138 glycans. Figure 71A shows trimer formation. Figure 71B and 71C shows antigenicity of CH0848.D1305.10.19 trimer to DH270UCA and DH270_I4 and DH270.6 (DH542).

[0137] Figure 72 shows that DH270-resistant CH0848 natural Env with a 17 aa V1 loop and no N133 and N138 glycan acquire V2 apex bnAb binding---Potential V3-glycan escape variant is recognized by V2 apex bnAbs (PGT145). Figure 72A shows DH270- reactive envelope CH0848.D0949.10.17. Figure 72B shows DH270-non reactive envelope CH0848.D1305.10.19.

[0138] Figure 73 shows DH270 UCA knock-in sera (see Figure 65) block V3-glycan bnAb binding to gp120.

[0139] Figure 74A-D show neutralization data from non-human primate study NHP-144. Arrows indicate immunizations at weeks 0, 4, 10, 16, 22. Samples tested for neutralization at weeks 0, 12, 18 or 24.

[0140] Figure 75A and 75B show the V1V2 loop sequence alignments show there are two glycosylation sites within the 10.17 V1 loop. The precise asparagines that are mutated in the 10.17DT Env design are underlined. The sequence for 10.17 is shown in relation to V1V2 loops of other viruses since V1 V2 amino acid numbering can vary depending on the alignment software, thus this alignment shows the exact position of each of the asparagines. Con-S V1 length is 22 aa. JRFL V1 length is 25aa. T250-4 V1 length is 22. CH0848.D0949.10.17 V1 length is 17aa.

[0141] Figure 76A-D shows binding data for a trimer comprising **CH848.3.D0949.10.17CHIM.6R.SOSIP.664v4.1 degly3 produced in 293F cells.** BLI sensor tips were coated with different bnAb precursors. Two DH270 UCA precursors were inferred (See e.g. Figure 21) and binding to CH0848 Envelope in solution was examined with BLI. Both DH270 UCAs bound to the Env. DH270 UCA3 bound at a higher magnitude and had a low dissociation rate so once it is bound it remains engaged with Env. V3 glycan bnAb precursors PGT121 and PGT128 did not bind. BnAb precursors to bnAb epitopes with the CD4bs, V1V2 glycan did not bind to this trimer.

[0142] Figure 77A-L shows sequences of various envelopes described in Table 4. Figure 77A shows the sequence of HV1301331_degly3 with N138, N133, and N301 glycans removed. These glycans were believed to prevent DH270 mAb binding by blocking access to HIV peptide binding. Figure 77B shows the sequence of HV1301331_N138T. This Env has a single V1 glycan removed. This Env would be used to sequentially add back glycans in the V1 loop to select antibodies capable of tolerating N301 and N133 glycans but not N138T. This Env could be used in a sequential Env vaccine where glycans are removed and added back sequentially. Figure 77C shows the sequence of HV1301345_D368R. This Env has

D368R mutation to reduce CD4 binding. CD4 binding could disrupt Env conformation in vivo. Figure 77D shows the sequence of HV1301331_N133DN138T_c-SORTA. This tagged Env that can be ligated to particles by sortase A enzyme. Figure 77E shows the sequence of HV1301522. This ferritin particle has a V1 glycan mutant Env attached as a fusion protein. Figure 77F shows the sequence of HV1301345_N133D_N138T_cSORTA. This tagged Env can be ligated to particles by sortase A enzyme reactions in vitro. Figure 77G shows the sequence of HV1301581, a full length gp160 HIV Env with V1 glycans removed to engender DH270 UCA binding. Figure 77H shows the sequence of HV1301345_TFV1loop with the 10.17 Env with a long V1 loop that was transplanted from the TF virus sequence. This can be used to select for antibodies capable of accommodating a long V1 loop. Figure 77I shows the sequence of HV1301345_N133D_N138T which is a stabilized trimer with V1 glycans removed to facilitate DH270 UCA binding. Figure 77J shows the sequence of HV1301262(has avi tag), a non-chimeric Env. Figure 77K shows the sequence of HV1301263(has avi tag), a chimeric DS Env without V1 glycan mutated. Figure 77L shows the sequence of HV1301264 (has avi tag), a non-chimeric DS stabilized CH0848 trimer.

[0143] Figure 78A-B shows annotated sequences of CH848.3.D0949.10.17.6R.SOSIP.664 envelope and CH848.3.D0949.10.17 SOSIPv5.2.8. Figure 78A shows the annotated sequence of CH848.3.D0949.10.17.6R.SOSIP.664. Figure 78B shows the annotated sequence of CH848.3.D0949.10.17 SOSIPv5.2.8.

[0144] Figure 79A-79L shows binding data for a trimer comprising **CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N133D_N138T produced in 293F cells.** BLI sensor tips were coated with different bnAb as indicated in the various panels. Binding was determined in the absence (79G-L) and presence (79A-79F) of 10um of Temsavir (BMS-626529). Vertical dotted line indicates response at the end of association

[0145] Figure 80 shows a summary of binding data (from Figures 79A-79L) for a trimer comprising **CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N133D_N138T** produced in 293F cells. Figure shows binding Ratio Relative to PGT151. Diamonds show antibody trimer binding without BMS-626529 and squares show trimer binding in the presence of BMS-626529.

[0146] Figure 81 shows a summary of BLI binding data for a trimer comprising **CH848.3.D0949.10.17.chim.6R.DS.SOSIP.664_N301A** produced in 293F cells. Figure shows binding Ratio Relative to PGT151. Diamonds show antibody trimer binding without BMS-626529 and squares show trimer binding in the presence of BMS-626529.

DETAILED DESCRIPTION

[0147] The third variable region, V3, of the envelope glycoprotein, gp120 of HIV-1 is a target for virus broad neutralizing antibodies. Several V3 glycan dependent broad neutralizing antibodies (bnAbs) have been isolated that neutralize diverse strains of difficult to neutralize viruses. A questions remains as to what form of Env could bind and initiate V3-glycan bnAb lineages. Soluble Env gp120 or cell surface Env trimers do not bind V3-glycan bnAb UCAs *(20)* (See Example 1). In some aspects the invention provides that the Man_9-V3glycopeptide (Example 2) as well as its aglycone (Example 2) form binds the UCA of the DH270V3-glycan bnAb lineage. Moreover, Man_9-V3/aglycone binds to the UCA of gp140-induced V3-glycan neutralizing mAb, DH501. With affinity maturation in both the DH270 bnAb and the DH501 lineages, binding to the aglycone-V3 diminished and binding to Man_9-V3 was dramatically enhanced. These observations raise the hypothesis that initiating immunogens for V3-glycan lineages may be denatured or Env fragments (Example 1 Bonsignori, M. et al. submitted).

[0148] The invention provides various methods to choose a subset of viral variants, including but not limited to envelopes, to investigate the role of antigenic diversity in serial samples. In other aspects, the invention provides compositions comprising viral variants, for example but not limited to envelopes, selected based on various criteria as described herein to be used as immunogens. In some embodiments, the immunogens are selected based on the envelope and/or peptide binding to the UCA, and/or intermediate antibodies. In some embodiments, the immunogens are selected based on UCA and/or intermediate antibodies neutralizing properties against viruses. In some embodiments the immunogens are selected based on their chronological appearance and/or sequence diversity during infection.

[0149] In other aspects, the invention provides immunization strategies using the selections of immunogens to induce cross-reactive neutralizing antibodies.

[0150] In certain aspects the invention provides an HIV-1 envelope sequence comprising non-glycosylatable amino acids in the V1 loop, at positions corresponding to N133 and/or N138 in the CH848.3.D0949.10.17 envelope sequence, wherein the envelope protomer sequence is based on the amino acid sequence of CH848.3.D0949.10.17 envelope; comprises amino acids from the CH848.3.D0949.10.17 envelope sequence, consists essentially of amino acids from CH848.3.D0949.10.17 envelope sequence and wherein the protomer is deglycosylated in the V1 loop (partially or completely in the V1 loop). In some embodiments, a deglycosylated envelope consists essentially of amino acids from

CH848.3.D0949.10.17 envelope sequence when the deglycosylated envelopes has all amino acids from CH848.3.D0949.10.17 envelope sequence except for the amino acids at positions N133 and/or N138. In some embodiments, it further comprises amino acid changes for trimer formation.

[0151] Using sequence alignment algorithms, a skilled artisan can readily determine whether a V1 loop deglycosylated envelope is based on CH848.3.D0949.10.17 envelope sequence.

[0152] Comparing the sequences of envelopes, a skilled artisan can readily determine sequence identity, compare sequence length and determine the % sequence identity and/or changes, including % sequence identity and/or changes in the sequences, as well as the specific positions and types of substitutions which can be tolerated while the V1 loop deglycosylated envelope sequence is based on CH848.3.D0949.10.17.

[0153] Various algorithms for sequence alignment are known in the art. The similarity between amino acid sequences is expressed in terms of the similarity between the sequences, otherwise referred to as sequence identity. Sequence identity is frequently measured in terms of percentage identity (or similarity or homology); the higher the percentage, the more similar the two sequences are. Homologs or variants of a polypeptide will possess a relatively high degree of sequence identity when aligned using standard methods.

[0154] Methods of alignment of sequences for comparison are well known in the art. Various programs and alignment algorithms are described in: Smith and Waterman, Adv. Appl. Math. 2:482, 1981; Needleman and Wunsch, J. Mol. Biol. 48:443, 1970; Pearson and Lipman, Proc. Natl. Acad. Sci. U.S.A. 85:2444, 1988; Higgins and Sharp, Gene 73:237, 1988; Higgins and Sharp, CABIOS 5:151, 1989; Corpet *et al.*, Nucleic Acids Research 16:10881, 1988; and Pearson and Lipman, Proc. Natl. Acad. Sci. U.S.A. 85:2444, 1988. Altschul *et al.*, Nature Genet. 6:119, 1994, presents a detailed consideration of sequence alignment methods and homology calculations.

[0155] The NCBI Basic Local Alignment Search Tool (BLAST) (Altschul *et al.*, J. Mol. Biol. 215:403, 1990) is available from several sources, including the National Center for Biotechnology Information (NCBI, Bethesda, Md.) and on the internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx. A description of how to determine sequence identity using this program is available on the NCBI website on the internet.

[0156] In some embodiments a deglycosylated envelope is based on CH848.3.D0949.10.17 envelope if it is characterized by possession of at least about 65%, 70%, 75%, for example at

least about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity counted over the full length alignment with the amino acid sequence of interest. When less than the entire sequence is being compared for sequence identity, a deglycosylated envelope could have at least 80% sequence identity over short windows of 10-20 amino acids, and may possess sequence identities of at least 85% or at least 90% or 95% depending on their similarity to the reference sequence. Methods for determining sequence identity over such short windows are available at the NCBI website on the internet. One of skill in the art will appreciate that these sequence identity ranges are provided for guidance only; it is entirely possible that strongly significant homologs could be obtained that fall outside of the ranges provided.

[0157] In some embodiments a deglycosylated envelope is based on CH848.3.D0949.10.17 envelope if it is characterized as having 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, 82%, 81%, 80%, 79%, 78%, 77%, 76%, 75.

[0158] In certain embodiments the envelope comprises amino acids substitutions within the CH848.3.D0949.10.17 sequence such that the envelope promoter forms a trimer. Any suitable envelope design or form is contemplated, so long as the envelope is based on CH848.3.D0949.10.17 sequence and the V1 loop is deglycosylated. In some embodiments short V1 loops of various length could be incorporated.

[0159] The invention provides amino acid or nucleic acids sequences encoding such deglycosylated proteins. Provided are also nucleic acids, including modified mRNAs which are stable and could be used as immunogens. Provided also are nucleic acids optionally designed as vectors, for example for recombinant expression and/or stable integration, e.g. but not limited, gp160 DNA encoding trimer for stable expression, or VLP incorporation.

[0160] In certain embodiments, the deglycosylated envelope is designed as a chimeric trimer chimeric (e.g incorporates amino acids and/or portions of envelope BG505). In certain embodiments, the deglycosylated envelopes are not chimeric, i.e. based on the sequence of envelope CH848.3.D0949.10.17 and comprising amino acids which help trimer formation. In certain embodiments, the envelope is designed as any suitable trimer, such as but not limited to various SOSIP designs, UFO trimers, or any other trimers. In certain embodiments, the envelopes of the invention comprising deglycosylated V1 positions binds and/or neutralizes DH270UCA3 and/or DH270UCA4. The envelope protomer, wherein the envelope is gp120, gp140, gp145, gp150 or gp160.

[0161] As Example 2 shows that a synthetic homogeneous Man_9-V3 glycopeptide mimics a HIV-1 Env V3-glycan bnAb epitope. Man9-V3 recognition by V3-glycan memory B cell and UCA BCR suggest that a minimal V3-glycan epitope construct may be a candidate for the induction of V3-glycan bnAb lineages. In HIV-1 infection, the DH270 V3-glycan bnAb lineage developed over ~4 years (Bonsignori, M et al. submitted), and V3-glycan-targeted antibodies took 4 years to develop in macaques repetitively immunized with Env gp140 (Saunders, K et al. submitted). Thus, while whole Env monomers or trimers do not bind to V3-glycan bnAb UCAs, the V3-glycopeptide does bind UCAs, suggesting that minimal Env epitopes may accelerate induction of V3-glycan bnAb B cell lineages.

[0162] Described herein are both the design and selections of immunogens to elicit neutralizing antibodies directed toward the V3 glycan epitope defined by V3 binding antibodies. Minimal V3 region glycopeptides bearing two glycans of appropriate structure can mimic the antigenic nature of this epitope, and can provide an effective platform for immunogen development. This concept--based on the "two glycans and a strand" paradigm of recognition suggested by x-ray analysis.sup.6--has been successfully applied to the V1V2 region anti-glycan BnAb site. Given the likely rarity of naive B cells relevant to BnAb ontogeny in the immune repertoire, preferred immunogens include those that exclude potentially interfering immunodominant epitopes. These immunogens can be evaluated not only based on their affinities for mature BnAbs, but also their germline precursors.

[0163] In certain embodiment, the invention provides a composition comprising any one of the inventive peptides, wherein the composition comprises purified homogenously glycosylated peptides. In certain embodiments, about 70%, 75%, 80%, 85%, 90%, 95%, 99%, or 99.9% of the peptides in the composition are homogenously glycosylated peptides. In certain embodiments, 70%, 75%, 80%, 85%, 90%, 95%, 99%, or 99.9% of the peptides in the composition are homogenously glycosylated peptides. In certain embodiments, 70%-75%, 75.1%-80%, 80.1%-85%, 85.1%-90%, 90.1%-95%, 95.1%-99%, 96%-99%, 97%-99%, 98%-99% or 99.9% of the peptides in the composition are homogenously glycosylated peptides. In certain embodiment, the glycosylation pattern is homogenous on all V3 peptides in the composition. In certain embodiment, the glycosylation pattern is substantially identical on all V3 peptides in the composition.

[0164] Various methods of determining the glycosylation pattern on a peptide are known in the art. In certain embodiments, glycosylation pattern on the peptides and % homogeneity can

be determined by Liquid chromatography--mass spectrometry (LC-MS, or alternatively HPLC-MS).

[0165] As indicated in the Examples that follow, V3 glycopeptides can be synthesized with well-defined glycans at N332 and N301 using clade B and clade C sequences (derived from Envs with known antigenicity toward V3 anti-glycan BnAbs). Variations of the peptide framework include full length vs. truncated V3 loops, as well as linear vs. constrained cyclic forms (via disulfide bond formation). Antigenicity testing provides the data needed to determine the peptide design motif that is optimal for binding to HIV-1 Env anti-glycan BnAbs. Using the best peptide "scaffold", derivatives can be synthesized bearing different glycans at N332 and N301 and the determination made as to the optimal carbohydrate design for anti-glycan BnAb binding. The constructs that exhibit the highest affinity for V3-directed anti-glycan BnAbs and their UCAs can be synthesized on larger scale and subjected to trials e.g., in non-human primates--immunogenicity can be evaluated for constructs both with and without conjugation to carrier protein.

[0166] The present invention thus relates, at least in part, to immunogens that focus the immune response to the V3 glycan epitope on gp120 that lead to BnAbs and away from epitopes that lead to non-neutralizing antibodies. Central to the present design strategy is making the immunogen as minimal in size as possible so as not to introduce diverting, non-neutralizing epitopes. Non-limiting embodiments of immunogens are described in the Examples below.

[0167] The immunogens can be formulated with appropriate carriers using standard techniques to yield compositions suitable for administration. The compositions can include an adjuvant, such as, for example, alum, poly IC, poly IC/LC, MF-59 or other squalene-based adjuvant, ASO1B or other liposomal based adjuvant suitable for protein immunization. Suitable vaccine strategies include, e.g., those described, for in the Examples that follow.

[0168] Nucleic acid sequences (e.g., DNA sequences) encoding the immunogens can also be administered to a subject (e.g., a human) under conditions such that the immunogen is expressed in vivo and BNAbs are produced. The DNA can be present as naked DNA with a potent promoter such as the CMV promoter as used in the pCMVr plasmid (Churchyard et al, PLoS One 6:e21225 (2011)) or as an insert in a vector, such as a rAdenoviral (Barouch, et al. Nature Med. 16: 319-23 (2010), recombinant mycobacterial (i.e., BCG or M smegmatis) (Yu et al. Clinical Vaccine Immunol. 14: 886-093 (2007); ibid 13: 1204-11 (2006), or recombinant vaccinia type of vector (Santra S. Nature Med. 16: 324-8 (2010)).

[0169] Immunogens of the invention, and nucleic acids (e.g., DNAs) encoding same, are suitable for use in generating an immune response (e.g., BNAbs) in a patient (e.g., a human patient) to HIV-1. The V3 N301, N332 peptide glycan can optimally be administered as a peptide-glycan formulated in a squalene based adjuvant such as MF59, or GLA-SE (Alving et al, Current Opinion in Immunology 24:310 (2012)). The mode of administration of the immunogen, or encoding sequence, can vary with the particular immunogen, the patient and the effect sought, similarly, the dose administered. Typically, the administration route is intramuscular or subcutaneous injection (intravenous and intraperitoneal can also be used). Additionally, the formulations can be administered via the intranasal route, or intrarectally or vaginally as a suppository-like vehicle. Optimum dosing regimens can be readily determined by one skilled in the art. The immunogens (and nucleic acids encoding same) are preferred for use prophylactically, however, their administration to infected individuals may reduce viral load.

[0170] The present invention includes the specific protein immunogens disclosed herein and nucleic acids comprising nucleotide sequences encoding same. The proteins can be expressed, for example, in 293T cells, 293F cells or CHO cells (Liao et al, Virology 353:268-82 (2006))

[0171] Peptides

[0172] The polypeptides of the present invention may be fused to or chemically linked with an appropriate carrier molecule, such as tetanus toxin, MLv gp70, cholera toxin, keyhole limpet haemocyanin or gp120. Alternatively, the polypeptides of the present invention may be inserted by genetic engineering techniques into permissible exposed loops of antigenic proteins.

[0173] Versions of the constructs that are conjugated to carrier protein will be produced for the purposes of comparison. Carrier proteins used in currently licensed vaccines include tetanus toxoid (TT), diphtheria toxoid (DT), CRM.sub.197 (cross-reactive material of diphtheria toxin.sub.197), N. meningitidis outer membrane protein (OMP), and H. influenzae protein D..sup.64 For the initial studies, CRM.sub.197, a non-toxic mutant (G52.fwdarw.D) of diphtheria toxin, will be selected which, unlike TT and DT, does not require chemical detoxification with formaldehyde. Thus, it is a well-defined, homogeneous 63 kD protein with a complete set of free, surface-exposed lysine chains (39 total), devoid of cross-linking, which are available for conjugation with potential haptens. Keyhole limpet hemocyanin (KLH) would be a potential alternative.

[0174] Alternatively the polypeptides of the present invention may be linked to amino acids derived from a T-helper epitope to enhance their immunogenicity.

[0175] A T-helper epitope is a peptide capable of activating a T helper cell. The T-helper epitope may be a human immunodeficiency virus (HIV) T helper epitope e.g. from the C4 domain of HIV gp120. According to one embodiment, the T helper epitope comprises about 16 consecutive residues from the C4 domain (about residues 421 to 436). According to another embodiment, the T-helper sequence is a variation of the above.

[0176] Contemplated T helper epitopes from the C4 domain are described in U.S. Pat. Appl. No. 20030147888, incorporated herein by reference. Other T helper determinants from HIV or from non-HIV proteins can also be used. For example, a further T helper epitope suitable for use in the invention is from HIV gag (e.g., residues 262-278). One such sequence is designated GTH1. Variants of this sequence can also be used.

[0177] Another contemplated T helper epitope is derived from murine HSP60 458-474.

[0178] In some embodiments, a carbohydrate such as the outer membrane protein of pneumococcus, or another carbohydrate or protein with immunogenic, T helper activity can be used.

[0179] The T-helper epitope amino acids may be linked to the V3 portion of the peptides of the present invention using any method known in the art so long as it does not decrease the immunogenic and antigenic properties of the peptide.

[0180] The amino acids of the V3 domain of gp120 are preferably linked C terminal to the amino acids of the T-helper epitope.

[0181] According to one embodiment, the V3 portion of the polypeptide is linked to the T helper epitope via a covalent bond (e.g. a peptide bond). According to another embodiment, the V3 portion of the polypeptide is linked to the T helper epitope via a non-covalent linker. The linkage may be direct or via bonding to an intervening linker element, such as a linker peptide or other chemical moiety, such as an organic polymer.

[0182] Any suitable method for conjugating the V3 portion with the T helper epitope portion are known in the art.

[0183] Natural aromatic amino acids, Trp, Tyr and Phe, may be substituted for synthetic non-natural acid such as Phenylglycine, TIC, naphthylelanine (Nol), ring-methylated derivatives of Phe, halogenated derivatives of Phe or o-methyl-Tyr.

[0184] In addition to the above, the polypeptides of the present invention may also include one or more modified amino acids or one or more non-amino acid moieties (e.g. lipids,

complex carbohydrates etc.). In some embodiments, these non-amino acid moieties are used to multimerize the peptides of the invention.

[0185] Amino acids incorporated in the peptides of the invention could include the 20 naturally occurring amino acids, D- and L-amino acids (stereoisomers); those amino acids often modified post-translationally in vivo, including, for example, hydroxyproline, phosphoserine and phosphothreonine; and other unusual amino acids including, but not limited to, 2-aminoadipic acid, hydroxylysine, isodesmosine, nor-valine, nor-leucine and ornithine.

[0186] Sequences/Clones

[0187] Described herein are nucleic and amino acids sequences of HIV-1 envelopes. The sequences for use as immunogens are in any suitable form. In certain embodiments, the described HIV-1 envelope sequences are gp160s. In certain embodiments, the described HIV-1 envelope sequences are gp120s. Other sequences, for example but not limited to stable SOSIP trimer designs, gp145s, gp140s, both cleaved and uncleaved, gp140 Envs with the deletion of the cleavage (C) site, fusion (F) and immunodominant (I) region in gp41--named as gp140ΔCFI (gp140CFI), gp140 Envs with the deletion of only the cleavage (C) site and fusion (F) domain -- named as gp140ΔCF (gp140CF), gp140 Envs with the deletion of only the cleavage (C)—named gp140ΔC (gp140C) (See e.g. Liao et al. Virology 2006, 353, 268-282), gp150s, gp41s, which are readily derived from the nucleic acid and amino acid gp160 sequences. In certain embodiments the nucleic acid sequences are codon optimized for optimal expression in a host cell, for example a mammalian cell, a rBCG cell or any other suitable expression system.

[0188] An HIV-1 envelope has various structurally defined fragments/forms: gp160; gp140--including cleaved gp140 and uncleaved gp140 (gp140C), gp140CF, or gp140CFI; gp120 and gp41. A skilled artisan appreciates that these fragments/forms are defined not necessarily by their crystal structure, but by their design and bounds within the full length of the gp160 envelope. While the specific consecutive amino acid sequences of envelopes from different strains are different, the bounds and design of these forms are well known and characterized in the art.

[0189] For example, it is well known in the art that during its transport to the cell surface, the gp160 polypeptide is processed and proteolytically cleaved to gp120 and gp41 proteins. Cleavages of gp160 to gp120 and gp41 occurs at a conserved cleavage site "REKR" (SEQ ID NO: 37). *See* Chakrabarti et al. Journal of Virology vol. 76, pp. 5357-5368 (2002) see for

example Figure 1, and Second paragraph in the Introduction on p. 5357; Binley et al. Journal of Virology vol. 76, pp. 2606-2616 (2002) for example at Abstract; Gao et al. Journal of Virology vol. 79, pp. 1154-1163 (2005); Liao et al. Virology vol. 353(2): 268–282 (2006).

[0190] The role of the furin cleavage site was well understood both in terms of improving cleave efficiency, *see* Binley et al. supra, and eliminating cleavage, s*ee* Bosch and Pawlita, Virology 64 (5):2337-2344 (1990); Guo et al. Virology 174: 217-224 (1990); McCune et al. Cell 53:55-67 (1988); Liao et al. J Virol. Apr;87(8):4185-201 (2013).

[0191] Likewise, the design ofgp140 envelope forms is also well known in the art, along with the various specific changes which give rise to the gp140C (uncleaved envelope), gp140CF and gp140CFI forms. Envelope gp140 forms are designed by introducing a stop codon within the gp41 sequence. *See* Chakrabarti et al. at Figure 1.

[0192] Envelope gp140C refers to a gp140 HIV-1 envelope design with a functional deletion of the cleavage (C) site, so that the gp140 envelope is not cleaved at the furin cleavage site. The specification describes cleaved and uncleaved forms, and various furin cleavage site modifications that prevent envelope cleavage are known in the art. In some embodiments of the gp140C form, two of the R residues in and near the furin cleavage site are changed to E, e.g., **R**RVVEREK**R** (SEQ ID NO: 38) is changed to **E**RVVEREK**E** (SEQ ID NO: 39), and is one example of an uncleaved gp140 form. Another example is the gp140C form which has the REKR site (SEQ ID NO: 37) changed to SEKS (SEQ ID NO: 40). *See* supra for references.

[0193] Envelope gp140CF refers to a gp140 HIV-1 envelope design with a deletion of the cleavage (C) site and fusion (F) region. Envelope gp140CFI refers to a gp140 HIV-1 envelope design with a deletion of the cleavage (C) site, fusion (F) and immunodominant (I) region in gp41. *See* Chakrabarti et al. Journal of Virology vol. 76, pp. 5357-5368 (2002) see for example Figure 1, and Second paragraph in the Introduction on p. 5357; Binley et al. Journal of Virology vol. 76, pp. 2606-2616 (2002) for example at Abstract; Gao et al. Journal of Virology vol. 79, pp. 1154-1163 (2005); Liao et al. Virology vol. 353(2): 268–282 (2006).

[0194] In certain embodiments, the envelope design in accordance with the present invention involves deletion of residues (e.g., 5-11, 5, 6, 7, 8, 9, 10, or 11 amino acids) at the N-terminus. For delta N-terminal design, amino acid residues ranging from 4 residues or even fewer to 14 residues or even more are deleted. These residues are between the maturation (signal peptide, usually ending with CXX, X can be any amino acid) and "VPVXXXX…". In one embodiments, CH0848.3.D0949.10.17 Delta11 gp120 is shown as an example in

Figure 3A. In certain embodiments, the invention relates generally to an immunogen, gp160, gp120 or gp140, without an N-terminal Herpes Simplex gD tag substituted for amino acids of the N-terminus of gp120, with an HIV leader sequence (or other leader sequence), and without the original about 4 to about 25, for example 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 amino acids of the N-terminus of the envelope (e.g. gp120). See WO2013/006688, e.g. at pages 10-12, the contents of which publication is hereby incorporated by reference in its entirety.

[0195] The general strategy of deletion of N-terminal amino acids of envelopes results in proteins, for example gpl20s, expressed in mammalian cells that are primarily monomeric, as opposed to dimeric, and, therefore, solves the production and scalability problem of commercial gp120 Env vaccine production. In other embodiments, the amino acid deletions at the N-terminus result in increased immunogenicity of the envelopes.

[0196] In certain embodiments, the invention provides envelope sequences, amino acid sequences and the corresponding nucleic acids, and in which the V3 loop is substituted with the following V3 loop sequence TRPNNNTRKSIRIGPGQTFY ATGDIIGNIRQAH (SEQ ID NO: 41). This substitution of the V3 loop reduced product cleavage and improves protein yield during recombinant protein production in CHO cells.

[0197] Soluble trimers comprising CH848 envelopes are contemplated by the invention and such trimer are contemplated for use in the methods of the invention. Various ways to form soluble envelope trimers are known in the art. *See* e.g. US Pub. 20100041875; US Pub 20110076298; US Pub. 20110250220; WO2016/037154, de Taeye et al. Cell. 2015 Dec 17;163(7):1702-15. doi: 10.1016/j.cell.2015.11.056.; Kwon et al. Nat Struct Mol Biol. 2015 Jul;22(7):522-31. doi: 10.1038/nsmb.3051. Epub 2015 Jun 22; Sharma et al. Cell Rep. 2015 Apr 28;11(4):539-50. doi: 10.1016/j.celrep.2015.03.047. Epub 2015 Apr 16, Kong et al. in Nat Commun. 2016 Jun 28;7:12040. doi: 10.1038/ncomms12040,all of these publications are incorporated by reference in their entirety.

[0198] The invention provides new chimeric designs, for example but not limited to CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 (Figure 41C). Non-limiting examples of trimer sequence designs are shown in Figures 39A-B, 40A-C, and 41A-C, Table 1, Table 3, and Table 4. In some embodiments, the HIV-1 envelope trimer complex incorporated some aspects of the SOSIP HIV-1 trimer design.

[0199] Properties of the trimer complexes of the invention can be determined by any suitable assay used to characterize trimer envelope complexes. Antigenicity of the trimers, for example binding to HIV-1 antibodies, including but not limited to antibodies described in the invention, conformational state of the trimers, i.e., "open" or "closed", immunogenicity can be determined by any suitable assay. For discussion on open versus closed envelope confirmation *see* de Taeye et al. Cell. 2015 Dec 17;163(7):1702-15; Munro et a.; Science 07 Nov 2014: Vol. 346, Issue 6210, pp. 759-763, DOI: 10.1126/science.1254426; Guttman et al., Nature Communications 6, Article number: 6144 doi:10.1038/ncomms7144.

[0200] In certain aspects, the invention provides composition and methods which use a selection of Envs, as gp120s, gp 140s cleaved and uncleaved, gp145s, gp150s and gp160s, as proteins, as monomers or trimers, as DNAs, as RNAs, or any combination thereof, administered as primes and boosts to elicit immune response. Envelopes as proteins could be co-administered with nucleic acid vectors containing Envs to amplify antibody induction. In certain embodiments, the compositions and methods include any immunogenic HIV-1 sequences to give the best coverage for T cell help and cytotoxic T cell induction. In certain embodiments, the compositions and methods include mosaic and/or consensus HIV-1 genes to give the best coverage for T cell help and cytotoxic T cell induction. In certain embodiments, the compositions and methods include mosaic group M and/or consensus genes to give the best coverage for T cell help and cytotoxic T cell induction. In some embodiments, the mosaic genes are any suitable gene from the HIV-1 genome. In some embodiments, the mosaic genes are Env genes, Gag genes, Pol genes, Nef genes, or any combination thereof. See e.g. US Patent No. 7951377. In some embodiments the mosaic genes are bivalent mosaics. In some embodiments the mosaic genes are trivalent. In some embodiments, the mosaic genes are administered in a suitable vector with each immunization with Env gene inserts in a suitable vector and/or as a protein. In some embodiments, the mosaic genes, for example as bivalent mosaic Gag group M consensus genes, are administered in a suitable vector, for example but not limited to HSV2, would be administered with each immunization with Env gene inserts in a suitable vector, for example but not limited to HSV-2.

[0201] In certain aspects the invention provides compositions and methods of Env genetic immunization either alone or with Env proteins to recreate the swarms of evolved viruses that have led to bnAb induction. Nucleotide-based vaccines offer a flexible vector format to

immunize against virtually any protein antigen. Currently, two types of genetic vaccination are available for testing—DNAs and mRNAs.

[0202] In certain aspects the invention contemplates using immunogenic compositions wherein immunogens are delivered as DNA. See Graham BS, Enama ME, Nason MC, Gordon IJ, Peel SA, et al. (2013) DNA Vaccine Delivered by a Needle-Free Injection Device Improves Potency of Priming for Antibody and CD8+ T-Cell Responses after rAd5 Boost in a Randomized Clinical Trial. PLoS ONE 8(4): e59340, page 9. Various technologies for delivery of nucleic acids, as DNA and/or RNA, so as to elicit immune response, both T-cell and humoral responses, are known in the art and are under developments. In certain embodiments, DNA can be delivered as naked DNA. In certain embodiments, DNA is formulated for delivery by a gene gun. In certain embodiments, DNA is administered by electroporation, or by a needle-free injection technologies, for example but not limited to Biojector® device. In certain embodiments, the DNA is inserted in vectors. The DNA is delivered using a suitable vector for expression in mammalian cells. In certain embodiments the nucleic acids encoding the envelopes are optimized for expression. In certain embodiments DNA is optimized, e.g. codon optimized, for expression. In certain embodiments the nucleic acids are optimized for expression in vectors and/or in mammalian cells. In non-limiting embodiments these are bacterially derived vectors, adenovirus based vectors, rAdenovirus (e.g. Barouch DH, et al. Nature Med. 16: 319-23, 2010), recombinant mycobacteria (e.g. rBCG or M smegmatis) (Yu, JS et al. Clinical Vaccine Immunol. 14: 886-093,2007; ibid 13: 1204-11,2006), and recombinant vaccinia type of vectors (Santra S. Nature Med. 16: 324-8, 2010), for example but not limited to ALVAC, replicating (Kibler KV et al., PLoS One 6: e25674, 2011 nov 9.) and non-replicating (Perreau M et al. J. virology 85: 9854-62, 2011) NYVAC, modified vaccinia Ankara (MVA)), adeno-associated virus, Venezuelan equine encephalitis (VEE) replicons, Herpes Simplex Virus vectors, and other suitable vectors.

[0203] In certain aspects the invention contemplates using immunogenic compositions wherein immunogens are delivered as DNA or RNA in suitable formulations. Various technologies which contemplate using DNA or RNA, or may use complexes of nucleic acid molecules and other entities to be used in immunization. In certain embodiments, DNA or RNA is administered as nanoparticles consisting of low dose antigen-encoding DNA formulated with a block copolymer (amphiphilic block copolymer 704). See Cany et al., Journal of Hepatology 2011 vol. 54 j 115–121; Arnaoty et al., Chapter 17 in Yves Bigot (ed.),

Mobile Genetic Elements: Protocols and Genomic Applications, Methods in Molecular Biology, vol. 859, pp293-305 (2012); Arnaoty et al. (2013) Mol Genet Genomics. 2013 Aug;288(7-8):347-63. Nanocarrier technologies called Nanotaxi® for immunogenic macromolecules (DNA, RNA, Protein) delivery are under development. See for example technologies developed by Incellart. In certain embodiments, the nucleic acids, for e.g. mRNAs encoding immunogens of the invention, are delivered by a lipid nanoparticle (LNP) technology. In non-limiting embodiments, the LNPs could comprise four different lipids that could self assemble to 80-100nm size particles.

[0204] In certain aspects the invention contemplates using immunogenic compositions wherein immunogens are delivered as recombinant proteins. Various methods for production and purification of recombinant proteins suitable for use in immunization are known in the art. In certain embodiments recombinant proteins are produced in CHO cells.

[0205] The immunogenic envelopes can also be administered as a protein boost in combination with a variety of nucleic acid envelope primes (e.g., HIV -1 Envs delivered as DNA expressed in viral or bacterial vectors).

[0206] Dosing of proteins and nucleic acids can be readily determined by a skilled artisan. A single dose of nucleic acid can range from a few nanograms (ng) to a few micrograms (μg) or milligram of a single immunogenic nucleic acid. Recombinant protein dose can range from a few μg micrograms to a few hundred micrograms, or milligrams of a single immunogenic polypeptide.

[0207] Administration: The compositions can be formulated with appropriate carriers using known techniques to yield compositions suitable for various routes of administration. In certain embodiments the compositions are delivered via intramascular (IM), via subcutaneous, via intravenous, via nasal, via mucosal routes, or any other suitable route of immunization.

[0208] The compositions can be formulated with appropriate carriers and adjuvants using techniques to yield compositions suitable for immunization. The compositions can include an adjuvant, such as, for example but not limited to, alum, poly IC, MF-59 or other squalene-based adjuvant, ASO1B, or other liposomal based adjuvant suitable for protein or nucleic acid immunization. In certain embodiments, the adjuvant is GSK AS01E adjuvant containing MPL and QS21. This adjuvant has been shown by GSK to be as potent as the similar adjuvant AS01B but to be less reactogenic using HBsAg as vaccine antigen [Leroux-Roels et al., IABS Conference, April 2013,9]. In certain embodiments, TLR agonists are used as

adjuvants. In other embodiment, adjuvants which break immune tolerance are included in the immunogenic compositions.

[0209] In certain embodiments, the compositions are formulated such that the immunoges are comprises in nanoparticles. In some embodiments, these are lipid nanoparticle immunogens. In some embodiments, these are liposomes comprising immunogens. In some embodiments these are lipid nanodiscs. The immunogens could be arranged as particulate, high-density array on liposomes or other particles, for example but not limited to nanoparticles. In non-limiting embodiment, the liposome comprises cholesterol, PC, PE, PA, or any combination thereof. See Alam et al. J Immunol. 2007 Apr 1;178(7):4424-35; Alam et al. J Virol. 2008 Jan;82(1):115-25; Alam et al. Proc Natl Acad Sci U S A. 2009 Dec 1;106(48):20234-9. doi: 10.1073/pnas.0908713106; Dennison et al. J Virol. 2009 Oct;83(19):10211-23. doi: 10.1128/JVI.00571-09; Dennison et al. PLoS One. 2011;6(11):e27824. doi: 10.1371/journal.pone.0027824. In some embodiments, the lipid composition of lipid nanoparticle comprises cholesterol, POPC, sphingomyelin, or any combination thereof. In some embodiments, the lipids could comprise POPC, POPE, DMPA, cholesterol, or any combination thereof. In some embodiments, the ratio is POPC:POPE:DMPA:Cholesterol 45:25:20:1.33. In some embodiments, the protein to lipid ratio is about 1:3000. In some embodiments, the peptide to lipid ratio used provides 50-100 mer V3 peptide units per 100-200nm lipid nanoparticle. In some embodiments the peptide:lipid ratio is 1:100. A skilled artisan can readily determine conditions and lipids to achieve different desired ratios.

[0210] In certain embodiments, the compositions and methods comprise any suitable agent or immune modulation which could modulate mechanisms of host immune tolerance and release of the induced antibodies. In non-limiting embodiments modulation includes PD-1 blockade; T regulatory cell depletion; anti-CD25 antibodies; CD40L hyperstimulation; anti-CTLA4 antibodies; soluble antigen administration, wherein the soluble antigen is designed such that the soluble agent eliminates B cells targeting dominant epitopes, or a combination thereof. In certain embodiments, an immunomodulatory agent is administered in at time and in an amount sufficient for transient modulation of the subject's immune response so as to induce an immune response which comprises broad neutralizing antibodies against HIV-1 envelope. Non-limiting examples of such agents is any one of the agents described herein: e.g. chloroquine (CQ), PTP1B Inhibitor - CAS 765317-72-4 - Calbiochem or MSI 1436 clodronate or any other bisphosphonate; a Foxo1 inhibitor, e.g. 344355 | Foxo1 Inhibitor, AS1842856 - Calbiochem; Gleevac, anti-CD25 antibody, anti-CCR4 Ab, an agent which

binds to a B cell receptor for a dominant HIV-1 envelope epitope, or any combination thereof. In non-limiting embodiments, the modulation includes administering an anti-CTLA4 antibody. Non-limiting examples are ipilimumab and tremelimumab. In certain embodiments, the methods comprise administering a second immunomodulatory agent, wherein the second and first immunomodulatory agents are different.

[0211] Table 1 Summary of some disclosure of proteins and sequences.

	gp160	gp120 delta11	chim.6R.SOSIP.664	chim.6R.DS.SOSIP.664	**CHIM.6R.SOSIP.664V4.1**	**CHIM.6R.SOSIP.664V4.2**
CH848.0949.10.17 aa					Fig 41A and 41C	Fig 41A
One embodiment of a nucleic acid					Fig 41B	Fig 41B
	gp160	**gp120 delta11**	**chim.6R.SOSIP.664**	**chim.6R.DS.SOSIP.664**	**6R.SOSIP.664**	**6R.DS.SOSIP.664**
CH848.0949.10.17 aa	Fig. 39A	Fig. 39A	Fig. 39A	Fig. 39A	Fig. 39A	Fig. 39A
One embodiment of a nucleic acid	Fig. 39B	Fig. 39B	Fig. 39B	Fig. 39B	Fig. 39B	Fig. 39B
	gp160	**gp120 delta11**	**CHIM.6R.SOSIP.664**	**CHIMDS.6R.SOSIP.664**	**CHIM.6R.SOSIP.664V4.1**	**CHIM.6R.SOSIP.664V4.2**
CH848.0836.10.31 aa	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A
One embodiment of a nucleic acid						
CH848.0358.80.06 aa	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A
One embodiment of a nucleic acid						
CH848.1432.5.41 aa	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A
One embodiment of a nucleic acid						
CH848.0526.25.02 aa	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A

One embodiment of a nucleic acid						
CH848.3. D0794.5.41 aa	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A
One embodiment of a nucleic acid						
CH848. 0526.25.09 aa	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A	Fig. 40A
One embodiment of a nucleic acid						
CH848. 1120.10.21 aa	Fig 41A	Fig 41A	Fig 41A	Fig 41A	Fig 41A	Fig 41A
One embodiment of a nucleic acid						
CH848. 1432.05.27 aa	Fig 41A	Fig 41A	Fig 41A	Fig 41A	Fig 41A	Fig 41A
One embodiment of a nucleic acid						
CH848. 0949.10.18 aa	Fig 41A	Fig 41A	Fig 41A	Fig 41A	Fig 41A	Fig 41A
One embodiment of a nucleic acid						
CH848 T/F	Fig 40C					

[0212] It is readily understood that the envelope glycoproteins referenced in various examples and figures comprise a signal/leader sequence. It is well known in the art that HIV-1 envelope glycoprotein is a secretory protein with a signal or leader peptide sequence that is removed during processing and recombinant expression (without removal of the signal peptide, the protein is not secreted). *See* for example Li et al. Control of expression, glycosylation, and secretion of HIV-1 gp120 by homologous and heterologous signal sequences. Virology 204(1):266-78 (1994) ("Li et al. 1994"), at first paragraph, and Li et al. Effects of inefficient cleavage of the signal sequence of HIV-1 gpl20 on its association with calnexin, folding, and intracellular transport. PNAS 93:9606-9611 (1996) ("Li et al. 1996"), at 9609. Any suitable signal sequence could be used. In some embodiments the leader sequence is the endogenous leader sequence. Most of the gp120 and gp160 amino acid

sequences include the endogenous leader sequence. In other non-limiting examples the leaders sequence is human Tissue Plasminogen Activator (TPA) sequence, human CD5 leader sequence (e.g. MPMGSLQPLATLYLLGMLVASVLA (SEQ ID NO: 42)). Most of the chimeric designs include CD5 leader sequence. A skilled artisan appreciates that when used as immunogens, and for example when recombinantly produced, the amino acid sequences of these proteins do not comprise the leader peptide sequences.

[0213] The invention is directed to HIV-1 envelope immunogens which comprises changes in the amino acid sequence of glycosylation sites such that the envelope is partially deglycosylated. In certain embodiments deglycosylation is in the V1 loop of the HIV-1 envelope. In certain embodiments these changes are at positions N133, N138, N156, N301, N332, or any combination thereof. In certain embodiments where the envelope is deglycosylated at positions N133 and/or N138, the envelope is not glycosylated at positions N301 and N332. Position number given with respect to HXB2. Any suitable amino acid change is contemplated so longs as glycosylation at that position is abolished. Non-limiting embodiments include amino acids which are naturally occurring at the respective position in other envelopes and the envelopes are deglycosylated. Non-limiting amino acid changes include change to alanine, or any of the following: N133D, N138T, N301A, N301S, N332A, N332T. Any envelope form, e.g. but not limited to stabilized SOSIP trimer designs, gp140s, etc. could be designed to comprise deglycosylation mutations. In some embodiments, the envelope is CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_N133DN138T. In other embodiments, the envelope is CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_N133DN138T and further comprises N301mut.

[0214] The invention provides compositions comprising these deglycosylated envelopes. The invention provides methods of inducing immune response in a subject comprising administering compositions comprising deglycosylated envelopes. In some embodiments these deglycosylated envelopes are administered as a prime. In some embodiments, the prime could be a nucleic acid encoding a deglycosylated The glycosylated envelopes could also be administered as a boost.

[0215] The invention is described in the following non-limiting examples.

[0216] Nomenclature for trimers: chim.6R.DS.SOSIP.664 is SOSIP.I CHIM.6R.SOSIP.664 is SOSIP.II; CHIM.6R.SOSIP.664V4.1 is SOSIP.III. Additional designs of envelopes

deglycosylated in the V1 loop are also contemplated and covered by the invention. Using the sequence information, annotations and listing of amino acid positions and changes, a skilled artisan can envision additional envelopes based on the sequence of CH848.3.D0949.10.17.

[0217] Non-limiting embodiments include chimeric trimer designs, which could comprise portions of BG505 envelope. Figure 41C shows a non-limiting embodiment of a chimeric trimer design of a 6R.SOSIP664v4.1. Using this annotated sequence which shows the amino acids derived from BG505, a person of skill in the art could design any other chimeric trimer design. Non-limiting embodiments include non-chimeric trimer designs. See for example Figure 54, 39A. Non-limiting embodiments of various deglycosylaton designs, trimer designs, chimeric or non-chimeric designs are summarized in Table 1, Table 3 and Table4. A non-limiting example of a non-SOSIP trimer design is described in Kong et al. in Nat Commun. 2016 Jun 28;7:12040. doi: 10.1038/ncomms12040.

EXAMPLES

[0218] The following specific examples are to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever. Without further elaboration, it is believed that one skilled in the art can, based on the description herein, utilize the present invention to its fullest extent.

Example 1 Staged induction of HIV-1 glycan-dependent broadly neutralizing antibodies

[0219] Stages of V3-glycan neutralizing antibody maturation are identified that explain the long duration required for their development.

[0220] Abstract

[0221] A preventive HIV-1 vaccine should induce HIV-1 specific broadly neutralizing antibodies (bnAbs). However, bnAbs generally require high levels of somatic hypermutation (SHM) to acquire breadth and current vaccine strategies have not been successful in inducing bnAbs. Since bnAbs directed against a glycosylated site adjacent to the third variable loop (V3) of the HIV-1 envelope protein require limited SHM, the V3 glycan epitope is a desirable vaccine target. By studying the cooperation among multiple V3-glycan B-cell lineages and their co-evolution with autologous virus throughout 5 years of infection, we identify here key events in the ontogeny of a V3-glycan bnAb. Two autologous neutralizing antibody lineages selected for virus escape mutations and consequently allowed initiation and affinity maturation of a V3-glycan bnAb lineage. The nucleotide substitution required to initiate the bnAb lineage occurred at a low probability site for activation-induced cytidine deaminase

activity. Cooperation of B-cell lineages and an improbable mutation critical for bnAb activity define the necessary events leading to V3-glycan bnAb development, explain why initiation of V3-glycan bnAbs is rare, and suggest an immunization strategy for inducing V3-glycan bnAbs.

[0222] Introduction

[0223] A vaccine to prevent HIV-1 infection should include immunogens that can induce broadly neutralizing antibodies (bnAbs) (*1, 2*). Of the five major targets for bnAbs, the glycan-rich apex of the HIV-1 envelope (Env) trimer and the base of the third variable loop (V3) are distinguished by the potency of antibodies directed against them (*3-8*). Although these antibodies have less breadth than those directed against the CD4 binding site (CD4bs) or the gp41 membrane-proximal region (MPER), one current goal of vaccine development is to elicit them in combination with other bnAb specificities to achieve broad coverage of transmitted/founder (TF) viruses to prevent HIV-1 integration upon exposure (*1, 2*).

[0224] Mapping the co-evolution of virus and antibody lineages over time informs vaccine design by defining the succession of HIV-1 Env variants that evolve *in vivo* during the course of bnAb development (*9-11*). Antibody lineages with overlapping specificities can influence each other's affinity maturation by selecting for synergistic or antagonistic escape mutations: an example of such "cooperating" lineages is provided by two CD4bs-directed bnAbs that we characterized previously (*11, 12*). Thus, cooperating antibody lineages and their viral escape mutants allow identification of the specific Envs, among the diverse repertoire of mutated Envs that develop within the autologous quasi-species in the infected individual, that stimulate bnAb development and that we wish to mimic in a vaccine.

[0225] Here we describe the co-evolution of an HIV-1 Env quasispecies and a memory B-cell lineage of gp120 V3-glycan directed bnAbs in an acutely infected individual followed over time as broadly neutralizing plasma activity developed. To follow virus evolution, we sequenced ~1,200 HIV-1 *env* genes sampled over a 5 year period; to follow the antibody response, we identified natural heavy- and light-chain pairs of six antibodies from a bnAb lineage, designated DH270, and augmented this lineage by next generation sequencing (NGS). Structural studies defined the position of the DH270 Fab on gp140 Env. We also found two B-cell lineages (DH272 and DH475) with neutralization patterns that likely selected for observed viral escape variants, which in turn stimulated the DH270 lineage to potent neutralization breadth. We found a mutation in the DH270 heavy chain that occurred early in affinity maturation at a disfavored activation-induced cytidine deaminase (AID) site

and that was necessary for bnAb lineage initiation. This improbable mutation can explain the long period of antigenic stimulation needed for initial expansion of the bnAb B-cell lineage in this individual.

[0226] Results

[0227] Three N332 V3-glycan dependent antibody lineages

[0228] We studied an African male from Malawi (CH848) followed from the time of infection to 5 years post-transmission. He was infected with a clade C virus, developed plasma neutralization breadth 3.5 years post-transmission and did not receive antiretroviral therapy during this time as per country treatment guidelines. Reduced plasma neutralization of N332A Env-mutated HIV-1 pseudoviruses and plasma neutralization fingerprinting demonstrated the presence of N332-sensitive broadly neutralizing antibodies (bnAbs) (Fig. 29) (*13*). To identify these antibodies, we studied memory B cells from weeks 205, 232, and 234 post-infection using memory B cell cultures (*14*) and antigen-specific sorting (*15, 16*) and found three N332-sensitive lineages, designated DH270, DH272 and DH475. Their genealogy was augmented by NGS of memory B-cell cDNA from seven time points spanning week 11 to week 240 post-transmission.

[0229] DH270 antibodies were recovered from memory B cells at all three sampling times (weeks 205, 232, and 234) and expansion of the clone did not occur until week 186 (Fig. 1A and Figs. 30A-C). Clonal expansion was concurrent with development of plasma neutralization breadth (Fig. 31), and members of the DH270 lineage also displayed neutralization breadth (Fig. 1B and Fig. 33). The most potent DH270 lineage bnAb (DH270.6) was isolated using a fluorophore-labeled Man_9-V3 glycopeptide that is a mimic of the V3-glycan bnAb epitope (*16*) comprising a discontinuous 30 amino acid residue peptide segment within gp120 V3 and representative of the PGT128-bound minimal epitope described by Pejchal et al. (*17*). The synthetic Man_9-V3 glycopeptide includes high mannose glycan residues (Man_9) each at N301 and N332 and was synthesized using a chemical process similar to that described previously (*18, 19*). V3 glycan bnAb PGT128 affinity for the Man_9-V3 glycopeptide was similar to that of PGT128 for the BG505 SOSIP trimer and Man_9-V3 glycopeptide was therefore an effective affinity bait for isolating of V3 glycan bnAbs (*16*). The lineage derived from a V_H1-2*02 rearrangement that produced a CDRH3 of 20 amino acid residues paired with a light chain encoded by $V_\lambda2$-23 (Figs. 7A-D). Neutralization assays and competition with V3-glycan bnAbs PGT125 and PGT128 confirmed lineage N332-dependence (Figs. 8A-C).

[0230] The DH475 mAb was recovered from memory B cells at week 232 post-transmission by antigen-specific sorting using the fluorophore-labeled Man9-V3 glycopeptide (*16*). The earliest DH475 lineage V_HDJ_H rearrangements were identified with NGS at week 64 post-transmission (Fig. 9A and Figs. 30A-C). Its heavy chain came from V_H3-23*01 (V_H mutation frequency = 10.1%) paired with a V□4-69*02 light chain (Fig. 9B).

[0231] The DH272 mAb came from cultured memory B cells obtained at week 205 post-transmission. DH272 lineage V_HDJ_H rearrangements were detected as early as 19 weeks post-transmission by NGS (Fig. 9A and Figs. 30A-C). The DH272 heavy chain used V_H1-2*02, as did DH270, but it paired with a Vκ 2-30 light chain. Its CDRH3 was 17 amino acids long; V_H mutation was 14.9%. DH272, an IgA isotype, had a 6-nt deletion in FRH3 (Fig. 9B).

[0232] For both DH272 and DH475 lineages, binding to CH848 TF Env gp120 depended on the N332 potential N-linked glycosylation (PNG) site (Fig. 9C). DH272 binding also depended on the N301 PNG site (Fig. 9C). Neither lineage had neutralization breadth (Fig. 9D).

[0233] Evolution of the CH848 virus quasispecies

[0234] We sequenced 1,223 HIV-1 3'-half single-genomes from virus in plasma collected at 26 time points over 246 weeks. Analysis of sequences from the earliest plasma sample indicated that CH848 had been infected with a single, subtype clade C founder virus, ~ 17 (CI 14-19) days prior to screening (Figs. 10 and 11A-B). By week 51 post-infection, 91% of the sequences had acquired an identical, 10-residue deletion in variable loop 1, a region that includes the PGT128-proximal residues 133-135 and 141 (Figs. 12 and 13A-B). Further changes accrued during the ensuing four years, including additional insertions and deletions (indels) in V1, mutations in the ^{324}GDIR^{327} motif (SEQ ID NO: 34) within the V3 loop, deletion or shifting of N-linked glycosylation sites at positions 301 and 322, and mutations at PGT128-proximal positions in V1, V3, and C4, but none of these escape variants went to fixation during 4.5 years of follow-up (Figs. 12-15).

[0235] Simultaneously with the first detection of DH270 lineage antibodies at week 186, four autologous virus clades emerged that defined distinct immunological resistance profiles of the CH848 autologous quasispecies (Fig. 12). The first clade included viruses that shifted the potential N-glycosylation (PNG) site at N332 to 334 (Fig. 12, open circles) and despite this mutation was associated with complete resistance to the DH270 lineage bnAbs, this clade was detected only transiently and at relatively low frequency (7-33% per sample), suggesting

a balance where immune escape was countered by a cost in virological fitness. Conversely, viruses in the other three clades retained N332 and persisted throughout the 5 years of sampling. Viruses in the second clade resisted DH270 lineage neutralization and comprised gp120 Envs that were not bound by the DH270 antibodies (Fig. 12, triangles and Figs. 34-35). The third and fourth clades defined autologous viruses whose gp120 Env was bound by DH270 lineage antibodies but that were either only weakly neutralized by the most mature members of the DH270 lineage (Fig. 12, "X" and Figs. 34-35) or were completely neutralization resistant (Fig. 12, "+" and Figs. 34-35), respectively. Persistence of four divergent clades in the CH848 Env, each with distinctive immunological resistance phenotypes, suggests that multiple distinctive immune escape routes were explored and selected, allowing continuing Env escape mutations to accrue in distinct frameworks and exposing the antibody to Env diversity that may have been necessary to acquire neutralization breadth.

[0236] Ontogeny of DH270 lineage and acquisition of neutralization breadth

[0237] As with other V3-glycan bnAbs, viral neutralization clade specificity and intra-clade breadth of DH270 depended primarily on the frequency of the N332 glycosylation site within the relevant clade (Fig. 2A). Only one of 62 pseudoviruses tested that lacked the PNG site at N332, the B clade virus 5768.04, was sensitive to DH270.5 and DH270.6 (Fig. 33). Across the full M group HIV-1 virus isolate panel used in neutralization assays, the loss of the PNG N332 sites accounted for 70% of the observed neutralization resistance. The circulating recombinant form CRF01 very rarely has this glycosylation site (3% of sequences in the Los Alamos database and 4% (1/23) in our test panel) and DH270 lineage antibodies did not neutralize CRF01 strains (Fig. 2A). As a consequence of the N332 PNG site requirement of V3 glycan bnAbs to neutralize, *in vitro* estimation of neutralizing breadth was impacted simply by the fraction of CRF01 viruses included in the panel. Other V3-glycan bnAbs (10-1074, PGT121 and PGT128) shared this N332 glycan dependency but PGT121 and PGT128 were not as restrictive (Fig. 33) (*5, 6, 8*). Antibody 10-1074 was similar to DH270.6 in that it more strictly required the N332 PNG site, and its neutralization potency correlated with that of DH270.6 (Pearson's $p = 8.0e^{-13}$, $r = 0.63$) (*8*).

[0238] Heterologous breadth and potency of DH270 lineage antibodies increased with accumulation of V_H mutations and although DH270.UCA did not neutralize heterologous HIV-1, five amino-acid substitutions in DH270.IA.4 (four in the heavy chain, one in the light

chain) were sufficient to initiate the bnAb lineage and confer heterologous neutralization (Figs. 2B, C and Figs. 34-35).

[0239] The capacity of the early DH270 lineage members to neutralize heterologous viruses correlated with the presence of short V1 loops (Fig. 2D). As the lineage evolved, it gained capacity to neutralize viruses with longer V1 loops, although with reduced potency (Fig. 2D and Figs. 16A-C). Neutralization of the same virus panel by V3 glycan bnAbs 10-1074, PGT121 and PGT128 followed the same inverse correlation between potency and V1 length (Figs. 16D-F).

[0240] Mutations in the DH270 antibody lineage that initiated heterologous neutralization

[0241] The likelihood of AID-generated somatic mutation in immunoglobulin genes has strong nucleotide-sequence dependence (*20*)(*21*). Moreover, we have recently shown for CD4bs bnAbs that V_H sites of high intrinsic mutability indeed determine many sites of somatic hypermutation (*11*). Like the VRC01-class CD4bs bnAbs, both DH270 and DH272 used V_H1-2*02 although unlike the CD4bs bnAbs, V3 glycan bnAbs in general can use quite disparate V_H gene segments (*3, 17, 22-25*), and antibodies in both lineages have mutations at the same amino acid positions that correspond to sites of intrinsic mutability that we identified in the V_H1-2*02 CD4bs bnAbs (*11*) (Fig. 17A). In HIV-1 negative individuals, we identified 20 aa that frequently mutate from the V_H1-2*02 germline sequence (Fig. 17A). Twelve of these 20 aa were also frequently mutated in DH270 lineage antibodies and 11 of these 12 aa mutated to one of the two most frequent aa mutated in non-HIV-1 V_H1-2*02 sequences (identity conformity). G57R was the lone exception. DH272 mutated in 6 of these 12 positions and CD4bs bnAb VRC01 mutated in 11 out of 12 positions (Fig. 17A).

[0242] Presence of the canonical V_H1-2*02 allele in individual CH848 was confirmed by genomic DNA sequencing (Fig. 17B). Four nucleotide changes in the DH270 UCA conferred heterologous neutralization activity to the next intermediate antibody (IA4). The G92A and G102A nucleotide mutations in DH270.IA4 (and in DH272) occurred at "canonical" AID hotspots (DGYW) and encoded amino acid substitutions G31D and M34I, respectively (Fig. 3A). G164C (G164A for DH272) was in a "non-canonical" AID hotspot with a comparable level of mutability (*20*) and encoded the S55T (N for DH272) substitution (Fig. 3A). In contrast, the G169C mutation in DH270.IA4, which encoded the G57R amino acid mutation, occurred at a site with a very low predicted level of mutability (*20*), generated a canonical cold spot (GTC) and disrupted the overlapping AID hotspot at G170 within the same codon, which was instead used by DH272 and resulted in the G57V substitution (Fig.

3A). Thus, while both the DH270 bnAb and DH272 autologous neutralizing lineages had mutations at Gly57, the substitution in the DH270 lineage (G57R) was an improbable event whereas the substitution (G57V) in the DH272 lineage was much more probable.

[0243] The G31D and M31I substitutions that occurred in AID hotspots became fixed in both lineages and S55T eventually became prevalent also in the DH272 lineage (Fig. 3B). By week 111 post-transmission, all DH272 lineage V_HDJ_H transcripts sequenced by NGS harbored a mutation in the Gly57 codon, which resulted in the predominance of an encoded aspartic acid (Fig. 3B). In contrast, only 6/758 (0.8%) DH270 lineage transcripts isolated 186 weeks post-transmission had Val57 or Asp57; 48/758 (6.3%) retained Gly57, while over two-thirds, 514/758 (67.8%), had G57R (Fig. 3B).

[0244] Since the rare G169C nucleotide mutation in DH270.IA4 introduced a cold spot and simultaneously disrupted the overlapping AID hotspot, it had a high probability once it occurred of being maintained, and indeed it was present in 523/758 (68%) DH270 lineage V_H sequences identified with NGS at week 186 post-transmission (Fig. 3C).

[0245] Reversion of Arg57 to Gly abrogated DH270.IA4 neutralization of autologous and heterologous HIV-1 isolates (Fig. 3D). A DH270.IA4 R57V mutant, with the base change that would have occurred had the overlapping AID hotspot been used, also greatly reduced DH270.IA4 neutralization, confirming that Arg57, rather than the absence of Gly57 was responsible for the acquired neutralizing activity (Fig. 3D). Finally, the DH270.UCA G57R mutant neutralized both autologous and heterologous viruses, confirming that G57R alone could confer neutralizing activity on the DH270 germline antibody (Fig. 3E). Thus, the improbable G169C mutation conferred reactivity against autologous virus and initiated acquisition of heterologous neutralization breadth in the DH270 lineage.

[0246] A search for an Env that might select for the critical G57R mutation in DH270 UCA or IA4-like antibodies yielded Env 10.17 from week 135 of infection (Figs. 18A, B), which derived from the only autologous virus Env that DH270.IA4 could bind. DH270.IA4 binding to Env 10.17 depended on presence of Arg57 and reversion of R57G was necessary and sufficient to abrogate binding (Fig. 18A). Also, binding to Env 10.17 was acquired by DH270.UCA upon introduction of the G57R mutation (Fig. 18B).

[0247] Autologous neutralizing antibody lineages that cooperated with DH270

[0248] Evidence for functional interaction among the three N332-dependent lineages came from the respective neutralization profiles against a panel of 90 autologous viruses from transmitted/founder to week 240 post-transmission (Fig. 4A and Figs. 34-35). Both DH475

and DH272 neutralized autologous viruses isolated during the first year of infection that were resistant to most DH270 lineage antibodies (only DH270.IA1 and DH270.4 neutralized weakly) (Fig. 4A). DH475 neutralized viruses from week 15 through week 39 and DH272 neutralized the CH848 transmitted/founder and all viruses isolated up to week 51, when viruses that resisted DH475 and DH272 became strongly sensitive to the more mature antibodies in the DH270 lineage (V_H nt mutation frequency ≥ 5.6%) (Fig. 4A).

[0249] The identification of specific mutations implicated in the switch of virus sensitivity was complicated by the high levels of mutations accumulated by virus Env over time (Fig. 19 and Fig. 36). We identified virus signatures that defined the DH270.1 and DH272/DH475 immunotypes and introduced four of them, in various combinations, into the DH272/DH475-sensitive virus that was closest in sequence to the DH270.1-sensitive immunotype: a 10 amino-acid residue deletion in V1 (Δ134-143); a D185N mutation in V2, which introduced an N-linked glycosylation site; an N413Y mutation in V4, which disrupted an N-linked glycosylation site; and a 2 amino-acid residue deletion (Δ4. 63-464) in V5.

[0250] The large V1 deletion was critical for DH270.1 neutralization, with smaller contributions from the other changes; the V1 deletion increased virus resistance to DH475 (3.5-fold increase). V1-loop-mediated resistance to DH475 neutralization increased further when combined with the Δ463-464 V5 deletion (5-fold increase) (Fig. 4B).

[0251] The V1 loop of the transmitted/founder virus (34 residues) was longer than the average V1 length of 28 residues (range 11 to 64) of HIV-1 Env sequences found in the Los Alamos Sequence Database (*26*). As we found for heterologous neutralization, DH270 lineage antibodies acquired the ability to neutralize larger fractions of autologous viruses as maturation progressed by gaining activity for viruses with longer V1 loops, although at the expense of lower potency (Figs. 20A-C). This correlation was less clear for gp120 binding (Figs. 20D-F), however, suggesting that the V1 loop-length dependency of V3 glycan bnAb neutralization has a conformational component. Thus, DH475 cooperated with the DH270 bnAb lineage by selecting viral escape mutants sensitive to bnAb lineage members.

[0252] For DH272, the viral variants that we made did not implicate a specific cooperating escape mutation. The Δ134-143 (V1 deletion) mutated virus remained sensitive to DH272 neutralization; both combinations of the V1 deletion in our panel that were resistant to DH272 and sensitive to DH270.1 included D185N, which on its own also caused DH272 resistance but did not lead to DH270.1 sensitivity (Fig. 4C). Thus, we have suggestive, but

not definitive, evidence that DH272 also participated in selecting escape mutants for the DH270 bnAb lineage.

[0253] Structure of DH270 lineage members

[0254] We determined crystal structures for the single-chain variable fragment of DH270.1 and the Fabs of DH270.UCA3, DH270.3, DH270.5 and DH270.6, as well as for DH272 (Fig. 32). Because of uncertainty in the inferred sequence of the germline precursor (Figs. 21A, B), we also determined the structure of DH270.UCA1, which has a somewhat differently configured CDR H3 loop (Fig. 21C); reconfiguration of this loop during early affinity maturation could account for the observed increase with respect to the UCA in heterologous neutralization by several intermediates. The variable domains of the DH270 antibodies superposed well, indicating that affinity maturation modulated the antibody-antigen interface without substantially changing the antibody conformation (Fig. 5A). Mutations accumulated at different positions for DH270 lineage bnAbs in distinct branches (Fig. 22), possibly accounting for their distinct neutralization properties. DH272 had a CDRH3 configured differently from that of DH270 lineage members and a significantly longer CDRL1 (Fig. 5B), compatible with their distinct neutralization profiles.

[0255] We also compared the structures of DH270 lineage members with those of other N332-dependent bnAbs. All appear to have one long CDR loop that can extend through the network of glycans on the surface of the gp120 subunit and contact the "shielded" protein surface. The lateral surfaces of the Fab variable module can then interact with the reconfigured or displaced glycans to either side. PGT128 has a long CDRH2 (Fig. 5C), in which a 6-residue insertion is critical for neutralization breadth and potency (*5, 17*). PGT124 has a shorter and differently configured CDR H2 loop, but a long CDR H3 instead (Fig. 5D) (*27*).

[0256] Structure of the DH270 – HIV Env Complex

[0257] We determined a three-dimensional (3D) image reconstruction, from negative-stain electron microscopy (EM), of the DH270.1 Fab bound with a gp140 trimer (92Br SOSIP.664) (Figs. 5E, F and Figs. 23A-B). The three DH270.1 Fabs project laterally, with their axes nearly normal to the threefold of gp140, in a distinctly more "horizontal" orientation than seen for PGT124, PGT135 and PGT128 (Figs. 5G, H and Fig. 24). This orientational difference is consistent with differences between DH270 and PGT124 or PGT128 in the lengths and configurations of their CDR loops, which required an alternative DH270 bnAb position when docked onto the surface of the Env trimer. We docked the BG505 SOSIP

coordinates (*28*) and the Fab into the EM reconstruction, and further constrained the EM reconstruction image by the observed effects of BG505 SOSIP mutations in the gp140 surface image (Figs. 23A-B and Figs. 25A-B). Asp325 was essential for binding DH270.1since it is a potential partner for Arg57 on the Fab. Mutating Asp321 led to a modest loss in affinity; R327A had no effect (Fig. 26A-C). These data further distinguish DH270 from PGT124 and PGT128. Mutating W101, Y105, D107, D115, Y116 or W117 in DH270.1 individually to alanine substantially reduced binding to the SOSIP trimer, as did pairwise mutation to alanines of S106 and S109. The effects of these mutations illustrate the critical role of the CDRH3 loop in binding with HIV-1 Env (Figs. 26A-C).

[0258] DH270 UCA binding

[0259] The DH270 UCA did not bind to any of the 120 CH848 autologous gp120 Env glycoproteins isolated from time of infection to 245 weeks post-infection, including the TF Env (Fig. 6A). DH270 UCA, as well as maturation intermediate antibodies, also did not recognize free glycans or cell surface membrane expressed gp160 trimers (Fig. 6B). Conversely, the DH270 UCA bound to the Man_9-V3 synthetic glycopeptide mimic of the V3-glycan bnAb gp120 epitope (Fig. 27A) and also bound to the aglycone form of the same peptide (Fig. 27B). Similarly, the early intermediate antibodies (IA4, IA3, IA2) each bound to both the Man_9-V3 glycopeptide and its aglycone form, and their binding was stronger to the aglycone V3 peptide than to the Man_9-V3 glycopeptide (Fig. 27B). Overall, DH270 UCA and early intermediate antibodies binding to the Man_9-V3 glycopeptide was low (>10μM) (Fig. 27A). DH270.1 (V_H nt mutation frequency: 5.6%) bound the glycopeptide with higher affinity than did the aglycone ($K_{d,glycopeptide}$ = 331nM) (Figs. 27A, B) and, as mutations accumulated, binding of the Man_9-V3 glycopeptide also increased, culminating in a K_d of 188 nM in the most potent bnAb, DH270.6, which did not bind to the aglycone-V3 peptide (Figs. 27A, B). Thus, both the Man_9-V3 glycopeptide and the aglycone-V3 peptide bound to the DH270 UCA, and antibody binding was independent of glycans until the DH270 lineage had acquired a nucleotide mutation frequency of ~6%.

[0260] Discussion

[0261] We can reconstruct from the data presented here a plausible series of events during the development of a V3-glycan bnAb in a natural infection. The DH272 and DH475 lineages neutralized the autologous TF and early viruses, and the resulting escape viruses were neutralized by the DH270 lineage. In particular, V1 deletions were necessary for neutralization of all but the most mature DH270 lineage antibodies. DH475 (and possibly

DH272) escape variants stimulated DH270 affinity maturation, including both somatic mutations at sites of intrinsic mutability (*11*) and a crucial, improbable mutation at an AID cold spot within CDRH2 (G57R). The G57R mutation initiated expansion of the DH270 bnAb lineage. The low probability of this heterologous neutralization-conferring mutation and the complex lineage interactions that occurred is one explanation for why it took 4.5 years for the DH270 lineage to expand.

[0262] The CH848 viral population underwent a transition from a long V1 loop in the TF (34 residues) to short loops (16-17 residues) when escaping DH272/DH475 and facilitating expansion of DH270, to restoration of longer V1 loops later in infection as resistance to DH270 intermediates developed. Later DH270 antibodies adapted to viruses with longer V1 loops, allowing recognition of a broader spectrum of Envs and enhancing breadth. DH270.6 could neutralize heterologous viruses regardless of V1 loop length, but viruses with long loops tended to be less sensitive to it. Association of long V1 loops with reduced sensitivity was evident for three other V3 glycan bnAbs isolated from other individuals and may be a general feature of this class.

[0263] The V1 loop deletions in CH848 autologous virus removed the PNG site at position 137. While the hypervariable nature of the V1 loop (which evolves by insertion and deletion, resulting in extreme length heterogeneity, as well as extreme variation in number of PNG sites) complicates the interpretation of direct comparisons among unrelated HIV-1 strains, it is worth noting that a PNG in this region specified as N137 was shown to be important for regulating affinity maturation of the PGT121 V3 glycan bnAb family, with some members of the lineage evolving to bind (PGT121-123) and others (PGT124) to accommodate or avoid this glycan (*29*).

[0264] Since we cannot foresee the susceptibility to a particular bnAb lineage of each specific potential transmitted/founder virus to which vaccine recipients will be exposed, it will be important for a vaccine to induce bnAbs against multiple epitopes on the HIV-1 Env to minimize transmitted/founder virus escape (*30, 31*). In particular, induction of bnAb specificities beyond the HIV-1 V3 glycan epitope is critical for use in Asian populations where CRF01 strains, which lack for the most part the N332 PNG required for efficient neutralization by V3 glycan bnAbs, is frequently observed.

[0265] Regarding what might have stimulated the UCA of the DH270 bnAb lineage, the absence of detectable binding to the CH848 TF Env raised at least two possibilities. One is that the lineage arose at the end of year 1, either from a primary response to viruses present at

that time (*e.g.*, with deletions in V1-V2) or from subversion of an antibody lineage initially elicited by some other antigen. The other is that some altered form of the CH848 TF envelope protein (*e.g.* shed gp120, or a fragment of it) exposed the V3 loop and the N301 and N332 glycans in a way that bound and stimulated the germline BCR, even though the native CH848 TF Env did not. Our findings suggest that a denatured, fragmented or otherwise modified form of Env may have initiated the DH270 lineage. We cannot exclude that the DH270 UCA could not bind to autologous Env as an IgG but could potentially be triggered as an IgM B cell receptor (BCR) on a cell surface.

[0266] It will be important to define how often an improbable mutation such as G57R determines the time it takes for a bnAb lineage in an HIV-1 infected individual to develop, and how many of the accompanying mutations are necessary for potency or breadth rather than being non-essential mutations at AID mutational hotspots (*11, 32*). Mutations of the latter type might condition the outcome or modulate the impact of a key, improbable mutation, without contributing directly to affinity. Should the occurrence of an unlikely mutation be rate-limiting for breadth or potency in many other cases, a program of rational immunogen design will need to focus on modified envelopes most likely to select very strongly for improbable yet critical antibody nucleotide changes

[0267] The following proposal for a strategy to induce V3 glycan bnAbs recreates the events that led to bnAb induction in CH848: start by priming with a ligand that binds the bnAb UCA, such as the synthetic glycopeptide mimic of the V3-glycan bnAb gp120 epitope, then boost with an Env that can select G57R CDR H2 mutants, followed by Envs with progressive V1 lengths (Fig. 28). We hypothesize that more direct targeting of V3-glycan UCAs and intermediate antibodies can accelerate the time of V3-glycan bnAb development in the setting of vaccination.

[0268] A limitation of this approach is that the selection of immunogens was based on the analysis of a single lineage from a single individual and how frequently DH270-like lineages are present in the general population is unknown. Finally, our study describes a general strategy for the design of vaccine immunogens that can select specific antibody mutations thereby directing antibody lineage maturation pathways.

[0269] MATERIAL AND METHODS

[0270] Study Design. The CH848 donor, from which the DH270, DH272 and DH475 antibody lineages were isolated, is an African male enrolled in the CHAVI001 acute HIV-1 infection cohort (*33*) and followed for 5 years, after which he started antiretroviral therapy.

During this time viral load ranged from 8,927 to 442,749 copies/ml (median = 61,064 copies/ml), and CD4 counts ranged from 288 to 624 cells/mm^3 (median = 350 cells/ mm^3). The time of infection was estimated by analyzing the sequence diversity in the first available sample using the Poisson Fitter tool as described in (*10*). Results were consistent with a single founder virus establishing the infection (*34*).

[0271] MAbs DH270.1 and DH270.3 were isolated from cultured memory B cells isolated 205 weeks post-transmission (*14*). DH270.6 and DH475 mAbs were isolated from Man9-V3 glycopeptide-specific memory B cells collected 232 and 234 weeks post-transmission, respectively, using direct sorting. DH270.2, DH270.4 and DH270.5 mAbs were isolated from memory B cells collected 232 weeks post-transmission that bound to Consensus C gp120 Env but not to Consensus C N332A gp120 Env using direct sorting

[0272] Statistical Analyses. Statistical analysis was performed using R. The specific tests used to determine significance are reported for each instance in the text.

[0273] Flow Cytometry, Memory B Cell Cultures and mAb Isolation

[0274] A total of 30,700 memory B cells from individual CH848 were isolated from PBMC collected 205 weeks post-transmission using magnetic-activated cell sorting as described in (14). Memory B cells were cultured at limiting dilution at a calculated concentration of 2 cells/well for 2 weeks as described in (11) using irradiated CD40L L cells (7,500 cGy) as feeder cells at a concentration of 5,000 cells/well; culture medium was refreshed 7 days after plating. Cell culture supernatants were screened for neutralization of autologous CH848.TF virus using the tzm-bl neutralization assay (14) and for binding to CH848.TF gp120 Env, CH848.TF gp140 Env, Consensus C gp120 Env and consensus C N332A gp120 Env. Concurrently, cells from each culture were transferred in RNAlater (Qiagen) and stored at -80°C until functional assays were completed.

[0275] MAbs DH270.1 and DH270.3 were isolated from cultures that bound to CH848.TF gp120 Env and Consensus C gp120 but did not bind to C N332A gp120 Env. DH272 was isolated from a culture that neutralized 99% CH848.TF virus infectivity. DH272 dependency to N332-linked glycans was first detected on the transiently transfected recombinant antibody tested at higher concentration and confirmed in the purified recombinant antibody. From the stored RNAlater samples, mRNA of cells from these cultures was extracted and retrotranscribed as previously described (14).

[0276] DH270.6 and DH475 mAbs were isolated from Man9-V3 glycopeptide-specific memory B cells collected 232 and 234 weeks post-transmission, respectively, using direct

sorting (16). Briefly, biotinylated Man9–V3 peptides were tetramerized via streptavidin that was conjugated with either AlexaFluor 647 (AF647; ThermoScientific) or Brilliant Violet 421 (BV421) (Biolegend) dyes. Peptide tetramer quality following conjugation was assessed by flow cytometry to a panel of well-characterized HIV-1 V3 glycan antibodies (PGT128, and 2G12) and linear V3 antibodies (F39F) attached to polymer beads. PBMCs from donor CH848 were stained with LIVE/DEAD Fixable Aqua Stain (ThermoScientific), anti-human IgM (FITC), CD3 (PE-Cy5), CD235a (PE-Cy5), CD19 (APC-Cy7), and CD27 (PE-Cy7) (BD Biosciences); anti-human antibodies against IgD (PE); anti-human antibodies against CD10 (ECD), CD38 (APC-AF700), CD19 (APC-Cy7), CD16 (BV570), CD14 (BV605) (Biolegend); and Man9GlcNac2 V3 tetramer in both AF647 and BV421. PBMCs that were Aqua Stain -, CD14-, CD16-, CD3-, CD235a-, positive for CD19+, and negative for surface IgD were defined as memory B cells; these cells were then gated for Man9–V3+ positivity in both AF647 and BV421, and were single-cell sorted using a BD FACS Aria II into 96-well plates containing 20μl of reverse transcriptase buffer (RT).

[0277] DH270.2, DH270.4 and DH270.5 mAbs were isolated from memory B cells collected 232 weeks post-transmission that bound to Consensus C gp120 Env but not to Consensus C N332A gp120 Env using direct sorting. Reagents were made using biotinylated Consensus C gp120 Env and Consensus C N332A gp120 Env by reaction with streptavidin that was conjugated with either AlexaFluor 647 (AF647; ThermoScientific) or Brilliant Violet 421 (BV421) (Biolegend) dyes, respectively. Env tetramer quality following conjugation was assessed by flow cytometry to a panel of well-characterized HIV-1 V3 glycan antibodies (PGT128, and 2G12) and linear V3 antibodies (F39F) attached to polymer beads. PBMCs were stained as outlined for DH475 and DH270.6, however these cells were then gated for Consensus C gp120 positivity and Consensus C N332A gp120 negativity in AF647 and BV421, respectively, and were single cell sorted and processed as outlined for DH475 and DH270.6.

[0278] For all antibodies, cDNA synthesis, PCR amplification, sequencing and V(D)J rearrangement analysis were conducted as previously described (11). Reported mutation frequency is calculated as frequency of nucleotide mutations in the V gene region of antibody sequence. CDRH3 lengths reported are defined as the number of residues after the invariant Cys in FR3 and before the invariant Trp in FR4.

[0279] Antibody production

[0280] Immunoglobulin genes of mAbs DH270.1 through DH270.6, DH272 and DH475 were amplified from RNA from isolated cells, expression cassettes made, and mAbs expressed as described (12, 14). Inference of unmutated common ancestor (UCA) and intermediate antibodies DH270.IA1 through DH270.IA4 was conducted using methods previously described (36).

[0281] Heavy chain plasmids were co-transfected with appropriate light chain plasmids at an equal ratio in Expi 293 cells using ExpiFectamine 293 transfection reagents (Thermo Fisher Scientific) according to the manufacturer's protocols. We used the enhancer provided with the kit, transfected cultures were incubated at 37°C 8% CO2 for 2-6 days, harvested, concentrated and incubated overnight with Protein A beads at 4°C on a rotating shaker before loading the bead mixture in columns for purification; following PBS/NaCl wash, eluate was neutralized with trizma hydrochloride and antibody concentration was determined by Nanodrop. Purified antibodies were tested in SDS-Page Coomassie and western blots, and stored at 4°C.

[0282] Next-generation sequencing

[0283] PBMC-extracted RNA from weeks 11, 19, 64, 111, 160, 186, and 240 post-infection were used to generate cDNA amplicons for next-generation sequencing (Illumina Miseq) as described previously (35). Briefly, RNA isolated from PBMCs was separated into two equal aliquots before cDNA production; cDNA amplification and NGS were performed on both aliquots as independent samples (denoted A and B). Reverse transcription (RT) was carried out using human IgG, IgA, IgM, Igκ and Igλ primers as previously described (12). After cDNA synthesis, IgG isotype IGHV1 and IGHV3 genes were amplified separately from weeks 11, 19, 64, 111, 160, and 186. IGHV1-IGHV6 genes were amplified at week 240. A second PCR step was performed to add Nextera index sequencing adapters (Illumina) and libraries were purified by gel extraction (Qiagen) and quantified by quantitative PCR using the KAPA SYBR FAST qPCR kit (KAPA Biosystems). Each replicate library was sequencing using the Illumina Miseq V3 2x 300bp kit.

[0284] NGS reads were computationally processed and analyzed as previously described (35). Briefly, forward and reverse reads were merged with FLASH with average read length and fragment read length parameters set to 450 and 300, respectively. Reads were quality filtered using FASTX (http://hannonlab.cshl.edu/fastx_toolkit/) for sequences with a minimum of 50 percent of bases with a Phred quality score of 20 or greater (corresponding to 99% base call accuracy). Primer sequences were discarded and only unique nucleotide

sequences were retained. To mitigate errors introduced during PCR amplification, reads detected in sample A and B with identical nucleotide VHDJH rearrangement sequences were delineated as replicated sequences. The total number of unique reads per sample and total number of replicated sequences ("Overlap") across samples for each time point is listed in Fig. 30. We used replicated sequences to define presence of antibody clonal lineages at any time-point.

[0285] We identified clonally-related sequences to DH270, DH272 and DH475 from the longitudinal NGS datasets by the following procedure. First, the CDR H3 of the probe-identified clonal parent sequence was BLASTed (E-value cutoff =.01) against the pooled sample A and B sequence sets at each time point to get a candidate set of putative clonal members ("candidate set"). Next we identified replicated sequences across samples A and B in the candidate set. We then performed a clonal kinship test with the Cloanalyst software package (computationalimmunology/research/software/) as previously described (35) on replicated sequences. Clonally-related sequences within Sample A and B (including non-replicated sequences) were identified by performing the same clonal kinship test with Cloanalyst on the candidate set prior to identifying replicated sequences.

[0286] Clonal lineage reconstruction was performed on the NGS replicated sequences and probe-identified sequences of each clone using the Cloanalyst software package. A maximum of 100 sequences were used as input for inferring phylogenetic trees of clonal lineages. Clonal sequence sets were sub-sampled down to 100 sequences by collapsing to one sequence within a 2 or 9 base pair difference radius for the DH272 and DH270 clones, respectively.

[0287] The pre-vaccination NGS samples that were analyzed in Fig. 17A were obtained from HIV-1 uninfected participants of the HVTN082 and HVTN204 trials as previously described (35).

[0288] Sequence Analysis of Antibody Clonal Lineages

[0289] Unmutated common ancestors (UCA) and ancestral intermediate sequences were computationally inferred with the Cloanalyst software package. Cloanalyst uses Bayesian inference methods to infer the full unmutated V(D)J rearrangement thereby including a predicted unmutated CDR3 sequence. For lineage reconstructions when only cultured or sorted sequences were used as input, the heavy and light chain pairing relationship was retained during the inference of ancestral sequences. UCA inferences were performed each time a new member of the DH270 clonal lineage was experimentally isolated and thus several

versions of the DH270 UCA were produced and tested. UCA1 and UCA3 were used for structural determination. UCA4 (referred to as DH270.UCA throughout the text), which was inferred using the most observed DH270 clonal members and had the lowest uncertainty of UCAs inferred (as quantified by the sum of the error probability over all base positions in the sequence), was used for binding and neutralization studies. Subsequently, the DH270 UCA was also re-inferred when NGS data became available. We applied a bootstrapping procedure to infer the UCA with the NGS data included, resampling clonal lineage trees 10 times with 100 input NGS sequences each. The UCA4 amino acid sequence was recapitulated by 7 out of 10 UCA inferences of the resampled NGS trees confirming support for UCA4.

[0290] Each inference of V(D)J calls is associated with a probability. The probability of the DH270 lineage to use the VH1-2 family gene was 99.99% and that of using allele 02 (VH1-2*02) was 98.26%. Therefore, there was a 0.01% probability that the family was incorrectly identified and a 1.74% probability that the allele was incorrectly identified. Therefore, we sequenced genomic DNA of individual CH848. As previously reported, positional conformity is defined as sharing a mutation at the same position in the V gene segment and identity conformity as sharing the same amino acid substitution at the same position (11).

[0291] We refer to the widely established AID hot and cold spots (respectively WRCY and SYC and their reverse-complements) as "canonical" and to other hot and cold spots defined by Yaari et al. as "non-canonical" (20, 37-39).

[0292] Sequencing of germline variable region from genomic DNA

[0293] Genomic DNA was isolated from donor CH848 from PBMCs 3 weeks after infection (QIAmp DNA Blood mini kit; Qiagen). IGVH1-2 and IGVL2-23 sequences were amplified using 2 independent primer sets by PCR. To ensure amplification of non-rearranged variable sequences, both primer sets reverse primers aligned to sequences present in the non-coding genomic DNA downstream the V-recombination site. The forward primer for set 1 resided in the IGVH1-2 and IGVL2-23 leader sequences and upstream of the leader in set 2. The PCR fragments were cloned into a pcDNA2.1 (TOPO-TA kit; Life technologies) and transformed into bacteria for sequencing of individual colonies. The following primers were used: VH1-2_1_S: tcctcttcttggtggcagcag (SEQ ID NO: 43); VH1-2_2_S: tacagatctgtcctgtgccct (SEQ ID NO: 44); VH1-2_1_tmAS: ttctcagccccagcacagctg (SEQ ID NO: 45); VH1-2_2_TmAS: gggtggcagagtgagactctgtcaca (SEQ ID NO: 46); VL2-23_2_S: agaggagcccaggatgctgat (SEQ ID NO: 47); VL2-23_1_S: actctcctcactcaggacaca (SEQ ID NO: 48); VL2-23_1_AS:

tctcaaggccgcgctgcagca (SEQ ID NO: 49); VL2-23_2_AS: agctgtccctgtcctggatgg (SEQ ID NO: 50).

[0294] We identified two variants of VH1-2*02: the canonical sequence and a variant that encoded a VH that differed by 9 amino acids. Of these 9 amino acids, only 1 was shared among DH270 antibodies whereas 8 amino acids were not represented in DH270 lineage antibodies (Fig. 17B). The VH1-2*02 variant isolated from genomic DNA did not encode an arginine at position 57. We conclude that between the two variants of VH1-2*02 identified from genomic DNA from this individual, the DH270 lineage is likely derived from the canonical VH1-2*02 sequence.

[0295] Direct binding ELISA

[0296] Direct-binding ELISAs were performed as described (11). Briefly, 384-well plates were blocked for 1 h at room temperature (RT) or overnight at 4°C (both procedures were previously validated); primary purified antibodies were tested at a starting concentrations of 100μg/ml, serially three-fold diluted and incubated for 1 h at RT; HRP-conjugated human IgG antibody was added at optimized concentration of 1:30,000 in assay diluent for 1 hour and developed using TMB substrate; plates were read at 450 nm in a SpectraMax 384 PLUS reader (Molecular Devices, Sunnyvale, CA); results are reported as logarithm area under the curve (LogAUC) unless otherwise noted.

[0297] For biotinylated avi-tagged antigens, plates were coated with streptavidin (2μg/ml); blocked plates were stored at -20°C until used and biotinylated avi-tagged antigens were added at 2 μg/ml for 30 minutes at RT.

[0298] Competition ELISAs were performed using 10μl of primary purified monoclonal antibody, starting at 100μg/ml and diluted in a two-fold concentration, incubated for 1 h at RT. Ten μl of biotinylated target Mab was added at the EC50 determined by a direct binding of biotinylated-Mab for one hour at RT. After background subtractions, percent inhibition was calculated as follows: 100-(test Ab triplicate mean/no inhibition control mean)*100.

[0299] Assessment of virus neutralization

[0300] Antibody and plasma neutralization was measured in TZM-bl cell-based assays. Neutralization breadth of DH270.1, DH270.5 and DH270.6 was assessed using the 384-well plate declination of the assay using an updated panel of 207 geographically and genetically diverse Env-pseudoviruses representing the major circulating genetic subtypes and recombinant forms as described (40). The data were calculated as a reduction in luminescence units compared with control wells, and reported as IC50 in μg/ml.

[0301] Single genome sequencing and pseudovirus production

[0302] 3' half genome single genome sequencing of HIV-1 from longitudinally collected plasma was performed as previously described (41, 42). Sequence alignment was performed using ClustalW (version 2.11) and was adjusted manually using Geneious 8 (version 8.1.6). Env amino acid sequences were then aligned and evaluated for sites under selection using code derived from the Longitudinal Antigenic Sequences and Sites from Intra-host Evolution (LASSIE) tool (43). Using both LASSIE-based analysis and visual inspection, 100 representative env genes were selected for pseudovirus production. CMV promoter-ligated env genes were prepared and used to generate pseudotyped viruses as previously described (44).

[0303] Generation of cell surface-expressed CH848 Env trimer CHO cell line

[0304] The membrane-anchored CH848 TF Env trimer was expressed in CHO-S cells. Briefly, the CH848 env sequence was codon-optimized and cloned into an HIV-1-based lentiviral vector. A heterologous signal sequence from CD5 was inserted replacing that of the HIV-1 Env. The proteolytic cleavage site between gp120 and gp41 was altered, substituting serine residues for Arg508 and Arg511, the tyrosine at residues 712 was changed to alanine (Y712A), and the cytoplasmic tail was truncated by replacing the Lys808 codon with a sequence encoding (Gly)3 (His)6 (SEQ ID NO: 51) followed immediately by a TAA stop codon. This env-containing sequences was inserted into the vector immediately downstream of the tetracycline (tet)-responsive element (TRE), and upstream of an internal ribosome entry site (IRES) and a contiguous puromycin (puro)-T2A-EGFP open reading frame (generating K4831), as described previously for the JRFL and CH505 Envs (45).

[0305] CHO-S cells (Invitrogen) modified to constitutively express the reverse tet transactivator (rtTA) were transduced with packaged vesicular stomatitis virus (VSV) G glycoprotein-pseudotyped CH848 Env expression vector. Transduced cells were incubated in culture medium containing 1μg/ml of doxycycline (dox) and selected for 7 days in medium supplemented with 25 μg/ml of puromycin, generating the Env expressor-population cell line termed D831. From D831, a stable, high-expressor clonal cell line was derived, termed D835. The integrity of the recombinant env sequence in the clonal cell lines was confirmed by direct (without cloning) sequence analysis of PCR amplicons.

[0306] Cell surface-expressed trimeric CH848 Env binding

[0307] D831 Selected TRE2.CH848.JF-8.IRS6A Chinese Hamster Ovary Cells were cultured in DMEM/F-12 supplemented with HEPES and L-glutamine (Thermo Fischer,

Cat#11330057) 10% heat inactivated fetal bovine serum [FBS] (Thermo Fischer, Cat#10082147) and 1% Penicillin-Streptomycin (Thermo Fischer, Cat#15140163) and harvested when 70-80% confluent by trypsinization. A total 75,000 viable cells/well were transferred in 24-well tissue culture plates. After a 24-to-30-hour incubation at 37°C/5% CO2 in humidified atmosphere, CH848 Envs expression was induced with 1μg/mL doxycycline (Sigma-Aldrich, Cat#D9891) treatment for 16-20 hours. Cells were then washed in Stain buffer [PBS/2% FBS] and incubated at 4°C for 30 minutes. Stain buffer was removed from cells and 0.2ml/well of DH270 lineage antibodies, palivizumab (negative control) or PGT128 (positive control) were added at optimal concentration of 5μg/mL for 30 minutes at 4°C. After a 2X wash, cells were stained with 40 ul of APC-conjugated mouse anti-Human IgG (BD Pharmigen, Cat#562025) per well (final volume 0.2 ml/well) for 30 minutes at 4°C. Unstained cells were used as further negative control. Cells were washed 3X and gently dissociated with 0.3ml/well PBS/5mM EDTA for 30 minutes at 4°C, transferred into 5mL Polystyrene Round-Bottom Tubes (Falcon, Cat#352054), fixed with 0.1mL of BD Cytofix/Cytoperm Fixation solution (BD Biosciences, Cat#554722) and kept on ice until analyzed using a BD LSRFortessa Cell Analyzer. Live cells were gated through Forward/Side Scatter exclusion, and then gated upon GFP+ and APC.

[0308] Oligomannose Arrays

[0309] Oligomannose arrays were printed with glycans at 100, 33, and 10 μM (Z Biotech). Arrays were blocked for 1h in Hydrazide glycan blocking buffer. Monoclonal antibodies were diluted to 50 μg/mL in Hydrazide Glycan Assay Buffer, incubated on an individual subarray for 1 h, and then washed 5 times with PBS supplemented with 0.05% tween-20 (PBS-T). Subarrays that received biotinylated Concanavalin A were incubated with streptavidin-Cy3 (Sigma), whereas all other wells were incubated with anti-IgG-Cy3 (Sigma) for 1h while rotating at 40 rpm covered from light. The arrays were washed 5 times with 70 μL of PBS-T and then washed once with 0.01X PBS. The washed arrays were spun dry and scanned with a GenePix 4000B (Molecular Devices) scanner at wavelength 532 nm using GenePix Pro7 software. The fluorescence within each feature was background subtracted using the local method in GenePix Pro7 software (Molecular Devices). To determine glycan specific binding, the local background corrected fluorescence of the print buffer alone was subtracted from each feature containing a glycan.

[0310] Synthesis of Man9-V3 glycopeptide

[0311] A 30-amino acid V3 glycopeptide with oligomannose glycans (Man9-V3), based on the clade B JRFL mini-V3 construct (16), was chemically synthesized as described earlier (18). Briefly, after the synthesis of the oligomannose glycans in solution phase (18), two partially protected peptide fragments were obtained by Fmoc-based solid phase peptide synthesis, each featuring a single unprotected aspartate residue. The Man9GlcNAc2 anomeric amine was conjugated to each fragment (D301 or D332) using our one-flask aspartylation/deprotection protocol yielding the desired N-linked glycopeptide. These two peptide fragments were then joined by native chemical ligation immediately followed by cyclization via disulfide formation to afford Man9-V3–biotin. The control peptide, aglycone V3-biotin, had identical amino acid sequence as its glycosylated counterpart.

[0312] Affinity measurements

[0313] Antibody binding kinetic rate constants (ka, kd) of the Man9-V3 glycopeptide and its aglycone form (16) were measured by Bio-layer Interferometry (BLI, ForteBio Octet Red96) measurements. The BLI assay was performed using streptavidin coated sensors (ForteBio) to capture either biotin-tagged Man9-V3 glycopeptide or Aglycone-V3 peptide. The V3 peptide immobilized sensors were dipped into varying concentrations of antibodies following blocking of sensors in BSA (0.1%). Antibody concentrations ranged from 0.5 to 150 μg/mL and non-specific binding interactions were subtracted using the control anti-RSV Palivizumab (Synagis) mAb. Rate constants were calculated by global curve fitting analyses to the Bivalent Avidity model of binding responses with a 10 min association and 15 min dissociation interaction time. The dissociation constant (Kd) values without avidity contribution were derived using the initial components of the association and dissociation rates (ka1 and kd1) respectively. Steady-state binding Kd values for binding to Man9-V3 glycopeptide with avidity contribution were derived using near steady-state binding responses at varying antibody concentrations (0.5-80μg/mL) and using a non-linear 4-paramater curve fitting analysis.

[0314] HIV-1 Env site-directed mutagenesis

[0315] Deletion Mutant of CH0848.d0274.30.07 env gene was constructed using In Fusion HD EcoDry Cloning kit (Clontech) as per manufacturer instructions. Quick Change II Site-Directed Mutagenesis kit (Agilent Technologies) was used to introduce point mutations. All final env mutants were confirmed by sequencing.

[0316] Antibody site-directed mutagenesis

[0317] Site-directed mutagenesis of antibody genes was performed using the Quikchange II lightening multi-site-directed mutagenesis kit following manufacturer's protocol (Agilent). Mutant plasmid products were confirmed by single-colony sequencing. Primers used for introducing mutations were: DH270_IA4_D31G: cccagtgtatatagtagccggtgaaggtgtatcca (SEQ ID NO: 52); DH270.IA4 I34M: tcgcacccagtgcatatagtagtcggtgaaggtgt (SEQ ID NO: 53); DH270.IA4 T55S: gatggatcaaccctaactctggtcgcacaaactat (SEQ ID NO: 54); DH270.IA4 R57G: tgtgcatagtttgtgccaccagtgttagggttgat (SEQ ID NO: 55); DH270.IA4 R57V: cttctgtgcatagtttgtgacaccagtgttagggttgatc (SEQ ID NO: 56); DH270.UCA G57R: atcaaccctaacagtggtcgcacaaactatgcaca (SEQ ID NO: 57).

[0318] Env glycoprotein expression

[0319] The codon-optimized CH848-derived env genes were generated by de novo synthesis (GeneScript, Piscataway, NJ) or site-directed mutagenesis in mammalian expression plasmid pcDNA3.1/hygromycin (Invitrogen) as described (10), and stored at −80°C until use.

[0320] Expression and purification of DH270 lineage members for crystallization studies

[0321] The heavy- and light-chain variable and constant domains of the DH270 lineage Fabs were cloned into the pVRC-8400 expression vector using Not1 and Nhe1 restriction sites and the tissue plasminogen activator signal sequence. The DH270.1 single chain variable fragment (scFv) was cloned into the same expression vector. The C terminus of the heavy-chain constructs and scFv contained a noncleavable 6x histidine tag (SEQ ID NO: 58). Site-directed mutagenesis was carried out, using manufacturer's protocols (Stratagene), to introduce mutations into the CDR regions of DH270.1. Fabs were expressed and purified as described previously (46). The DH270.1 scFv was purified the same way as the Fabs.

[0322] Crystallization, structure determination, and refinement

[0323] All His-tagged Fabs and scFv were crystallized at 20-25mg/mL. Crystals were grown in 96-well format using hanging drop vapor diffusion and appeared after 24–48 h at 20 °C. Crystals were obtained in the following conditions: 2.5M ammonium sulfate and 100mM sodium acetate, pH 5.0 for DH272; 1.5M ammonium sulfate and 100mM sodium acetate pH 4.0 for UCA1; 20% PEG 4K, 100mM sodium acetate, pH 5 and 100mM magnesium sulfate for UCA3; 100mM sodium acetate, pH 4.5, 200mM lithium sulfate, and 2.5M NaCl for DH270.1; 1.4M lithium sulfate and 100mM sodium acetate, pH 4.5 for DH270.3; 40% PEG 400 and 100mM sodium citrate, pH 4.0 for DH270.5; and 30% PEG 4K, 100mM PIPES pH 6, 1M NaCl for DH270.6. All crystals were harvested and cryoprotected by the addition of 20–25% glycerol to the reservoir solution and then flash-cooled in liquid nitrogen.

[0324] Diffraction data were obtained at 100 K from beam lines 24-ID-C and 24-ID-E at the Advanced Photon Source using a single wavelength. Datasets from individual crystals (multiple crystals for UCA1, DH270.1 and DH270.5) were processed with HKL2000. Molecular replacement calculations for the free Fabs were carried out with PHASER, using I3.2 from the CH103 lineage [Protein Data Bank (PDB) ID 4QHL] (46) or VRC01 from the VRC01/gp120 complex [Protein Data Bank (PDB) ID 4LST] (47) as the starting models. Subsequent structure determinations were performed using DH270 lineage members as search models. The Fab models were separated into their variable and constant domains for molecular replacement.

[0325] Refinement was carried out with PHENIX, and all model modifications were carried out with Coot. During refinement, maps were generated from combinations of positional, group B-factor, and TLS (translation/libration/screw) refinement algorithms. Secondary-structure restraints were included at all stages for all Fabs; noncrystallographic symmetry restraints were applied to the DH270.1 scFv and UCA3 Fab throughout refinement. The resulting electron density map for DH270.1 was further improved by solvent flattening, histogram matching, and non-crystallographic symmetry averaging using the program PARROT. Phase combination was disabled in these calculations. After density modification, restrained refinement was performed using Refmac in Coot. Structure validations were performed periodically during refinement using the MolProbity server. The final refinement statistics are summarized in Fig. 32.

[0326] Design of the 92BR SOSIP.664 construct

[0327] To generate the clade B HIV-1 92BR SOSIP.664 expression construct we followed established SOSIP design parameters (48). Briefly, the 92BR SOSIP.664 trimer was engineered with a disulfide linkage between gp120 and gp41 by introducing A501C and T605C mutations (HxB2 numbering system) to covalently link the two subunits of the heterodimer (48). The I559P mutation was included in the heptad repeat region 1 (HR1) of gp41 for trimer stabilization, and part of the hydrophobic membrane proximal external region (MPER), in this case residues 664–681 of the Env ectodomain, was deleted (48). The furin cleavage site between gp120 and gp41 (508REKR511 (SEQ ID NO: 37)) was altered to 506RRRRRR511 (SEQ ID NO: 59) to enhance cleavage (48). The resulting, codon-optimized 92BR SOSIP.664 env gene was obtained from GenScript (Piscataway, NJ) and cloned into pVRC-8400 as described above for Fabs using Nhe1 and NotI.

[0328] Purification of Envs for analysis by biolayer interferometry and negative stain EM

[0329] SOSIP.664 constructs were transfected along with a plasmid encoding the cellular protease furin at a 4:1 Env:furin ratio in HEK 293F cells. Site-directed mutagenesis was performed using manufacturer's protocols (Stratagene) for mutations in the V3 region and glycosylation sites. The cells were allowed to express soluble SOSIP.664 trimers for 5–7 days. Culture supernatants were collected and cells were removed by centrifugation at 3,800 x g for 20 min, and filtered with a 0.2μm pore size filter. SOSIP.664 proteins were purified by flowing the supernatant over a lectin (Galanthus nivalis) affinity chromatography column overnight at 4°C. The lectin column was washed with 1x PBS and proteins were eluted with 0.5M methyl-α-D-mannopyranoside and 0.5M NaCl. The eluate was concentrated and loaded onto a Superdex 200 10/300 GL column (GE Life Sciences) prequilibrated in a buffer of 10mM Hepes, pH 8.0, 150mM NaCl and 0.02% sodium azide for EM, or in 2.5mM Tris, pH 7.5, 350mM NaCl, 0.02% sodium azide for binding analysis, to separate the trimer-size oligomers from aggregates and gp140 monomers.

[0330] Electron Microscopy

[0331] Purified 92BR SOSIP.664 trimer was incubated with a five molar excess of DH270.1 Fab at 4 °C for 1 hour. A 3μL aliquot containing ~0.01 mg/ml of the Fab - 92BR SOSIP.664 complex was applied for 15 s onto a carbon coated 400 Cu mesh grid that had been glow discharged at 20 mA for 30s, followed by negative staining with 2% uranyl formate for 30 s. Samples were imaged using a FEI Tecnai T12 microscope operating at 120kV, at a magnification of 52,000x that resulted in a pixel size of 2.13 Å at the specimen plane. Images were acquired with a Gatan 2K CCD camera using a nominal defocus of 1,500 nm at 10° tilt increments, up to 50°. The tilts provided additional particle orientations to improve the image reconstructions.

[0332] Negative Stain Image Processing and 3D Reconstruction

[0333] Particles were picked semi-automatically using EMAN2 and put into a particle stack. Initial, reference-free, two-dimensional (2D) class averages were calculated and particles corresponding to complexes (with three Fabs bound) were selected into a substack for determination of an initial model. The initial model was calculated in EMAN2 using 3-fold symmetry and EMAN2 was used for subsequent refinement using 3-fold symmetry. In total, 5,419 particles were included in the final reconstruction for the 3D average of 92BR SOSIP.664 trimer complex with DH270.1. The resolution of the final model was determined using a Fourier Shell Correlation (FSC) cut-off of 0.5.

[0334] Model fitting into the EM reconstructions

[0335] The cryo-EM structure of PGT128-liganded BG505 SOSIP.664 (PDB ID: 5ACO) (28) and crystal structure of DH270.1 were manually fitted into the EM density and refined by using the UCSF Chimera 'Fit in map' function.

[0336] Biolayer Interferometry

[0337] Kinetic measurements of Fab binding to Envs were carried out using the Octet QKe system (ForteBio); 0.2mg/mL of each His-tagged Fab was immobilized onto an anti-Human Fab-CH1 biosensor until it reached saturation. The SOSIP.664 trimers were tested at concentrations of 200nM and 600nM in duplicate. A reference sample of buffer alone was used to account for any signal drift that was observed during the experiment. Association and dissociation were each monitored for 5 min. All experiments were conducted in the Octet instrument at 30°C in a buffer of 2.5mM Tris, pH 7.5, 350mM NaCl and 0.02% sodium azide with agitation at 1,000 rpm. Analyses were performed using nonlinear regression curve fitting using the Graphpad Prism software, version 6.

[0338] Protein Structure Analysis and Graphical Representations

[0339] The Fabs and their complexes analyzed in this study were superposed by least squares fitting in Coot. All graphical representations with protein crystal structures were made using PyMol.

[0340] Definition of immunological virus phenotypes and virus signature analysis

[0341] The maximum likelihood trees depicting the heterologous virus panel and the full set of Env sequences for the subject CH848 were created using the Los Alamos HIV database PhyML interface. HIV substitution models (49) were used and the proportion of invariable sites and the gamma parameters were estimated from the data. Illustrations were made using the Rainbow Tree interface that utilizes Ape. The analysis that coupled neutralization data with the within-subject phylogeny based on Envs that were evaluated for neutralization sensitivity was performed using LASSIE (43). Signature analysis was performed using the methods fully described in (50, 51).

[0342] Heat maps and logo plots

[0343] Heat maps and logo plots were generated using the Los Alamos HIV database web interfaces (www.hiv.lanl.gov, version Dec. 2015, HEATMAP and Analyze Align).

[0344] Selection of CH848 Env signatures for antibody lineage cooperation studies.

[0345] We previously studied cooperation between lineages that occurred soon after infection, at a time when diversity in the autologous quasispecies was limited (12). In contrast, in CH848 the earliest autologous quasispecies transition in sensitivity to

DH272/DH475 neutralization to DH270 lineage members occurred between week 39 and week 51, when multiple virus variants were circulating. Viral diversity made it impractical to test all the possible permutations or mutations from the transmitted founder virus. To select a smaller pool of candidate mutations, we sought the two most similar CH848 Env sequences at the amino acid level with opposite sensitivity to DH272/DH475 and DH270.1 neutralization around week 51 and identified clones CH0848.3.d0274.30.07 and CH0848.3.d0358.80.06 being the most similar (sim: 0.98713). Among the differences in amino acid sequences between these two clones, the four that we selected (Δ134-143 in V1); D185N in V2; N413Y in V4; Δ463-464 in V5) were the only ones consistently different among all clones with differential sensitivity to DH272 and DH270.1. We elected to use DH270.1 for these cooperating studies as the least mutated representative of DH270 antibodies that gained autologous neutralization at week 51. The D185N and N413Y mutations were also identified by the signature analysis shown in Fig. 19 and Fig. 36.

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[0347] Data and materials availability.

[0348] The V(D)J rearrangement sequences of DH272, DH475 and the DH270 lineage antibodies (DH270.UCA, DH270.IA1 through IA4, and DH270.1 through 6) have been deposited in GenBank with accession numbers KY354938 through KY354963. NGS sequence data for clones DH270, DH272 and DH475 have been deposited in GenBank with accession numbers KY347498 through KY347701. Coordinates and structure factors for UCA1, UCA3, DH270.1, DH270.3, DH270.5, DH270.6, and DH272 have been deposited in the Protein Data Bank with accession code 5U0R, 5U15, 5U0U, 5TPL, 5TPP, 5TQA, and 5TRP, respectively. The EM map of the 92BR SOSIP.664 trimer in complex with DH270.1 has been deposited in the EM Data Bank with accession code EMD-8507.

Example 2 Man_9-V3 glycopeptides and aglycone peptides

[0349] This example provides non-limiting embodiments of V3 peptides which can be used in the immunogenic compositions and methods.

[0350] The crystal structure of the HIV-1 V3 bnAb PGT128 in complex with gp120 outer domain containing a truncated V3 loop revealed the key antibody contacts with its glycosylated epitope (R. Pejchal et al., *Science* (New York, N.Y.) **334**, 1097 (2011)).. We constructed a glycosylated peptide (Man_9-V3) that is comprised of the discontinuous epitope of PGT128 with deletion of residues 305-320, retention of P^{321}, and stabilization by a disulfide bridge between C^{296} and C^{331} (**Figure 38A-E**) (R. Pejchal et al., *Science* (New York, N.Y.) **334**, 1097 (2011)). Man_9-V3 glycopeptide was synthesized using a similar synthetic approach used to produce V1V2 glycopeptides (B. Aussedat et al., *J Am Chem Soc* **135**, 13113 (2013)). As controls, a biotinylated aglycone-V3 peptide with no high mannose glycans (**Fig. 38C**) and a biotinylated Man_9 free glycan (**Fig. 38A**) were also synthesized.

[0351] V3-glycan bnAb DH270 unmutated common ancestor binding to the peptide component of Man_9-V3 glycopeptide

[0352] The unmutated common ancestor (UCA) and the earlier intermediates in the DH270 lineage showed no detectable binding to either soluble or to cell surface Env. However, the DH270 bnAb UCA did bind to Man_9V3 (**Figure 27A)** and, as well, bound to the aglycone-V3 (**Figures 27B**). Similarly, the early intermediate antibodies (IA4, IA3, IA2) each bound to both Man_9V3 and aglycone-V3, and their binding was stronger to the aglycone-V3 compared to the Man_9-V3glycopeptide (**Figures 27B**). Binding to the Man_9-V3 glycopeptide remained low (>10μM) up to the DH270.1 bnAb lineage member (**Figures 27A**), when the affinity increased (coincident with nucleotide mutations up to a frequency of 5.6%) to a K_d of 331nM with better binding to the glycopeptide than to aglycone-V3 (**Figures 27A-B**). Thereafter in the DH270 bnAb lineage as mutations accumulated, binding to the Man_9-V3 glycopeptide increased, culminating in a K_d of 188 nM in the most potent bnAb, DH270.6, and no binding to aglycone-V3 peptide (**Figures 27A-B**). Thus, both the Man_9-V3 glycopeptide and the aglycone-V3 peptide bound the DH270.UCA with the lineage member binding independent of glycans until the DH270 lineage acquired a frequency of ~6% nucleotide mutations.

[0353] Additional V3 peptides contemplated by the invention are listed in Table 2.

Table 2 below includes non-limiting examples of V3 peptides

CH848.TF_V3_293-321-biotin	EIVCTRPGNNTRKSVRIGPGQTFYATGK
CH848.TF_V3_297-324-biotin	TRPGNNTRKSVRIGPGQTFYATGDIIGK
CH848.TF_V3_303-330-biotin	TRKSVRIGPGQTFYATGDIIGDIRQAHK
CH848.TF_V3_307-334-biotin	VRIGPGQTFYATGDIIGDIRQAHCNISK
CH848.TF_V3_315-340-biotin	QTFYATGDIIGDIRQAHCNISERQWNKK
CH848.TF_V3_biotin-315-340	KQTFYATGDIIGDIRQAHCNISERQWNK
CH848.0949.10.17_V3_293-321-biotin	EIVCTRPNNNTRKSVRIGPGQTFYATGK
CH848.0949.10.17_V3_297-324-biotin	TRPNNNTRKSVRIGPGQTFYATGDIIGK
CH848.0949.10.17_V3_303-330-biotin	TRKSVRIGPGQTFYATGDIIGDIKQAHK
CH848.0949.10.17_V3_307-334-biotin	VRIGPGQTFYATGDIIGDIKQAHCNISK
CH848.0949.10.17_V3_315-340-biotin	QTFYATGDIIGDIKQAHCNISEEKWNDK
CH848.0949.10.17_V3_biotin-315-340	KQTFYATGDIIGDIKQAHCNISEEKWND

[0354] Peptide sequences above in order of appearance in Table 2 are SEQ ID Nos: 2 to 13. Peptides sequence from Table 2 without N-or C-terminal biotinylation lysine are SEQ ID NOs: 14 to 25.

[0355] Any of the peptides could be biotinylated. In some embodiments, the peptides are biotinylated on the C terminus, except CH848.TF_V3_biotin-315-340 and CH848.0949.10.17_V3_biotin-315-340, which are biotinylated on the N terminus.

[0356] The peptides of the invention can be synthesized by any known method. V3 aglycone of and Man9V3 and their synthesis are provided in Figure 38A. See also WO2014//172366.

[0357] In some embodiments, the peptides are:

CH848.TF_V3_293-321-biotin EIVCTRPGNNTRKSVRIGPGQTFYATGK-Biotin (SEQ ID NO: 2)

CH848.TF_V3_297-324-biotin TRPGNNTRKSVRIGPGQTFYATGDIIGK-Biotin (SEQ ID NO: 3)

CH848.TF_V3_303-330-biotin TRKSVRIGPGQTFYATGDIIGDIRQAHK-Biotin (SEQ ID NO: 4)

CH848.TF_V3_307-334-biotin VRIGPGQTFYATGDIIGDIRQAHCNISK-Biotin (SEQ ID NO: 5)

CH848.TF_V3_315-340-biotin QTFYATGDIIGDIRQAHCNISERQWNKK-Biotin (SEQ ID NO: 6)

[0358] It is readily understood that peptides which are not biotinylated do not include an N- or C-terminal lysine (or other specific functional groups or residues) for targeting with biotynalation reagents.

[0359] V3 (+ the base containing N332 NGS) of CH848 transmitted founder and CH0848.0949.10.17 are shown below:

TF EIVC**TRPGNNTRKSVRIGPGQTFYATGDIIGDIRQAH**CNISERQWNK

(SEQ ID NO: 26 with lysine and SEQ ID NO: 27 without terminal lysine).

CH0848.0949.10.17 EIVC**TRPNNNTRKSVRIGPGQTFYATGDIIGDIKQAH**CNISEE KWND (SEQ ID NO: 28).

[0360] Non-limiting embodiments of V3 peptides variants include:

[0361] a. Wildtype EINCTRPNNNTRPGEIIGDIRQAHCNISRA (SEQ ID NO: 29)

[0362] b. GAIA (SEQ ID NO: 510): EINCTRPNNNTRPGEIIGAIAQAHCNISRA (SEQ ID NO: 30)

[0363] c. GDIA (SEQ ID NO: 511): EINCTRPNNNTRPGEIIGDIRQAHCNISRA (SEQ ID NO: 31)

[0364] d. GAIR (SEQ ID NO: 512): EINCTRPNNNTRPGEIIGAIRQAHCNISRA (SEQ ID NO: 32)

[0365] e. ADAR (SEQ ID NO: 513): EINCTRPNNNTRPGEIIADARQAHCNISRA (SEQ ID NO: 33)

[0366] The peptides of the invention could be glycosylated at either or both positions N301 and N332. In some embodiments the glycan is Man9GlcNAc2.

[0367] It is readily understood that peptides which are not biotinylated do not include an N- or C-terminal lysine (or other specific functional groups or residues) for targeting with biotynaltion reagents.

[0368] The invention also contemplates peptides which comprise T-cell helper epitope. One non-limiting embodiment includes GTH1 helper epitope. The helper epitope(s) could be at the N-or C-terminus of the peptide.

[0369] The peptides of the invention could be multimerized. In some embodiments, the peptides are biotinylated or multimerized. In some embodiments, the multimeric peptides comprise a T-helper epitope, e.g. but not limited to GTH1 epitope. The helper epitope(s) could be at the N-or C-terminus of the peptide. In some embodiments, the peptides are conjugated to a lipid and then multimerized. The lipids could be pegylated. A non-limiting example is V3 (SEQ ID NO: 1) Peg-GTH1-DPPE peptide.

Example 3: Selections of immunogens to induce and boost V3 antibodies

[0370] The following example provides non-limiting embodiments of immunogens and combination of immunogens for use in various immunization schedules.

[0371] All selections need a prime which engages the UCA. Non-limiting examples are Some of the general considerations in choosing immunogens for boost in induction of V3 glycan antibodies are as follows: (i) -- activate IA4, select for rare mutation; (ii) -- select for

antibodies that favor the trimer, expand the variation in the autologous signature residue to potentially expand recognition of diversity in the population; (iii) –expose the maturing antibodies to longer loops, even though these viruses are not bound or neutralized as well as viruses with shooter loops, as this is the main constrain on heterologous population breadth and that is what is needed. In some embodiments, immunogens are selected which can do (i) and (iii). In other embodiments, the selection includes immunogens which can do (ii).

[0372] Any suitable form of the envelope could be used for prime and/or boost. The envelope used in the compositions and methods of the invention can be a gp160, gp150, gp145, gp140, gp120, gp41, N-terminal deletion variants as described herein, cleavage resistant variants as described herein, or codon optimized sequences thereof. In certain embodiments the composition comprises envelopes as trimers. In certain embodiments, envelope proteins are multimerized, for example trimers are attached to a particle such that multiple copies of the trimer are attached and the multimerized envelope is prepared and formulated for immunization in a human. In certain embodiments, the compositions comprise envelopes, including but not limited to trimers as particulate, high-density array on liposomes or other particles, for example but not limited to nanoparticles. In some embodiments, the trimers are in a well ordered, near native like or closed conformation. In some embodiments the trimer compositions comprise a homogenous mix of native like trimers.

[0373] Near-native soluble trimers using the 6R.SOSIP.664 design are capable of generating autologous tier 2 neutralizing plasma antibodies in the plasma (Sanders et al. 2015), which provides a starting point for designing immunogens to elicit broadly neutralizing antibodies. While these trimers are preferentially antigenic for neutralizing antibodies they still possess the ability to expose the V3 loop, which generally results in strain-specific binding and neutralizing antibodies after vaccination. Using the unliganded structure the BG505.6R.SOSIP.664 has been stabilized by adding cysteines at position 201 and 433 to constrain the conformational flexibility such that the V3 loop is maintained unexposed (Kwon et al. 2015).

[0374] Stabilized Trimer Immunogen Design. Several SOSIP trimer designs have been generated: 6R.SOSIP.664, disulfide stabilized (DS) 6R.SOSIP.664 (Kwon et al Nature Struc Mol Biol 2015), 6R.SOSIP.664v4.1 (DeTaeye et al. Cell 2016), and 6R.SOSIP.664v4.2 (DeTaeye et al. Cell 2016). The CH848 SOSIP is made as a chimera of C.CH848 and A.BG505. Sequences of various CH848 envelope trimer designs are illustrated in Figures

39A-B, 40A-C, and 41A-C. Any one of the CH848 envelope sequences from WO2015/153638 could be designed as SOSIP trimers.

[0375] In some embodiments the CHIM.6R.SOSIP.664V4.1 and/or CHIM.6R.SOSIP.664V4.1design is expected to be in closed stabilized conformation. This design is expected to show preferential binding to broad neutralizing antibodies compared to binding to non-neutralizing antibodies. This design is expected to bind to antibodies from the V3 antibodies of Example 1.

[0376] The gp120 of C.CH848 envelope was fused with the BG505 inner domain gp120 sequence within the alpha helix 5 (alpha5) to result in a chimeric protein. The chimeric gp120 is disulfide linked to the A.BG505 gp41 as outlined by Sanders et al. (PLOS Path 2013). In some embodiments the immunogens were designed as chimeric proteins that possess the BG505 gp41 connected to the CH848 gp120, since the BG505 strain is particularly adept at forming well-folded, closed state trimers (See Figure 41C). This envelope design retains the CH848 base of the V3 loop and glycan(s) that are targeted by the DH270 lineage of broadly neutralizing antibody lineages that were isolated from CH848 (Example 1).

[0377] Provided are non-limiting examples of selections of envelopes for immunization to induce neutralizing HIV-1 antibodies, including but not limited to broadly neutralizing antibodies with the specificity of antibodies from the DH270 lineage. One non-limiting embodiment of the V3 peptide used as a prime is:
EINCTRPNNNTRPGEIIGDIRQAHCNISRA (SEQ ID NO: 1) as aglycone or as Man9GlcNAc2 glycosylated at both N301 and N332.

[0378] The envelopes could be administered in any suitable form, as nucleic acids, amino acids and/or combination. a gp160, gp150, gp145, any suitable form of a trimer, for example but not limited to SOSIP trimers, preferably in a closed conformation , gp140 (including but not limited to gp140C, gp140CF, gp140CFI), gp120, gp41, N-terminal deletion variants (e.g. delta 11 deletions) as described herein, cleavage resistant variants, or codon optimized sequences thereof. Non-limiting examples of sequences are provided in Figures 39A-B, 40A-C, and 41A-C. The boost could be sequential or additive.

[0379] Selection I: V3 glycopeptide and/or aglycone peptide (SEQ ID NO: 1) as a prime; Boost: CH848.0949.10.17; CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02. See Figure 37A and Figure 28 in Example 1.

[0380] Selection II: V3 glycopeptide and/or aglycone peptide as a prime; Boost: CH848.0949.10.17; CH848.0836.10.31; CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02. See Figure 37A and Figures 27A-B, 18A-B, and 28 in Example 1.

[0381] Selection III: V3 glycopeptide and/or aglycone peptide as a prime; Boost: CH848.0949.10.17; CH848.d1120.10.21; CH848.d1432.05.27. See Figure 37B.

[0382] Selection IV: V3 glycopeptide and/or aglycone peptide as a prime; Boost: CH848.0949.10.17; CH848.d1120.10.21; CH848d0949.10.18; CH848.d1432.05.27. See Figure 37C.

[0383] Selection V: V3 glycopeptide and/or aglycone peptide as a prime; Boost: CH848.0949.10.17; CH848.0794.05.14; CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.09; CH848.0526.25.02.

[0384] Selection VI: CH848.0949.10.17 trimer as a prime, boost: CH848.0949.10.17; optionally CH848.0836.10.31; CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02.

[0385] Selection VII: CH848.0949.10.17 trimer as a prime; could be a V1 loop deglycosylated envelope, boost: CH848.0949.10.17; optionally CH848.0836.10.31; CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02; CH0848.3.d1651.10.07.

[0386] In any of the above selections the prime could be selected from any of the contemplated envelope designs that show binding to the DH270UCA.

[0387] In any one of the above selections, the boost could include CH848.d1305.10.13 and CH0848.3.d1651.10.07 envelope designs to increase the breadth of antibodies.

[0388] This example describes additional considerations for selecting CH848 envelopes and modifications of such envelopes for use as immunogens.

[0389] CRF02_AG.T250 is an envelope which is very sensitive to V2glycan and V3glycan antibodies, and resistant to CD4bs antibodies. Short positively charged V1 V2's are highly associated with sensitivity, and T250 has among the shortest V1 V2 regions--So do CH848.d0949.10.17 envelope. T250's V1 V2 region could be introduced in any of the envelopes describe herein, e.g. in CH0848.d0949.021.10.17.

[0390] The best antibody from the DH270 lineage is DH270.6. Like most V3 antibodies, it requires the N332 PNGS. In addition, D325N is highly associated with resistance, and is a common circulating mutation. Other V3glycan bNAbs can tolerate the mutation, and it arose in CH848 after DH270 lineage antibodies were isolated, likely possibly as an escape from our DH270 lineage. An N325 CH848 envelope isolate could be included in the vaccine to potentially extend breadth when DH270-like linages is started. There are several candidates,

but only two had any binding or neutralizing activity CH848.d1305.10.13 and CH0848.3.d1651.10.07. Figures 42,43, and 35. As CH848.d1305.10.13 has a proline after the N, GDIR -> GNPR (SEQ ID NOS 34 and 35, respectively), which is rare, CH0848.3.d1651.10.07 based envelopes are better vaccine option.

[0391] Figures 44A, 44B, and 44D show additional envelope designs, to introduce changes in the sequence of CH0848.3.D0949.10.17 to increase the sensitivity of these envelopes to antibodies in the DH270 lineage. Some of the changes affect glycans while others do not impact glycosylation positions.

[0392] Table 3 provides a listing of reagents for use as prime(s)/DH270 lineage germline binders and/or boosts (Amino acid sequences of these envelopes are provided in Figure 45). Reference to amino acid positions is with respect to HXB2 envelope sequence.

	Protein	**Explanation**
1.	AG.T250-4 Delta10 gp120	Long V1 loops confers resistance to DH270 antibodies. T250-4 was chosen since the V1 length is very short compared to all other Envs in the HIV sequence database.
2.	T250-4chim.6R.SOSIP.664 v4.1	Chimeric SOSIP of the above AG.T250 envelope. Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers
3.	BG505 SOSIP MUT11B	Selected as a potential binder to DH270 UCA or other lineage members. See Steichen JM, et al. HIV Vaccine Design to Target Germline Precursors of Glycan-Dependent Broadly Neutralizing Antibodies. *Immunity*. 2016;45(3):483-496. doi:10.1016/j.immuni.2016.08.016.
4.	CH0848.3.D0949.10.17gp140c	Long V1 loops confers resistance to DH270 antibodies. Autologous Env with a short V1 loop.
5.	CH0848.3.D0836.10.31gp140C	DH270 antibodies recognize the GDIR motif (SEQ ID NO: 34) at the base of the V3 loop. The D325 makes critical contact with R57 in the DH270. The UCA of DH270 is G57 not R57. CH0848.3.D0836.10.31 has a N325 change that may bind better to the R57 of the UCA.
6.	CH848.3.D0949.10.17_GT1_D11gp120	Mutations that were helpful in getting 11MUTB to bind to PGT121 were analyzed and similar mutations were constructed into CH848 D949.10.17 to create an Env that might bind to the DH270 UCA. See Steichen JM, et al. HIV Vaccine Design to Target Germline Precursors of Glycan-Dependent Broadly Neutralizing Antibodies. *Immunity*. 2016;45(3):483-496. doi:10.1016/j.immuni.2016.08.016.
7.	BG505_MUT11B D11 gp120	Selected as a potential binder to DH270 UCA or other lineage members. See Steichen JM, et al. HIV Vaccine Design to Target Germline Precursors

		of Glycan-Dependent Broadly Neutralizing Antibodies. *Immunity*. 2016;45(3):483-496. doi:10.1016/j.immuni.2016.08.016.
8.	B.JRFLgp140CF_V1_3Q	V1 glycans block PGT121 from binding to the V3 glycan site (Garces et al. Cell. 2014 Sep 25;159(1):69-79. doi: 10.1016/j.cell.2014.09.009; Garces et al. Immunity. 2015 Dec 15; 43(6): 1053–1063). A virus and an Env were constructed where three potential N-linked sites in V1 are deleted. The N is changed to Q hence 3Q.
9.	CON-Sgp140CFI_V1_4Q	V1 glycans block PGT121 from binding to the V3 glycan site (Garces et alSupra). A virus and an Env were constructed where four potential N-linked sites in are V1 deleted. The N is changed to Q hence 4Q.
10	CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. autologous Env made as a stable trimer.
11	CH0848.3.D0836.10.31CHIM.6R.SOSIP.664V4.1	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. autologous Env made as a stable trimer.
12	CH0848.3.D0358.80.06CHIM.6R.SOSIP.664V4.1	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. autologous Env made as a stable trimer.
13	CH848.3.D1432.5.41CHIM.6R.SOSIP.664V4.1	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. autologous Env made as a stable trimer.
14	CH848.3.D0526.25.02CHIM.6R.SOSIP.664V4.1	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. autologous Env made as a stable trimer.
15	CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_GT1	Mutations that were helpful in getting 11MUTB to bind to PGT121 were analyzed and similar mutations were constructed into CH848 D949.10.17 to create an Env that might bind to the DH270 UCA. Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers thus we made the Env as a stable trimer. Also for immunization the native stable trimer has less exposure of nonneutralizing epitopes.
16	B.JRFL gp120core_mini-V3_v2	This construct is already published (Kong et al. (2013) Nat.Struct.Mol.Biol. **20**: 796-803), but we have been treating the protein with deglycosylases under denaturing and non-denaturing conditions since the UCA of DH270 does not bind free glycan and may interfere with the UCA being able to bind to the base of the V3 loop. This is gp120 with the variable loops 1 and 2 deleted. A truncated V3 loop remains.

17	CH848.3.D0949.10.17chim.6R.DS.SOSIP.664	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. autologous Env made as a stable trimer.
18	CH848.3.D0949.10.17chim.6R.DS.SOSIP.664	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. autologous Env made as a stable trimer.
19	CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N301AN332A	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. This is an autologous Env made as a stable trimer. We then removed the glycans at the base of the V3 loop since the UCA of DH270 does not bind free glycan and the glycans at N301 and N332 may interfere with the UCA being able to bind to the base of the V3 loop. Glycans were removed by mutation of the indicated amino acid position(s).
20	CH848.3.D0949.10.17chim.6R.DS.SOSIP.664__N332A	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. This is an autologous Env made as a stable trimer. We then removed the N332 glycan at the base of the V3 loop since the UCA of DH270 does not bind free glycan and may interfere with the UCA being able to bind to the base of the V3 loop. Glycans were removed by mutation of the indicated amino acid position(s).
21	CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N301A	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. This is an autologous Env made as a stable trimer. We then removed the N301 glycan at the base of the V3 loop since the UCA of DH270 does not bind free glycan and may interfere with the UCA being able to bind to the base of the V3 loop. Glycans were removed by mutation of the indicated amino acid position(s).
22	CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N301A	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. This is an autologous Env made as a stable trimer. We then removed the N301 glycan at the base of the V3 loop since the UCA of DH270 does not bind free glycan and may interfere with the UCA being able to bind to the base of the V3 loop. Glycans were removed by mutation of the indicated amino acid position(s).
23	CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_V1A	Long V1 loops confers resistance to DH270 antibodies. Autologous Env that started with a short V1 loop and we replaced the loop with a GlySerGly linker.
24	CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_V1B	Long V1 loops confers resistance to DH270 antibodies. Autologous Env that started with a short V1 loop and we replaced the middle 11 amino acids of the V1 loop with a GlySerGly linker.
25	CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_V1D	Long V1 loops confers resistance to DH270 antibodies. Autologous Env that started with a short V1 loop and we replaced the middle 7 amino acids of the V1 loop with a GlySerGly linker.

26	CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1degly4	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. Autologous Env made as a stable trimer. We then removed the N301 and N332 glycan at the base of the V3 loop since the UCA of DH270 does not bind free glycan and may interfere with the UCA being able to bind to the base of the V3 loop. V1 glycans block PGT121 from binding to the V3 glycan site (Garces et al. see supra). So we made an Env with N137 and N141 potential glycosylation sites in V1 removed. Glycans were removed by mutation of the indicated amino acid position(s).
27	CH0848.3.D0949.10.17gp140C_degly4	Some bnAb precursor antibodies bind stronger to trimer than gp120 monomers. Autologous Env made as a uncleaved trimer. We then removed the N301 and N332 glycan at the base of the V3 loop since the UCA of DH270 does not bind free glycan and may interfere with the UCA being able to bind to the base of the V3 loop. V1 glycans block PGT121 from binding to the V3 glycan site (Garces et al Immunity). So we made an Env with N137 and N141 potential glycosylation sites in V1 removed. Glycans were removed by mutation of the indicated amino acid position(s).
28	B.JRFL gp140C_3QN301SN332T	V1 glycans block PGT121 from binding to the V3 glycan site (Garces et al Immunity). So we made a virus and an Env with three potential N-linked sites in V1 deleted. The N is changed to Q hence 3Q. We then removed the glycans at the base of the V3 loop since the UCA of DH270 does not bind free glycan and the glycans at N301 and N332 may interfere with the UCA being able to bind to the base of the V3 loop. Glycans were removed by mutation of the indicated amino acid position(s).
29	B.JRFL gp120core_mini-V3_v2_degly	This is gp120 with the variable loops 1 and 2 deleted. A truncated V3 loop remains. We removed the N295A, N301A, N332A glycans at the base of the V3 loop since the UCA of DH270 does not bind free glycan and the glycans at N295A, N301 and N332 may interfere with the UCA being able to bind to the base of the V3 loop. Glycans were removed by mutation of the indicated amino acid position(s).

[0393] Provided and contemplated are envelopes and modified version thereof for use as DH270 lineage germline binders:

[0394] Envelope (HV1301265)_JRFL gp140_3QN301SN332T --

[0395] Envelope CH848 703010848.3.d0949.10.17_signature_opt_filled_rare_holes_a_ CD5ss gp140C. Contemplated is also a SOSIP design of the envelope CH848 703010848.3.d0949.10.17_signature_opt_filled_rare_holes_a_.

[0396] Envelope CH0848.3.d1651.10.07_CD5ss gp140C

[0397] Envelope CH848 703010848.3.d0949.10.17_signature_opt_b_T250.4_V1V2_CD5ss _gp140C. Envelope CH848 703010848.3.d0949.10.17_signature_opt_b_CD5ss gp140C. Contemplated is also a SOSIP design of this envelope.

[0398] Envelope T250-4 gp140C

[0399] Envelope T250-4chim.6R.SOSIP.664v4.1

[0400] Envelope CH848 703010848.3.d0949.10.17_signature_opt_b_CD5ss gp140C. Contemplated is also a SOSIP design of this envelope.

[0401] Envelope CH848 703010848.3.d0949.10.17_signature_opt_filled_rare_holes_a_ CD5ss gp140C

[0402] Envelope CH8448 703010848.3.d0949.10.17_signature_opt_filled_rare_holes_a_ CD5ss_N133AN138A

[0403] Envelope T250-4 gp140C_N133AN138A –

[0404] Envelope JRFL Core with miniV3 (293F produced/KIF treated/EndoH treated). Signature_opt_filled_rare_holes_a designs are also referred to as SOFA design. Additional designs are also contemplated and covered by the invention. Non-limiting embodiments include chimeric trimer designs, which could comprise portions of BG505 envelope (See Figure 41C for example). Non-limiting embodiments include non-chimeric trimer designs. See for example Figure 54, **Example 3B.**

[0405] The example describes CH848 envelopes, trimers and additional envelopes, modifications and designs. This example shows that stabilized HIV-1 Env trimer immunogens show enhanced antigenicity. See Figures 48A-48B. In some embodiments and are not recognized by non-neutralizing antibodies. In some embodiments these envelopes, including but not limited to trimers are further mutlimerized, and/or used as particulate, high-density array in liposomes or other particles, for example but not limited to nanoparticles. Any one of the envelopes of the invention could be designed and expressed as described herein. The envelopes of the invention are engineered and tested for binding to various antibodies from the DH270 lineage.

[0406] Elicitation of neutralizing antibodies is one goal for antibody-based vaccines. Neutralizing antibodies target the native trimeric HIV-1 Env on the surface virions. The trimeric HIV-1 envelope protein consists of three protomers each containing a gp120 and gp41 heterodimer. Recent immunogen design efforts have generated soluble near-native mimics of the Env trimer that bind to neutralizing antibodies but not non-neutralizing antibodies. The recapitulation of the native trimer could be a key component of vaccine

induction of neutralizing antibodies. Neutralizing Abs target the native trimeric HIV-1 Env on the surface of viruses (Poignard et al. J Virol. 2003 Jan;77(1):353-65; Parren et al. J Virol. 1998 Dec;72(12):10270-4.; Yang et al. J Virol. 2006 Nov;80(22):11404-8.). The HIV-1 Env protein consists of three protomers of gp120 and gp41 heterodimers that are noncovalently linked together (Center et al. J Virol. 2002 Aug;76(15):7863-7.). Soluble near-native trimers preferentially bind neutralizing antibodies as opposed to non-neutralizing antibodies (Sanders et al. PLoS Pathog. 2013 Sep; 9(9): e1003618).

[0407] Provided here are non-limiting embodiments of well-folded trimers or other engieneered forms of envelopes, which bind to the DH270UCA, and/or other DH270 lineage antibodies and are useful for Env immunizations as prime(s) and/or boosts.

[0408] Near-native soluble trimers using the 6R.SOSIP.664 design are capable of generating autologous tier 2 neutralizing plasma antibodies in the plasma (Sanders et al. 2015), which provides a starting point for designing immunogens to elicit broadly neutralizing antibodies. While these trimers are preferentially antigenic for neutralizing antibodies they still possess the ability to expose the V3 loop, which generally results in strain-specific binding and neutralizing antibodies after vaccination. Using the unliganded structure the BG505.6R.SOSIP.664 has been stabilized by adding cysteines at position 201 and 433 to constrain the conformational flexibility such that the V3 loop is maintained unexposed (Kwon et al. Nat Struct Mol Biol. 2015 Jul; 22(7): 522–531.).

[0409] Immunogen design. Provided are engineered trimeric envelopes, for use as immunogens, wherein the envelopes are based on multiple viruses from CH848, and other viruses with suitable characteristics, e.g. V1 loop length, as described.

[0410] We generated chimeric 6R.SOSIP.664, chimeric disulfide stabilized (DS) 6R.SOSIP.664 (Kwon et al Nat Struct Mol Biol. 2015 Jul; 22(7): 522–531.), chimeric 6R.SOSIP.664v4.1 (DeTaeye et al. Cell. 2015 Dec 17;163(7):1702-15. doi: 10.1016/j.cell.2015.11.056), and chimeric 6R.SOSIP.664v4.2 (DeTaeye et al. Cell. 2015 Dec 17;163(7):1702-15. doi: 10.1016/j.cell.2015.11.056). The 6R.SOSIP.664 is the basis for all of these designs and is made as a chimera of C.CH0505 and A.BG505. The gp120 of C.CH848 was fused with the BG505 inner domain gp120 sequence within the alpha helix 5 (α5) to result in the chimeric protein. The chimeric gp120 is disulfide linked to the A.BG505 gp41 as outlined by Sanders et al. (PLoS Pathog. 2013 Sep; 9(9): e1003618). These immunogens were designed as chimeric proteins that possess the BG505 gp41 connected to the CH848 gp120, since the BG505 strain is particularly adept at forming well-folded, closed trimers.

This envelope design are expected to retain and expose features of the envelopes recognized by DH270 by broadly neutralizing antibody lineages that were isolated from CH848.

[0411] Figures 39A-B, 40A-C, and 41A-C show nucleic acid and amino acid and sequences of various CH848 and other envelope trimer designs. Figure 41C shows an annotated sequence of the SOSIP.III design. Based on the various SOSIP designs, any other suitable envelope, for example but not limited to CH848 envelopes as described in WO2015/153638 can be designed.

[0412] Recombinant envelopes as trimers could be produced and purified by any suitable method. For a non-limiting example of purification methods see Ringe RP, Yasmeen A, Ozorowski G, Go EP, Pritchard LK, Guttman M, Ketas TA, Cottrell CA, Wilson IA, Sanders RW, Cupo A, Crispin M, Lee KK, Desaire H, Ward AB, Klasse PJ, Moore JP. 2015. Influences on the design and purification of soluble, recombinant native-like HIV-1 envelope glycoprotein trimers. J Virol 89:12189 -12210. doi:10.1128/JVI.01768-15.

[0413] Multimeric Envelopes

[0414] Presentation of antigens as prticulates reduces the B cell receptor affinity necessary for signal transduction and expansion (See Baptista et al. EMBO J. 2000 Feb 15; 19(4): 513–520). Displaying multiple copies of the antigen on a particle provides an avidity effect that can overcome the low affinity between the antigen and B cell receptor. The initial B cell receptor specific for pathogens can be low affinity, which precludes vaccines from being able to stimulate and expand B cells of interest. In particular, very few naïve B cells from which HIV-1 broadly neutralizing antibodies arise can bind to soluble HIV-1 Envelope. Provided are envelopes, including but not limited to trimers as particulate, high-density array on liposomes or other particles, for example but not limited to nanoparticles. See e.g. He et al. Nature Communications 7, Article number: 12041 (2016), doi:10.1038/ncomms12041; Bamrungsap et al. Nanomedicine, 2012, 7 (8), 1253-1271.

[0415] To improve the interaction between the naïve B cell receptor and CH848 SOSIP trimer protein we created to two constructs that can be presented on particles. The first construct was made by fusing HIV-1 Envelope trimer CH848 to ferritin. Ferritin protein self assembles into a small nanoparticle with three fold axis of symmetry. At these axis CH848 envelope protein was fused. Therefore the assembly of the three-fold axis also clusters three HIV-1 envelope protomers together to form an envelope trimer. Each ferritin particle has 6 axis which equates to 6 CH848 trimers being displayed per particle. See e.g. Sliepen et al. Retrovirology201512:82, DOI: 10.1186/s12977-015-0210-4.

[0416] Another approach to multimerize expression constructs uses staphylococcus Sortase A transpeptidase ligation to conjugate CH848 envelope trimers to cholesterol. The CH848 trimers can then be embedded into liposomes via the conjugated cholesterol. To conjugate the CH848 trimer to cholesterol either a C-teminal LPXTG tag (SEQ ID NO: 60) or a N-terminal pentaglycine repeat tag (SEQ ID NO: 61) was added to the CH505 envelope trimer gene. Cholesterol was also synthesized with these two tags. Sortase A was then used to covalently bond the tagged CH505 envelope to the cholesterol. The sortase A-tagged trimer protein can also be used to conjugate the trimer to other peptides, proteins, or fluorescent labels.

[0417] The invention provides design of envelopes and trimer designs wherein the envelope comprises a linker which permits addition of a lipid, such as but not limited to cholesterol, via a Sortase A reaction. See e.g. Tsukiji, S. and Nagamune, T. (2009), Sortase-Mediated Ligation: A Gift from Gram-Positive Bacteria to Protein Engineering. ChemBioChem, 10: 787–798. doi:10.1002/cbic.200800724; Proft, T. Sortase-mediated protein ligation: an emerging biotechnology tool for protein modification and immobilisation. Biotechnol Lett (2010) 32: 1. doi:10.1007/s10529-009-0116-0; Lena Schmohl, Dirk Schwarzer, Sortase-mediated ligations for the site-specific modification of proteins, Current Opinion in Chemical Biology, Volume 22, October 2014, Pages 122-128, ISSN 1367-5931, dx.doi.org/10.1016/j.cbpa.2014.09.020; Tabata et al. Anticancer Res. 2015 Aug;35(8):4411-7.

[0418] The lipid modified envelopes and trimers could be formulated as liposomes. Any suitable liposome composition is contemplated.

[0419] Non-limiting embodiments of envelope designs for use in Sortase A reaction are shown in **Figure 47B-C**.

[0420] Design of trimers with readthrough codons

[0421] The development of clonal cell lines that highly express trimeric HIV-1 Envelope will facilitate manufacturing of high quality proteins for clinical and research purposes. However, it is challenging to identify the cells that express trimeric protein among the many cells making various forms of HIV-1 Envelope with in the cell population. To identify cells expressing trimeric HIV-1 Envelope protein, we designed an expression construct that simultaneously produces both secreted Envelope protein as well as membrane anchored Envelope protein. The secreted Envelope protein can be purified using standard methods and results in unaltered soluble envelope. The membrane-anchored Envelope protein serves to mark the cells within a population of cells that expresses trimeric Envelope. More

specifically, the trimeric Envelope expressing cells are sorted by fluorescence-activated cell sorting using a HIV-1 trimer specific antibody. The sorted cells can then be used to initiate clonal populations of cells that have been phenotypically shown to express the protein of interest.

[0422] The expression construct is designed by taking advantage of the amber stop codon UAG in messenger RNA. The codon UAG usually signifies the end of the polypeptide sequence, but at a low rate the ribosome can readthrough this stop codon and continue to elongate the polypeptide chain. We incorporated this stop codon into our protein construct followed by the natural BG505 gp41 transmembrane and cytoplasmic tail sequence ended with two stop codons. Therefore, when the stop codon is readthrough a membrane-anchored gp120/gp41 heterodimer is formed. Loughran et al. (Nucleic Acids Res. 2014 Aug;42(14):8928-38. doi: 10.1093/nar/gku608) identified that the efficiency of readthrough could be increased by flanking the amber stop codon with the nucleotides CTA. Readthrough could be even further augmented with the addition of CTAG nucleotides after the amber stop codon. We engineered expression constructs with both modifications to ensure an optimal ratio of membrane-anchored and secreted trimeric Envelope protein. Since the CTAG creates a shift in reading frame we added GC nucleotides after the CTAG motif to preserve the original reading frame. The addition of CTAGGC results in the membrane anchored protein having a leucine and glycine residue expressed before the transmembrane domain. Any one of the envelopes of the invention could be designed and expressed as readthrough envelopes.

Example 4: Animal studies

[0423] Various selections of immunogens will be tested in animal models. Any suitable animal model will be used. Such animal models include mouse models, including humanized mice carrying human immunoglobulin locus, guinea pigs, rabbits, non-human primates, or any other model. Adults and neonates could be used in the studies.

[0424] Mouse study: prime with Man9 V3 (SEQ ID NO: 1) glycan monomer with adjuvant LASTS. Boost at least twice with CH848 d0949.10.17Δ11 gp120 with adjuvant, e.g.LASTS.

[0425] Mouse study: prime with V3 (SEQ ID NO: 1) aglycan monomer with adjuvant LASTS. Boost at least twice with CH848 d0949.10.17Δ11 gp120 with adjuvant LASTS.

[0426] In the immunogenic methods of the invention, the first boost after the prime comprises CH848 d0949.10.17 envelope either as a protein or nucleic acid in any suitable form.

[0427] The adjuvant in the above studies could be any suitable adjuvant, for example but no limited to polyIC or polyIC/LC.

[0428] **Example 5**: Modification of HIV Env glycosylation augments binding to unmutated common ancestor and intermediate antibodies of V3-glycan broadly neutralizing antibody lineages. This example investigates whether envelope designs with a short V1 loop and no glycans near N137 engage the DH270 UCA.

[0429] Example 5 shows data for one non-limited embodiment of a deglycosylated envelope. These data include antigenic and immunogenic characterization of the envelope, and characterization of immunogenic responses in animals immunized with the deglycosylated envelope CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_N133DN138T.

[0430] Additional trimer designs based on CH848.3.D0949.10.17 envelope are also contemplated as deglycosylated immunogens.

[0431] The recombinant envelopes in this example are expressed in mammalian cells and purified by methods known in the art.

[0432] In a study described in Example 1 (Bonsignori et al. *Sci. Transl. Med.* **9**, eaai7514 (2017)), we described the antibody lineage called DH270 that was isolated from an HIV-infected individual called CH0848. We isolated this lineage using memory B cell cultures and single B cell sorting followed by RT-PCR. In total we isolated 6 natural antibody heavy chain and light chain pairs. The most potent and broad neutralizing antibody of the lineage neutralized 71% of viruses tested. Using these antibodies, we inferred a unmutated common ancestor or UCA antibody using the Cloanalyst program. The UCA lacks any somatic mutation and is our best approximation of the germline starting point for the DH270 lineage. In this study, autologous Envs were isolated from CH0848 covering 4.5 years of infection. A subset of these Envs were used to identify Envs that were engaged by various members of the DH270 lineage throughout its developmental pathway. The identified Envs are being used to design B cell lineage sequential vaccines. However, no Env was identified that bound the DH270 UCA antibody. Antibody DH270 binding and neutralization inversely correlates with HIV-1 Env V1 loop length. V1 glycans inhibit V3-glycan bnAb inter-PGT122 lineages and the N137 glycan in the V1 loop needs to be accommodated for early lineage member binding to BG505 SOSIP. Garces F. et al. *Immunity* 43, 1053-1063 (2015); Garces et al. Cell 159, 69-78 (2014); Steichen et al. Immunity 45, 483-496 (2016).

[0433] An autologous Env from the CH0848 individual was identified—this envelope called CH0848.D0949.10.17, which possessed a 17 amino acid V1 loop. It had glycosylation sites

within the V1 loop at positions 133, 138 and N156. We removed the N133 and N138 glycans by substituting in amino acids that naturally occur at those sites. We made a SOSIP trimer derived from the CH0848.10.17 sequence (see for example Figure 49A as a non-limiting embodiment). We also made a CH0848 10.17 SOSIP trimer lacking the N-linked glycosylation sites at positions 133 and 138 (see for example Figure 49A as a non-limiting embodiment). Figure 58shows analysis of trimer formation by negative stain electron microscopy. Shown here are the 2D class averages of each of the soluble trimers—for the 32 classes, both Envs were trimeric.

[0434] **Figure 59** shows analysis of the antigenicity of the trimers. As part of our initial characterization of the trimers we analyze binding of 19 different antibodies targeting diverse epitopes on Env in biolayer interferometry assays. Shown here are four of the 19 antibodies, including trimer-specific broadly neutralizing antibody PGT151, and non-neutralizing antibodies A32, CH58, and 17B, which target the C1, linear V2 peptide, and coreceptor binding site on Env. Both of the trimers bound strongly to PGT151 as indicated by the red curves. The nonneutralizing antibodies against the various epitopes showed no binding, which suggested these Envs were not in the CD4 induced conformation.

[0435] This example investigated whether soluble, recombinant Env proteins derived from CH0848.D0949.10.17 engage the DH270 UCA. **Figure 60** shows that DH270 UCA binds SOSIP trimers, but not uncleaved gp140 oligomers or monomeric gp120. We performed SPR assays where the DH270 UCA Fab captured on BiaCore sensor chips and serial dilutions of the different forms of WT CH0848.D0949.10.17 Envs were flowed over the antibody. Interestingly we observed that only the SOSIP trimer bound to the UCA. The binding was weak but was calculated to be 2600 nM affinity. Our earlier binding screens were performed with monomeric gp120s, with which we would have missed this interaction.

[0436] We also investigated whether DH270 UCA binding to CH0848.D0949.10.17 SOSIP could be limited by the V1 glycans at N133 and N138. Figure 61 shows that CH0848 10.17 N133D N138T SOSIP engages the DH270 UCA Fab with 29 nM affinity. We tested the binding of the DH270 UCA Fab using BIACore as I previously described. The binding results are summarized in the table on the left and the data for the N133D N138T mutant Env is shown on the left where each curve represents a different concentration of CH0848.10.17 N133D N138T SOSIP. Removal of the glycosylation sites at position 133 and 138 resulted in a 100-fold improvement in DH270 UCA affinity as highlighted in blue. The SOSIP trimers

are mimics of the native, thus we wondered whether the V1 glycans inhibited DH270 UCA binding to CH0848.D949.10.17 native trimers on virions.

[0437] Figure 62A shows that V1 glycans inhibit DH270 UCA recognition of native Env trimers. We made a pseudovirus expressing the wildtype 10.17 Env with the glycans or expressing the N133D N138T mutant version of 10.17. The DH270 UCA did not neutralize the wildtype 10.17 virus, however, the broadly neutralizing antibody DH270.7 potently neutralized the virus. When removed the two glycans at position N133 and N138 the DH270 UCA was now able to neutralize at a IC50 titer of 1.7 ug/mL. Also, the bnAb DH270.6 more potently neutralized the V1 glycan modified virus. Figure 62B shows that V1 glycan deletion was not solely sufficient for neutralization sensitivity since we performed the same experiment with JR-FL pseudoviruses and despite removing the V1 glycans at three positions the DH270 UCA still could not neutralize the virus. We also did not detect any binding to JR-FL N135Q N137Q N141Q SOSIPs. Therefore, the DH270 UCA binding and neutralization of the autologous virus likely requires specific amino acids in addition to the removal of glycans.

[0438] We investigated the structural basis for N133 and N138 glycan inhibition of DH270 UCA binding to trimer. **Figure 63** shows a model of DH270.6 binding to SOSIP trimer and potential N137 glycan interference. The crystal structure of the most broad and potent DH270 antibody called DH270.6 in complex with a glycosylated peptide antigen bearing the N332 and N301 glycans solved. We used that structure to model the DH270.6 interaction with the glycosylated BG505 SOSIP. In this model the N137 glycan shown in orange clashed with the heavy chain. Thus elimination of this glycan would be predicted to improve antibody:Env interaction. We saw that the N133 glycan was not directly clashing with the antibody. However, we found that the N133 glycan interacts with the V1 loop. We hypothesize that the N133 glycan would buttress the V1 loop and limit its flexibility.

[0439] We investigated whether CH0848 N133D N138T trimer stimulate B cells encoding the DH270 UCA. **Figure 64** shows that CH0848 N133D N138T SOSIP induces Ca2+ flux in DH270 UCA and DH270 Ramos cell lines. We first performed calcium flux assays where the DH270 UCA, DH270.1, or a negative control Flu antibody was expressed on Ramos B cells. We added the trimer and measured calcium flux using FuraRed. The cells expressing the flu antibody showed no Calcium flux where the cells expressing either the DH270 UCA or DH270.1 neutralizing antibody fluxed calcium.

[0440] Figure 65 shows DH270 UCA knock-in (DH270 UCA $VH^{+/-}$, DH270 UCA $VL^{+/-}$) mice SOSIP immunization regimen. We next examined whether the soluble trimer could activate the DH270 UCA in vivo. DH270 UCA knock-in mouse model was created for these immunization studies. In this mouse the rearranged DH270 UCA variable region is knocked in for both the heavy chain and the light chain and the mouse is heterozygous for the knock-in genes. We immunized this mouse every two weeks six times with 25 micrograms of the CH848.D0949.10.17 N133D/N138T SOSIP. The immunized group was compared to control animals that received the GLA-SE adjuvant only.

[0441] Figure 66 shows that immunization with N133D/N138T SOSIP induced SOSIP-binding antibodies in DH270 UCA knock in mice. We first looked at the binding antibodies elicited against the CH848 10.17 N133D N138T by the vaccination. Using ELISA we measured binding titers represented as log area under the curve and observed that autologous binding antibodies were elicited in all five mice by the third immunization. The binidng titers continued to be boosted with subsequent immunizations. This response was specific to the Env immunogen since the adjuvant only mice did not mount any binding responses. We wondered whether the glycans have to be removed in order for the antibodies to bind.

[0442] Figure 67 shows that DH270 UCA knock-in mouse serum antibodies can bind to CH0848.D949.10.17 in the presence of N133 and N138 glycans. We added the V1 glycans back to the Env, and while titers decreased they were still detectable in all of the mice.

[0443] We investigated whether vaccine-induced antibodies possess autologous neutralizing activity. **Figure 68** shows that DH270 UCA knock-in mouse sera neutralize CH0848.D0949.10.17 lacking the N133/N138 glycans. The pre-immune sera and the sera one week after the sixth and final boost were tested for neutralization of the 10.17DT virus. Neutralization titers are shown here as serum reciprocal dilution that neutralized 50% of viral replication. The trimer immunized animals are shown on top and the adjuvant only group is shown on the bottom. None of the serum samples neutralized the negative control virus, Murine leukemia virus. All 5 mice potently neutralized the CH0848DT (CH0848.3.D949.10.17 N133D/N138T) virus that matched the immunogen with titers ranging from 7,500 to 126,000.

[0444] Figure 69 shows that DH270 UCA knock-in mouse sera neutralize tier 2 virus CH0848.D0949.10.17 with N133/N138 glycan. We next tested the neutralization activity against the tier 2 virus CH0848 10.17 virus that has the V1 glycosylation site present. The presence of the glycans reduced neutralization of the 10.17 virus, but titers still ranged from

141 to 1118. Thus, neutralizing antibodies elicited after six vaccinations of DH270 UCA mice with a glycan modified immunogen were able to neutralize the wildtype virus with the natural glycan shield.

[0445] Experiments in this example show that DH270 UCA preferentially bound autologous SOSIP trimers, but not gp120 or uncleaved gp140 versions of the same Env; that the glycans in the V1 loop are not only inhibitory for PGT121, but also are inhibitory for other V3 glycan antibodies such as DH270; that the CH0848 10.17N133DN138T SOSIP elicited binding and neutralizing antibodies against the unmodified, WT CH0848 10.17 virus in rearranged DH270 UCA knock in mice.

[0446] We investigated whether N133 /N138 lacking viruses are found in circulation in CH0848 individual envelope sampling. Natural Envs with 17 aa V1 loops lacking N133/ N138 glycans are present during in CH0848 infection. Figure 70 shows that a CH0848 natural Env with a 17 aa V1 loop and naturally lackingN133 and N138 glycan has eliminated the N295, N301, and N332 glycans. Figure 70 shows JRFL, CH0848.D1305.10.19, and CH0848.D949.10.17 V3 loop alignment. See Figure 49B for sequence of CH0848.D1305.10.19. Figure 71 shows that DH270 UCA does not bind CH0848 natural Env that has a 17 aa V1 loop and lacks N133 and N138 glycans. Figure 72 shows that DH270-resistant CH0848 natural Env with a 17 aa V1 loop and no N133 and N138 glycan acquire V2 apex bnAb binding (PGT145). Figure 73 shows that DH270 UCA knock-in sera block V3-glycan bnAb binding to gp120.

[0447] NHP 144: CH0848 10.17N133DN138T SOSIP was used as an immunogen in a non-human primate study. Regimen was as follows: **week 0**—all groups CH848.d949.10.17_N301A_SOSIP (100 ug), IM injection in GLA-LSQ; **week 4-- Group 1:** CH65 IgG (α-HA) 10 mg/kg IV infusion, **Group 2:** Ipilimumab (α-CTLA-4) 10 mg/kg IV infusion, **Group 3:** RH anti-tac 1 mg IV infusion, **Group 4:** Ipilimumab (α-CTLA-4) 10 mg/kg IV infusion + RH anti-tac 1 mg IV infusion) +CH848.d949.10.17_N301A_SOSIP (100 ug), IM injection in GLA-LSQ; **week 10-- Group 1:** CH65 IgG (α-HA) 10 mg/kg IV infusion, **Group 2**:Ipilimumab (α-CTLA-4) 10 mg/kg IV infusion, **Group 3:** RH anti-tac 1 mg IV infusion , **Group 4:** Ipilimumab (α-CTLA-4) 10 mg/kg IV infusion + RH anti-tac 1 mg IV infusion) + **CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_N133DN138T** (100 ug) IM injection in GLA-LSQ; week 16-- **Group 1:** CH65 IgG (α-HA) 10 mg/kg IV infusion + CH848.d949.10.17 SOSIP (100 ug) IM injection in GLA-LSQ, **Group 2 :** Ipilimumab (α-CTLA-4) 10 mg/kg IV infusion +CH848.d949.10.17 SOSIP (100 ug) IM injection in GLA-

LSQ, **Group 3-4 :** CH848.d949.10.17 SOSIP (100 ug) IM injection in GLA-LSQ; week 22—all groups CH848.d8369.10.31 SOSIP (100 ug) IM injection in GLA-LSQ.

[0448] Following two immunizations with CH848.d949.10.17_N301A_SOSIP and a third immunization with CH848.d949.10.17_N133DN138T _SOSIP that have been demonstrated to bind to the germline precursor of the V3-glycan bnAb DH270 lineage as a priming immunization regimen, then boosting with the CH848.d949.10.17 with all glycan sites intact we can detect serum antibody neutralization (Figure 74D) of the CH848.d949.10.17_N133DN138T pseudovirus in the TZM-bl neutralization assay at weeks 18 and/or 24 for 3 of the 4 animals in the anti-CTLA-4 blocking antibody group, 2 of the 4 animals in the rhesus anti-CD25 (RH anti-tac) antibody groups and 1 of 4 animals in the combination antibody treated group. None of the control antibody treated animals (CH65) developed neutralization of this double glycan deleted virus. Additionally, none of the antibody treated animals that could neutralize the CH848.d949.10.17_N133DN138T virus could neutralize the CH848.d949.10.17 virus with both glycan sites added back. This indicates targeting of the neutralizing antibody response to a similar V3-glycan site as the DH270 bnAb, but antibody maturation has not occurred that allows accommodation of the N133 and N138 glycan sites. No neutralization was detected against control SVA-MLV virus. Samples from additional weeks, e.g. Weeks 6 and 12, are tested for neutralization to determine if neutralization was induced after the N301A prime.

[0449] SOFA deglycosylated envelopes (See Example 3 and Figure 50) will be analyzed in mouse and non-human primate immunization studies.

[0450] Table 4 is summary of various designs of V1 deglycosylated envelopes

	Envelope	**Figure**
1.	CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_N133DN138T (amino acid)	Figure 49A
2.	Alignment of CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_N133DN138T And CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1	
3.	>CH0848.3.d1305.10.19gp160 (Amino acid and nucleic acid)	49B
4.	>CH848.3.D1305.10.19ch.DS.SOSIP.664 (Amino acid)	50A
5.	>CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T (amino acid)	50B
6.	>CH848.3.D0949.10.17SOFA.DS.chSOSIP (amino acid)	50B
7.	>CH848.3.D0949.10.17SOFA.DS.chSOSIP_N133N138A	50B

	(amino acid)	
8.	>JRFL_SOSIPv6_V1_PNGS (removed V1 glycosylation sites except N156) (Amino acid)	50C
9.	>CON-Schim.6R.DS.SOSIP.664_OPT_N130D_N135K_N138S_N141S (amino acid)	50D
10.	>CON-Schim.6R.DS.SOSIP.664_OPT_N138S_N141S (amino acid)	50D
11.	T250-4CHIMSOSIPV5.2.8	51
12.	T250-4CHIMSOSIPV5.2.8_N160K	51
13.	CH848.3.D0949.10.17CHIM.SOSIPV5.2.8	51
14.	WITOCHIM.SOSIPV5.2.8	51
15.	ZM233CHIM.SOSIPV5.2.8	51
16.	A.Q23_17CHIM.SOSIPV5.2.8	51
17.	CM244CHIM.SOSIPV5.2.8	51
18.	CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T	51
19.	CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N301A	51
20.	>CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160 (Amino acid)	52
21.	Alignment of amino acids of: >CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160 And >CH848d949.10.17_N133DN138T_SOSIPv5.2.8	52
22.	>CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T	53A
23.	>CH848.3.D949.10.17_N133DN138TchimericSOSIP CH848.3.D949.10.17_N133DN138T as a first generation .664 SOSIP Amino acid	54A
24.	>CH848.3.D949.10.17_N133DN138TSOSIP.664 CH848.3.D949.10.17_N133DN138T as a first generation .664 SOSIP Amino acid	54A
25.	>CH848.3.D949.10.17_N133DN138TchimericDS.SOSIP CH848.3.D949.10.17_N133DN138T plus the disulfide that blocks CD4 induced conformational changes Amino acid	54B
26.	>CH848.3.D949.10.17_N133DN138TDS.SOSIP CH848.3.D949.10.17_N133DN138T plus the disulfide that blocks CD4 induced conformational changes Amino acid	54B
27.	>CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP CH848.3.D949.10.17_N133DN138T plus the disulfide that blocks CD4 induced conformational changes and Rich Wyatt's .8 mutations: D47, E49, K65, T106, L165, R429, Q432, R500 Amino acid	54C
28.	>CH848.3.D949.10.17_N133DN138TTD8.DS.SOSIP.664 CH848.3.D949.10.17_N133DN138T plus the disulfide that blocks CD4 induced conformational changes and Rich Wyatt's .8 mutations: D47, E49, K65, T106, L165, R429, Q432, R500 Amino acid	54C
29.	Schematic diagram of CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP	54D

30.	Annotates amino acid sequence of CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP	54E
31.	Alignment of amino acid sequences in Figures 54A, B and C	54F
32.	>CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1degly3 HV1301331_degly3: This Env has N138, N133, and N301 glycans removed. These glycans were believed to prevent DH270 mAb binding by blocking access to HIV peptide binding	77A
33.	>CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_N138T HV1301331_N138T: this Env has a single V1 glycan removed. This Env would be used to sequentially add back glycans in the V1 loop to select antibodies capable of tolerating N301 and N133 glycans but not N138T. This Env could be used in a sequential Env vaccine where glycans are removed and added back sequentially	77B
34.	>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_D368R HV1301345_D368R: Env has D368R mutation to reduce CD4 binding. CD4 binding could disrupt Env conformation in vivo	77C
35.	>CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T_c-SORTA HV1301331_N133DN138T_c-SORTA: Tagged Env that can be ligated to particles by sortase A enzyme	77D
36.	>CH848.3.D0949.10.17chDS.SOSIP_N133DN138T-ferritin HV1301522: Ferritin particle with V1 glycan mutant Env attached as a fusion protein	77E
37.	>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N133D_N138T_cSORTA HV1301345_N133D_N138T_cSORTA: Tagged Env that can be ligated to particles by sortase A enzyme reactions in vitro.	77F
38.	>CH848.3.D0949.10.17N133D138T_CD5ss gp160 opt HV1301581: Full length gp160 HIV Env with V1 glycans removed to engender DH270 UCA binding.	77G
39.	>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_TFV1loop HV1301345_TFV1loop: The 10.17 Env with a long V1 loop that was transplanted from the TF virus sequence. This can be used to select for antibodies capable of accommodating a long V1 loop	77H
40.	>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N133DN138T HV1301345_N133D_N138T: Stabilized trimer with V1 glycans removed to facilitate DH270 UCA binding	77I
41.	> CH848.3.D0949.10.17.6R.SOSIP.664 (no avi tag) HV1301262(has avi tag): Non-chimeric Env	77J
42.	> CH848.3.D0949.10.17chim.6R.DS.SOSIP.664 (no avi tag) HV1301263(has avi tag): Chimeric DS Env without V1 glycan mutated	77K
43.	> CH848.3.D0949.10.17.6R.DS.SOSIP.664 (no avi tag) HV1301264 (has avi tag): Non-chimeric DS stabilized CH0848 trimer	77L
44.	Annotated sequence of CH848.3.D0949.10.17.6R.SOSIP.664	78A
45.	Annotated sequence of CH848.3.D0949.10.17 SOSIPv5.2.8	78B

[0451] CH848.3.D0949.10.17 SOSIP trimers were also analyzed for their antigenicity in the presence of BMS compound(s) which inhibit binding of CD4 to the envelope. See e.g. Langley et al. Proteins 2015; 83:331–350. Trimer antigenicity in the presence of the inhibitor was not affected—see Figures 79 and 80.

[0452] Animal studies comparing immunogenicity of envelopes in the presence and absence of BMS- 626529 CD4 binding inhibitors will be conducted.

CLAIMS

What is claimed is:

1. A recombinant HIV-1 envelope polypeptide, comprising non-glycosylatable amino acids in the V1 loop at positions corresponding to N133 and/or N138 in the CH848.3.D0949.10.17 envelope sequence, wherein the remaining envelope sequence comprises the amino acid sequence of the CH848.3.D0949.10.17 envelope.
2. The recombinant envelope of claim 1, wherein the envelope comprises amino acids substitutions within the CH848.3.D0949.10.17 sequence such that the envelope protomer forms a trimer.
3. A nucleic acid encoding any one of the polypeptides of claim 1 or 2.
4. An immunogenic composition comprising the recombinant HIV-1 envelope polypeptide of claim 1 or claim 2 and a carrier.
5. An immunogenic composition comprising the nucleic acid of claim 3 and a carrier.
6. The composition of claim 4 or 5 further comprising an adjuvant.
7. The composition of claim 3 or 5 wherein the nucleic acid is operably linked to a promoter inserted in an expression vector.
8. A method of inducing an immune response in a subject comprising administering a composition comprising an HIV-1 envelope polypeptide(s) in an amount sufficient to induce an immune response from one or more of the following groups:
   (a) deglycosylated envelope polypeptide form(s) of CH848.0949.10.17 designed to bind DH270UCA (Table 1, Table 3, Table 4, Ex. 3, Ex. 5), or any combination thereof as a prime;

   and wherein the administration step can alternatively, or in addition, comprise administering any suitable form of a nucleic acid(s) encoding an HIV-1 envelope polypeptide(s) in an amount sufficient to induce an immune response from one or more of the following groups:

   (b) deglycosylated envelope polypeptide form(s) of CH848.0949.10.17 designed to bind DH270UCA (Table 1, Table 3, Table 4, Ex. 3, Ex. 5), or any combination thereof as a prime.
9. A method of inducing an immune response in a subject comprising administering a composition comprising an HIV-1 envelope polypeptide(s) in an amount sufficient to induce an immune response from one or more of the following groups:

(a) deglycosylated envelope polypeptide form(s) of CH848.0949.10.17 designed to bind DH270UCA (Table 1, Table 3, Table 4, Ex. 3, Ex. 5), or any combination thereof as a prime;

(b) envelope polypeptide(s) CH848.0949.10.17, CH848.0836.10.31, CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02 (Figure 37A), or any combination thereof

(c) envelope polypeptide CH0848.3.d1651.10.07;

and wherein the administration step can alternatively, or in addition, comprise administering any suitable form of a nucleic acid(s) encoding an HIV-1 envelope polypeptide(s) in an amount sufficient to induce an immune response from one or more of the following groups:

(d) deglycosylated envelope polypeptide form(s) of CH848.0949.10.17 designed to bind DH270UCA (Table 1, Table 3, Table 4, Ex. 3, Ex. 5), or any combination thereof as a prime;

(e) envelope polypeptide(s) CH848.0949.10.17, CH848.0836.10.31, CH848.0358.80.06; CH848.1432.5.41; CH848.0526.25.02 (Figure 37A), or any combination thereof;

(f) envelope polypeptide CH0848.3.d1651.10.07.

10. The method of claim 8 wherein the nucleic acid encodes a gp120 envelope, gp120D11 envelope, a gp140 envelope (gp140C, gp140CF, gp140CFI) as soluble or stabilized protomer of a trimer, a gp145 envelope, a gp150 envelope, or a transmembrane bound envelope.
11. The method of claim 8 wherein the polypeptide is gp120 envelope, gp120D11 envelope, a gp140 envelope (gp140C, gp140CF, gp140CFI) as soluble or stabilized protomer of a trimer, a gp145 envelope, a gp150 envelope, or a transmembrane bound envelope.
12. The method of claim 8, wherein the composition further comprises an adjuvant.
13. The method of claim 8, further comprising administering an agent which modulates host immune tolerance.
14. The method of claim 8, wherein the polypeptide administered is multimerized in a liposome or nanoparticle.
15. The method of claim 8, further comprising administering one or more additional HIV-1 immunogens to induce a T cell response.

16. The method of claim 8, wherein the first boost administered after the prime comprises HIV-1 envelope polypeptide CH848.0949.10.17 in any suitable form.
17. The method of claim 8, wherein the deglycosylated form of CH848.0949.10.17 (N133mut N138mut) envelope is administered multiple times.
18. The method of claim 8, wherein the prime is a deglycosylated form of CH848.0949.10.17 (N133mut N138mut) and boost is selected from Selections I, II, II, IV, V, VI or VII.
19. The recombinant HIV-1 envelope polypeptide of claim 2, wherein the polypeptide does not include a signal peptide.

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CECI EST LE TOME 1 DE 2
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CONTAINING PAGES 1 TO 173

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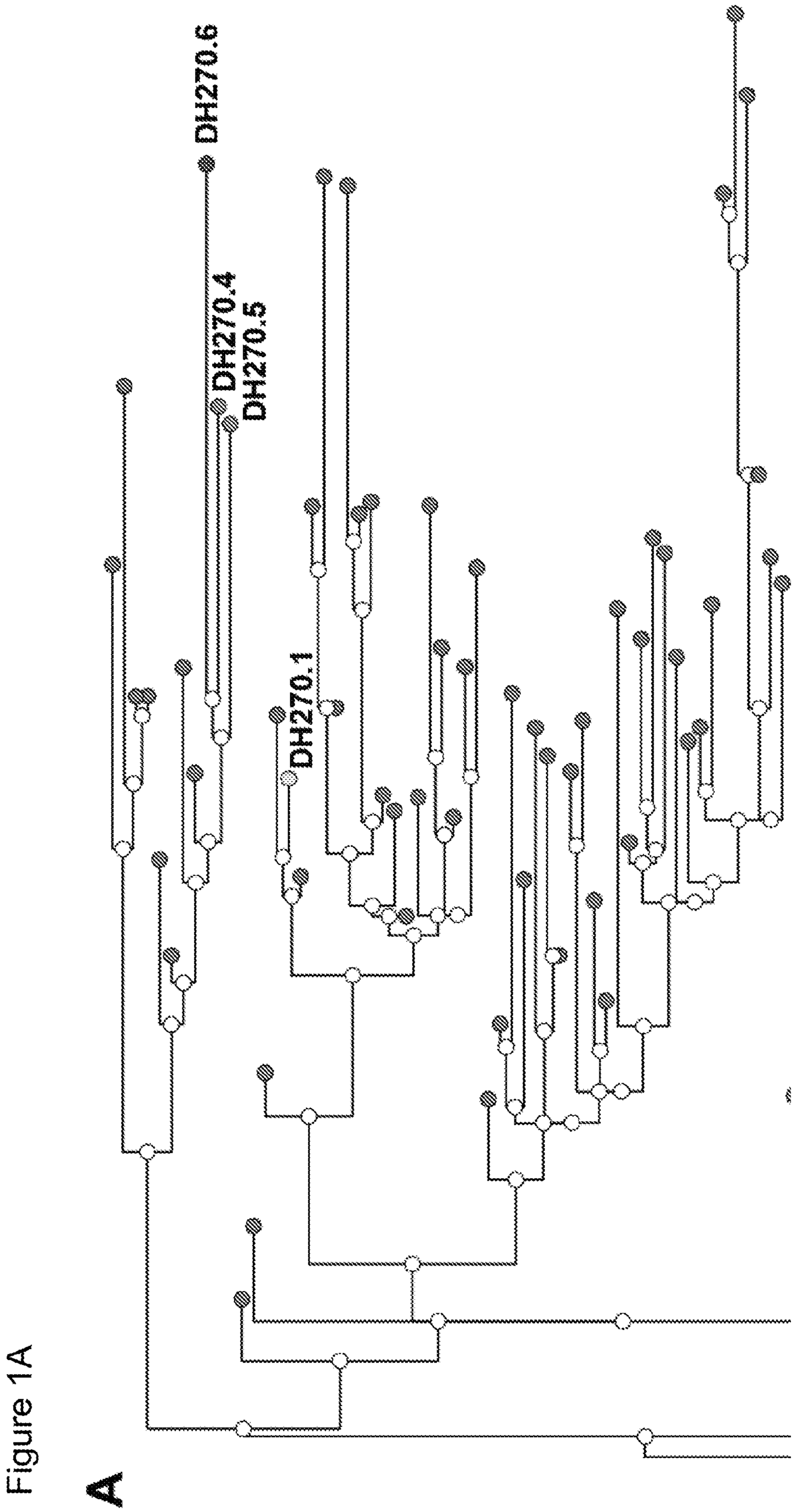


Figure 1A

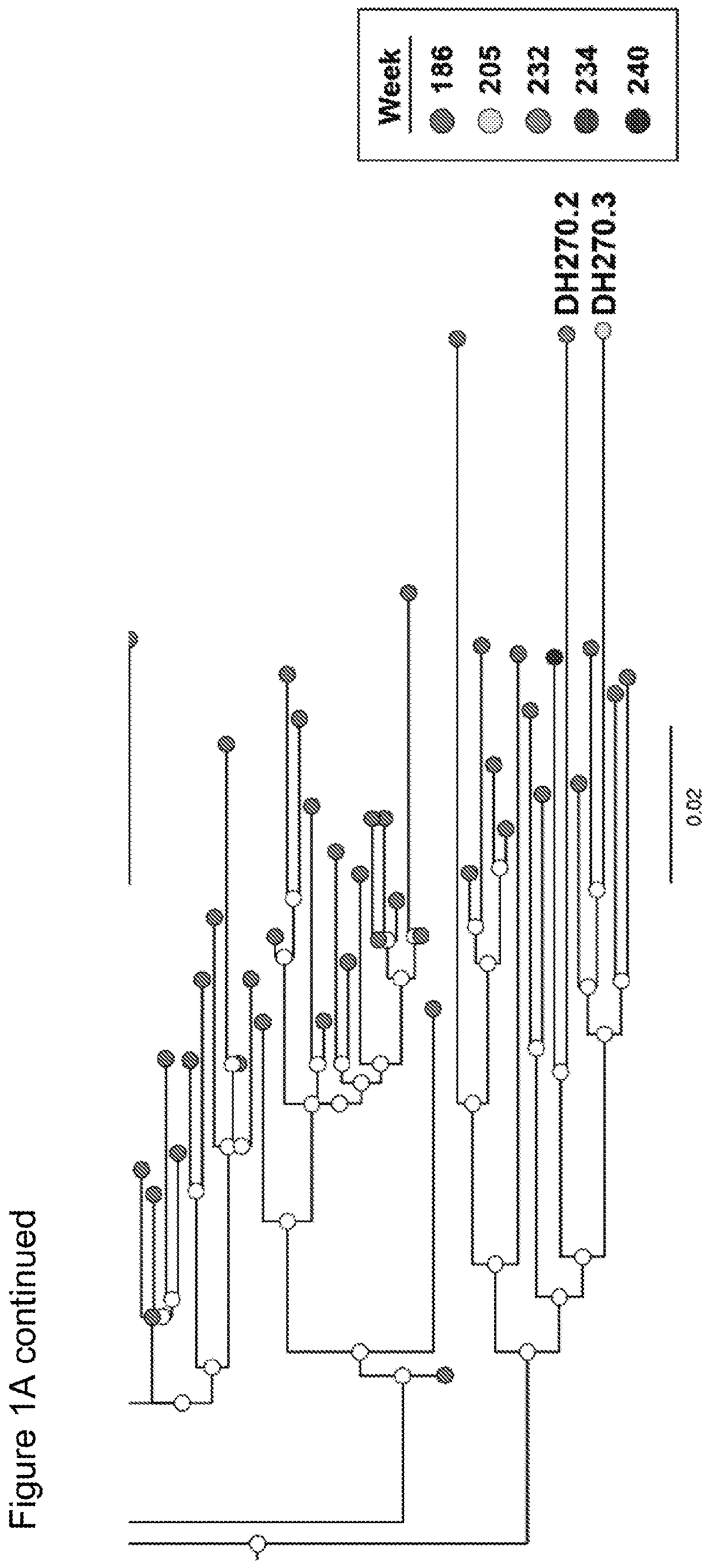


Figure 1A continued

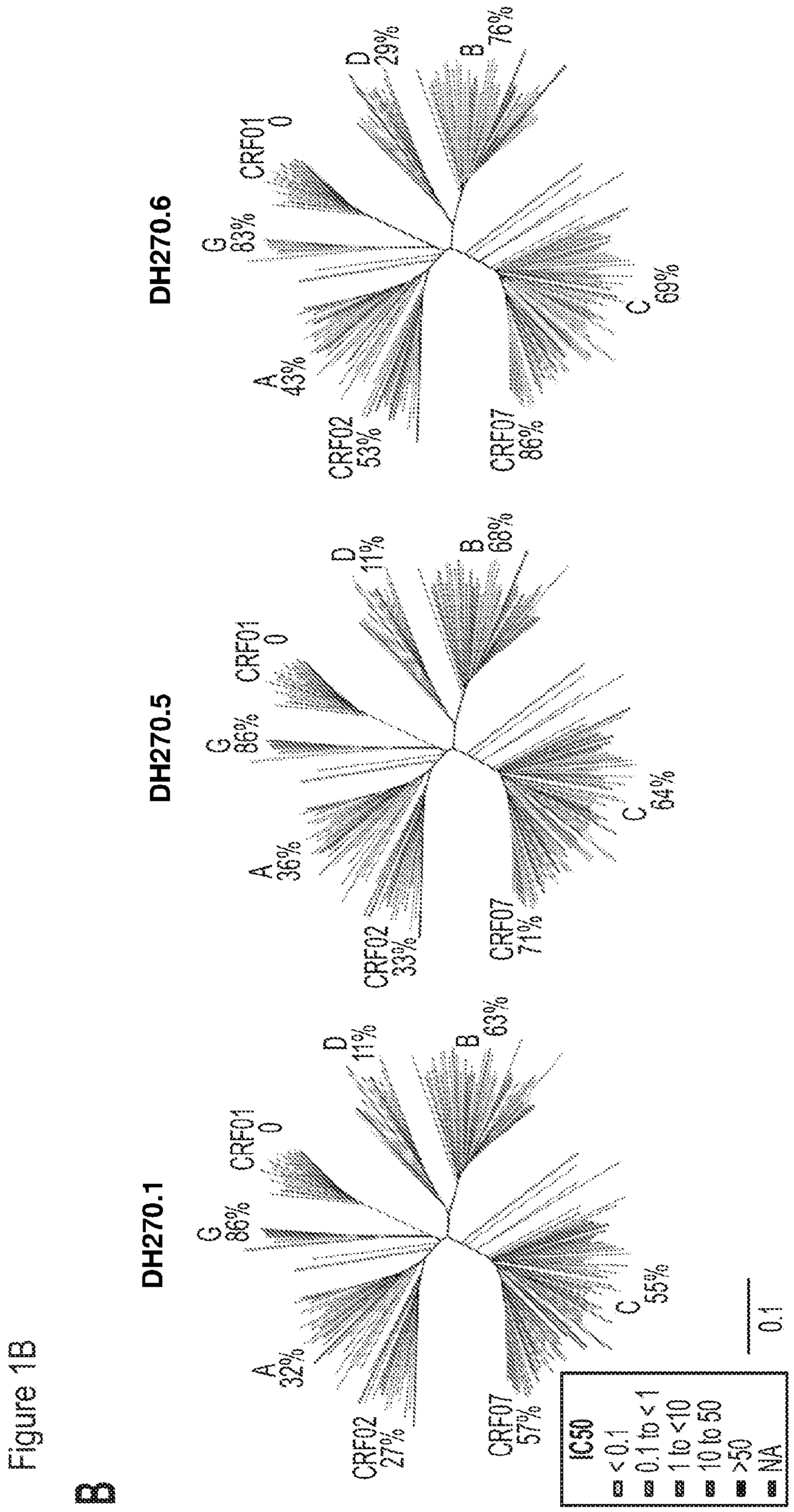

DH270.6
CRF01
0
D
29%
B
76%
G
83%
A
43%
CRF02
53%
CRF07
86%
C
69%
DH270.5
CRF01
0
D
11%
B
68%
G
86%
A
36%
CRF02
33%
CRF07
71%
C
64%
DH270.1
CRF01
0
D
11%
B
63%
G
86%
A
32%
CRF02
27%
CRF07
57%
C
55%
IC50
< 0.1
0.1 to < 1
1 to < 10
10 to 50
>50
NA
0.1

Figure 1B

Figure 2A

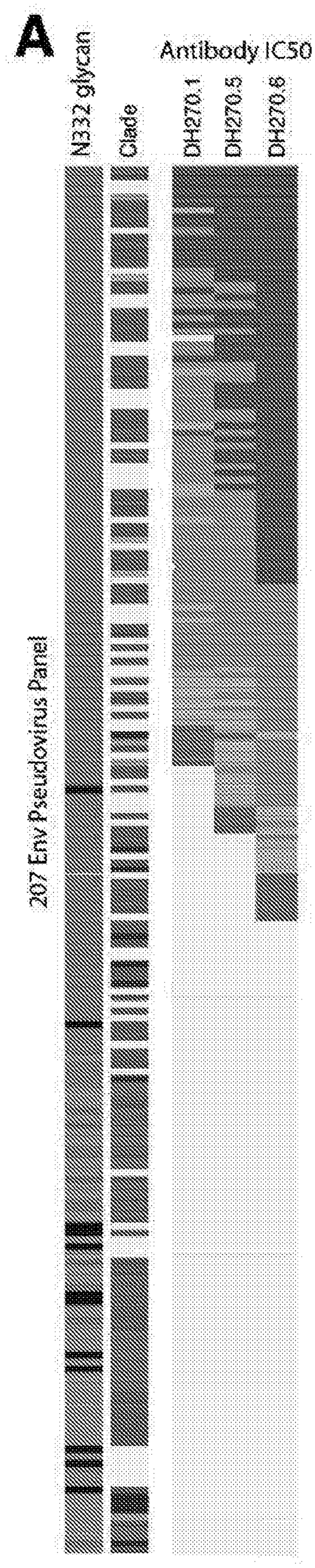

A
Antibody IC50
N332 glycan
Clade
DH270.1
DH270.5
DH270.6
207 Env Pseudovirus Panel

Figure 2B

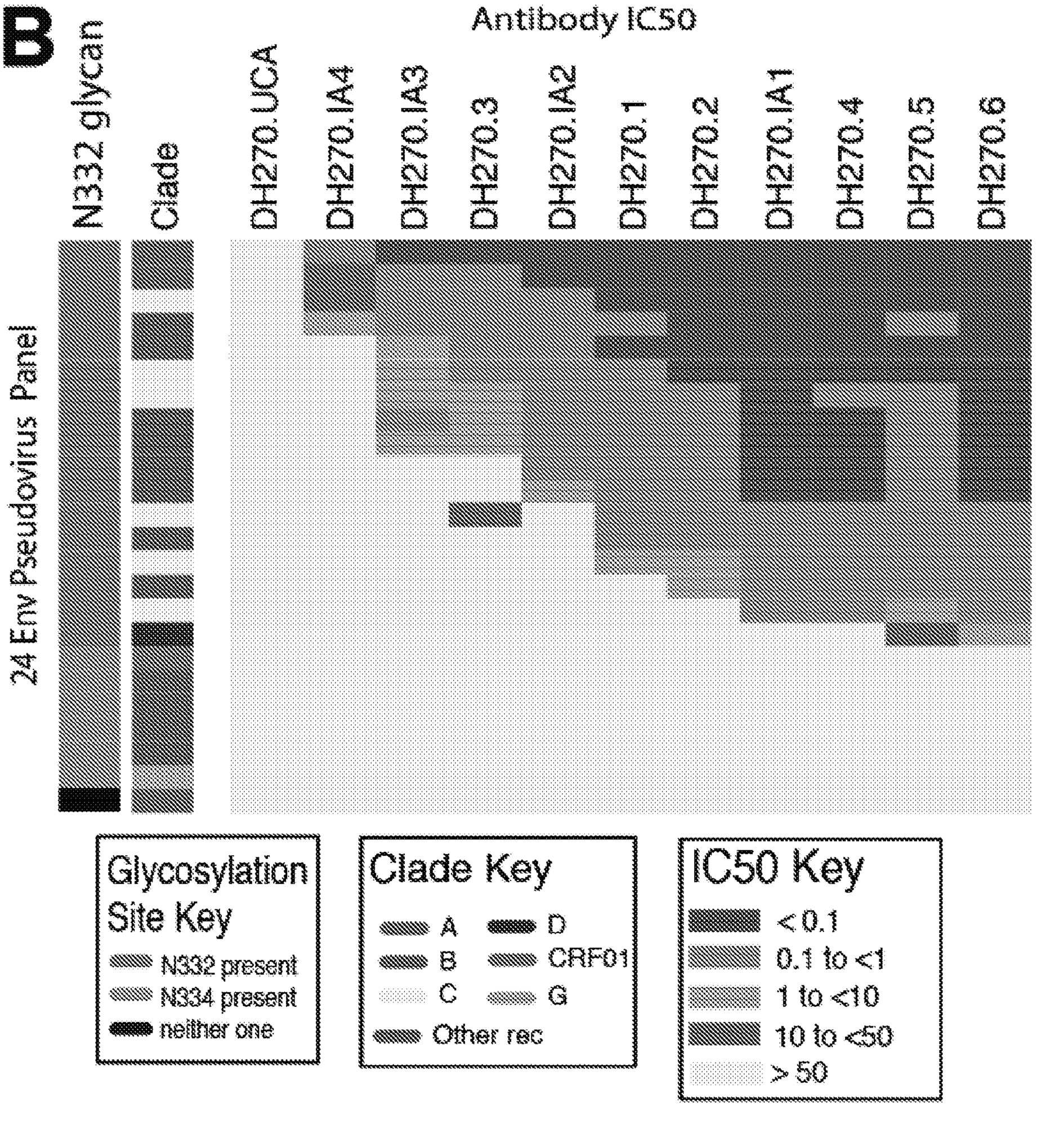

B
Antibody IC50
N332 glycan
Clade
24 Env Pseudovirus Panel
DH270.UCA
DH270.IA4
DH270.IA3
DH270.3
DH270.IA2
DH270.1
DH270.2
DH270.IA1
DH270.4
DH270.5
DH270.6
Glycosylation Site Key
N332 present
N334 present
neither one
Clade Key
A
B
C
D
CRF01
G
Other rec
IC50 Key
< 0.1
0.1 to <1
1 to <10
10 to <50
> 50

Figure 2C

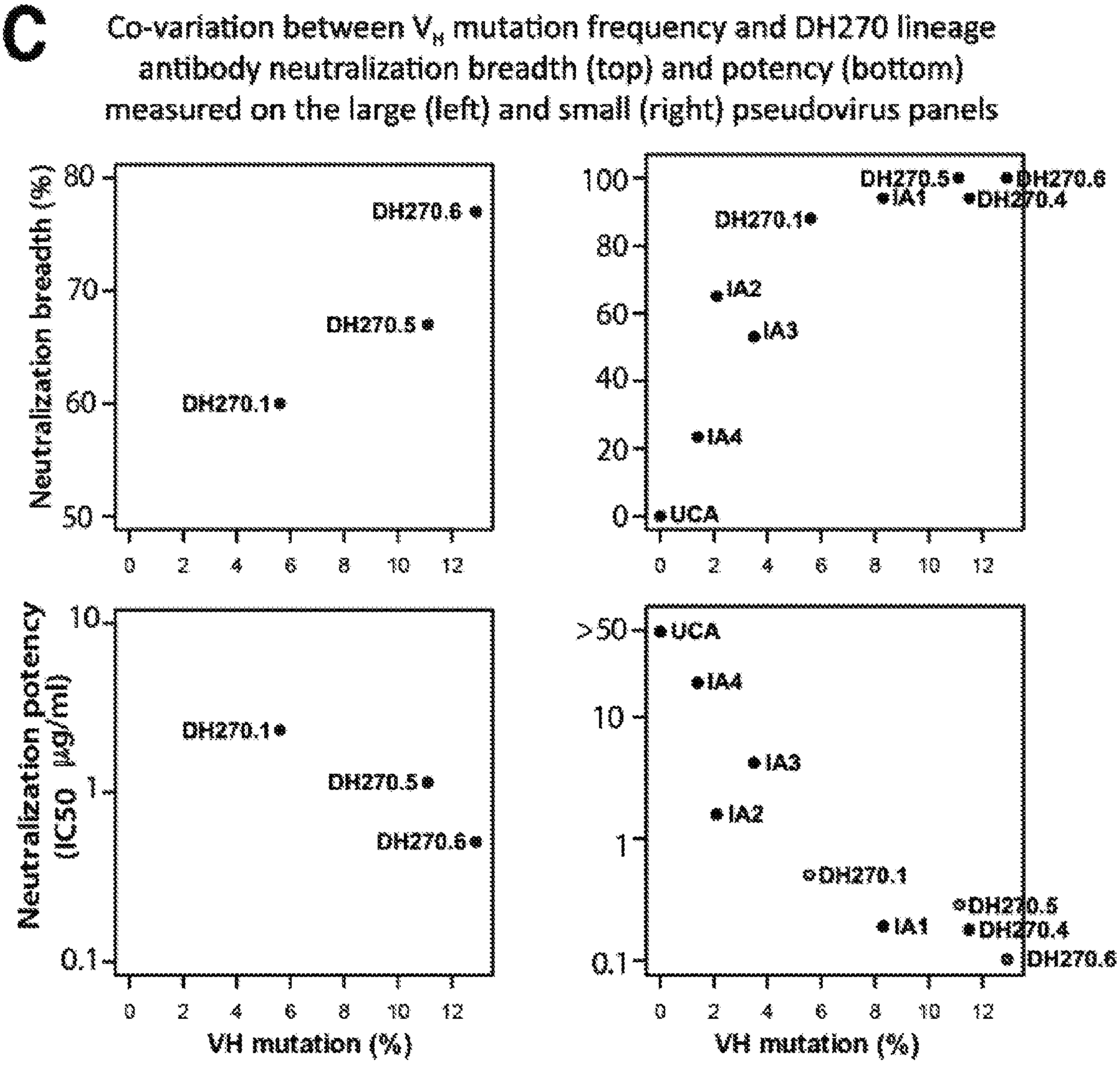

C
Co-variation between V_H mutation frequency and DH270 lineage antibody neutralization breadth (top) and potency (bottom) measured on the large (left) and small (right) pseudovirus panels
Neutralization breadth (%)
80
70
60
50
DH270.6
DH270.5
DH270.1
100
80
60
40
20
0
DH270.5
DH270.6
IA1
DH270.4
DH270.1
IA2
IA3
IA4
UCA
0 2 4 6 8 10 12
Neutralization potency (IC50 µg/ml)
10
1
0.1
>50
DH270.1
DH270.5
DH270.6
UCA
IA4
IA3
IA2
IA1
DH270.4
VH mutation (%)

Figure 2D

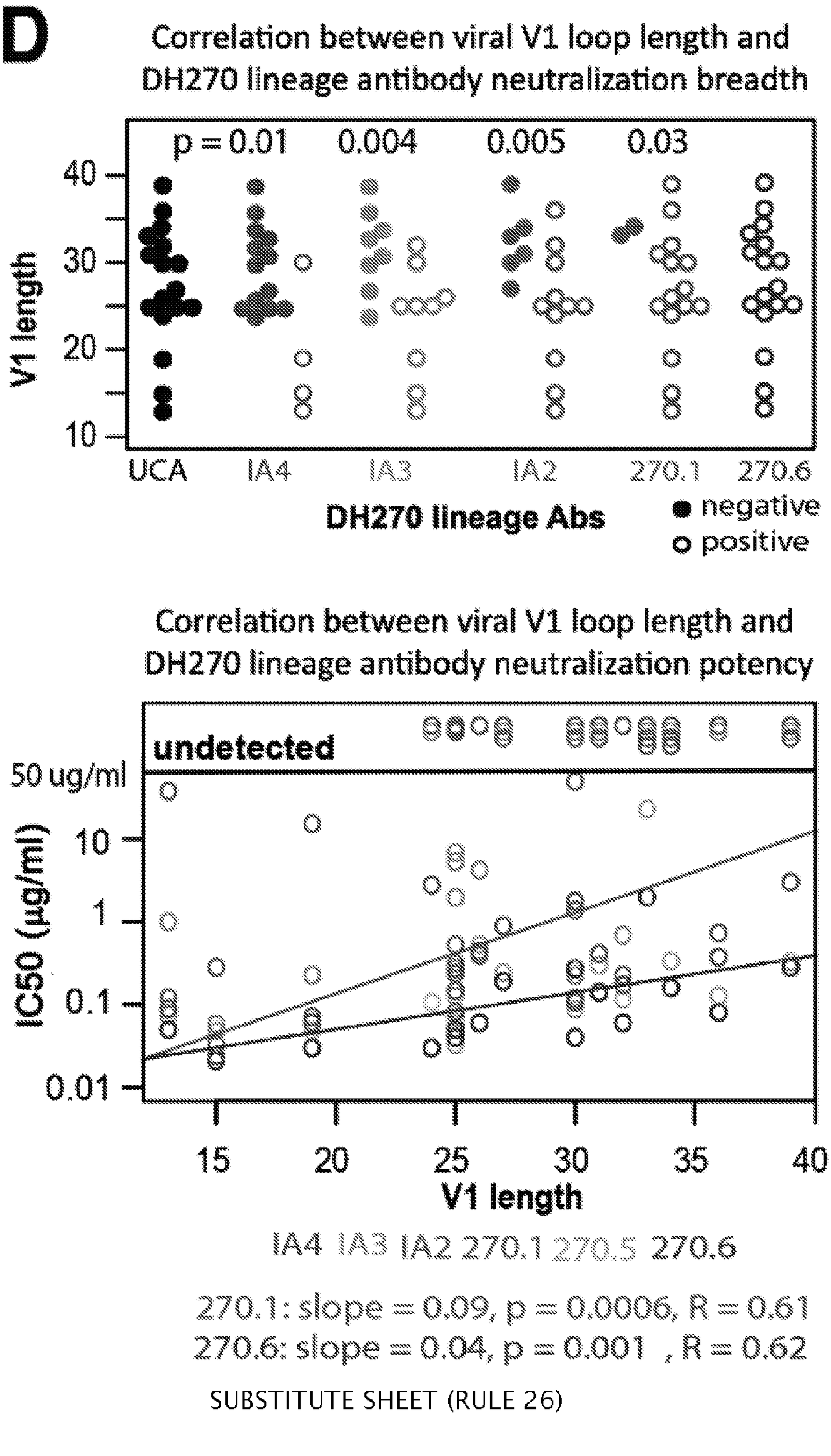
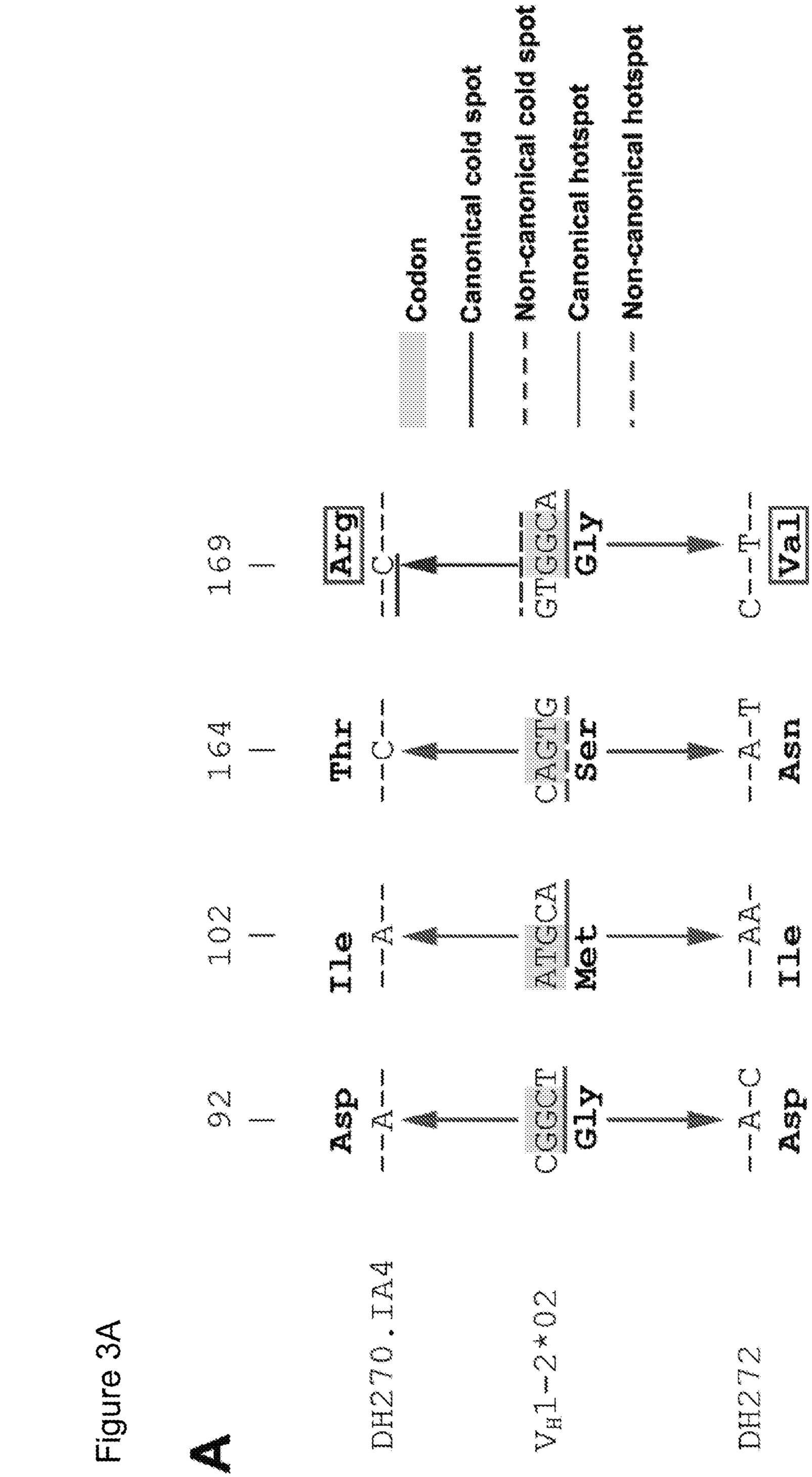
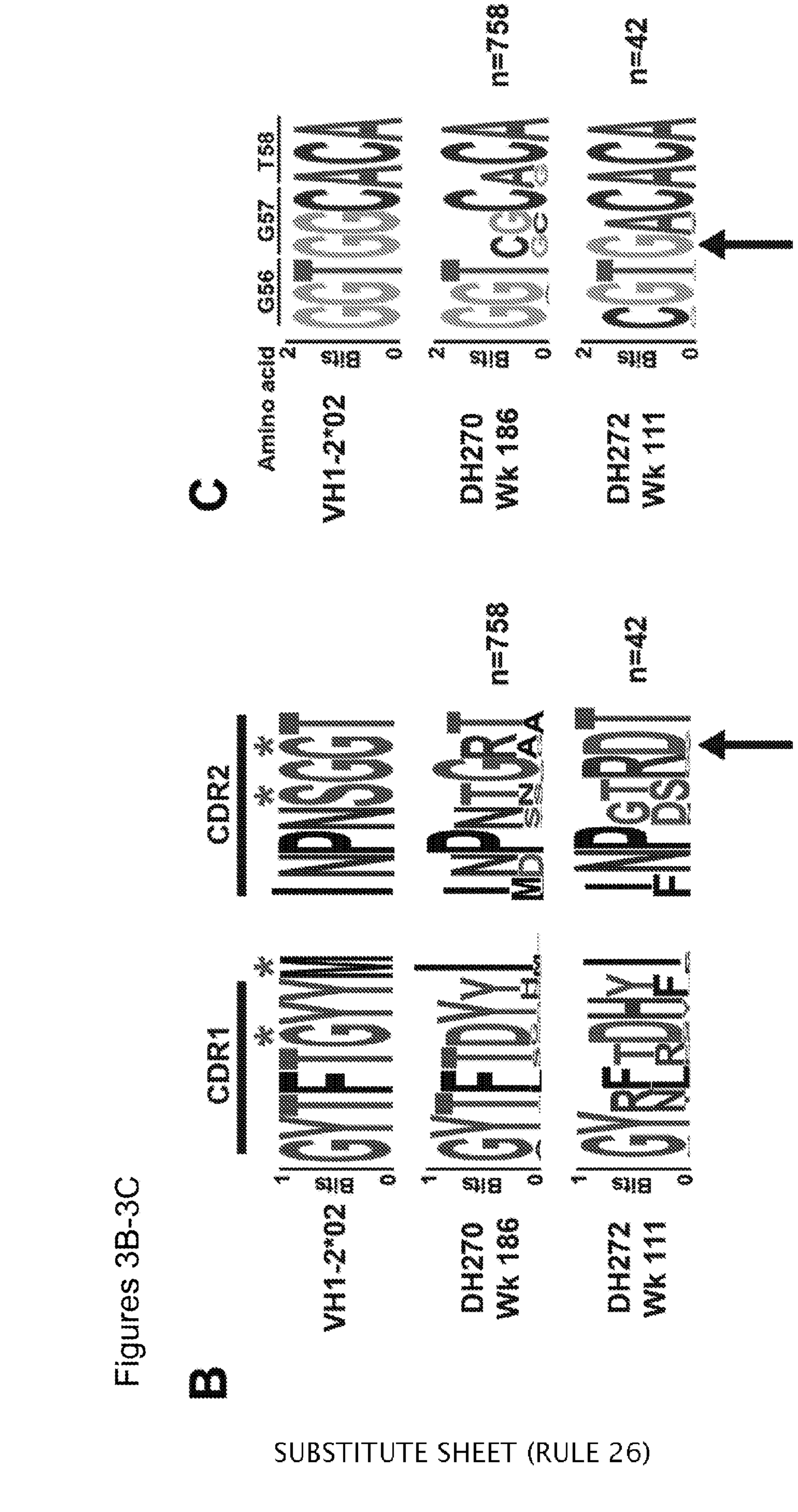
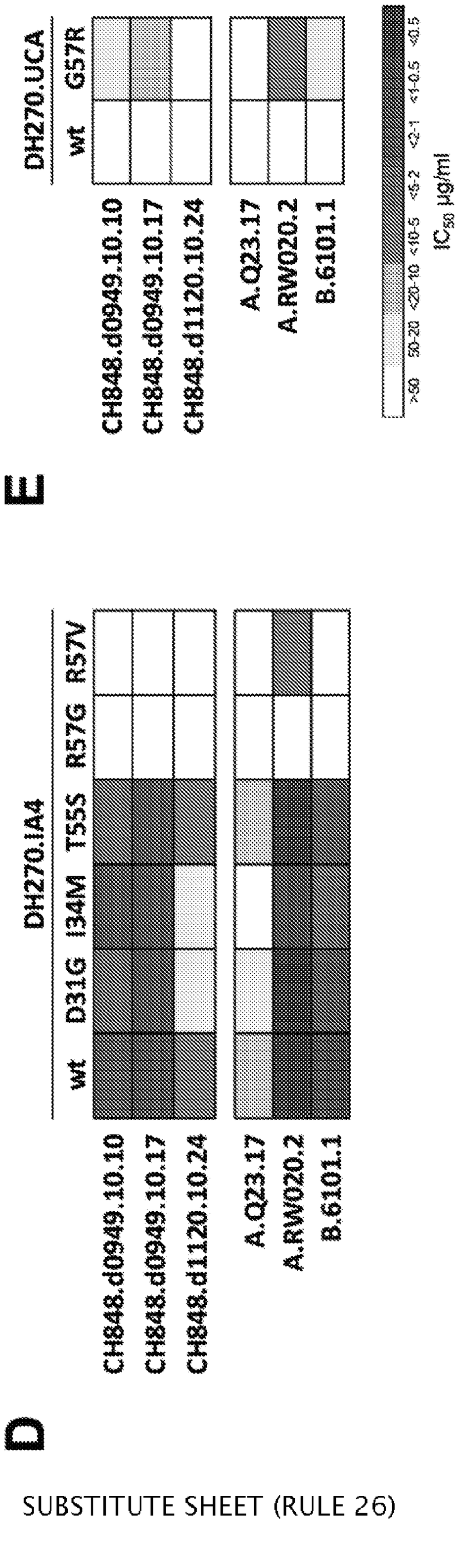

D
Correlation between viral V1 loop length and DH270 lineage antibody neutralization breadth
p = 0.01
0.004
0.005
0.03
40
30
20
10
V1 length
UCA
IA4
IA3
IA2
270.1
270.6
DH270 lineage Abs
negative
positive
Correlation between viral V1 loop length and DH270 lineage antibody neutralization potency
undetected
50 ug/ml
10
1
0.1
0.01
IC50 (µg/ml)
15
20
25
30
35
40
V1 length
IA4 IA3 IA2 270.1 270.5 270.6
270.1: slope = 0.09, p = 0.0006, R = 0.61
270.6: slope = 0.04, p = 0.001 , R = 0.62

Figure 3A

A


DH270.1A4
VH1-2*02
DH272
92
102
164
169
Asp
Ile
Thr
Arg
GCCT
ATGCA
CAGTG
GTCCCA
Gly
Met
Ser
Gly
Codon
Canonical cold spot
Non-canonical cold spot
Canonical hotspot
Non-canonical hotspot


Figures 3B-3C
B
C
CDR1
CDR2
Amino acid
bits
VH1-2*02
DH270
Wk 186
DH272
Wk 111
n=758
n=42
G56
G57
T58



Figures 3D-3E

Figure 4A

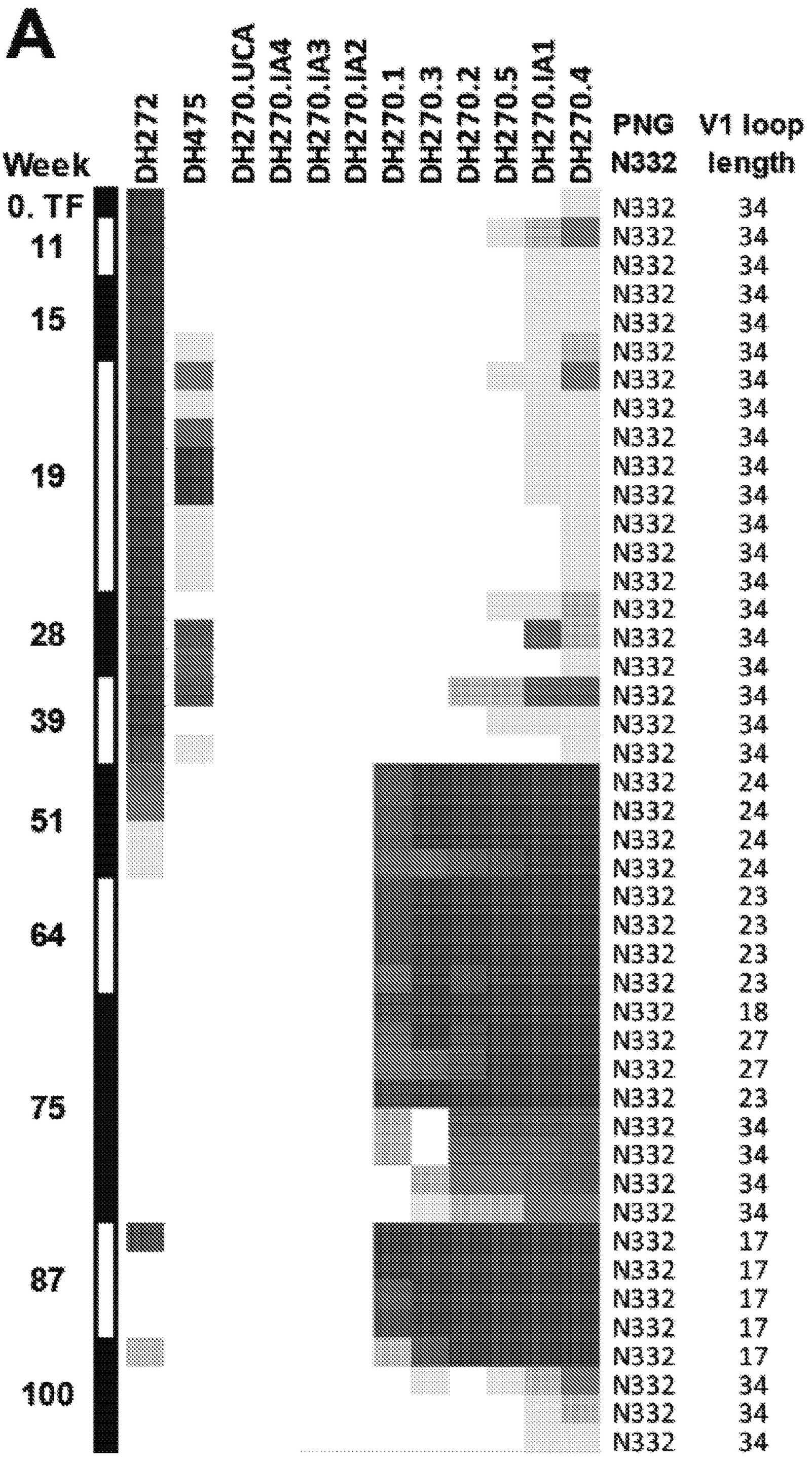
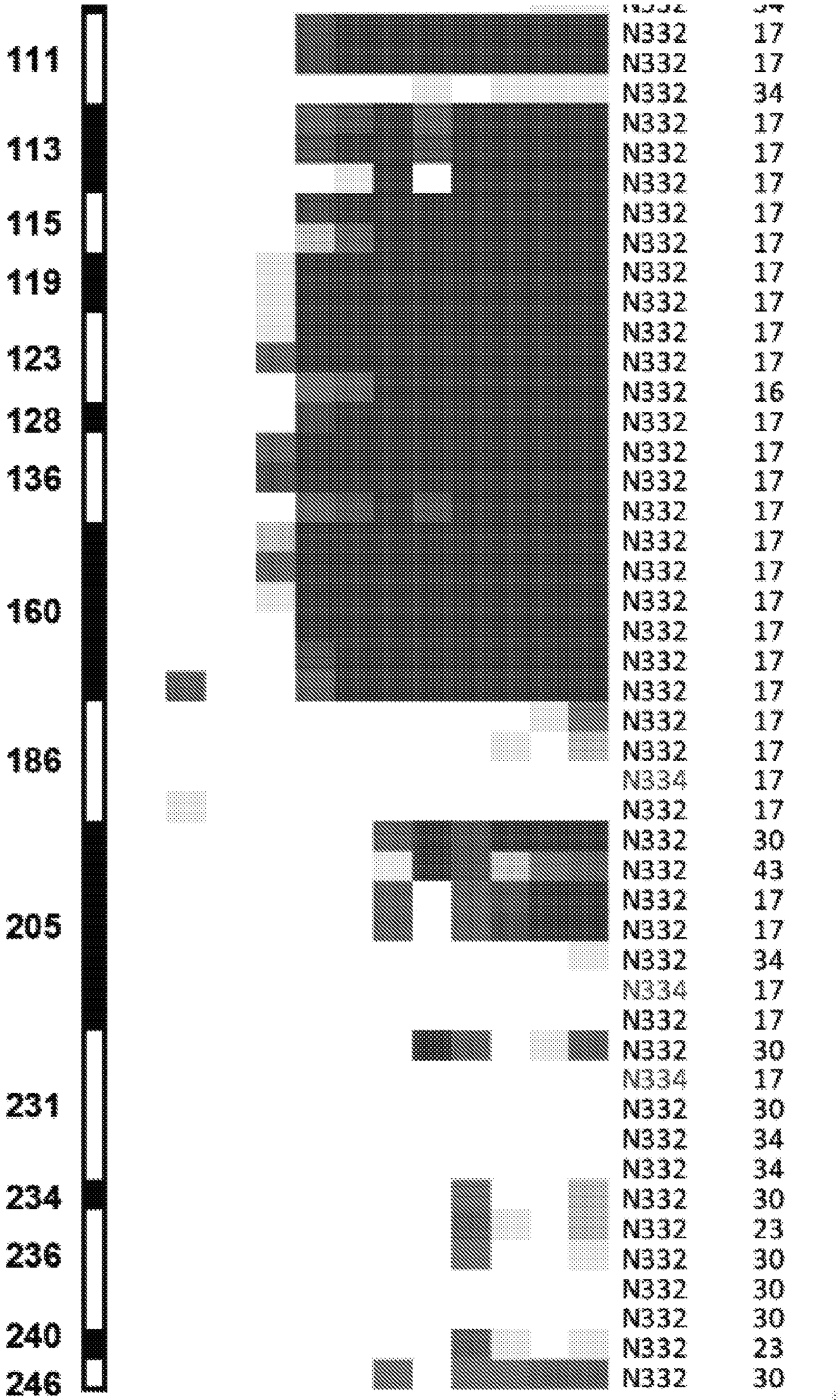
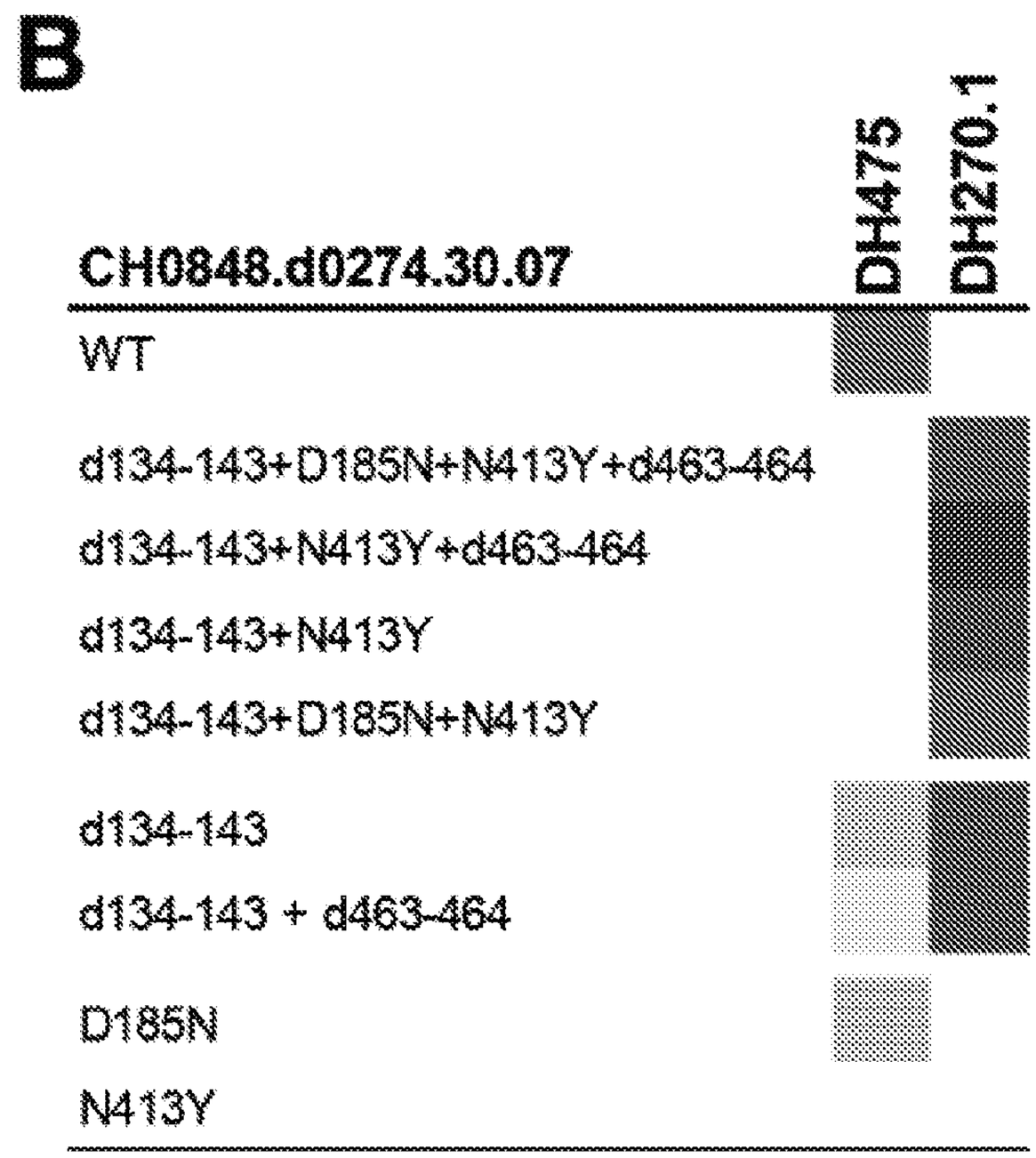
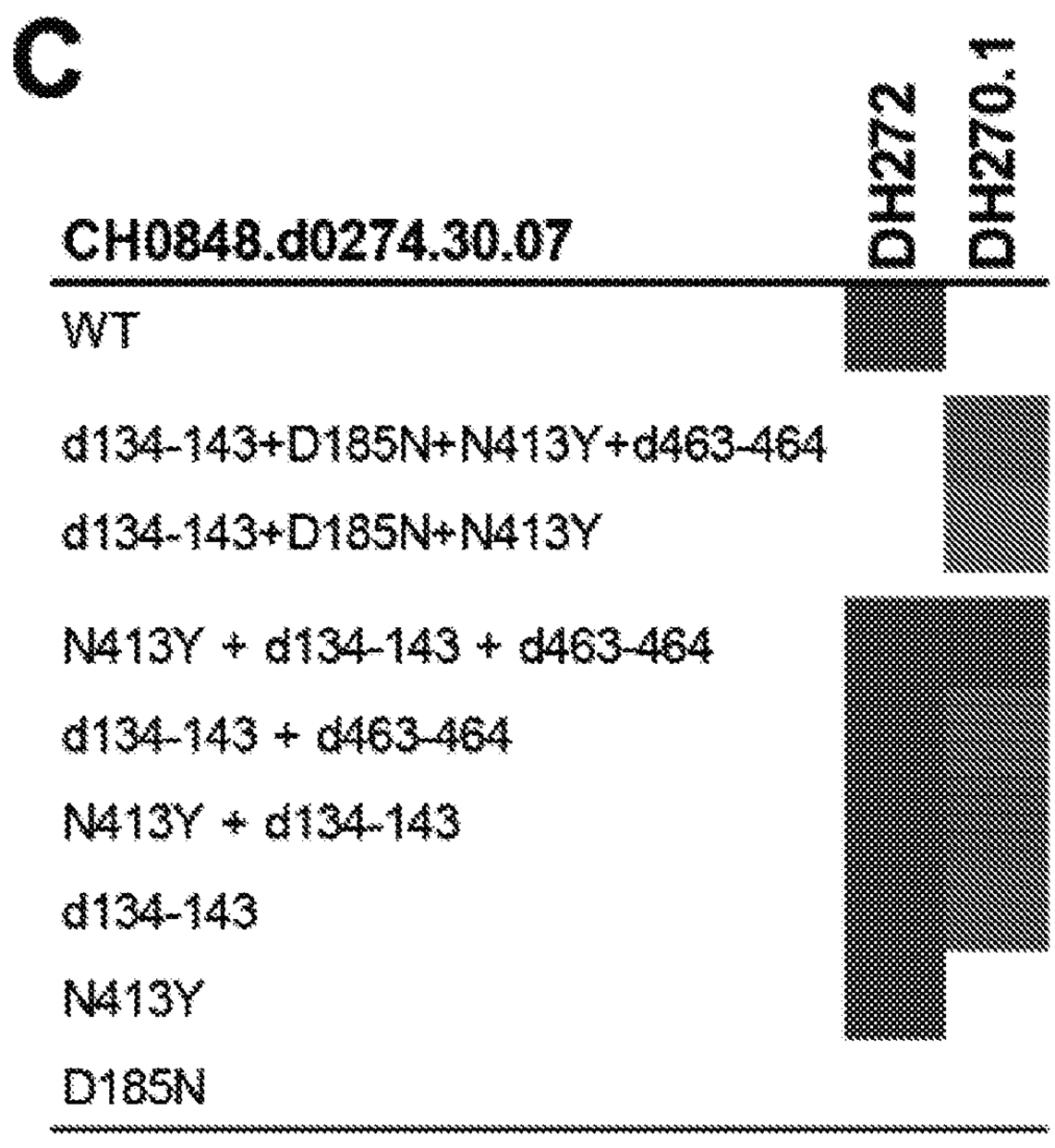

A
Week
DH272
DH475
DH270.UCA
DH270.iA4
DH270.iA3
DH270.iA2
DH270.1
DH270.3
DH270.2
DH270.5
DH270.iA1
DH270.4
PNG N332
V1 loop length
0. TF
11
15
19
28
39
51
64
75
87
100
N332 34
N332 24
N332 23
N332 18
N332 27
N332 17

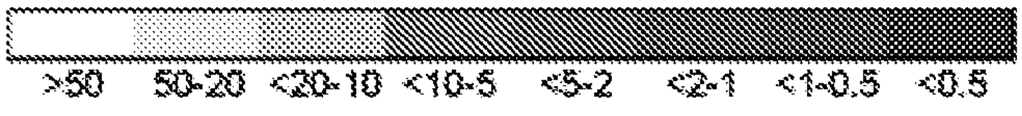
Figure 4A continued

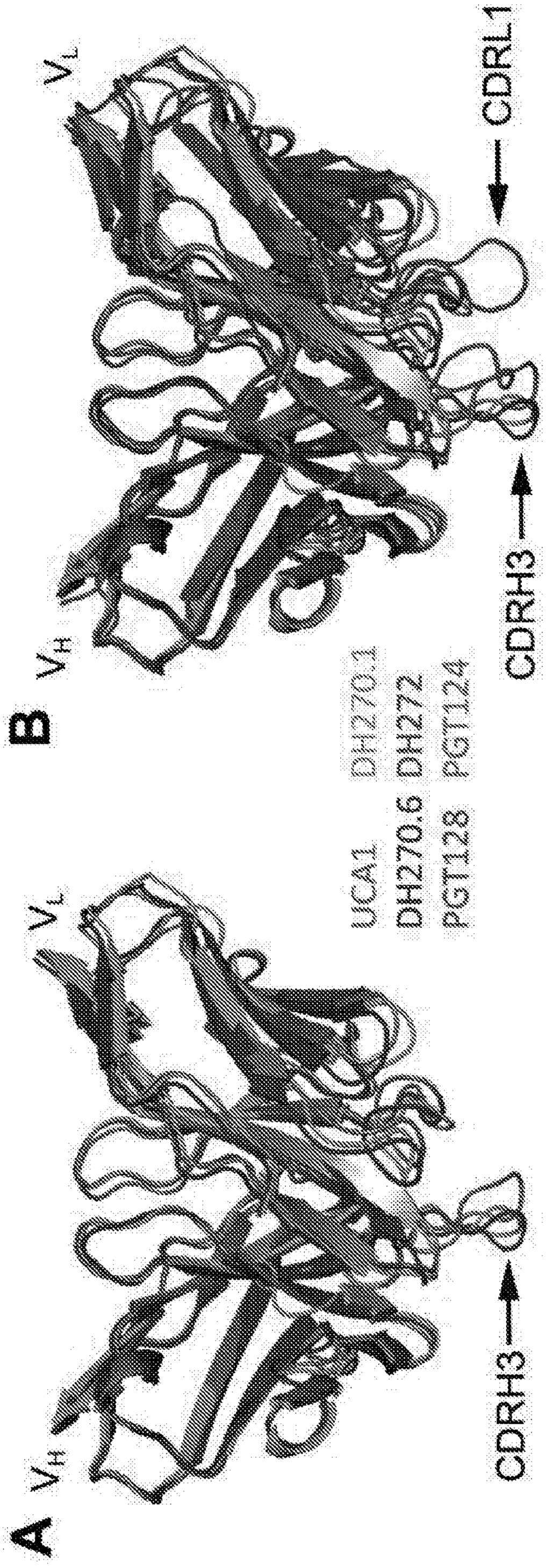


Figures 4B-4C

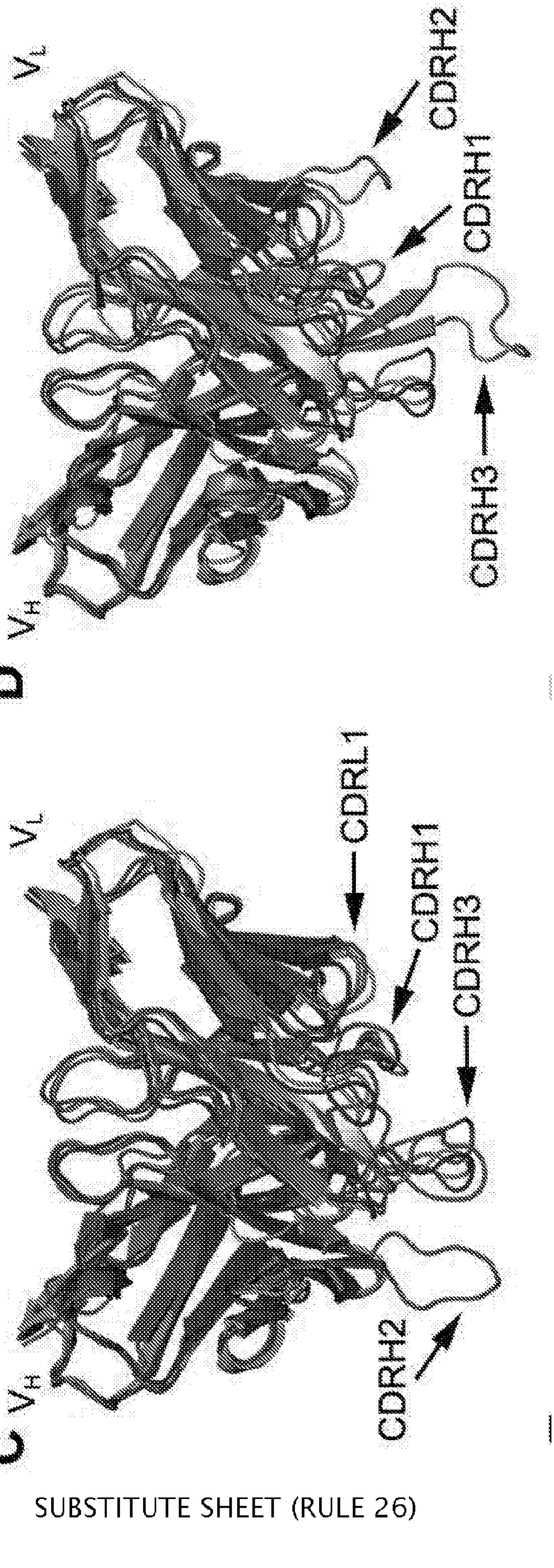




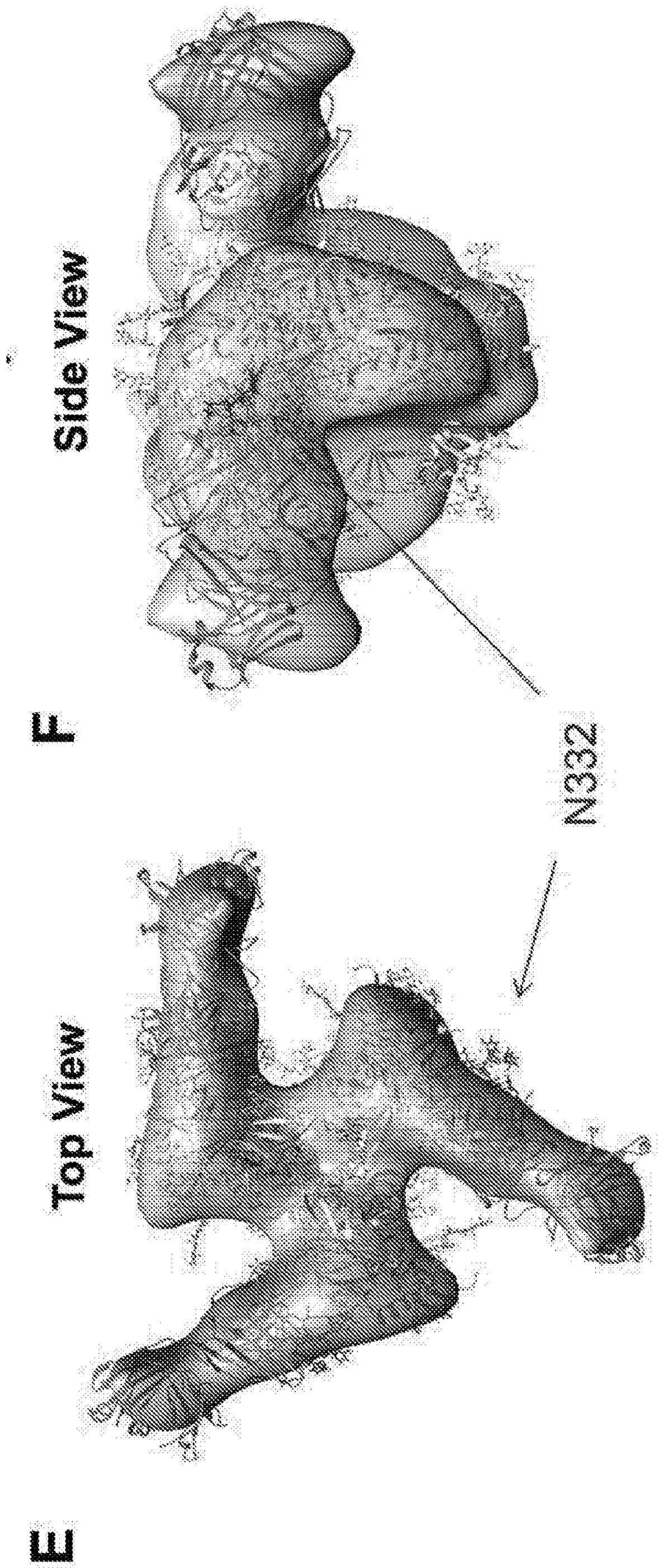




Figures 5A-5B

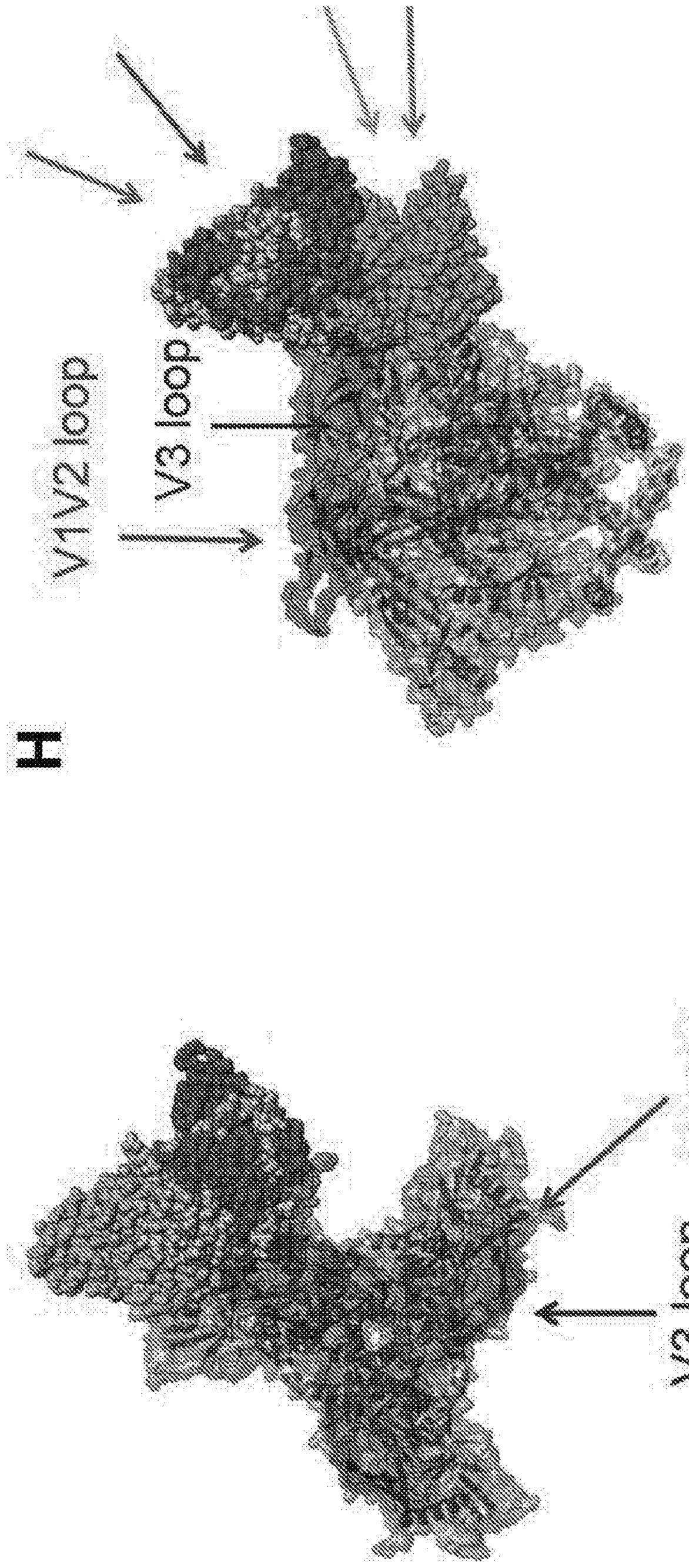


Figures 5C-5D



Figures 5E-5F

E



Figures 5G-5H

Figure 6A

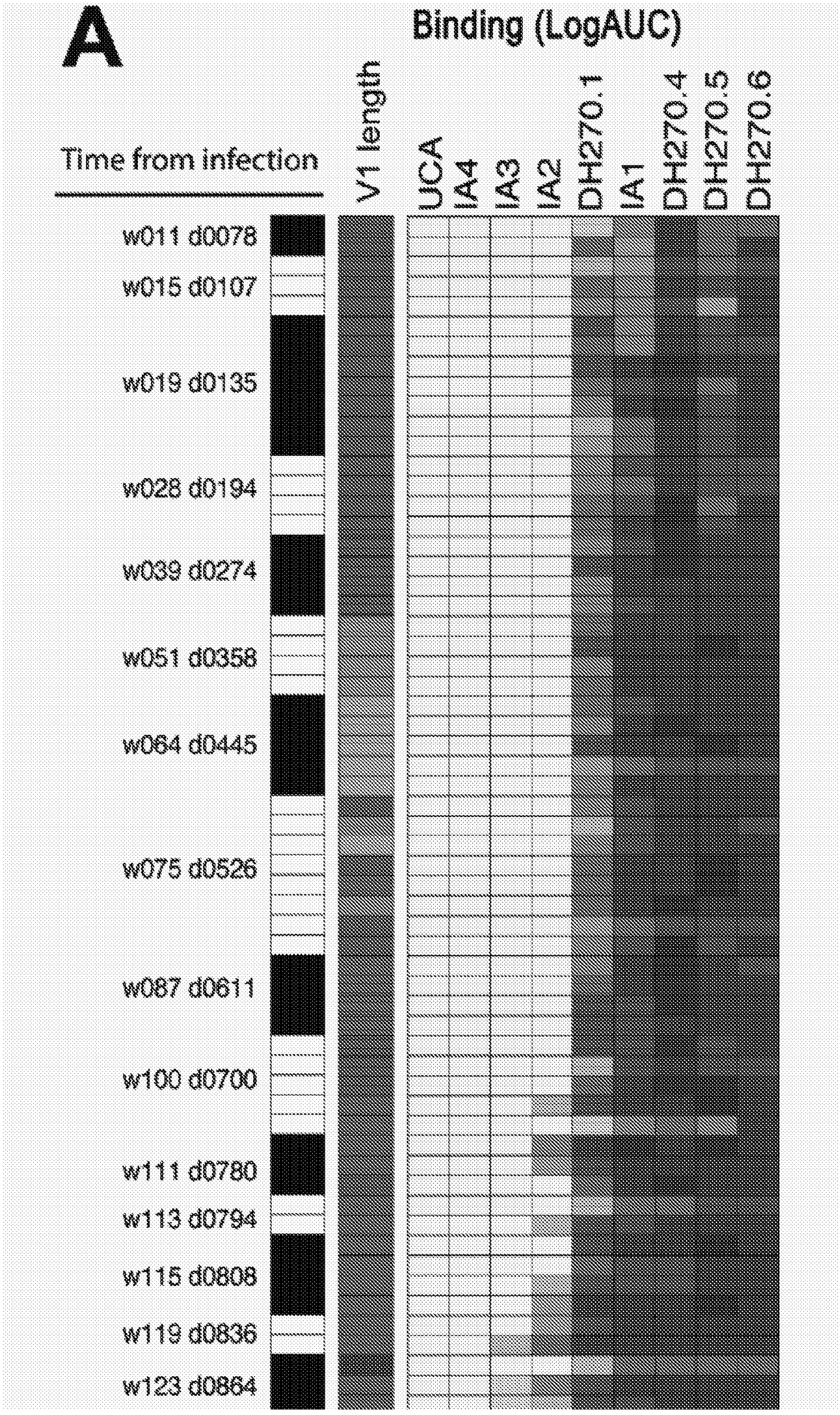

A
Binding (LogAUC)
Time from infection
V1 length
UCA
IA4
IA3
IA2
DH270.1
IA1
DH270.4
DH270.5
DH270.6
w011 d0078
w015 d0107
w019 d0135
w028 d0194
w039 d0274
w051 d0358
w064 d0445
w075 d0526
w087 d0611
w100 d0700
w111 d0780
w113 d0794
w115 d0808
w119 d0836
w123 d0864

Figure 6A continued

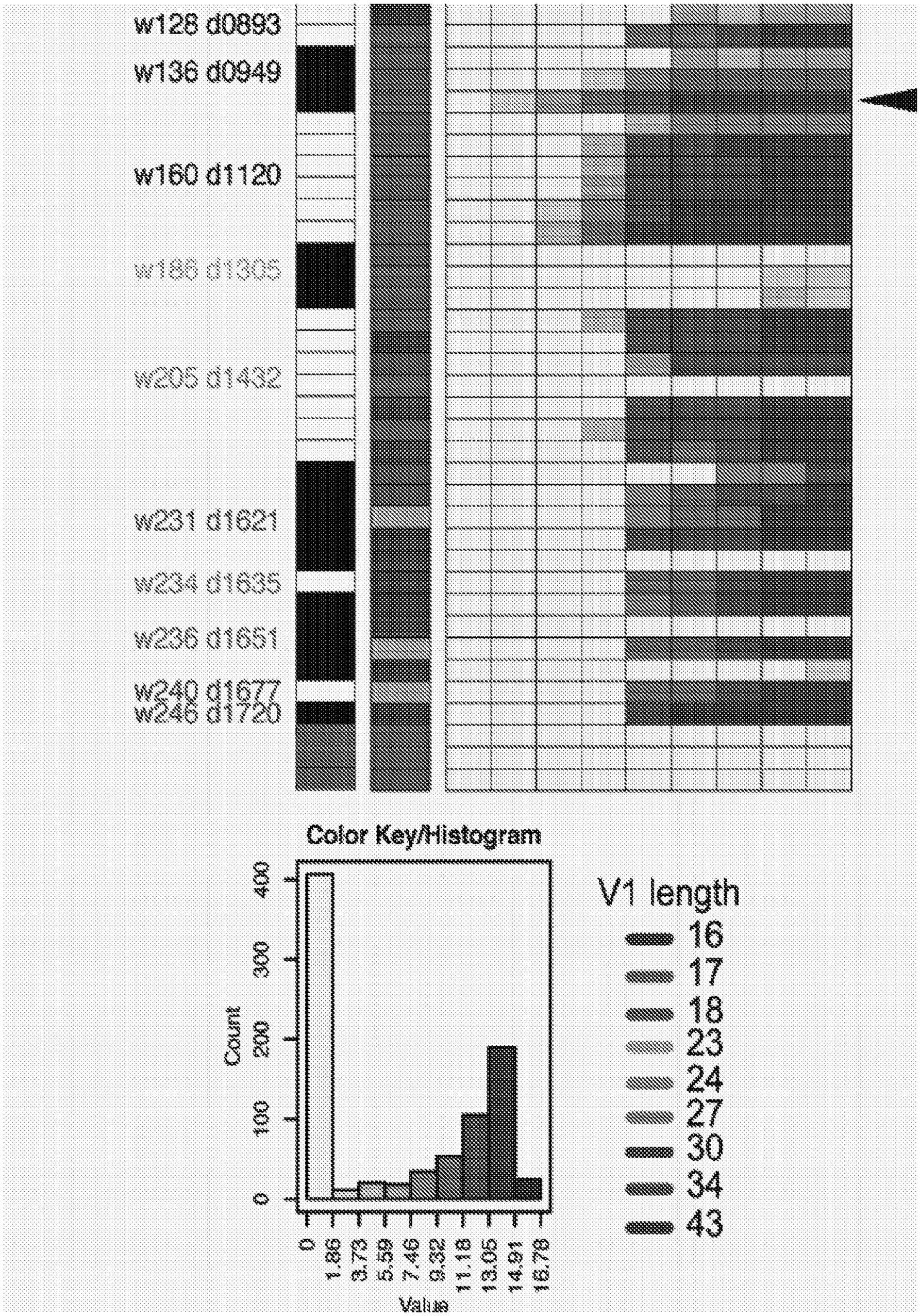


Figure 6B

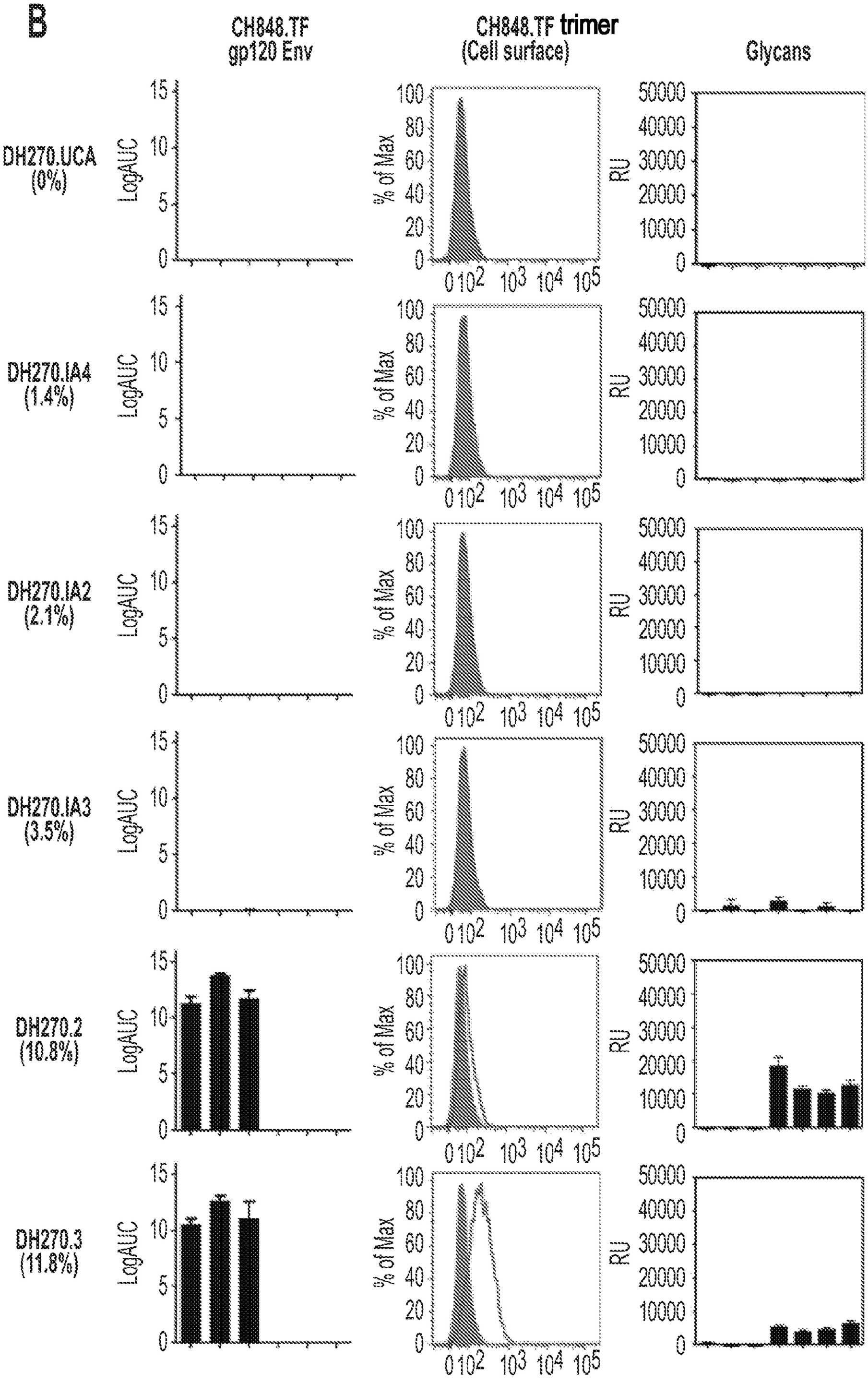

B
CH848.TF gp120 Env
CH848.TF trimer (Cell surface)
Glycans
DH270.UCA (0%)
DH270.IA4 (1.4%)
DH270.IA2 (2.1%)
DH270.IA3 (3.5%)
DH270.2 (10.8%)
DH270.3 (11.8%)
LogAUC
% of Max
RU
0 5 10 15
0 20 40 60 80 100
0 10000 20000 30000 40000 50000
0 10^2 10^3 10^4 10^5

Figure 6B continued

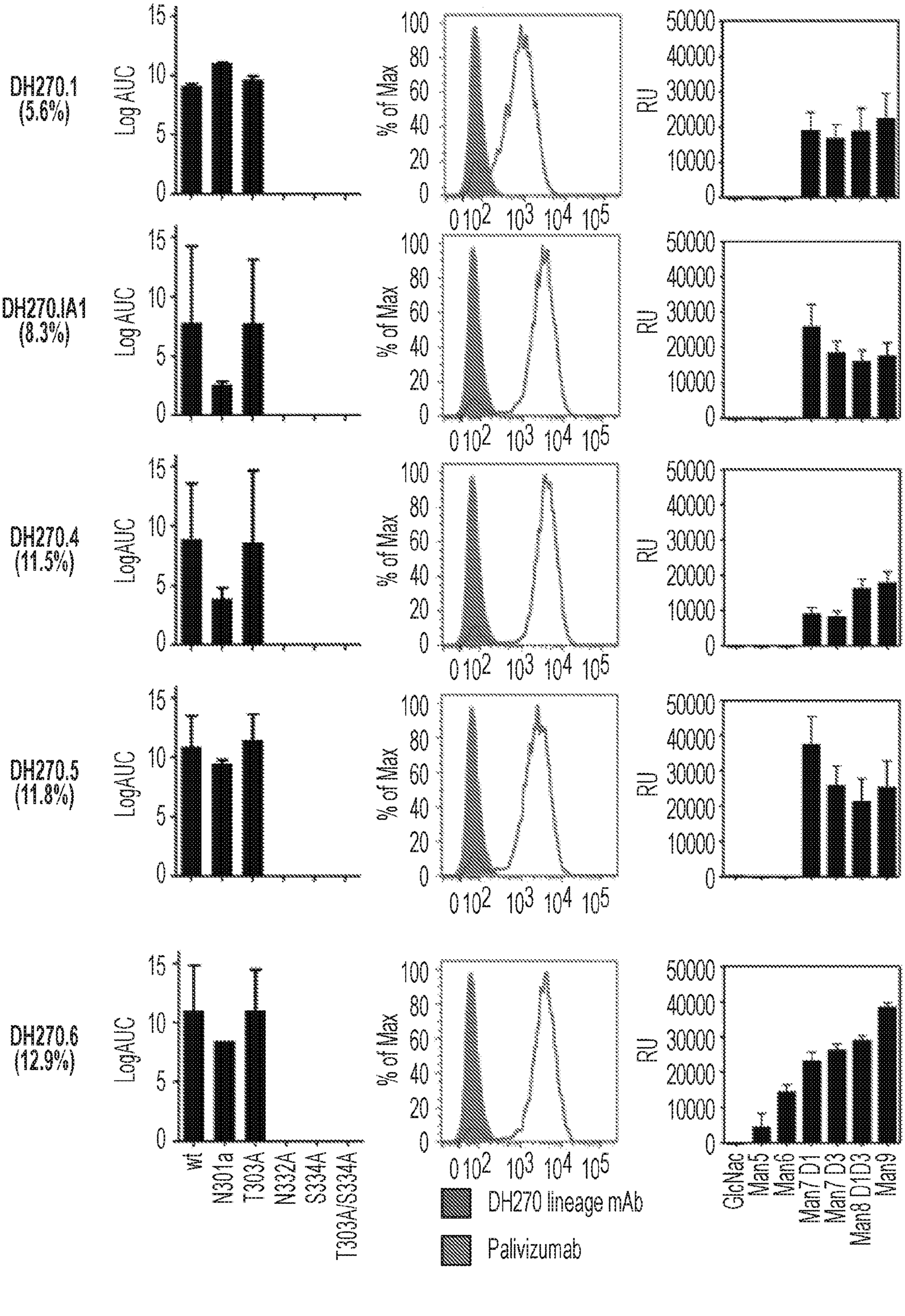


Figure 7A

Antibody ID	V_H	D	J_H	Mutation frequency V_H	Mutation frequency V_HDJ_H nt	Mutation frequency V_HDJ_H aa	CDRH3 length	VL	JL	Mutation frequency V_L	Mutation frequency V_LJ_L nt	Mutation frequency V_LJ_L aa	CDRL3 length	Week of isolation	Inser dele
DH270.UCA	1-2*02	3-22*01	4*02	0.0%	0 (0%)	0 (0%)	20	2-23*02	2*01	0.0%	0 (0%)	0 (0%)	10	-	no
DH270.IA4	1-2*02	3-22*01	4*02	1.4%	4/381 (1.0%)	4/127 (3.1%)	20	2-23*02	2*01	0.7%	2/330 (0.6%)	1/110 (0.9%)	10	-	no
DH270.IA2	1-2*02	3-22*01	4*02	2.1%	7/381 (1.8%)	7/127 (5.5%)	20	2-23*02	2*01	2.1%	6/330 (1.8%)	3/110 (2.7%)	10	-	no
DH270.IA3	1-2*02	3-22*01	4*02	3.5%	16/381 (4.2%)	11/127 (8.7%)	20	2-23*02	2*01	1.4%	4/330 (1.2%)	2/110 (1.8%)	10	-	no
DH270.1	1-2*02	3-22*01	4*02	5.6%	21/381 (5.5%)	18/127 (14.2%)	20	2-23*02	2*01	5.2%	21/330 (6.3%)	11/110 (10.0%)	10	205	no
DH270.IA1	1-2*02	3-22*01	4*02	8.3%	33/381 (8.7%)	22/127 (17.3%)	20	2-23*02	2*01	6.9%	26/330 (7.9%)	14/110 (12.7%)	10	-	no
DH270.2	1-2*02	3-22*01	4*02	10.8%	46/381 (12.1%)	27/127 (21.3%)	20	2-23*02	2*01	3.8%	13/330 (3.9%)	7/110 (6.4%)	10	232	no
DH270.3	1-2*02	3-22*01	4*02	11.8%	48/381 (12.6%)	27/127 (21.3%)	20	2-23*02	2*01	8.3%	27/330 (8.2%)	16/110 (14.5%)	10	205	no
DH270.4	1-2*02	3-22*01	4*02	11.5%	44/381 (11.6%)	28/127 (22.0%)	20	2-23*02	2*01	8.0%	29/330 (8.8%)	16/110 (14.5%)	10	232	no
DH270.5	1-2*02	3-22*01	4*02	11.1%	45/381 (11.8%)	26/127 (20.5%)	20	2-23*02	2*01	11.5%	41/330 (12.4%)	22/110 (20.0%)	10	232	no
DH270.6	1-2*02	3-22*01	4*02	12.9%	47/381 (12.3%)	28/127 (22.0%)	20	2-23*02	2*01	7.6%	39/330 (11.8%)	17/110 (15.5%)	10	234	no

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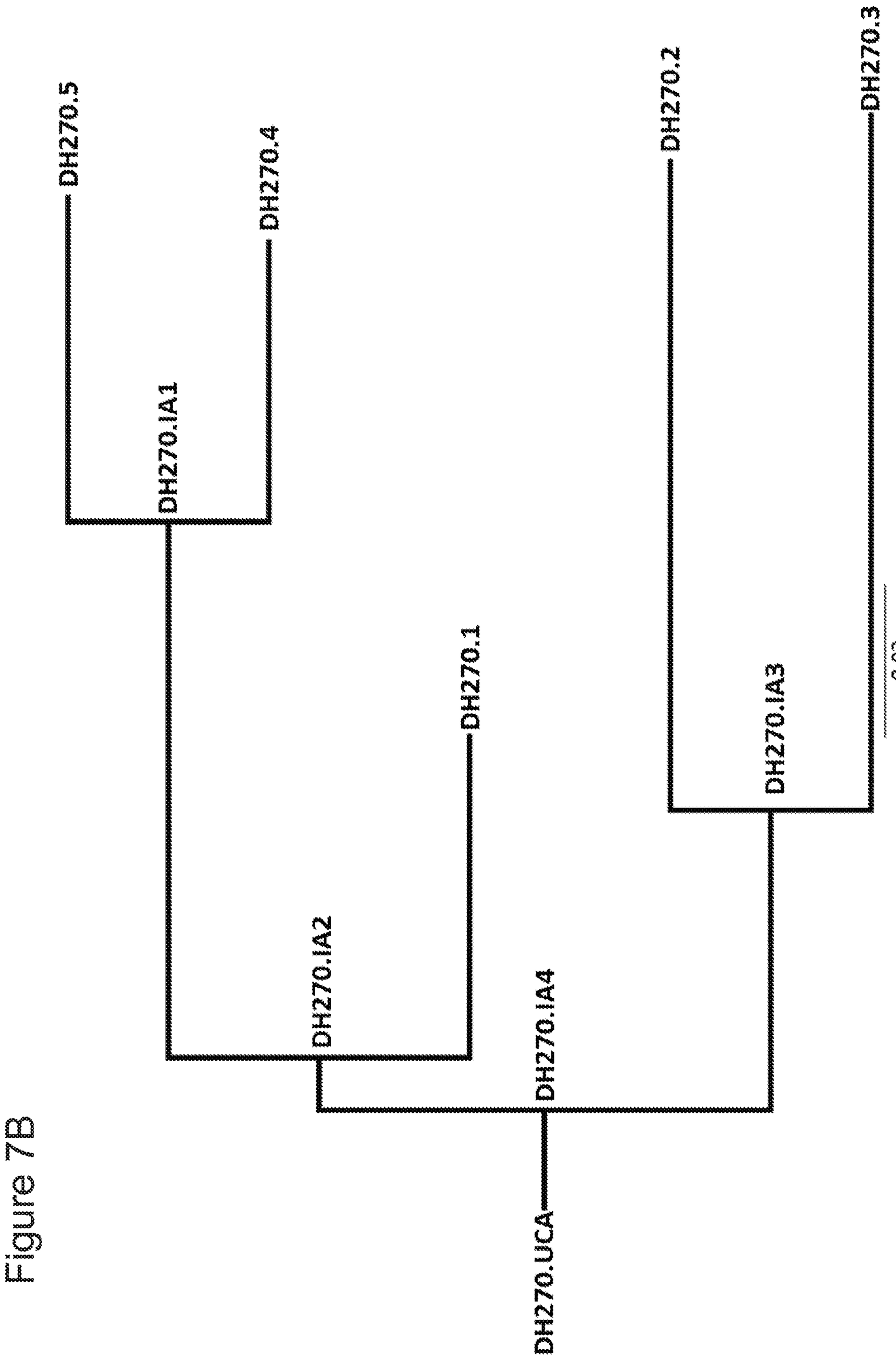

DH270.5
DH270.4
DH270.IA1
DH270.2
DH270.3
DH270.1
DH270.IA3
DH270.IA2
DH270.IA4
DH270.UCA
0.02

Figure 7B

Figure 7C

Amino Acid Sequence Alignment of DH270 Lineage Antibodies V_HDJ_H rearrangements

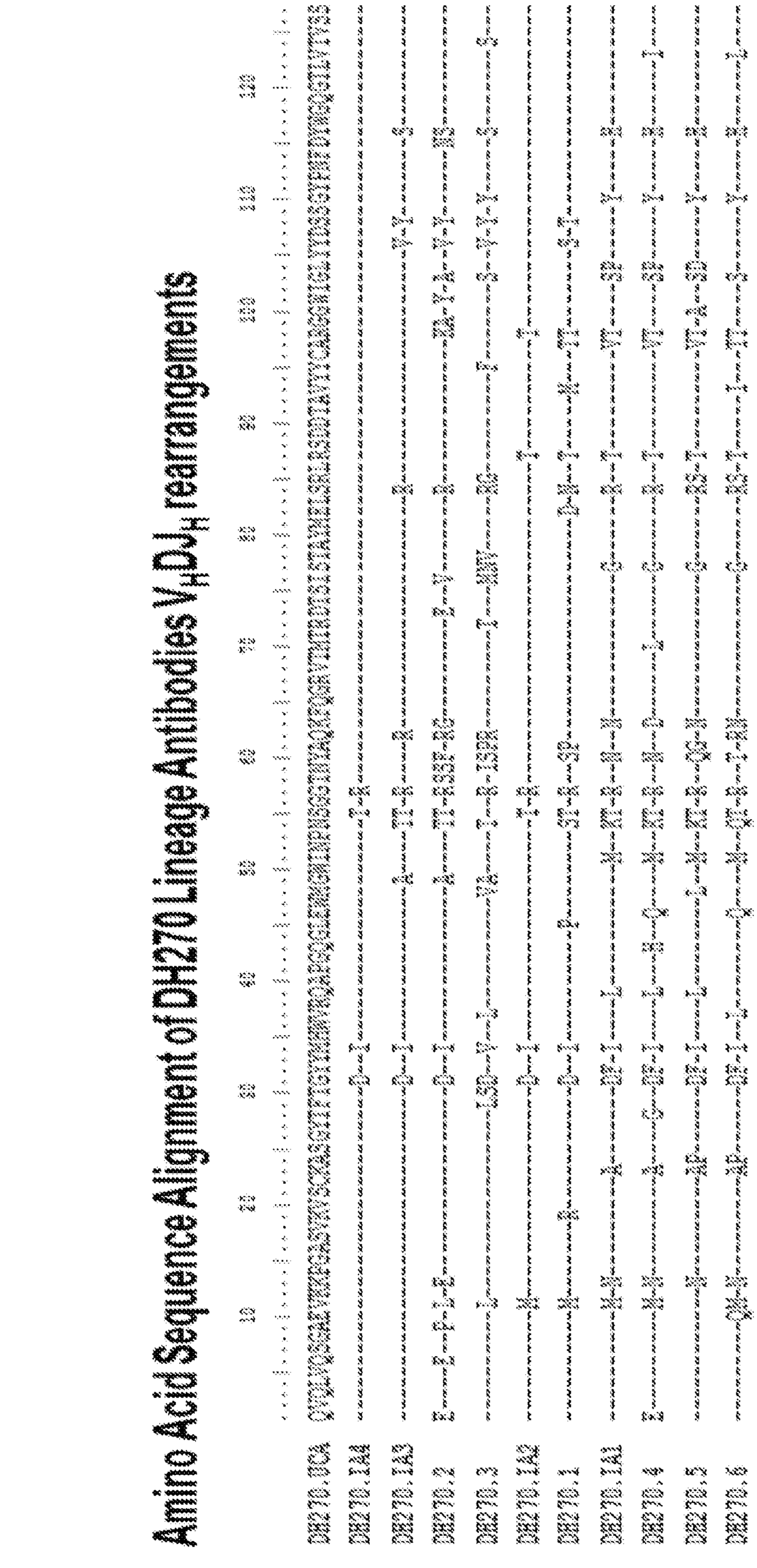


Figure 7D

Amino Acid Sequence Alignment of DH270 Lineage Antibodies VH1-1 rearrangements

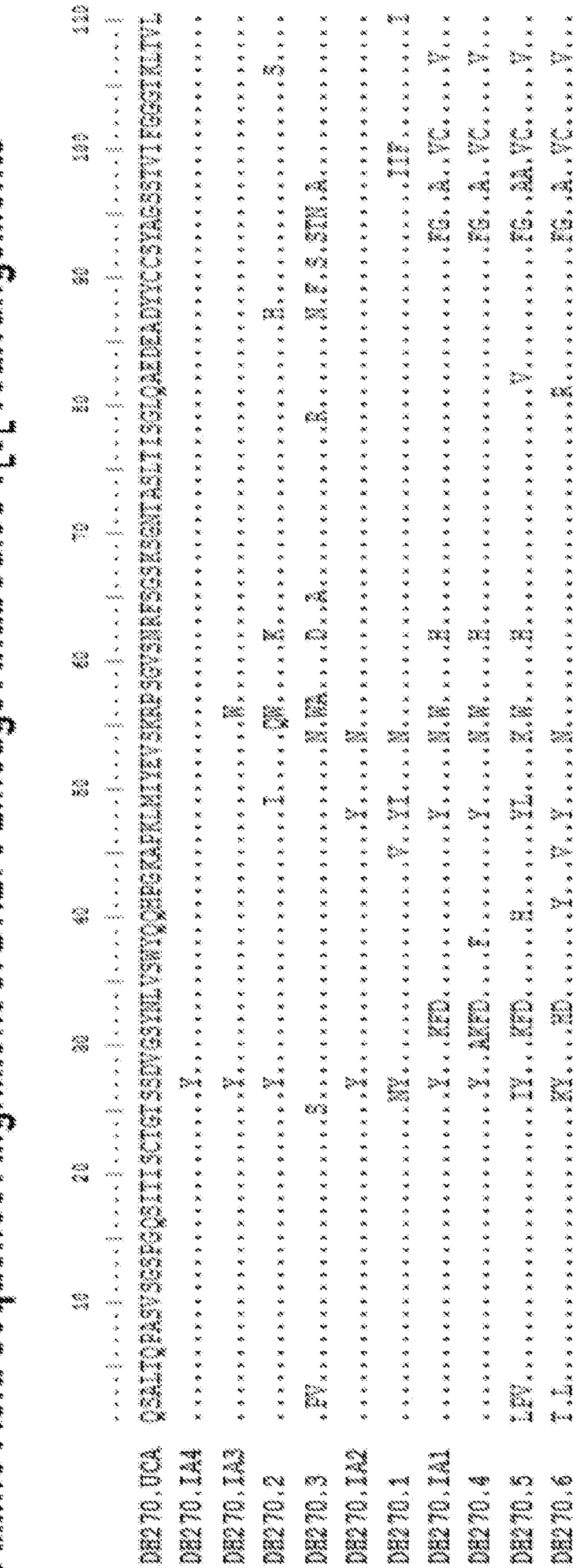


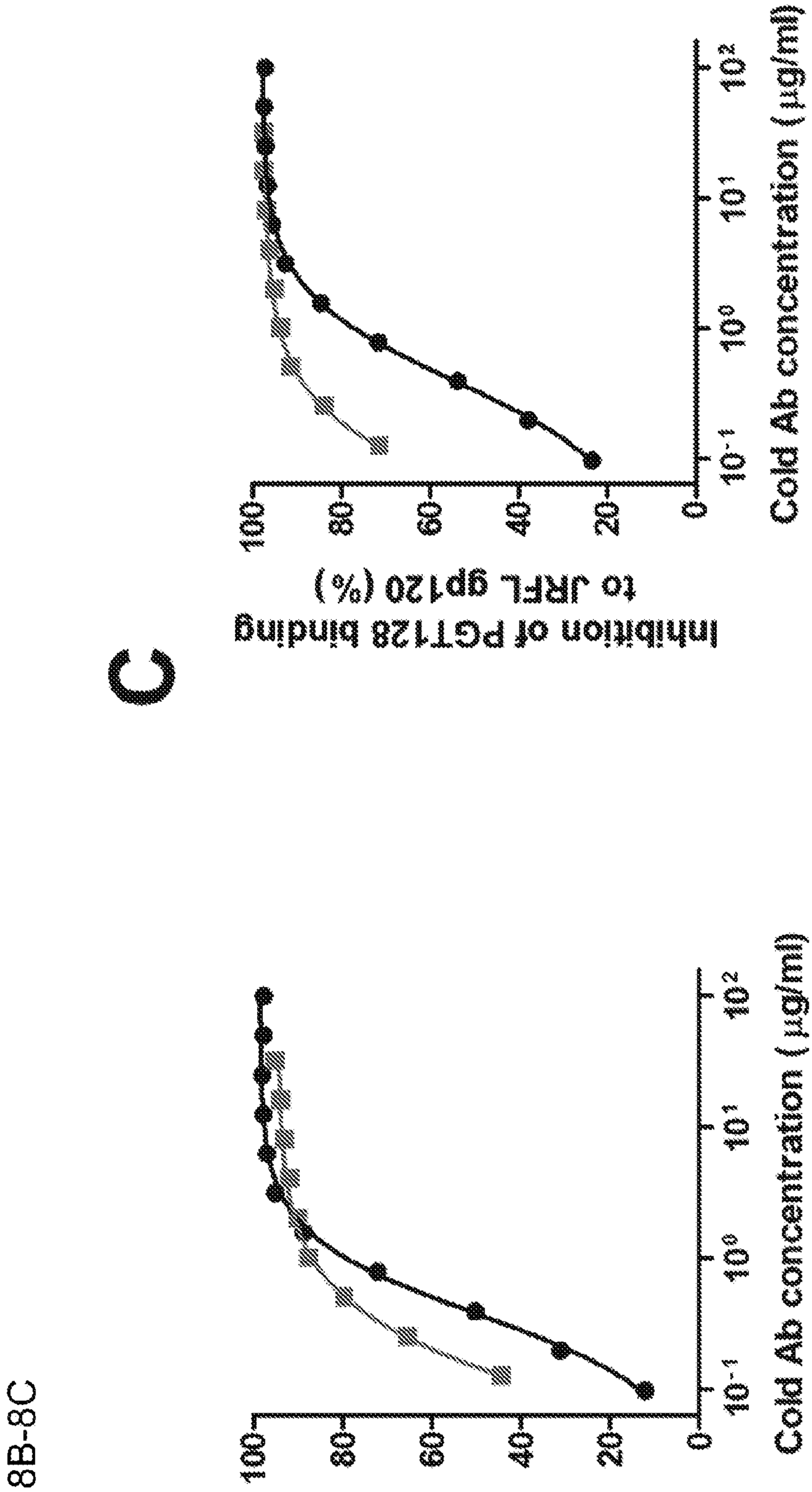
Figure 8A

A

	Neutralization IC_{50} μg/ml									
	AC13.8		PVO.4		TRO.11		AC10.029		RHPA.4259	
	wt	N332A	wt	N332A	wt	N332A	wt	N332A	wt	N332A
DH270.UCA	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50
DH270.IA4	>50	>50	42	>50	43	>50	>50	>50	>50	>50
DH270.IA3	>50	>50	>50	>50	0.2	>50	>50	>50	6.6	>50
DH270.IA2	>50	>50	>50	>50	0.1	>50	>50	>50	6.4	>50
DH270.1	>50	>50	0.2	>50	0.08	>50	1.9	>50	0.2	>50
DH270.IA1	>50	>50	0.07	>50	0.05	32.4	<0.02	>50	0.04	>50
DH270.2	21	>50	0.3	>50	0.06	>50	0.3	>50	0.1	>50
DH270.3	>50	>50	23	>50	0.3	>50	43	>50	42	>50
DH270.4	15	>50	0.1	>50	0.04	14	<0.02	>50	0.05	>50
DH270.5	41	>50	0.1	>50	0.07	>50	<0.02	>50	0.04	>50
DH270.6	1.4	>50	0.03	>50	0.02	>50	<0.02	>50	<0.02	>50

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Figures 8B-8C

Figure 9A

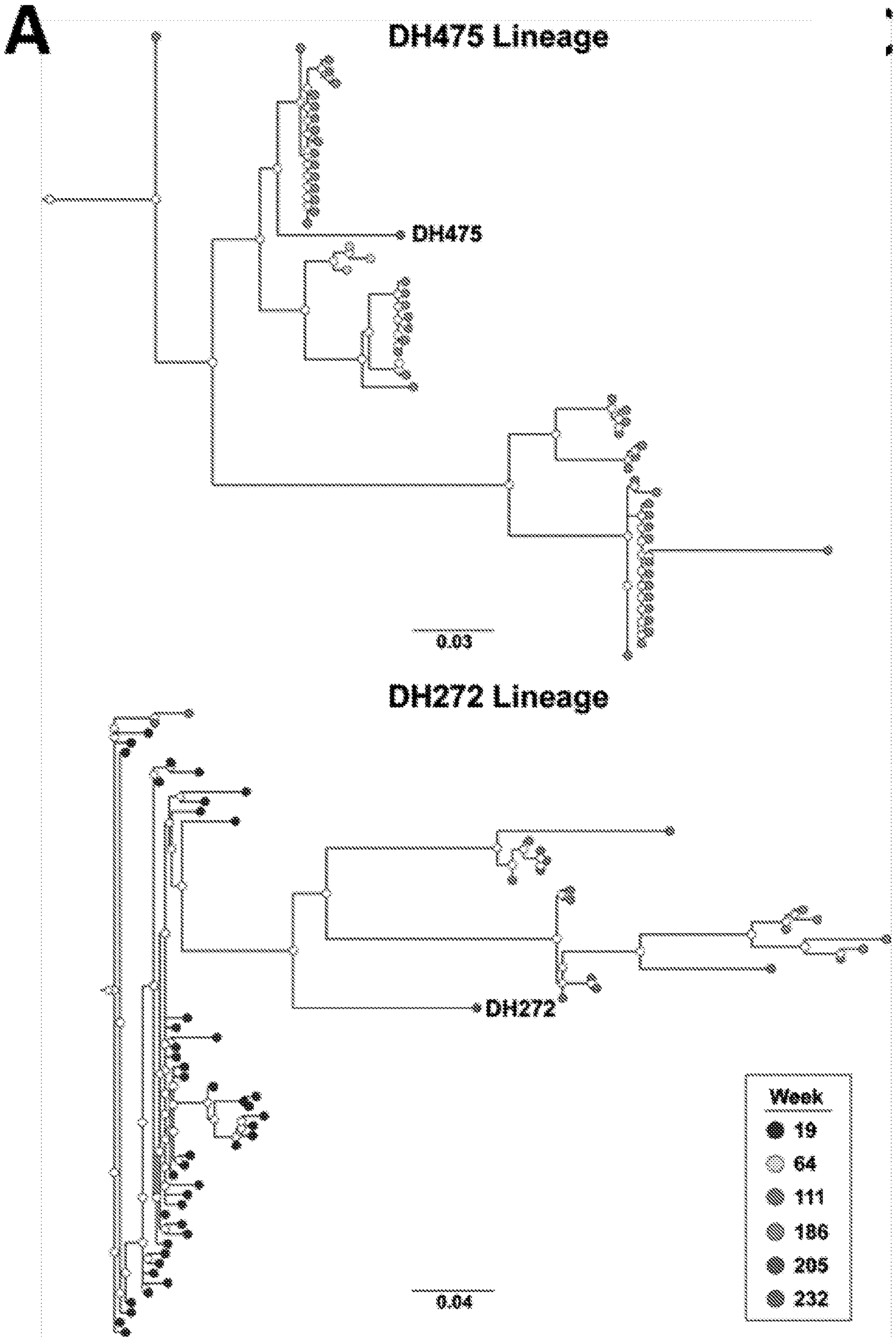

A
DH475 Lineage
DH475
0.03
DH272 Lineage
DH272
0.04
Week
19
64
111
186
205
232

Figure 9B

B

Antibody ID	V_H	D	J_H	V_H mutation frequency	CDRH3 length	V_L	J_L	κ/λ	V_L mutation frequency	CDRL3 length	Week of isolation	Insertions/ deletions
DH475	3-23*01	2-8*02	3*01	10.1%	19	4-69*02	1*01	λ	10.9%	9	232	none
DH272	1-2*02	3-3*01	4*02	14.9%	17	2-30*02	2*02	κ	5.1%	9	205	-6 FRH3

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Figures 9C-9D

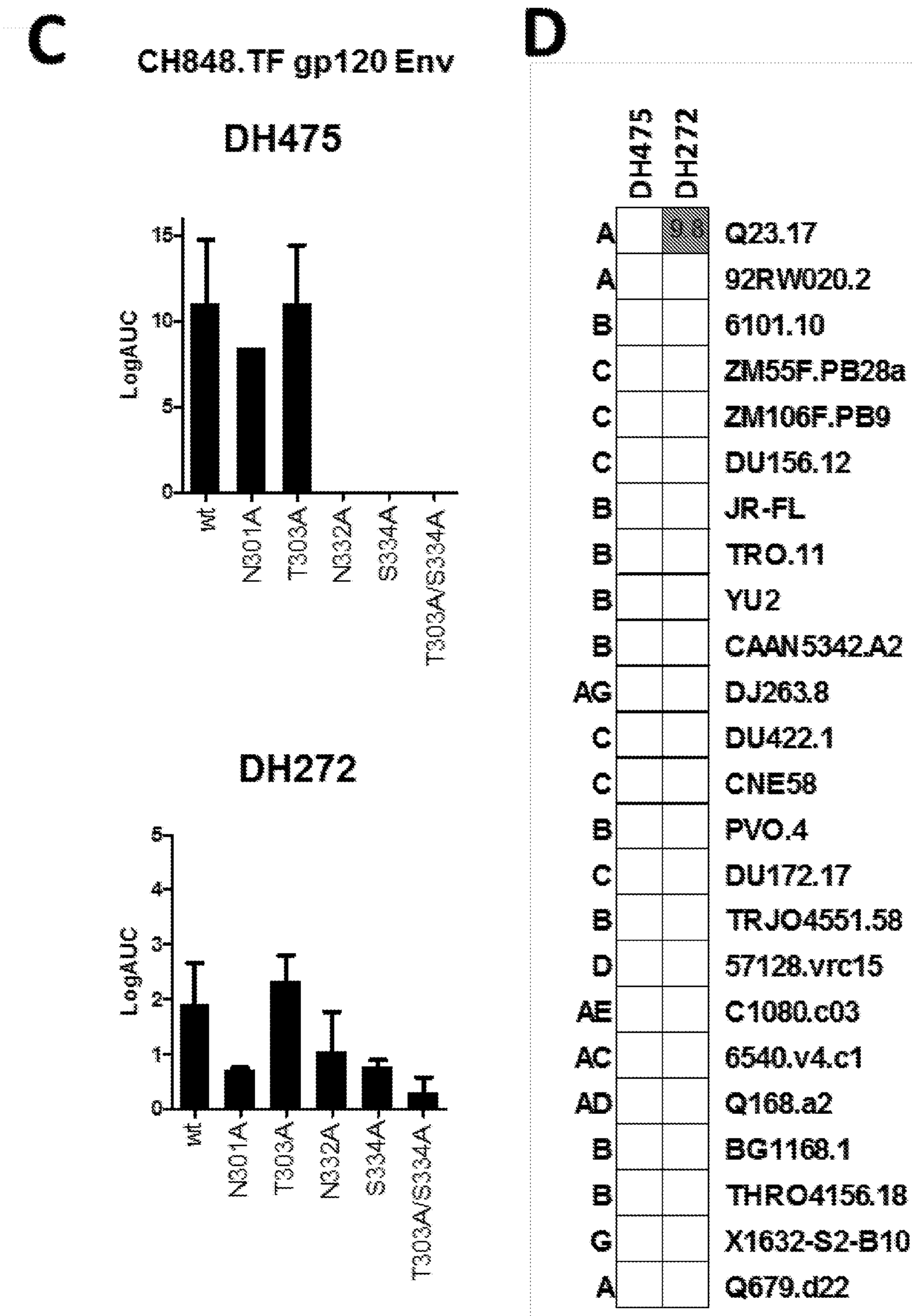
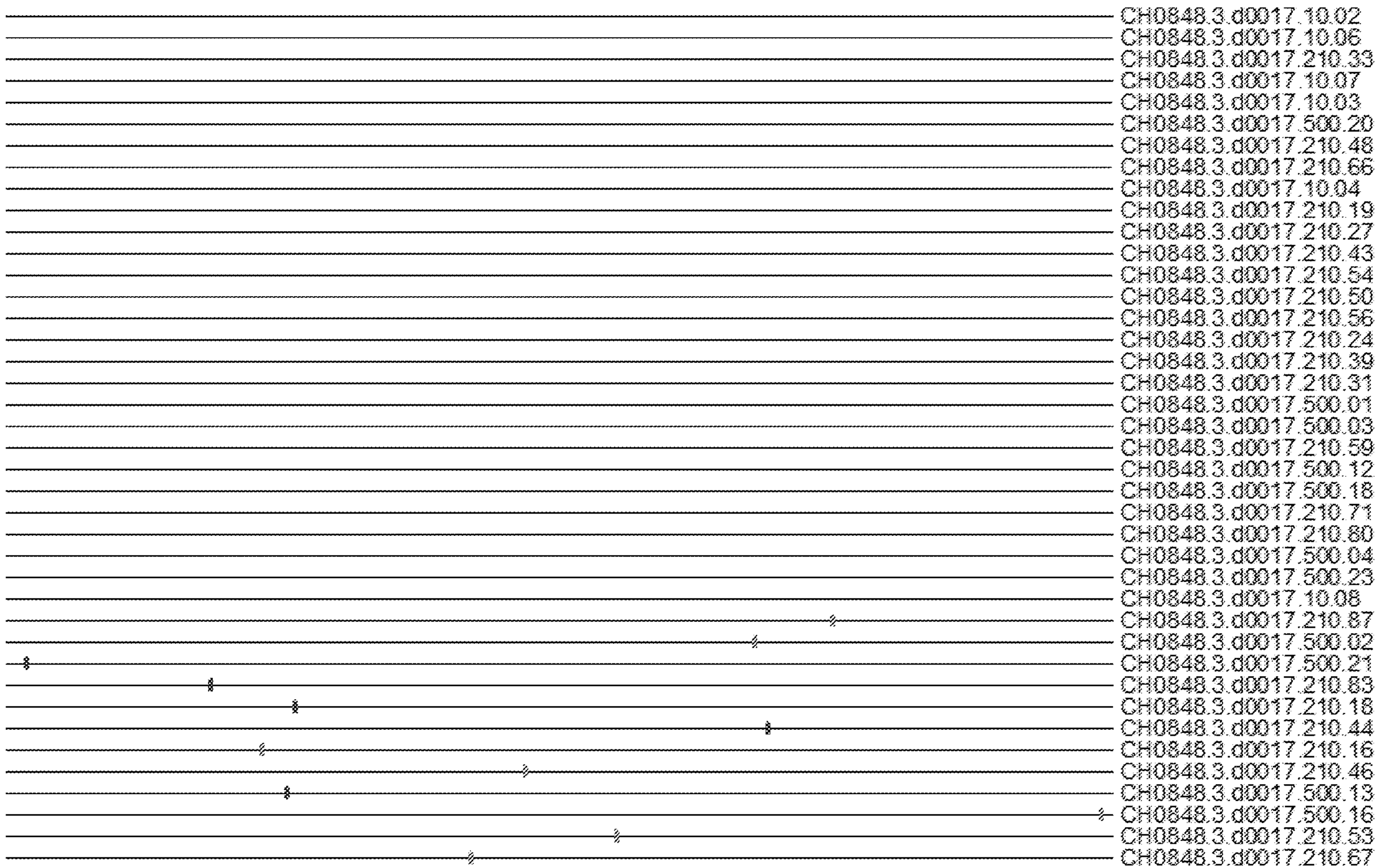


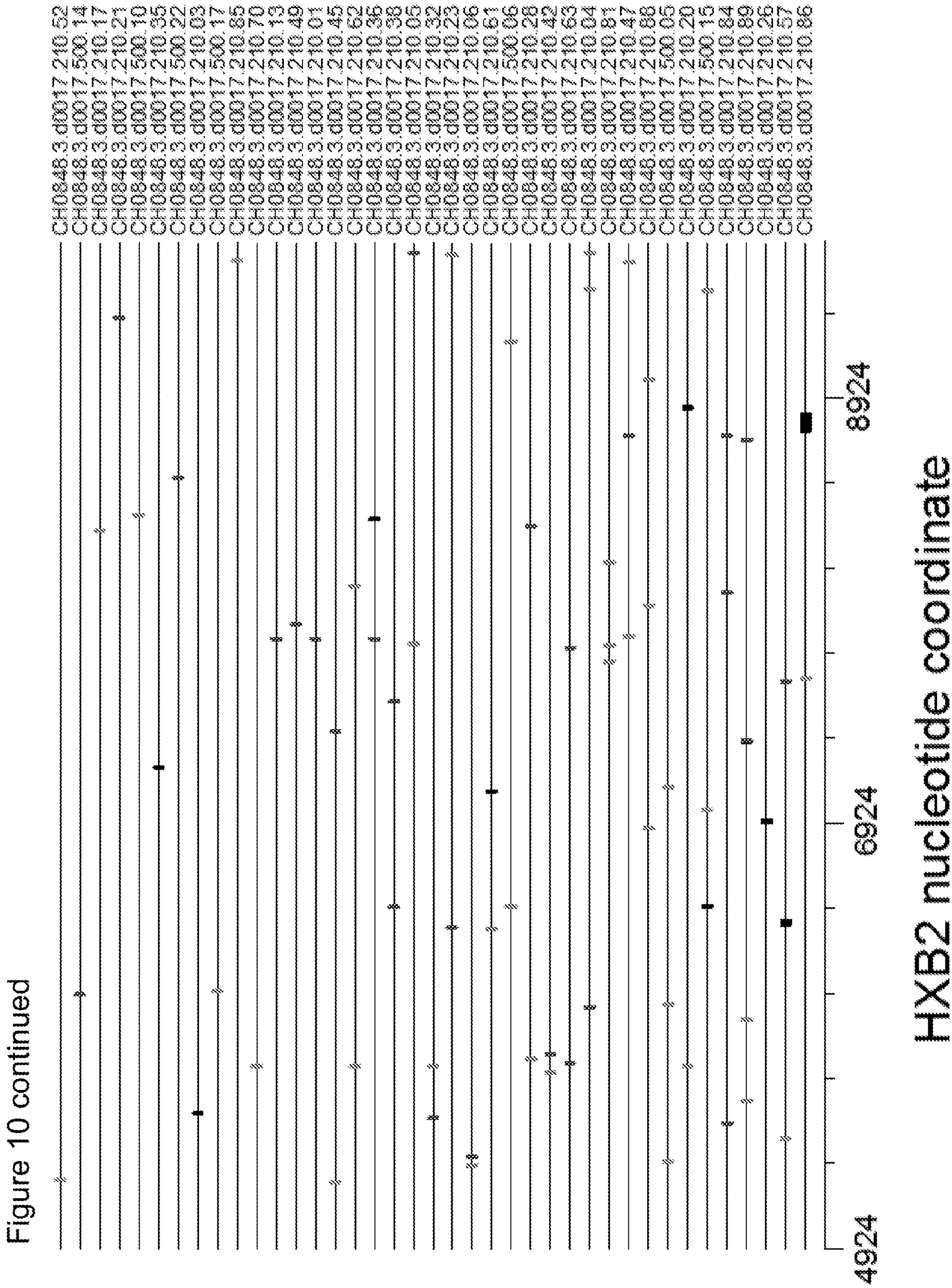
Figure 10

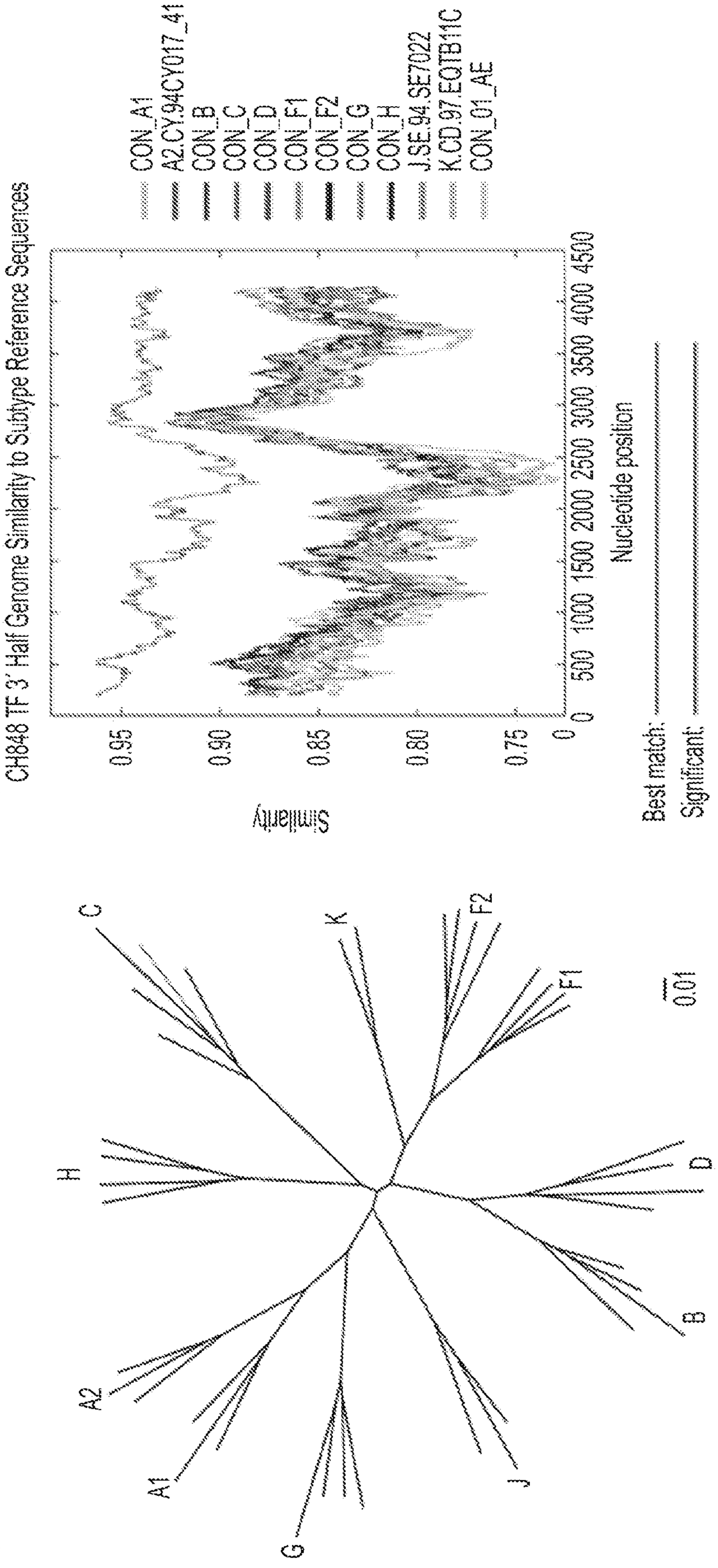
A:Green, T:Red, G:Orange, C:Light blue, Gaps:Gray



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Figure 10 continued
HXB2 nucleotide coordinate
8924
6924
4924



Figures 11A-11B

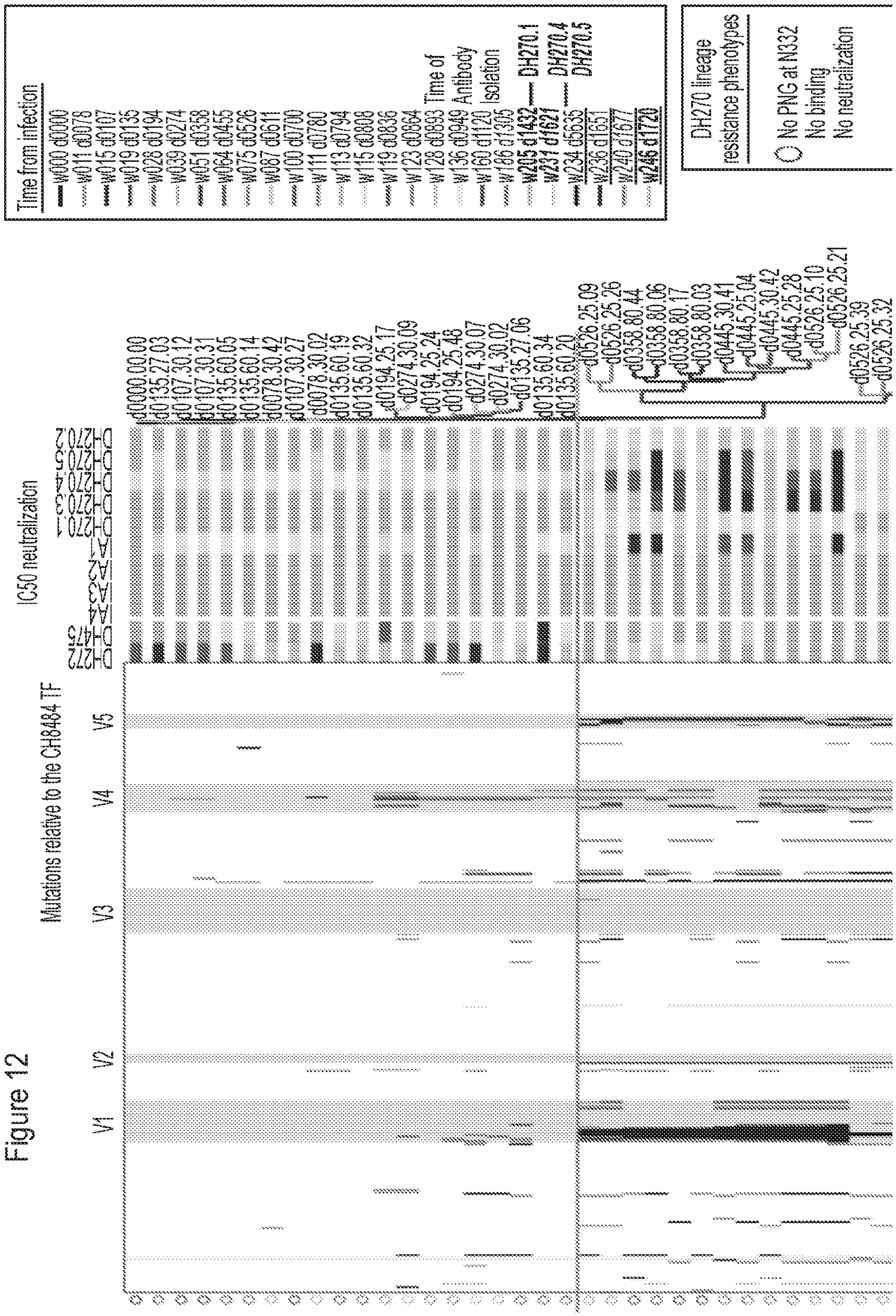

Time from infection
w000 d0000
w011 d0078
w015 d0107
w019 d0135
w028 d0194
w039 d0274
w051 d0358
w064 d0455
w075 d0526
w087 d0611
w100 d0700
w111 d0780
w113 d0794
w115 d0808
w119 d0836
w123 d0864
w128 d0893 Time of
w136 d0949 Antibody
w160 d1120 Isolation
w186 d1305
w205 d1432 DH270.1
w231 d1621 DH270.4
w234 d5635 DH270.5
w236 d1651
w240 d1677
w246 d1720
DH270 lineage resistance phenotypes
No PNG at N332
No binding
No neutralization
IC50 neutralization
Mutations relative to the CH8484 TF
V1
V2
V3
V4
V5
d0000.00.00
d0135.27.03
d0107.30.12
d0107.30.31
d0135.60.05
d0135.60.14
d0078.30.42
d0107.30.27
d0078.30.02
d0135.60.19
d0135.60.32
d0194.25.17
d0274.30.09
d0194.25.24
d0194.25.48
d0274.30.07
d0274.30.02
d0135.27.06
d0135.60.34
d0135.60.20
d0526.25.09
d0526.25.26
d0358.80.44
d0358.80.06
d0358.80.17
d0358.80.03
d0445.30.41
d0445.25.04
d0445.30.42
d0445.25.28
d0526.25.10
d0526.25.21
d0526.25.39
d0526.25.32

Figure 12

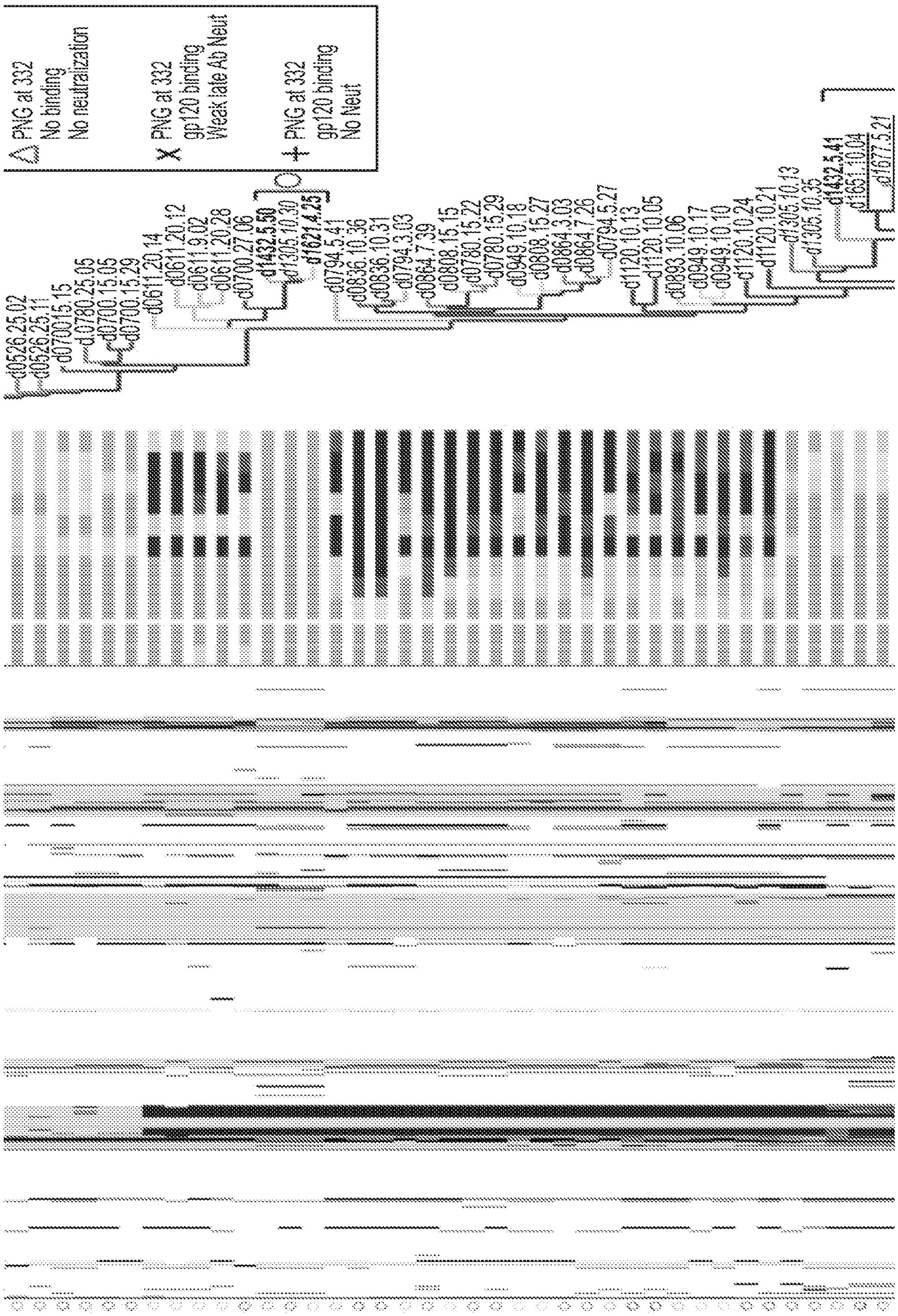


Figure 12 continued

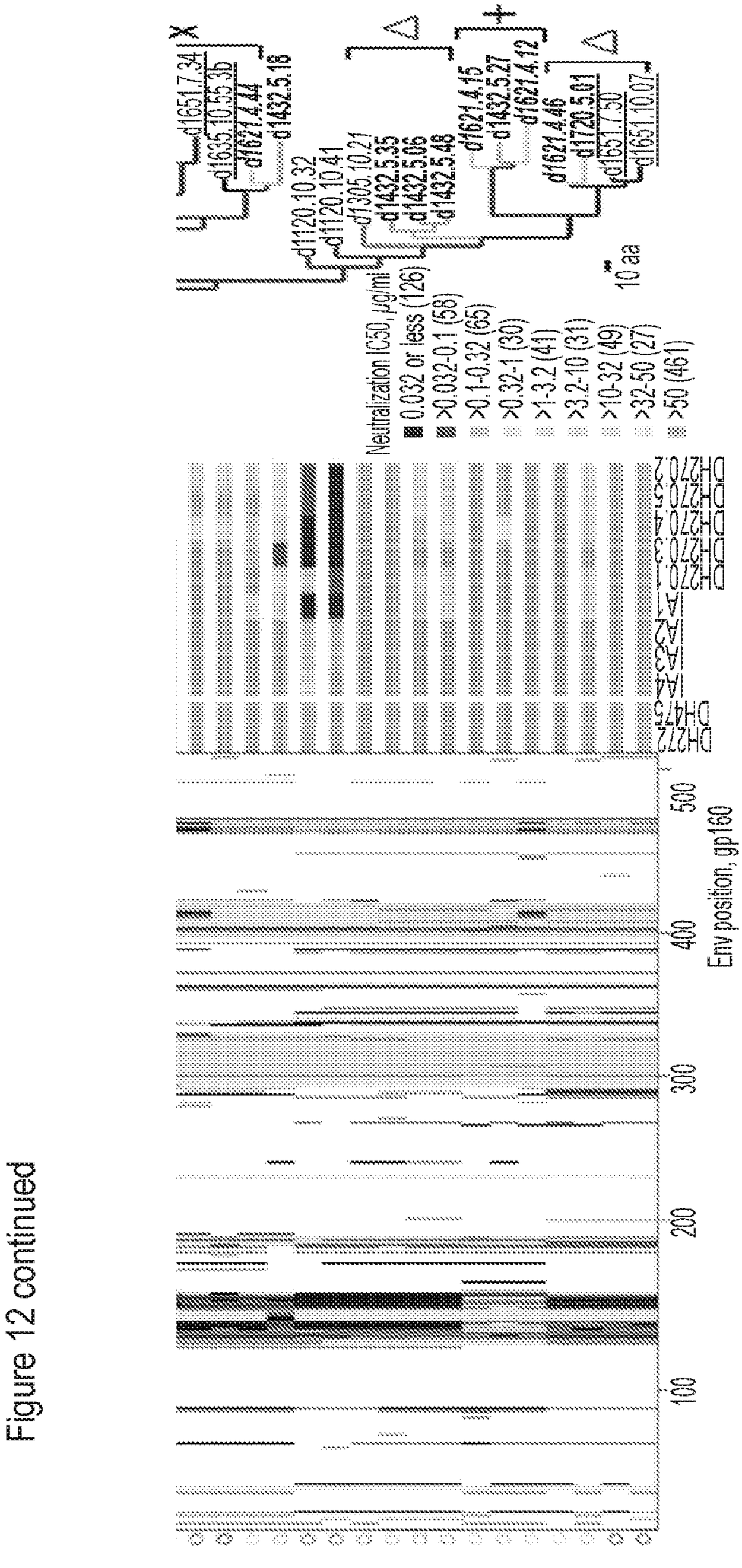


Figure 12 continued

Figures 13A-13B

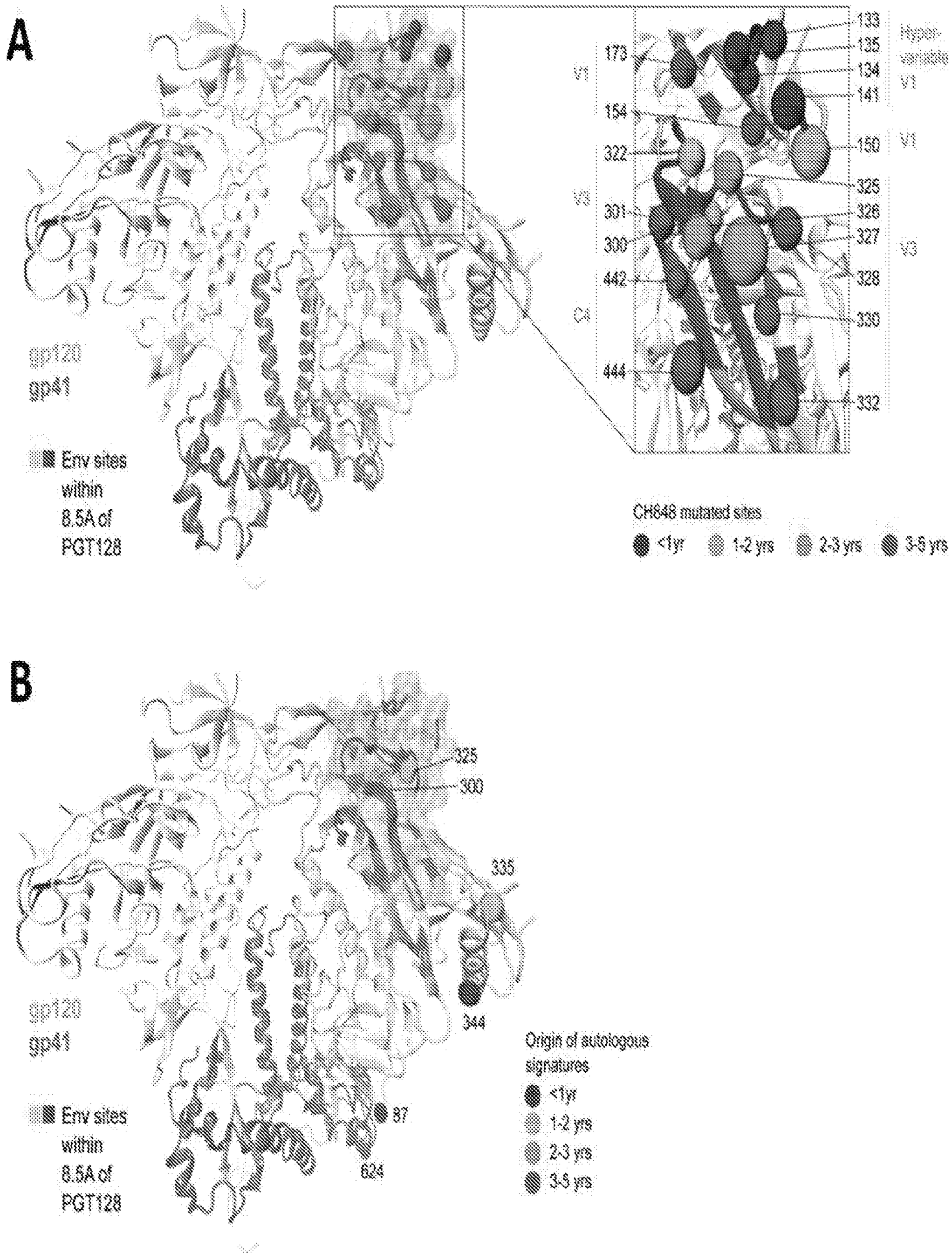


Figure 14

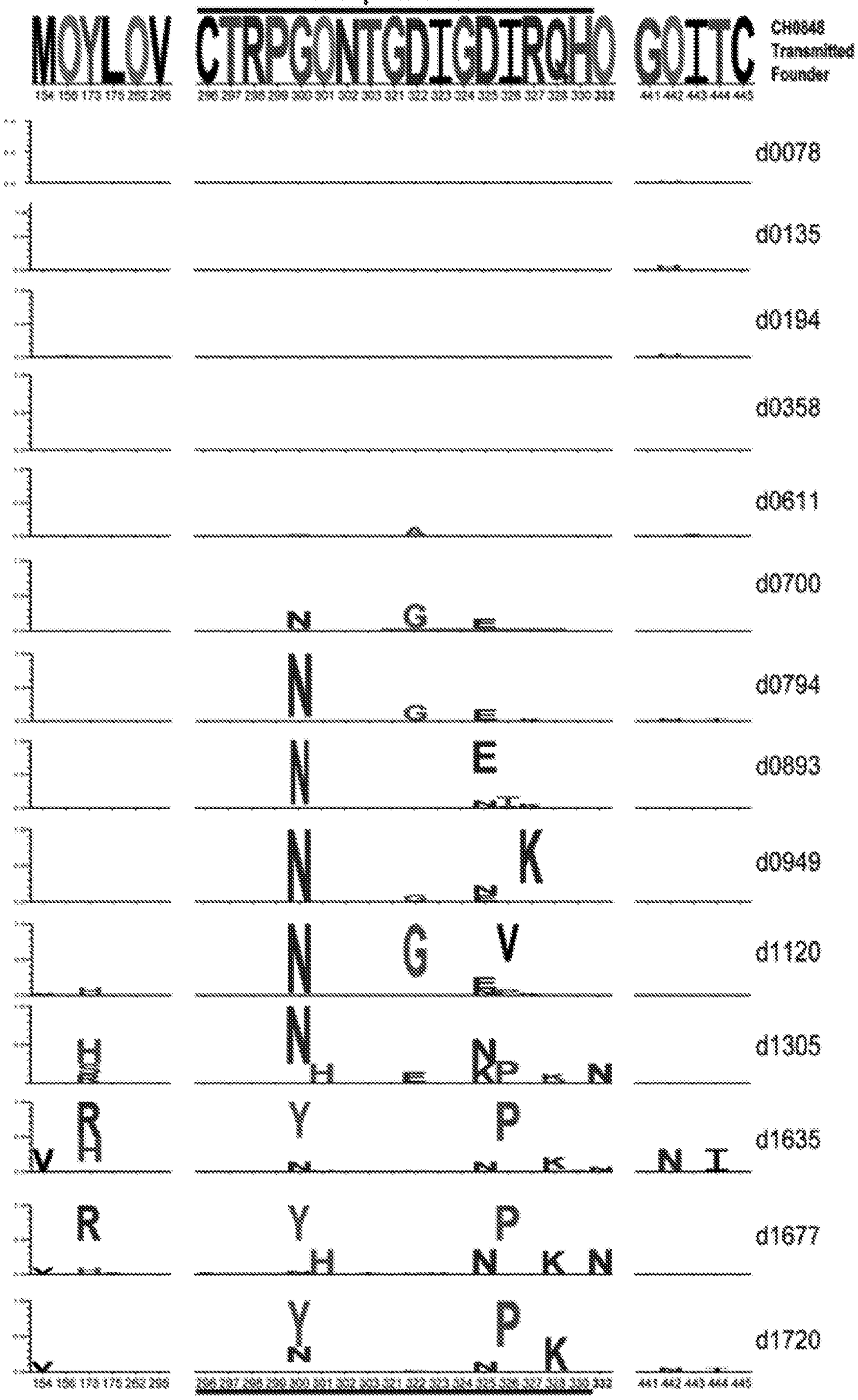
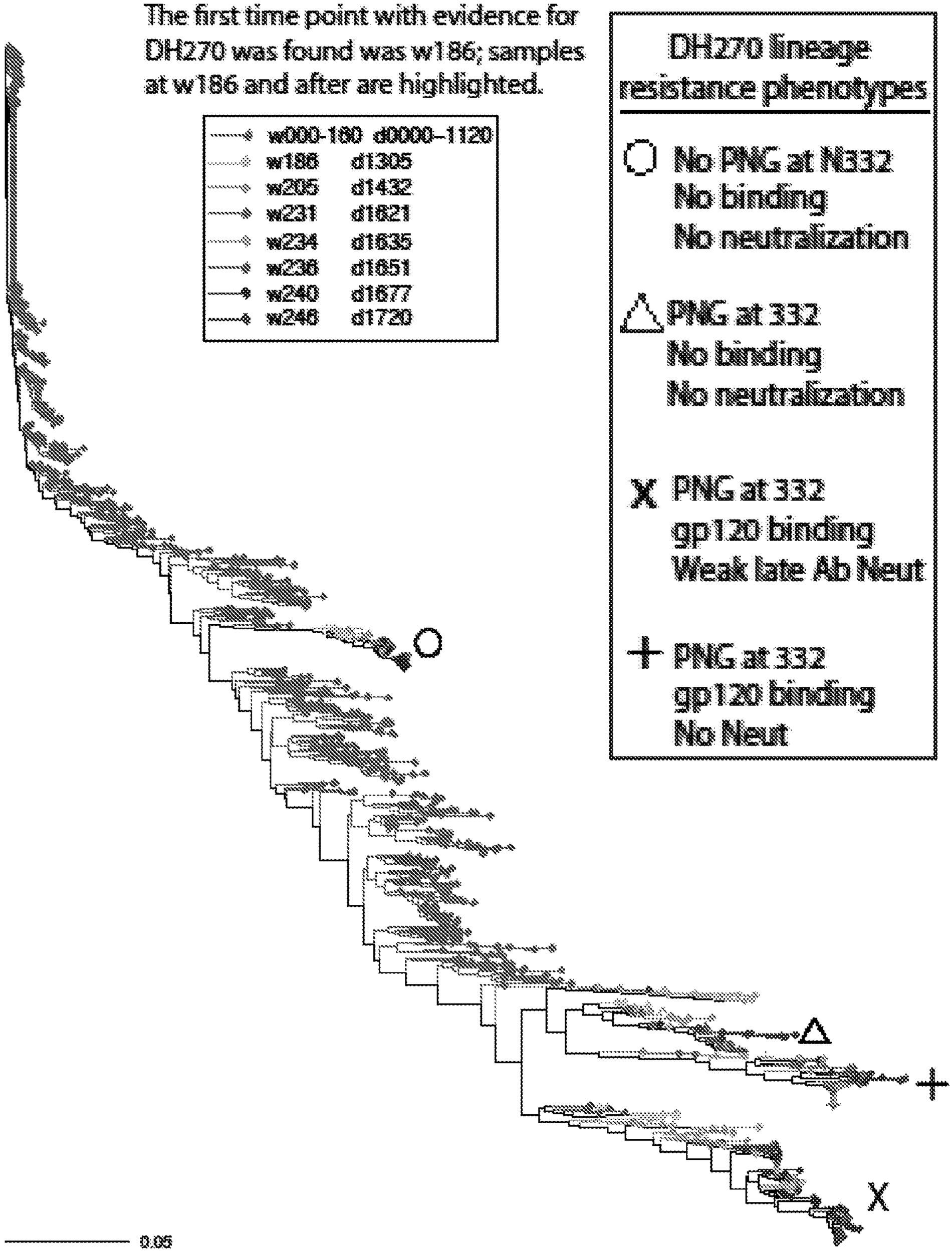

V3 loop residues
MOYLOV CTRPGNTGDIGDIRQHC GCITC
CH0848 Transmitted Founder
d0078
d0135
d0194
d0358
d0611
d0700
d0794
d0893
d0949
d1120
d1305
d1635
d1677
d1720
Env positions < 8.5 A from PGT128

Figure 15


The first time point with evidence for DH270 was found was w186; samples at w186 and after are highlighted.
w000-180 d0000-1120
w186 d1305
w205 d1432
w231 d1621
w234 d1635
w236 d1651
w240 d1677
w246 d1720
DH270 lineage resistance phenotypes
No PNG at N332
No binding
No neutralization
PNG at 332
No binding
No neutralization
PNG at 332
gp120 binding
Weak late Ab Neut
PNG at 332
gp120 binding
No Neut
0.05

Figures 16A-16F

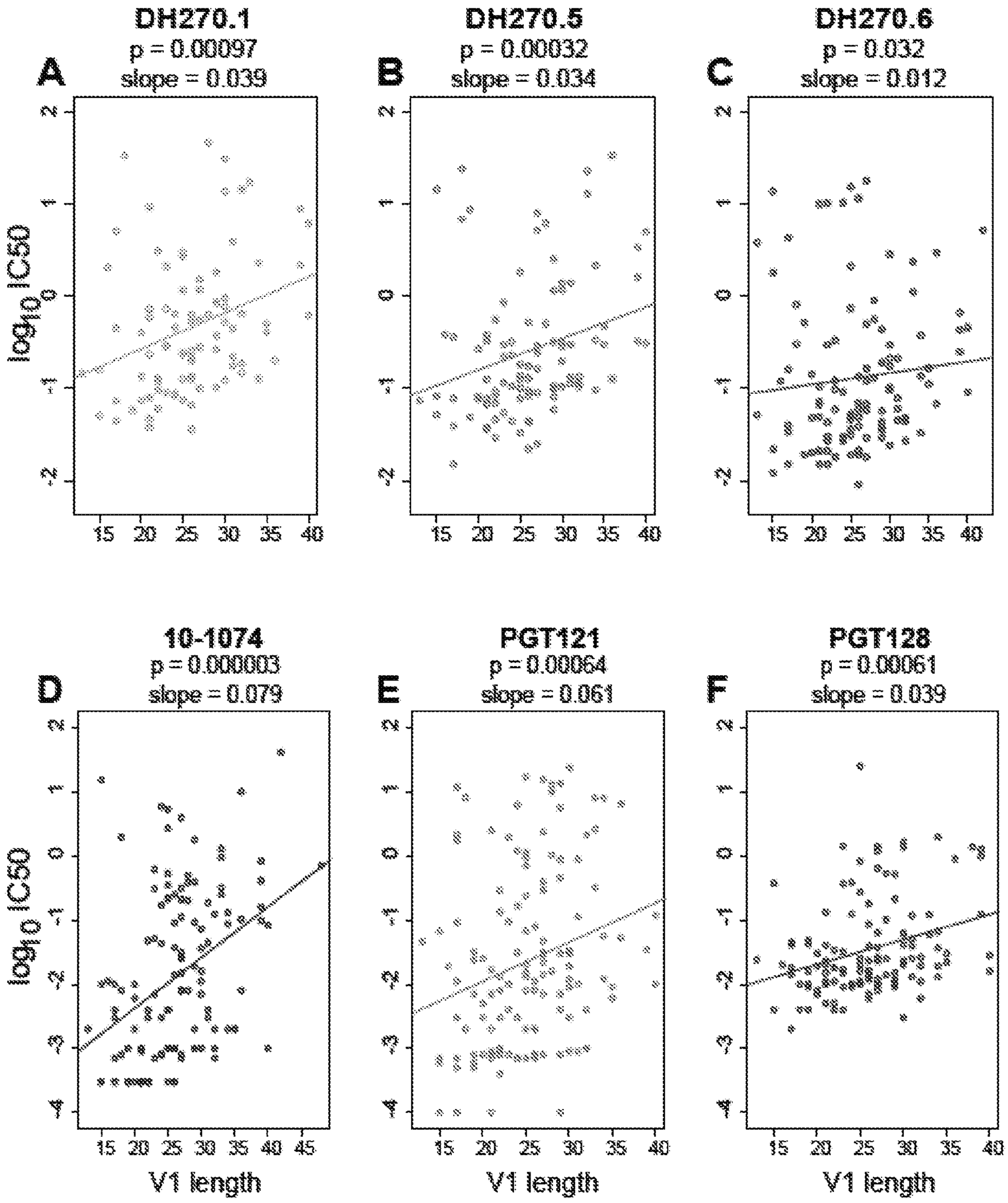
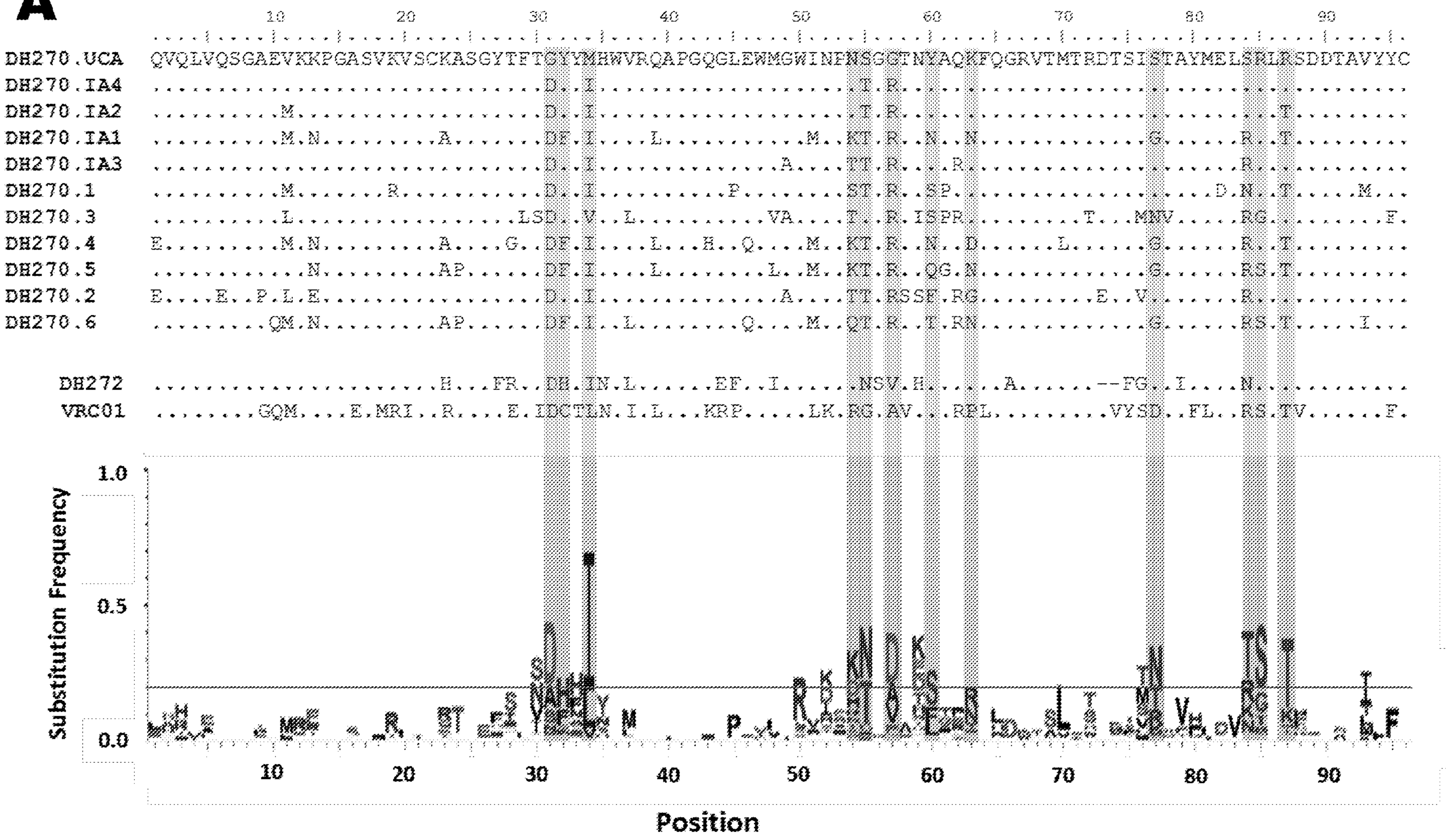


Figure 17A



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Figure 17B

B

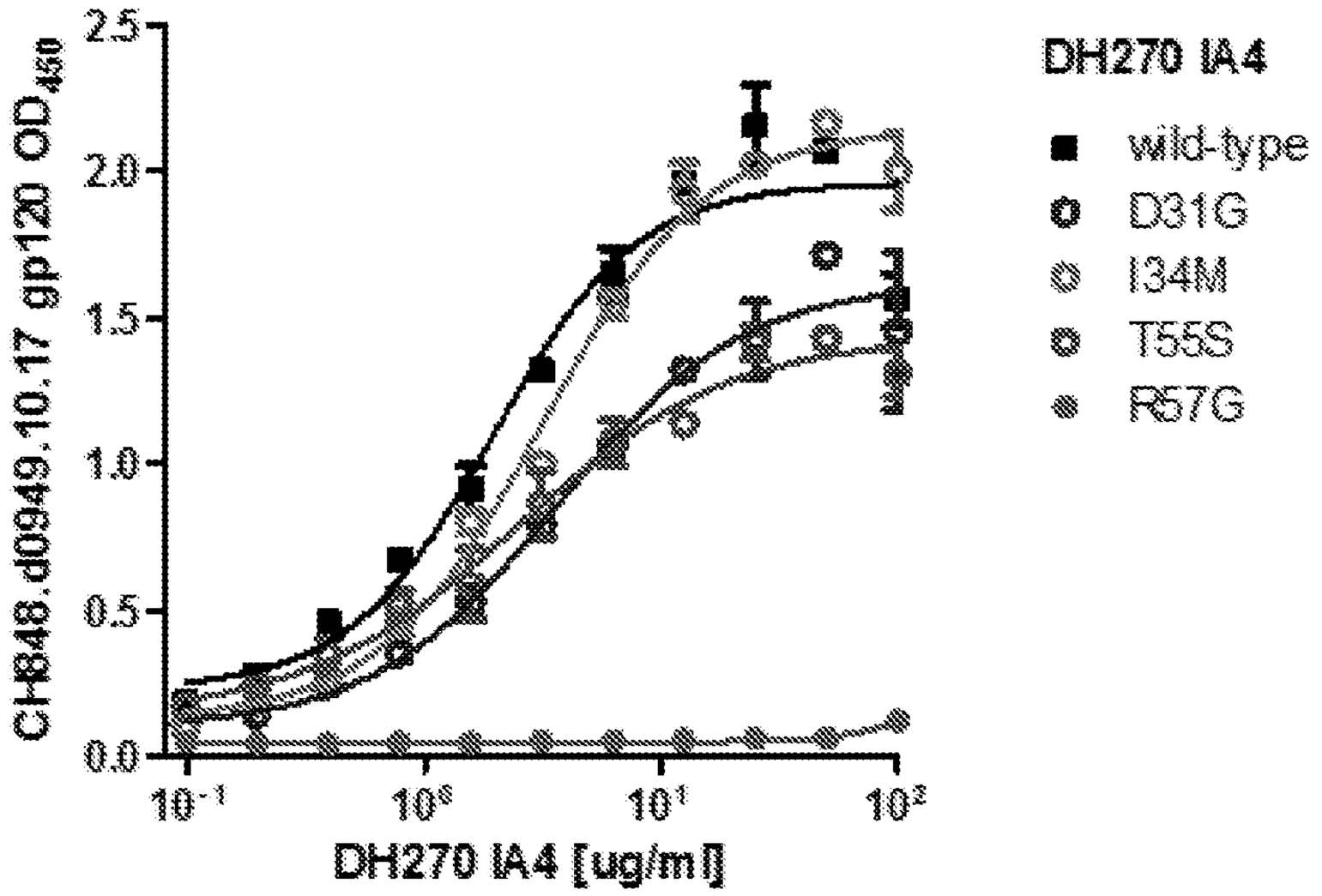
```
                    10        20        30        40        50        60        70        80        90
                    |....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|...
DH270.UCA           QVQLVQSGAE VKKPGASVKV SCKASGYTFT GYYMHWVRQA PGQGLEWMGW INPNSGGTNY AQKFQGRVTM TRDTSISTAY MELSRLRSDD TAVYYCAR
DH270.IA4           .......... .......... .......... D..I...... .......... ....T.R... .......... .......... .......... .......
DH270.IA2           .......... M......... .......... D..I...... .......... ....T.R... .......... .......... ......T... .......T
DH270.IA1           .......... M.N....... ..A....... DF.I....L. .......... M..KT.R..N ..N....... .......G.. ...R..T... ......VT
DH270.IA3           .......... .......... .......... D..I...... ........A. ...TT.R... .R........ .......... ...R...... ........
DH270.1             .......... M........R. .......... D..I...... ....P..... ...ST.R..S P......... .......... .D.N..T... ..M...TT
DH270.3             .......... L......... ........LS D..V..L... .......VA. ...T..R.IS FR........ .T...MNV.. ...RG..... ....F...
DH270.4             E......... M.N....... ..A....G.. DF.I....L. ..H..Q.... M..KT.R..N ..D......L .......G... ...R..T... ......VT
DH270.5             .......... ..N....... ..AP...... DF.I....L. ........L.. M..KT.R..Q G.N..... .......G... ...RS.T... ......VT
DH270.2             E....E..P. L.E....... .......... D..I...... ........A. ...TT.RSSF .RG..... ..E..V.... ...R...... .......K
DH270.6             .........Q M.N....... ..AP...... DF.I..L... .....Q.... M..QT.R..T .RM..... .......G... ...RS.TV.. ....F.TT

VH1-2*02            .......... .......... .......... .......... .......... .......... .......... .......... .......... ........
Genomic DNA         .......... .......... .......I.. D......... ...E.G...R .......... .......... .......... T...S...E. ..T.....
```

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Figures 18A-18B

A



B

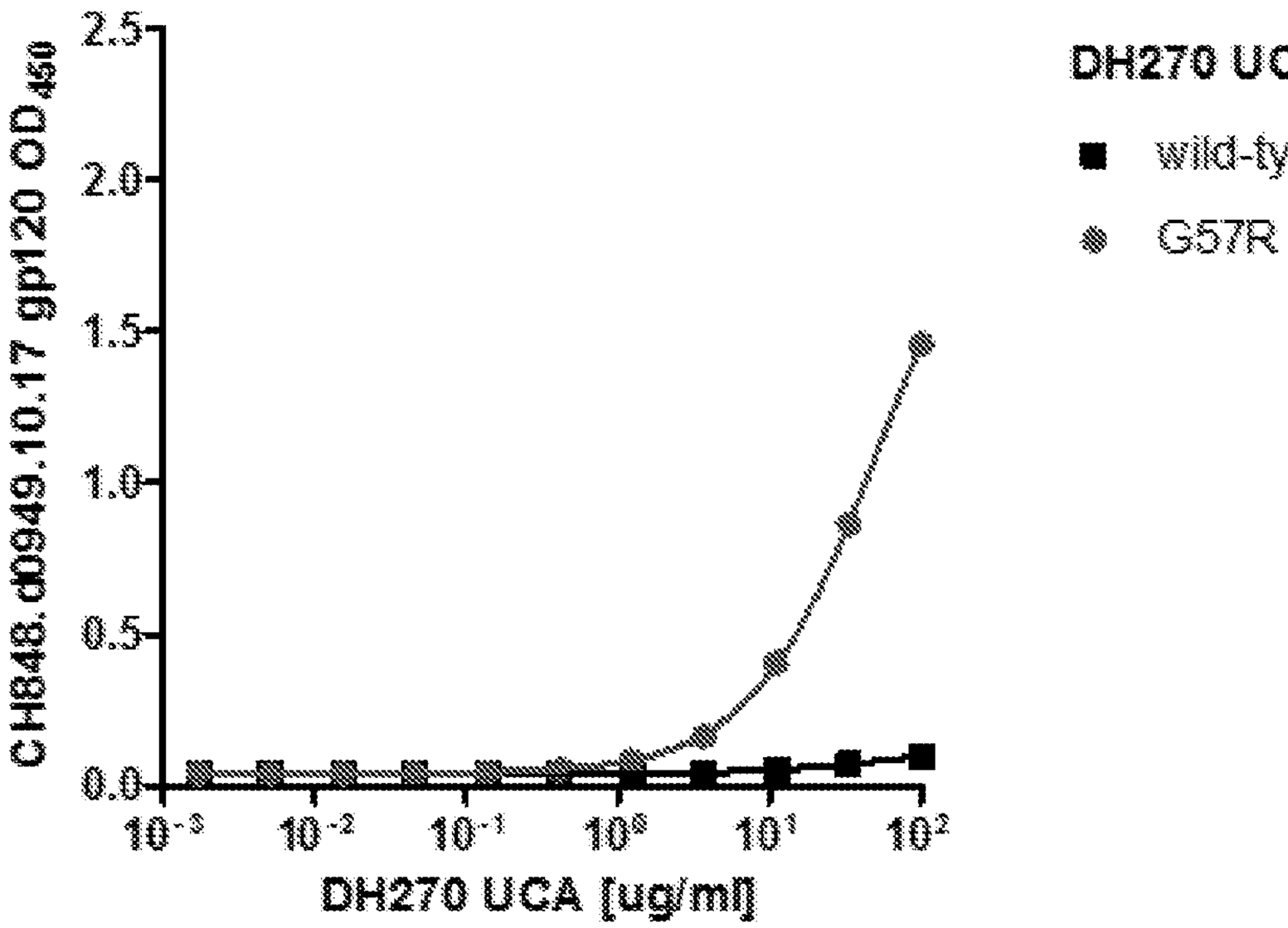
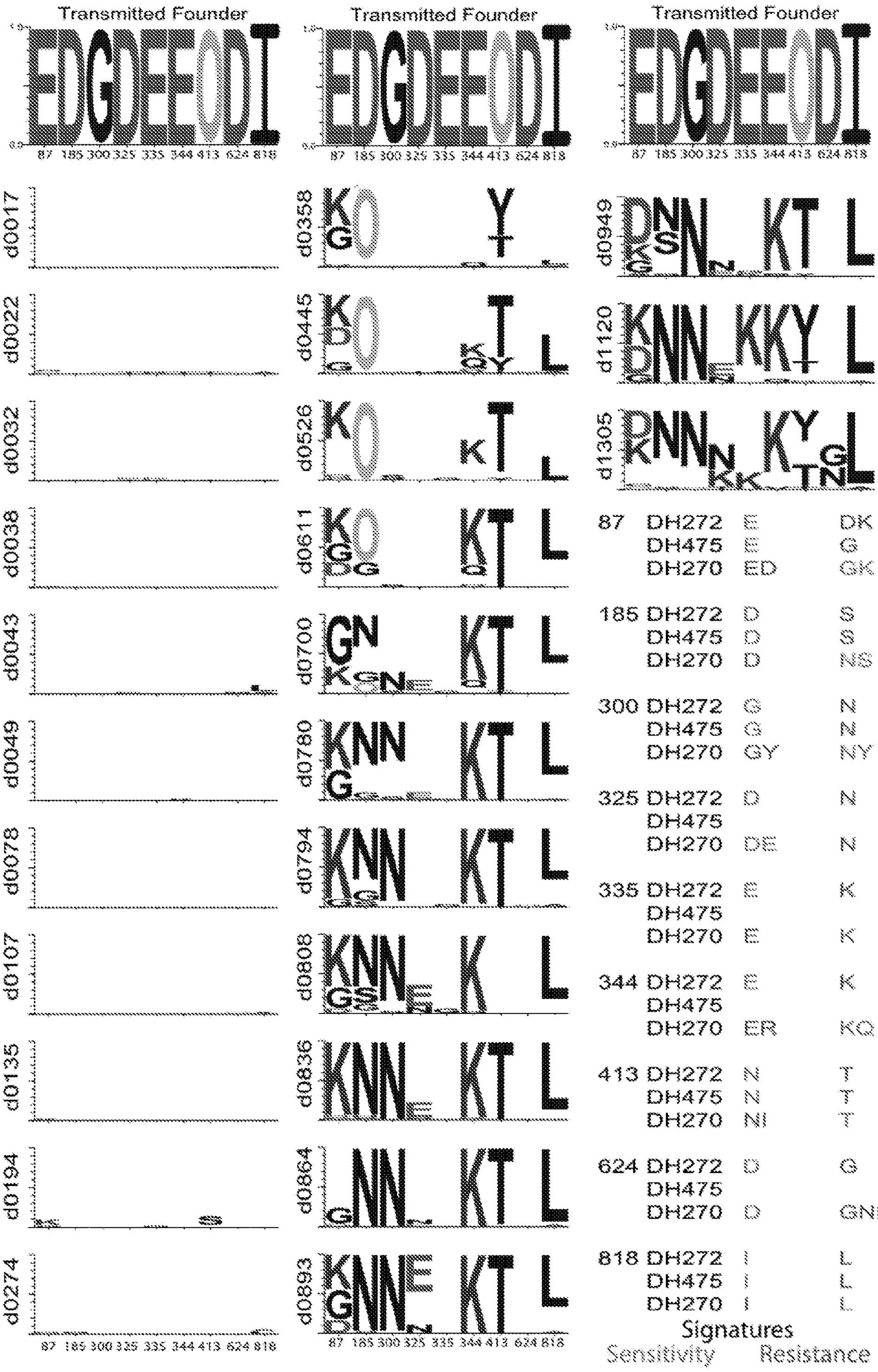
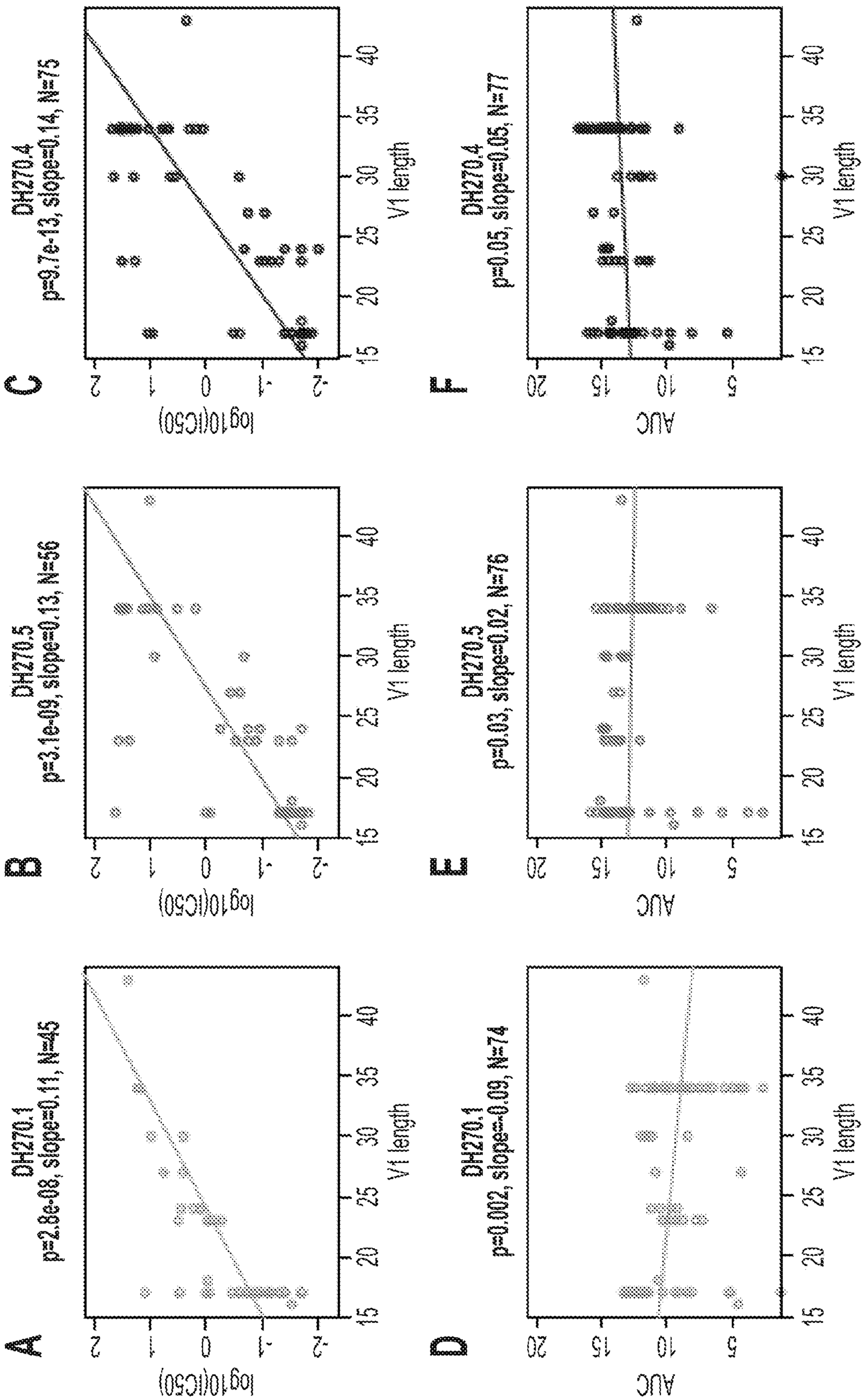


Figure 19


Transmitted Founder
Transmitted Founder
Transmitted Founder
d0017
d0022
d0032
d0038
d0043
d0049
d0078
d0107
d0135
d0194
d0274
d0358
d0445
d0526
d0611
d0700
d0780
d0794
d0808
d0836
d0864
d0893
d0949
d1120
d1305
87 185 300 325 335 344 413 624 818
87 DH272 E DK
DH475 E G
DH270 ED GK
185 DH272 D S
DH475 D S
DH270 D NS
300 DH272 G N
DH475 G N
DH270 GY NY
325 DH272 D N
DH475
DH270 DE N
335 DH272 E K
DH475
DH270 E K
344 DH272 E K
DH475
DH270 ER KQ
413 DH272 N T
DH475 N T
DH270 NI T
624 DH272 D G
DH475
DH270 D GNE
818 DH272 I L
DH475 I L
DH270 I L
Signatures
Sensitivity Resistance



Figures 20A-20F

Figures 21A-21B

A

```
UCA1_HC     QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY
UCA3_HC     QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY
UCA4_HC     QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY
            ************************************************************

UCA1_HC     AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCATGGWIGLYYDSSGYPNFDYWGQG
UCA3_HC     AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGWISLYYDSSGYPNFDYWGQG
UCA4_HC     AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGWIGLYYDSSGYPNFDYWGQG
            ************************************ **** ******************

UCA1_HC     TLVTVS
UCA3_HC     TLVTVS
UCA4_HC     TLVTVS
            ******
```

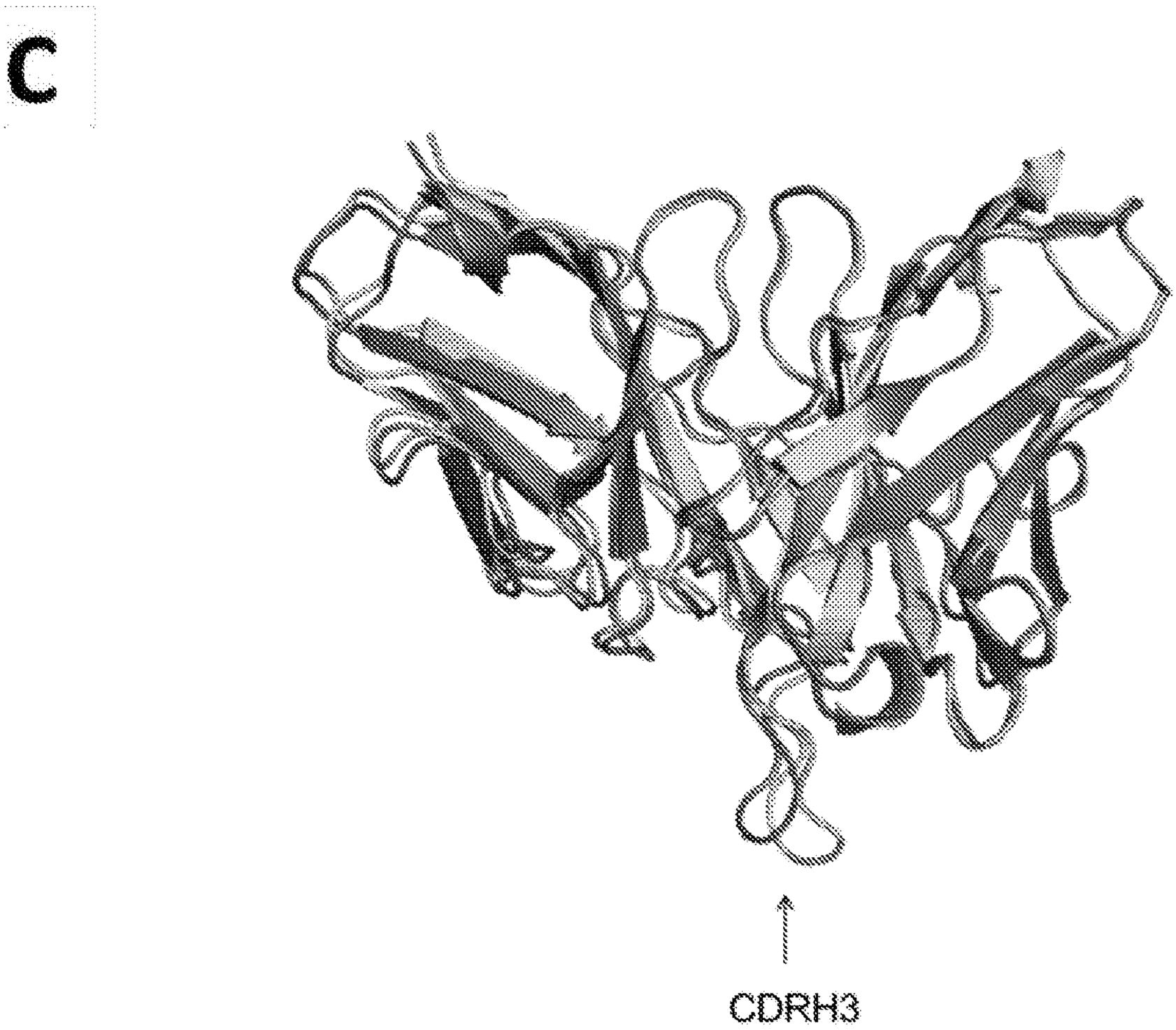
B

```
UCA3_LC     QSALTQPASVSGSPGQSITISCTGTSSDVGSYNLVSWYQQHPGKAPKLMIYEVSKRPSGV
UCA1_LC     QSALTQPASVSGSPGQSITISCTGTSSDVGSYNLVSWYQQHPGKAPKLMIYEVSKRPSGV
            ************************************************************

UCA3_LC     SNRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSSTVIFGGGTKLTVL
UCA1_LC     SNRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSSIILFGGGTKLTVL
            ************************************ :: **********
```

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Figure 21C



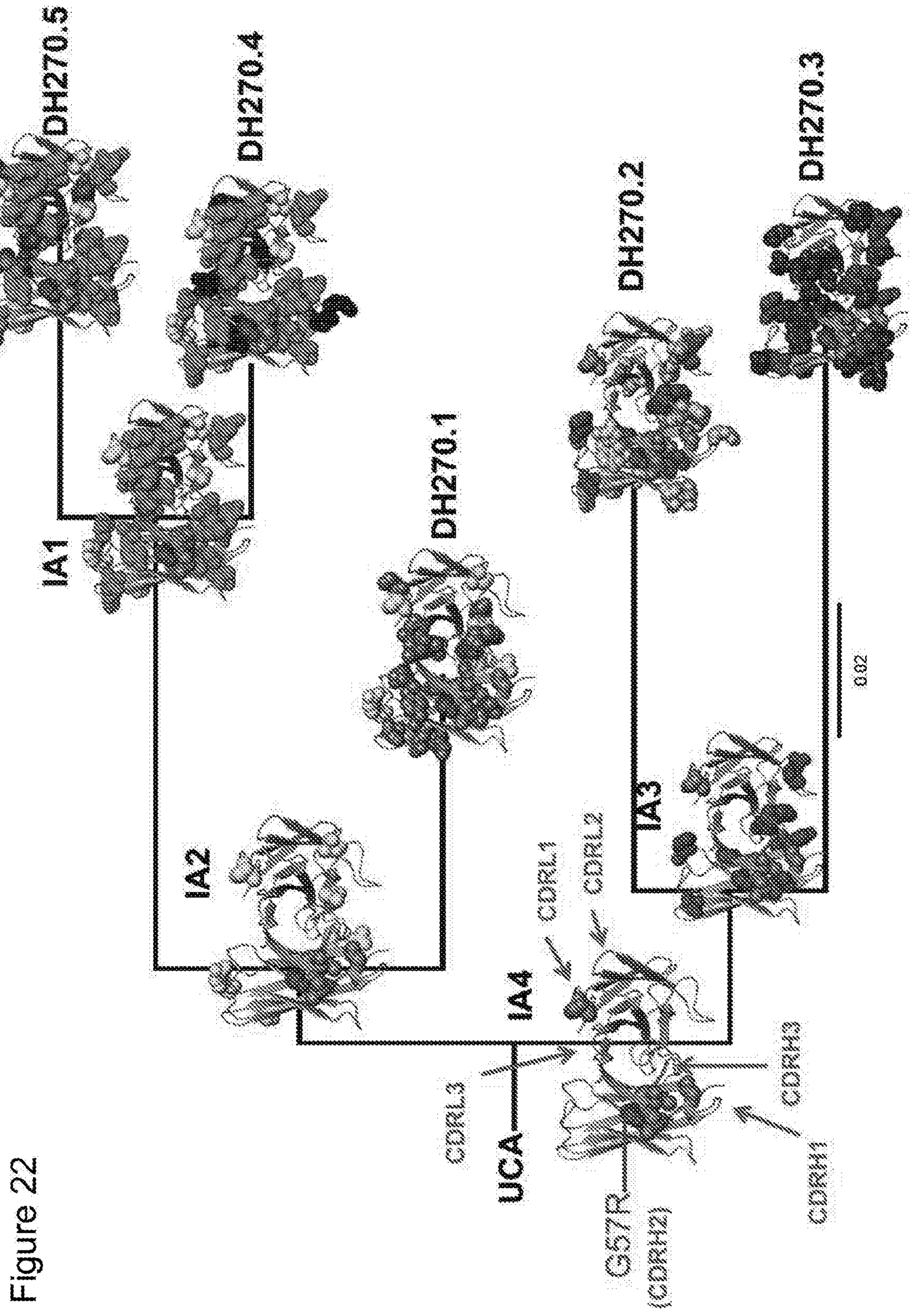
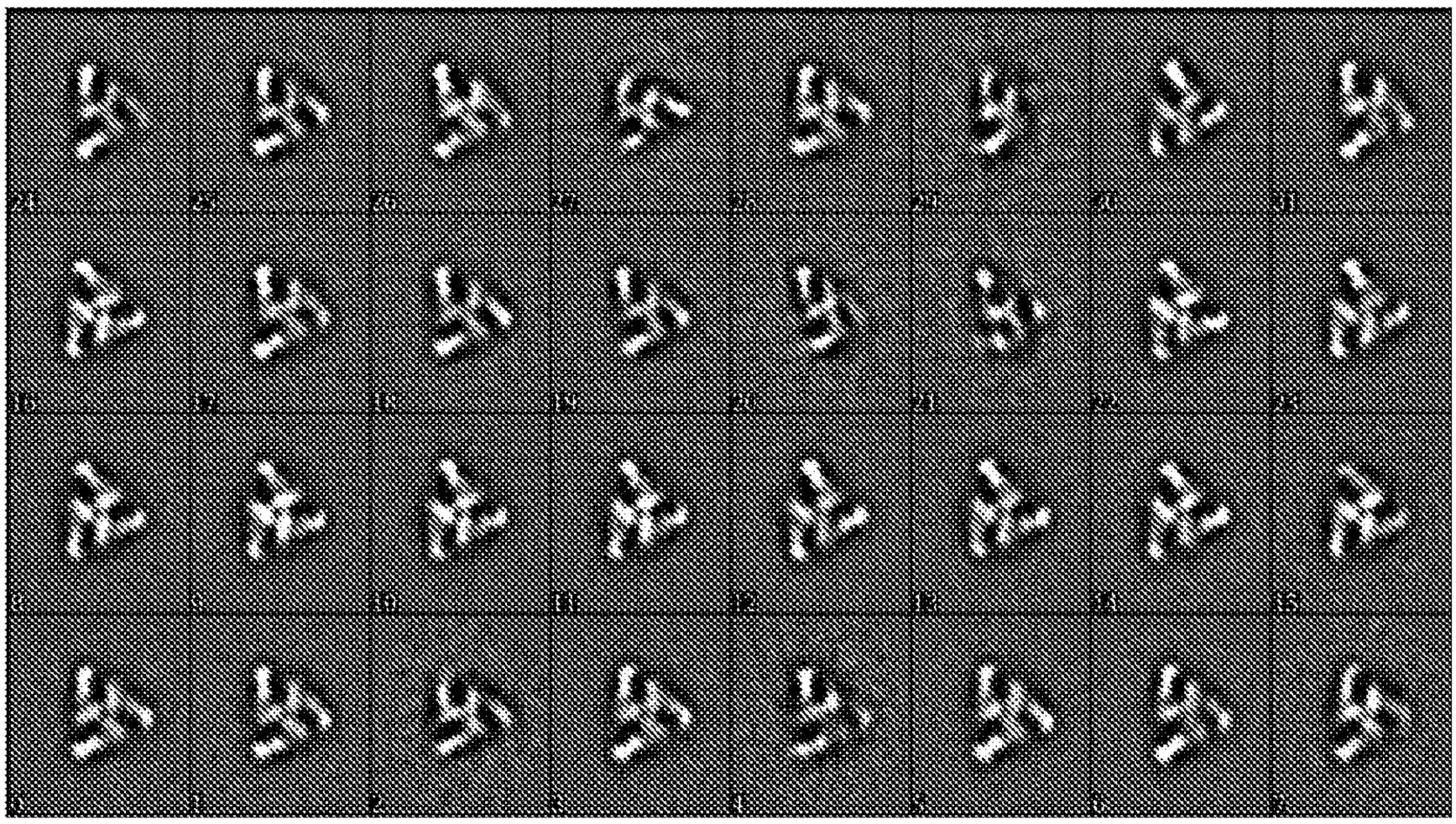

DH270.5
DH270.4
DH270.3
DH270.2
DH270.1
IA1
IA2
IA3
IA4
UCA
CDRL1
CDRL2
CDRL3
CDRH3
G57R
(CDRH2)
0.02

Figure 22

Figures 23A-23B

A



B

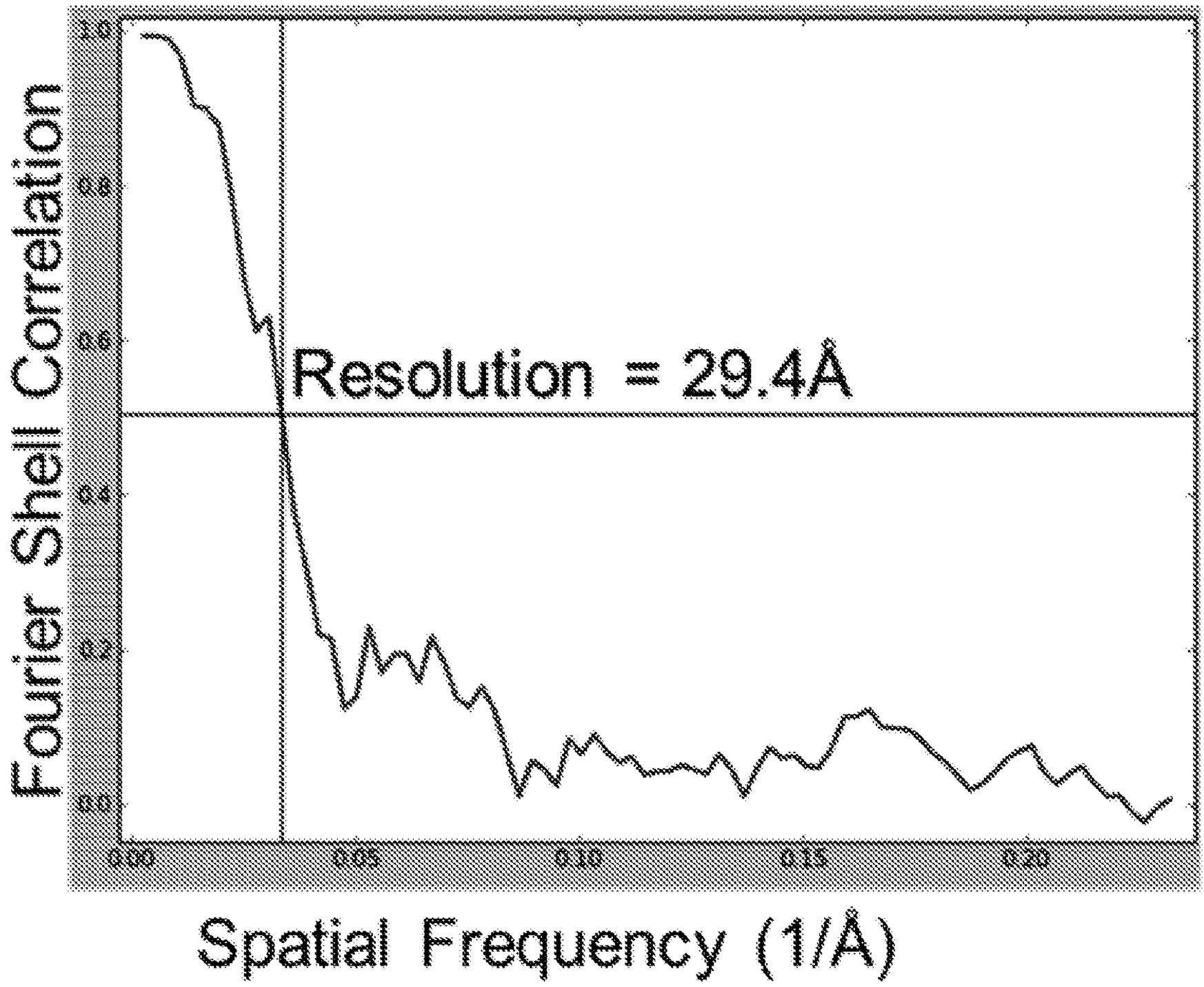


Figure 24

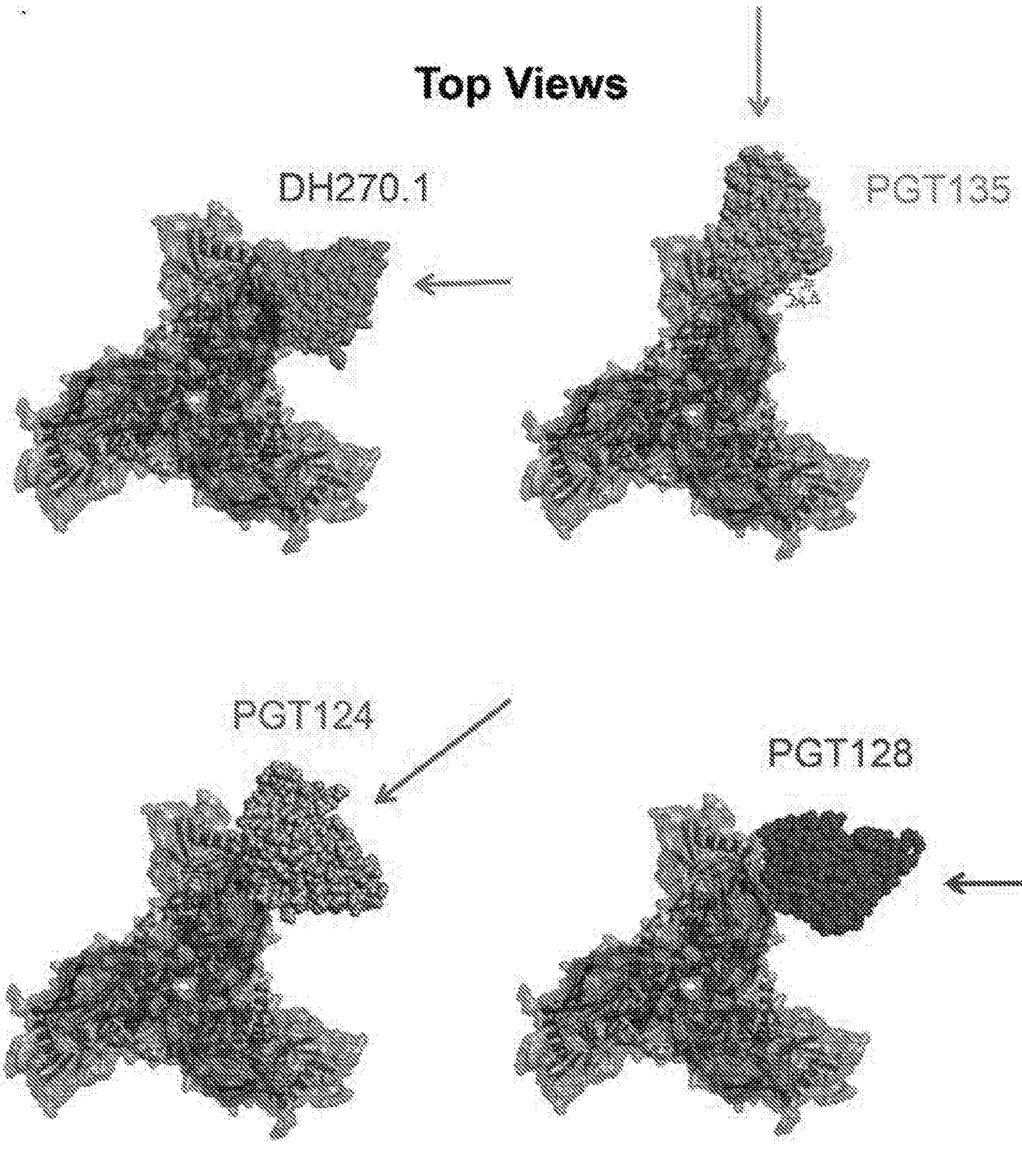
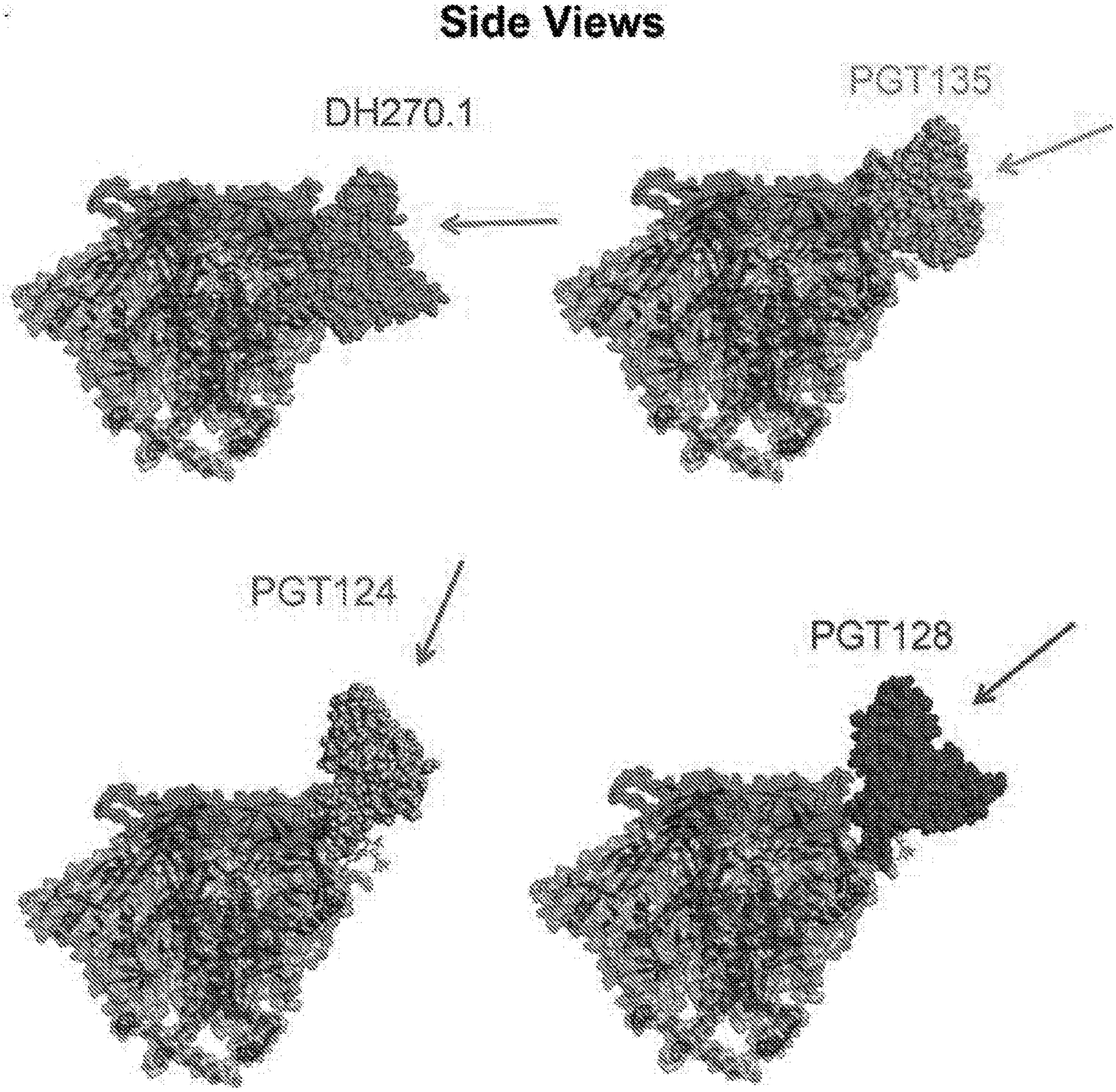
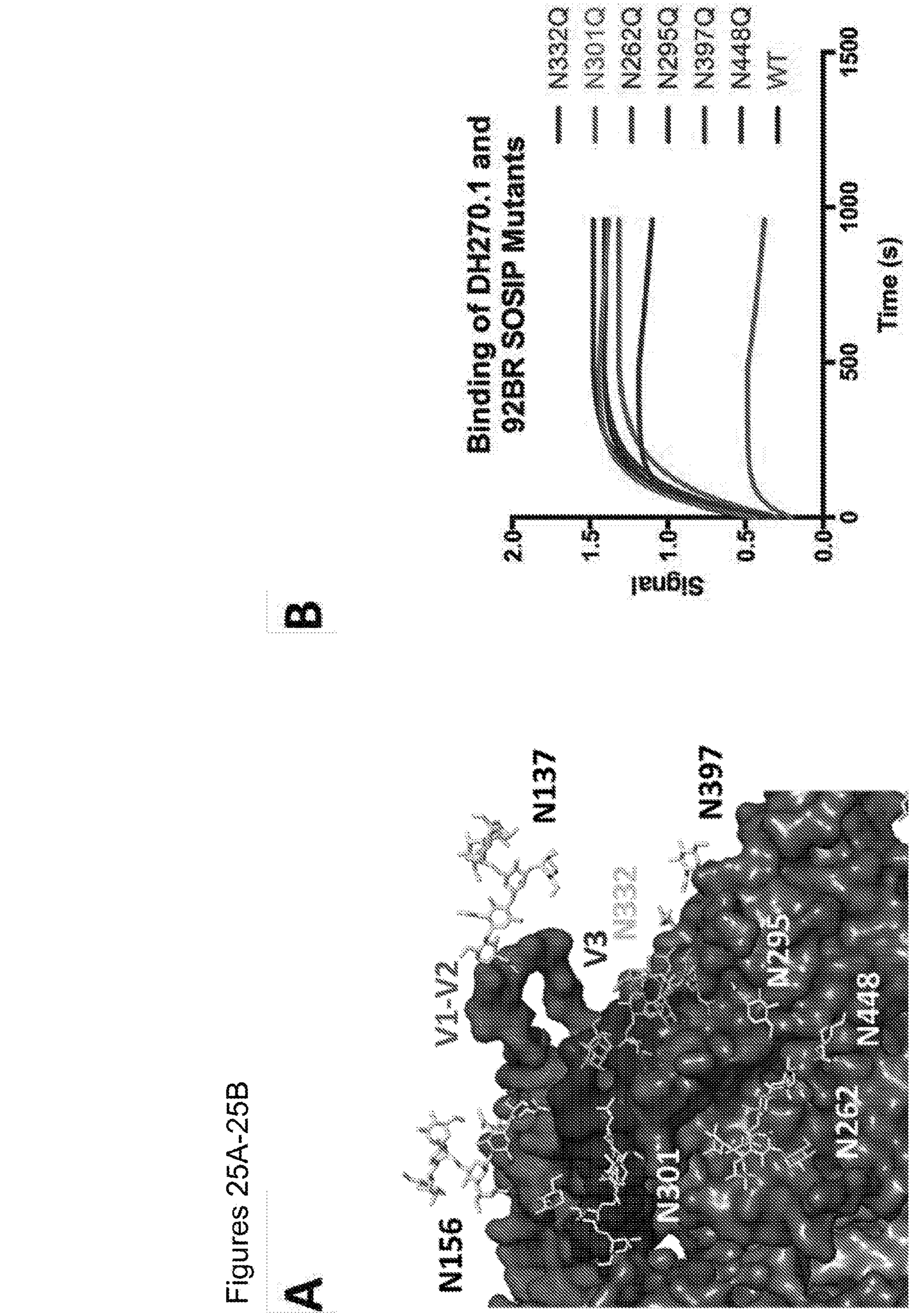


Figure 24 continued





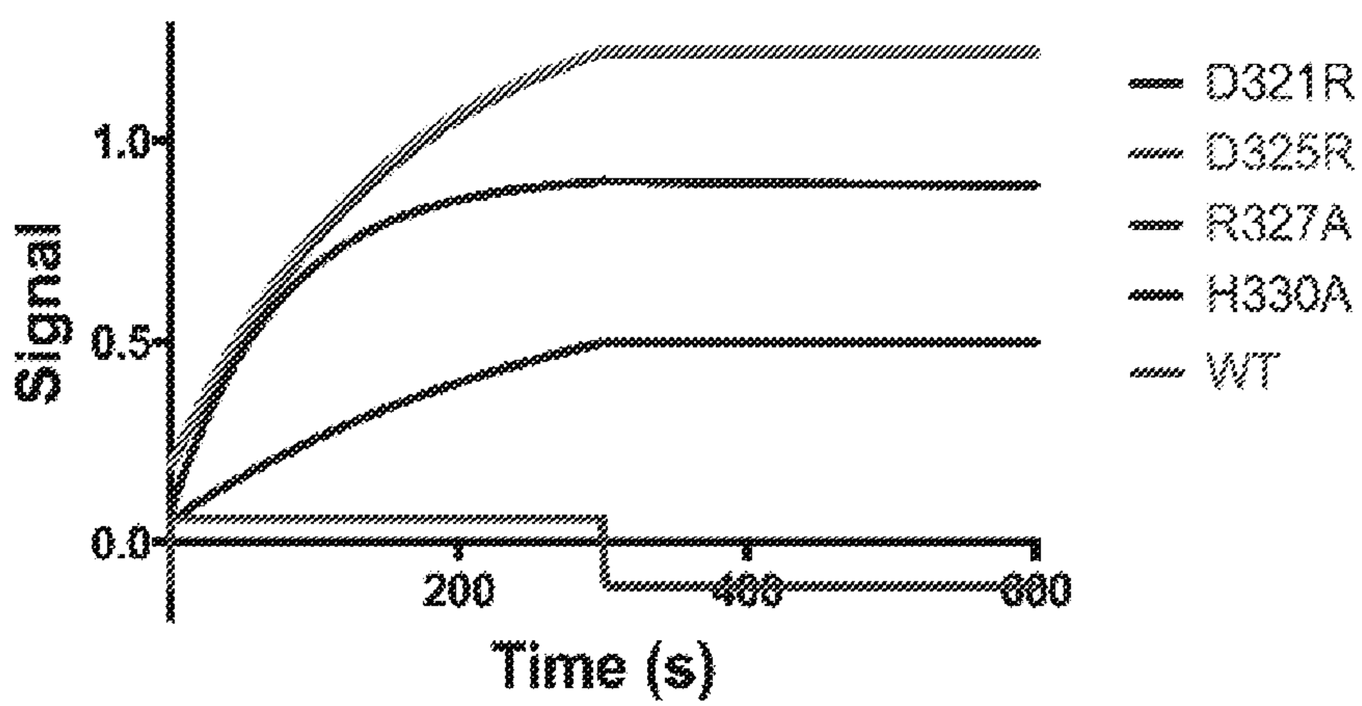
Figures 25A-25B

Figures 26A-26C

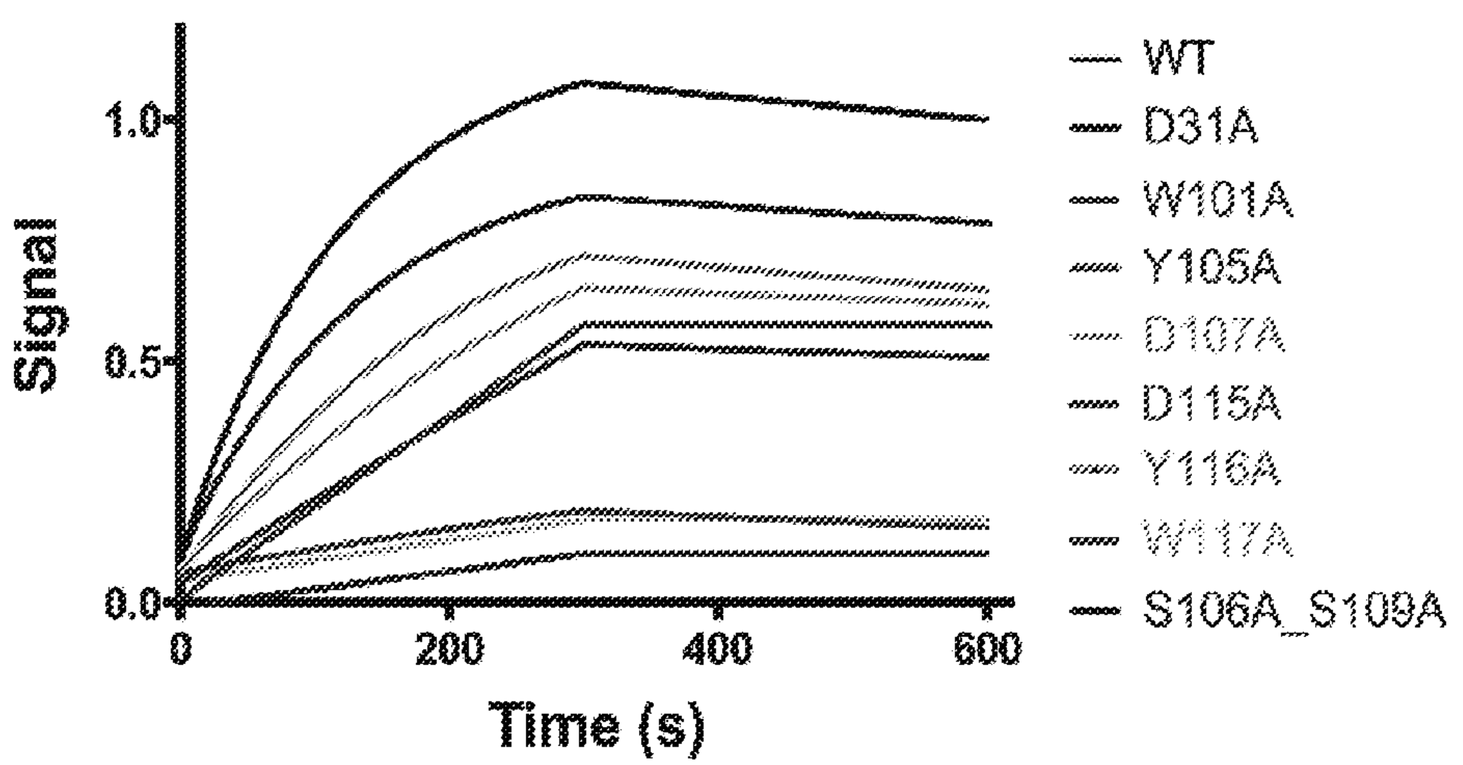
A.



B.



C.



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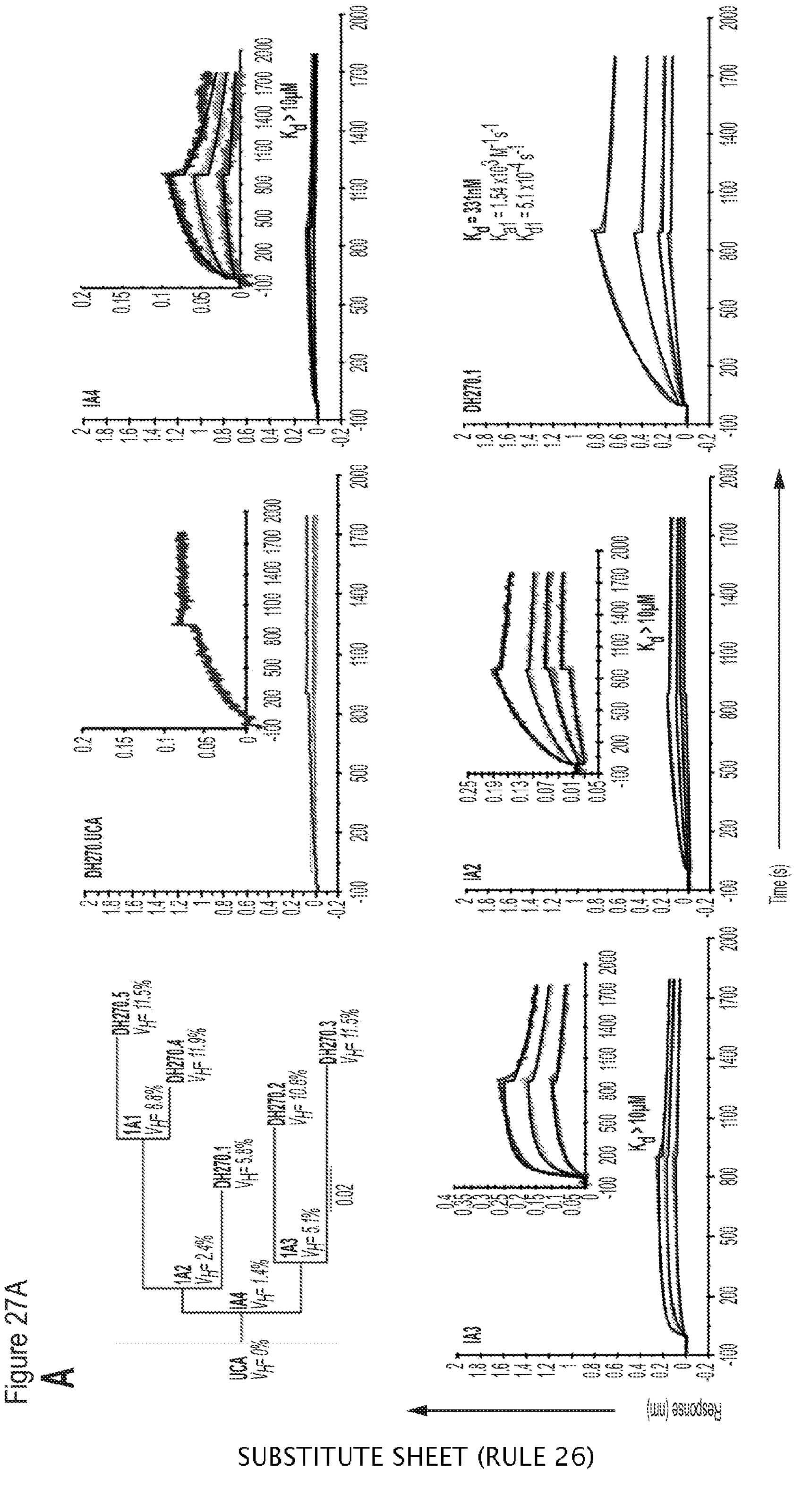
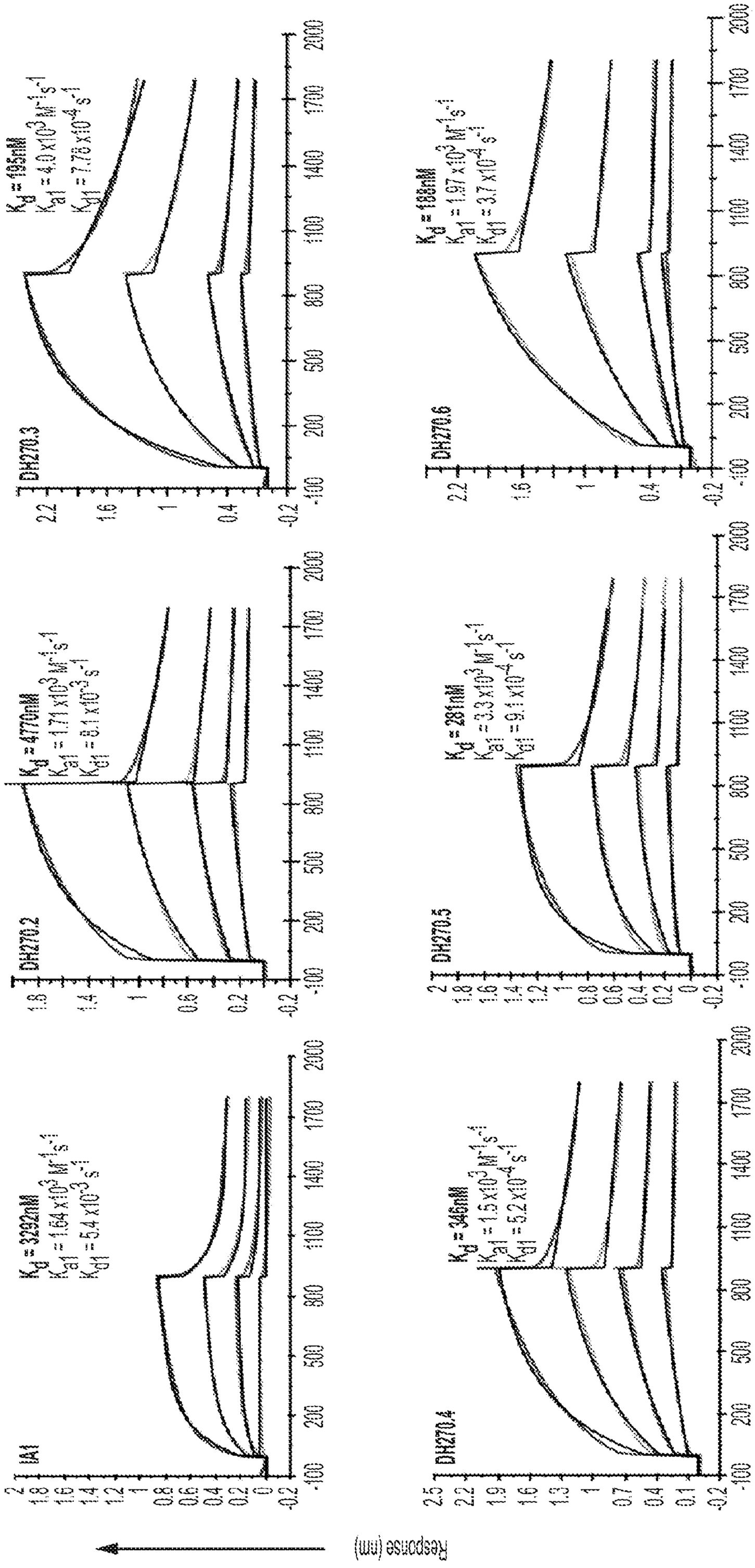


Figure 27A

SUBSTITUTE SHEET (RULE 26)

Figure 27A continued

A



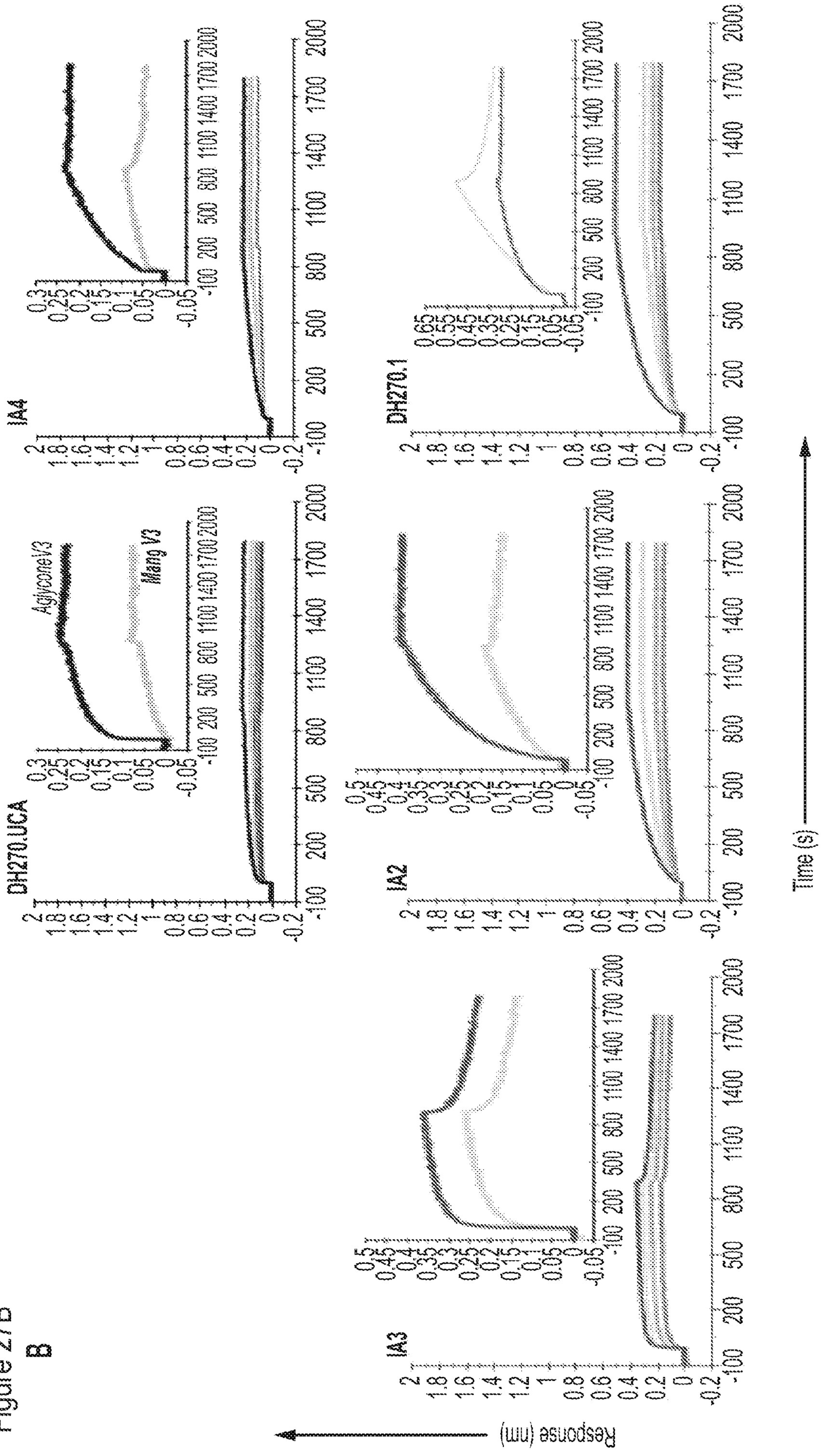

IA4
DH270.1
Agilcone V3
Mang V3
DH270.UCA
IA2
IA3
Response (nm)
Time (s)

Figure 27B

B

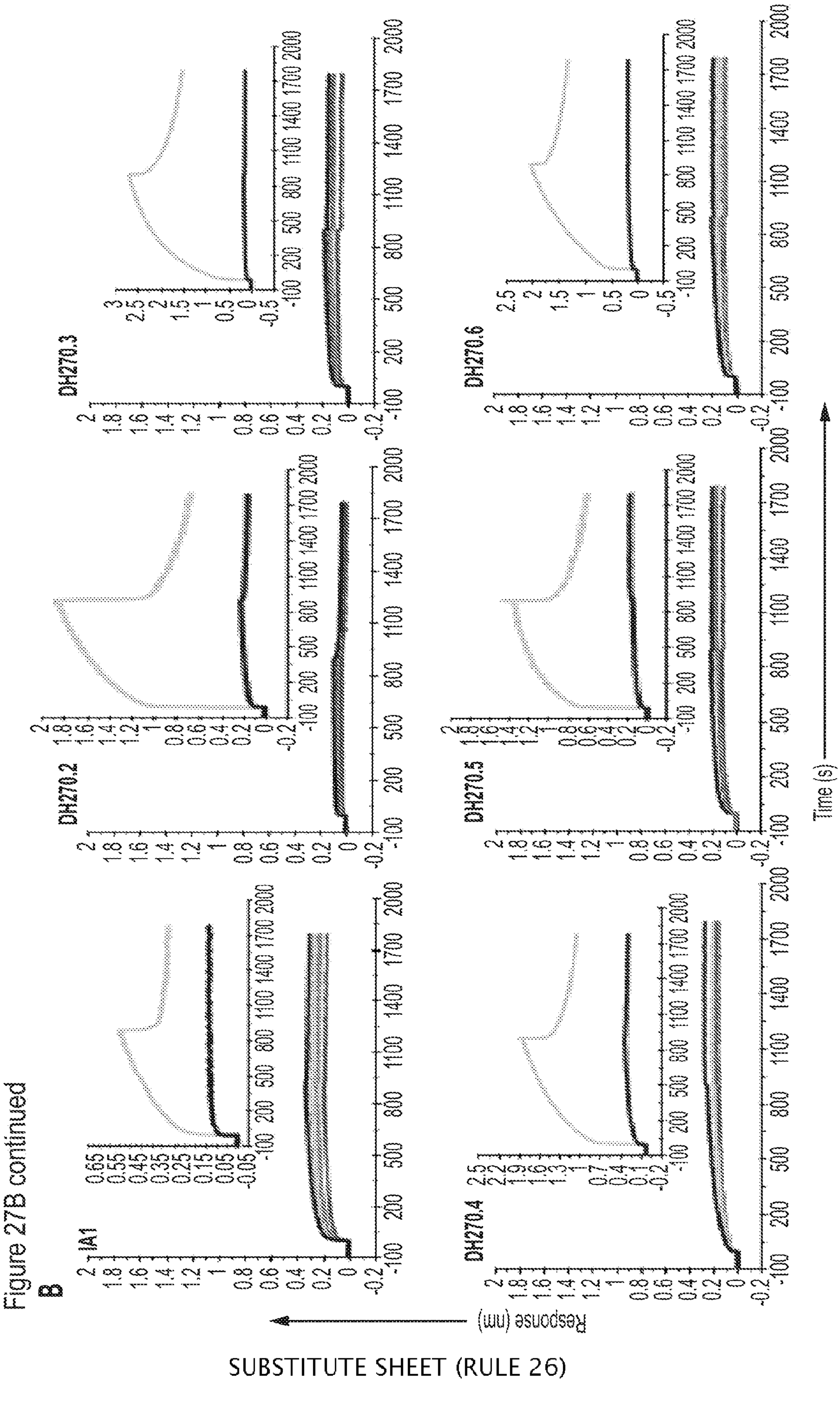


Figure 27B continued

B

Figure 28

		gp120 Binding AUC									Neutralization IC50								
Boost	Subject.day.clone	UCA	IA4	IA3	IA2	I	IA1	4	5	6	UCA	IA4	IA3	IA2	I	IA1	4	5	V1 loop length
i.	CH848.0949.10.17	0	2.5	6.3	9.4	12.9	13.6	14.3	14.6	14.3	>50	0.64	0.2	0.14	0.18	<0.02	0.03	0.05	17
ii.	CH848.0836.10.31	0	0.0	4.9	9.4	13.2	13.5	13.2	14.5	14.2	>50	45.68	0.07	<0.02	<0.02	<0.02	<0.02	<0.02	17
iii.	CH848.0358.80.06	0	0.0	0.0	0.3	11.2	13.5	14.9	15.3	13.9	>50	>50	>50	>50	1.3	0.02	<0.02	<0.02	24
iii.	CH848.1432.5.41	0	0.0	0.0	0.8	11.7	12.7	12.7	14.5	14.3	>50	>50	>50	>50	2.6	0.33	0.26	0.21	30
iii.	CH848.0526.25.02	0	0.0	0.0	0.0	8.8	12.0	13.6	13.8	13.5	>50	>50	>50	>50	18.7	1.4	1.1	1.6	34

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Figure 29

	CH848 plasma neutralization, week 186 post-transmission (EC_{50} titer)		
HIV-1 strain	**Wild-type A**	**N332A mutant**	**Fold-difference**
Q23.17	962	150	6
Du156	170	<40	4
TRO.11	204	<40	5
Consensus C	4,261	1,569	3

Figures 30A-30C

A. DH270 Lineage

Week[a]	Sample A	Sample B	Overlap[d]	Total[e]
11	0	0	0	32,732
19	0	0	0	31,179
64	1	0	0	19,383
111	0	0	0	87,224
160	0	0	0	114,729
186	9,365	14,268	776	161,104
240[c]	3	251	1	171,012

B. DH272 Lineage

Week[a]	Sample A	Sample B	Overlap	Total
11	0	0	0	32,732
19	1,634	2,782	105	31,179
64	48	0	0	19,383
111	558	684	42	87,224
160	0	0	0	114,729
186	596	509	36	161,104
240[c]	0	7	0	171,012

C. DH475 Lineage

Week[b]	Sample A	Sample B	Overlap	Total
11	0	0	0	30,764
19	0	0	0	39,784
64	378	276	3	21,353
111	0	0	0	30,925
160	0	0	0	96,301
186	788	1590	50	37,648
240[c]	0	0	0	171,012

a Reads from V_H1 family-targeted Illumina
b Reads from V_H3 family-targeted Illumina
c Reads from V_H1 through V_H6 families-targeted Illumina
d Number of clonally-related V_HDJ_H sequences that replicated across samples A and B
e Total number of replicated sequences at each timepoint

Figure 31

HIV-1 strain	Week post-transmission, neutralization IC_{50} µg/ml							
	51	100	111	113	136	160	186	205
Du172.17	31	81	117	95	61	101	83	415
6535.3	<10	<10	<10	32	<10	115	460	1,363
Q23.17	<10	<10	<10	<10	64	<10	37	1,483
Du156.12	<10	<10	<10	<10	<10	25	280	682
SC422661.8	<10	<10	<10	<10	<10	38	92	207
Q842.d12	<10	<10	<10	<10	<10	50	74	54
QH0692.42	<10	<10	<10	<10	<10	<10	56	100
PVO.4	<10	<10	<10	<10	<10	<10	32	251
AC10.0.29	<10	<10	<10	<10	<10	<10	21	209
RHPA4259.7	<10	<10	<10	<10	<10	<10	59	250
Du422.1	<10	<10	<10	<10	<10	<10	152	341
ZM197M.PB7	<10	<10	<10	<10	<10	<10	43	105
Q259.d2.17	<10	<10	<10	<10	<10	<10	<10	112
ZM214M.PL15	<10	<10	<10	<10	<10	<10	<10	37
Q769.d22	<10	<10	<10	<10	<10	<10	<10	<10
CAP45.2.00.G3	<10	<10	<10	<10	<10	<10	<10	<10
SVA-MLV	<10	<10	<10	<10	<10	<10	<10	<10

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Figure 32

Data Collection							
	UCA1	**UCA3**	**DH270.1**	**DH270.3**	**DH270.5**	**DH270.6**	**DH272**
Resolution (Å)	50 - 3.31 (3.37 - 3.31)	50 - 2.26 (2.30 - 2.26)	50 - 3.47 (3.53 - 3.47)	50 - 2.50 (2.54 - 2.50)	50 - 1.85 (1.88 - 1.85)	50 - 2.73 (2.78 - 2.73)	50 - 2.68 (2.73 - 2.68)
Space group	R 3 2	C 1 2 1	C 1 2 1	P 21 21 21	C 1 2 1	P 1 21 1	I 2 2 2
Unit cell a,b,c (Å)	209.1, 209.1, 83.5	98.5, 76.9, 137.1	156.873 111.284 89.134	63.2, 69.3, 115.2	135.1, 68.8, 59.5	67.1, 73.7, 112.7	60.9, 124.5, 146.2
Unit cell α, β, γ (°)	90 90 120	90, 102, 90	90, 120.46, 90	90, 90, 90	90, 113, 90	90, 107, 90	90, 90, 90
Total reflections	65247	142800	32526	57856	126544	57894	47496
Unique reflections	10410	46692	14420	17599	42441	27592	15439
Redundancy	6.3 (5.0)	3.1 (3.0)	2.3 (2.2)	3.3 (3.0)	3.0 (2.1)	2.1 (2.1)	1.7 (1.6)
Completeness (%)	97.6 (90.5)	99.1 (98.9)	80.9 (77.0)	97.1 (98.4)	96.2 (83.9)	97.2 (92.8)	97.5 (94.4)
$\langle I/\sigma_I \rangle$	7.0 (1.9)	7.3 (1.5)	4.6 (1.4)	6.8 (1.9)	5.6 (1.7)	6.00 (1.4)	9.3 (2.6)
R_{merge}	21.0 (88.3)	9.6 (87.8)	23.3 (50.3)	12.9 (56.9)	15.3 (54.6)	11.2 (64.2)	11.9 (63.8)
Refinement							
R_{work}/R_{free} (%)	24.5/27.3 (33.1/39.4)	21.6/25.5 (33.0/35.2)	25.4/28.2 (32.2/33.4)	21.5/24.9 (33.0/43.3)	17.9/21.2 (24.1/26.9)	19.1/20.9 (31.7/32.4)	21.1/25.6 (34.6/37.0)
No. atoms							
Protein	3195	6290	7157	3250	3313	6582	3361
Ligand	10	0			16		33
Water	3	274	0	114	415	107	75
R.M.S. deviations							
Bond lengths (Å)	0.006	0.005	0.005	0.010	0.007	0.004	0.003
Bond angles (°)	0.98	1.13	0.89	1.33	1.25	0.91	0.81
B-factors (Å^2)							
Protein	53.40	56.80	61.20	41.80	25.60	55.20	51.00
Ligand	98.00				47.60		61.50
Solvent	60.00	49.50	39.20	39.20	40.90	42.00	40.10

Statistics for the highest-resolution shell are shown in parentheses.

Figure 33

Virus ID	Clade or CRF	Clade	331-336	N332 glycan	LengthV1	DH270.1	DH270.5	DH270.6	10-1074	PGT128	PGT121
398-F1_F6_20	A	A	CNVSKA	332	21	0.038	0.036	0.021	0.2091	0.905	0.0307
RW020.2	A	A	CNVSRA	332	15	0.051	0.052	0.012	0.3053	0.904	0.0307
Q23.17	A	A	CNVTRS	332	19	0.056	0.049	0.019	0.0003	0.910	0.0025
KNH1209.18	A	A	CNVSRS	332	24	0.065	0.044	0.028	0.0003	0.909	0.0307
BI369.9A	A	A	CNVSRS	332	35	0.407	0.301	0.112	0.302	0.930	0.096
MI369.A5	A	A	CNVSRS	332	35	0.501	0.480	0.166	0.302	0.922	0.039
UG037.8	A	A	CNVSGS	332	27	1.53	0.290	0.058	0.031	0.922	0.011
0260.v5.c36	A	A	CNVSKA	332	44	2.32	2.18	0.378	0.130	0.937	0.056
KER2008.12	A	A	CNVSKS	332	32	1.16	0.133	0.047	0.123	>50	2.10
0330.v4.c3	A	A	CNVSGT	332	15	>50	1.16	1.83	0.319	0.377	0.067
3365.v2.c20	A	A	CNVSQT	332	22	>50	>50	1.04	0.003	>50	0.133
BS208.B1	A	A	CNVSGS	332	15	>50	>50	1.83	0.1	>50	>25
BB201.B42	A	A	CNVSRS	332	19	>50	>50	>50	0.0003	0.904	0.0308
3415.v1.c1	A	A	CNVSRK	332	24	>50	>50	>50	>50	0.910	>25
0439.v5.c1	A	A	CNVSKT	332	48	>50	>50	>50	>50	1.38	>25
MS208.A1	A	A	CNVSGS	332	23	>50	>50	>50	>50	>50	>25
Q259.17	A	A	CTVNRT	334	18	>50	>50	>50	1.94	>50	>25
MB201.A1	A	A	CKVNRS	334	19	>50	>50	>50	>50	0.909	0.0308
Q842.d12	A	A	CNVNRT	334	19	>50	>50	>50	>50	0.942	0.097
MB539.2B7	A	A	CTVNRT	334	23	>50	>50	>50	>50	1.41	>25
3718.v3.c11	A	A	CHVNKT	334	25	>50	>50	>50	>50	>50	1.12
KER2018.11	A	A	CVVNRT	334	24	>50	>50	>50	>50	>50	>25
QH209.14M.A2	A	A	CIVNKT	334	28	>50	>50	>50	>50	>50	>25
BB539.2B13	A	A	CTVNRT	334	22	>50	>50	>50	>50	>50	>25
Q461.e2	A	AD	CVVNRT	334	27	>50	>50	>50	>50	>50	>25
BG505.W6M.C2	A	A	CTVSKA	none	19	>50	>50	>50	>50	0.948	0.124
Q769.d22	A	A	CNVNRQ	none	24	>50	>50	>50	>50	>50	>25
Q769.h5	A	A	CNVNRQ	none	26	>50	>50	>50	>50	>50	>25
BJOX028000.10.3	CRF01-AE	AE	CNISRT	332	31	>50	>50	>50	>50	0.924	>25
C3347.c11	CRF01-AE	AE	CEINGT	334	32	>50	>50	>50	>50	0.904	>25
BJOX009000.02.4	CRF01-AE	AE	CEINGT	334	27	>50	>50	>50	>50	0.908	2.36
TH966.8	CRF01-AE	AE	CEINGT	334	29	>50	>50	>50	>50	0.905	>25
CM244.ec1	CRF01-AE	AE	CEINGT	334	34	>50	>50	>50	>50	0.912	>25
C2101.c1	CRF01-AE	AE	CEINET	334	28	>50	>50	>50	>50	0.914	>25
CNE8	CRF01-AE	AE	CEINRT	334	26	>50	>50	>50	>50	0.914	>25
CNE5	CRF01-AE	AE	CEINGT	334	30	>50	>50	>50	>50	0.962	>25
C1080.c3	CRF01-AE	AE	CEINGT	334	28	>50	>50	>50	>50	0.100	>25
CNE56	CRF01-AE	AE	CKINGT	334	27	>50	>50	>50	>50	1.18	>25
R2184.c4	CRF01-AE	AE	CVINGT	334	30	>50	>50	>50	>50	1.36	>25
BJOX010000.06.2	CRF01-AE	AE	CKINAT	334	34	>50	>50	>50	>50	1.97	>25
620345.c1	CRF01-AE	AE	CEINGT	334	29	>50	>50	>50	>50	>50	>25
BJOX025000.01.1	CRF01-AE	AE	CEINGT	334	28	>50	>50	>50	>50	>50	>25

Figure 33 continued

Virus ID	Clade or CRF	Clade	331-336	N332 glycan	LengthV1	DH270.1	DH270.5	DH270.6		10-1074	PGT128	PGT121
CNE3	CRF01-AE	AE	CEINRT	334	37	>50	>50	>50		>50	>50	>25
CNE59	CRF01-AE	AE	CEINGT	334	27	>50	>50	>50		>50	>50	>25
R1166.c1	CRF01-AE	AE	CEINRT	334	31	>50	>50	>50		>50	>50	>25
R3265.c6	CRF01-AE	AE	CEINQT	334	29	>50	>50	>50		>50	>50	>25
TH976.17	CRF01-AE	AE	CEINET	334	34	>50	>50	>50		>50	>50	>25
M02138	CRF01-AE	AE	CKINGT	334	27	>50	>50	>50		>50	>50	>25
TH023.6	CRF01-AE	AE	CEINGA	334	29	>50	>50	>50		>50	0.176	>25
C4118.09	CRF01-AE	AE	CEIDGT	none	29	>50	>50	>50		>50	>50	>25
CNE55	CRF01-AE	AE	CEIDGT	none	25	>50	>50	>50		>50	>50	>25
DJ263.8	CRF02-AG	AG	CNVSRS	332	33	0.201	0.129	0.062		0.308	>50	0.053
269-12	CRF02-AG	AG	CNVSTT	332	25	2.74	0.184	0.036		0.184	0.810	0.236
235-47	CRF02-AG	AG	CNVSST	332	22	3.11	0.557	0.301		0.084	>50	0.289
T266-60	CRF02-AG	AG	CNVSGK	332	40	6.21	5.04	0.462		0.362	0.316	0.118
263-8	CRF02-AG	AG	CNVSKG	332	29	>50	2.56	0.191		0.092	0.211	0.872
928-28	CRF02-AG	AG	CNVSKI	332	25	>50	>50	2.12		0.530	>50	6.11
T251-18	CRF02-AG	AG	CNVSRG	332	24	>50	>50	14.1		0.169	>50	6.17
T278-50	CRF02-AG	AG	CNVSGT	332	26	>50	>50	1.16		0.247	0.038	>25
T250-4	CRF02-AG	AG	CNVSKR	332	22	>50	>50	>50		0.3003	0.004	0.0134
T255-34	CRF02-AG	AG	CNVSK-	332	28	>50	>50	>50		0.380	>50	1.21
T253-11	CRF02-AG	AG	CNVSKT	332	25	>50	>50	>50		2.70	>50	>25
271-11	CRF02-AG	AG	CEVNRT	334	30	>50	>50	>50		>50	>50	3.14
242-14	CRF02-AG	AG	CVVNKT	334	24	>50	>50	>50		>50	>50	>25
T257-31	CRF02-AG	AG	CKVNKT	334	33	>50	>50	>50		>50	>50	>25
T33-7	CRF02-AG	AG	CEVNRT	334	30	>50	>50	>50		>50	>50	>25
BJOX002000.03.2	CRF07_BC	BC	CNISGK	332	22	0.096	0.046	0.021		0.311	0.918	0.098
CH119.10	CRF07_BC	BC	CNIS--	332	21	0.235	0.077	0.049		0.029	0.926	0.017
CNE21	CRF07_BC	BC	CNISET	332	26	0.535	0.129	0.060		0.014	0.912	0.032
CH181.12	CRF07_BC	BC	CNISRD	332	30	0.773	0.320	0.102		0.011	0.922	0.012
CNE19	CRF07_BC	BC	CNISKD	332	22	>50	0.093	0.030		0.027	>50	0.0093
CNE20	CRF07_BC	BC	CNISEN	332	17	>50	>50	4.32		0.3093	0.902	0.0907
CH117.4	CRF07_BC	BC	CNINRT	334	24	>50	>50	>50		>50	>50	>25
SF162.LS	B	B	CNISGE	332	26	0.036	0.022	0.009		0.0093	0.906	0.0907
CNE14	B	B	CNLSRT	332	26	0.066	0.043	0.021		0.0093	0.913	0.0908
BX08.16	B	B	CNISRT	332	20	0.074	0.078	0.020		0.0093	0.907	0.0908
JRFL.JB	B	B	CNISRA	332	25	0.079	0.033	0.019		0.0210	0.910	0.048
SS1196.01	B	B	CNISRK	332	21	0.060	0.067	0.021		0.0093	0.911	0.0908
CAAN.A2	B	B	CNISGE	332	24	0.056	0.106	0.027		0.0906	0.124	0.092
3988.25	B	B	CNISRT	332	23	0.040	0.034	0.019		0.0907	0.904	0.0908
45_01dG5	B	B	CNISKA	332	27	0.094	0.060	0.029		0.0906	0.910	0.0909
6535.3	B	B	CNISRA	332	29	0.102	0.039	0.029		0.0210	0.911	0.0908
6101.10	B	B	CNISRG	332	30	0.124	0.104	0.024		0.0210	0.903	0.0909

Figure 33 continued

Virus ID	Clade or CRF	Clade	331-336	N332 glycan	LengthV1	DH270.1	DH270.5	DH270.6		10-1074	PGT128	PGT121
CNE12	B	B	CNLSRA	332	26	0.126	0.033	0.049		0.0010	0.016	0.002
CNE57	B	B	CNLSIA	332	20	0.135	0.081	0.048		0.006	0.008	0.005
Bal.01	B	B	CNLSRA	332	31	0.176	0.131	0.043		0.003	0.117	0.0309
TRO.11	B	B	CNISRT	332	32	0.189	0.116	0.044		0.0010	0.019	0.0010
BaL.26	B	B	CNLSRA	332	31	0.221	0.113	0.048		0.004	0.050	0.010
89.6.DG	B	B	CNISRA	332	29	0.267	0.321	0.035		0.002	0.010	0.007
7165.18	B	B	CNLSRA	332	27	0.281	0.163	0.048		0.006	0.012	0.014
RHPA7	B	B	CNISRE	332	23	0.285	0.116	0.054		0.007	0.032	0.010
PVO.04	B	B	CNLSRA	332	31	0.447	0.299	0.070		0.044	0.013	0.113
ADA.DG	B	B	CNISRT	332	24	0.463	0.231	0.050		0.003	0.010	0.031
YU2.DG	B	B	CNLSKT	332	26	0.634	0.524	0.135		0.269	0.065	0.079
SC422.8	B	B	CNLSSA	332	24	0.646	0.321	0.052		0.043	0.384	0.165
X2278.C2.B6	B	B	CNISAT	332	29	0.855	0.108	0.038		0.015	0.012	0.004
JRCSF.JB	B	B	CNISRA	332	25	1.17	0.100	0.046		0.004	0.011	0.020
AC10.29	B	B	CNISRQ	332	27	1.18	0.025	0.016		0.025	0.010	0.029
QH0692.42	B	B	CNLSSV	332	31	3.96	1.40	0.212		0.185	0.539	0.891
TRJO.58	B	B	CNISEA	332	24	>50	0.335	0.167		0.098	0.019	7.82
CNE4	B	B	CNLSST	332	28	>50	12.9	2.99		0.102	0.898	6.42
QH0515.01	B	B	CNLSRA	332	28	>50	>50	0.907		0.200	>50	9.88
CNE10	B	B	CNLSRT	332	21	>50	>50	11.1		0.0009	0.010	0.0030
BL01.DG	B	B	CNLSRA	332	25	>50	>50	12.5		5.28	>50	>25
BR07.DG	B	B	CNLSRT	332	27	>50	>50	>50		0.015	0.636	0.396
WITO.33	B	B	CNISTE	332	25	>50	>50	>50		0.213	>50	0.705
HT593.1	B	B	CNISRA	332	26	>50	>50	>50		0.704	>50	>25
MN.3	B	B	CNISRA	332	33	>50	>50	>50		1.29	>50	>25
HXB2.DG	B	B	CNISRA	332	27	>50	>50	>50		3.91	>50	>25
REJO.67	B	B	CTINES	334	29	>50	>50	>50		>50	>50	12.4
BG1168.01	B	B	CTLNST	334	34	>50	>50	>50		>50	>50	>25
HO86.8	B	B	CNVNKT	334	23	>50	>50	>50		>50	>50	>25
THRO.18	B	B	CTVNGT	334	35	>50	>50	>50		>50	>50	>25
5768.04	B	B	CNINRA	none	27	>50	5.23	0.164		0.314	1.41	0.293
57128.vrc15	D	D	CNISRK	332	33	17.4	24.8	2.40		0.252	0.859	2.60
6405.v4.c34	D	D	CNVSRV	332	30	>50	>50	2.88		0.607	1.63	0.039
A07412M1.vrc12	D	D	CNVSKV	332	25	>50	>50	>50		0.0033	24.7	0.013
A03349M1.vrc4a	D	D	CNISGA	332	20	>50	>50	>50		0.210	0.319	0.025
231965.c1	D	D	CNISRK	332	36	>50	>50	>50		1.14	>50	>25
UG021.16	D	D	CNISGE	332	21	>50	>50	>50		0.468	>50	2.49
191821.E6.1	D	D	CNVSRT	332	17	>50	>50	6.91		>50	0.035	>25
UG024.2	D	D	CNISEA	332	27	>50	>50	>50		0.111	>50	>25
NKU3006.ec1	D	D	CEINGT	334	41	>50	>50	>50		>50	>50	>25
3016.v5.c45	D	D	CTIDGT	none	23	>50	>50	>50		>50	>50	>25
P1981.C5.3	G	G	CNISKS	332	21	0.047	0.038	0.015		0.2003	0.515	0.007

Figure 33 continued

Virus ID	Clade or CRF	Clade	331-336	N332 glycan	LengthV1	DH270.1	DH270.5	DH270.6		10-1074	PGT128	PGT121
X2088.c9	G	G	CNVTRG	332	15	0.158	0.053	0.022		0.0003	>50	0.0006
X1254.c3	G	G	CNISGT	332	26	0.259	0.174	0.070		0.027	0.023	0.038
X2131.C1.B5	G	G	CNISKT	332	30	0.972	0.197	0.046		0.021	0.029	0.033
P0402.c2.11	G	G	CNISGA	332	24	14.5	2.81	0.107		0.006	0.007	0.0007
X1193.c1	G	G	CNISKT	332	30	11.2	1.19	0.213		0.036	0.029	0.019
X1632.S2.B10	G	G	CNINGS	334	27	>50	>50	>50		>50	>50	>25
3817.v2.c59	unique	CD	CNISRG	332	23	0.736	0.856	0.332		0.308	0.917	>25
3337.V2.C6	unique	CD	CNISAT	332	18	34.0	6.88	0.305		0.006	0.004	8.10
T280-5	unique	AG	CNVSKA	332	17	0.044	0.015	0.034		0.0003	0.014	0.033
CH038.12	unique	BC	CNISRE	332	26	0.217	0.093	0.039		0.0010	0.007	0.002
0815.V3.C3	unique	ACD	CNVSRA	332	28	0.635	0.508	0.131		0.008	0.025	0.016
CH070.1	unique	07C	CNISKD	332	40	0.621	0.310	0.091		0.0010	0.028	0.010
3589.V1.C4	unique	AC	CNVSRT	332	23	>50	>50	>50		>50	0.906	>25
CNE7	unique	BC	CNIS--	332	22	>50	>50	>50		0.048	0.034	0.013
CNE40	unique	BC	CNISRS	332	33	>50	>50	>50		0.964	>50	0.321
6095.V1.C10	unique	ACD	CNISSK	332	20	>50	>50	>50		>50	>50	>25
3468.V1.C12	unique	AD	CNVSGT	332	27	>50	>50	>50		0.0007	>50	0.047
3326.V4.C3	unique	CD	CNINGT	334	19	>50	>50	>50		>50	>50	>25
6540.v4.c1	unique	AC	CTVNRT	334	25	>50	>50	>50		>50	0.815	>25
6545.V4.C1	unique	AC	CTVNRT	334	25	>50	>50	>50		>50	>50	>25
246-F3.C10.2	unique	AC	CTVNKT	334	22	>50	>50	>50		>50	0.903	>25
247-23	unique	DU	CTINKT	334	21	>50	>50	>50		>50	>50	>25
Q168.a2	unique	AD	CTVNGS	334	24	>50	>50	>50		>50	>50	>25
CNE15	unique	BC	CSINAG	none	23	>50	>50	>50		>50	>50	>25
BR025.9	C	C	CNISRT	332	22	0.060	0.029	0.015		0.0003	0.905	0.0016
SO18.18	C	C	CNISES	332	17	0.073	0.039	0.016		0.0007	0.041	0.0035
286.36	C	C	CNISRE	332	22	0.119	0.049	0.027		0.0003	0.011	0.0009
ZM106.9	C	C	CNISEE	332	25	0.127	0.079	0.031		0.0010	0.025	0.0007
6644.V2.C33	C	C	CNISAS	332	34	0.128	0.095	0.033		0.002	0.906	0.012
CAP256.206.C9	C	C	CNISEI	332	22	0.126	0.094	0.043		0.030	0.918	0.003
MW965.26	C	C	CNISTI	332	26	0.135	0.091	0.019		0.0010	0.179	0.0008
ZM55.28a	C	C	CNISIE	332	13	0.145	0.074	0.052		0.002	0.924	0.046
288.38	C	C	CNISGD	332	32	0.148	0.114	0.048		0.0007	0.911	0.034
25711-2.4	C	C	CNISEG	332	26	0.200	0.044	0.021		0.0010	0.916	0.011
DU156.12	C	C	CNISRN	332	25	0.234	0.126	0.053		0.0010	0.920	0.002
6785.V5.C14	C	C	CNISAR	332	25	0.247	0.138	0.060		0.004	0.916	0.015
Ce1176.A3	C	C	CNVSKQ	332	23	0.294	0.222	0.096		0.024	0.915	0.004
3873.V1.C24	C	C	CNISGA	332	29	0.374	0.100	0.042		0.019	0.915	0.030
CNE53	C	C	CNISES	332	20	0.406	0.272	0.143		0.002	0.930	0.003
CE703010217.B6	C	C	CNISEK	332	17	0.457	0.073	0.040		0.004	0.943	0.0007
DU123.06	C	C	CNISKT	332	30	0.531	0.238	0.175		0.072	0.961	0.032
DU422.01	C	C	CNISRE	332	27	0.554	0.243	0.120		0.027	0.964	0.022

Figure 33 continued

Virus ID	Clade or CRF	Clade	331-336	N332 glycan	LengthV1	DH270.1	DH270.5	DH270.6		10-1074	PGT128	PGT121
96ZM651.02	C	C	CNISRT	332	32	0.660	0.103	0.027		0.002	0.026	0.010
16936-2.21	C	C	CNISEA	332	21	0.725	0.380	0.072		0.003	0.023	0.032
3168.V4.C10	C	C	CNISEK	332	29	0.856	1.16	0.440		0.391	>50	0.453
3301.V1.C24	C	AC	CNITRN	332	21	0.587	0.331	0.105		0.0010	0.131	0.007
TZBD.02	C	C	CNISKD	332	29	1.82	0.091	0.027		0.0010	>50	0.0021
25710-2.43	C	C	CNISKD	332	16	2.07	0.383	0.120		0.011	0.020	0.013
ZM135.10a	C	C	CNISGE	332	23	2.12	0.302	0.122		0.052	>50	1.94
CNE58	C	C	CNITKS	332	32	2.20	0.323	0.250		0.397	0.988	>25
CNE30	C	C	CNISRN	332	25	3.02	1.84	0.742		0.222	0.269	0.069
ZM215.8	C	C	CNISKK	332	17	5.13	0.361	0.161		0.004	0.045	0.011
TV1.29	C	C	CNISTD	332	33	8.94	1.62	0.670		0.410	0.122	0.035
ZA012.29	C	C	CNISES	332	21	9.33	0.125	0.026		0.0010	0.040	0.0008
DU172.17	C	C	CNISRK	332	30	13.2	1.39	0.300		0.316	0.941	0.042
ZM214.15	C	C	CNISKD	332	28	40.9	6.22	0.563		0.491	0.522	1.03
426c	C	C	CNTSGL	332	29	>50	0.916	0.197		0.068	>50	>25
6471.V1.C16	C	C	CNISKV	332	43	>50	3.43	0.429		0.827	>50	>25
ZM176.66	C	C	CNISEE	332	27	>50	8.01	0.504		0.209	0.026	5.44
25925-2.22	C	C	CNISRD	332	19	>50	8.78	0.519		0.0010	0.016	0.032
16845-2.22	C	C	CNISEA	332	33	>50	15.1	1.12		0.318	0.121	7.98
DU151.02	C	C	CNISKS	332	18	>50	24.2	0.820		0.0036	0.010	0.032
0921.V2.C14	C	C	CNISKH	332	13	>50	>50	3.86		>50	>50	>25
CAP244.D3	C	C	CNIDKG	332	46	>50	>50	5.23		6.78	>50	>25
001428-2.42	C	C	CNISEK	332	27	>50	>50	44.2		0.008	0.037	0.097
ZM233.6	C	C	CNISAS	332	17	>50	>50	>50		0.003	>50	2.13
26191-2.48	C	C	CNISKE	332	17	>50	>50	>50		0.010	0.010	0.041
6631.V3.C10	C	C	CNISRE	332	39	>50	>50	>50		0.158	1.25	>25
CNE31	C	C	CNISEE	332	25	>50	>50	>50		0.348	>50	0.947
TZA125.17	C	C	CNISRS	332	29	>50	>50	>50		1.77	0.511	5.55
0013095-2.11	C	C	CNISEE	332	24	>50	>50	>50		5.84	>50	>25
ZM249.1	C	C	CNISKE	332	23	>50	>50	>50		>50	0.363	>25
ZM109.4	C	C	CKINGS	332	17	>50	>50	>50		>50	>50	9.17
3637.V5.C3	C	C	CNISKG	332	18	>50	>50	>50		>50	>50	>25
CAP210.E8	C	C	CNISEK	332	19	>50	>50	>50		>50	>50	>25
CAP45.G3	C	C	CNINNS	334	17	>50	>50	>50		>50	>50	1.74
0077_V1.C16	C	C	CNINES	334	29	>50	>50	>50		>50	>50	>25
6322.V4.C1	C	C	CKINGT	334	25	>50	>50	>50		>50	>50	>25
6838.V1.C35	C	C	CTIETE	none	23	>50	>50	>50		0.611	>50	0.032
ZM53.12	C	C	CIINKA	none	15	>50	>50	>50		>50	>50	0.040
16055-2.3	C	C	CNIKKD	none	24	>50	>50	>50		>50	>50	1.18
00836-2.5	C	C	CDISED	none	22	>50	>50	>50		>50	>50	>25
ZM197.7	C	C	CDLSKS	none	43	>50	>50	>50		>50	>50	>25
SIVmac251.30.SG3	neg control					>50	>50	>50		>50	>50	>25
SVA.MLV	neg controal					>50	>50	>50		>50	>50	>25

Figure 33 continued

Column B:
Clade or CRF
Clade designation used in Figs. 1 and 2. CRF's refer to circulating recombinant forms (see: http://www.hiv.lanl.gov/content/sequence/HIV/CRFs/CRFs.html, April 2016, for a complete description)

Reassigned clades in this panel are indicated below:

Here is why we altered some designations:

CH070.1	This was previously designated BC, but our analysis indicated it was a CRF07/C recombinant, which would be all C in Env.
247-23	This was previously designated D, but our analysis indicated it was only part D-like, part a recombinant with a virus of unknown origin, very dissimilar to D and to other strains in Env
3301.V1.C24	This is sometimes designated AC, but designated C in the database and here; it has a short possible A like region near the 5' end, hence the ambiguity
Q461.e2 ADA	This is sometimes designated AD, but designated A in the database and here; it has a short possible D like region near the 5' end, hence the ambiguity

Column C: Clade: Parental clades associated with the virus.

CRF01 is an AE recombinant that is essentially E in Env, and very common in parts of Asia
CRF02 is a AG recombinant, that is essentially A in Env, and common in West and Central Africa

CRF07is a BC recombinant that is essentially C in Env, and common in China

Column D: Positions 331-336

These are the amino acids for each virus (based on HXB2 numbering) in positions that frame the key glycosylations site at 332.
A potential N-linked glycosylation sites requires the sequence motif: Nx[ST], where N is followed by "x", any amino acids except proline, and then by a Ser or Thr.

C331 is the perfectly preserved Cys the closes the V3 loop in HIV-1
The critical glycosylation site for V3 glycan antibodies is at N332 -- the DH270 lineage requires it, other V3 glycan antibodies tend to prefer it.
The site is lost by 2 common mechanisms: The [ST] in the third position of the motif changed to an N, shifting the glycosylation site to N334, or the complete loss of either site.

Column E:
N332 glycan

Based on the amino acid patterns in Column D, one of three outcomes in indicated

332	The N332 glycosyation site is intact
334	The N332 site is lost and shifted to N334
none	No glycosylation site is found at either 332 or 334.

Column F: Length V1: The number of amino acids within the V1 loop region.

Shorter loops are associated with greater potency and required for senstivity by early antibodies in the lineage

<21
21 to 30
31 - 40
>40

Columns G-I: IC50 values for antibodies in the DH270 lineage using the TZM bl assay to explore heterologous reactivity.

Figure 33 continued

Columns K-M: IC50 values for antibodies isolsated from other subjects that also recognize the V3 glycan epitope.

Above the threshold of detection

Figure 34

Virus ID	Clade or CRF	N332 glycan	Length V1*	DH270.UCA	DH270.IA4	DH270.IA3	DH270.3	DH270.IA2	DH270.1
92RW020.2	A	332	15	>50	0.282	0.958	0.038	0.033	0.024
Q23.17	A	332	19	>50	15.3	0.227	0.128	0.071	0.056
ZM55F.PB28a	C	332	13	>50	37.8	0.998	0.677	0.121	0.089
6101.10	B	332	30	>50	1.77	0.225	0.341	0.119	0.116
JR-FL	B	332	25	>50	>50	5.31	0.109	0.237	0.082
ZM106F.PB9	C	332	25	>50	>50	6.83	0.255	0.315	0.147
DU156.12	C	332	25	>50	>50	1.97	1.46	0.527	0.25
TRO.11	B	332	32	>50	>50	0.686	1.51	0.226	0.173
YU2	B	332	26	>50	>50	4.22	2.07	0.443	0.395
DJ263.8	CRF02.AG	332	36	>50	>50	>50	>50	0.734	0.374
CAAN5342.A2	B	332	24	>50	>50	>50	>50	2.78	0.109
DU422.1	C	332	27	>50	>50	>50	46.7	>50	0.891
PVO.4	B	332	34	>50	>50	>50	>50	>50	0.41
CNE58	C	332	39	>50	>50	>50	>50	>50	3.01
TRJO4551.58	B	332	34	>50	>50	>50	>50	>50	>50
DU172.17	C	332	30	>50	>50	>50	>50	>50	49.8
57128.vrc15	D	332	33	>50	>50	>50	>50	>50	>50
C1080.c03	CRF01.AE	334	28	>50	>50	>50	>50	>50	>50
6540.v4.c1	AC	334	25	>50	>50	>50	>50	>50	>50
Q168.a2	AD	334	24	>50	>50	>50	>50	>50	>50
BG1168.1	B	334	42	>50	>50	>50	>50	>50	>50
THRO4156.18	B	334	35	>50	>50	>50	>50	>50	>50
X1632-S2-B10	G	334	27	>50	>50	>50	>50	>50	>50
Q769.d22	A	none	24	>50	>50	>50	>50	>50	>50

Figure 34 continued

Virus ID	DH270.2	DH270.IA1	DH270.4	DH270.5	DH270.6	DH272	DH475	CH01+CH31
92RW020.2	0.022	0.014	0.016	0.052	0.021	>50	>50	1.672
Q23.17	0.056	0.035	0.036	0.049	0.03	9.802	>50	0.078
ZM55F.PB28a	0.071	0.068	0.093	0.074	0.05	>50	>50	2.87
6101.10	0.079	0.035	0.031	0.104	0.04	>50	>50	>25
JR-FL	0.039	0.011	0.016	0.033	0.04	>50	>50	0.916
ZM106F.PB9	0.083	0.047	0.052	0.078	0.05	>50	>50	11.577
DU156.12	0.202	0.093	0.115	0.126	0.07	>50	>50	0.591
TRO.11	0.121	0.089	0.079	0.116	0.06	>50	>50	0.256
YU2	0.215	0.075	0.074	0.524	0.06	>50	>50	0.072
DJ263.8	0.158	0.076	0.027	0.128	0.08	>50	>50	0.36
CAAN5342.A2	0.197	0.05	0.044	0.106	0.03	>50	>50	0.089
DU422.1	0.486	0.225	0.266	0.243	0.19	>50	>50	0.025
PVO.4	0.618	0.115	0.138	0.299	0.14	>50	>50	0.095
CNE58	2.04	0.343	0.483	0.325	0.28	>50	>50	0.245
TRJO4551.58	5.35	0.216	0.127	0.335	0.16	>50	>50	0.307
DU172.17	>50	0.877	0.701	1.39	0.27	>50	>50	>50
57128.vrc15	>50	>50	>50	23	2	>50	>50	0.574
C1080.c03	>50	>50	>50	>50	>50	>50	>50	>25
6540.v4.c1	>50	>50	>50	>50	>50	>50	>50	0.458
Q168.a2	>50	>50	>50	>50	>50	>50	>50	0.015
BG1168.1	>50	>50	>50	>50	>50	>50	>50	0.141
THRO4156.18	>50	>50	>50	>50	>50	>50	>50	2.816
X1632-S2-B10	>50	>50	>50	>50	>50	>50	>50	0.086
Q769.d22	>50	>50	>50	>50	>50	>50	>50	0.033

IC50 neturalization scores for a series of antibodies from the DH270 lineage tested against a panel of 24 Tier 2 HIV-1 pseudo viruses in the TZMbl assay.
*Note that having a N332 PNG site was critical to outome, and that sensitivity to early antibodies in the lineage was associated with short V1 loops.

Column B: Clade or CRF: Clade designation used in Figs. 1 and 2

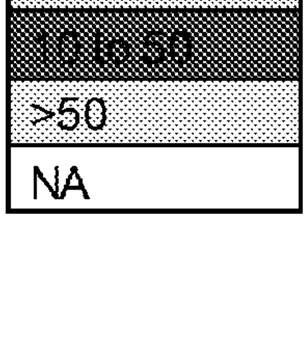
Column C: N332 glycan

Based on the amino acid patterns in Column D, one of three outcomes in indicated

332	The N332 glycosyation site is intact
334	The N332 site is lost and shifted to N334
none	No glycosylation site is found at either 332 or 334.

Figure 34 continued

Column D: Length V1: The number of amino acids within the V1 loop region.
Shorter loops are associated with greater potency and required for senstivity by early antibodies in the lineage



Columns E-O: IC50 values for antibodies in the DH270 lineage using the TZMbl assay to explore heterologous reactivity.
Columns P, Q: IC50 values for antibodies DH272 and DH475 isolated from the same subject that also recognize the V3 glycan epitope but do not belong to the DH270 lineage.
Column R: IC50 values for positive control antibodies CH01, a V2 glycan broadly neutralizing antibody, and CH31 a CD4bs broadly neutralizing antibody.

Above the threshold of detection

Not tested

Figure 35

	Autologous gp120 Binding Data												
							wk 205		wk 232	wk 232	wk234	wk 205	wk 232
Subject.day.clone	DH272	DH475	DH270.UCA	DH270.IA4	DH270.IA3	DH270.IA2	DH270.I	DH270.IA1	DH270.4	DH270.5	DH270.6	DH270.3	DH270.2
CH848.0000.TF	1.155	13.549	0	0	0	0	8.909	14.244	13.549	13.469	14.807	10.025	10.69
CH848.0078.30.02	0.589	13.315	0	0	0	0	2.674	8.519	13.816	11.105	10.423	3.194	8.023
CH848.0078.30.42	0.327	12.57	0	0	0	0	10.109	6.335	13.426	10.359	13.214	8.062	7.636
CH848.0107.30.12	1.159	10.256	0	0	0	0	4.137	5.834	12.791	9.877	11.765	4.642	5.183
CH848.0107.30.27	0.391	12.937	0	0	0	0	9.712	8.718	13.964	11.25	13.5	10.391	8.565
CH848.0107.30.31	0.157	12.203	0	0	0	0	8.756	8.657	12.003	6.603	13.399	9.155	1.795
CH848.0135.27.03													
CH848.0135.27.06	0.12	15.15	0	0	0	0	11.615	9.242	14.151	11.406	13.632	9.014	9.677
CH848.0135.60.05	0.439	12.284	0	0	0	0	10.101	9.306	14.29	11.809	12.779	10.349	9.78
CH848.0135.60.14	0.351	12.931	0	0	0	0	12.733	14.628	16.776	14.405	14.543	11.497	14.619
CH848.0135.60.19	0.392	13.775	0	0	0	0	10.309	11.97	14.636	10.961	13.859	9.95	8.167
CH848.0135.60.20	0.357	14.234	0	0	0	0	9.064	13.778	16.508	12.811	14.004	9.057	12.346
CH848.0135.60.32	0.651	12.798	0	0	0	0	4.452	10.233	13.773	12.256	13.782	7.745	9.12
CH848.0135.60.34	0.377	15.642	0	0	0.088	0	5.599	10.58	13.876	11.43	13.899	7.505	7.917
CH848.0194.25.17	1.625	9.807	0	0	0	0	7.477	12.496	14.715	12.212	12.63	7.843	10.506
CH848.0194.25.21	0.255	8.705	0	0	0	0	7.532	10.992	13.806	11.218	11.911	6.883	9.655
CH848.0194.25.24	0.15	13.849	0	0	0	0	10.911	12.025	14.933	10.99	13.929	10.368	8.513
CH848.0194.25.48	0.687	14.116	0	0	0	0.081	11.173	14.131	16.276	12.983	14.203	9.849	12.02
CH848.0274.30.02	0.141	13.637	0	0	0	0	8.542	12.814	15.26	13.575	13.768	8.58	10.84
CH848.0274.30.07	0.198	14.476	0	0	0	0	12.378	13.469	15.075	14.803	14.371	11.512	12.235
CH848.0274.30.09	1.907	10.068	0	0	0	0	8.087	13.87	14.297	14.773	14.07	9.643	12.776
CH848.0274.30.14	1.202	8.162	0	0	0	0	9.097	12.633	13.815	13.451	13.558	10.092	13.038
CH848.0358.80.03	0.145	5.612	0	0	0	0	9.693	13.888	14.564	14.878	13.537	9.783	14.196
CH848.0358.80.06	1.189	8.276	0	0	0	0.284	11.203	13.456	14.866	14.991	13.899	11.122	14.556
CH848.0358.80.17	0.528	8.157	0	0	0	0	9.226	13.590	14.485	14.629	13.245	9.631	13.293
CH848.0358.80.44	0.525	7.732	0	0	0	0.099	10.495	13.91	14.455	14.802	13.875	10.342	14.195
CH848.0445.25.04	0.2	7.868	0	0	0	0	10.396	12.357	13.912	14.202	14.323	10.505	13.368
CH848.0445.25.18	0.361	11.239	0	0	1.469	0	8.756	13.323	14.938	14.545	13.337	9.127	13.593
CH848.0445.25.26	1.172	7.876	0	0	0	0	11.781	13.911	14.358	14.954	14.594	11.667	14.197
CH848.0445.30.41	0.112	8.839	0	0	0	0	7.311	10.781	12.109	12.091	12.654	7.04	10.905
CH848.0445.30.42	0.551	8.706	0	0	0	0	9.262	13.358	14.464	14.761	14.104	9.889	13.094

Figure 35 continued

CH848.0526.25.02	0.104	7.02	0	0	0	0	8.821	11.957	13.561	13.794	13.628	9.888	12.58
CH848.0526.25.09	0.091	7.874	0	0	0	0	4.326	12.187	14.065	13.574	11.551	7.18	12.3
CH848.0526.25.10	0.102	6.492	0	0	0	0	7.786	12.924	13.424	13.533	13.143	7.746	12.705
CH848.0526.25.11	0.206	6.889	0	0	0	0.304	10.851	14.16	14.664	15.437	14.218	8.912	13.769
CH848.0526.25.21	0.522	6.881	0	0	0	0.111	10.69	13.559	14.249	15.101	13.458	10.082	13.921
CH848.0526.25.26	0.867	7.295	0	0	0	0.118	10.876	14.078	15.638	14.009	13.151	9.551	13.895
CH848.0526.25.32	0	5.914	0	0	0	0	6.529	11.176	12.661	11.756	12.154	6.692	11.034
CH848.0526.25.39	0.205	7.713	0	0	0	0.196	8.835	12.356	15.689	12.943	13.515	8.967	13.699
CH848.0611.09.02	0.755	5.853	0	0	0	0.153	9.121	14.51	16.072	14.781	12.829	9.995	15.77
CH848.0611.20.12	0.346	6.673	0	0	0	0.444	10.343	13.113	15.688	13.541	13.532	9.335	14.581
CH848.0611.20.14	0.256	7.209	0	0	0	0	11.935	12.402	15.278	13.066	14.691	12.773	13.362
CH848.0611.20.28	0.262	5.535	0	0	0	0.284	11.604	12.983	14.387	14.146	14.76	11.208	13.671
CH848.0700.15.05	0.143	7.471	0	0	0	0	11.761	12.785	14.931	12.506	14.038	11.691	12.114
CH848.0700.15.15	0.116	6.165	0	0	0	0	4.91	11.497	14.424	11.984	12.435	6.341	12.103
CH848.0700.15.29	0.226	6.133	0	0	0	0.093	10.103	14.26	15.244	15.272	13.22	10.095	13.724
CH848.0700.15.34	0.599	3.562	0	0	0.722	4.95	12.286	13.564	14.906	15.647	13.353	10.66	14.864
CH848.0700.27.06	0.63	0.549	0	0	0.088	0	8.1	11.772	12.939	12.822	13.916	8.842	10.28
CH848.0700.27.06	0.305	7.529	0	0	0	0	3.401	8.894	10.501	8.32	13.375	5.99	8.433
CH848.0780.15.22	0	3.618	0	0	1.621	8.839	13.34	15.012	14.465	15.896	14.345	13.002	14.785
CH848.0780.15.22/293VRC	0	5.904	0	0	1.141	9.782	13.356	15.668	16.047	16.874	14.706	12.487	15.696
CH848.0780.15.29	0	1.874	0	0	1.206	7.257	12.594	13.202	13.053	14.192	14.319	11.211	12.993
CH848.0780.25.05	0.147	7.028	0	0	0	0	11.075	13.816	16.068	13.814	14.059	10.58	13.889
CH848.0794.03.03	0	6.282	0	0	0	0.097	5.29	10.834	10.767	11.34	12.376	1.496	10.442
CH848.0794.05.41	0.098	6.336	0	0	0.685	4.705	12.051	12.633	13.381	13.479	14.196	8.638	11.959
CH848.0794.5.27													
CH848.0808.15.15	0.09	2.1	0	0	0.654	5.213	12.677	13.02	12.679	14.232	13.779	10.426	12.47
CH848.0808.15.25	0	2.649	0	0	0	0.111	12.638	14.614	14.431	16.074	13.547	10.781	13.808
CH848.0808.15.27	0	2.458	0	0	0.547	7.204	12.946	13.3	14.344	14.169	14.392	10.051	13.358
CH848.0808.15.43	0	0.257	0	0	0	1.105	11.031	12.017	12.494	13.123	13.729	9.533	11.154
CH848.0836.10.31	0	1.235	0	0	4.946	9.379	13.228	13.514	13.184	14.549	14.15	11.41	13.392
CH848.0836.10.36	0.09	3.091	0	0	1.432	6.854	13.276	14.168	14.372	15.399	13.851	13.124	13.983
CH848.0864.3.03	0.098	0.282	0	0	0	0.189	4.557	9.487	9.813	9.5	10.511	1.5	10.28
CH848.0864.7.26	0	2.228	0	0	3.317	7.974	12.992	13.409	14.054	14.623	14.708	11.567	14.406
CH848.0864.7.39	0	1.241	0	0	2.189	4.419	11.379	12.728	14.285	14.599	14.66	11.695	13.991
CH848.0893.10.05	0	0.2	0	0	0	0	1.594	5.893	5.178	5.714	5.617	0	4.266
CH848.0893.10.06	0.102	5.427	0	0	0.248	1.512	9.393	10.986	12.682	13.148	13.798	7.228	11.735

Figure 35 continued

CH848.0949.10.10	0	0	0	0	0	0	1.314	5.748	5.389	5.786	6.083	0	5.059
CH848.0949.10.17	0	2.488	0	2.484	6.311	9.4	12.9	13.606	14.346	14.625	14.288	13.249	13.386
CH848.0949.10.18	0	0.324	0	0	0.348	2.878	8.422	10.427	9.743	9.744	10.895	0	10.148
CH848.1120.10.05	0	0.504	0	0	1.363	5.495	11.793	11.85	11.826	13.163	13.76	8.953	11.488
CH848.1120.10.13	0.13	3.176	0	0	0.105	0.23	5.139	8.753	8.114	7.651	8.858	0.749	8.252
CH848.1120.10.21	0	12.046	0	0	0.228	3.731	12.083	12.74	13.236	14.466	14.187	13.549	13.708
CH848.1120.10.24	0	2.771	0	0	1.736	6.607	12.153	12.773	12.447	13.506	14.072	8.065	12.372
CH848.1120.10.32	0	9.799	0	0.069	5.258	10.07	13.333	13.6	13.265	14.723	14.048	14.122	13.709
CH848.1120.10.41	0	4.948	0	0.064	3.535	7.483	12.536	13.741	13.337	14.853	14.413	13.657	13.757
CH848.1305.10.13	0	4.237	0	0	0	0	0	0	0.511	2.701	2.345	0	5.796
CH848.1305.10.21	0	12.053	0	0	0	0	0	0	0	0.712	0.154	0	3.81
CH848.1305.10.30	0	1.824	0	0	0	0	0	0	0	0	0	0	0
CH848.1305.10.35	0	3.481	0	0	0	0	0	0.216	0.785	3.823	2.97	0	5.851
CH848.1432.5.06	0.095	7.656	0	0	0	3.823	12.103	12.345	12.45	13.446	13.713	8.785	10.971
CH848.1432.5.18	0	2.199	0	0	0	0.646	11.791	11.372	12.292	13.482	13.94	13.656	13.976
CH848.1432.5.27	0	0	0	0	0.09	0.857	7.03	11.724	11.653	12.192	12.901	1.481	11.783
CH848.1432.5.35	0	7.242	0	0	0	0	0	0	0.139	0.968	0.5	0	3.984
CH848.1432.5.41	0	2.086	0	0	0	0.779	11.712	12.73	12.747	14.55	14.034	13.606	13.765
CH848.1432.5.48	0.088	7.064	0	0	0	4.146	12.239	12.558	12.491	13.398	13.94	8.748	11.149
CH848.1432.5.50	0	3.015	0	0	0	0	0	0	0	0	0	0	0
CH848.1432.5.56	0.097	0	0	0	0	0.136	11.264	10.958	12.193	13.148	13.275	13.771	14.469
CH848.1621.4.12	0	1.662	0	0	0	0	0	0.266	9.087	8.975	11.808	8.1	9.969
CH848.1621.4.15	0	6.84	0	0	0	0	8.482	10.843	12.735	12.677	13.791	8.777	9.827
CH848.1621.4.25	0	9.443	0	0	0	0	0	0	0	0.155	0.208	0	3.892
CH848.1621.4.31	0	2.926	0	0	0	0	8.349	9.536	11.146	13.454	13.703	12.463	13.673
CH848.1621.4.44	0	1.807	0	0	0	0.743	11.496	11.232	12.098	13.421	13.719	13.445	13.937
CH848.1621.4.46	0	2.668	0	0	0	0	0	0	0	0	0	0	0
CH848.1635.10.55	0	2.037	0	0	0	0.342	11.14	11	11.906	13.121	13.856	13.16	14.183
CH848.1651.07.34	0	3.553	0	0	0	0	8.411	9.728	11.197	13.524	13.265	12.666	13.799
CH848.1651.10.04	0	2.992	0	0	0	0	10.247	10.855	11.592	13.976	14.076	12.703	13.762
CH848.1651.10.07	0	11.175	0	0	0	0	0.394	0.642	1.258	0.769	2.096	0	0
CH848.1651.7.50	0.181	10.336	0	0	0	0	0	0	0	0	0.147	0	0
CH848.1677.05.21	0	2.166	0	0	0	0	9.551	10.067	11.335	13.701	13.604	12.835	13.622
CH848.1720.05.01	0	10.784	0	0	0	0.559	12.018	13.701	13.794	14.808	13.345	9.382	10.695

Figure 35 continued

	Autologous Neutralization Data IC50												
							wk 205		wk 232	wk 234	wk 205		
Subject.day.clone	DH272	DH475	DH270.UCA	DH270.IA4	DH270.IA3	DH270.IA2	DH270.1	DH270.IA1	DH270.5	DH270.4	DH270.3	PNG N332	V1 loop length
CH848.0000.TF	0.06	>50	>50	>50	>50	>50	>50	>50	>50	30.30	>50	N332	34
CH848.0078.30.02	<0.02	>50	>50	>50	>50	>50	>50	10.65	25.23	5.02	>50	N332	34
CH848.0078.30.42	0.17	>50	>50	>50	>50	>50	>50	46.11	>50	36.33	>50	N332	34
CH848.0107.30.12	0.04	>50	>50	>50	>50	>50	>50	37.01	>50	22.24	>50	N332	34
CH848.0107.30.27	0.12	>50	>50	>50	>50	>50	>50	45.36	>50	35.52	>50	N332	34
CH848.0107.30.31	0.07	>50	>50	>50	>50	>50	>50	44.23	>50	17.20	>50	N332	34
CH848.0135.27.03	<0.02	>50	>50	>50	>50	>50	>50	27.74	24.41	5.54	>50	N332	34
CH848.0135.27.06	0.12	23.37	>50	>50	>50	>50	>50	>50	>50	32.86	>50	N332	34
CH848.0135.60.05	0.05	24.24	>50	>50	>50	>50	>50	45.47	>50	25.81	>50	N332	34
CH848.0135.60.14	0.14	37.44	>50	>50	>50	>50	>50	32.25	>50	22.95	>50	N332	34
CH848.0135.60.19	0.13	26.14	>50	>50	>50	>50	>50	>50	>50	33.07	>50	N332	34
CH848.0135.60.20	0.14	30.02	>50	>50	>50	>50	>50	42.58	>50	28.90	>50	N332	34
CH848.0135.60.32	0.17	4.04	>50	>50	>50	>50	>50	>50	>50	26.55	>50	N332	34
CH848.0135.60.34	<0.02	0.05	>50	>50	>50	>50	>50	44.77	>50	31.15	>50	N332	34
CH848.0194.25.17	0.11	0.05	>50	>50	>50	>50	>50	20.02	3.54	10.56	>50	N332	34
CH848.0194.25.21												N332	34
CH848.0194.25.24	0.10	7.36	>50	>50	>50	>50	>50	>50	>50	34.69	>50	N332	34
CH848.0194.25.48	0.07	>50	>50	>50	>50	>50	>50	3.60	>50	18.07	>50	N332	34
CH848.0274.30.02	0.55	3.14	>50	>50	>50	>50	>50	>50	>50	31.05	>50	N332	34
CH848.0274.30.07	<0.02	1.97	>50	>50	>50	>50	>50	4.10	16.56	4.59	>50	N332	34
CH848.0274.30.09	0.23	>50	>50	>50	>50	>50	>50	23.81	30.14	22.15	>50	N332	34
CH848.0274.30.14												N332	34
CH848.0358.80.03	25.67	>50	>50	>50	>50	>50	2.82	0.19	0.56	0.21	3.53	N332	24
CH848.0358.80.06	4.62	7.11	>50	>50	>50	>50	1.27	0.02	<0.02	<0.02	0.09	N332	24
CH848.0358.80.17	24.86	>50	>50	>50	>50	>50	1.25	0.15	0.18	0.01	0.08	N332	24
CH848.0358.80.44	5.62	>50	>50	>50	>50	>50	1.69	0.03	0.11	0.04	0.26	N332	24
CH848.0445.25.04	>50	4.06	>50	>50	>50	>50	0.53	0.04	0.05	0.05	<0.02	N332	23
CH848.0445.25.18	>50	>50	>50	>50	>50	>50	0.96	0.12	0.18	0.09	0.03	N332	23
CH848.0445.25.26												N332	23
CH848.0445.30.41	>50	>50	>50	>50	>50	>50	0.67	0.06	0.03	<0.02	<0.02	N332	23
CH848.0445.30.42	>50	>50	>50	>50	>50	>50	3.12	0.12	0.30	0.11	0.15	N332	23

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Figure 35 continued

CH848.0526.25.02	>50	>50	>50	>50	>50	>50	15.71	1.42	1.56	1.14	>50	N332	34
CH848.0526.25.09	>50	>50	>50	>50	>50	>50	5.76	0.26	0.37	0.18	2.06	N332	27
CH848.0526.25.10	>50	>50	>50	>50	>50	>50	0.69	0.13	0.13	0.07	0.03	N332	23
CH848.0526.25.11	>50	>50	>50	>50	>50	>50	14.63	2.34	3.27	1.98	>50	N332	33
CH848.0526.25.21	>50	>50	>50	>50	>50	>50	0.94	0.02	0.04	<0.02	0.03	N332	18
CH848.0526.25.26	>50	>50	>50	>50	>50	>50	2.6	0.14	0.25	0.08	0.11	N332	27
CH848.0526.25.32	>50	>50	>50	>50	>50	>50	>50	2.94	7.4	1.48	18.39	N332	33
CH848.0526.25.39	>50	>50	>50	>50	>50	>50	>50	6.59	13.7	5.93	37.73	N332	34
CH848.0611.09.02	0.91	>50	>50	>50	>50	>50	0.35	<0.02	<0.02	<0.02	0.05	N332	17
CH848.0611.20.12	>50	>50	>50	>50	>50	>50	0.26	<0.02	0.03	<0.02	<0.02	N332	17
CH848.0611.20.14	>50	>50	>50	>50	>50	>50	1.03	<0.02	<0.02	<0.02	<0.02	N332	17
CH848.0611.20.28	>50	>50	>50	>50	>50	>50	0.86	<0.02	0.04	<0.02	<0.02	N332	17
CH848.0700.15.05	>50	>50	>50	>50	>50	>50	>50	21.97	>50	12.1	>50	N332	34
CH848.0700.15.15	>50	>50	>50	>50	>50	>50	>50	15.55	29.6	6.19	23.38	N332	34
CH848.0700.15.29	>50	>50	>50	>50	>50	>50	>50	41.64	>50	22.58	>50	N332	34
CH848.0700.15.34												N332	17
CH848.0700.27.06	11.44	>50	>50	>50	>50	>50	1.43	<0.02	0.05	<0.02	1.94	N332	17
CH848.0700.27.06												N332	17
CH848.0780.15.22	>50	>50	>50	>50	1.18	0.13	0.05	<0.02	<0.02	<0.02	<0.02	N332	17
CH848.0780.15.22/293VRC												N332	17
CH848.0780.15.29	>50	>50	>50	>50	0.92	0.15	0.04	<0.02	<0.02	<0.02	<0.02	N332	17
CH848.0780.25.05	>50	>50	>50	>50	>50	>50	>50	44.03	36.61	20.04	27.75	N332	34
CH848.0794.03.03	>50	>50	>50	>50	>50	27.61	0.26	<0.02	<0.02	<0.02	>50	N332	17
CH848.0794.05.41	>50	>50	>50	>50	1.68	0.32	<0.02	<0.02	0.03	<0.02	1.82	N332	17
CH848.0794.5.27	>50	>50	>50	>50	3.95	1.86	0.04	<0.02	<0.02	<0.02	4.7	N332	17
CH848.0808.15.15	>50	>50	>50	>50	0.62	0.1	0.02	<0.02	<0.02	<0.02	<0.02	N332	17
CH848.0808.15.25												N332	17
CH848.0808.15.27	>50	>50	>50	>50	10.54	2.3	0.04	<0.02	<0.02	<0.02	0.02	N332	17
CH848.0808.15.43												N332	17
CH848.0836.10.31	>50	>50	>50	15.69	0.07	<0.02	<0.02	<0.02	<0.02	<0.02	<0.02	N332	17
CH848.0836.10.36	>50	>50	>50	2.69	0.05	0.03	<0.02	<0.02	<0.02	<0.02	<0.02	N332	17
CH848.0864.3.03	>50	>50	>50	>50	7.08	2.21	0.03	<0.02	<0.02	<0.02	0.04	N332	16
CH848.0864.7.26	>50	>50	>50	26.53	0.22	0.1	0.05	<0.02	0.03	<0.02	<0.02	N332	17
CH848.0864.7.39	>50	>50	>50	4.75	0.1	0.05	0.06	<0.02	<0.02	<0.02	<0.02	N332	17
CH848.0893.10.05												N332	16
CH848.0893.10.06	>50	>50	>50	>50	0.89	0.13	0.02	<0.02	<0.02	0.04	0.09	N332	17

Figure 35 continued

CH848.0949.10.10	>50	>50	>50	2.01	0.13	0.05	0.08	<0.02	0.04	0.02	<0.02	N332	17
CH848.0949.10.17	>50	>50	>50	0.64	0.2	0.14	0.18	<0.02	0.05	0.03	<0.02	N332	17
CH848.0949.10.18	>50	>50	>50	>50	2.16	1.63	0.19	<0.02	0.04	<0.02	1.4	N332	17
CH848.1120.10.05	>50	>50	>50	12.59	0.32	0.14	0.12	0.03	<0.02	0.04	<0.02	N332	17
CH848.1120.10.13	>50	>50	>50	>50	1.06	0.29	0.12	<0.02	0.04	<0.02	0.09	N332	17
CH848.1120.10.21	>50	>50	>50	>50	2.96	0.17	0.05	<0.02	<0.02	<0.02	<0.02	N332	17
CH848.1120.10.24	>50	>50	>50	4.05	0.31	0.2	0.15	0.04	0.04	0.03	<0.02	N332	17
CH848.1120.10.32	>50	>50	>50	24.87	0.29	0.11	0.11	<0.02	0.04	<0.02	<0.02	N332	17
CH848.1120.10.41	>50	>50	>50	>50	0.28	0.14	0.04	<0.02	<0.02	<0.02	<0.02	N332	17
CH848.1305.10.13	>50	>50	>50	>50	>50	>50	>50	21.41	>50	9.08	>50	N332	17
CH848.1305.10.21	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	N332	17
CH848.1305.10.30	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	N334	17
CH848.1305.10.35	>50	>50	>50	>50	>50	>50	>50	>50	41.66	10.82	>50	N332	17
CH848.1432.5.06	>50	3.75	>50	>50	>50	>50	3.03	0.25	0.83	0.25	>50	N332	17
CH848.1432.5.18	>50	>50	>50	>50	>50	>50	24.34	9.75	10.17	2.27	0.07	N332	44
CH848.1432.5.27	>50	>50	>50	>50	>50	>50	>50	>50	**>50**	48.58	>50	N332	34
CH848.1432.5.35	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	N332	17
CH848.1432.5.41	>50	41.41	>50	>50	>50	>50	2.56	0.33	0.21	0.26	0.13	N332	30
CH848.1432.5.48	>50	>50	>50	>50	>50	>50	2.98	0.36	1.02	0.33	>50	N332	17
CH848.1432.5.50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	N334	17
CH848.1432.5.56												N332	30
CH848.1621.4.12	>50	>50	>50	>50	>50	>50	>50	>50	**>50**	>50	>50	N332	34
CH848.1621.4.15	>50	>50	>50	>50	>50	>50	>50	>50	**>50**	>50	>50	N332	34
CH848.1621.4.25	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	N334	17
CH848.1621.4.31												N332	23
CH848.1621.4.44	>40	>50	>50	>50	>50	>50	>50	29.1	**>50**	4.37	0.22	N332	30
CH848.1621.4.46	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	N332	30
CH848.1635.10.55	>50	>50	>50	>50	>50	>50	>50	>50	**>50**	19.72	>50	N332	30
CH848.1651.07.34	>50	>50	>50	>50	>50	>50	>50	>50	**>50**	45.26	>50	N332	30
CH848.1651.10.04	>50	>50	>50	>50	>50	>50	>50	>50	23.53	10.63	>50	N332	23
CH848.1651.10.07	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	N332	30
CH848.1651.7.50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	N332	30
CH848.1677.05.21	>50	>50	>50	>50	>50	>50	>50	>50	36.39	31.74	>50	N332	23
CH848.1720.05.01	>50	>50	>50	>50	>50	>50	9.56	4.37	8.36	3.49	>50	N332	30

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Figure 36

The 9 autologous signature patterns shown are each very highly significantly associated with patterns of autologous antibody resistance or sensitivity.

All amino acids at all sites, as well as glycosylation sites, were evaluated, and the q-value reflects the full set of thousands of comparisons.
To be included in this table of the most statisically interesting signature sites, a site had to have a two pieces of supporting evidence:
a phylogenetically corrected q-value of <0.05 (Table T3 and T2), as well as a very strong simple Fisher p value of < 0.001 (T1)
or be within 8.5 angstroms of the bound PGT128 antibody, as well as a very strong simple Fisher p value of < 0.001 (T1)
Once a site meets the above criteria to be deemed of interest, other patterns with q < 0.2 are included in the summary, to get a more comprehensive view of the impact of the mutation on the V3 glycan lineages in this study.

If the senstivity/resistance profile is the opposite (the reds and blues are inverted) it suggests potential cooperativity for the DH2727/DH475 and DH270 lineage

			Amino acid associated with:			r = row, c = column, for contingency tables						Distance if in the contact region	
Test data	see examples	**position**	sensitivity resistance										
Run	**Table**	**HXB2aa Env**	**test**	**Antibody**	**p-value**	**r1c1**	**r1c2**	**r2c1**	**r2c2**	**qvalue**	**oddsRatio**	**Distance**	
Site 87: Cooperative pattern suggested by signatures: DH272 drives escape from E->K, DH475 from E->G, G and K are susceptible for 270.													
AutNeut	T1	87	E	DH270.IA4	0.027	9	0	51	30	0.055	Inf		
AutNeut	T1	87	E	DH270.IA3	9.80E-05	21	0	39	30	0.00048	Inf		
AutNeut	T1	87	E	DH270.IA2	4.20E-05	22	0	38	30	0.00022	Inf		
AutNeut	T1	87	E	DH270.1	0.00028	39	7	21	23	0.0012	6		
AutNeut	T1	87	E	DH270.5	0.0048	45	13	15	17	0.013	3.9		
AutNeut	T1	87	E	DH270.2	7.30E-05	45	9	15	21	0.00035	6.8		
AutNeut	T1	87	E	DH270.3	0.004	37	8	18	17	0.011	4.3		
AutNeut	T3	87	E	DH270.IA3	0.0002	8	0	11	29	0.0064	Inf		
AutNeut	T3	87	E	DH270.IA2	0.0002	8	0	11	29	0.0064	Inf		

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Figure 36 continued

Test data	see examples	position	Amino acid associated with: sensitivity resistance			r = row, c = column, for contingency tables						Distance if in the contact region	
Run	**Table**	**HXB2aa Env**	**test**	**Antibody**	**p-value**	**r1c1**	**r1c2**	**r2c1**	**r2c2**	**qvalue**	**oddsRatio**	**Distance**	
Site 87: Cooperative pattern suggested by signatures: DH272 drives escape from E->K, DH475 from E->G, G and K are susceptible for 270.													
AutNeut	T3	87	E	DH270.1	7.60E-05	16	7	3	22	0.0064	16		
AutNeut	T3	87	E	DH270.5	0.00048	18	13	1	16	0.0081	21		
AutNeut	T3	87	E	DH270.2	0.00039	16	9	3	20	0.0095	11		
AutNeut	T3	87	E	DH270.3	0.00043	17	8	2	16	0.0088	16		
AutNeut	T1	87	D	DH270.4	0.018	73	7	6	4	0.04	6.7		
AutNeut	T1	87	G	DH270.IA4	0.039	5	4	70	11	0.075	0.2		
AutNeut	T1	87	G	DH270.IA3	0.00086	12	9	63	6	0.0032	0.13		
AutNeut	T1	87	G	DH270.IA2	0.0013	13	9	62	6	0.0043	0.14		
AutNeut	T1	87	G	DH270.IA1	0.018	52	15	22	0	0.039	0		
AutNeut	T1	87	G	DH270.1	0.0036	33	13	42	2	0.011	0.12		
AutNeut	T1	87	G	DH270.5	0.075	45	13	30	2	0.13	0.23		
AutNeut	T1	87	G	DH270.2	0.023	41	13	34	2	0.047	0.19		
AutNeut	T1	87	G	DH270.3	0.0095	32	13	33	2	0.023	0.15		
AutNeut	T1	87	K	DH270.2	0.015	28	26	28	8	0.036	0.31		
AutNeut	T1	87	K	DH270.5	0.073	32	26	24	8	0.13	0.41		
AutNeut	T1	87	E	DH272	5.50E-08	6	20	54	10	5.10E-07	0.058		
AutNeut	T3	87	E	DH272	0.001	3	19	16	10	0.019	0.1		
AutNeut	T1	87	D	DH272	0.03	26	0	53	11	0.06	Inf		
AutNeut	T1	87	K	DH272	0.0076	22	4	34	30	0.019	4.8		
AutNeut	T1	87	E	DH475	0.00036	4	11	56	17	0.0014	0.11		

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Figure 36 continued

Test data	see examples	position	Amino acid associated with: sensitivity resistance			r = row, c = column, for contingency tables						Distance if in the contact region	
Run	**Table**	**HXB2aa Env**	**test**	**Antibody**	**p-value**	**r1c1**	**r1c2**	**r2c1**	**r2c2**	**qvalue**	**oddsRatio**	**Distance**	
Site 87: Cooperative pattern suggested by signatures: DH272 drives escape from E->K, DH475 from E->G, G and K are susceptible for 270.													
AutNeut	T3	87	E	DH475	0.016	1	10	18	17	0.17	0.099		
AutNeut	T1	87	G	DH475	0.064	15	0	58	15	0.12	Inf		
Site 185 cooperative pattern													
AutNeut	T1	185	D	DH270.IA3	0.12	17	4	41	28	0.2	2.9		
AutNeut	T1	185	D	DH270.IA2	0.072	18	4	40	28	0.12	3.1		
AutNeut	T1	185	D	DH270.1	5.40E-05	39	7	19	25	0.00028	7.2		
AutNeut	T1	185	D	DH270.5	0.0011	45	13	13	19	0.0037	5		
AutNeut	T1	185	D	DH270.2	9.70E-07	46	8	12	24	7.80E-06	11		
AutNeut	T1	185	D	DH270.3	0.00032	38	7	16	19	0.0013	6.3		
AutNeut	T1	185	N	DH270.1	0.0011	10	36	25	19	0.0037	0.22		
AutNeut	T1	185	N	DH270.2	1.80E-05	11	43	24	12	0.00011	0.13		
AutNeut	T1	185	N	DH270.3	0.0047	10	35	19	16	0.013	0.25		
AutNeut	T1	185	N	DH270.5	0.0062	16	42	19	13	0.016	0.26		
AutNeut	T1	185	S	DH270.IA2	0.058	20	2	68	0	0.1	0		
AutNeut	T1	185	S	DH270.IA3	0.052	19	2	69	0	0.097	0		
AutNeut	T1	185	D	DH272	2.10E-08	5	21	53	11	2.30E-07	0.052		
AutNeut	T1	185	N	DH272	1.80E-08	22	4	13	51	2.00E-07	21		
AutNeut	T1	185	D	DH475	6.50E-06	2	13	56	17	4.40E-05	0.049		

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Figure 36 continued

Test data	see examples	position	Amino acid associated with: sensitivity resistance			r = row, c = column, for contingency tables						Distance if in the contact region	
Run	**Table**	**HXB2aa Env**	**test**	**Antibody**	**p-value**	**r1c1**	**r1c2**	**r2c1**	**r2c2**	**qvalue**	**oddsRatio**	**Distance**	
Site 87: Cooperative pattern suggested by signatures: DH272 drives escape from E->K, DH475 from E->G, G and K are susceptible for 270.													
AutNeut	T1	185	N	DH475	2.80E-05	13	2	20	53	0.00015	17		
Site 300: cooperative pattern													
AutNeut	T1	300	G	DH270.IA4	0.00039	9	0	31	50	0.0015	Inf	6.35	
AutNeut	T1	300	G	DH270.IA3	7.70E-10	21	0	19	50	1.30E-08	Inf	6.35	
AutNeut	T1	300	G	DH270.IA2	2.10E-10	22	0	18	50	3.90E-09	Inf	6.35	
AutNeut	T1	300	G	DH270.1	0.0016	28	18	12	32	0.005	4.1	6.35	
AutNeut	T1	300	G	DH270.5	0.027	31	27	9	23	0.056	2.9	6.35	
AutNeut	T1	300	G	DH270.2	0.0001	33	21	7	29	0.00049	6.4	6.35	
AutNeut	T1	300	G	DH270.3	0.11	24	21	12	23	0.2	2.2	6.35	
AutNeut	T1	300	Y	DH270.IA1	0.031	65	2	18	4	0.064	7	6.35	
AutNeut	T1	300	Y	DH270.1	0.11	45	1	39	5	0.18	5.7	6.35	
AutNeut	T1	300	N	DH270.IA4	5.50E-05	0	9	57	24	0.00028	0	6.35	
AutNeut	T1	300	N	DH270.IA3	2.10E-12	0	21	57	12	4.60E-11	0	6.35	
AutNeut	T1	300	N	DH270.IA2	3.60E-13	0	22	57	11	7.30E-12	0	6.35	
AutNeut	T1	300	N	DH270.1	7.30E-05	20	26	37	7	0.00035	0.15	6.35	
AutNeut	T1	300	N	DH270.2	0.0073	28	26	29	7	0.018	0.26	6.35	
AutNeut	T1	300	N	DH270.5	0.012	31	27	26	6	0.028	0.27	6.35	
AutNeut	T1	300	Y	DH270.2	0.077	48	6	36	0	0.13	0	6.35	

Figure 36 continued

Test data	see examples	position	Amino acid associated with: sensitivity resistance			r = row, c = column, for contingency tables						Distance if in the contact region
Run	**Table**	**HXB2aa Env**	**test**	**Antibody**	**p-value**	**r1c1**	**r1c2**	**r2c1**	**r2c2**	**qvalue**	**odds Ratio**	**Distance**
Site 300: cooperative pattern												
AutNeut	T1	300	G	DH272	6.90E-09	0	26	40	24	7.70E-08	0	6.35
AutNeut	T1	300	N	DH272	4.70E-07	26	0	31	33	4.00E-06	Inf	6.35
AutNeut	T1	300	G	DH475	0.0089	2	13	38	35	0.021	0.14	6.35
AutNeut	T1	300	N	DH475	0.042	13	2	42	31	0.078	4.7	6.35
site 325: mutual resistance for N, a late mutation												
AutNeut	T1	325	E	DH270.IA3	0.025	17	4	67	2	0.051	0.13	2.73
AutNeut	T1	325	E	DH270.IA2	0.003	17	5	67	1	0.0089	0.053	2.73
AutNeut	T1	325	E	DH270.1	0.026	40	6	44	0	0.055	0	2.73
AutNeut	T1	325	E	DH270.5	0.085	52	6	32	0	0.15	0	2.73
AutNeut	T1	325	E	DH270.2	0.077	48	6	36	0	0.13	0	2.73
AutNeut	T1	325	D	DH270.IA1	0.037	7	60	7	15	0.072	0.25	2.73
AutNeut	T1	325	D	DH270.IA1	0.037	7	60	7	15	0.072	0.25	2.73
AutNeut	T3	325	D	DH270.4	0.018	5	71	3	4	0.17	0.099	2.73
AutNeut	T1	325	D	DH270.4	0.00072	8	72	6	4	0.0028	0.078	2.73
AutNeut	T1	325	N	DH270.IA1	0.00017	66	1	15	7	0.00078	29	2.73
AutNeut	T1	325	N	DH270.1	0.0023	46	0	36	8	0.0066	Inf	2.73
AutNeut	T1	325	N	DH270.2	0.00039	54	0	28	8	0.0016	Inf	2.73
AutNeut	T1	325	N	DH270.3	0.00081	45	0	27	8	0.003	Inf	2.73

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Figure 36 continued

Test data	see examples	position	Amino acid associated with: sensitivity resistance			r = row, c = column, for contingency tables						Distance if in the contact region	
Run	**Table**	**HXB2aa Env**	**test**	**Antibody**	**p-value**	**r1c1**	**r1c2**	**r2c1**	**r2c2**	**qvalue**	**oddsRatio**	**Distance**	
site 325: mutual resistance for N, a late mutation													
AutNeut	T1	325	N	DH270.4	8.70E-06	78	2	4	6	5.40E-05	51	2.73	
AutNeut	T1	325	N	DH270.5	0.0027	57	1	25	7	0.0079	15	2.73	
AutNeut	T2	325	N	DH270.2	0.0064	0	54	5	28	0.19	0	2.73	
AutNeut	T2	325	N	DH270.4	0.0031	2	78	3	4	0.18	0.038	2.73	
AutNeut	T1	325	D	DH272	0.059	1	25	13	51	0.11	0.16	2.73	
AutNeut	T1	325	N	DH272	0.099	26	0	56	8	0.16	Inf	2.73	
Site 335: cooperative pattern:													
AutNeut	T1	335	K	DH270.IA4	0.059	6	3	74	7	0.11	0.19		
AutNeut	T2	335	K	DH270.IA4	0.0035	3	6	1	73	0.13	33		
AutNeut	T2	335	K	DH270.IA3	0.0033	4	17	0	62	0.15	Inf		
AutNeut	T2	335	K	DH270.IA2	0.004	4	18	0	61	0.12	Inf		
AutNeut	T1	335	E	DH270.IA4	0.059	3	6	7	74	0.11	5.1		
AutNeut	T3	335	E	DH270.IA4	0.0035	3	6	1	73	0.058	33		
AutNeut	T3	335	E	DH270.IA3	0.0033	4	17	0	62	0.058	Inf		
AutNeut	T3	335	E	DH270.IA2	0.004	4	18	0	61	0.059	Inf		
AutNeut	T1	335	E	DH272	0.057	0	26	10	54	0.1	0		
AutNeut	T1	335	K	DH272	0.057	26	0	54	10	0.1	Inf		

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Figure 36 continued

Test data	see examples	position	Amino acid associated with: sensitivity resistance			r = row, c = column, for contingency tables						Distance if in the contact region	
Run	**Table**	**HXB2aa Env**	**test**	**Antibody**	**p-value**	**r1c1**	**r1c2**	**r2c1**	**r2c2**	**qvalue**	**odds Ratio**	**Distance**	
Site 344: cooperative pattern:													
AutNeut	T1	344	E	DH270.IA4	0.01	9	0	45	36	0.024	Inf		
AutNeut	T1	344	E	DH270.IA3	4.50E-06	21	0	33	36	2.80E-05	Inf		
AutNeut	T1	344	E	DH270.IA2	1.90E-06	22	0	32	36	1.40E-05	Inf		
AutNeut	T3	344	E	DH270.1	0.012	4	10	0	25	0.16	Inf		
AutNeut	T1	344	E	DH270.1	0.0005	36	10	18	26	0.002	5.1		
AutNeut	T1	344	E	DH270.3	0.096	34	11	20	15	0.16	2.3		
AutNeut	T1	344	E	DH270.5	0.0072	41	17	13	19	0.018	3.5		
AutNeut	T1	344	E	DH270.2	0.017	38	16	16	20	0.038	2.9		
AutNeut	T1	344	E	DH270.4	0.046	45	35	9	1	0.084	0.15		
AutNeut	T1	344	K	DH270.1	0.011	15	31	27	17	0.025	0.31		
AutNeut	T1	344	K	DH270.IA2	1.00E-07	0	22	42	26	9.00E-07	0		
AutNeut	T1	344	K	DH270.IA3	1.30E-07	0	21	42	27	1.30E-06	0		
AutNeut	T1	344	K	DH270.4	0.098	40	40	2	8	0.16	3.9		
AutNeut	T1	344	K	DH270.IA4	0.003	0	9	42	39	0.0089	0		
AutNeut	T1	344	K	DH270.5	0.029	22	36	20	12	0.06	0.37		
AutNeut	T1	344	K	DH270.2	0.086	21	33	21	15	0.15	0.46		
AutNeut	T1	344	Q	DH270.1	0.056	41	5	44	0	0.1	0		
AutNeut	T1	344	Q	DH270.2	0.081	49	5	36	0	0.14	0		
AutNeut	T1	344	R	DH270.4	0.11	80	0	9	1	0.18	Inf		

Figure 36 continued

Test data	see examples	position	Amino acid associated with: sensitivity resistance			r = row, c = column, for contingency tables						Distance if in the contact region	
Run	**Table**	**HXB2aa Env**	**test**	**Antibody**	**p-value**	**r1c1**	**r1c2**	**r2c1**	**r2c2**	**qvalue**	**odds Ratio**	**Distance**	
Site 344: cooperative pattern:													
AutNeut	T1	344	E	DH272	2.00E-09	3	23	51	13	2.70E-08	0.035		
AutNeut	T1	344	K	DH272	1.50E-08	24	2	18	46	1.60E-07	29		
AutNeut	T1	344	E	DH475	4.40E-05	2	13	52	21	0.00023	0.064		
AutNeut	T1	344	K	DH475	0.0005	13	2	27	46	0.0019	11		
Site 413: cooperative pattern:													
AutNeut	T1	413	T	DH270.IA3	0.012	5	16	39	30	0.029	0.24		
AutNeut	T1	413	T	DH270.IA2	0.0065	5	17	39	29	0.016	0.22		
AutNeut	T1	413	T	DH270.IA1	4.60E-05	24	43	19	3	0.00024	0.091		
AutNeut	T1	413	T	DH270.1	2.10E-07	10	36	34	10	1.90E-06	0.085		
AutNeut	T1	413	T	DH270.2	1.10E-05	16	38	28	8	7.00E-05	0.12		
AutNeut	T1	413	T	DH270.3	4.00E-07	8	37	26	9	3.30E-06	0.078		
AutNeut	T1	413	T	DH270.5	6.50E-06	18	40	26	6	4.40E-05	0.11		
AutNeut	T1	413	I	DH270.IA1	0.0032	66	1	17	5	0.0095	19		
AutNeut	T1	413	I	DH270.1	0.011	46	0	38	6	0.027	Inf		
AutNeut	T1	413	N	DH270.IA3	0.0041	19	2	39	30	0.011	7.2		
AutNeut	T1	413	N	DH270.IA2	0.004	20	2	38	30	0.011	7.7		
AutNeut	T1	413	N	DH270.IA1	0.0094	49	18	9	13	0.022	3.9		
AutNeut	T1	413	N	DH270.1	5.90E-07	41	5	17	27	4.90E-06	13		

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Figure 36 continued

Test data	see examples	position	Amino acid associated with: sensitivity resistance			r = row, c = column, for contingency tables						Distance if in the contact region	
Run	**Table**	**HXB2aa Env**	**test**	**Antibody**	**p-value**	**r1c1**	**r1c2**	**r2c1**	**r2c2**	**qvalue**	**oddsRatio**	**Distance**	
Site 413: cooperative pattern:													
AutNeut	T1	413	N	DH270.3	5.50E-10	43	2	11	24	8.70E-09	44		
AutNeut	T1	413	N	DH270.5	1.90E-06	48	10	10	22	1.40E-05	10		
AutNeut	T1	413	N	DH270.2	3.20E-09	48	6	10	26	3.60E-08	20		
AutNeut	T1	413	N	DH272	3.40E-07	6	20	52	12	2.60E-06	0.072		
AutNeut	T1	413	T	DH272	0.00015	21	5	23	41	0.00071	7.3		
AutNeut	T1	413	N	DH475	4.90E-09	0	15	58	15	5.40E-08	0		
AutNeut	T1	413	T	DH475	3.10E-06	15	0	27	46	2.00E-05	Inf		
Site 624: mutual resistnace, late escape from DH270 lineage, similar association with DH272													
AutNeut	T1	624	D	DH270.IA3	0.0095	0	21	17	52	0.022	0		
AutNeut	T1	624	D	DH270.IA2	0.0095	0	22	17	51	0.023	0		
AutNeut	T1	624	D	DH270.IA1	5.20E-07	4	63	13	9	4.40E-06	0.047		
AutNeut	T1	624	D	DH270.1	0.0027	3	43	14	30	0.008	0.15		
AutNeut	T1	624	D	DH270.3	0.0017	2	43	11	24	0.0052	0.1		
AutNeut	T1	624	D	DH270.4	1.10E-05	9	71	8	2	6.90E-05	0.034		
AutNeut	T1	624	D	DH270.5	0.0015	5	53	12	20	0.0047	0.16		
AutNeut	T3	624	D	DH270.IA1	0.012	3	63	4	9	0.16	0.11		
AutNeut	T3	624	D	DH270.3	0.016	1	43	6	24	0.16	0.096		
AutNeut	T3	624	D	DH270.4	0.0039	4	71	3	2	0.064	0.042		

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Figure 36 continued

Test data	see examples	position	Amino acid associated with: sensitivity resistance			r = row, c = column, for contingency tables						Distance if in the contact region	
Run	**Table**	**HXB2aa Env**	**test**	**Antibody**	**p-value**	**r1c1**	**r1c2**	**r2c1**	**r2c2**	**qvalue**	**oddsRatio**	**Distance**	
Site 624: mutual resistnace, late escape from DH270 lineage, similar association with DH272													
AutNeut	T1	624	E	DH270.3	0.08	45	0	32	3	0.14	Inf		
AutNeut	T1	624	G	DH270.IA1	0.0025	65	2	16	6	0.0072	12		
AutNeut	T1	624	G	DH270.4	0.042	75	5	7	3	0.078	6.2		
AutNeut	T1	624	N	DH270.IA1	0.0032	66	1	17	5	0.0095	19		
AutNeut	T1	624	N	DH270.1	0.011	46	0	38	6	0.027	Inf		
AutNeut	T1	624	N	DH270.4	0.0011	78	2	6	4	0.0038	24		
AutNeut	T1	624	N	DH270.5	0.0015	58	0	26	6	0.0046	Inf		
AutNeut	T1	624	D	DH272	0.0022	0	26	17	47	0.0062	0		
AutNeut	T1	624	G	DH272	0.099	26	0	56	8	0.16	Inf		
Site 818: cooperative pattern:													
AutNeut	T1	818	L	DH270.1	0.089	16	30	24	20	0.15	0.45		
AutNeut	T1	818	L	DH270.IA2	0.001	3	19	37	31	0.0037	0.14		
AutNeut	T1	818	L	DH270.IA3	0.0021	3	18	37	32	0.0062	0.15		
AutNeut	T1	818	L	DH270.IA4	0.0039	0	9	40	41	0.011	0		
AutNeut	T1	818	L	DH270.2	0.051	19	35	21	15	0.092	0.39		
AutNeut	T1	818	L	DH270.4	0.0019	40	40	0	10	0.0058	Inf		
AutNeut	T1	818	L	DH270.IA1	0.087	33	34	6	16	0.15	2.6		
AutNeut	T1	818	I	DH270.4	0.0019	40	40	10	0	0.0058	0		

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Figure 36 continued

Test data	see examples	position	Amino acid associated with: sensitivity resistance			r = row, c = column, for contingency tables						Distance if in the contact region	
Run	**Table**	**HXB2aa Env**	**test**	**Antibody**	**p-value**	**r1c1**	**r1c2**	**r2c1**	**r2c2**	**qvalue**	**odds Ratio**	**Distance**	
Site 818: cooperative pattern:													
AutNeut	T1	818	I	DH270.IA1	0.087	34	33	16	6	0.15	0.39		
AutNeut	T1	818	I	DH270.1	0.089	30	16	20	24	0.15	2.2		
AutNeut	T1	818	I	DH270.IA2	0.001	19	3	31	37	0.0037	7.4		
AutNeut	T1	818	I	DH270.IA3	0.0021	18	3	32	37	0.0062	6.8		
AutNeut	T1	818	I	DH270.IA4	0.0039	9	0	41	40	0.011	Inf		
AutNeut	T1	818	I	DH270.2	0.051	35	19	15	21	0.092	2.6		
AutNeut	T3	818	I	DH272	0.01	0	24	5	13	0.17	0		
AutNeut	T1	818	I	DH272	2.70E-09	2	24	48	16	3.10E-08	0.029		
AutNeut	T1	818	L	DH272	2.70E-09	24	2	16	48	3.10E-08	34		
AutNeut	T1	818	I	DH475	0.0003	2	13	48	25	0.0012	0.082		
AutNeut	T1	818	L	DH475	0.0003	13	2	25	48	0.0012	12		

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Figure 36 continued

Examples of how to read contingency tables

How to read a phylogenetically corrected T3 contingency table:

pos 87, T3 LA2 E	E -> !E	E -> E
DH473 pos	8	0
DH473 neg	11	29

Fisher's exact p = 0.0002

In this case, T3 is tracking the evolution of an ancestral state of E, to not-E(!E), any other amino acid, at position 87.

If E is lost, changes to an amino acid that is not E, the phenotype tends to be associatied nd with IA2 activity.

Infinite and 0 are important cases of perfect associations, other values indicate relative levels of enrichment.

How to read a simple (not phylogenetically corrected) T1 contingency table:

position 87 T1 IA3 G	!G	G
IA3 pos	12	9
IA3 neg	63	6

Fisher's exact p = 0.00086

In this case, T1 is tracking the presence of G, and not not-G(!G), any other amino acid, at position 87, in all sequences tested.

Odds Ratio = 0.13: for T1, OR > 1 indicates an amino acid associated with resistance, <1 senstivity

Infinite and 0 are important cases of perfect associations, other values (like 0.13) indicate relative levels of enrichment.

How to read a phylogenetically corrected T2 contingency table:

T2 DH473 N	!N->N	!N->!N
DH473 pos	0	54
DH473 neg	5	28

Fisher's exact p = 0.0064

In this case, T2 is tracking the evolution of an ancestral state of not-N (!N, any other amino acid), to N, at position 325.

Odds Ratio = 0: for T2, OR < 1 indicates an amino acid associated with resistance

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Figure 37A

A

		gp120 Binding AUC									Neutralization IC50								
Boost	**Subject.day.clone**	**UCA**	**IA4**	**IA3**	**IA2**	**I**	**IA1**	**4**	**5**	**6**	**UCA**	**IA4**	**IA3**	**IA2**	**I**	**IA1**	**4**	**5**	**V1 loop length**
i.	CH848.0949.10.17	0	2.5	6.3	9.4	12.9	13.6	14.3	14.6	14.3	>50	0.64	0.2	0.14	0.18	<0.02	0.03	0.05	17
ii.	CH848.0836.10.31	0	0.0	4.9	9.4	13.2	13.5	13.2	14.5	14.2	>50	45.68	0.07	<0.02	<0.02	<0.02	<0.02	<0.02	17
iii.	CH848.0358.80.06	0	0.0	0.0	0.3	11.2	13.5	14.9	15.0	13.9	>50	>50	>50	>50	1.3	0.02	<0.02	<0.02	24
iii.	CH848.1432.5.41	0	0.0	0.0	0.8	11.7	12.7	12.7	14.6	14.0	>50	>50	>50	>50	2.6	0.33	0.26	0.21	30
iii.	CH848.0526.25.02	0	0.0	0.0	0.0	8.8	12.0	13.6	13.8	13.6	>50	>50	>50	>50	16.7	1.4	1.1	1.6	34

Figure 37B

B

Prime

1. Engage UCA
Man9 V3 glycopeptide

N301 N332

R1 = R2 =

AcHN-EINCTRPNNNTRPGETIGDIRQAHCNISR 293 301 332

2. Select for intermediates with G57R (CH848.d949.10.17 gp120)

Boost

V3 $Man_9GlcNAc_2$

CH848.d949.10.17 gp120

AcHN-EINCTRPNNNTRPGETIGDIRQAHCNISRA-NH2 293 301 332 336

3. Drive maturation toward DH270.6 and away from DH270.3

CH848.d1120.10.21 gp120
CH848.d1432.05.27 gp120

DH270.UCA
DH270.IA4
DH270.IA3
DH270.IA2
DH270.1
DH270.3
DH270.2
DH270.IA1
DH270.5
DH270.4
DH270.6

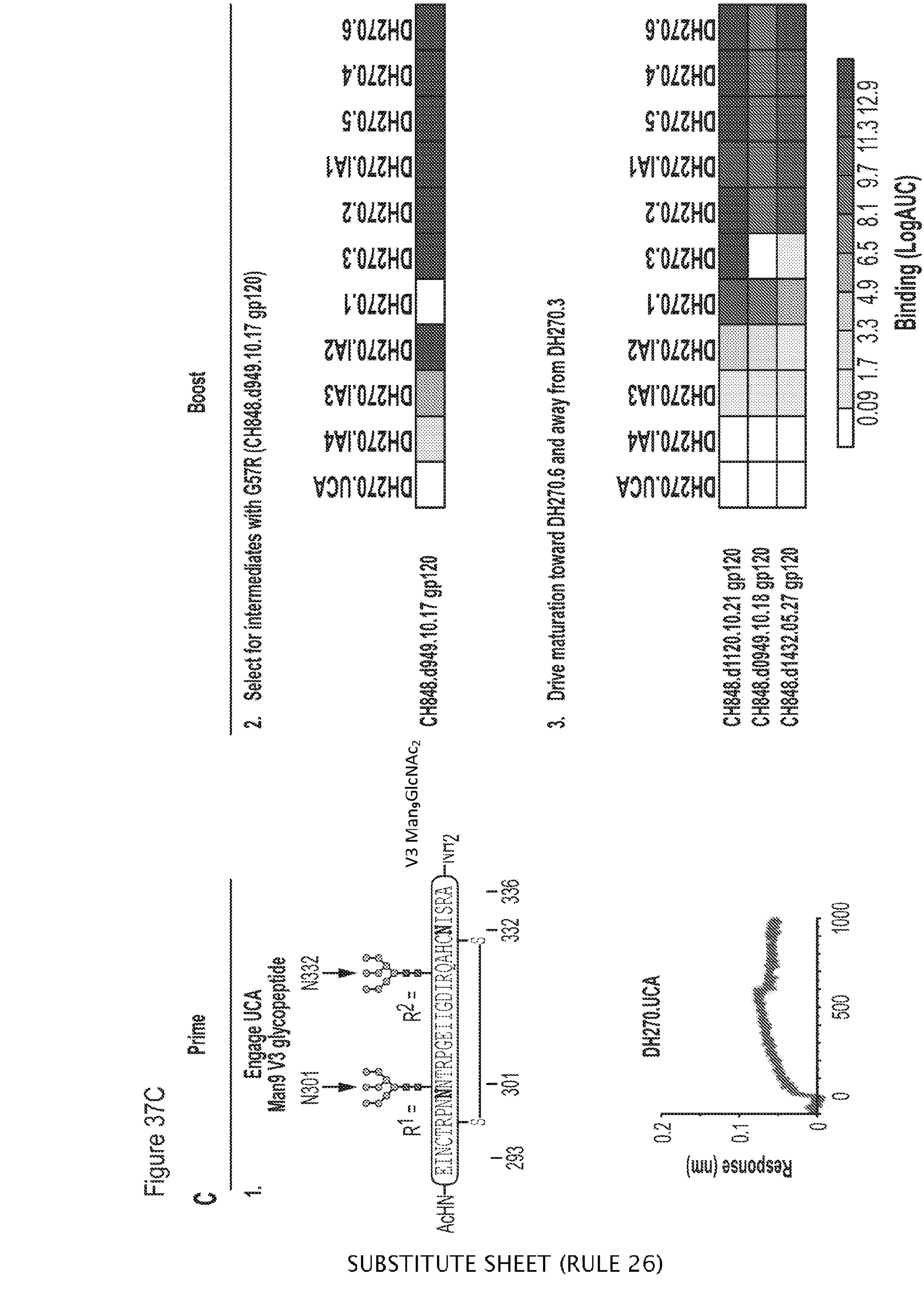
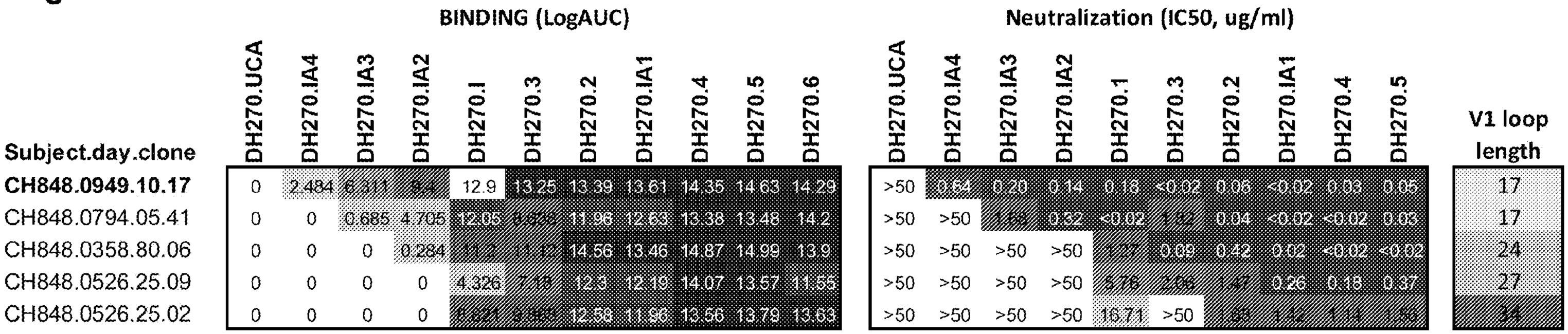
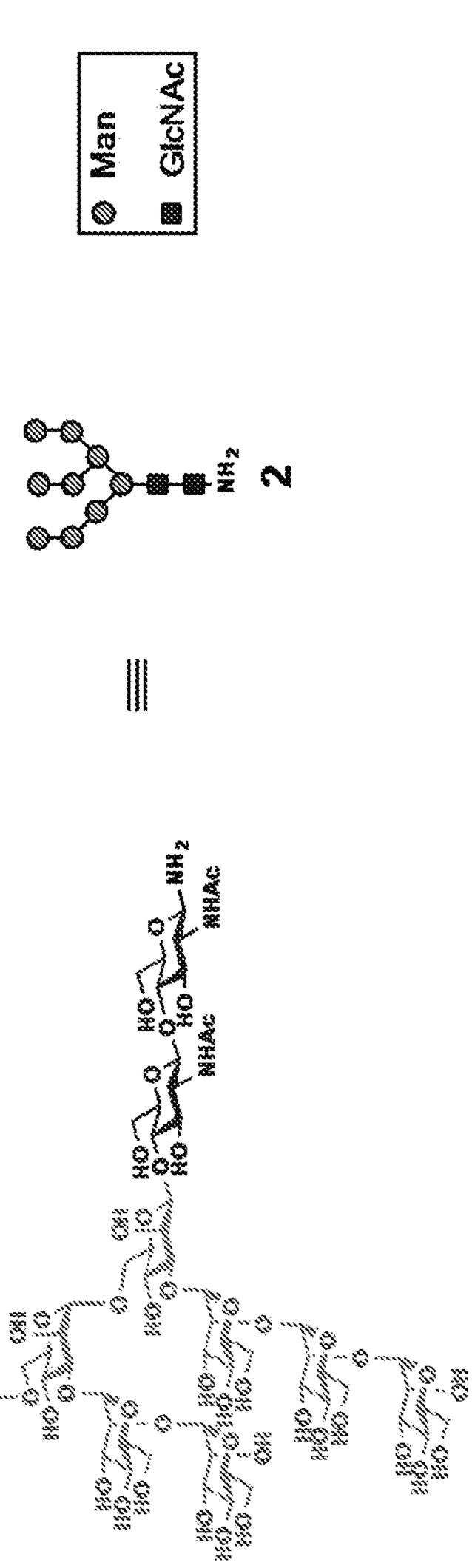

Boost
2. Select for intermediates with G57R (CH848.d949.10.17 gp120)
DH270.UCA
DH270.1A4
DH270.1A3
DH270.1A2
DH270.1
DH270.3
DH270.2
DH270.1A1
DH270.5
DH270.4
DH270.6
CH848.d949.10.17 gp120
V3 Man9GlcNAc2
N332
N301
AcHN-EINCTRPNNNTRPGEIIGDIRQAHCNISRA
293
301
332
336
3. Drive maturation toward DH270.6 and away from DH270.3
CH848.d1120.10.21 gp120
CH848.d0949.10.18 gp120
CH848.d1432.05.27 gp120
Binding (LogAUC)
0.09 1.7 3.3 4.9 6.5 8.1 9.7 11.3 12.9
Figure 37C
C
Prime
1. Engage UCA
Man9 V3 glycopeptide
DH270.UCA
Response (nm)
0.2
0.1
0
0
500
1000

Figure 37D


BINDING (LogAUC)
Neutralization (IC50, ug/ml)
Subject.day.clone
DH270.UCA
DH270.IA4
DH270.IA3
DH270.IA2
DH270.1
DH270.3
DH270.2
DH270.IA1
DH270.4
DH270.5
DH270.6
V1 loop length
CH848.0949.10.17
CH848.0794.05.41
CH848.0358.80.06
CH848.0526.25.09
CH848.0526.25.02


Man
GlcNAc
2
NH2
NHAc
NH2
NHAc
HO
HO
HO
O
O
O

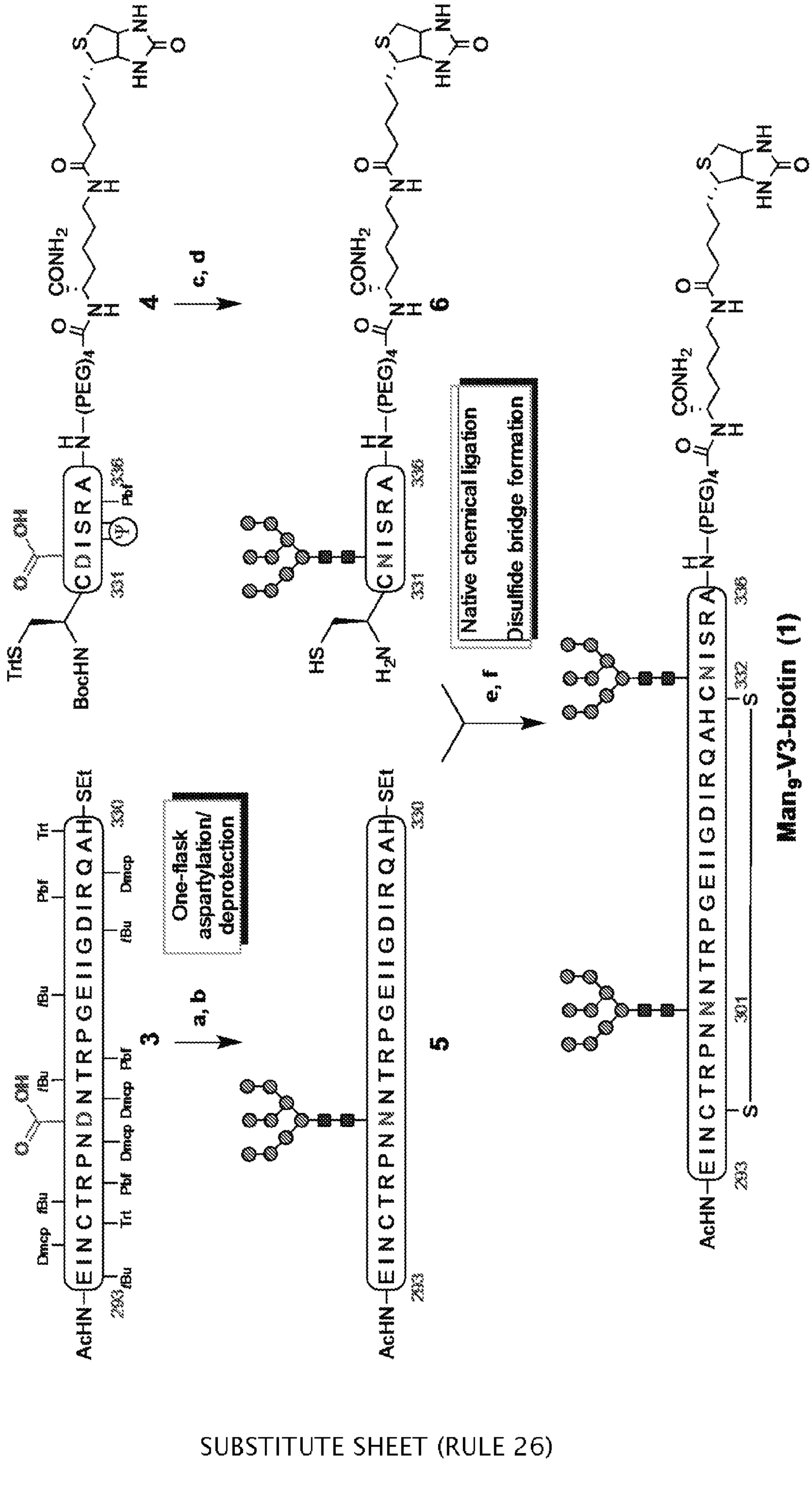
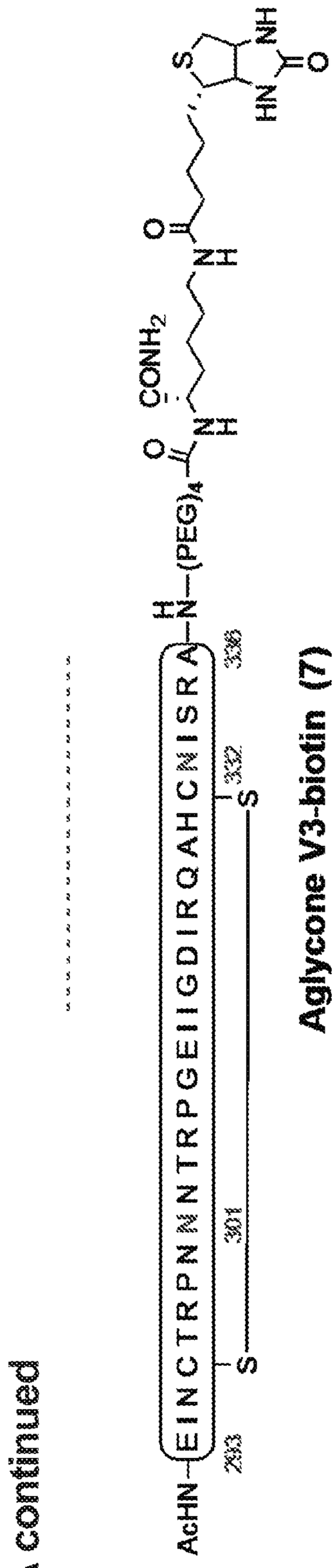
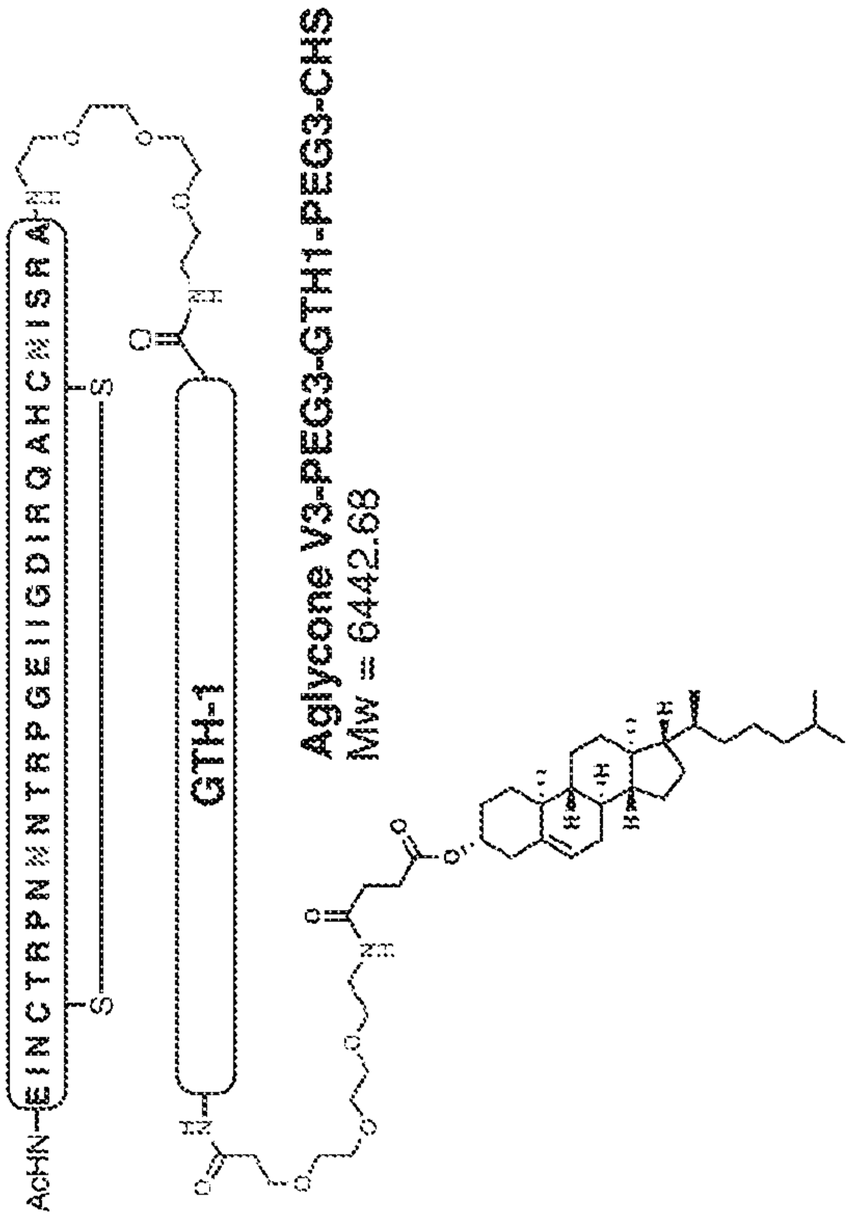
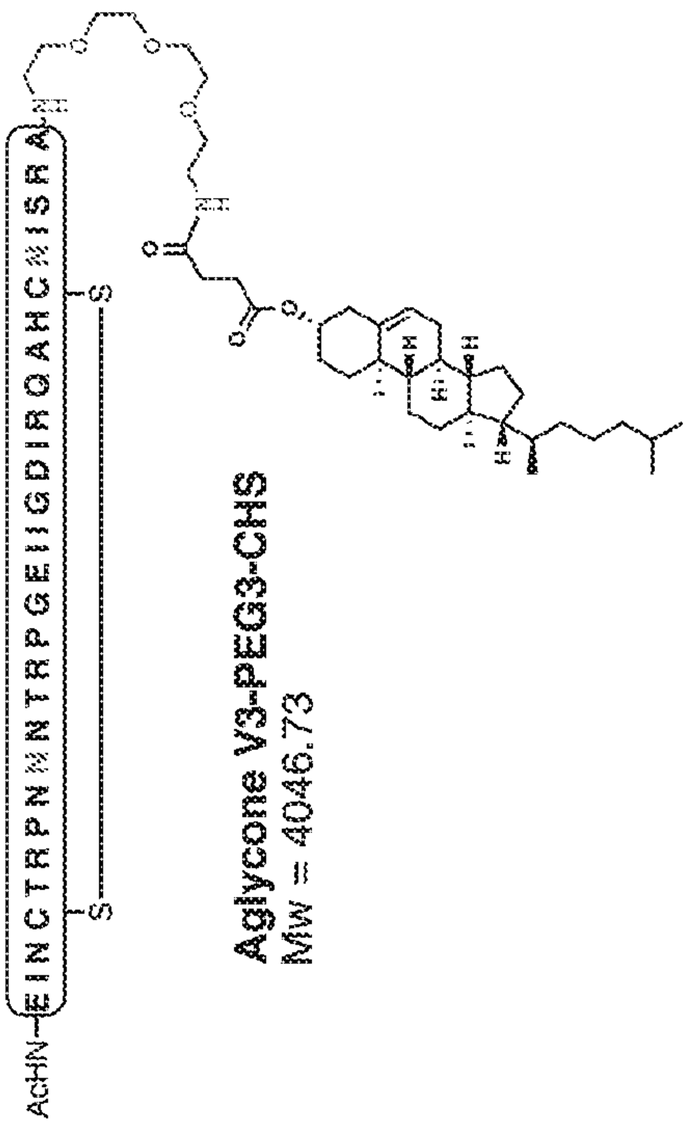
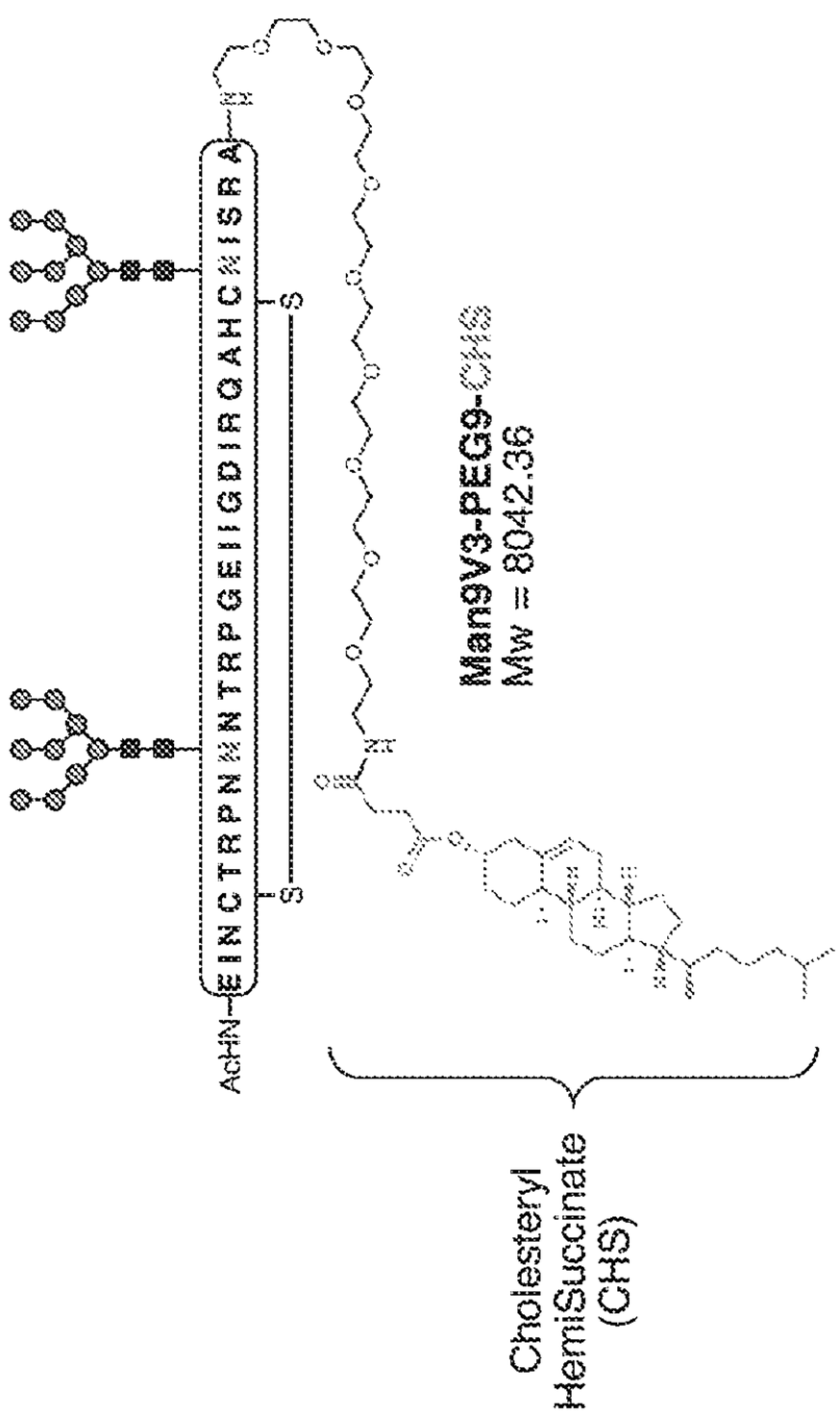


Figure 38A continued


AcHN
EINCTRPNNTRPGEIIGDIRQAHCNISR
293
301
332
S
S
S


AcHN—EINCTRPN%NTRPGEIIGDIRQAHC%ISRA
S
GTH-1
Aglycone V3-PEG3-GTH1-PEG3-CHS
MW = 6442.68


AcHN—EINCTRPN%NTRPGEIIGDIRQAHC%ISRA
S
Aglycone V3-PEG3-CHS
MW = 4046.73


AcHN—EINCTRPN%NTRPGEIIGDIRQAHC%ISRA
S
Man9V3-PEG9-CHS
MW = 8042.36
Cholesteryl
HemiSuccinate
(CHS)

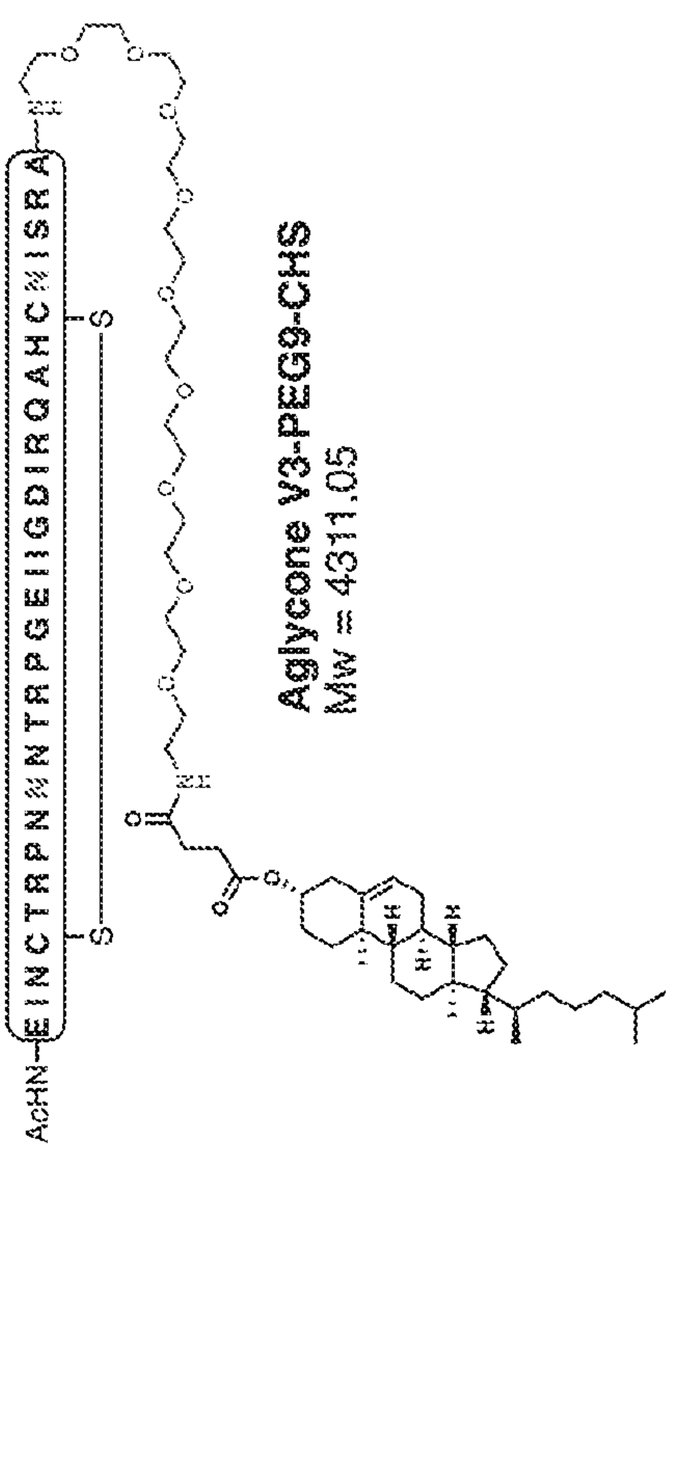
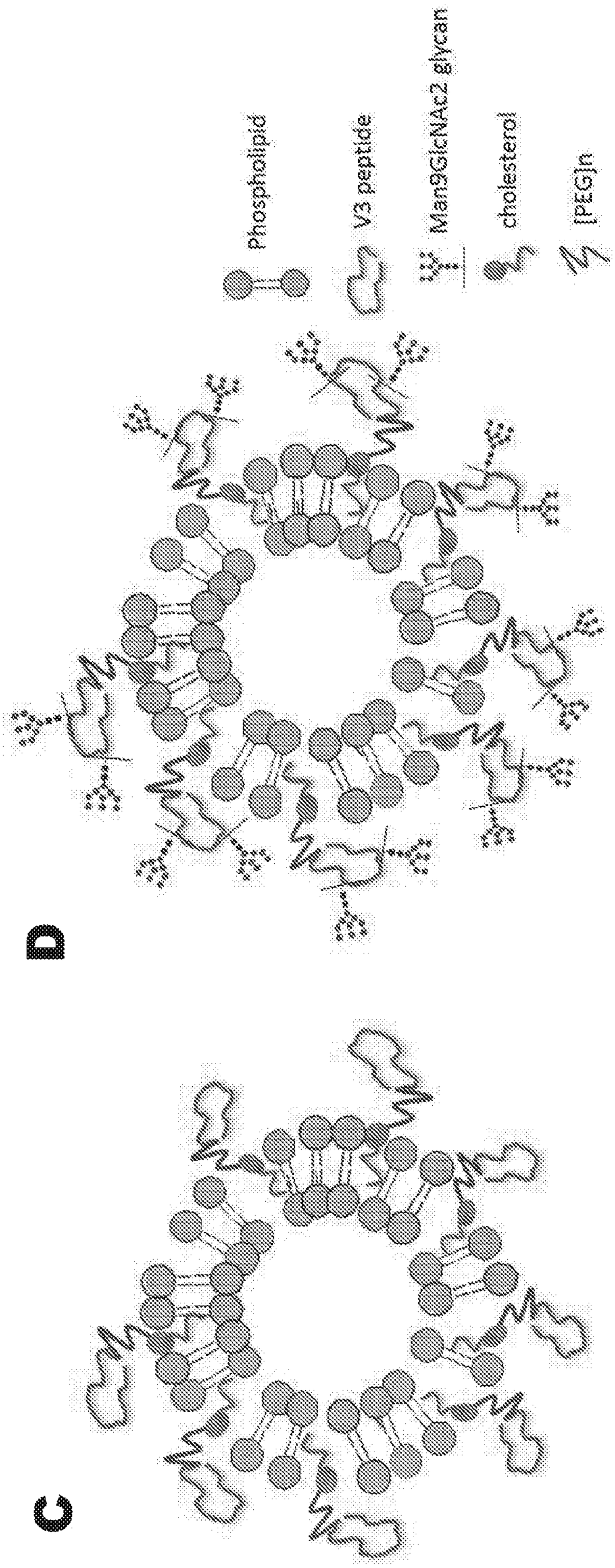

AcHN—EINCTRPN%NTRPGEIIGDIRQAHC%ISRA
S
Aglycone V3-PEG9-CHS
MW = 4311.05

Figure 38B



Figures 38C-38D

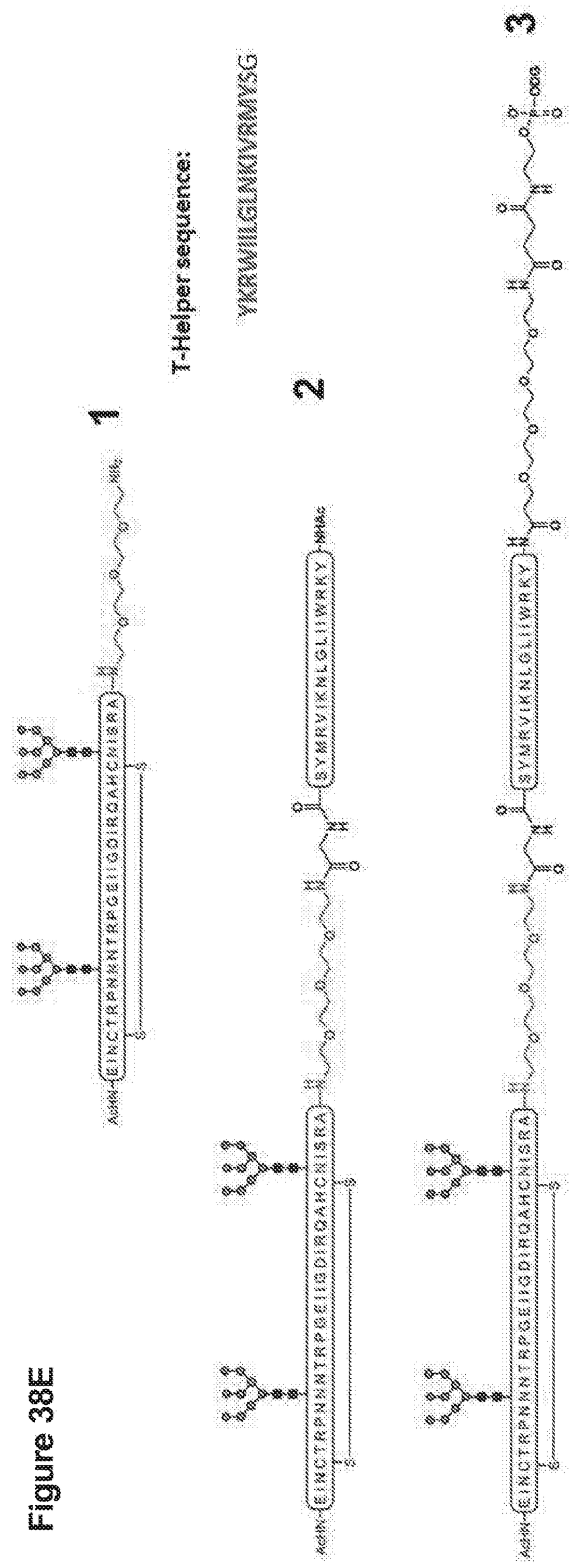

T-Helper sequence:
YYWWLGLMKNNGK
1
2
3
EINCTRPNNNTRPGEIIGDIRQAHCNISRA
KNLGLIIWRRKY
SYWRVIKNNGK

Figure 38E

Figure 39A

Name	SEQ ID NO	Feature
>HV1301262, CH848.3.D0949.10.17.6R.SOSIP.664	323	
>HV1301264, CH848.3.D0949.10.17.6R.DS.SOSIP.664	324	
>HV1301263, CH848.3.D0949.10.17chim.6R.DS.SOSIP.664	325	MGSLQPLATLYLLGMLVASVLA (Signal sequence)
>HV1301261, CH848.3.D0949.10.17chim.6R.SOSIP.664	326	
>CH0848.3.D0949.10.17 gp160	327	MRVMGILKNYPQWWIWGILGFWMLMICNG (Signal sequence)
>CH0848.3.D0949.10.17 Delta11 gp120	328	MRVMGILKNYPQWWIWGILGFWMLMICNG (Signal sequence)

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Figure 39B

Name	SEQ ID NO
>HV1301262, CH848.3.D0949.10.17.6R.SOSIP.664	329
>HV1301264, CH848.3.D0949.10.17.6R.DS.SOSIP.664	330
>HV1301263, CH848.3.D0949.10.17chim.6R.DS.SOSIP.664	331
>HV1301261, CH848.3.D0949.10.17chim.6R.SOSIP.664	332
>CH0848.3.D0949.10.17 gp160	333
>CH0848.3.D0949.10.17 Delta11 gp120	334

Figure 40A

Name	SEQ ID NO
>CH0848.3.D0836.10.31 GP160	335
>CH0848.3.D0836.10.31 D11 GP120	336
>CH0848.3.D0836.10.31CHIM.6R.SOSIP.664	337
>CH0848.3.D0836.10.31CHIM.DS.6R.SOSIP.664	338
>CH0848.3.D0836.10.31CHIM.6R.SOSIP.664V4.1	339
>CH0848.3.D0836.10.31CHIM.6R.SOSIP.664V4.2	340
>CH0848.3.D0358.80.06 GP160	341
>CH0848.3.D0358.80.06 D11 GP120	342
>CH0848.3.D0358.80.06CHIM.6R.SOSIP.664	343
>CH0848.3.D0358.80.06CHIM.DS.6R.SOSIP.664	344
>CH0848.3.D0358.80.06CHIM.6R.SOSIP.664V4.1	345
>CH0848.3.D0358.80.06CHIM.6R.SOSIP.664V4.2	346
>CH848.3.D0794.5.41 GP160	347
>CH848.3.D0794.5.41 D11 GP120	348
>CH848.3.D0794.5.41 CHIM.6R.SOSIP.664	349
> CH848.3.D0794.5.41 CHIM.DS.6R.SOSIP.664	350
>CH848.3.D0794.5.41 CHIM.6R.SOSIP.664V4.1	351
>CH848.3.D0794.5.41 CHIM.6R.SOSIP.664V4.2	352
>CH848.3.D0526.25.09 GP160	353
>CH848.3.D0526.25.09 D11 GP120	354
>CH848.3.D0526.25.09 CHIM.6R.SOSIP.664	355
>CH848.3.D0526.25.09 CHIM.DS.6R.SOSIP.664	356
>CH848.3.D0526.25.09 CHIM.6R.SOSIP.664V4.1	357
>CH848.3.D0526.25.09 CHIM.6R.SOSIP.664V4.2	358
>CH848.3.D0526.25.02 GP160	359

Figure 40A continued

Name	SEQ ID NO
>CH848.3.D0526.25.02 D11 GP120	360
>CH848.3.D0526.25.02CHIM.6R.SOSIP.664	361
>CH848.3.D0526.25.02CHIM.DS.6R.SOSIP.664	362
>CH848.3.D0526.25.02CHIM.6R.SOSIP.664V4.1	363
>CH848.3.D0526.25.02CHIM.6R.SOSIP.664V4.2	364
>CH848.3.D1432.5.41 GP160	365
>HV1300954 CH848.3.D1432.5.41 D11 GP120	366
>CH848.3.D1432.5.41CHIM.6R.SOSIP.664	367
>CH848.3.D1432.5.41CHIM.DS.6R.SOSIP.664	368
>CH848.3.D1432.5.41CHIM.6R.SOSIP.664V4.1	369
>CH848.3.D1432.5.41CHIM.6R.SOSIP.664V4.2	370

Figure 40B

Name	SEQ ID NO
>CH0848.3.D0836.10.31 GP160	371
>CH0848.3.D0836.10.31 D11 GP120	372
>CH0848.3.D0836.10.31CHIM.6R.SOSIP.664	373
>CH0848.3.D0836.10.31CHIM.DS.6R.SOSIP.664	374
>CH0848.3.D0836.10.31CHIM.6R.SOSIP.664V4.1	375
>CH0848.3.D0836.10.31CHIM.6R.SOSIP.664V4.2	376
>CH0848.3.D0358.80.06 GP160	377
>CH0848.3.D0358.80.06 D11 GP120	378
>CH0848.3.D0358.80.06CHIM.6R.SOSIP.664	379
>CH0848.3.D0358.80.06CHIM.DS.6R.SOSIP.664	380
>CH0848.3.D0358.80.06CHIM.6R.SOSIP.664V4.1	381
>CH0848.3.D0358.80.06CHIM.6R.SOSIP.664V4.2	382
>CH848.3.D0794.5.41 GP160	383
>CH848.3.D0794.5.41 D11 GP120	384
>CH848.3.D0794.5.41 CHIM.6R.SOSIP.664	385
> CH848.3.D0794.5.41 CHIM.DS.6R.SOSIP.664	386
>CH848.3.D0794.5.41 CHIM.6R.SOSIP.664V4.1	387
>CH848.3.D0794.5.41 CHIM.6R.SOSIP.664V4.2	388
>CH848.3.D0526.25.09 GP160	389
>CH848.3.D0526.25.09 D11 GP120	390
>CH848.3.D0526.25.09 CHIM.6R.SOSIP.664	391
>CH848.3.D0526.25.09 CHIM.DS.6R.SOSIP.664	392
>CH848.3.D0526.25.09 CHIM.6R.SOSIP.664V4.1	393
>CH848.3.D0526.25.09 CHIM.6R.SOSIP.664V4.2	394
>CH848.3.D0526.25.02 GP160	395

Figure 40B continued

Name	SEQ ID NO
>CH848.3.D0526.25.02 D11 GP120	396
>CH848.3.D0526.25.02CHIM.6R.SOSIP.664	397
>CH848.3.D0526.25.02CHIM.DS.6R.SOSIP.664	398
>CH848.3.D0526.25.02CHIM.6R.SOSIP.664V4.1	399
>CH848.3.D0526.25.02CHIM.6R.SOSIP.664V4.2	400
>CH848.3.D1432.5.41 GP160	401
>HV1300954 CH848.3.D1432.5.41 D11 GP120	402
>CH848.3.D1432.5.41CHIM.6R.SOSIP.664	403
>CH848.3.D1432.5.41CHIM.DS.6R.SOSIP.664	404
>CH848.3.D1432.5.41CHIM.6R.SOSIP.664V4.1	405
>CH848.3.D1432.5.41CHIM.6R.SOSIP.664V4.2	406

Figure 40C

Name	SEQ ID NO
>CH0848.3.d0000.TF	407

Figure 41A

Name	SEQ ID NO
>CH0848.3.D1120.10.21 GP160	408
>CH0848.3.D0949.10.18 GP160	409
>CH0848.3.D1432.5.27 GP160	410
>CH0848.3.D1432.5.27 D11 GP120	411
>CH0848.3.D0949.10.18 D11 GP120	412
>CH0848.3.D1120.10.21 D11 GP120	413
>CH0848.3.D1120.10.21CHIM.6R.SOSIP.664	414
>CH0848.3.D1120.10.21CHIM.DS.6R.SOSIP.664	415
>CH0848.3.D1120.10.21CHIM.6R.SOSIP.664V4.1	416
>CH0848.3.D1120.10.21CHIM.6R.SOSIP.664V4.2	417
>CH0848.3.D1432.5.27CHIM.6R.SOSIP.664	418
>CH0848.3.D1432.5.27CHIM.DS.6R.SOSIP.664	419
>CH0848.3.D1432.5.27CHIM.6R.SOSIP.664V4.1	420
>CH0848.3.D1432.5.27CHIM.6R.SOSIP.664V4.2	421
>CH0848.3.D0949.10.18CHIM.6R.SOSIP.664	422
>CH0848.3.D0949.10.18CHIM.DS.6R.SOSIP.664	423
> CH0848.3.D0949.10.18CHIM.6R.SOSIP.664V4.1	424
>CH0848.3.D0949.10.18CHIM.6R.SOSIP.664V4.2	425
>CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 (annotated sequence in Figure 5C)	426
>CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.2	427

Figure 41B

Name	SEQ ID NO
>CH0848.3.D1120.10.21 GP160	428
>CH0848.3.D0949.10.18 GP160	429
>CH0848.3.D1432.5.27 GP160	430
>CH0848.3.D1432.5.27 D11 GP120	431
>CH0848.3.D0949.10.18 D11 GP120	432
>CH0848.3.D1120.10.21 D11 GP120	433
>CH0848.3.D1120.10.21CHIM.6R.SOSIP.664	434
>CH0848.3.D1120.10.21CHIM.DS.6R.SOSIP.664	435
>CH0848.3.D1120.10.21CHIM.6R.SOSIP.664V4.1	436
>CH0848.3.D1120.10.21CHIM.6R.SOSIP.664V4.2	437
>CH0848.3.D1432.5.27CHIM.6R.SOSIP.664	438
>CH0848.3.D1432.5.27CHIM.DS.6R.SOSIP.664	439
>CH0848.3.D1432.5.27CHIM.6R.SOSIP.664V4.1	440
>CH0848.3.D1432.5.27CHIM.6R.SOSIP.664V4.2	441
>CH0848.3.D0949.10.18CHIM.6R.SOSIP.664	442
>CH0848.3.D0949.10.18CHIM.DS.6R.SOSIP.664	443
> CH0848.3.D0949.10.18CHIM.6R.SOSIP.664V4.1	444
>CH0848.3.D0949.10.18CHIM.6R.SOSIP.664V4.2	445
>CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1	446
>CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.2	447

Figure 41C

>CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 annotated

Human CD5 leader sequence: *MPMGSLQPLATLYLLGMLVASVLA;*
Amino acids from strain BG505;
Start of gp41 from BG505;
Sequence between right and left arrows is from CH848 except for the v4.1 mutations;
V4.1 mutation shows the position of the lysine mutation correspondnng to E64K and the position of the A316W mutation (See de Taeye et al. (2015) Cell 163, 1702-1715.

*MPMGSLQPLATLYLLGMLVASVLA***AENL**WVTVYYGVPVWKEAKTTLFCASDARAYEKKVHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDIIS

LWDQSLKPCVKLTPLCVTLICSNATVKNGTVEEMKNCSFNTTTEIRDKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNDET

FNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQWFYATGDIIGDIKQAHCNISEEKWNDTLQKV

GIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRAMYAPPIAGNITCRSNITGLLLTRDGG

TNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQH

LLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD*

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CA 03055204 2019-08-30

Figure 42

Starting place

		Autologous gp120 binding											Autologous Neutralization									
	day.clone	DH270.UCA	DH270.IA4	DH270.IA3	DH270.IA2	DH270.1	DH270.IA1	DH270.4	DH270.5	DH270.6	DH270.3	DH270.2	DH270.UCA	DH270.IA4	DH270.IA3	DH270.IA2	DH270.1	DH270.IA1	DH270.5	DH270.4	DH270.3	V1 loop length
	0000.TF	0	0	0	0	8.91	14.2	13.5	13.5	14.8	10	10.7	>50	>50	>50	>50	>50	>50	>50	38.3	>50	34
I	0949.10.17	0	2.6	6.3	9.4	12.9	13.6	14.3	14.6	14.3	13	13.4	>50	0.64	0.2	0.14	0.18	<0.02	0.05	0.03	<0.02	17
II	0836.10.31	0	0	4.9	9.4	13.2	13.5	13.2	14.5	14.2	11	13.4	>50	48.2	1.07	<0.02	<0.02	<0.02	<0.02	<0.02	<0.02	17
III	0358.80.06	0	0	0	0.3	11.2	13.5	14.9	15	13.9	11	14.8	>50	>50	>50	>50	1.27	0.02	<0.02	<0.02	0.06	24
III	1432.05.41	0	0	0	0.8	11.7	12.7	12.7	14.6	14	14	13.8	>50	>50	>50	>50	2.56	0.33	0.21	0.26	0.13	30
III	0526.25.02	0	0	0	0	8.62	12	13.6	13.8	13.6	9.8	12.6	>50	>50	>50	>50	16.7	1.42	1.56	1.14	>50	34
	1305.10.13								2.7	2.3		5.8						2.4		9.1		17

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Figure 43

contacts

		i0yl00ctrp n0ntgdigdi rgh0g0itc
CH0848.0949.10.17	D	m---y--- ---di--- k-------
CH0848.0836.10.31	D	m---y--- ---di--- --------
CH0848.0358.80.06	D	m---y--- g--di--- --------
CH0848.1432.5.41	D	m---y--- ---di--p -k-------
CH0848.0526.25.02	D	m---y--- g--di--- --------
CH0848.1305.10.13	N	m---y--- ---di--np --------

1305 is one of 2 CH848 Envs with D325N that has some binding affinity and sensitivity to DH270 lineage antibodies

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Figure 44A

>703010848.3.d0949.10.17_signature_opt_b gp160

TRVMGILKNYPQWWIWGILGFWMLMICNGKGKLWVTVYYGVPVWKEAKTTLFCASDARAYEKEVH
NVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLIC
SNATVKNGTVEEMKNCSFNTTTEIRDKEKKEYALFYKPDIVPISETNNTSEYRLINCDTSAVTQA
CPKVTFEPIPIHYCAPAGYAILKCNNETFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEKE
IVIRSENLTNNAKIIIVHLKTPVEINCTRPNNNTRKSIRIGPGQTFYATGDIIGDIKQAHCNISE
AKWNDTLQNVSIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCDTSNLFNGTYNGTYIS
TNSSANSTSTITLQCRIKQIINMWQGVGRAMYAPPIAGNITCRSSITGLLLTRDGGTNSNETETF
RPAGGDMRDNWRSELYKYKVVEIQPLGIAPTGAKRRVVEREKRAAGLGALFLGFLGAAGSTMGAA
SITLTVQARQLLSGIVQQQSNLLRAIEAQQHMLQLTVWGIKQLQARVLAIERYLKDQQLLGMWGC
SGKLICTTNVPWNASWSNKSETDIWDNMTWMQWEREISNYTETIYKLLEDSQNQQERNEQDLLAL
DSWNSLWNWFNITKWLWYIKIFIMIVGGLIGLRIVFAVLSIVNRVRQGYSPLSLQTLTPNPREPD
RLRGIEEEGGEQDRDRSGRLVHGFLPIVWDDLRSLCLFSYHQLRDLLLLAARVVELLGRSSLRGL
QRGWEVLKYLGSLVQYWGLELKKSAISLFDTLAIAVAEGTDRIIELIQRICRAIRNIPTRIRQGF
EASLL

1. Replace signal peptide with CD5

>703010848.3.d0949.10.17_signature_opt_b_CD5ss gp160

MPMGSLQPLATLYLLGMLVASCLG*KGKLWVTVYYG*VPVWKEAKTTLFCASDARAYEKEVHNVWAT
HACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICSNATV
KNGTVEEMKNCSFNTTTEIRDKEKKEYALFYKPDIVPISETNNTSEYRLINCDTSAVTQACPKVT
FEPIPIHYCAPAGYAILKCNNETFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRS
ENLTNNAKIIIVHLKTPVEINCTRPNNNTRKSIRIGPGQTFYATGDIIGDIKQAHCNISEAKWND
TLQNVSIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCDTSNLFNGTYNGTYISTNSSA
NSTSTITLQCRIKQIINMWQGVGRAMYAPPIAGNITCRSSITGLLLTRDGGTNSNETETFRPAGG
DMRDNWRSELYKYKVVEIQPLGIAPTGAKRRVVEREKRAAGLGALFLGFLGAAGSTMGAASITLT
VQARQLLSGIVQQQSNLLRAIEAQQHMLQLTVWGIKQLQARVLAIERYLKDQQLLGMWGCSGKLI
CTTNVPWNASWSNKSETDIWDNMTWMQWEREISNYTETIYKLLEDSQNQQERNEQDLLALDSWNS
LWNWFNITKWLWYIKIFIMIVGGLIGLRIVFAVLSIVNRVRQGYSPLSLQTLTPNPREPDRLRGI
EEEGGEQDRDRSGRLVHGFLPIVWDDLRSLCLFSYHQLRDLLLLAARVVELLGRSSLRGLQRGWE
VLKYLGSLVQYWGLELKKSAISLFDTLAIAVAEGTDRIIELIQRICRAIRNIPTRIRQGFEASLL

2. Delete N-terminal residues

>703010848.3.d0949.10.17_signature_opt_b_CD5ss delta11 gp160

MPMGSLQPLATLYLLGMLVASCLGVPVWKEAKTTLFCASDARAYEKEVHNVWATHACVPTDPSPQ
ELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICSNATVKNGTVEEMKNC
SFNTTTEIRDKEKKEYALFYKPDIVPISETNNTSEYRLINCDTSAVTQACPKVTFEPIPIHYCAP
AGYAILKCNNETFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAKIII
VHLKTPVEINCTRPNNNTRKSIRIGPGQTFYATGDIIGDIKQAHCNISEAKWNDTLQNVSIELQK
HFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCDTSNLFNGTYNGTYISTNSSANSTSTITLQCR
IKQIINMWQGVGRAMYAPPIAGNITCRSSITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELY
KYKVVEIQPLGIAPTGAKRRVVEREKRAAGLGALFLGFLGAAGSTMGAASITLTVQARQLLSGIV
QQQSNLLRAIEAQQHMLQLTVWGIKQLQARVLAIERYLKDQQLLGMWGCSGKLICTTNVPWNASW
SNKSETDIWDNMTWMQWEREISNYTETIYKLLEDSQNQQERNEQDLLALDSWNSLWNWFNITKWL
WYIKIFIMIVGGLIGLRIVFAVLSIVNRVRQGYSPLSLQTLTPNPREPDRLRGIEEEGGEQDRDR
SGRLVHGFLPIVWDDLRSLCLFSYHQLRDLLLLAARVVELLGRSSLRGLQRGWEVLKYLGSLVQY
WGLELKKSAISLFDTLAIAVAEGTDRIIELIQRICRAIRNIPTRIRQGFEASLL

3. Mutate furin site

>703010848.3.d0949.10.17_signature_opt_b_CD5ss delta11 gp160C

MPMGSLQPLATLYLLGMLVASCLGVPVWKEAKTTLFCASDARAYEKEVHNVWATHACVPTDPSPQ
ELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICSNATVKNGTVEEMKNC
SFNTTTEIRDKEKKEYALFYKPDIVPISETNNTSEYRLINCDTSAVTQACPKVTFEPIPIHYCAP

Figure 44A continued

AGYAILKCNNETFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAKIII
VHLKTPVEINCTRPNNNTRKSIRIGPGQTFYATGDIIGDIKQAHCNISEAKWNDTLQNVSIELQK
HFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCDTSNLFNGTYNGTYISTNSSANSTSTITLQCR
IKQIINMWQGVGRAMYAPPIAGNITCRSSITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELY
KYKVVEIQPLGIAPTGAKERVVEREKEAAGLGALFLGFLGAAGSTMGAASITLTVQARQLLSGIV
QQQSNLLRAIEAQQHMLQLTVWGIKQLQARVLAIERYLKDQQLLGMWGCSGKLICTTNVPWNASW
SNKSETDIWDNMTWMQWEREISNYTETIYKLLEDSQNQQERNEQDLLALDSWNSLWNWFNITKWL
WYIKIFIMIVGGLIGLRIVFAVLSIVNRVRQGYSPLSLQTLTPNPREPDRLRGIEEEGGEQDRDR
SGRLVHGFLPIVWDDLRSLCLFSYHQLRDLLLLAARVVELLGRSSLRGLQRGWEVLKYLGSLVQY
WGLELKKSAISLFDTLAIAVAEGTDRIIELIQRICRAIRNIPTRIRQGFEASLL

4. Truncate to gp120

>703010848.3.d0949.10.17_signature_opt_b_CD5ss delta11 gp120
MPMGSLQPLATLYLLGMLVASCLGVPVWKEAKTTLFCASDARAYEKEVHNVWATHACVPTDPSPQ
ELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICSNATVKNGTVEEMKNC
SFNTTTEIRDKEKKEYALFYKPDIVPISETNNTSEYRLINCDTSAVTQACPKVTFEPIPIHYCAP
AGYAILKCNNETFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAKIII
VHLKTPVEINCTRPNNNTRKSIRIGPGQTFYATGDIIGDIKQAHCNISEAKWNDTLQNVSIELQK
HFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCDTSNLFNGTYNGTYISTNSSANSTSTITLQCR
IKQIINMWQGVGRAMYAPPIAGNITCRSSITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELY
KYKVVEIQPLGIAPTGAKERVVEREKE

5. Codon optimize sequence with liao codon converter

>703010848.3.d0949.10.17_signature_opt_b_CD5ss delta11 gp120
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ACGCCCGCGCCTACGAGAAGGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCC
ACCGACCCCTCCCCCCAGGAGCTGGTGCTGGGCAACGTGACCGAGAACTTCAACATGTG
GAAGAACGACATGGTGGACCAGATGCACGAGGACATCATCTCCCTGTGGGACCAGTCCC
TGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTGACCCTGATCTGCTCCAACGCCACC
GTGAAGAACGGCACCGTGGAGGAGATGAAGAACTGCTCCTTCAACACCACCACCGAGAT
CCGCGACAAGGAGAAGAAGGAGTACGCCCTGTTCTACAAGCCCGACATCGTGCCCATCT
CCGAGACCAACAACACCTCCGAGTACCGCCTGATCAACTGCGACACCTCCGCCGTGACC
CAGGCCTGCCCCAAGGTGACCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGG
CTACGCCATCCTGAAGTGCAACAACGAGACCTTCAACGGCACCGGCCCCTGCACCAACG
TGTCCACCGTGCAGTGCACCCACGGCATCCGCCCCGTGGTGTCCACCCAGCTGCTGCTG
AACGGCTCCCTGGCCGAGAAGGAGATCGTGATCCGCTCCGAGAACCTGACCAACAACGC
CAAGATCATCATCGTGCACCTGAAGACCCCCGTGGAGATCAACTGCACCCGCCCCAACA
ACAACACCCGCAAGTCCATCCGCATCGGCCCCGGCCAGACCTTCTACGCCACCGGCGAC
ATCATCGGCGACATCAAGCAGGCCCACTGCAACATCTCCGAGGCCAAGTGGAACGACAC
CCTGCAGAACGTGTCCATCGAGCTGCAGAAGCACTTCCCCAACAAGACCATCAAGTACA
ACCAGTCCGCCGGCGGCGACATGGAGATCACCACCCACTCCTTCAACTGCGGCGGCGAG
TTCTTCTACTGCGACACCTCCAACCTGTTCAACGGCACCTACAACGGCACCTACATCTC
CACCAACTCCTCCGCCAACTCCACCTCCACCATCACCCTGCAGTGCCGCATCAAGCAGA
TCATCAACATGTGGCAGGGCGTGGGCCGCGCCATGTACGCCCCCCCCATCGCCGGCAAC
ATCACCTGCCGCTCCTCCATCACCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACTC
CAACGAGACCGAGACCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACTGGCGCTCCG
AGCTGTACAAGTACAAGGTGGTGGAGATCCAGCCCCTGGGCATCGCCCCCACCGGCGCC
AAGGAGCGCGTGGTGGAGCGCGAGAAGGAG

Figure 44B

>703010848.3.d0949.10.17_signature_opt_filled_rare_holes_a gp160

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SNATVKNGTVEEMKNCSFNTTTEIRDKEKKEYALFYKPDIVPISETNNTSEYRLINCNTSAVTQA
CPKVTFEPIPIHYCAPAGYAILKCNNETFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEKE
IVIRSENLTNNAKIIIVHLNTSVEINCTRPNNNTRKSIRIGPGQTFYATGDIIGDIKQAHCNISE
AKWNDTLQNVSIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYIS
TNSSANSTSTITLQCRIKQIINMWQGVGRAMYAPPIAGNITCRSSITGLLLTRDGGTNSNETETF
RPAGGDMRDNWRSELYKYKVVEIQPLGIAPTGAKRRVVEREKRAAGLGALFLGFLGAAGSTMGAA
SITLTVQARQLLSGIVQQQSNLLRAIEAQQHMLQLTVWGIKQLQARVLAIERYLKDQQLLGMWGC
SGKLICTTNVPWNASWSNKSETDIWDNMTWMQWEREISNYTETIYKLLEDSQNQQERNEQDLLAL
DSWNSLWNWFNITKWLWYIKIFIMIVGGLIGLRIVFAVLSIVNRVRQGYSPLSLQTLTPNPREPD
RLRGIEEEGGEQDRDRSGRLVHGFLPIVWDDLRSLCLFSYHQLRDLLLLAARVVELLGRSSLRGL
QRGWEVLKYLGSLVQYWGLELKKSAISLFDTLAIAVAEGTDRIIELIQRICRAIRNIPTRIRQGF
EASLL

1. Replace signal peptide with CD5

>703010848.3.d0949.10.17_signature_opt_filled_rare_holes_a_CD5ss
gp160

MPMGSLQPLATLYLLGMLVASCLG*KGKLWVTVYYG*VPVWKEAKTTLFCASDARAYEKEVHNVWAT
HACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICSNATV
KNGTVEEMKNCSFNTTTEIRDKEKKEYALFYKPDIVPISETNNTSEYRLINCNTSAVTQACPKVT
FEPIPIHYCAPAGYAILKCNNETFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRS
ENLTNNAKIIIVHLNTSVEINCTRPNNNTRKSIRIGPGQTFYATGDIIGDIKQAHCNISEAKWND
TLQNVSIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSA
NSTSTITLQCRIKQIINMWQGVGRAMYAPPIAGNITCRSSITGLLLTRDGGTNSNETETFRPAGG
DMRDNWRSELYKYKVVEIQPLGIAPTGAKRRVVEREKRAAGLGALFLGFLGAAGSTMGAASITLT
VQARQLLSGIVQQQSNLLRAIEAQQHMLQLTVWGIKQLQARVLAIERYLKDQQLLGMWGCSGKLI
CTTNVPWNASWSNKSETDIWDNMTWMQWEREISNYTETIYKLLEDSQNQQERNEQDLLALDSWNS
LWNWFNITKWLWYIKIFIMIVGGLIGLRIVFAVLSIVNRVRQGYSPLSLQTLTPNPREPDRLRGI
EEEGGEQDRDRSGRLVHGFLPIVWDDLRSLCLFSYHQLRDLLLLAARVVELLGRSSLRGLQRGWE
VLKYLGSLVQYWGLELKKSAISLFDTLAIAVAEGTDRIIELIQRICRAIRNIPTRIRQGFEASLL

2. Delete N-terminal residues

>703010848.3.d0949.10.17_signature_opt_filled_rare_holes_a_CD5ss_
delta11 gp160

MPMGSLQPLATLYLLGMLVASCLGVPVWKEAKTTLFCASDARAYEKEVHNVWATHACVPTDPSPQ
ELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICSNATVKNGTVEEMKNC
SFNTTTEIRDKEKKEYALFYKPDIVPISETNNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAP
AGYAILKCNNETFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAKIII
VHLNTSVEINCTRPNNNTRKSIRIGPGQTFYATGDIIGDIKQAHCNISEAKWNDTLQNVSIELQK
HFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCR
IKQIINMWQGVGRAMYAPPIAGNITCRSSITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELY
KYKVVEIQPLGIAPTGAKRRVVEREKRAAGLGALFLGFLGAAGSTMGAASITLTVQARQLLSGIV
QQQSNLLRAIEAQQHMLQLTVWGIKQLQARVLAIERYLKDQQLLGMWGCSGKLICTTNVPWNASW
SNKSETDIWDNMTWMQWEREISNYTETIYKLLEDSQNQQERNEQDLLALDSWNSLWNWFNITKWL
WYIKIFIMIVGGLIGLRIVFAVLSIVNRVRQGYSPLSLQTLTPNPREPDRLRGIEEEGGEQDRDR
SGRLVHGFLPIVWDDLRSLCLFSYHQLRDLLLLAARVVELLGRSSLRGLQRGWEVLKYLGSLVQY
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3. Mutate furin site

Figure 44B continued

>703010848.3.d0949.10.17_signature_opt_filled_rare_holes_a_CD5ss_delta11 gp160

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ELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICSNATVKNGTVEEMKNC
SFNTTTEIRDKEKKEYALFYKPDIVPISETNNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAP
AGYAILKCNNETFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAKIII
VHLNTSVEINCTRPNNNTRKSIRIGPGQTFYATGDIIGDIKQAHCNISEAKWNDTLQNVSIELQK
HFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCR
IKQIINMWQGVGRAMYAPPIAGNITCRSSITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELY
KYKVVEIQPLGIAPTGAKERVVEREKEAAGLGALFLGFLGAAGSTMGAASITLTVQARQLLSGIV
QQQSNLLRAIEAQQHMLQLTVWGIKQLQARVLAIERYLKDQQLLGMWGCSGKLICTTNVPWNASW
SNKSETDIWDNMTWMQWEREISNYTETIYKLLEDSQNQQERNEQDLLALDSWNSLWNWFNITKWL
WYIKIFIMIVGGLIGLRIVFAVLSIVNRVRQGYSPLSLQTLTPNPREPDRLRGIEEEGGEQDRDR
SGRLVHGFLPIVWDDLRSLCLFSYHQLRDLLLLAARVVELLGRSSLRGLQRGWEVLKYLGSLVQY
WGLELKKSAISLFDTLAIAVAEGTDRIIELIQRICRAIRNIPTRIRQGFEASLL

4. Truncate to gp120

>703010848.3.d0949.10.17_signature_opt_filled_rare_holes_a_CD5ss_delta11 gp120

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ELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICSNATVKNGTVEEMKNC
SFNTTTEIRDKEKKEYALFYKPDIVPISETNNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAP
AGYAILKCNNETFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAKIII
VHLNTSVEINCTRPNNNTRKSIRIGPGQTFYATGDIIGDIKQAHCNISEAKWNDTLQNVSIELQK
HFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCR
IKQIINMWQGVGRAMYAPPIAGNITCRSSITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELY
KYKVVEIQPLGIAPTGAKERVVEREKE

5. Codon optimize sequence

>703010848.3.d0949.10.17_signature_opt_filled_rare_holes_a_CD5ss_delta11 gp120

ATGCCCATGGGCTCCCTGCAGCCCCTGGCCACCCTGTACCTGCTGGGCATGCTGGTGGC
CTCCTGCCTGGGCGTGCCCGTGTGGAAGGAGGCCAAGACCACCCTGTTCTGCGCCTCCG
ACGCCCGCGCCTACGAGAAGGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCC
ACCGACCCCTCCCCCCAGGAGCTGGTGCTGGGCAACGTGACCGAGAACTTCAACATGTG
GAAGAACGACATGGTGGACCAGATGCACGAGGACATCATCTCCCTGTGGGACCAGTCCC
TGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTGACCCTGATCTGCTCCAACGCCACC
GTGAAGAACGGCACCGTGGAGGAGATGAAGAACTGCTCCTTCAACACCACCACCGAGAT
CCGCGACAAGGAGAAGAAGGAGTACGCCCTGTTCTACAAGCCCGACATCGTGCCCATCT
CCGAGACCAACAACACCTCCGAGTACCGCCTGATCAACTGCAACACCTCCGCCGTGACC
CAGGCCTGCCCCAAGGTGACCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGG
CTACGCCATCCTGAAGTGCAACAACGAGACCTTCAACGGCACCGGCCCCTGCACCAACG
TGTCCACCGTGCAGTGCACCCACGGCATCCGCCCCGTGGTGTCCACCCAGCTGCTGCTG
AACGGCTCCCTGGCCGAGAAGGAGATCGTGATCCGCTCCGAGAACCTGACCAACAACGC
CAAGATCATCATCGTGCACCTGAACACCTCCGTGGAGATCAACTGCACCCGCCCCAACA
ACAACACCCGCAAGTCCATCCGCATCGGCCCCGGCCAGACCTTCTACGCCACCGGCGAC
ATCATCGGCGACATCAAGCAGGCCCACTGCAACATCTCCGAGGCCAAGTGGAACGACAC
CCTGCAGAACGTGTCCATCGAGCTGCAGAAGCACTTCCCCAACAAGACCATCAAGTACA
ACCAGTCCGCCGGCGGCGACATGGAGATCACCACCCACTCCTTCAACTGCGGCGGCGAG
TTCTTCTACTGCAACACCTCCAACCTGTTCAACGGCACCTACAACGGCACCTACATCTC

Figure 44B continued

CACCAACTCCTCCGCCAACTCCACCTCCACCATCACCCTGCAGTGCCGCATCAAGCAGA
TCATCAACATGTGGCAGGGCGTGGGCCGCGCCATGTACGCCCCCCCCATCGCCGGCAAC
ATCACCTGCCGCTCCTCCATCACCGGCCTGCTGCTGACCCGCGACGGCGGCACCAACTC
CAACGAGACCGAGACCTTCCGCCCCGCCGGCGGCGACATGCGCGACAACTGGCGCTCCG
AGCTGTACAAGTACAAGGTGGTGGAGATCCAGCCCCTGGGCATCGCCCCCACCGGCGCC
AAGGAGCGCGTGGTGGAGCGCGAGAAGGAG

Figure 44C

>CH0848.3.d1651.10.07 gp160

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EEISHALARNSTTEEMKNCSFNTTTEIRDKEKKEYALFYRPDIVPLNNKTSNISEYRLINCNTSTVTQAC
PKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEKGIVIRSE
NLTNNAKIIIVQLNANASVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGNIRQAHCNISEKKWNETLQK
VGIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTAKLFNSTYNGTYISTNSINSTLNITLQC
RIKQIINMWQGVGRAMYAPPIAGNITCRSNITGLLLTRDGGIHNDSNVTETFRPAGGDMRDNWRSELYKY
KVVEIQPLGIAPTGAKRRVVERGKRAAGLGALFLGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLL
RAIEAQQHMLQLTVWGIKQLQARVLALERYLKDQQLLGIWGCSGKLICTTNVPWNTSWSNKSEMDIWNNM
TWMQWEREISNYTGTIYKLLEDSQNQQERNEQDLLALDSWNSLWNWFDITKWLWYIKIFIMIVGGLIGLR
IVFAVLSIVNRVRQGYSPLSLQTLTPNPREPDRLRGIEEEGGEQDRDKSIRLVNGFLPIVWDDLRSLCLF
SYHRLRDFLLLAARVVELLGRSSLRGLQRGWEVLKYLGSLVQYWGLELKKSAISLFDTLAVAVAEGTDRI
IELIQGFCRAIRNIPRRIRQGFEASLL

1. Replace signal peptide with CD5

>CH0848.3.d1651.10.07_CD5ss gp160

MPMGSLQPLATLYLLGMLVASCLG*EGNLWVTVYYG*VPVWKEAKTTLFCASDAKAYVKEVHNVWATHACVP
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ALARNSTTEEMKNCSFNTTTEIRDKEKKEYALFYRPDIVPLNNKTSNISEYRLINCNTSTVTQACPKVTF
EPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEKGIVIRSENLTNN
AKIIIVQLNANASVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGNIRQAHCNISEKKWNETLQKVGIEL
QKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTAKLFNSTYNGTYISTNSINSTLNITLQCRIKQI
INMWQGVGRAMYAPPIAGNITCRSNITGLLLTRDGGIHNDSNVTETFRPAGGDMRDNWRSELYKYKVVEI
QPLGIAPTGAKRRVVERGKRAAGLGALFLGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAIEA
QQHMLQLTVWGIKQLQARVLALERYLKDQQLLGIWGCSGKLICTTNVPWNTSWSNKSEMDIWNNMTWMQW
EREISNYTGTIYKLLEDSQNQQERNEQDLLALDSWNSLWNWFDITKWLWYIKIFIMIVGGLIGLRIVFAV
LSIVNRVRQGYSPLSLQTLTPNPREPDRLRGIEEEGGEQDRDKSIRLVNGFLPIVWDDLRSLCLFSYHRL
RDFLLLAARVVELLGRSSLRGLQRGWEVLKYLGSLVQYWGLELKKSAISLFDTLAVAVAEGTDRIIELIQ
GFCRAIRNIPRRIRQGFEASLL

2. Delete N-terminal residues

>CH0848.3.d1651.10.07_CD5ss_Delta11 gp160

MPMGSLQPLATLYLLGMLVASCLGVPVWKEAKTTLFCASDAKAYVKEVHNVWATHACVPTDPSPQELVLD
NVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLNCSNAIVKNSTTEEISHALARNSTTEEM
KNCSFNTTTEIRDKEKKEYALFYRPDIVPLNNKTSNISEYRLINCNTSTVTQACPKVTFEPIPIHYCAPA
GYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEKGIVIRSENLTNNAKIIIVQLNAN
ASVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGNIRQAHCNISEKKWNETLQKVGIELQKHFPNKTIKY
NQSAGGDMEITTHSFNCGGEFFYCNTAKLFNSTYNGTYISTNSINSTLNITLQCRIKQIINMWQGVGRAM
YAPPIAGNITCRSNITGLLLTRDGGIHNDSNVTETFRPAGGDMRDNWRSELYKYKVVEIQPLGIAPTGAK
RRVVERGKRAAGLGALFLGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAIEAQQHMLQLTVWG
IKQLQARVLALERYLKDQQLLGIWGCSGKLICTTNVPWNTSWSNKSEMDIWNNMTWMQWEREISNYTGTI
YKLLEDSQNQQERNEQDLLALDSWNSLWNWFDITKWLWYIKIFIMIVGGLIGLRIVFAVLSIVNRVRQGY
SPLSLQTLTPNPREPDRLRGIEEEGGEQDRDKSIRLVNGFLPIVWDDLRSLCLFSYHRLRDFLLLAARVV
ELLGRSSLRGLQRGWEVLKYLGSLVQYWGLELKKSAISLFDTLAVAVAEGTDRIIELIQGFCRAIRNIPR
RIRQGFEASLL

3. Mutate furin site

>CH0848.3.d1651.10.07_CD5ss_Delta11 gp160C

MPMGSLQPLATLYLLGMLVASCLGVPVWKEAKTTLFCASDAKAYVKEVHNVWATHACVPTDPSPQELVLD
NVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLNCSNAIVKNSTTEEISHALARNSTTEEM
KNCSFNTTTEIRDKEKKEYALFYRPDIVPLNNKTSNISEYRLINCNTSTVTQACPKVTFEPIPIHYCAPA

Figure 44C continued

GYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEKGIVIRSENLTNNAKIIIVQLNAN
ASVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGNIRQAHCNISEKKWNETLQKVGIELQKHFPNKTIKY
NQSAGGDMEITTHSFNCGGEFFYCNTAKLFNSTYNGTYISTNSINSTLNITLQCRIKQIINMWQGVGRAM
YAPPIAGNITCRSNITGLLLTRDGGIHNDSNVTETFRPAGGDMRDNWRSELYKYKVVEIQPLGIAPTGAK
ERVVERGKEAAGLGALFLGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAIEAQQHMLQLTVWG
IKQLQARVLALERYLKDQQLLGIWGCSGKLICTTNVPWNTSWSNKSEMDIWNNMTWMQWEREISNYTGTI
YKLLEDSQNQQERNEQDLLALDSWNSLWNWFDITKWLWYIKIFIMIVGGLIGLRIVFAVLSIVNRVRQGY
SPLSLQTLTPNPREPDRLRGIEEEGGEQDRDKSIRLVNGFLPIVWDDLRSLCLFSYHRLRDFLLLAARVV
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4. Truncate to gp120

>CH0848.3.d1651.10.07_CD5ss_Delta11 gp120

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GYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEKGIVIRSENLTNNAKIIIVQLNAN
ASVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGNIRQAHCNISEKKWNETLQKVGIELQKHFPNKTIKY
NQSAGGDMEITTHSFNCGGEFFYCNTAKLFNSTYNGTYISTNSINSTLNITLQCRIKQIINMWQGVGRAM
YAPPIAGNITCRSNITGLLLTRDGGIHNDSNVTETFRPAGGDMRDNWRSELYKYKVVEIQPLGIAPTGAK
ERVVERGKE

>CH0848.3.d1651.10.07_CD5ss_Delta11 gp120

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CTACGTGAAGGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCTCCCCC
CAGGAGCTGGTGCTGGACAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACC
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CCTGTGCGTGACCCTGAACTGCTCCAACGCCATCGTGAAGAACTCCACCACCGAGGAGATCTCC
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AGATCCGCGACAAGGAGAAGAAGGAGTACGCCCTGTTCTACCGCCCCGACATCGTGCCCCTGAA
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TCCTGAAGTGCAACGACGAGACCTTCAACGGCACCGGCCCCTGCTCCAACGTGTCCACCGTGCA
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Figure 44C continued

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Figure 44D

>703010848.3.d0949.10.17_signature_opt_b_T250.4_V1V2
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IVNRVRQGYSPLSLQTLTPNPREPDRLRGIEEEGGEQDRDRSGRLVHGFLPIVWDDLRSLCLFSYHQLRD
LLLLAARVVELLGRSSLRGLQRGWEVLKYLGSLVQYWGLELKKSAISLFDTLAIAVAEGTDRIIELIQRI
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1. Replace signal peptide with CD5

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IVHLKTPVEINCTRPNNNTRKSIRIGPGQTFYATGDIIGDIKQAHCNISEAKWNDTLQNVSIELQKHFPN
KTIKYNQSAGGDMEITTHSFNCGGEFFYCDTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQ
GVGRAMYAPPIAGNITCRSSITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVEIQPLGIAP
TGAKRRVVEREKRAAGLGALFLGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAIEAQQHMLQL
TVWGIKQLQARVLAIERYLKDQQLLGMWGCSGKLICTTNVPWNASWSNKSETDIWDNMTWMQWEREISNY
TETIYKLLEDSQNQQERNEQDLLALDSWNSLWNWFNITKWLWYIKIFIMIVGGLIGLRIVFAVLSIVNRV
RQGYSPLSLQTLTPNPREPDRLRGIEEEGGEQDRDRSGRLVHGFLPIVWDDLRSLCLFSYHQLRDLLLLA
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2. Delete N-terminal residues

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LTPNPREPDRLRGIEEEGGEQDRDRSGRLVHGFLPIVWDDLRSLCLFSYHQLRDLLLLAARVVELLGRSS
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ASLL

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Figure 44D continued

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ASLL

4. Truncate to gp120

>703010848.3.d0949.10.17_signature_opt_b_T250.4_V1V2_CD5ss_Delta11
gp120

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TCAAGTACAACCAGTCCGCCGGCGGCGACATGGAGATCACCACCCACTCCTTCAACTGCGGCGG
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ACATGTGGCAGGGCGTGGGCCGCGCCATGTACGCCCCCCCCCATCGCCGGCAACATCACCTGCCG
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Figure 44D continued

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GGAG

Figure 45

>AG.T250-4 Delta10 gp120

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>T250-4chim.6R.SOSIP.664v4.1

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VSTQLLLNGSLAEEEVIIRSENITNNAKNILVQLNTPVQINCTRPNNNTVKSIRIGPGQAFYYFGDIIGDIRMAHCNVSKATWNET
LGKVVKQLRKHFGNNTIIRFAQSSGGDLEVTTHSFNCGGEFFYCNTSGLFNSTWISNTSVQGSNSTGSNDSIVLPCRIKQIINMW
QRIGQAMYAPPIQGVIRCVSNITGLILTRDGGSTNSTTETFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRR
RRAVGIGAVSLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEPQQHLLKDTHWGIKQLQARVLAVEHYLRDQ
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EYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVS
TQLLLNGSLAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGDIKQAHCNISEEKWNDTLQK
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Figure 45 continued

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>CH0848.3.D0836.10.31gp140C

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YALFYRPDIVPLNNETSNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVS
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GS*

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Figure 45 continued

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KPVVSTQLLLNGSLAEEEIIIRSENITNNAKTIIVQLNESVEINCTRPNNNTRKSIRIGPGQAFYATGDIIGDIRQAHCNISGTKWNK
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IVQQQSNLLRAIEAQQHLLQLTVWGIKQLQARVLAVERYLKDQQLEIWDNMTWMEWEREINNYTDIIYSLIEESQNQQEKNE
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> CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1

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IVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSL
AEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQWFYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHF
PNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRAMYAPPIA
GNITCRSNITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFLGF
LGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLIC
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> CH0848.3.D0836.10.31CHIM.6R.SOSIP.664V4.1

MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEAKTTLFCASDAKAYKKKVHNVWATHACVPTDPSPQELFLK
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IVPLNNETSNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
LAEKGIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQWFYATGDIIGDIRQAHCNISESKWNETLQKVGKELQK
HFPNKTIKYAQSAGGDMEITTHSFNCGGEFFYCNTAKLFNGTYNGTDISTNSSTNSNPTITLQCRIKQIINMWQGVGRAMYAP
PIAGNITCKSNITGLLLTRDGGTNSSGKEEIFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVF
LGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGK
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> CH0848.3.D0358.80.06CHIM.6R.SOSIP.664V4.1

Figure 45 continued

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EYALFYKPDVVPLNETSNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNNKTFNGTGPCSNVSTVQCTHGIRPVV
STQLLLNGSLAEKEIVIRSENLTNNAKIIIVHLNTSVEIVCTRPGNNTRKSVRIGPGQWFYATGDIIGDIRQAHCNISEGQWNKTLH
EVSKELQKHFPNKTIKYERSAGGDMEIATHSFNCGGEFFYCNTSNLFNGTYNGTYINTSSTSYITLQCRIKQIINMWQGVGRAM
YAPPIAGNITCKSNITGLLLTRDGGTKNNSNEETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGI
GAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWG
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>CH848.3.D1432.5.41CHIM.6R.SOSIP.664V4.1

MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEAKTTLFCASDAKAYKKKVHNVWATHACVPTDPSPQELFLK
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KEKKEYALFYRPDIVPLNNETGNISEYRLINCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGI
RPVVSTQLLLNGSLAKEEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQWFYATGDIIGDPRKAHCNISEKDW
NKTLQEVGKELQKHFPNKTIRYNQSAGGDMEITTHSFNCGGEFFYCNTSKLFNSTYNDTYISTNSSANNSSTITLQCRIKQIINM
WQGVGRAMYAPPIAGNITCKSNITGLLLTRDGGPDSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGR
RRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLR
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>CH848.3.D0526.25.02CHIM.6R.SOSIP.664V4.1

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NVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICSNATVNNRTAYDTRSNVNVTSINNTIMGEMKNCSFNT
TTEIRDKEKKEYALFYKPDIVPLNETSNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNNETFNGTGPCSNVSTVQ
CTHGIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAKIIIVHLNTSVEIVCTRPGNNTRKSVRIGPGQWFYATGDIIGDIRQAHCNISE
KQWNETLQKVGKELQKHFPNKTIKYERSAGGDMEIATHSFNCGGEFFYCNTSKLFNGTYNGTDINISTNSNSTITLQCRIKQIIN
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GRRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERY
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>CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1_GT1

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VPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSL
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LGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEPQQHLLKDTHWGIKQLQARVLAVEHYLRDQQLLGIWGCSGKLIC
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Figure 45 continued

> CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N332A

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LSETNNTSEYRLINCNTSACTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEK
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TIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPPIAGNIT
CRSNITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFLGFLGAA
GSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNV
PWNSSWSNRNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALDGS*

>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N301A

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LSETNNTSEYRLINCNTSACTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEK
EIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNANTRKSVRIGPGQTFYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNK
TIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPPIAGNIT
CRSNITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFLGFLGAA
GSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNV
PWNSSWSNRNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALDGS*

> CH848.3.D0949.10.17chim.6R.DS.SOSIP.664

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LSETNNTSEYRLINCNTSACTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEK
EIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNK
TIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPPIAGNIT
CRSNITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFLGFLGAA
GSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNV
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> B.JRFL gp120core_mini-V3_v2

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QLKESVEINCTRPNNNTRPGEIIGDIRQAHCNISRAKWNDTLKQIVIKLREQFENKTIVFNHSSGGDPEIVMHSFNCGGEFFYCN

Figure 45 continued

STQLFNSTWNNNTEGSNNTEGNTITLPCRIKQIINMWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGINENGTEIFRPGGGD
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>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664

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LSETNNTSEYRLINCNTSACTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEK
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>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N301AN332A

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LSETNNTSEYRLINCNTSACTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEK
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GSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNV
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>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N301A

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TIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPPIAGNIT
CRSNITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFLGFLGAA
GSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNV
PWNSSWSNRNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD*

>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_V1A

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Figure 45 continued

CNTSACTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAK
IIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAGGDME
ITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPPIAGNITCRSNITGLLLTRDG
GTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLT
VQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLS
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> CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_V1B

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YRLINCNTSACTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRSENLT
NNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAG
GDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPPIAGNITCRSNITGLL
LTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFLGFLGAAGSTMGAA
SMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWS
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> CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_V1D

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QSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPPIAGNITCRSNI
TGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFLGFLGAAGSTM
GAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNS
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>CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1degly4

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IVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSL
AEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNDNTRKSVRIGPGQWFYATGDIIGDIKQAHCXHLRGEVERHPAEGGHRAAEA
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VRPPHRRQHHLPLQHHRPAADPRRRHQLQRDRDLPPRRRRHARQLALRAVQVQGGEDRAPGRGPHPLQAPRGGPPPPPPR
RGHRRRVPGLPGRRRLHHGRRLHDPDRAGPQPAVRHRAAAVQPAARPRGPAAPAEADRVGHQAAAGPRAGRGALPARPA
AAGHLGLLRQADLLHQRALELLLVQPQPVRDLGQHDLAAVGQGDLQLHPDHLRPAGGVPEPAGEERAGPAGPGLVSGRGS*

Figure 45 continued

>CH0848.3.D0949.10.17gp140C_degly4

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SPQELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTEIRDKEKKE
YALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVST
QLLLNGSLAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNDNTRKSVRIGPGQTFYATGDIIGDIKQAHCTISEEKWNDTLQKV
GIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRA
MYAPPIAGNITCRSNITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVEIQPLGIAPTGAKERVVEREKEAAGLGA
LFLGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAIEAQQHMLQLTVWGIKQLQARVLALERYLKDQQLLGMWGCS
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WYIK*

>B.JRFL gp140C_3QN301SN332T

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REQFENKTIVFNHSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNNNTEGSNNTEGNTITLPCRIKQIINMWQEVGKAMYA
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>B.JRFL gp120core_mini-V3_v2_degly

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TCTRPNDNTRPGEIIGDIRQAHCTISRAKWNDTLKQIVIKLREQFENKTIVFNHSSGGDPEIVMHSFNCGGEFFYCNSTQLFNST
WNNNTEGSNNTEGNTITLPCRIKQIINMWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGINENGTEIFRPGGGDMRDNWR
SELYKYKVVKIE**

Figure 46

HV1301263_V1A

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>HV1301263_V1B

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VTLICSNGSGKNCSFNTTTEIRDKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSACT

QACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLN

GSLAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQTFYATGDII

GDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFY

CNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPPIAGNITCR

SNITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVV

GRRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQH

LLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLSEIWD

NMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD*

Figure 46 (continued)

>HV1301263_V1D

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VTLICSNATGSGEMKNCSFNTTTEIRDKEKKEYALFYKPDIVPLSETNNTSEYRLINCNT

SACTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQ

LLLNGSLAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQTFYAT

GDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGG

EFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPPIAGN

ITCRSNITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCK

RRVVGRRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPE

AQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLS

EIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD*

Figure 47A

>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_C-SORTA
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AACCTGTGGGTGACCGTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCAAGACCACCCTGTTCTGCGCCTCCGACGCC
CGCGCCTACGAGAAGGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCTCCCCCCAGGAGCTG
GTGCTGGGCAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACCAGATGCACGAGGACATCATCTCC
CTGTGGGACCAGTCCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTGACCCTGATCTGCTCCAACGCCACCGTG
AAGAACGGCACCGTGGAGGAGATGAAGAACTGCTCCTTCAACACCACCACCGAGATCCGCGACAAGGAGAAGAAGGAG
TACGCCCTGTTCTACAAGCCCGACATCGTGCCCCTGTCCGAGACCAACAACACCTCCGAGTACCGCCTGATCAACTGC
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TACGCCATCCTGAAGTGCAACGACGAGACCTTCAACGGCACCGGCCCCTGCTCCAACGTGTCCACCGTGCAGTGCACC
CACGGCATCCGCCCCGTGGTGTCCACCCAGCTGCTGCTGAACGGCTCCCTGGCCGAGAAGGAGATCGTGATCCGCTCC
GAGAACCTGACCAACAACGCCAAGATCATCATCGTGCACCTGCACACCCCCGTGGAGATCGTGTGCACCCGCCCCAAC
AACAACACCCGCAAGTCCGTGCGCATCGGCCCCGGCCAGACCTTCTACGCCACCGGCGACATCATCGGCGACATCAAG
CAGGCCCACTGCAACATCTCCGAGGAGAAGTGGAACGACACCCTGCAGAAGGTGGGCATCGAGCTGCAGAAGCACTTC
CCCAACAAGACCATCAAGTACAACCAGTCCGCCGGCGGCGACATGGAGATCACCACCCACTCCTTCAACTGCGGCGGC
GAGTTCTTCTACTGCAACACCTCCAACCTGTTCAACGGCACCTACAACGGCACCTACATCTCCACCAACTCCTCCGCC
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>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_C-SORTA
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Figure 47A continued

>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N-SORTA

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GCCTACGAGAAGGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCCACCGACCCCTCCCCCCA
GGAGCTGGTGCTGGGCAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACCAGATGC
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CACCACCACCGAGATCCGCGACAAGGAGAAGAAGGAGTACGCCCTGTTCTACAAGCCCGACATCGTGC
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GCCTGCCCCAAGGTGACCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCGCCGGCTACGCCATCCT
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CGTGTGCACCCGCCCCAACAACAACACCCGCAAGTCCGTGCGCATCGGCCCCGGCCAGACCTTCTACG
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ACCCTGCAGAAGGTGGGCATCGAGCTGCAGAAGCACTTCCCCAACAAGACCATCAAGTACAACCAGTC
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TCCGGCATCGTGCAGCAGCAGTCCAACCTGCTGCGCGCCCCCGAGGCCCAGCAGCACCTGCTGAAGCT
GACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGCTGGCCGTGGAGCGCTACCTGCGCGACCAGC
AGCTGCTGGGCATCTGGGGCTGCTCCGGCAAGCTGATCTGCTGCACCAACGTGCCCTGGAACTCCTCC
TGGTCCAACCGCAACCTGTCCGAGATCTGGGACAACATGACCTGGCTGCAGTGGGACAAGGAGATCTC
CAACTACACCCAGATCATCTACGGCCTGCTGGAGGAGTCCCAGAACCAGCAGGAGAAGAACGAGCAGG
ACCTGCTGGCCCTGGACTAG

>CH848.3.D0949.10.17chim.6R.DS.SOSIP.664_N-SORTA

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GTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFLG
FLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERY
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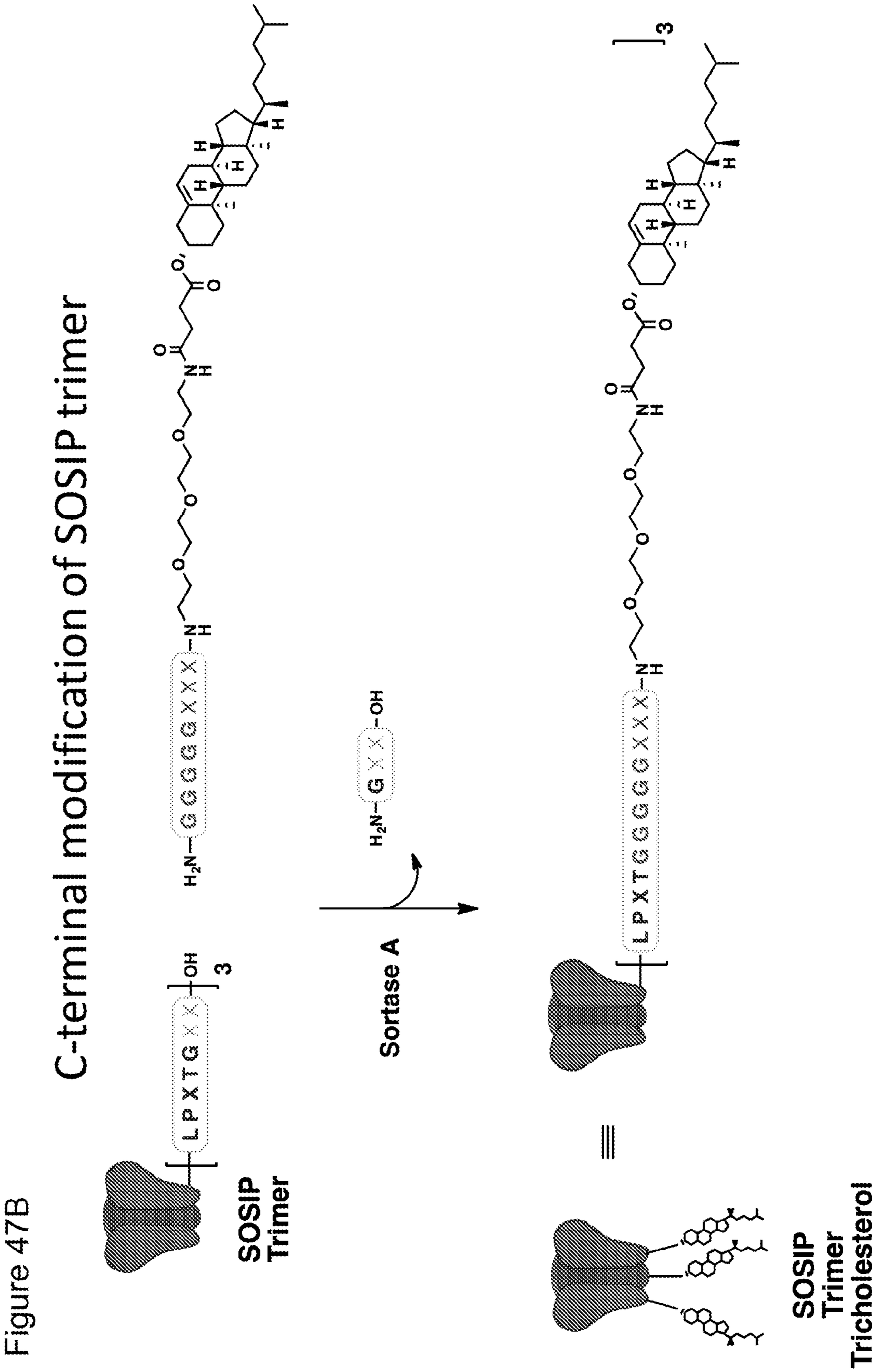

C-terminal modification of SOSIP trimer
L P X T G X X
OH
3
Sortase A
H2N
G G G G G X X X
SOSIP
Trimer
H2N
G X X
OH
L P X T G G G G X X X
N
H
3
SOSIP
Trimer
Tricholesterol

Figure 47B

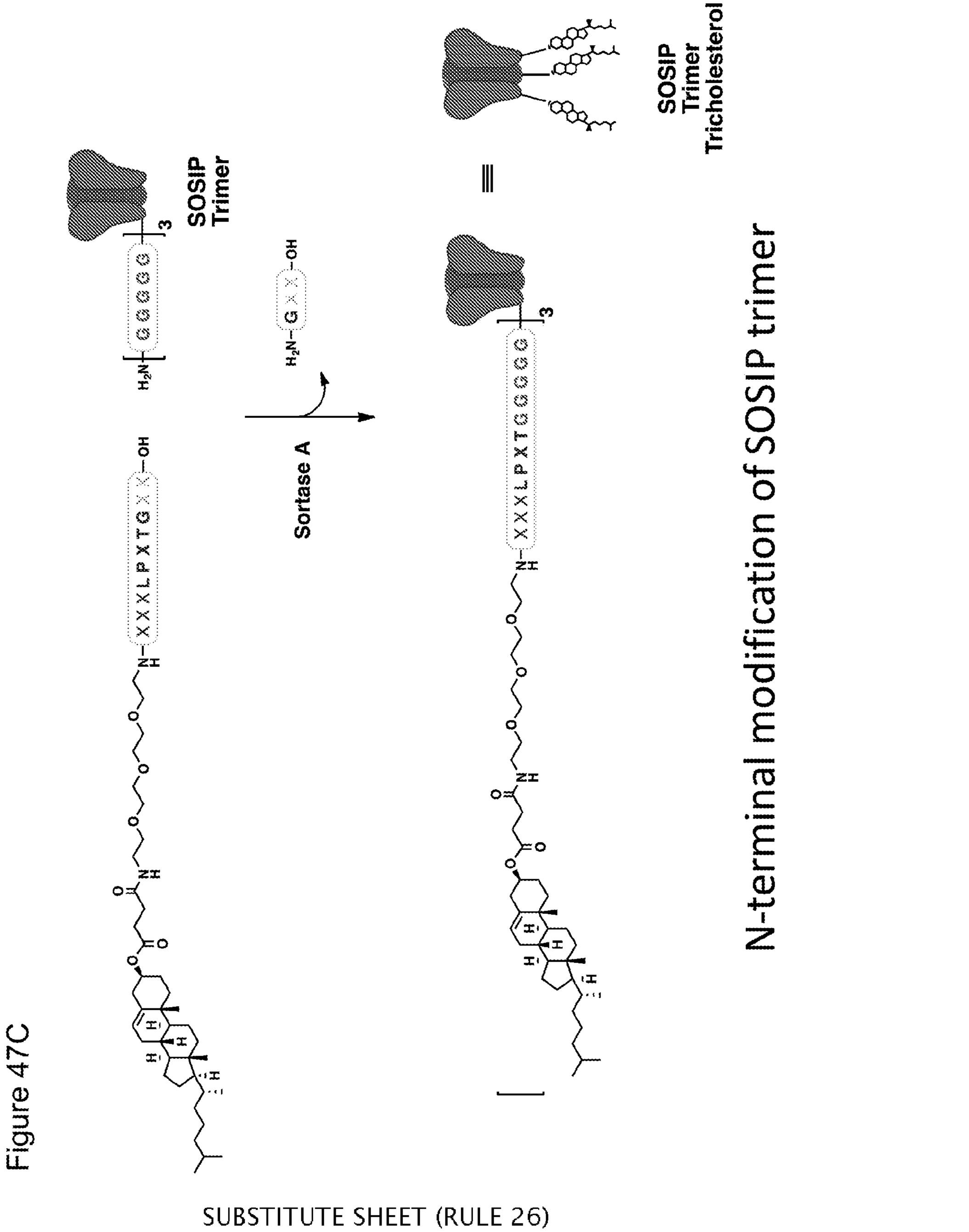

SOSIP trimer
N-terminal modification of
SOSIP
Trimer
Tricholesterol
SOSIP
Trimer
Sortase A
H2N
OH
XXXLPXTGXX
XXXLPXTGGGG
3

Figure 47C

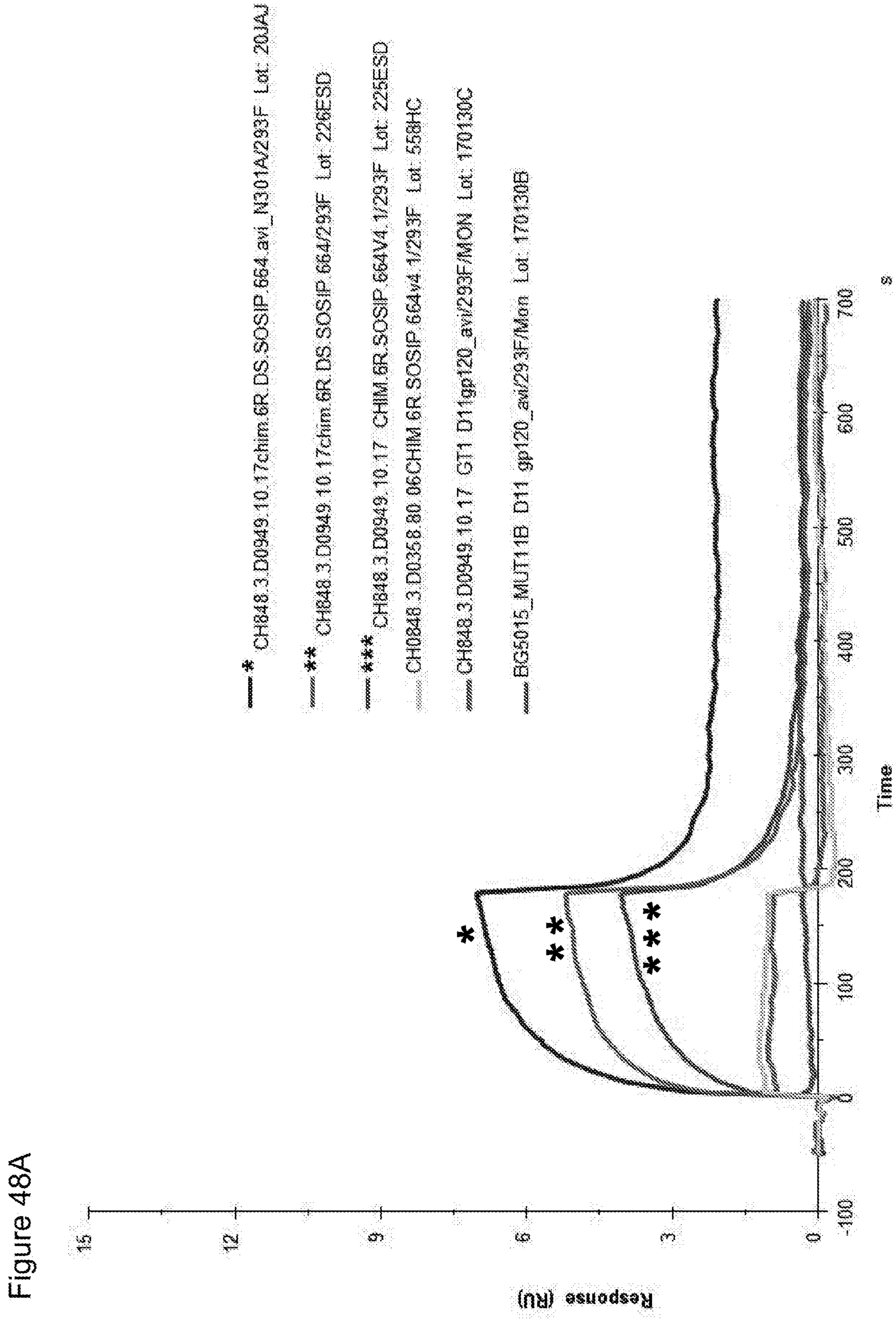

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CH0848.3.D0358.80.06CHIM.6R.SOSIP.664v4.1/293F Lot: 558HC
CH848.3.D0949.10.17 GT1.D11gp120_avi/293F/MON Lot: 170130C
BG5015_MUT11B D11 gp120_avi/293F/Mon Lot: 170130B
*
**
***
Response (RU)
Time
15
12
9
6
3
0
-100
0
100
200
300
400
500
600
700
s

Figure 48A

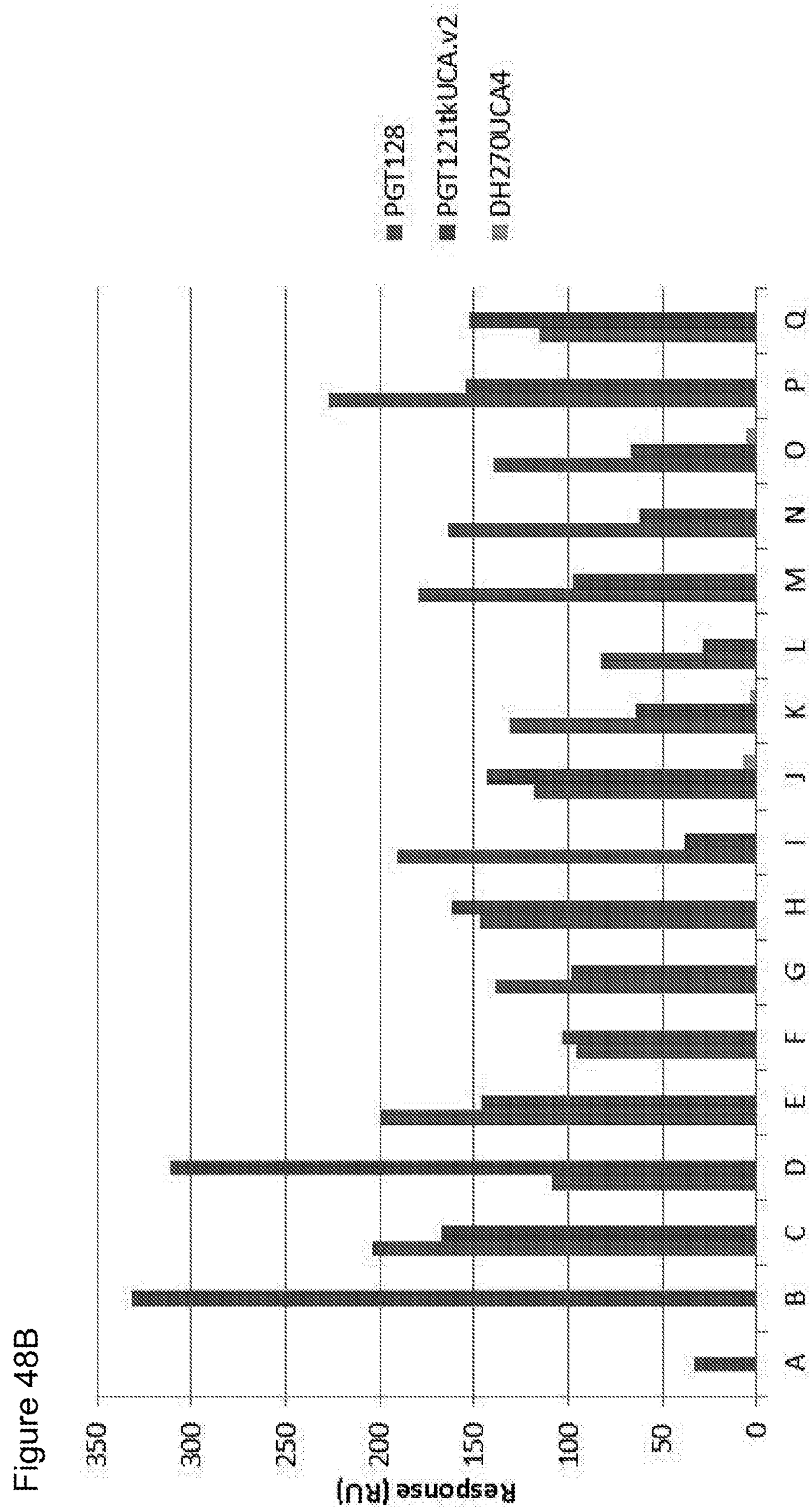

PGT128
PGT121tkJCA.v2
DH270JCA4
A
B
C
D
E
F
G
H
I
J
K
L
M
N
O
P
Q
0
50
100
150
200
250
300
350
Response (RU)

Figure 48B

>HV1301331 N133DN138T,CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 N133DN138T

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NVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLC
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NCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPV
VSTQLLLNGSLAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQW
FYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAGGDMEITTHSF
NCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRAMYAPP
IAGNITCRSNITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAP
TRCKRRVVGRRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLL
RAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD**

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                                    1                                                 50
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (1)  MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEAKTTLFCAS
                HV1301331_N133DN138T       (1)  MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEAKTTLFCAS
                           Consensus       (1)  MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEAKTTLFCAS
                                   51                                                100
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (51) DARAYEKKVHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHE
                HV1301331_N133DN138T       (51) DARAYEKKVHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHE
                           Consensus       (51) DARAYEKKVHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHE
                                  101                                                150
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (101) DIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTEIR
                HV1301331_N133DN138T       (101) DIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTEIR
                           Consensus       (101) DIISLWDQSLKPCVKLTPLCVTLICS ATVK GTVEEMKNCSFNTTTEIR
                                  151                                                200
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (151) DKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIP
                HV1301331_N133DN138T       (151) DKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIP
                           Consensus       (151) DKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIP
                                  201                                                250
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (201) IHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
                HV1301331_N133DN138T       (201) IHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
                           Consensus       (201) IHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
                                  251                                                300
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (251) LAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQW
                HV1301331_N133DN138T       (251) LAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQW
                           Consensus       (251) LAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQW
                                  301                                                350
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (301) FYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAG
                HV1301331_N133DN138T       (301) FYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAG
                           Consensus       (301) FYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAG
                                  351                                                400
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (351) GDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQC
                HV1301331_N133DN138T       (351) GDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQC
                           Consensus       (351) GDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQC
                                  401                                                450
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (401) RIKQIINMWQGVGRAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETF
                HV1301331_N133DN138T       (401) RIKQIINMWQGVGRAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETF
                           Consensus       (401) RIKQIINMWQGVGRAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETF
                                  451                                                500
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (451) RPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIG
                HV1301331_N133DN138T       (451) RPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIG
                           Consensus       (451) RPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIG
                                  501                                                550
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (501) AVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLL
                HV1301331_N133DN138T       (501) AVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLL
                           Consensus       (501) AVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLL
                                  551                                                600
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (551) KLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
                HV1301331_N133DN138T       (551) KLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
                           Consensus       (551) KLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
                                  601                                                648
CH848.3.D0949.10.17chim.6R.SOSIP.664v4.1   (601) RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD
                HV1301331_N133DN138T       (601) RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD
                           Consensus       (601) RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD
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Figure 49A

>CH0848.3.d1305.10.19gp160

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>HV1301509, CH0848.3.d1305.10.19gp160

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TTGACCCCACTCTGTGTCACTTTAATTTGTAGTACTGCTACTGTTAACAATAGAGCAGTTGA
TGAAATGAAAAATTGCTCCTTCAATACAACCACAGAAATAAGAGATAAGAAAAAGAAGGAA
TATGCACTTTTTTTATAGATCTGATGTAGTACCACTTGATGAAACAAACAATACCAGTGAGTA
TAGATTAATAAATTGTAATACCTCAGCCGTAACACAAGCCTGTCCAAAGGTCACTTTTGAAC
CAATTCCTATACATTATTGTGCTCCAGCTGGTTATGCGATTCTAAAGTGCAATGATGAGACA
TTCAATGGAACAGGACCATGCAGTAATGTCAGCACAGTACAATGTACACATGGAATTAGGCC
AGTGGTATCAACCCAACTACTGTTAAATGGTAGTCTGGCAGAAAAAGAGATAGTAATTAGAT
CTGAAAACCTGACAAACAATGCCAAAATAATAATAGTCCATCTTCACACCCCTGTAGAAATT
GTGTGTACAAGGCCCGGCCATAATACAAGGAAAAGTGTGAGAATAGGCCCAGGACAAACATT
CTATGCAACAGGAGACATAATAGGAGATATAAGACAAGCACATTGTAACATTAATGAAAGTA
AATGGAATGAAACTTTACAAAAGGTAGGTATAGAATTGCAAAAACACTTCCCTAATAAGACA
ATAAAGTATAACCAATCCGCAGGAGGAGACATGGAAATTACAACACATAGCTTTAATTGTGG
AGGAGAATTTTTCTATTGCAATACATCAAAGCTGTTTAATAGTACATACAATGGTACATACA
TAAGTACAAACAGCACAAACAGTACTTCATACATCACGCTTCAATGCAGAATAAAACAAATT
ATAAACATGTGGCAGGGGGTAGGAAGAGCAATGTATGCTCCTCCCATTGCAGGAAACATAAC
ATGTAGATCAAATATCACAGGGCTACTATTGACACGTGATGGAGGGATCAATAATGTTAGCA
ACGAGACAGAGACATTCAGGCCTGCAGGAGGAGATATGAGGGATAATTGGAGAAGTGAATTA
TATAAATATAAAGTAGTAGAAGTTCAGCCATTAGGAATAGCACCAACTGGTGCAAAAAGGAG
AGTGGTGGAGAGAGAAAAAAGAGCAGCAGGACTAGGAGCTTTGTTCCTTGGGTTCTTGGGAG
CAGCAGGAAGCACTATGGGCGCAGCATCAATAACGCTGACGGTACAGGCCAGACAATTGTTG
TCTGGTATAGTGCAACAGCAAAGCAATTTGCTGAGGGCTATAGAGGCGCAACAGCATATGTT
GCAACTCACGGTCTGGGGCATCAAGCAGCTCCAGGCAAGAGTCCTGGCTCTGGAAAGATACCT

Figure 49B

AAAGGATCAACAGCTCCTAGGGATGTGGGGCTGCTCTGGAAAACTCATCTGCACCACTAATG
TGCCTTGGAACACTAGTTGGAGTAATAAATCTGAAATGGATATTTGGAATAACATGACATGG
ATGCAGTGGGAAAGAGAAATTAGCAATTACACAGAGACAATATACATGTTGCTTGAAGACTC
GCAACGCCAGCAGGAGAGAAATGAAAAAGATTTACTAGCATTGGACAGTTGGAACAGTCTGT
GGAATTGGTTTAACATAACAAACTGGCTGTGGTATATAAAAATATTCATAATGATAGTAGGG
GGCTTGATAGGTTTAAGAATAGTTTTTGCTGTGCTATCTATAGTGAATAGAGTCAGGCAGGG
ATACTCACCTTTGTCGTTGCAGACCCTTACCCCAAACCCGAGGGAACCCGACAGGCTCAGAGG
AATCGAAGAAGAAGGTGGAGAGCAAGACAGAGACAGATCCATTCGATTAGTGAGCGGATTCT
TGCCAATTGTCTGGGACGACCTGCGGAGCCTGTGCCTCTTCAGTTACCACCGATTGAGAGACT
TTCTATTGCTGGCAGCGAGAGTGGTGGAACTTCTGGGACACAGCAGTCTCAGGGGACTGCAG
AGGGGGTGGGAAGTCCTTAAGTATCTGGGAAGTCTTGTGCAGTATTGGGGTCTGGAACTAAA
AAGGAGTGCTATTAGTCTTTTTGATACCCTAGCAATAGCAGTAGCTGAAGGAACAGATAGGA
TTATAGAATTAATACAAGGATTTTGTAGAGCTATCCGCAACATACCTACAAGAATAAGACAA
GGCTTTGAAGCATCTTTGCTATAATGATCTAGA

Figure 49B continued

>CH848.3.D1305.10.19ch.DS.SOSIP.664
MGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEAKTTLFCASDAKAYKKEVHNV
WATHACVPTDPSPQELFLENVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVT
LICSTATVNNRAVDEMKNCSFNTTTEIRDKKKKEYALFYRSDVVPLDETNNTSEYRLINC
NTSACTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVS
TQLLLNGSLAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPGHNTRKSVRIGPGQTFY
ATGDIIGDIRQAHCNINESKWNETLQKVGIELQKHFPNKTIKYNQSAGGDMEITTHSFNC
GGEFFYCNTSKLFNSTYNGTYISTNSTNSTSYITLQCRIKQIINMWQGVGRCMYAPPIAG
NITCRSNITGLLLTRDGGINNVSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPT
RCKRRVVGRRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLR
APEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNR
NLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD**

Figure 50A

>CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T
MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKDAETTLFCASDARAYEKKKRN
VWATHCCVPTDPSPQELVLGNVTENFNMWKNDMVDQMHTDIISLWDQSLKPCVKLTPLCVT
LICSDATVKTGTVEEMKNCSFNTTTELRDKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSA
VTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSL
AEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQWFYATGDIIGDIKQAHC
NISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTY
NGTYISTNSSANSTSTITLQCRIKQIINMWQRVGQAMYAPPIAGNITCRSNITGLLLTRDGGTNS
NETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFLGF
LGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPECQQHLLKLTVWGIKQLQARVLAVE
RYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLSEIWDNMTWLQWDKEISNYTQIIYGLL
EESQNQQEKNEQDLLALD**

>CH848.3.D0949.10.17SOFA.DS.chSOSIP
MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEAKTTLFCASDARAYEKEVH
NVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLC
VTLICSNATVKNGTVEEMKNCSFNTTTEIRDKEKKEYALFYKPDIVPISETNNTSEYRLI
NCNTSACTQACPKVTFEPIPIHYCAPAGYAILKCNNETFNGTGPCTNVSTVQCTHGIRPV
VSTQLLLNGSLAEKEIVIRSENLTNNAKIIIVHLNTSVEINCTRPNNNTRKSIRIGPGQT
FYATGDIIGDIKQAHCNISEAKWNDTLQNVSIELQKHFPNKTIKYNQSAGGDMEITTHSF
NCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPP
IAGNITCRSSITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAP
TRCKRRVVGRRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLL
RAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD**

>CH848.3.D0949.10.17SOFA.DS.chSOSIP_N133N138A
MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEAKTTLFCASDARAYEKEVH
NVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLC
VTLICSAATVKAGTVEEMKNCSFNTTTEIRDKEKKEYALFYKPDIVPISETNNTSEYRLI
NCNTSACTQACPKVTFEPIPIHYCAPAGYAILKCNNETFNGTGPCTNVSTVQCTHGIRPV
VSTQLLLNGSLAEKEIVIRSENLTNNAKIIIVHLNTSVEINCTRPNNNTRKSIRIGPGQT
FYATGDIIGDIKQAHCNISEAKWNDTLQNVSIELQKHFPNKTIKYNQSAGGDMEITTHSF
NCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPP
IAGNITCRSSITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAP
TRCKRRVVGRRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLL
RAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD**

Figure 50B

>JRFL_SOSIPv6_V1_PNGS (removed V1 glycosylation sites except N156)
MGSLQPLATLYLLGMLVASCLGVEKLWVTVYYGVPVWKEACTTLFCASDAKAYDTKVRNV
WATHCCVPTDPNPQEVVLENVTEHFNMWKNNMVEQMQEDIISLWDQSLKPCVKLTPLCVT
LNCKDVKATSTTSDSEGTMERGEIKNCSFNITTSIRDKVQKEYALFYKLDVVPIDNNNTS
YRLISCDTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKTFNGKGPCKNVSTVQCTHG
IRPVVSTQLLLNGSLAEEEVVIRSDNFTNNAKTIIVQLKESVEINCTRPNNNTRKSIHIG
PGRWFYTTGEIIGDIRQAHCNISRAKWNDTLKQIVIKLREQFENKTIVFNHSSGGDPEIV
MHSFNCGGEFFYCNSTQLFNSTWNNNTEGSNNTEGNTITLPCRIKQIINMWQEIGKAMYA
PPIRGQIRCSSNITGLLLTRDGGINENGTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGV
APTKCKRRVVGRRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARQLLSGIVQQQNN
CLRAPECQQRMLQLTVWGIKQLQARVLAVERYLGDQQLLGIWGCSGKLICCTAVPWNASW
SNKSLDRIWNNMTWMEWEREIDNYTSEIYTLIEESQNQQEKNEQELLELD**

Figure 50C

>HV1301521(originally HV1301405_N130D_N135K_N138S_N141S)CON-Schim.6R.DS.SOSIP.664_OPT_N130D_N135K_N138S_N141S
MGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEANTTLFCASDAKAYDTEVHNVW
ATHACVPTDPNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLD
CTNVKVTSTTSNTEEKGEIKNCSFNITTEIRDKKQKVYALFYRLDVVPIDDNNNNSSNYRLINC
NTSACTQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGTGPCKNVSTVQCTHGIKPVVSTQLLL
NGSLAEEEIIIRSENITNNAKTIIVQLNESVEINCTRPNNNTRKSIRIGPGQAFYATGDIIGDIRQA
HCNISGTKWNKTLQQVAKKLREHFNNKTIIFKPSSGGDLEITTHSFNCRGEFFYCNTSGLFNST
WIGNGTKNNNNTNDTITLPCRIKQIINMWQGVGQCMYAPPIEGKITCKSNITGLLLTRDGGNN
NTNETEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFL
GFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLA
VERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLSEIWDNMTWLQWDKEISNYTQIIYG
LLEESQNQQEKNEQDLLALD**

>HV1301405_N138S_N141S;CON-Schim.6R.DS.SOSIP.664_OPT_N138S_N141S
MGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEANTTLFCASDAKAYDTEVHNV
WATHACVPTDPNPQEIVLENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVT
LNCTNVNVTSTTSNTEEKGEIKNCSFNITTEIRDKKQKVYALFYRLDVVPIDDNNNNSSN
YRLINCNTSACTQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGTGPCKNVSTVQCTHG
IKPVVSTQLLLNGSLAEEEIIIRSENITNNAKTIIVQLNESVEINCTRPNNNTRKSIRIG
PGQAFYATGDIIGDIRQAHCNISGTKWNKTLQQVAKKLREHFNNKTIIFKPSSGGDLEIT
THSFNCRGEFFYCNTSGLFNSTWIGNGTKNNNNTNDTITLPCRIKQIINMWQGVGQCMYA
PPIEGKITCKSNITGLLLTRDGGNNNTNETEIFRPGGGDMRDNWRSELYKYKVVKIEPLG
VAPTRCKRRVVGRRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQS
NLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSS
WSNRNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD**

Figure 50D

DHVI pjt20171030_Saunders_SOSIPv5.2.8
Use purchase number: PPF

Task 1: Gene synthesis of 1 gene including
SHIVSF162P3.5chim.6R.DS.SOSIP.664 per sequence below.

>T250-4CHIMSOSIPV5.2.8
GTCGACGCCACCATGCCTATGGGATCTCTGCAGCCTCTGGCCACACTGTACCTGCTGGGAATGCTGGTGGCTTCT
GTGCTGGCCGCCGAGAATCTGTGGGTCACAGTGTACTATGGCGTGCCCGTTTGGAGGGACGCCGAGACAACACTG
TTTTGTGCCTCCGACGCCAAGGGCTACGACACCAAGGCTAGAAACGTGTGGGCCACACACTGCTGCGTGCCCACA
GATCCTAGACCTCAAGAGATGTACCTGGAAAACGTGACCGAGAACTTCAACATGTGGAAGAACAGCATGGTCGAG
CAGATGCACACCGACATCATCAGCCTGTGGGACGAGAGCCTGAAGCCTTGCGTGAAGCTGACCCCTCTGTGCGTG
ACCCTGGATTGCCAGGCCTTCAATAGCAGCAGCCACACCAACAGCTCTATCGCCATGCAAGAGATGAAGAACTGC
AGCTTCAACGTGACCACCGAGCTGCGGGACAAGAAGAAGAAAGAGTACAGCTTCTTCTACAAGACCGACATTGAG
CAGATCAACAAGAACGGCCGGCAGTACCGGCTGATCAACTGCAACACAAGCGCCATCACACAGGCTTGCCCCAAG
GTGTCCTTCGAGCCTATTCCTATCCACTTCTGTGCCCCTGCCGGCTTCGCCATCCTGAAGTGCAATGAGAAGCAC
TTCAACGGCAAGGGCCCCTGCAAGAACGTGTCCACCGTGCAGTGTACCCACGGCATCAAGCCAGTGGTGTCTACC
CAGCTGCTGCTGAATGGCTCTCTGGCCGAAGAAGAGGTGGTCATCAGAGTGGAAAACACCATCGACAACGCCAAG
ACCATCATCGTGCAGCTGGCTAAGCCCGTGAAGATCAATTGCACCCGGCCTAACAACAACACCAGAAAGAGCATC
CGGATCGGCCCTGGCCAGTGGTTTTATGCCACCGGCGATATCATCGGCAACATCCGGAAGGCCTACTGCAATGTG
TCCAAGAGAGAGTGGAACAATACCCTGCAGCAGGTCGCCGCTCAGCTGTCCAAGTCCTTCAACAATACCAAGATC
GTGTTCGAGAAGCACAGCGGAGGCGACCTGGAAGTGATCACCCACAGCTTTGTGTGTGGCGGCGAGTTCTTCTAC
TGTAACACCAGCGGCCTGTTCAACTCCACCTGGACCAACAGCACCTGGACAAACTCTACCACCGGCAGCAATGGC
ACCGAGAGCAACGACACCATCACTCTGCAGTGCGAGATCAAGCAGTTCATCAATATGTGGCAGCGCGTCGGCCAG
GCTATGTACGCTCCTCCTATTCCTGGCGTGATCAGATGCGAGAGCGACATCACAGGCCTGCTGCTCACAAGAGAT
GGCCCCAATAGCACCCAGAACGAGACATTCAGACCTGGCGGCGGAGACATGAGAGACAATTGGAGAAGCGAGCTG
TACAAGTACAAGGTGGTCAAGATCGAGCCCCTGGGCGTCGCACCTACACGGTGCAAGAGAAGAGTCGTGGGCCGT
CGTAGAAGGCGGAGAGCCGTTGGAATTGGCGCCGTGTTCCTGGGCTTTCTGGGAGCCGCTGGATCTACAATGGGC
GCTGCCAGCATGACCCTGACAGTGCAGGCAAGAAATCTGCTGAGCGGAATCGTCCAGCAGCAGAGCAACCTGCTG
AGAGCCCCTGAGTGTCAGCAGCACCTCCTGAAACTGACCGTGTGGGGAATCAAGCAGCTGCAGGCTAGAGTGCTG
GCTGTGGAAAGATACCTGCGGGACCAGCAGCTCCTCGGCATCTGGGGATGTTCTGGCAAGCTGATCTGCTGCACC
AACGTGCCCTGGAACAGCTCCTGGTCCAACAGAAACCTGAGCGAGATCTGGGACAACATGACCTGGCTGCAGTGG
GACAAAGAGATCAGCAACTACACCCAGATCATCTACGGCCTGCTGGAAGAGAGCCAGAACCAGCAAGAGAAAAAC
GAGCAGGACCTGCTGGCCCTGGACTGATAAGGATCC

>CH848.3.D0949.10.17CHIM.SOSIPV5.2.8
GTCGACGCCACCATGCCTATGGGATCTCTGCAGCCTCTGGCCACACTGTACCTGCTGGGAATGCTGGTGGCTTCT
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TTTTGCGCCTCCGATGCCAGAGCCTACGAGAAGAAAAAGCGGAACGTGTGGGCCACACACTGCTGCGTGCCAACC
GATCCATCTCCTCAAGAGCTGGTGCTGGGCAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGAC
CAGATGCACACCGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCTTGCGTGAAGCTGACCCCTCTGTGCGTG
ACCCTGATCTGCAGCAATGCCACCGTGAAGAACGGCACCGTGGAAGAGATGAAGAACTGCAGCTTCAACACCACC
ACCGAGCTGCGCGACAAAGAGAAGAAAGAGTACGCCCTGTTCTACAAGCCCGACATCGTGCCCCTGAGCGAGACA
AACAACACCAGCGAGTACCGGCTGATCAACTGCAACACCTCCGCCGTGACACAGGCTTGCCCCAAAGTGACCTTC
GAGCCCATTCCTATCCACTACTGTGCCCCTGCCGGCTACGCCATCCTGAAGTGCAACGACGAGACATTCAACGGC
ACAGGCCCCTGCTCCAATGTGTCCACCGTGCAGTGTACCCACGGCATCAGACCAGTGGTGTCTACCCAGCTGCTG
CTGAATGGAAGCCTGGCCGAGAAAGAAATCGTGATCAGAAGCGAGAACCTGACCAACAACGCCAAGATCATCATC
GTGCATCTGCACACCCCTGTGGAAATCGTGTGCACCCGGCCTAACAACAACACCCGGAAGTCTGTGCGGATCGGC
CCTGGCCAGTGGTTTTATGCCACCGGCGATATCATCGGCGACATCAAGCAGGCCCACTGCAACATCAGCGAGGAA
AAGTGGAACGACACCCTGCAGAAAGTGGGCATCGAGCTGCAGAAGCACTTCCCCAACAAGACCATCAAGTACAAC
CAGAGCGCTGGCGGCGACATGGAAATCACCACACACAGCTTCAATTGTGGCGGCGAGTTCTTCTACTGCAATACC
AGCAACCTGTTCAACGGGACCTACAATGGC

Figure 51

ACCTACATCAGCACCAACAGCAGCGCCAACTCCACCAGCACCATCACTCTGCAGTGCCGGATCAAGCAGATCATC
AATATGTGGCAGCGCGTTGGCCAGGCTATGTACGCCCCTCCTATCGCCGGCAACATCACCTGTCGGAGCAATATC
ACAGGCCTGCTGCTCACCAGAGATGGCGGCACCAATAGCAACGAGACAGAAACCTTCAGACCTGCCGGCGGAGAC
ATGAGAGACAATTGGAGAAGCGAGCTGTACAAGTACAAGGTGGTCAAGATCGAGCCCCTGGGCGTCGCACCTACA
CGGTGCAAGAGAAGAGTCGTGGGCCGTCGTAGAAGGCGGAGAGCCGTTGGAATTGGCGCCGTGTTCCTGGGCTTT
CTGGGAGCCGCTGGATCTACAATGGGCGCTGCCAGCATGACCCTGACAGTGCAGGCTAGAAATCTGCTGAGCGGC
ATCGTGCAGCAGCAGAGCAATCTGCTCAGAGCCCCTGAGTGCCAGCAGCATCTGCTGAAACTGACCGTGTGGGGA
ATCAAGCAGCTGCAGGCAAGAGTGCTGGCTGTGGAAAGATACCTGCGGGACCAGCAGCTCCTCGGCATCTGGGGA
TGTTCTGGCAAGCTGATCTGCTGCACCAACGTGCCCTGGAACAGCTCCTGGTCCAACCGGAATCTGTCCGAGATC
TGGGATAACATGACCTGGCTGCAGTGGGACAAAGAAATCAGCAACTACACCCAGATCATCTACGGCCTGCTGGAA
GAGAGCCAGAACCAGCAAGAGAAAAACGAGCAGGACCTGCTGGCCCTGGACTGATAAGGATCC

>WITOCHIM.SOSIPV5.2.8

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TTTTGTGCCTCCGACGCCAAGGCCTACGACACCAAGAAACGGAACGTGTGGGCCACACACTGCTGCGTGCCAACA
GACCCCAATCCTCAAGAGGTGGTCATGGGCAACGTGACCGAGGACTTCAACATGTGGAAGAACAACATGGTCGAG
CAGATGCACACCGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCTTGCGTGAAGCTGACCCCTCTGTGTGTG
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AAGAACTGCAGCTTCAACACCACCACCGTGCTGCGGGACAAGATCCAGAAAGAGTACGCCCTGTTCTACAAGCTG
GACATCGTGCCCATCGAGGGCAAGAACACCAACACCGGCTACCGGCTGATCAACTGCAACACCAGCGTGATCACC
CAGGCCTGTCCTAAGGTGTCCTTCGAGCCCATTCCTATCCACTACTGTGCCCCTGCCGGCTTCGCCATCCTGAAG
TGCAACAACAAGACCTTCAACGGCAAGGGCCCCTGCAGAAACGTGTCCACCGTGCAGTGTACCCACGGCATCAAG
CCAGTGGTGTCTACCCAGCTGCTGCTGAATGGCTCTCTGGCCGAAGAGGATATCATCATCAGAAGCGAGAACTTC
ACCAACAACGGGAAGAACATCATCGTGCAGCTGAAAGAACCCGTGAAGATCAATTGCACCCGGCCTGGCAACAAC
ACCCGGCGGTCTATCAATATCGGCCCTGGCAGATGGTTCTACGCCACCGGCGCCATCATCGGCGATATCAGAAAG
GCCCACTGCAACATCTCTACCGAGCAGTGGAACAACACACTGACCCAGATCGTGGACAAGCTGAGAGAGCAGTTC
GGCAACAAGACGATCATCTTCAACCAGAGCAGCGGAGGCGACCCCGAGGTTGTGATGCACACATTCAATTGTGGC
GGCGAGTTCTTCTACTGCAACAGCACCCAGCTGTTCAACTCCACCTGGTTCAACAACGGCACCAGCACCTGGAAT
AGCACCGCCGACAATATCACCCTGCCTTGCCGGATCAAGCAAGTGATCAATATGTGGCAGCGCGTCGGCCAGGCT
ATGTACGCCCCTCCTATCAGAGGCCAGATCGACTGCAGCAGCAACATCACCGGCCTGATCCTGACAAGAGATGGC
GGCAGCAACTCCAGCCAGAACGAGACATTCAGACCCGGCGGAGGCAACATGAAGGACAATTGGAGAAGCGAGCTG
TACAAGTACAAGGTGGTCAAGATCGAGCCCCTGGGCGTCGCACCTACACGGTGCAAGAGAAGAGTCGTGGGCCGT
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GCTGCCAGCATGACCCTGACAGTGCAGGCTAGAAATCTGCTGAGCGGCATCGTCCAGCAGCAGAGCAATCTGCTC
AGAGCCCCTGAGTGCCAGCAGCATCTGCTGAAACTGACCGTGTGGGGAATCAAGCAGCTGCAGGCAAGAGTGCTG
GCTGTGGAAAGATACCTGCGGGACCAGCAGCTCCTCGGCATCTGGGGATGTTCTGGCAAGCTGATCTGCTGCACC
AACGTGCCCTGGAACAGCTCCTGGTCCAACAGAAACCTGAGCGAGATCTGGGACAACATGACCTGGCTGCAGTGG
GACAAAGAGATCAGCAACTACACCCAGATCATCTACGGCCTGCTGGAAGAGAGCCAGAACCAGCAAGAGAAAAAC
GAGCAGGACCTGCTGGCCCTGGACTGATAAGGATCC

>ZM233CHIM.SOSIPV5.2.8

GTCGACGCCACCATGCCTATGGGATCTCTGCAGCCTCTGGCCACACTGTACCTGCTGGGAATGCTGGTGGCTTCT
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TTTTGTGCCTCCGACGCCAAGGCCTACGAGACAAAAAAACGCAGCGTGTGGGCCACTCACTGCTGCGTGCCAACC
GATCCTAATCCTCAAGAGATGGTGCTGGAAAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGAC
CAGATGCACACCGACGTGATCAGCATCTGGGACCAGAGCCTGAAGCCTTGCGTGAAGCTGACCCCTCTGTGCGTG
ACACTGGACTGCAGCACCTACAACAACACCCACAACATCAGCAAAGAGATGAAGATCTGCAGCTTCAATATGACC
ACCGAGCTGCGGGACAAGAAACGGAAAGTGAACGTGCTGTTCTACAAGCTGGACCTGGTGCCTCTGACCAACAGC
AGCAACACCACCAACTACAGACTGATCAGCTGCAACACCTCCACCATCACACAGGCTTGCCCCAAGGTGTCCTTC
GATCCCATTCCTATCCACTACTGTGCCCCTGCCGGCTACGCCATCCTGAAGTGCAACAACAAGACCTTCAACGGC
ACAGGCCCCTGCAACAACGTGTCCACCGTGCAGTGTACCCACGGCATCAAGCCAGTGGTGTCTACCCAGCTGCTG
CTGAATGGCTCTCTGGCCGAGGAAGAGATCATCATCAGATTCGAGAACCTGACCGACAACGTGAAGATCATTATC
GTGCAGCTGAACGAGACAATCAACATCACATGCACCCGGCCGAACAACAATACCAGAAAGAGCATCCGGATCGGC
CCTGGCCAGTGGTTTTATGCCACC

Figure 51 continued

GGCGAGATCGTGGGCAACATCAGAGAGGCCCACTGCAATATCAGCGCCAGCAAGTGGAACAAGACCCTGGAAAGA
GTGCGGACCAAGCTGAAAGAGCACTTCCCTAACAAGACCATCGAGTTCGAGCCCAGCTCTGGCGGCGACCTGGAA
ATCACCACACACAGCTTTAACTGTGGCGGCGAGTTCTTCTACTGTAACACCAGCGGCCTGTTCAACAGCGCCATC
AATGGCACCCTGACCAGCAATGTGACCCTGCCTTGCCGGATCAAGCAGATCATCAATATGTGGCAGAGAGAAGTC
GGCCAGGCTATGTACGCCCCTCCTATCGCCGGCAACATTACCTGCAAGAGCAACATCACCGGCCTGCTGCTCACC
AGAGATGGCGGAGAGAATAGCAGCTCCACCACCGAGACATTCAGACCCACAGGCGGCGACATGAAGAACAACTGG
CGGAGCGAGCTGTACAAGTACAAGGTGGTCAAGATCGAGCCCCTGGGCGTCGCACCAACACGGTGCAAGAGAAGA
GTCGTGGGCCGTCGTAGAAGGCGGAGAGCCGTTGGAATTGGCGCCGTGTTCCTGGGCTTTCTGGGAGCCGCTGGA
TCTACAATGGGCGCTGCCAGCATGACCCTGACAGTGCAGGCTAGAAATCTGCTGAGCGGCATTGTGCAGCAGCAG
AGCAACCTGCTGAGAGCCCCTGAGTGTCAGCAGCACCTCCTGAAACTGACCGTGTGGGGAATCAAGCAGCTGCAG
GCAAGAGTGCTGGCTGTGGAAAGATACCTGCGGGACCAGCAGCTCCTCGGCATCTGGGGATGTTCTGGCAAGCTG
ATCTGCTGCACCAACGTGCCCTGGAACAGCTCCTGGTCCAACAGAAACCTGAGCGAGATCTGGGATAACATGACC
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CAAGAGAAAAACGAGCAGGACCTGCTGGCCCTGGATGGATCC

>A.Q23_17CHIM.SOSIPV5.2.8

GTCGACGCCACCATGCCTATGGGATCTCTGCAGCCTCTGGCCACACTGTACCTGCTGGGAATGCTGGTGGCTTCT
GTGCTGGCCGCCGAGAATCTGTGGGTCACAGTGTACTATGGCGTGCCCGTTTGGAGGGACGCCGAGACAACACTG
TTTTGTGCCTCCGACGCCAAGGCCTACGAGACAAAGAAACGGAACGTGTGGGCCACACACTGCTGCGTGCCAACA
GACCCCAATCCTCAAGAGATCCACCTGGACAACGTGACCGAGAAGTTCAACATGTGGAAGAACAACATGGTCGAG
CAGATGCACACCGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCTTGCGTGAAGCTGACCCCTCTGTGTGTG
ACCCTGCACTGCACCAATGTGACCAGCGTGAACACCACCGGCGATAGAGAGGGCCTGAAGAACTGCAGCTTCAAC
ATGACCACCGAGCTGCGGGACAAGCGGCAGAAGGTGTACAGCCTGTTCTACCGGCTGGACATCGTGCCCATCAAC
GAGAATCAGGGCAGCGAGTACCGGCTGATCAACTGCAACACCAGCGCCATCACTCAGGCCTGTCCTAAGGTGTCC
TTCGAGCCCATTCCTATCCACTACTGTACCCCTGCCGGCTTCGCCATCCTGAAGTGCAAGGACGAGGGCTTCAAT
GGCACCGGCCTGTGCAAGAATGTGTCCACCGTGCAGTGTACCCACGGCATCAAGCCAGTGGTGTCTACCCAGCTG
CTGCTGAATGGAAGCCTGGCCGAGAAGAACATCACCATCAGAAGCGAGAATATCACCAACAACGCCAAGATCATC
ATCGTGCAGCTGGTGCAGCCCGTGACCATCAAGTGCATCAGACCCAACAACAACACCCGGAAGTCCATCAGAATC
GGCCCTGGCCAGTGGTTTTACGCCACCGGGGATATCATCGGCGACATCAGACAGGCCCACTGCAACGTGACACGG
TCCAGATGGAACAAGACCCTGCAAGAGGTGGCCGAAAAGCTGCGGACCTACTTCGGCAACAAGACCATCATCTTC
GCCAACAGCTCTGGCGGCGACCTGGAAATCACCACACACAGCTTCAATTGTGGCGGCGAGTTCTTCTACTGCAAT
ACCTCCGGCCTGTTCAACAGCACTTGGTACGTGAACAGCACCTGGAACGACACCGACAGCACCCAAGAGAGCAAC
GACACCATCACACTGCCCTGCCGGATCAAGCAGATCATCAATATGTGGCAGCGCGCAGGCCAGGCTATGTACGCT
CCTCCTATTCCTGGCGTGATCAAGTGCGAGAGCAACATCACAGGCCTGCTGCTCACAAGAGATGGCGGCAAGGAC
AACAACGTGAACGAAACCTTCAGACCCGGCGGAGGCGACATGAGAGACAATTGGAGAAGCGAGCTGTACAAGTAC
AAGGTGGTCAAGATCGAGCCCCTGGGCGTCGCACCTACACGGTGCAAGAGAAGAGTCGTGGGCCGTCGTAGAAGG
CGGAGAGCCGTTGGAATTGGCGCCGTGTTCCTGGGCTTTCTGGGAGCCGCTGGATCTACAATGGGCGCTGCCAGC
ATGACCCTGACAGTGCAGGCTAGAAATCTGCTGAGCGGCATCGTCCAGCAGCAGAGCAATCTGCTCAGAGCCCCT
GAGTGCCAGCAGCATCTGCTGAAACTGACCGTGTGGGGAATCAAGCAGCTGCAGGCAAGAGTGCTGGCTGTGGAA
AGATACCTGCGGGACCAGCAGCTCCTCGGCATCTGGGGATGTTCTGGCAAGCTGATCTGCTGCACCAACGTGCCC
TGGAACAGCTCCTGGTCCAACAGAAACCTGAGCGAGATCTGGGACAATATGACCTGGCTGCAGTGGGACAAAGAG
ATCAGCAACTACACCCAGATCATCTACGGCCTGCTGGAAGAGAGCCAGAACCAGCAAGAGAAAAACGAGCAGGAC
CTGCTGGCCCTGGACTGATAAGGATCC

>CM244CHIM.SOSIPV5.2.8

GTCGACGCCACCATGCCTATGGGATCTCTGCAGCCTCTGGCCACACTGTACCTGCTGGGAATGCTGGTGGCTTCT
GTGCTGGCCGCCGAGAATCTGTGGGTCACAGTGTACTATGGCGTGCCCGTTTGGAGGGACGCCGAGACAACACTG
TTTTGCGCCTCCGATGCCAAGGCTCACGAGACAAAGAAACGGAACGTGTGGGCCACACACTGCTGCGTGCCAACA
GACCCCAATCCTCAAGAGATCGACCTGGAAAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGTCGAG
CAGATGCAGACCGACGTGATCAGCCTGTGGGACCAGAGCCTGAAGCCTTGCGTGAAGCTGACCCCTCTGTGTGTG
ACCCTGCACTGCACCAACGCCAATCTGACCAAGGCCAACCTGACAAACGTGAACAACCGGACCAACGTGTCCAAC
ATCATCGGCAACATCACCGACGAAGTGCGGAACTGCAGCTTCAATATGACCACCGAGCTGCGGGACAAGAAACAG
AAGGTGCACGCCCTGTTCTACAAGCTGGACATCGTGCCCATCGAGGACAACAACGACAACAGCAAGTACCGGCTG
ATCAACTGCAACACCAGCGTGATCAAGCAGGCCTGTCCTAAGATCAGCTTCGACCCCATTCCTATCCACTACTGC
ACCCCTGCCGGCTACGCC

Figure 51 continued

ATCCTGAAGTGCAACGACAAGAATTTCAACGGCACAGGCCCCTGCAAGAACGTGTCCTCTGTGCAGTGTACCCAC
GGCATCAAGCCCGTGGTGTCTACACAGCTGCTGCTGAATGGCAGCCTGGCCGAGGAAGAGATCATCATCAGAAGC
GAGGACCTGACCAACAACGCCAAGACCATCATCGTGCACCTGAACAAGAGCGTGGTCATCAATTGCACCCGGCCT
AGCAACAACACCCGGACCAGCATCACAATCGGCCCTGGCCAGTGGTTCTACAGAACCGGCGATATCATCGGAGAC
ATCCGGAAGGCCTACTGCGAGATCAATGGCACCGAGTGGAACAAGGCCCTGAAGCAAGTGACAGAGAAGCTGAAA
GAGCACTTCAACAACAAGCCCATCATCTTCCAGCCTCCATCTGGCGGCGATCTGGAAATCACCATGCACCACTTC
AACTGCAGAGGCGAGTTCTTCTACTGCAATACCACCAGGCTGTTCAACAATACCTGTATCGCCAACGGCACCATC
GAGGGCTGCAACGGCAATATCACCCTGCCTTGCAAGATTAAGCAGATCATCAATATGTGGCAGCGCGCAGGCCAG
GCTATGTACGCCCCTCCTATCAGCGGCACAATCAACTGCGTGTCCAATATTACCGGCATCCTGCTGACCAGAGAT
GGCGGAGCCACCAACAACACAAACAACGAGACATTCAGACCCGGCGGAGGAAACATCAAGGACAACTGGCGGAGC
GAGCTGTACAAGTACAAGGTGGTCAAGATCGAGCCCCTGGGCGTCGCACCTACACGGTGCAAGAGAAGAGTCGTG
GGCCGTCGTAGAAGGCGGAGAGCCGTTGGAATTGGCGCCGTGTTCCTGGGCTTTCTGGGAGCCGCTGGATCTACA
ATGGGCGCTGCCAGCATGACCCTGACAGTGCAGGCTAGAAATCTGCTGAGCGGCATCGTGCAGCAGCAGAGCAAT
CTGCTCAGAGCCCCTGAGTGCCAGCAGCATCTGCTGAAACTGACCGTGTGGGGAATCAAGCAGCTGCAGGCAAGA
GTGCTGGCTGTGGAAAGATACCTGCGGGACCAGCAGCTCCTCGGCATCTGGGGATGTTCTGGCAAGCTGATTTGC
TGCACCAATGTGCCCTGGAACAGCAGCTGGTCCAACCGGAATCTGAGCGAGATCTGGGACAACATGACCTGGCTG
CAGTGGGACAAAGAGATCAGCAACTACACCCAGATCATCTACGGCCTGCTGGAAGAGAGCCAGAACCAGCAAGAG
AAAAACGAGCAGGACCTGCTGGCCCTGGATGGATCC

Task 2: Subclone the synthesized genes including, into into plasmid **HV10004** at unique SalI and BamHI sites (remove the original insert).

HV10004 plasmid is Kanamycin resistant and has been sent to GenScript and used in the order#165286 by GeneScript.

Task 3 template: CH848.3.D0949.10.17CHIM.SOSIPV5.2.8 in **HV10004** vector was previously produced by GenScript as item 1 of this order.

>CH848.3.D0949.10.17CHIM.SOSIPV5.2.8

GTCGACGCCACCATGCCTATGGGATCTCTGCAGCCTCTGGCCACACTGTACCTGCTGGGAATGCTGGTGGCTTCT
GTGCTGGCCGCCGAGAATCTGTGGGTCACAGTGTACTATGGCGTGCCCGTGTGGAAGGACGCCGAGACAACACTG
TTTTGCGCCTCCGATGCCAGAGCCTACGAGAAGAAAAAGCGGAACGTGTGGGCCACACACTGCTGCGTGCCAACC
GATCCATCTCCTCAAGAGCTGGTGCTGGGCAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGAC
CAGATGCACACCGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCTTGCGTGAAGCTGACCCCTCTGTGCGTG
ACCCTGATCTGCAGCAATGCCACCGTGAAGAACGGCACCGTGGAAGAGATGAAGAACTGCAGCTTCAACACCACC
ACCGAGCTGCGCGACAAAGAGAAGAAAGAGTACGCCCTGTTCTACAAGCCCGACATCGTGCCCCTGAGCGAGACA
AACAACACCAGCGAGTACCGGCTGATCAACTGCAACACCTCCGCCGTGACACAGGCTTGCCCCAAAGTGACCTTC
GAGCCCATTCCTATCCACTACTGTGCCCCTGCCGGCTACGCCATCCTGAAGTGCAACGACGAGACATTCAACGGC
ACAGGCCCCTGCTCCAATGTGTCCACCGTGCAGTGTACCCACGGCATCAGACCAGTGGTGTCTACCCAGCTGCTG
CTGAATGGAAGCCTGGCCGAGAAAGAAATCGTGATCAGAAGCGAGAACCTGACCAACAACGCCAAGATCATCATC
GTGCATCTGCACACCCCTGTGGAAATCGTGTGCACCCGGCCTAACAACAACACCCGGAAGTCTGTGCGGATCGGC
CCTGGCCAGTGGTTTTATGCCACCGGCGATATCATCGGCGACATCAAGCAGGCCCACTGCAACATCAGCGAGGAA
AAGTGGAACGACACCCTGCAGAAAGTGGGCATCGAGCTGCAGAAGCACTTCCCCAACAAGACCATCAAGTACAAC
CAGAGCGCTGGCGGCGACATGGAAATCACCACACACAGCTTCAATTGTGGCGGCGAGTTCTTCTACTGCAATACC
AGCAACCTGTTCAACGGGACCTACAATGGCACCTACATCAGCACCAACAGCAGCGCCAACTCCACCAGCACCATC
ACTCTGCAGTGCCGGATCAAGCAGATCATCAATATGTGGCAGCGCGTTGGCCAGGCTATGTACGCCCCTCCTATC
GCCGGCAACATCACCTGTCGGAGCAATATCACAGGCCTGCTGCTCACCAGAGATGGCGGCACCAATAGCAACGAG
ACAGAAACCTTCAGACCTGCCGGCGGAGACATGAGAGACAATTGGAGAAGCGAGCTGTACAAGTACAAGGTGGTC
AAGATCGAGCCCCTGGGCGTCGCACCTACACGGTGCAAGAGAAGAGTCGTGGGCCGTCGTAGAAGGCGGAGAGCC
GTTGGAATTGGCGCCGTGTTCCTGGGCTTTCTGGGAGCCGCTGGATCTACAATGGGCGCTGCCAGCATGACCCTG
ACAGTGCAGGCTAGAAATCTGCTGAGCGGCATCGTGCAGCAGCAGAGCAATCTGCTCAGAGCCCCTGAGTGCCAG
CAGCATCTGCTGAAACTGACCGTGTGGGGAATCAAGCAGCTGCA

Figure 51 continued

GGCAAGAGTGCTGGCTGTGGAAAGATACCTGCGGGACCAGCAGCTCCTCGGCATCTGGGGATGTTCTGGCAAGCT
GATCTGCTGCACCAACGTGCCCTGGAACAGCTCCTGGTCCAACCGGAATCTGTCCGAGATCTGGGATAACATGAC
CTGGCTGCAGTGGGACAAAGAAATCAGCAACTACACCCAGATCATCTACGGCCTGCTGGAAGAGAGCCAGAACCA
GCAAGAGAAAAACGAGCAGGACCTGCTGGCCCTGGACTGATAAGGATCC

Task 3: Using CH848.3.D0949.10.17CHIM.SOSIPV5.2.8 as a template, perform site directed mutagenesis to change:

The A to G at nucleotide position 391
The T to C at nucleotide position 393
The A to G at nucleotide positions 407

The final product should be named
CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T
and have the sequence indicated below between the SalI and BamHI sites in **HV10004** vector.

>CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T
GTCGACGCCACCATGCCTATGGGATCTCTGCAGCCTCTGGCCACACTGTACCTGCTGGGAATGCTGGTGGCTTCT
GTGCTGGCCGCCGAGAATCTGTGGGTCACAGTGTACTATGGCGTGCCCGTGTGGAAGGACGCCGAGACAACACTG
TTTTGCGCCTCCGATGCCAGAGCCTACGAGAAGAAAAAGCGGAACGTGTGGGCCACACACTGCTGCGTGCCAACC
GATCCATCTCCTCAAGAGCTGGTGCTGGGCAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGAC
CAGATGCACACCGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCTTGCGTGAAGCTGACCCCTCTGTGCGTG
ACCCTGATCTGCAGCGACGCCACCGTGAAGACCGGCACCGTGGAAGAGATGAAGAACTGCAGCTTCAACACCACC
ACCGAGCTGCGCGACAAAGAGAAGAAAGAGTACGCCCTGTTCTACAAGCCCGACATCGTGCCCCTGAGCGAGACA
AACAACACCAGCGAGTACCGGCTGATCAACTGCAACACCTCCGCCGTGACACAGGCTTGCCCCAAAGTGACCTTC
GAGCCCATTCCTATCCACTACTGTGCCCCTGCCGGCTACGCCATCCTGAAGTGCAACGACGAGACATTCAACGGC
ACAGGCCCCTGCTCCAATGTGTCCACCGTGCAGTGTACCCACGGCATCAGACCAGTGGTGTCTACCCAGCTGCTG
CTGAATGGAAGCCTGGCCGAGAAAGAAATCGTGATCAGAAGCGAGAACCTGACCAACAACGCCAAGATCATCATC
GTGCATCTGCACACCCCTGTGGAAATCGTGTGCACCCGGCCTAACAACAACACCCGGAAGTCTGTGCGGATCGGC
CCTGGCCAGTGGTTTTATGCCACCGGCGATATCATCGGCGACATCAAGCAGGCCCACTGCAACATCAGCGAGGAA
AAGTGGAACGACACCCTGCAGAAAGTGGGCATCGAGCTGCAGAAGCACTTCCCCAACAAGACCATCAAGTACAAC
CAGAGCGCTGGCGGCGACATGGAAATCACCACACACAGCTTCAATTGTGGCGGCGAGTTCTTCTACTGCAATACC
AGCAACCTGTTCAACGGGACCTACAATGGCACCTACATCAGCACCAACAGCAGCGCCAACTCCACCAGCACCATC
ACTCTGCAGTGCCGGATCAAGCAGATCATCAATATGTGGCAGCGCGTTGGCCAGGCTATGTACGCCCCTCCTATC
GCCGGCAACATCACCTGTCGGAGCAATATCACAGGCCTGCTGCTCACCAGAGATGGCGGCACCAATAGCAACGAG
ACAGAAACCTTCAGACCTGCCGGCGGAGACATGAGAGACAATTGGAGAAGCGAGCTGTACAAGTACAAGGTGGTC
AAGATCGAGCCCCTGGGCGTCGCACCTACACGGTGCAAGAGAAGAGTCGTGGGCCGTCGTAGAAGGCGGAGAGCC
GTTGGAATTGGCGCCGTGTTCCTGGGCTTTCTGGGAGCCGCTGGATCTACAATGGGCGCTGCCAGCATGACCCTG
ACAGTGCAGGCTAGAAATCTGCTGAGCGGCATCGTGCAGCAGCAGAGCAATCTGCTCAGAGCCCCTGAGTGCCAG
CAGCATCTGCTGAAACTGACCGTGTGGGGAATCAAGCAGCTGCAGGCAAGAGTGCTGGCTGTGGAAAGATACCTG
CGGGACCAGCAGCTCCTCGGCATCTGGGGATGTTCTGGCAAGCTGATCTGCTGCACCAACGTGCCCTGGAACAGC
TCCTGGTCCAACCGGAATCTGTCCGAGATCTGGGATAACATGACCTGGCTGCAGTGGGACAAAGAAATCAGCAAC
TACACCCAGATCATCTACGGCCTGCTGGAAGAGAGCCAGAACCAGCAAGAGAAAAACGAGCAGGACCTGCTGGCC
CTGGACTGATAAGGATCC

Task 4 template: CH848.3.D0949.10.17CHIM.SOSIPV5.2.8 in **HV10004** vector was previously produced by GenScript as item 1 of this order.

>CH848.3.D0949.10.17CHIM.SOSIPV5.2.8
GTCGACGCCACCATGCCTATGGGATCTCTGCAGCCTCTGGCCACACTGTACCTGCTGGGAATGCTGGTGGCTTCT
GTGCTGGCCGCCGAGAATCTGTGGGTCACAGTGTACTATGGCGTGCCCGTGTGGAAGGACGCCGAGACAACACTG
TTTTGCGCCTCCGATGCCAGAGCCTACGAGAAGAAAAAGCGGAACGTGTGGGCCACACACTGCTGCGTGCCAACC
GATCCA

Figure 51 continued

TCTCCTCAAGAGCTGGTGCTGGGCAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACCAGATG
CACACCGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCTTGCGTGAAGCTGACCCCTCTGTGCGTGACCCTG
ATCTGCAGCAATGCCACCGTGAAGAACGGCACCGTGGAAGAGATGAAGAACTGCAGCTTCAACACCACCACCGAG
CTGCGCGACAAAGAGAAGAAAGAGTACGCCCTGTTCTACAAGCCCGACATCGTGCCCCTGAGCGAGACAAACAAC
ACCAGCGAGTACCGGCTGATCAACTGCAACACCTCCGCCGTGACACAGGCTTGCCCCAAAGTGACCTTCGAGCCC
ATTCCTATCCACTACTGTGCCCCTGCCGGCTACGCCATCCTGAAGTGCAACGACGAGACATTCAACGGCACAGGC
CCCTGCTCCAATGTGTCCACCGTGCAGTGTACCCACGGCATCAGACCAGTGGTGTCTACCCAGCTGCTGCTGAAT
GGAAGCCTGGCCGAGAAAGAAATCGTGATCAGAAGCGAGAACCTGACCAACAACGCCAAGATCATCATCGTGCAT
CTGCACACCCCTGTGGAAATCGTGTGCACCCGGCCTAACAACAACACCCGGAAGTCTGTGCGGATCGGCCCTGGC
CAGTGGTTTTATGCCACCGGCGATATCATCGGCGACATCAAGCAGGCCCACTGCAACATCAGCGAGGAAAAGTGG
AACGACACCCTGCAGAAAGTGGGCATCGAGCTGCAGAAGCACTTCCCCAACAAGACCATCAAGTACAACCAGAGC
GCTGGCGGCGACATGGAAATCACCACACACAGCTTCAATTGTGGCGGCGAGTTCTTCTACTGCAATACCAGCAAC
CTGTTCAACGGGACCTACAATGGCACCTACATCAGCACCAACAGCAGCGCCAACTCCACCAGCACCATCACTCTG
CAGTGCCGGATCAAGCAGATCATCAATATGTGGCAGCGCGTTGGCCAGGCTATGTACGCCCCTCCTATCGCCGGC
AACATCACCTGTCGGAGCAATATCACAGGCCTGCTGCTCACCAGAGATGGCGGCACCAATAGCAACGAGACAGAA
ACCTTCAGACCTGCCGGCGGAGACATGAGAGACAATTGGAGAAGCGAGCTGTACAAGTACAAGGTGGTCAAGATC
GAGCCCCTGGGCGTCGCACCTACACGGTGCAAGAGAAGAGTCGTGGGCCGTCGTAGAAGGCGGAGAGCCGTTGGA
ATTGGCGCCGTGTTCCTGGGCTTTCTGGGAGCCGCTGGATCTACAATGGGCGCTGCCAGCATGACCCTGACAGTG
CAGGCTAGAAATCTGCTGAGCGGCATCGTGCAGCAGCAGAGCAATCTGCTCAGAGCCCCTGAGTGCCAGCAGCAT
CTGCTGAAACTGACCGTGTGGGGAATCAAGCAGCTGCAGGCAAGAGTGCTGGCTGTGGAAAGATACCTGCGGGAC
CAGCAGCTCCTCGGCATCTGGGGATGTTCTGGCAAGCTGATCTGCTGCACCAACGTGCCCTGGAACAGCTCCTGG
TCCAACCGGAATCTGTCCGAGATCTGGGATAACATGACCTGGCTGCAGTGGGACAAAGAAATCAGCAACTACACC
CAGATCATCTACGGCCTGCTGGAAGAGAGCCAGAACCAGCAAGAGAAAAACGAGCAGGACCTGCTGGCCCTGGAC
TGATAAGGATCC

Task 4: Using CH848.3.D0949.10.17CHIM.SOSIPV5.2.8 as a template, perform site directed mutagenesis to change:

The AA to GC at nucleotide position 871-872

The final product should be named CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N301A and have the sequence indicated below between the SalI and BamHI sites in **HV10004** vector.

>CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N301A
GTCGACGCCACCATGCCTATGGGATCTCTGCAGCCTCTGGCCACACTGTACCTGCTGGGAATGCTGGTGGCTTCT
GTGCTGGCCGCCGAGAATCTGTGGGTCACAGTGTACTATGGCGTGCCCGTGTGGAAGGACGCCGAGACAACACTG
TTTTGCGCCTCCGATGCCAGAGCCTACGAGAAGAAAAAGCGGAACGTGTGGGCCACACACTGCTGCGTGCCAACC
GATCCATCTCCTCAAGAGCTGGTGCTGGGCAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGAC
CAGATGCACACCGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCTTGCGTGAAGCTGACCCCTCTGTGCGTG
ACCCTGATCTGCAGCAATGCCACCGTGAAGAACGGCACCGTGGAAGAGATGAAGAACTGCAGCTTCAACACCACC
ACCGAGCTGCGCGACAAAGAGAAGAAAGAGTACGCCCTGTTCTACAAGCCCGACATCGTGCCCCTGAGCGAGACA
AACAACACCAGCGAGTACCGGCTGATCAACTGCAACACCTCCGCCGTGACACAGGCTTGCCCCAAAGTGACCTTC
GAGCCCATTCCTATCCACTACTGTGCCCCTGCCGGCTACGCCATCCTGAAGTGCAACGACGAGACATTCAACGGC
ACAGGCCCCTGCTCCAATGTGTCCACCGTGCAGTGTACCCACGGCATCAGACCAGTGGTGTCTACCCAGCTGCTG
CTGAATGGAAGCCTGGCCGAGAAAGAAATCGTGATCAGAAGCGAGAACCTGACCAACAACGCCAAGATCATCATC
GTGCATCTGCACACCCCTGTGGAAATCGTGTGCACCCGGCCTAACGCCAACACCCGGAAGTCTGTGCGGATCGGC
CCTGGCCAGTGGTTTTATGCCACCGGCGATATCATCGGCGACATCAAGCAGGCCCACTGCAACATCAGCGAGGAA
AAGTGGAACGACACCCTGCAGAAAGTGGGCATCGAGCTGCAGAAGCACTTCCCCAACAAGACCATCAAGTACAAC
CAGAGCGCTGGCGGCGACATGGAAATCACCACACACAGCTTCAATTGTGGCGGCGAGTTCTTCTACTGCAATACC
AGCAACCTGTTCAACGGGACCTACAATGGCACCTACATCAGCACCAACAGCAGCGCCAACTCCACCAGCACCATC
ACTCTGCAGTGCCGGATCAAGCAGATCATCAATATGTGGCAGCGCGTTGGCCAGGCTATGTACGCCCCTCCTATC
GCCGGCAACATCACCTGTCGGAGCAATATCACAGGCCTGCTGCTCACCAGAGATGGCGGCACCAATAGCAACGAG
ACAGAAACCTTCAGACCTGCCGGCGGAGACATGAGAGACAATTGGAGAAGCGAGCTGTACAAGTACAAGGTGGTC
AAGATCGAGCCCCTGGGCGTCGCACCTACACGGTGCAA

Figure 51 continued

GAGAAGAGTCGTGGGCCGTCGTAGAAGGCGGAGAGCCGTTGGAATTGGCGCCGTGTTCCTGGGCTTTCTGGGAGC
CGCTGGATCTACAATGGGCGCTGCCAGCATGACCCTGACAGTGCAGGCTAGAAATCTGCTGAGCGGCATCGTGCA
GCAGCAGAGCAATCTGCTCAGAGCCCCTGAGTGCCAGCAGCATCTGCTGAAACTGACCGTGTGGGGAATCAAGCA
GCTGCAGGCAAGAGTGCTGGCTGTGGAAAGATACCTGCGGGACCAGCAGCTCCTCGGCATCTGGGGATGTTCTGG
CAAGCTGATCTGCTGCACCAACGTGCCCTGGAACAGCTCCTGGTCCAACCGGAATCTGTCCGAGATCTGGGATAA
CATGACCTGGCTGCAGTGGGACAAAGAAATCAGCAACTACACCCAGATCATCTACGGCCTGCTGGAAGAGAGCCA
GAACCAGCAAGAGAAAAACGAGCAGGACCTGCTGGCCCTGGACTGATAAGGATCC

Figure 51 continued

>CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160
MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKDAETTLFCASDARAYEKKKRNVWATHCCVPTDPSP
QELVLGNVTENFNMWKNDMVDQMHTDIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTELR
DKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPC
SNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQW
FYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLF
NGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQRVGQAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETF
RPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQA
RNLLSGIVQQQSNLLRAPECQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALDKWASLWNWFDISNWLWYIKIFIMIVGG
LIGLRIVFAVLSVIHRVRQGYSPLSFQTHTPNPRGLDRPERIEEEDGEQDRGRSTRLVSGFLALAWDDLRSLCLF
CYHRLRDFILIAARIVELLGHSSLKGLRLGWEGLKYLWNLLAYWGRELKISAINLFDTIAIAVAEWTDRVIEIGQ
RLCRAFLHIPRRIRQGLERALL**

Figure 52A

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                                                1                                                  50
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8     (1) MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKDAETTLFCAS
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160     (1) MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKDAETTLFCAS
                                      Consensus     (1) MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKDAETTLFCAS
                                               51                                                 100
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8    (51) DARAYEKKKRNVWATHCCVPTDPSPQELVLGNVTENFNMWKNDMVDQMHT
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160    (51) DARAYEKKKRNVWATHCCVPTDPSPQELVLGNVTENFNMWKNDMVDQMHT
                                      Consensus    (51) DARAYEKKKRNVWATHCCVPTDPSPQELVLGNVTENFNMWKNDMVDQMHT
                                              101                                                 150
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8   (101) DIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTELR
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160   (101) DIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTELR
                                      Consensus   (101) DIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTELR
                                              151                                                 200
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8   (151) DKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIP
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160   (151) DKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIP
                                      Consensus   (151) DKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIP
                                              201                                                 250
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8   (201) IHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160   (201) IHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
                                      Consensus   (201) IHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
                                              251                                                 300
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8   (251) LAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQW
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160   (251) LAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQW
                                      Consensus   (251) LAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQW
                                              301                                                 350
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8   (301) FYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAG
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160   (301) FYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAG
                                      Consensus   (301) FYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAG
                                              351                                                 400
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8   (351) GDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQC
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160   (351) GDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQC
                                      Consensus   (351) GDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQC
                                              401                                                 450
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8   (401) RIKQIINMWQRVGQAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETF
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160   (401) RIKQIINMWQRVGQAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETF
                                      Consensus   (401) RIKQIINMWQRVGQAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETF
```

Figure 52B

```
                                          451                                                 500
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8  (451) RPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIG
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160  (451) RPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIG
                                  Consensus  (451) RPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIG
                                          501                                                 550
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8  (501) AVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPECQQHLL
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160  (501) AVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPECQQHLL
                                  Consensus  (501) AVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPECQQHLL
                                          551                                                 600
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8  (551) KLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160  (551) KLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
                                  Consensus  (551) KLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
                                          601                                                 650
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8  (601) RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD--
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160  (601) RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALDKW
                                  Consensus  (601) RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD
                                          651                                                 700
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8  (649) --------------------------------------------------
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160  (651) ASLWNWFDISNWLWYIKIFIMIVGGLIGLRIVFAVLSVIHRVRQGYSPLS
                                  Consensus  (651)
                                          701                                                 750
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8  (649) --------------------------------------------------
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160  (701) FQTHTPNPRGLDRPERIEEEDGEQDRGRSTRLVSGFLALAWDDLRSLCLF
                                  Consensus  (701)
                                          751                                                 800
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8  (649) --------------------------------------------------
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160  (751) CYHRLRDFILIAARIVELLGHSSLKGLRLGWEGLKYLWNLLAYWGRELKI
                                  Consensus  (751)
                                          801                                                 849
     CH848d949.10.17_N133DN138T_SOSIPv5.2.8  (649) ---------------------------------------------------
CH848d949.10.17_N133DN138T_SOSIPv5.2.8gp160  (801) SAINLFDTIAIAVAEWTDRVIEIGQRLCRAFLHIPRRIRQGLERALL--
                                  Consensus  (801)
```

Figure 52B continued

>CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T
MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKDAETTLF
CASDARAYEKKKRNVWATHCCVPTDPSPQELVLGNVTENFNMWKNDM
VDQMHTDIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNC
SFNTTTELRDKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVT
QACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTH
GIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAKIIIVHLHTPVEIVC
TRPNNNTRKSVRIGPGQWFYATGDIIGDIKQAHCNISEEKWNDTLQK
VGIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFN
GTYNGTYISTNSSANSTSTITLQCRIKQIINMWQRVGQAMYAPPIAG
NITCRSNITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKV
VKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAVFLGFLGAAGSTMGAA
SMTLTVQARNLLSGIVQQQSNLLRAPECQQHLLKLTVWGIKQLQARV
LAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLSEIWDNMT
WLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD**

Figure 53A

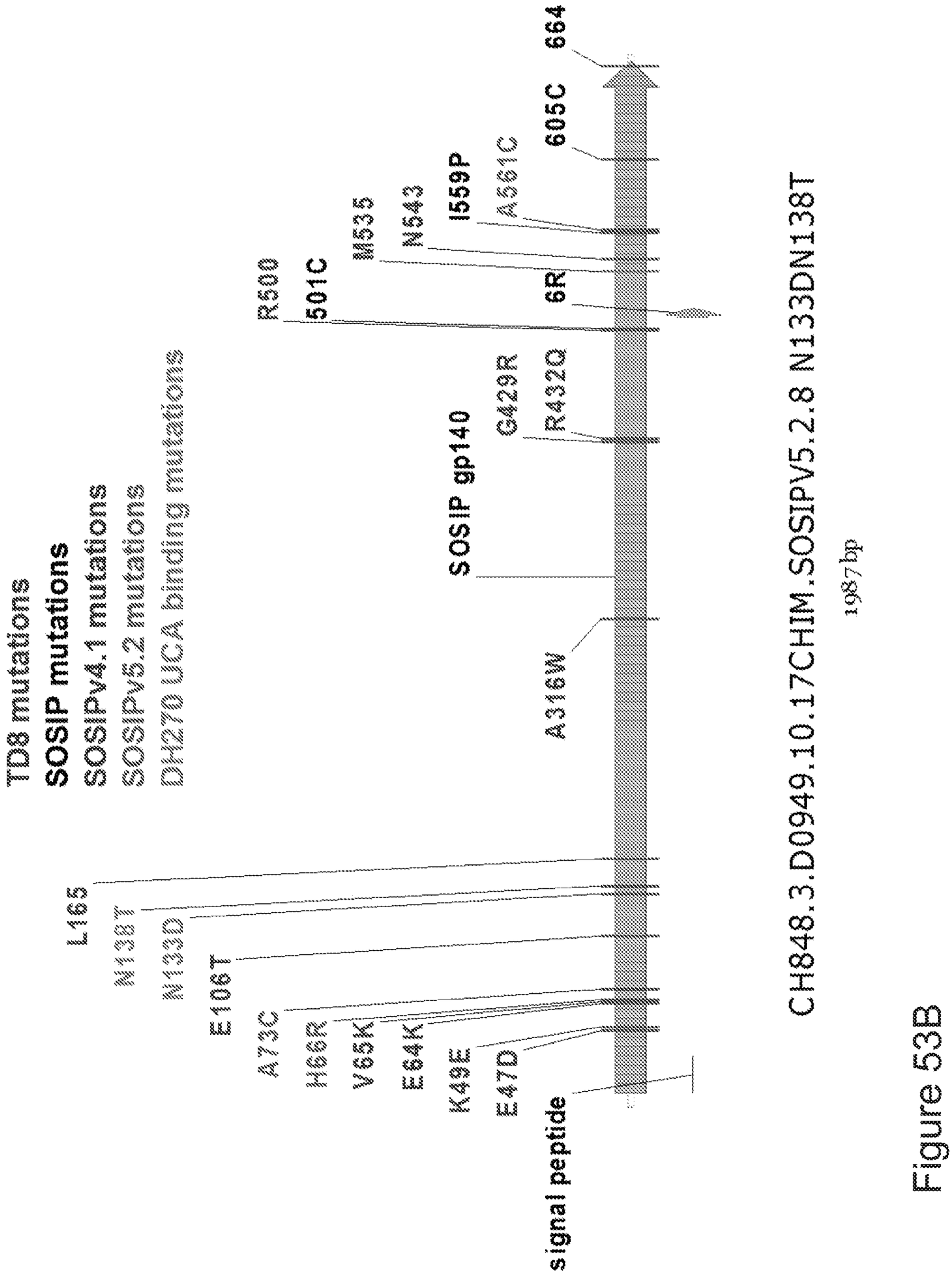

TD8 mutations
SOSIP mutations
SOSIPv4.1 mutations
SOSIPv5.2 mutations
CH848.3.D0949.10.17CHIM.SOSIPV5.2.8 N133DN138T
1987 bp
signal peptide
SOSIP gp140
L165
N133T
N133D
E106T
A75C
H66R
V65K
E64K
K49E
E47D
G429R
R432Q
A316W
R500
501C
M535
N543
I559P
A561C
6R
664

Figure 53B

Mutations to make v5.2.8

A501C-T605C
I559P
R6
664
I535M
L543N/Q
A316W
E64K
H66R
A73-A561C

L165
Q432
R429
K65
T106
E49
D47
R500

Figure 53C

```
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...    (1) ----------------------------AENLWVTVYYGVPVWKEAKTTLFCAS
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...    (1) ----------------------------AENLWVTVYYGVPVWKEAKTTLFCAS
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T     (1) MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKDAETTLFCAS
                                                Consensus (1)                          AENLWVTVYYGVPVWKEAKTTLFCAS
                                                               51                                                100

 CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...   (27) DARAYEKKVHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHE
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...    (27) DARAYEKKVHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHE
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T     (51) DARAYEKKKRNVWATHCCVPTDPSPQELVLGNVTENFNMWKNDMVDQMHT
                                                Consensus (51) DARAYEKKVHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHE
                                                              101                                               150

 CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...   (77) DIISLWDQSLKPCVKLTPLCVTLICSNATVKNGTVEEMKNCSFNTTTEIR
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...    (77) DIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTEIR
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T    (101) DIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTELR
                                                Consensus (101) DIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTEIR
                                                              151                                               200

 CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...   (127) DKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIP
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...    (127) DKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIP
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T    (151) DKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIP
                                                Consensus (151) DKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAVTQACPKVTFEPIP
                                                              201                                               250

 CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...   (177) IHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...    (177) IHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T    (201) IHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
                                                Consensus (201) IHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
                                                              251                                               300

 CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...   (227) LAEKEIVIRSENLTNNAKIIIVHLNTPVEIVCTRPNNNTRKSVRIGPGQW
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...    (227) LAEKEIVIRSENLTNNAKIIIVHLNTPVEIVCTRPNNNTRKSVRIGPGQW
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T    (251) LAEKEIVIRSENLTNNAKIIIVHLNTPVEIVCTRPNNNTRKSVRIGPGQW
                                                Consensus (251) LAEKEIVIRSENLTNNAKIIIVHLNTPVEIVCTRPNNNTRKSVRIGPGQW
                                                              301                                               350

 CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...   (277) FYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAG
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...    (277) FYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAG
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T    (301) FYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAG
                                                Consensus (301) FYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAG
                                                              351                                               400

 CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...   (327) GDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQC
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...    (327) GDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQC
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T    (351) GDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQC
                                                Consensus (351) GDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYISTNSSANSTSTITLQC
                                                              401                                               450
```

Figure 53D

SUBSTITUTE SHEET (RULE 26)

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CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...  (377) RIKQIINMWQGVGRAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETF
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...  (377) RIKQIINMWQGVGRAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETF
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T   (401) RIKQIINMWQRVGQAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETF
                                           Consensus   (401) RIKQIINMWQGVGRAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETF
                                                              451                                             500
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...  (427) RPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIG
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...  (427) RPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIG
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T   (451) RPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIG
                                           Consensus   (451) RPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIG
                                                              501                                             550
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...  (477) AVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLL
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...  (477) AVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLL
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T   (501) AVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPECQQHLL
                                           Consensus   (501) AVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLL
                                                              551                                             600
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...  (527) KLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...  (527) KLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T   (551) KLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
                                           Consensus   (551) KLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSN
                                                              601                                             650
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1 no signal...  (577) RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD---
CH848.3.D0949.10.17CHIM.6R.SOSIP.664V4.1N133DN138T...  (577) RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD---
      CH848.3.D0949.10.17CHIM.SOSIPV5.2.8_N133DN138T   (601) RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD---
                                           Consensus   (601) RNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD
```

Figure 53D continued

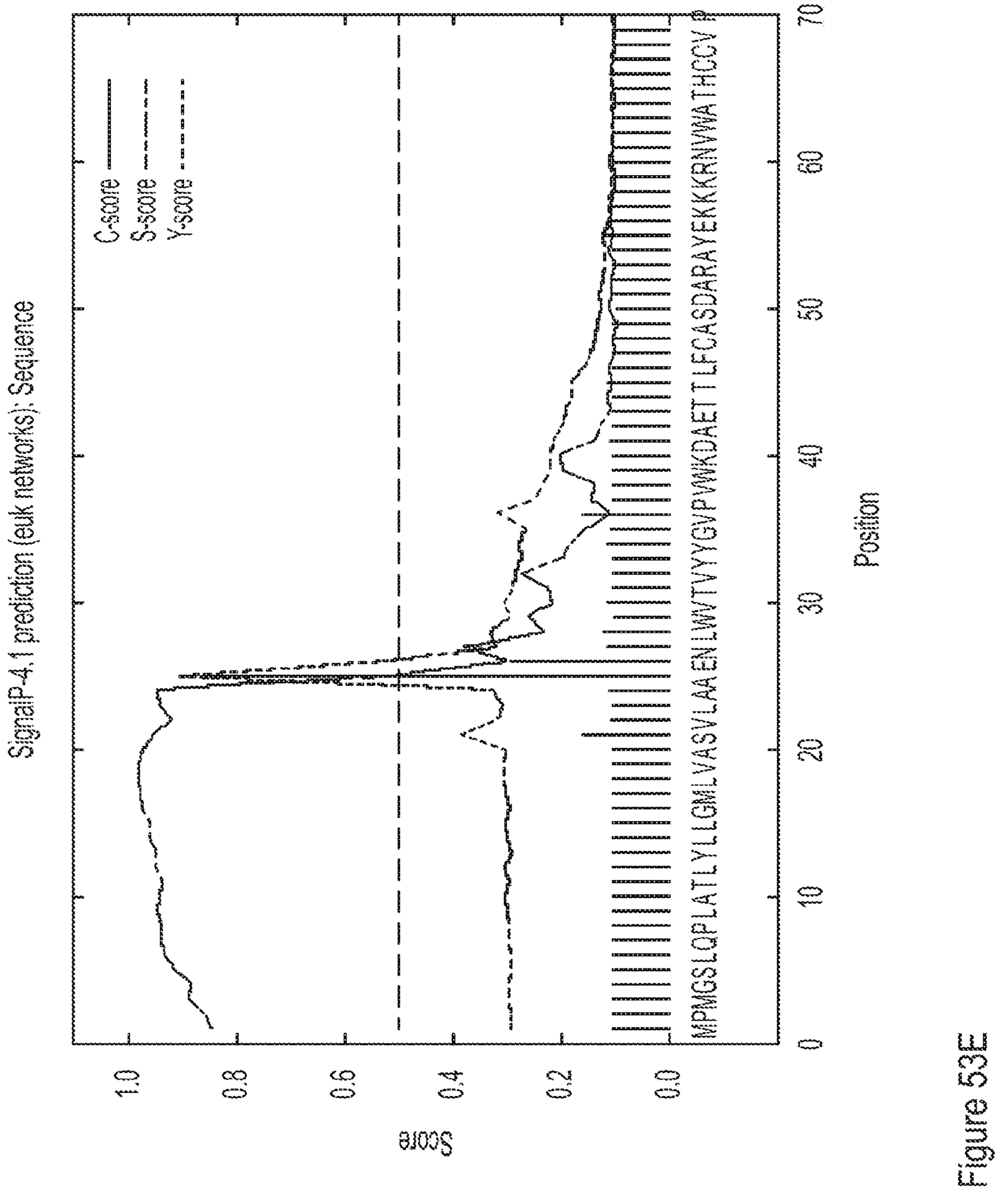

SignalP-4.1 prediction (euk networks): Sequence
C-score
S-score
Y-score
Score
Position
MPMGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKDAETTLFCASDARAYEKKRNVWATHACV
0
10
20
30
40
50
60
70
0.0
0.2
0.4
0.6
0.8
1.0

Figure 53E

1. CH848.3.D949.10.17_N133DN138T as a first generation .664 SOSIP

>CH848.3.D949.10.17_N133DN138TchimericSOSIP

MGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEAKTTLFCASDARAYEKEVHNVWA
THACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICS
DATVKTGTVEEMKNCSFNTTTEIRDKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAIT
QACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
LAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGDIK
QAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNL
FNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRAMYAPPIAGNITCRSNITGLLL
TRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVG
IGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQL
QARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLSEIWDNMTWLQWDKEISNY
TQIIYGLLEESQNQQEKNEQDLLALD**

>CH848.3.D949.10.17_N133DN138TSOSIP.664

MGSLQPLATLYLLGMLVASVLAKGKLWVTVYYGVPVWKEAKTTLFCASDARAYEKEVHNVWA
THACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICS
DATVKTGTVEEMKNCSFNTTTEIRDKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAIT
QACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
LAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGDIK
QAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNL
FNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRAMYAPPIAGNITCRSNITGLLL
TRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVEIQPLGIAPTGCKRRVVERRRRRRAAG
LGALFLGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAPEAQQHMLQLTVWGIKQL
QARVLALERYLKDQQLLGMWGCSGKLICCTNVPWNTSWSNKSETDIWDNMTWMQWEREISNY
TETIYKLLEDSQNQQERNEQDLLALD**

Figure 54A

2. CH848.3.D949.10.17_N133DN138T plus the disulfide that blocks CD4 induced conformational changes

>CH848.3.D949.10.17_N133DN138TchimericDS.SOSIP

MGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEAKTTLFCASDARAYEKEVHNVWA
THACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICS
DATVKTGTVEEMKNCSFNTTTEIRDKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSACT
QACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
LAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGDIK
QAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNL
FNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPPIAGNITCRSNITGLLL
TRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVG
IGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQL
QARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLSEIWDNMTWLQWDKEISNY
TQIIYGLLEESQNQQEKNEQDLLALD**

>CH848.3.D949.10.17_N133DN138TDS.SOSIP

MGSLQPLATLYLLGMLVASVLAKGKLWVTVYYGVPVWKEAKTTLFCASDARAYEKEVHNVWA
THACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVKLTPLCVTLICS
DATVKTGTVEEMKNCSFNTTTEIRDKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSACT
QACPKVTFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGS
LAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTRKSVRIGPGQTFYATGDIIGDIK
QAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNL
FNGTYNGTYISTNSSANSTSTITLQCRIKQIINMWQGVGRCMYAPPIAGNITCRSNITGLLL
TRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVEIQPLGIAPTGCKRRVVERRRRRRAAG
LGALFLGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAPEAQQHMLQLTVWGIKQL
QARVLALERYLKDQQLLGMWGCSGKLICCTNVPWNTSWSNKSETDIWDNMTWMQWEREISNY
TETIYKLLEDSQNQQERNEQDLLALD**

Figure 54B

3. CH848.3.D949.10.17_N133DN138T plus the disulfide that blocks CD4 induced conformational changes and Rich Wyatt's .8 mutations: D47, E49, K65, T106, L165, R429, Q432, R500

>CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP

MGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKDAETTLFCASDARAYEKEKHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQM
HTDIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTELRDKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSACTQACPKV
TFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTR
KSVRIGPGQTFYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYIST
NSSANSTSTITLQCRIKQIINMWQRVGQCMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVKIEPLGVAPTR
CKRRVVGRRRRRRAVGIGAVFLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLG
IWGCSGKLICCTNVPWNSSWSNRNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD**

>CH848.3.D949.10.17_N133DN138TTD8.DS.SOSIP.664

MGSLQPLATLYLLGMLVASVLAKGKLWVTVYYGVPVWKDAETTLFCASDARAYEKEKHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQM
HTDIISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTELRDKEKKEYALFYKPDIVPLSETNNTSEYRLINCNTSACTQACPKV
TFEPIPIHYCAPAGYAILKCNDETFNGTGPCSNVSTVQCTHGIRPVVSTQLLLNGSLAEKEIVIRSENLTNNAKIIIVHLHTPVEIVCTRPNNNTR
KSVRIGPGQTFYATGDIIGDIKQAHCNISEEKWNDTLQKVGIELQKHFPNKTIKYNQSAGGDMEITTHSFNCGGEFFYCNTSNLFNGTYNGTYIST
NSSANSTSTITLQCRIKQIINMWQRVGQCMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETFRPAGGDMRDNWRSELYKYKVVEIQPLGIAPTR
CKRRVVERRRRRRAAGLGALFLGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAPEAQQHMLQLTVWGIKQLQARVLALERYLKDQQLLG
MWGCSGKLICCTNVPWNTSWSNKSETDIWDNMTWMQWEREISNYTETIYKLLEDSQNQQERNEQDLLALD**

Figure 54C

SUBSTITUTE SHEET (RULE 26)

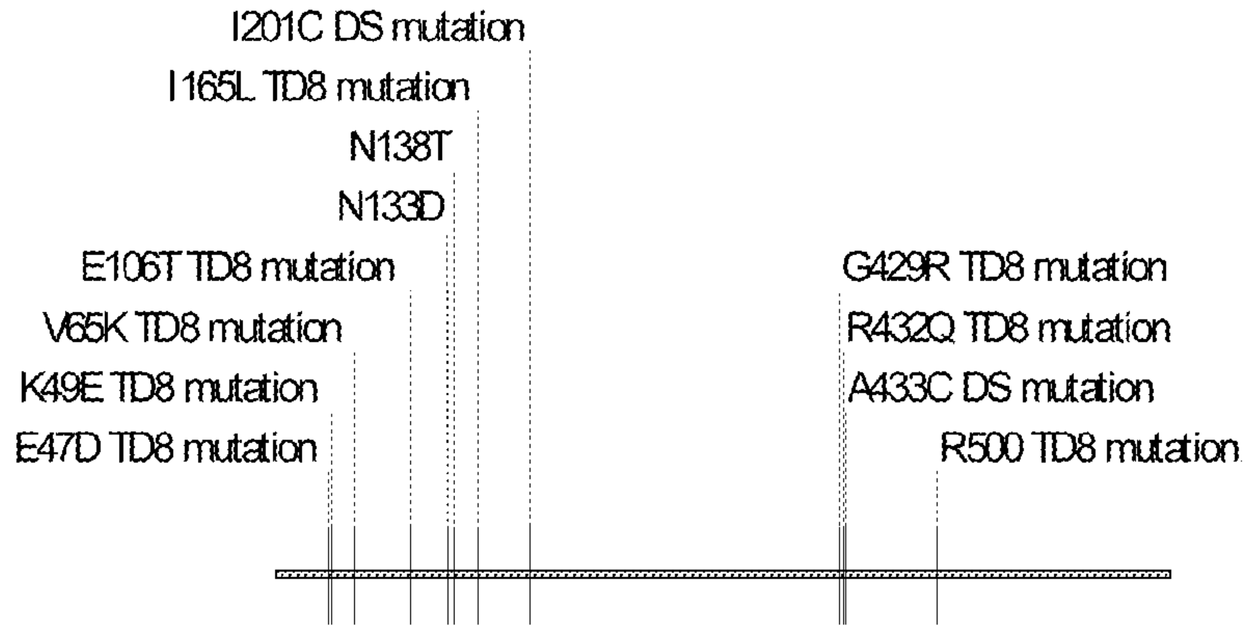


Figure 54D

```
                                        E47D TD8 mutation    V65K TD8 mutation
                                        ~                    ~
                                           K49E TD8 mutation                                                    E106T TD8 mutation
                                           ~                                                                    ~
  1  MGSLQPLATL YLLGMLVASV LAAENLWVTV YYGVPVWKDA ETTLFCASDA RAYEKEKHNV WATHACVPTD PSPQELVLGN VTENFNMWKN DMVDQMHTDI
                                    N138T
                                    ~~
                                  N133D                  I165L TD8 mutation                          I201C DS mutation
                                  ~                      ~                                           ~
101  ISLWDQSLKP CVKLTPLCVT LICSDATVKT GTVEEMKNCS FNTTTELRDK EKKEYALFYK PDIVPLSETN NTSEYRLINC NTSACTQACP KVTFEPIPIH
201  YCAPAGYAIL KCNDETFNGT GPCSNVSTVQ CTHGIRPVVS TQLLLNGSLA EKEIVIRSEN LTNNAKIIIV HLHTPVEIVC TRPNNNTRKS VRIGPGQTFY
301  ATGDIIGDIK QAHCNISEEK WNDTLQKVGI ELQKHFPNKT IKYNQSAGGD MEITTHSFNC GGEFFYCNTS NLFNGTYNGT YISTNSSANS TSTITLQCRI
                A433C DS mutation
                ~
               R432Q TD8 mutation
               ~
          G429R TD8 mutation                                                                  R500 TD8 mutation
          ~                                                                                   ~~
401  KQIINMWQRV GQCMYAPPIA GNITCRSNIT GLLLTRDGGT NSNETETFRP AGGDMRDNWR SELYKYKVVK IEPLGVAPTR CKRRVVGRRR RRRAVGIGAV
501  FLGFLGAAGS TMGAASMTLT VQARNLLSGI VQQQSNLLRA PEAQQHLLKL TVWGIKQLQA RVLAVERYLR DQQLLGIWGC SGKLICCTNV PWNSSWSNRN
601  LSEIWDNMTW LQWDKEISNY TQIIYGLLEE SQNQQEKNEQ DLLALD**
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Figure 54E

SUBSTITUTE SHEET (RULE 26)

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                                                1                                                  50
CH848.3.D949.10.17_N133DN138TchimericDS.SOSIP  (1) MGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEAKTTLFCASDA
   CH848.3.D949.10.17_N133DN138TchimericSOSIP  (1) MGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKEAKTTLFCASDA
CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP  (1) MGSLQPLATLYLLGMLVASVLAAENLWVTVYYGVPVWKDAETTLFCASDA
         CH848.3.D949.10.17_N133DN138TDS.SOSIP  (1) MGSLQPLATLYLLGMLVASVLAKGKLWVTVYYGVPVWKEAKTTLFCASDA
       CH848.3.D949.10.17_N133DN138TSOSIP.664  (1) MGSLQPLATLYLLGMLVASVLAKGKLWVTVYYGVPVWKEAKTTLFCASDA
CH848.3.D949.10.17_N133DN138TTD8.DS.SOSIP.664  (1) MGSLQPLATLYLLGMLVASVLAKGKLWVTVYYGVPVWKDAETTLFCASDA
                                     Consensus  (1) MGSLQPLATLYLLGMLVASVLAKGNLWVTVYYGVPVWKEAKTTLFCASDA
                                                51                                                 100
CH848.3.D949.10.17_N133DN138TchimericDS.SOSIP  (51) RAYEKEVHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDI
   CH848.3.D949.10.17_N133DN138TchimericSOSIP  (51) RAYEKEVHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDI
CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP  (51) RAYEKEKHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHTDI
         CH848.3.D949.10.17_N133DN138TDS.SOSIP  (51) RAYEKEVHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDI
       CH848.3.D949.10.17_N133DN138TSOSIP.664  (51) RAYEKEVHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDI
CH848.3.D949.10.17_N133DN138TTD8.DS.SOSIP.664  (51) RAYEKEKHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHTDI
                                     Consensus  (51) RAYEKEVHNVWATHACVPTDPSPQELVLGNVTENFNMWKNDMVDQMHEDI
                                                101                                                150
CH848.3.D949.10.17_N133DN138TchimericDS.SOSIP  (101) ISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTEIRDK
   CH848.3.D949.10.17_N133DN138TchimericSOSIP  (101) ISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTEIRDK
CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP  (101) ISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTELRDK
         CH848.3.D949.10.17_N133DN138TDS.SOSIP  (101) ISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTEIRDK
       CH848.3.D949.10.17_N133DN138TSOSIP.664  (101) ISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTEIRDK
CH848.3.D949.10.17_N133DN138TTD8.DS.SOSIP.664  (101) ISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTELRDK
                                     Consensus  (101) ISLWDQSLKPCVKLTPLCVTLICSDATVKTGTVEEMKNCSFNTTTEIRDK
                                                151                                                200
CH848.3.D949.10.17_N133DN138TchimericDS.SOSIP  (151) EKKEYALFYKPDIVPLSETNNTSEYRLINCNTSACTQACPKVTFEPIPIH
   CH848.3.D949.10.17_N133DN138TchimericSOSIP  (151) EKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAITQACPKVTFEPIPIH
CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP  (151) EKKEYALFYKPDIVPLSETNNTSEYRLINCNTSACTQACPKVTFEPIPIH
         CH848.3.D949.10.17_N133DN138TDS.SOSIP  (151) EKKEYALFYKPDIVPLSETNNTSEYRLINCNTSACTQACPKVTFEPIPIH
       CH848.3.D949.10.17_N133DN138TSOSIP.664  (151) EKKEYALFYKPDIVPLSETNNTSEYRLINCNTSAITQACPKVTFEPIPIH
CH848.3.D949.10.17_N133DN138TTD8.DS.SOSIP.664  (151) EKKEYALFYKPDIVPLSETNNTSEYRLINCNTSACTQACPKVTFEPIPIH
                                     Consensus  (151) EKKEYALFYKPDIVPLSETNNTSEYRLINCNTSACTQACPKVTFEPIPIH
                                                201                                                250
```

Figure 54F

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CH848.3.D949.10.17_N133DN138TchimericDS.SOSIP   (401) KQIINMWQGVGRCMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETFRP
CH848.3.D949.10.17_N133DN138TchimericSOSIP      (401) KQIINMWQGVGRAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETFRP
CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP (401) KQIINMWQRVGQCMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETFRP
CH848.3.D949.10.17_N133DN138TDS.SOSIP           (401) KQIINMWQGVGRCMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETFRP
CH848.3.D949.10.17_N133DN138TSOSIP.664          (401) KQIINMWQGVGRAMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETFRP
CH848.3.D949.10.17_N133DN138TTD8.DS.SOSIP.664   (401) KQIINMWQRVGQCMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETFRP
                                                Consensus (401) KQIINMWQGVGRCMYAPPIAGNITCRSNITGLLLTRDGGTNSNETETFRP
                                                                451                                         500
CH848.3.D949.10.17_N133DN138TchimericDS.SOSIP   (451) AGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAV
CH848.3.D949.10.17_N133DN138TchimericSOSIP      (451) AGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAV
CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP (451) AGGDMRDNWRSELYKYKVVKIEPLGVAPTRCKRRVVGRRRRRRAVGIGAV
CH848.3.D949.10.17_N133DN138TDS.SOSIP           (451) AGGDMRDNWRSELYKYKVVEIQPLGIAPTGCKRRVVERRRRRRAAGLGAL
CH848.3.D949.10.17_N133DN138TSOSIP.664          (451) AGGDMRDNWRSELYKYKVVEIQPLGIAPTGCKRRVVERRRRRRAAGLGAL
CH848.3.D949.10.17_N133DN138TTD8.DS.SOSIP.664   (451) AGGDMRDNWRSELYKYKVVEIQPLGIAPTRCKRRVVERRRRRRAAGLGAL
                                                Consensus (451) AGGDMRDNWRSELYKYKVVKIQPLGIAPTRCKRRVVGRRRRRRAVGIGAL
                                                                501                                         550
CH848.3.D949.10.17_N133DN138TchimericDS.SOSIP   (501) FLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKL
CH848.3.D949.10.17_N133DN138TchimericSOSIP      (501) FLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKL
CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP (501) FLGFLGAAGSTMGAASMTLTVQARNLLSGIVQQQSNLLRAPEAQQHLLKL
CH848.3.D949.10.17_N133DN138TDS.SOSIP           (501) FLGFLGAAGSTMGAASITLTVQAROLLSGIVQQQSNLLRAPEAQQHMLQL
CH848.3.D949.10.17_N133DN138TSOSIP.664          (501) FLGFLGAAGSTMGAASITLTVQAROLLSGIVQQQSNLLRAPEAQQHMLQL
CH848.3.D949.10.17_N133DN138TTD8.DS.SOSIP.664   (501) FLGFLGAAGSTMGAASITLTVQAROLLSGIVQQQSNLLRAPEAQQHMLQL
                                                Consensus (501) FLGFLGAAGSTMGAASITLTVQARNLLSGIVQQQSNLLRAPEAQQHLLQL
                                                                551                                         600
CH848.3.D949.10.17_N133DN138TchimericDS.SOSIP   (551) TVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRN
CH848.3.D949.10.17_N133DN138TchimericSOSIP      (551) TVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRN
CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP (551) TVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRN
CH848.3.D949.10.17_N133DN138TDS.SOSIP           (551) TVWGIKQLQARVLALERYLKDQQLLGMWGCSGKLICCTNVPWNTSWSNKS
CH848.3.D949.10.17_N133DN138TSOSIP.664          (551) TVWGIKQLQARVLALERYLKDQQLLGMWGCSGKLICCTNVPWNTSWSNKS
CH848.3.D949.10.17_N133DN138TTD8.DS.SOSIP.664   (551) TVWGIKQLQARVLALERYLKDQQLLGMWGCSGKLICCTNVPWNTSWSNKS
                                                Consensus (551) TVWGIKQLQARVLALERYLKDQQLLGIWGCSGKLICCTNVPWNSSWSNKS
                                                                601                                         648
```

Figure 54F continued

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CH848.3.D949.10.17_N133DN138TchimericDS.SOSIP   (601) LSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD--
  CH848.3.D949.10.17_N133DN138TchimericSOSIP    (601) LSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD--
CH848.3.D949.10.17_N133DN138TchimericTD8.DS.SOSIP (601) LSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLALD--
       CH848.3.D949.10.17_N133DN138TDS.SOSIP    (601) ETDIWDNMTWMQWEREISNYTETIYKLLEDSQNQQERNEQDLLALD--
     CH848.3.D949.10.17_N133DN138TSOSIP.664     (601) ETDIWDNMTWMQWEREISNYTETIYKLLEDSQNQQERNEQDLLALD--
CH848.3.D949.10.17_N133DN138TTD8.DS.SOSIP.664   (601) ETDIWDNMTWMQWEREISNYTETIYKLLEDSQNQQERNEQDLLALD--
                                    Consensus   (601) LSDIWDNMTWLQWDKEISNYTQTIYKLLEDSQNQQEKNEQDLLALD
```

Figure 54F continued

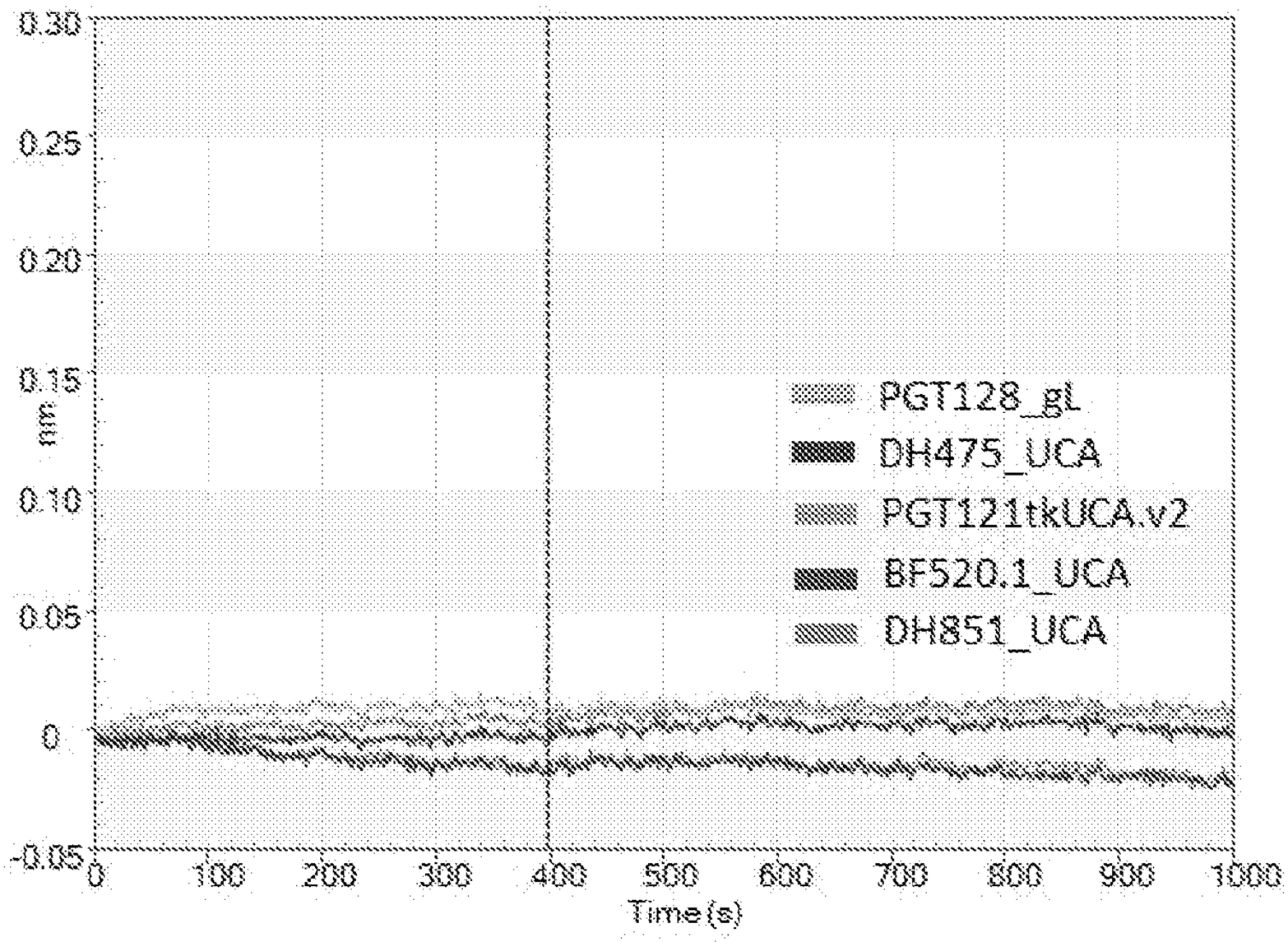


Figure 55A

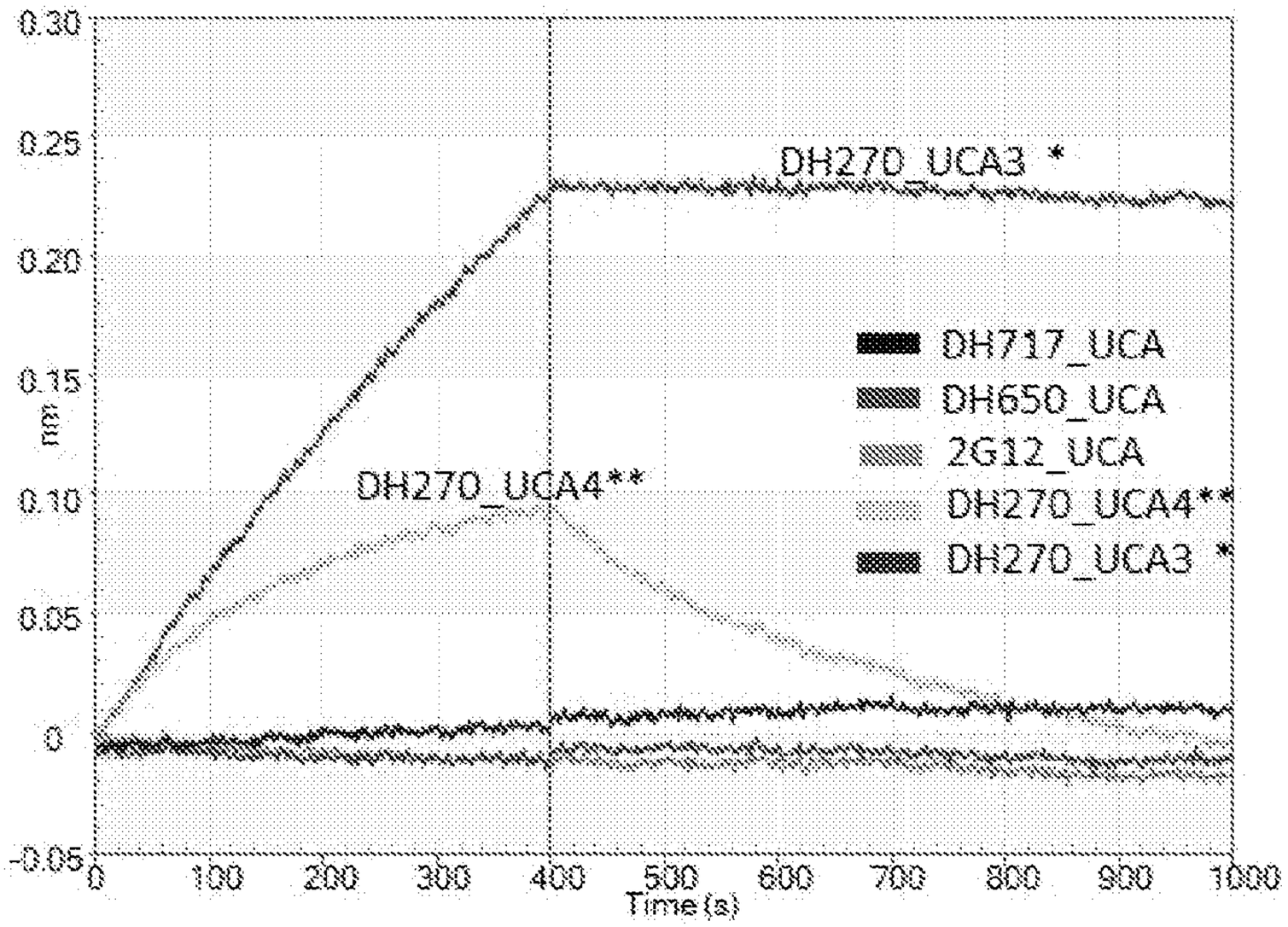


Figure 55B

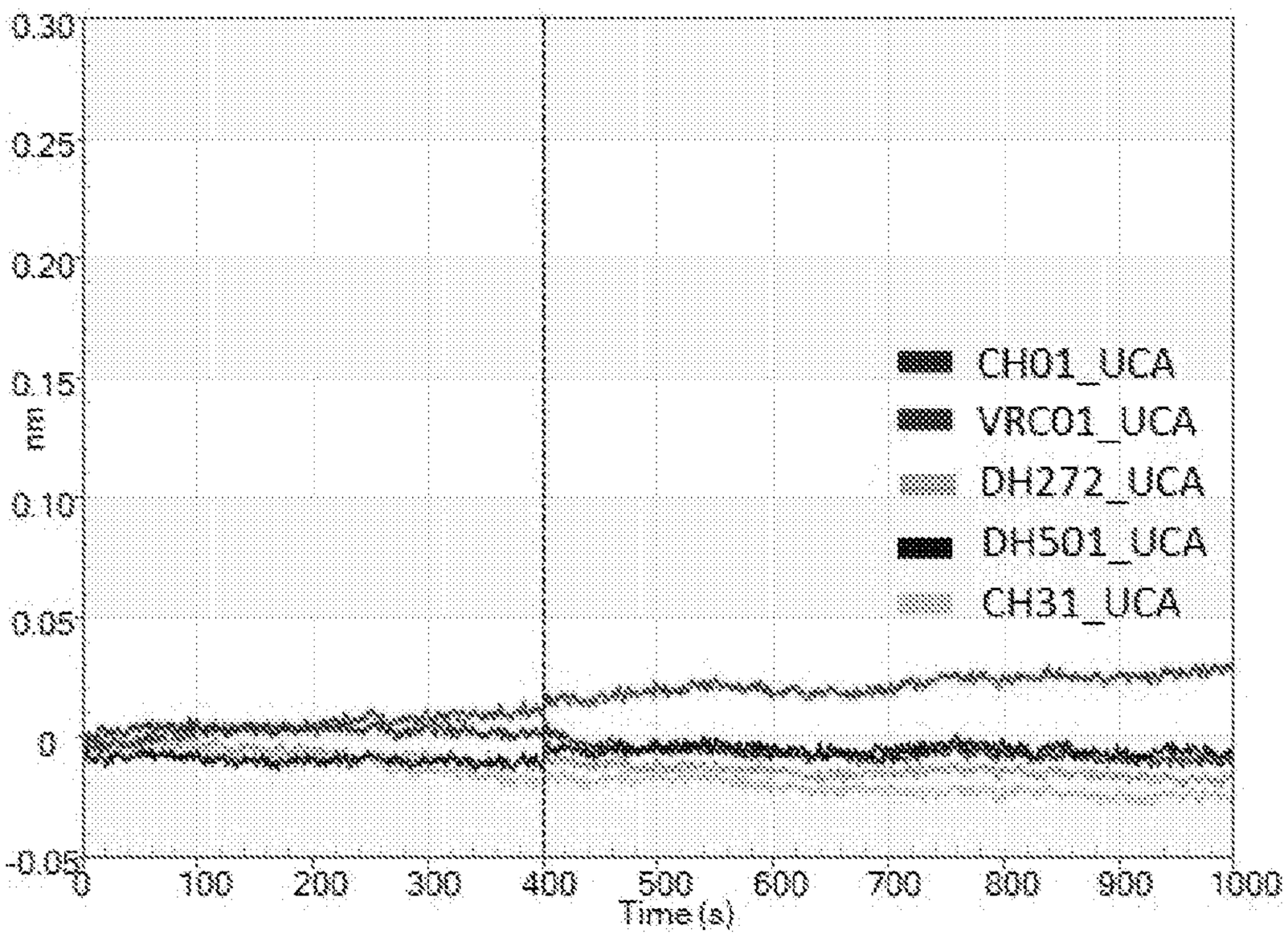


Figure 55C

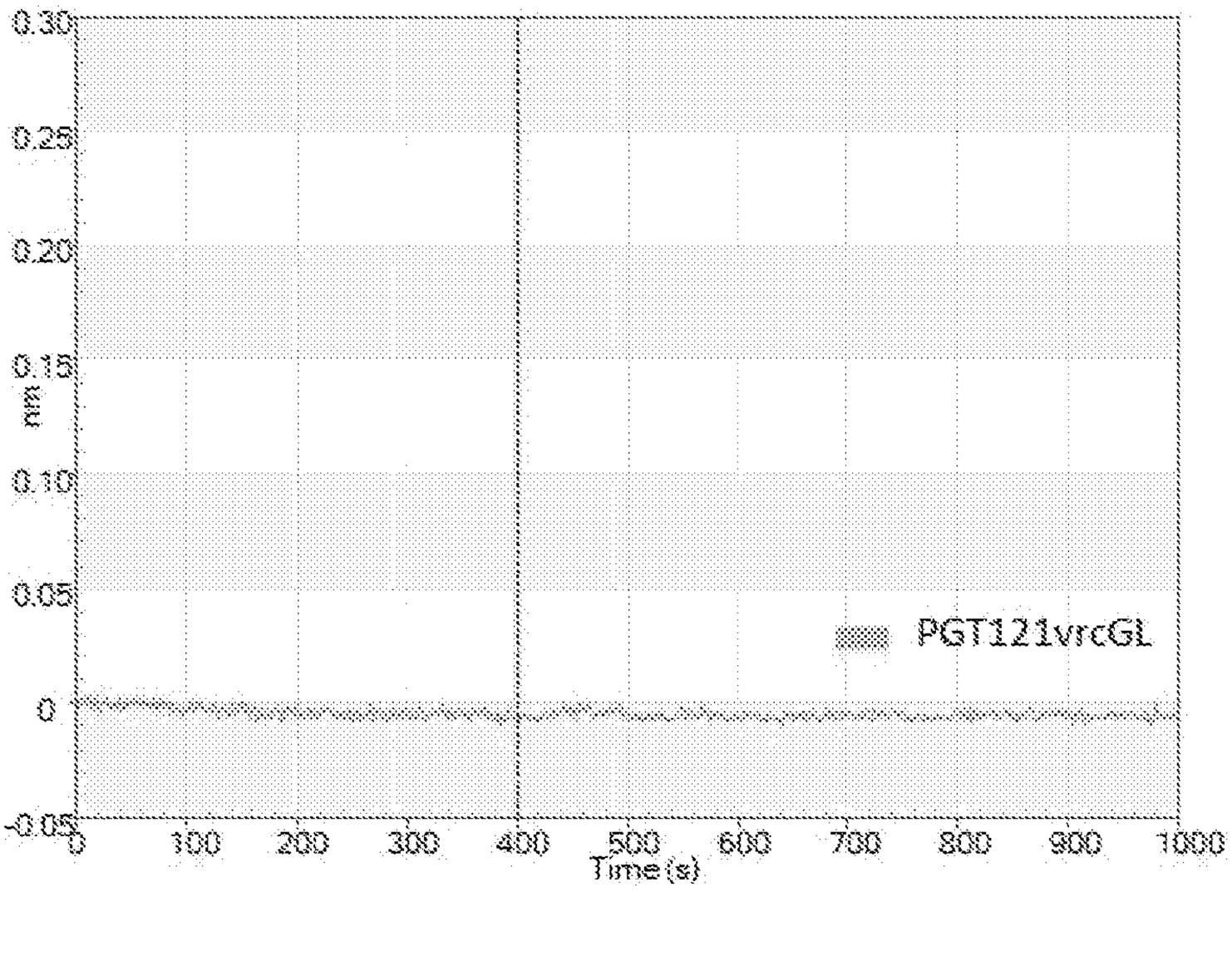


Figure 55D

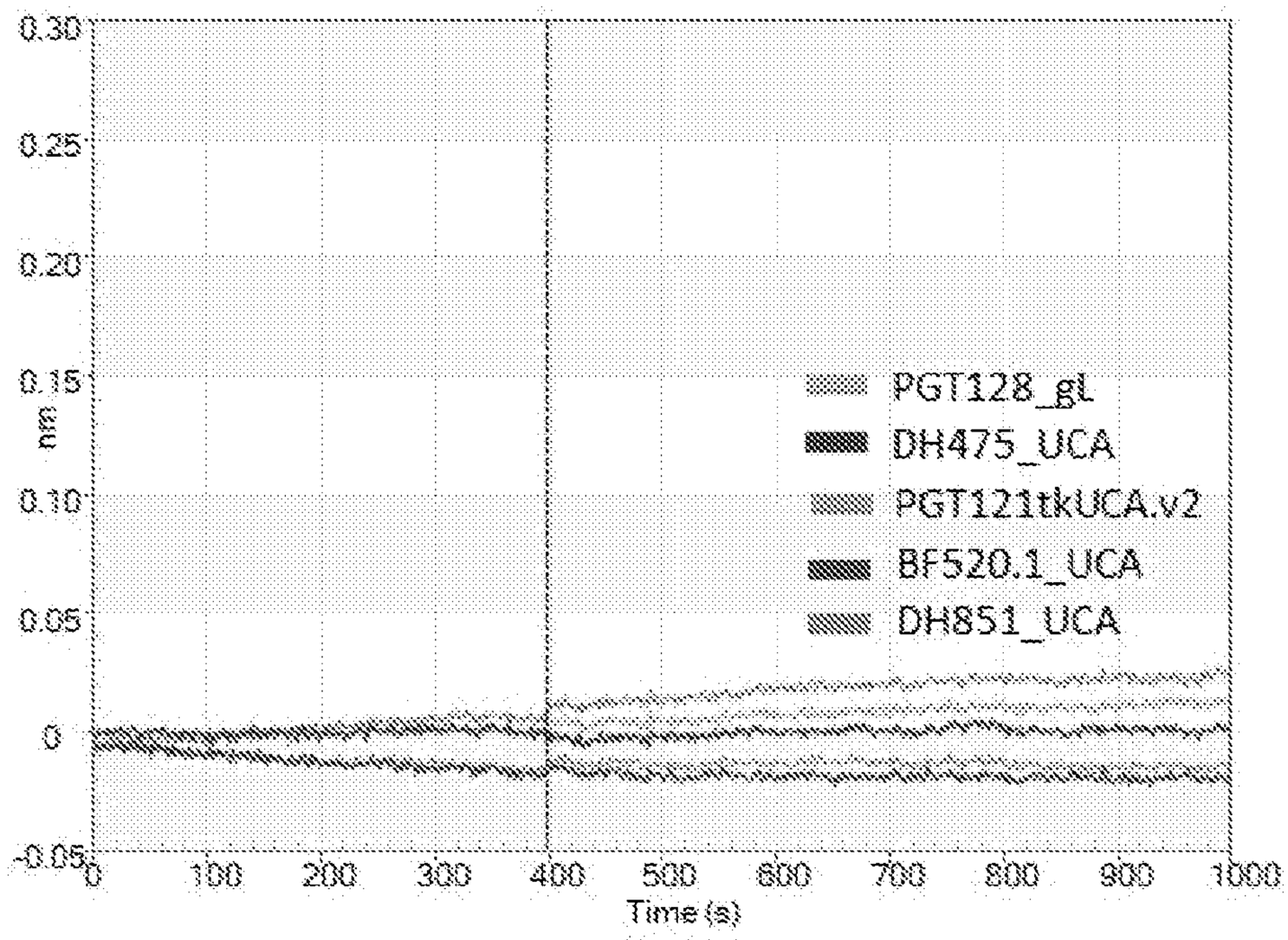


Figure 56A

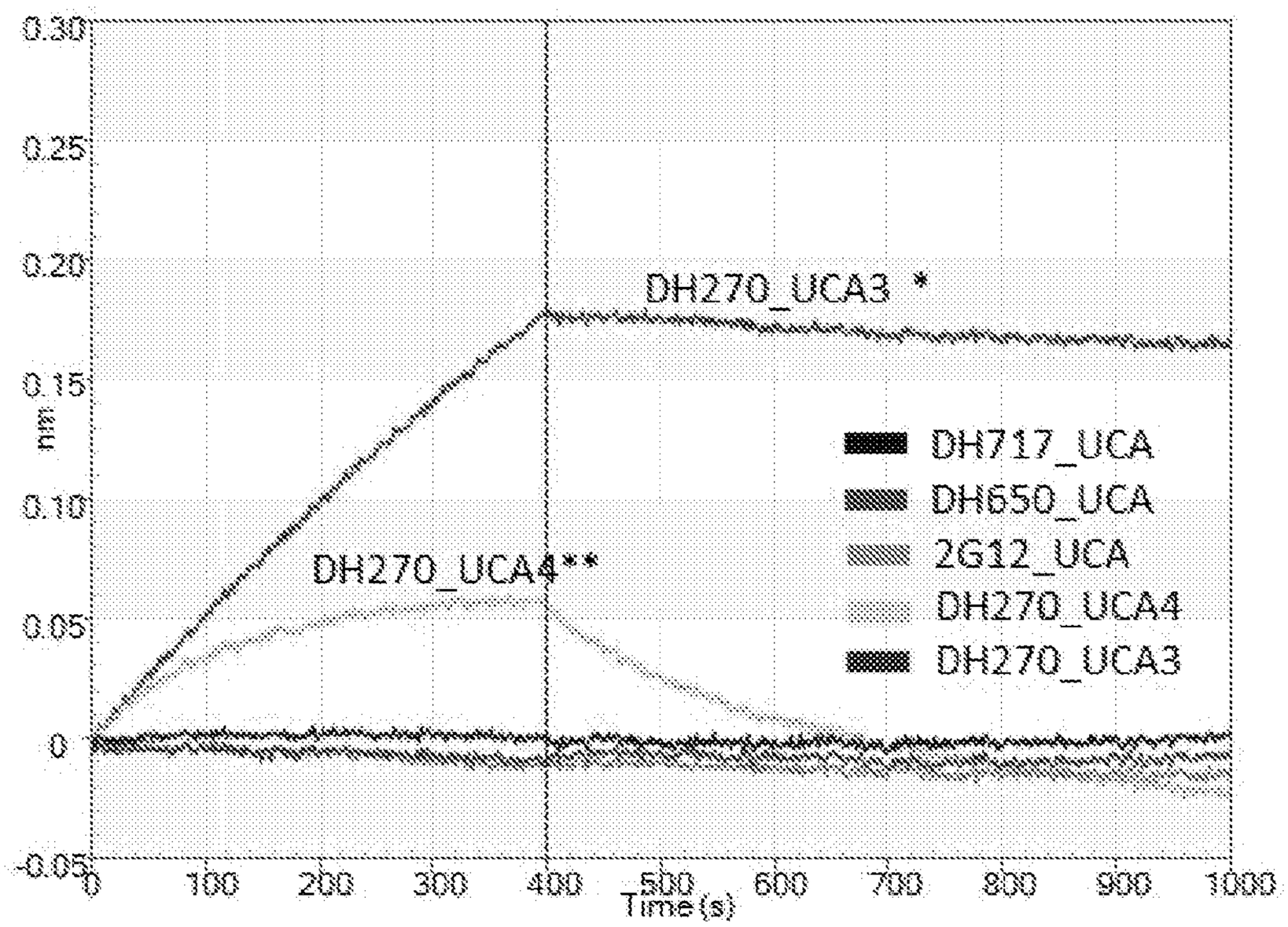


Figure 56B

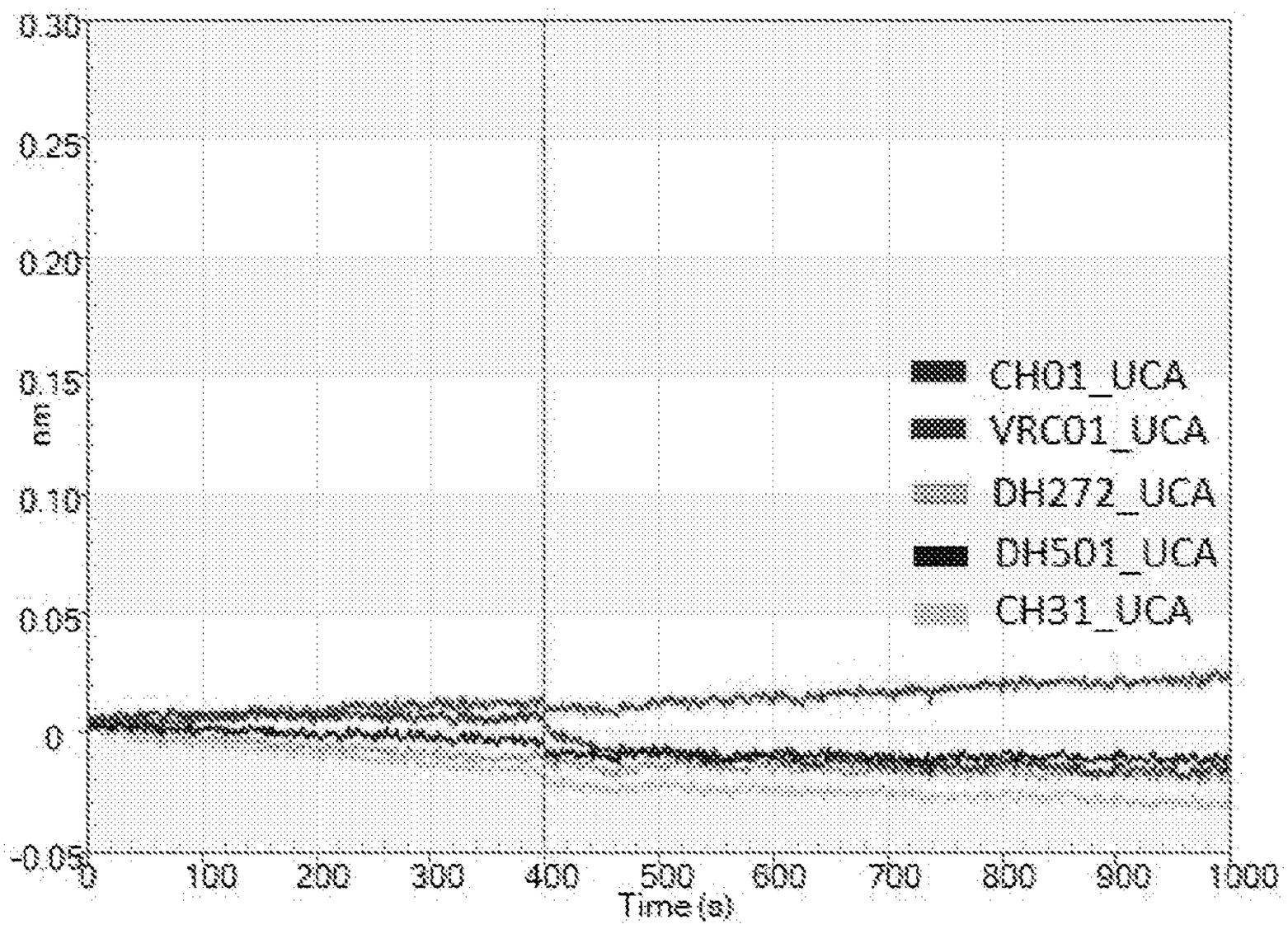


Figure 56C

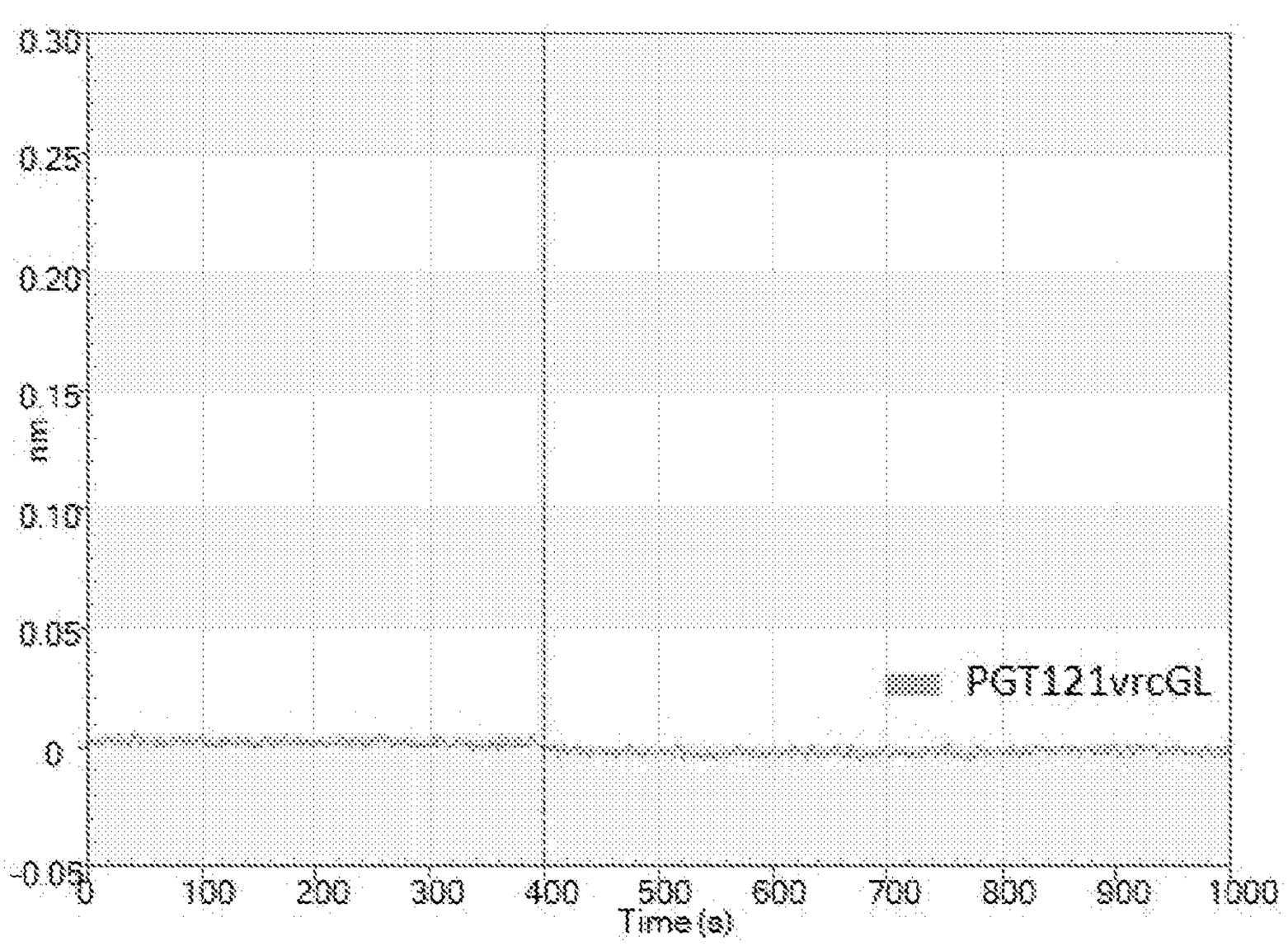


Figure 56D

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 2
CONTENANT LES PAGES 1 À 173

NOTE : Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

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THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 173

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NOM DU FICHIER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

Figure 1A

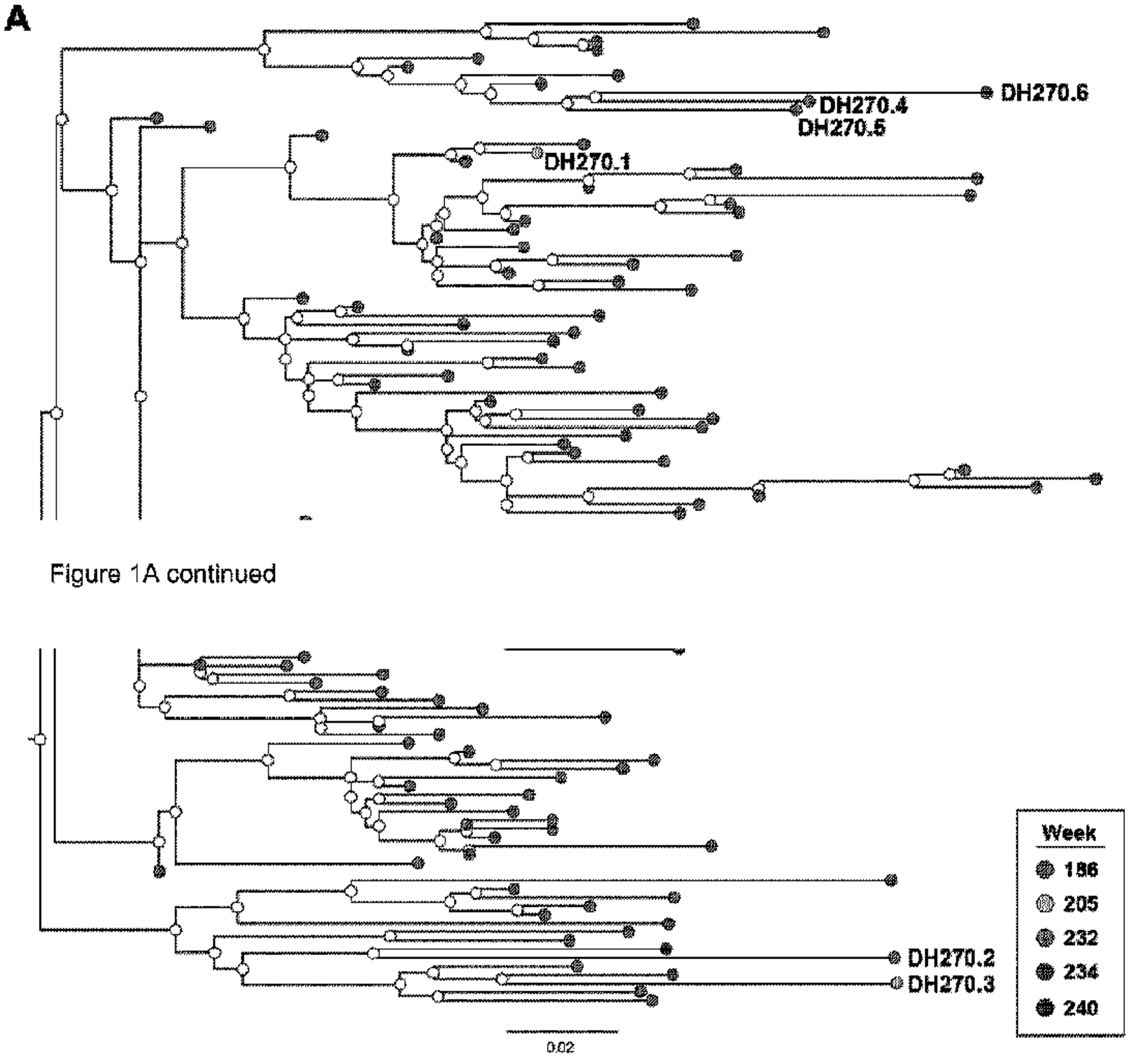


Figure 1A continued