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(54) Title: LIPID NANOPARTICLES FOR DELIVERING MRNA VACCINES

(57) Abstract: Provided are novel lipid nanoparticles for delivering nucleic acids such as mRNA. Also provided are methods of making and using lipid nanoparticles for delivering nucleic acids such as mRNA.

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Lipid Nanoparticles for Delivering mRNA Vaccines

RELATED APPLICATIONS

[001] This application claims the benefit of priority of U.S. Provisional Application No. 63/110,965, filed November 6, 2020, U.S. Provisional Application No. 63/212,523, filed June 18, 2021, and EP Priority Application No. 21315198.8, filed October 13, 2021, the content of each incorporated by reference in their entirety for all purposes.

BACKGROUND OF THE INVENTION

[002] Messenger RNA (mRNA)-based vaccines provide a promising alternative to traditional subunit vaccines, which contain antigenic proteins derived from a pathogen. Antigenic proteins are usually recombinantly made and require bacterial fermentation and/or cell culture, as well as complex purification. Vaccines based on mRNA allow *de novo* expression of complex antigens in the vaccinated subject, which in turn allows proper post-translational modification and presentation of the antigen in its natural conformation. Unlike traditional technologies, the manufacture of mRNA vaccines does not require complex and costly bacterial fermentation, tissue culture, and purification processes. Moreover, once established, the manufacturing process for mRNA vaccines can be used for a variety of antigens, enabling rapid development and deployment of mRNA vaccines. Further, mRNA vaccines are inherently safe delivery vectors as they express the antigens only transiently and do not integrate into the host genome. Because antigens encoded by mRNAs are produced *in vivo* in the vaccinated individual, mRNA vaccines are especially effective in eliciting both humoral and T cell mediated immunity.

[003] RNA, however, is unstable and subject to rapid degradation. There also are no natural cell surface receptors that facilitate cellular uptake of RNA. Indeed, development of mRNA vaccines has been hampered by inefficient *in vivo* delivery of mRNA. Thus, there remains a need to develop vaccine formulations that can improve mRNA delivery *in vivo*.

SUMMARY OF THE INVENTION

[004] The present disclosure provides a pharmaceutical composition comprising nucleic acid molecules (e.g., mRNA molecules) encapsulated in lipid nanoparticles (LNPs), wherein each LNP comprises a cationic lipid at a molar ratio between 35% and 45%, a polyethylene glycol (PEG) conjugated (PEGylated) lipid at a molar ratio between 0.25% and 2.75%, a cholesterol-based lipid at a molar ratio between 20% and 35%, and a helper lipid at a molar ratio of between 25% and 35%, wherein all the molar ratios are relative to the total lipid content of the LNP. The composition may be used as a vaccine to elicit immune protection in subjects (e.g., human subjects) in need thereof.

[005] In some embodiments, the cationic lipid is OF-02, cKK-E10, GL-HEPES-E3-E10-DS-3-E18-1, GL-HEPES-E3-E12-DS-4-E10, or GL-HEPES-E3-E12-DS-3-E14.

[006] In some embodiments, the LNP comprises a cationic lipid at a molar ratio of 40%, a PEGylated lipid at a molar ratio of 1.5%, a cholesterol-based lipid at a molar ratio of 28.5%, and a helper lipid at a molar ratio of 30%.

[007] In some embodiments, the cationic lipid is OF-02, cKK-E10, GL-HEPES-E3-E10-DS-3-E18-1, GL-HEPES-E3-E12-DS-4-E10, or GL-HEPES-E3-E12-DS-3-E14, the PEGylated lipid is dimyristoyl-PEG2000 (DMG-PEG2000), the cholesterol-based lipid is cholesterol, and/or the helper lipid is 1,2-dioleoyl-SN-glycero-3-phosphoethanolamine (DOPE). In particular embodiments, the LNP comprises OF-02, cKK-E10, GL-HEPES-E3-E10-DS-3-E18-1, GL-HEPES-E3-E12-DS-4-E10, or GL-HEPES-E3-E12-DS-3-E14 at a molar ratio of 40%, DMG-PEG2000 at a molar ratio of 1.5%, cholesterol at a molar ratio of 28.5%, and DOPE at a molar ratio of 30%.

[008] In some embodiments, the LNP comprises 1-20, optionally 5-10 or 6-8, nucleic acid molecules. In some embodiments, the LNP comprises one or more mRNA molecules encoding an antigen (e.g., a viral antigen such as an influenza viral antigen, or a bacterial antigen).

[009] In some embodiments, the LNP comprises two or more mRNA molecules, wherein each mRNA molecule encodes a different antigen, optionally wherein the different antigens are from the same pathogen or from different pathogens. In some embodiments, the composition comprises two or more LNPs, wherein each LNP comprises an mRNA encoding a different antigen, optionally wherein the different antigens are from the same pathogen or from different pathogens.

[0010] For example, the composition may comprise two, three, four, five, six, seven, eight, nine, or more mRNA molecules encoding (i) different hemagglutinin (HA) antigens, (ii) different neuraminidase (NA) antigens, or (iii) at least one HA antigen and at least one NA antigen.

[0011] In some embodiments, mRNA molecule comprises an open reading frame (ORF) encoding a respiratory syncytial virus (RSV) F protein antigen.

[0012] In some embodiments, the RSV F protein antigen comprises an amino acid sequence with at least 98% identity to SEQ ID NO: 16 or consists of an amino acid sequence of SEQ ID NO: 16.

[0013] In some embodiments, the RSV F protein antigen is a pre-fusion protein.

[0014] In some embodiments, the ORF is codon optimized.

[0015] In some embodiments, the mRNA molecule comprises at least one 5' untranslated region (5' UTR), at least one 3' untranslated region (3' UTR), and at least one polyadenylation (poly(A)) sequence.

[0016] In some embodiments, the mRNA comprises at least one chemical modification.

[0017] In some embodiments, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of the uracil nucleotides in the mRNA are chemically modified.

[0018] In some embodiments, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of the uracil nucleotides in the ORF are chemically modified.

[0019] In some embodiments, the chemical modification is selected from the group consisting of pseudouridine, N1-methylpseudouridine, 2-thiouridine, 4'-thiouridine, 5-methylcytosine, 2-thio-l-methyl-1-deaza-pseudouridine, 2-thio-l-methyl-pseudouridine, 2-thio-5-aza-uridine, 2-thio-dihydropseudouridine, 2-thio-dihydrouridine, 2-thio-pseudouridine, 4-methoxy-2-thio-pseudouridine, 4-methoxy-pseudouridine, 4-thio-l-methyl-pseudouridine, 4-thio-pseudouridine, 5-aza-uridine, dihydropseudouridine, 5-methyluridine, 5-methyluridine, 5-methoxyuridine, and 2'-O-methyl uridine.

[0020] In some embodiments, the chemical modification is selected from the group consisting of pseudouridine, N1-methylpseudouridine, 5-methylcytosine, 5-methoxyuridine, and a combination thereof.

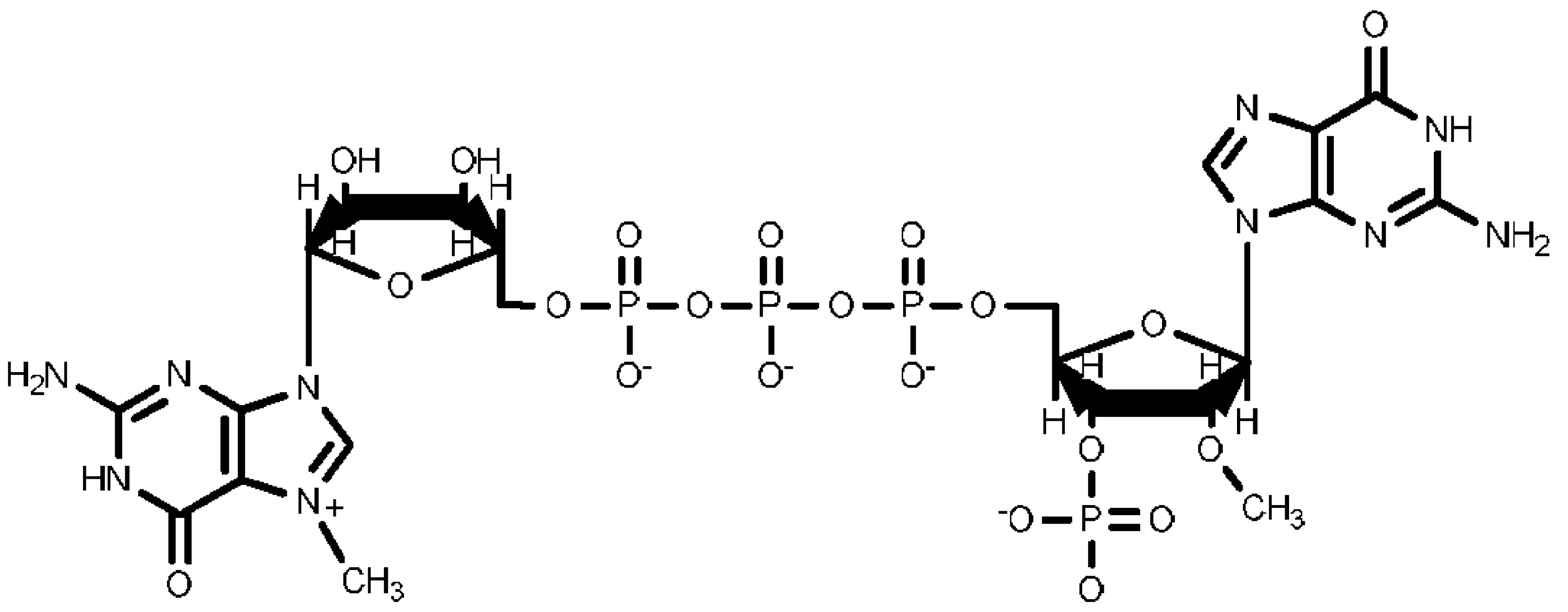
[0021] In some embodiments, the chemical modification is N1-methylpseudouridine.

[0022] In some embodiments, the mRNA comprises a nucleic acid sequence with at least 80% identity to a nucleic acid sequence set forth in SEQ ID NO: 17.

[0023] In some embodiments, the mRNA comprises a nucleic acid sequence with at least 80% identity to a nucleic acid sequence set forth in SEQ ID NO: 21.

[0024] In some embodiments, the mRNA comprises of the following structural elements:

(i) a 5' cap with the following structure:


;

(ii) a 5′ untranslated region (5’ UTR) having the nucleic acid sequence of SEQ ID NO: 19;

(iii) a protein coding region having the nucleic acid sequence of SEQ ID NO: 17;

(iv) a 3’ untranslated region (3’ UTR) having the nucleic acid sequence of SEQ ID NO: 20; and

(v) a poly(A) tail.

[0025] In some embodiments, the LNP has an average diameter of 30-200 nm (e.g., 80-150 nm). In some embodiments, the composition comprises 1-10, optionally 1, mg/mL of the LNP. The composition may be formulated for intramuscular or intradermal injection and may comprise a phosphate-buffer saline. In some embodiments, the composition comprising trehalose, optionally at 10% (w/v) of the composition.

[0026] In another aspect, the present disclosure provides a method of preparing the LNP composition herein, comprising providing an aqueous buffered solution comprising the nucleic acid molecule, providing an amphiphilic solution comprising the cationic lipid, the PEGylated lipid, the cholesterol-based lipid, and the helper lipid, and mixing the aqueous buffered solution and the amphiphilic solution at a ratio of 5:1 to 3:1, optionally 4:1. The aqueous buffered solution may be, for example an acidic buffered solution (e.g., comprising 1 mM citrate and 150 mM sodium chloride with a pH of about 4.5). The amphiphilic solution may be, e.g., an ethanol solution.

[0027] In another aspect, the present disclosure provides a method of eliciting an immune response in a subject in need thereof, comprising administering to the subject, optionally intramuscularly, intranasally, intravenously, subcutaneously, or intradermally, a prophylactically effective amount of the present LNP composition. In some embodiments, the subject is treated with one or more (e.g., two) doses of the composition, each dose comprising 1-250, optionally 2.5., 5, 15, 45, or 135, μg of mRNA. The doses may be given at an interval of 2-24, optionally 4, 8, 12, 16, or 20 weeks, or one, two, three, four, five, or six months.

[0028] Also provided herein are use of the present composition for the manufacture of a medicament for use in treating a subject in need thereof, as well as the composition for use for use in treating a subject in need thereof|.

[0029] The present disclosure also provides a kit comprising a container comprising a single-use or multi-use dosage of the present, optionally wherein the container is a vial or a pre-filled syringe or injector.

[0030] In another aspect, the disclosure provides a pharmaceutical composition comprising a mRNA molecule encapsulated in a lipid nanoparticle (LNP), wherein the LNP comprises:

a cationic lipid at a molar ratio between 35% and 45%,

a polyethylene glycol (PEG) conjugated (PEGylated) lipid at a molar ratio between 0.25% and 2.75%,

a cholesterol-based lipid at a molar ratio between 20% and 35%, and

a helper lipid at a molar ratio of between 25% and 35%,

wherein all the molar ratios are relative to the total lipid content of the LNP;

wherein the mRNA molecule comprises an open reading frame (ORF) encoding an antigen derived from influenza virus.

[0031] In another aspect, the disclosure provides a pharmaceutical composition comprising a mRNA molecule encapsulated in a lipid nanoparticle (LNP), wherein the LNP comprises:

a cationic lipid at a molar ratio between 35% and 45%,

a polyethylene glycol (PEG) conjugated (PEGylated) lipid at a molar ratio between 0.25% and 2.75%,

a cholesterol-based lipid at a molar ratio between 20% and 35%, and

a helper lipid at a molar ratio of between 25% and 35%,

wherein all the molar ratios are relative to the total lipid content of the LNP;

wherein the mRNA molecule comprises an open reading frame (ORF) encoding a respiratory syncytial virus (RSV) F protein antigen.

[0032] Other features, objects, and advantages of the invention are apparent in the detailed description that follows. It should be understood, however, that the detailed description, while indicating embodiments and aspects of the invention, is given by way of illustration only, not limitation. Various changes and modification within the scope of the invention will become apparent to those skilled in the art from the detailed description

BRIEF DESCRIPTION OF THE DRAWINGS

[0033] **FIG. 1A** is a pair of graphs showing the expression of human erythropoietin (hEPO) in mice treated with various LNP formulations of hEPO mRNA. Panel a): LNP formulations “Lipid A” and “Lipid B” compared to MC3. Bars represent means and standard deviations. Panel b): Formulation made with cationic lipid OF-02. PEG: DMG-PEG2000. Cholest: cholesterol. “Lipid A”: LNP composition containing OF-02, DMG-PEG2000, cholesterol, and DOPE, in this order, at a molar ratio of 40:1.5:28.5:30, unless otherwise indicated. “Lipid B”: LNP composition containing cKK-E10, DMG-PEG2000, cholesterol, and DOPE, in this order, at a molar ratio of 40:1.5:28.5:30.

[0034] **FIG. 1B** is a pair of graphs showing expression of hEPO in mice and non-human primates (NHPs) using LNP formulations Lipid A and Lipid B.

[0035] **FIG. 2A** and **2B** are a pair of graphs showing that Lipid A and Lipid B LNP formulations with mRNA encoding hemagglutinin (HA) of strain A/California/7/2009 (H1N1) (CA09) induced robust functional antibodies (**FIG. 2A**) and protected mice against death or severe weight loss (more than 20%) when challenged with a pandemic strain of influenza virus (**FIG. 2B**). Hemagglutinin inhibition (HAI) titers are reported as log10 for serum samples taken at study days 0, 14, 28, 42, 56, 92, and 107. Bars are geometric means and geometric standard deviations. Daily weights were measured after intranasal challenge (day 93) with $4LD_{50}$ of A/Belgium/2009 (H1N1) (Belgium09). Weights are presented as the percentage of weight lost from the day of challenge. Euthanasia occurred for mice losing more than 20% of their starting body weight and for all mice 14 days post-infection (day 107). rHA: recombinant hemagglutinin. AF03: an oil-in-water emulsion adjuvant. Diluent = PBS. LLOQ = lower limit of quantitation. 1/40 = 1/40 minimum target, which refers to HAI antibody titers associated with 50% reduction in the risk of influenza infection or disease in healthy adults (Coudeville et al., *BMC Med Res Methodol.* (2010) 10:18). Dashed line in **FIG. 2B** = 20% weight loss cut off with respect to weight on the day of challenge.

[0036] **FIG. 3A** and **3B** are a pair of graphs showing that A/Michigan/45/2015 (Mich15) neuraminidase (NA) mRNA formulated with Lipid A LNP induced robust functional antibodies (**FIG. 3A**) and protected mice against weight loss and death when challenged with a pandemic strain of influenza virus (**FIG. 3B**). Neuraminidase inhibition (NAI) titers are reported as log10 for serum samples taken at study days 14, 28, 42, 56, 88, and 114. Daily weights were observed after intranasal challenge (day 89 for the one-dose groups or day 117 for the two-dose groups) with 4LD$_{50}$ of Belgium09. Weights are presented as the percentage of weight lost from the day of challenge. Euthanasia occurred for mice losing more than 20% of their starting body weight and for all mice 14 days post-infection (day 103 for the 1 dose groups or day 131 for the 2 dose groups). Bars are means and standard deviations. Upper dashed line in **FIG. 3A** = upper limit of quantitation. Lower dashed line in **FIG. 3A** = lower limit of quantitation. Dashed line in **FIG. 3B** = 20% weight loss cut off with respect to weight on the day of challenge. mRNA dosed: 0.4 or 0.016 µg mRNA encoding Mich15 NA. Control: 0.6 µg mRNA encoding hEPO or diluent (PBS).

[0037] **FIG. 4** is a graph showing that Lipid A and Lipid B LNP formulations with CA09 HA mRNA (10 µg) induced robust functional antibodies in cynomolgus macaque monkeys. HAI titers are reported as log2 for serum samples taken at study days 0, 14, 28, 42, and 56.

[0038] **FIGs. 5A-C** show the MRT1400 mRNA encoding for influenza virus A/Singapore/ INFIMH160019/2016 (Sing16; H3N2) HA hemagglutinin. **FIG. 5A**: an alignment of the wildtype (WT) gene and a codon-optimized gene (MRT10279) for the HA antigen. **FIG. 5B**: the structure of the mRNA. **FIG. 5C**: the sequence of the mRNA.

[0039] **FIG. 6** is a pair of graphs showing that Lipid A and Lipid B LNP formulations with MRT1400 or NA mRNA induced robust functional antibodies in mice. First injection was given at study day 0 and second injection was given at study day 28. Left Panel: HAI titers are reported as log10 for serum samples taken at study days 14, 28, 42, and 56. Right Panel: NAI titers are reported as log10 for serum samples taken at study days 14, 28, 42, and 56. Bars are geometric means and geometric standard deviations. Dashed line = lower limit of quantitation.

[0040] **FIG. 7A** is a graph showing that Lipid A and Lipid B LNP formulations with MRT 1400 induced robust functional antibodies in NHPs. HAI titers are reported as log2 for serum samples taken at study days 0, 14, 28, 42, and 56. First injection was given at study day 0 and second injection was given at study day 28. Bars are means and standard deviation. Upper dashed line = 1/40 minimum target. Lower dashed line = lower limit of detection.

[0041] **FIG. 7B** and **7C** are a pair of graphs showing that a Lipid A LNP formulation (MRT5400) containing MRT1400 mRNA induced functional antibodies (**FIG. 7B**) and robust ELISA titers (**FIG. 7C**) in cynomolgus macaque monkeys at four dose levels: 15, 45, 135 and 250 µg of mRNA. HAI and ELISA titers are reported as log2 for serum samples taken at study days 0, 14, 28, 42, and 56. First injection was given at study day 0 and second injection given at study day 28. Bars are means and standard deviations. Dash line = 1/40 minimum target.

[0042] **FIGs. 8A** and **8B** are panels of graphs showing the T cell cytokine response of cynomolgus macaques after a second vaccination with Lipid A LNP formulation MRT5400 in three dose level groups (250 µg, 135 µg, and 45 µg of mRNA). IFN-γ and IL-13 induced by re-stimulation with either the recombinant HA (rHA) protein (left panel) or the pooled peptides (right panel) were assessed in peripheral blood mononuclear cells (PMBC) on day 42 by ELISPOT assays. The frequencies of PBMC secreting IFN-γ (**FIG. 8A**) or IL-13 (**FIG. 8B**) were calculated as spots forming cells (SFC) per million PBMC. Each symbol represents an individual sample, and the bar represents the standard deviation.

[0043] **FIG. 9A** is a pair of graphs showing that Lipid A LNP formulations containing modified and unmodified CA09 HA mRNA were comparable as indicated by HAI titers in vaccinated mice. HAI titers are reported as log2 for serum samples taken at study days 14, 28, 42, and 56. First injection was given at study day 0 and second injection was given at study day 28. Bars are means and standard deviation. Upper dashed line = 1/40 minimum target. Lower dashed line = lower limit of quantitation.

[0044] **FIG. 9B** is a pair of graphs showing that Lipid A LNP formulations containing modified and unmodified CA09 HA mRNA were comparable as indicated by ELISA titers in mice. Total IgG ELISA titers are reported as log10 for serum samples taken at study days 14, 28, 42, and 56. First injection was given at study day 0 and second injection was given at study day 28. Dashed line = lower limit of quantitation.

[0045] **FIGs. 10A** and **10B** are a pair of graphs showing that bivalent Lipid A LNP formulations with CA09 HA mRNA and Sing16 HA mRNA induced robust functional antibodies as assessed by HAI titers (CA09 (**FIG. 10A**) and Sing16 (**FIG. 10B**)) in Balb/c mice at a dose of 0.4 µg of total mRNA. 0.4 µg mRNA was dosed as a co-encapsulated mRNA-LNP formulation, or each HA mRNA was separately administered with 0.2 µg going into each leg. Each HA mRNA was also co-encapsulated into a formulation with non-coding mRNA to control for total mRNA packing into the LNP. The diluent group received mRNA-LNP diluent buffer. HAI titers are reported for serum samples taken at study days -2 (baseline), 14, 28, and 42. **FIG. 10B** only shows study days -2 (baseline from pooled sera) and 42. First injection was given at study day 0 and second injection given at study day 28. Bars are geometric means and geometric standard deviations. Dashed line = lower limit of quantitation.

[0046] **FIG. 11** shows the functional verification of mRNA-LNP Formulations. **Panel (a)** is a graph showing the expression of firefly (FF) luciferase in BALB/c mice: a single dose of Luciferase FF mRNA-LNP (5, 1, 0.1, 0.05 μg) was injected in mice (n=4) by IM route. Luciferin (3 mg) was injected at the time of whole animal imaging, using IVIS Spectrum, Perkin Elmer recording bioluminescence intensity. Images of whole animal average radiance at 6, 24, 48 and 72h after injection were taken. Radiance recorded for 1, 0.5, 0.1 and 0.05 μg dose administrations of Luc mRNA-LNP are shown in the graph. **Panel (b)** shows whole animal images indicating total flux of luminescence, at 6 to 72 hours. Total flux of luminescence in groups of mice (n=4) receiving 0.1 μg dose of FF-LNP are shown. **Panel (c)** shows the expression of hEPO in BALB/c mice. A single dose of hEPO mRNA-LNP (0.1 μg) was injected in BALB/c mice by IM route. hEPO expression was quantified in serum at 6 hours and 24 hours after administration using ELISA. Bars represent means and standard deviations. **Panel (d)** shows the expression of hEPO in NHP. A single dose of hEPO mRNA-LNP (10 μg) was injected in Cynomolgus macaques by IM route. hEPO expression was quantified in serum at 6, 24, 48, 72, and 96 hours after administration, using ELISA. Bars represent means and standard deviations.

[0047] **FIG. 12** shows the serological evaluation of HA mRNA-LNP vaccine in mice. BALB/c mice (n=8 per group) were immunized twice IM, 4 weeks apart with 2, 0.4, 0.08, and 0.016 μg of either Cal09 HA mRNA-LNP or Sing16 HA mRNA-LNP. ELISA titers recorded for sera collected at days 14, 28, 42, 56 against CA09 (Cal09) H1N1 influenza virus recombinant HA (left panel) and Sing16 H3N2 influenza virus recombinant HA (right panel) are shown.

[0048] **FIG. 13** shows the serological evaluation of HA mRNA-LNP vaccine in mice. BALB/c mice (n=8 per group) were immunized twice IM, 4 weeks apart with 2, 0.4, 0.08 and 0.016 μg of either CA09 HA mRNA-LNP or Sing16 HA mRNA-LNP. Log_{10} HAI titers recorded against CA09 H1N1 influenza virus (left panel) and Sing16 H3N2 influenza virus (right panel) are shown.

[0049] **FIG. 14** shows the serological evaluation of NA mRNA-LNP vaccine in mice. BALB/c mice (n=8 per group) were immunized twice IM 4 weeks apart with 2, 0.4, 0.08, and 0.016 μg of either Mich15 NA mRNA-LNP or Sing16 NA mRNA-LNP. Total IgG titers recorded for sera collected at days 0, 14, 28, 42, 56 against Mich15 N1 influenza virus recombinant NA (left panel) and Sing16 N2 virus recombinant NA (right panel) are shown

[0050] **FIG. 15** shows the serological evaluation of NA mRNA-LNP vaccine in mice. BALB/c mice (n=8 per group) were immunized twice IM 4 weeks apart with 2, 0.4, 0.08 and 0.016 µg of either Mich15 NA mRNA-LNP or Sing16 NA mRNA-LNP. Log_{10} NAI (ELLA) titers recorded for sera against Mich2015 (N1): A/Mallard/Sweden/2002 (H6) chimeric influenza virus (left panel) and Sing16 (N2): A/Mallard/Sweden/2002 (H6) chimeric virus (right panel) are shown.

[0051] **FIGs. 16A** and **16B** show the protective efficacy of CA09 HA mRNA-LNP vaccine in mice after lethal A/Belgium/2009 H1N1 virus challenge. Mice (n=8) received two IM doses of CA09 HA mRNA-LNP (0.4 µg each) on day 0 and day 28. Control animals received two IM doses of diluent on day 0 and day 28. **FIG. 16A** shows the HAI titers reported as Log_{10} for serum samples taken at study days 0, 14, 28, 42, 56, 92, and 107. **FIG. 16B** shows daily weights after intranasal challenge on day 93 with $4LD_{50}$ of A/Belgium/2009 H1N1 strain. Weights are presented as the percentage of weight lost from the day of challenge. Individual lines represent each animal.

[0052] **FIGs. 17A-B** show the protective efficacy of a single dose of unmodified Mich15 NA mRNA-LNP in mice after lethal A/Belgium/2009 H1N1 virus challenge. Mice (n=16) were injected by the IM route with 0.4 µg or 0.016 µg of Mich15 NA mRNA-LNP. Half of the mice only received one injection (1 dose) on study day 0, while the other half (2 doses) received two injections given at study day 0 and day 28. Control animals received two IM doses of hEPO mRNA-LNP (0.6 µg) on day 0 and day 28. **FIG. 17A** shows the NAI titers are reported as Log_{10} for serum samples taken at study days 0, 14, 28, 42, 56, 88, and 114. **FIG. 17B** shows the daily weight change after intranasal challenge on day 89 for single dose group and day 117 (89 days after second dose) for two dose group with 4LD50 of Belgium09 H1N1. Weights are presented as the percentage of weight lost from the day of challenge. Individual lines represent each animal.

[0053] **FIG. 18** shows the serological evaluation of HA Sing16 HA mRNA-LNP vaccine in NHP. Cynomolgus macaques (n=6 per group) were injected twice, 4 weeks apart by IM route, with 15, 45 or 135 µg of Sing16 HA mRNA-LNP. Serum samples were collected at days -6, 14, 28, 42, and 56. Log_{10} IgG titers against recombinant HA protein of Sing16 virus are shown.

[0054] **FIGs. 19A** and **19B** show the serological evaluation of HA Sing16 HA mRNA-LNP vaccine in NHP. Cynomolgus macaques (n=6 per group) were injected twice, 4 weeks apart by IM route, with 15, 45 or 135 µg of Sing16 HA mRNA-LNP. Serum samples were collected at days 0, 14, 28, 42, and 56. Log_{10} HAI titers (**FIG. 19A**) and Log_{10} micro-neutralization (MN) titers (**FIG. 19B**) against Sing2016 virus are shown.

[0055] **FIGs. 20A** and **20B** show T cell responses in NHP vaccinated with Sing16 HA mRNA-LNP vaccine. Cynomolgus macaques (n=6 per group) were injected twice, 4 weeks apart by IM route, with 45, 135, or 250 μg of Sing16 HA mRNA-LNP. T cells were determined by ELISPOT on day 42 in PBMC stimulated in vitro with peptide pools to represent the entire HA open reading frame. The responses of PBMC secreting IFN-γ (**FIG. 20A**) or IL-13 (**FIG. 20B**) calculated as spots forming cells (SFC) per million PBMC are shown. Each symbol represents an individual sample, and the bar represent the geometric mean for the group.

[0056] **FIG. 21** shows the secretion of Sing16 H3-specific IgG by memory B cells on day 180 in NHP vaccinated with Sing16 HA mRNA-LNP vaccine. Cynomolgus macaques (n=6 per group) were injected twice, 4 weeks apart by IM route, with 15 or 45 μg of Sing16 HA mRNA-LNP. The Human IgG single-color memory B cell ELISPOT kit (CAT# NC1911372, CTL) was used to measure Sing16/H3-specific and total IgG^+ antibody-secreting cells (ASCs). Differentiation of MBCs into ASCs was performed in PBMC collected at day 180 by using a stimulation cocktail provided by the kit. The number of IgG^+ and number of Sing16/H3-specific ASCs was calculated per million of PBMCs for each animal and the frequency of antigen-specific ASCs is shown.

[0057] **FIG. 22** shows the delivery of bivalent combinations of influenza vaccine in mice. BALB/c mice (n=8 per group) were immunized twice IM, 4 weeks apart with a total 0.4 μg of bivalent combinations co-encapsulated mRNA transcripts (1:1 wt/wt, half volume per each leg) or 0.2 μg each monovalent which was separately formulated and immunized different legs. H1H3 combo constituting CA09 HA mRNA-LNP, Sing16 HA mRNA-LNP; H3N2 combo of Sing16 HA mRNA-LNP and Sing16 NA mRNA-LNP and N1N2 combo of Mich15 NA mRNA-LNP and Perth09 NA mRNA-LNP were tested in sera collected a day 0, 14, 28, 42, against corresponding virus. **Panel (a)** shows HAI titers recorded against CA09 H1N1 influenza virus and Sing2016 H3N2. **Panel (b)** shows the HAI and NAI titers recorded against Sing2016 H3N2 and A/Mallard/Sweden/2002 (H6) chimeric influenza virus and H6N2 A/Perth/09 virus F1919D (N2) virus, respectfully. **Panel (c)** shows NAI titers recorded against Mich15 (N1): A/Mallard/Sweden/2002 (H6) chimeric influenza virus and H6N2 A/Perth/09 virus F1919D (N2) virus.

[0058] **FIG. 23** shows the delivery of quadrivalent combinations of influenza vaccines in NHP. Cynomolgus macaques (n=6 per group) were immunized twice IM, 4 weeks apart with a total 10 μg of quadrivalent combinations of co-encapsulated mRNA transcripts (1:1:1:1 wt/wt).

H2H3N1N2 combo consisting of CA09 HA mRNA, Sing16 HA mRNA, Mich15 NA mRNA, and Perth09 NA mRNA. H1H3 combo constituting CA09 HA mRNA, Sing16 HA mRNA and 2x non-coding mRNA (ncmRNA); H3N2 combo of Sing16 HA mRNA and Perth09 NA mRNA and 2x non-coding mRNA. N1N2 combo of Mich15 NA mRNA, Perth09 NA mRNA-LNP, and 2x non-coding mRNA. H1 consisting of CA09 HA mRNA and 3x non-coding mRNA. H3 consisting of Sing16 HA mRNA and 3x non-coding mRNA. N1 consisting of Mich15 NA mRNA and 3x non-coding mRNA. N2 consisting of Perth09 NA mRNA and 3x non-coding mRNA. Inhibitory titers were tested in sera collected a day 0, 14, 28, 42, against corresponding virus. **Panel (a)** shows the HAI titers recorded against CA09 H1N1 influenza virus and Sing16 H3N2. **Panel (b)** shows the NAI titers recorded against Mich15 (N1): A/Mallard/Sweden/2002 (H6) chimeric influenza virus and H6N2 Perth/09 virus F1919D (N2) virus.

[0059] **FIG. 24** depicts a graph showing the expression of human erythropoietin (hEPO) in mice treated with various LNP formulations of hEPO mRNA. LNP formulations “Lipid A,” “Lipid B,” “Lipid C,” “Lipid D,” and “Lipid E” are shown. Bars represent means and standard deviations. The LNP compositions contain the cationic lipid, DMG-PEG2000, cholesterol, and DOPE, in this order, at a molar ratio of 40:1.5:28.5:30.

[0060] **FIG. 25** depicts a graph showing the expression of hEPO in non-human primates (NHPs) treated with various LNP formulations of hEPO mRNA. LNP formulations “Lipid A,” “Lipid B,” “Lipid C,” “Lipid D,” and “Lipid E” are shown. Bars represent means and standard deviations. The LNP compositions contain the cationic lipid, DMG-PEG2000, cholesterol, and DOPE, in this order, at a molar ratio of 40:1.5:28.5:30.

[0061] **FIG. 26** depicts a graph showing HAI titers at day 28 and day 42 post injection with various LNP formulations of HA mRNA. LNP formulations “Lipid A,” “Lipid B,” “Lipid C,” “Lipid D,” and “Lipid E” are shown. Bars represent means and standard deviations. The LNP compositions contain the cationic lipid, DMG-PEG2000, cholesterol, and DOPE, in this order, at a molar ratio of 40:1.5:28.5:30.

[0062] **FIG. 27** depicts a graph showing Cal09 H1 HAI titers at day 28 and day 42 post injection with various LNP formulations of HA mRNA. LNP formulations “Lipid A,” “Lipid B,” “Lipid C,” “Lipid D,” and “Lipid E” are shown. Bars represent means and standard deviations. The LNP compositions contain the cationic lipid, DMG-PEG2000, cholesterol, and DOPE, in this order, at a molar ratio of 40:1.5:28.5:30.

[0063] **FIG. 28** depicts a graph showing Sing16 H3 HAI titers at day 28 and day 42 post injection with various LNP formulations of HA mRNA. LNP formulations "Lipid A," "Lipid B," "Lipid C," "Lipid D," and "Lipid E" are shown. Bars represent means and standard deviations. The LNP compositions contain the cationic lipid, DMG-PEG2000, cholesterol, and DOPE, in this order, at a molar ratio of 40:1.5:28.5:30.

[0064] **FIG. 29** depicts RSV F protein antibody titers in NHPs immunized with the FD3 F protein expressing mRNA. The mRNA was delivered with lipid nanoparticles (LNPs) containing one of several cationic lipids. The antibody titers were measured at day 0, 21, and 35 for each antigenic composition.

[0065] **FIG. 30** depicts RSV neutralization titers in NHPs immunized with the FD3 F protein expressing mRNA. The mRNA was delivered with lipid nanoparticles (LNPs) containing one of several cationic lipids. The antibody titers were measured at day 0, 21, and 35 for each antigenic composition.

[0066] **FIG. 31** depicts HAI titers for quadrivalent and octavalent mRNA-LNP vaccines administered to mice for 4 different influenza strains.

[0067] **FIG. 32** depicts HINT values for quadrivalent and octavalent mRNA-LNP vaccines, administered to ferrets for 4 different influenza strains.

[0068] **FIG. 33** depicts NAI titers for quadrivalent and octavalent mRNA-LNP vaccines, administered to mice for 4 different influenza strains.

[0069] **FIG. 34** depicts NAI titers for quadrivalent and octavalent mRNA-LNP vaccines, administered to ferrets for 4 different influenza strains. Samples were obtained on day 20 (D20) after the second dose of vaccine.

[0070] **FIG. 35** depicts NAI titers for quadrivalent and octavalent mRNA-LNP vaccines, administered to ferrets for 4 different influenza strains. Samples were obtained on day 42 (D42) after the second dose of vaccine.

[0071] **FIG. 36** depicts microneutralization titers for Sing16HA-encoding mRNA in a Lipid A LNP formulation, administered to NHPs at 15 µg and 45 µg doses. Samples were obtained on day 6 (D6) and day42 (D42) after the second dose of vaccine.

[0072] **FIG. 37** depicts microneutralization titers for Sing16HA-encoding mRNA in a Lipid B LNP formulation, administered to NHPs at 15 µg and 45 µg doses. Samples were obtained on day 6 (D6) and day42 (D42) after the second dose of vaccine.

DETAILED DESCRIPTION OF THE INVENTION

[0073] The present disclosure provides novel lipid nanoparticle (LNP) formulations for delivering mRNA vaccines *in vivo* and methods of making the vaccines. The LNPs are made of a mixture of four lipids: a cationic lipid, a polyethylene glycol (PEG)-conjugated lipid, a cholesterol-based lipid, and a helper lipid. The LNPs encapsulate mRNA molecules. The encapsulated mRNA molecules can be comprised of naturally-occurring ribonucleotides, chemically modified nucleotides, or a combination thereof, and can each or collectively code for one or more proteins.

[0074] The inventors have discovered the present formulations through screening combinatorial libraries of lipid components. The present LNPs encapsulate and protect the mRNA payload from degradation and facilitate cellular uptake of the encapsulated mRNA. The LNPs described herein have enhanced transfection efficiency, promote endosomal escape of the mRNA, and consequently have improved potency as demonstrated by enhanced expression *in vivo* and *in vitro* when compared to industrial formulations described in literature. For example, the LNPs disclosed herein have superior stability and/or potency profiles compared to known LNPs, e.g., heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino)butanoate (aka DLin-MC3-DMA or MC3; Semple et al., *Nat Biotechnol.* (2010) 28:172-6) or di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy) heptadecanedioate (aka L319; Maier et al., *Mol Ther.* (2013) 21(8):1570-8). As further described below, the present formulations encapsulating an mRNA encoding hEPO, when delivered *in vivo*, led to high levels of erythropoietin circulating in blood at 6 hours and 24 hours, with an up to 12-fold increase, relative to the industrial standard, the MC3 LNP formulation. Similarly, high potency has been found with other mRNAs, such as those encoding influenza antigens, in both murine and non-human primate models.

[0075] The mRNA vaccines as formulated herein can be used to induce a balanced immune response comprising both cellular and humoral immunity. Because the advantages of the present LNP formulations are not sequence-specific, these formulations can be used to deliver mRNAs that encode a variety of antigens, allowing rapid deployment in epidemic or pandemic situations.

Further, the present LNP-formulated mRNA vaccines are highly immunogenic and therefore provide significant dose sparing possibility.

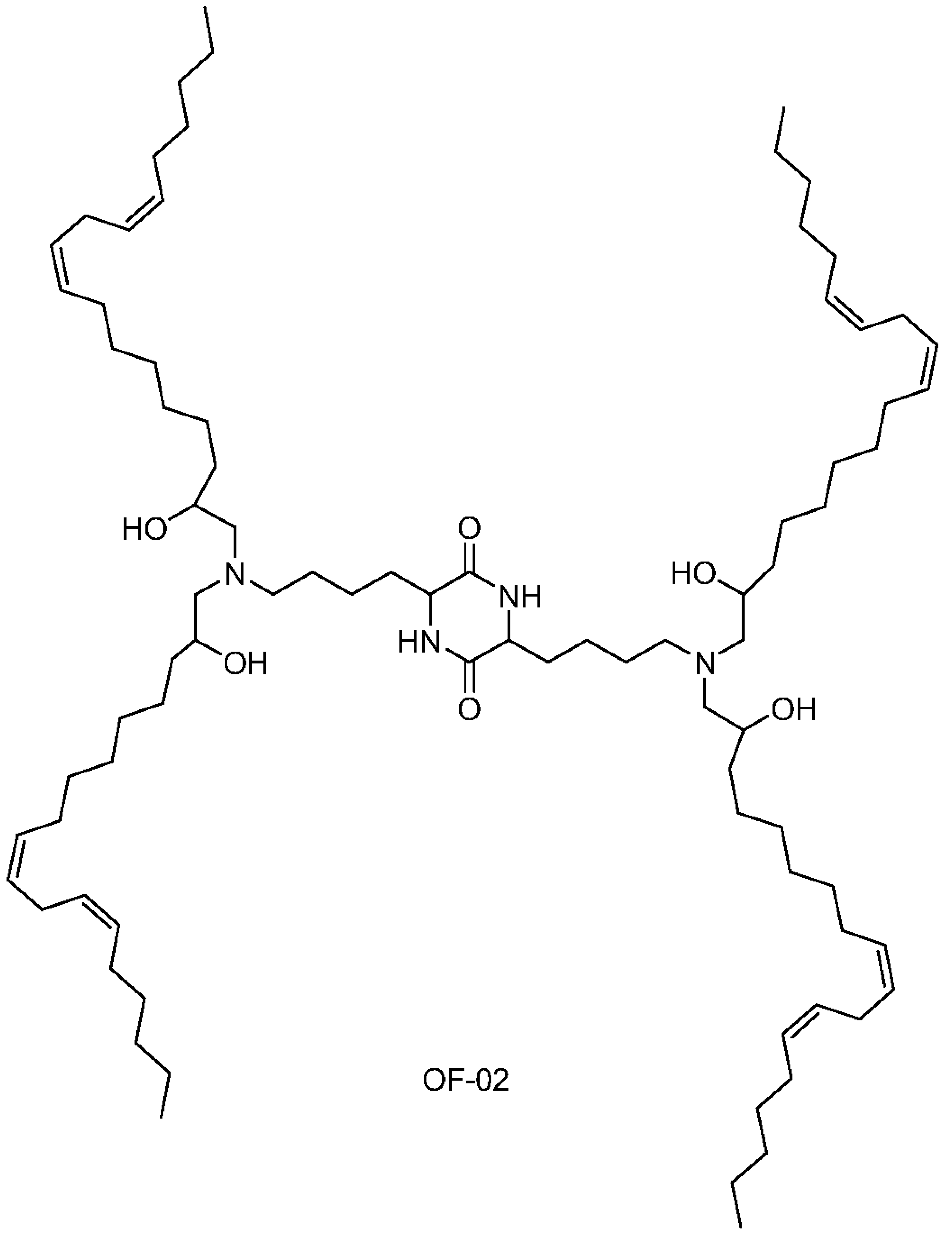
I. Compositions of the Present Lipid Nanoparticles

[0076] The present LNPs comprise four categories of lipids: (i) an ionizable lipid; (ii) a PEGylated lipid; (iii) a cholesterol-based lipid, and (iv) a helper lipid.

A. Ionizable Lipids

[0077] An ionizable lipid facilitates mRNA encapsulation and may be a cationic lipid. A cationic lipid affords a positively charged environment at low pH to facilitate efficient encapsulation of the negatively charged mRNA drug substance.

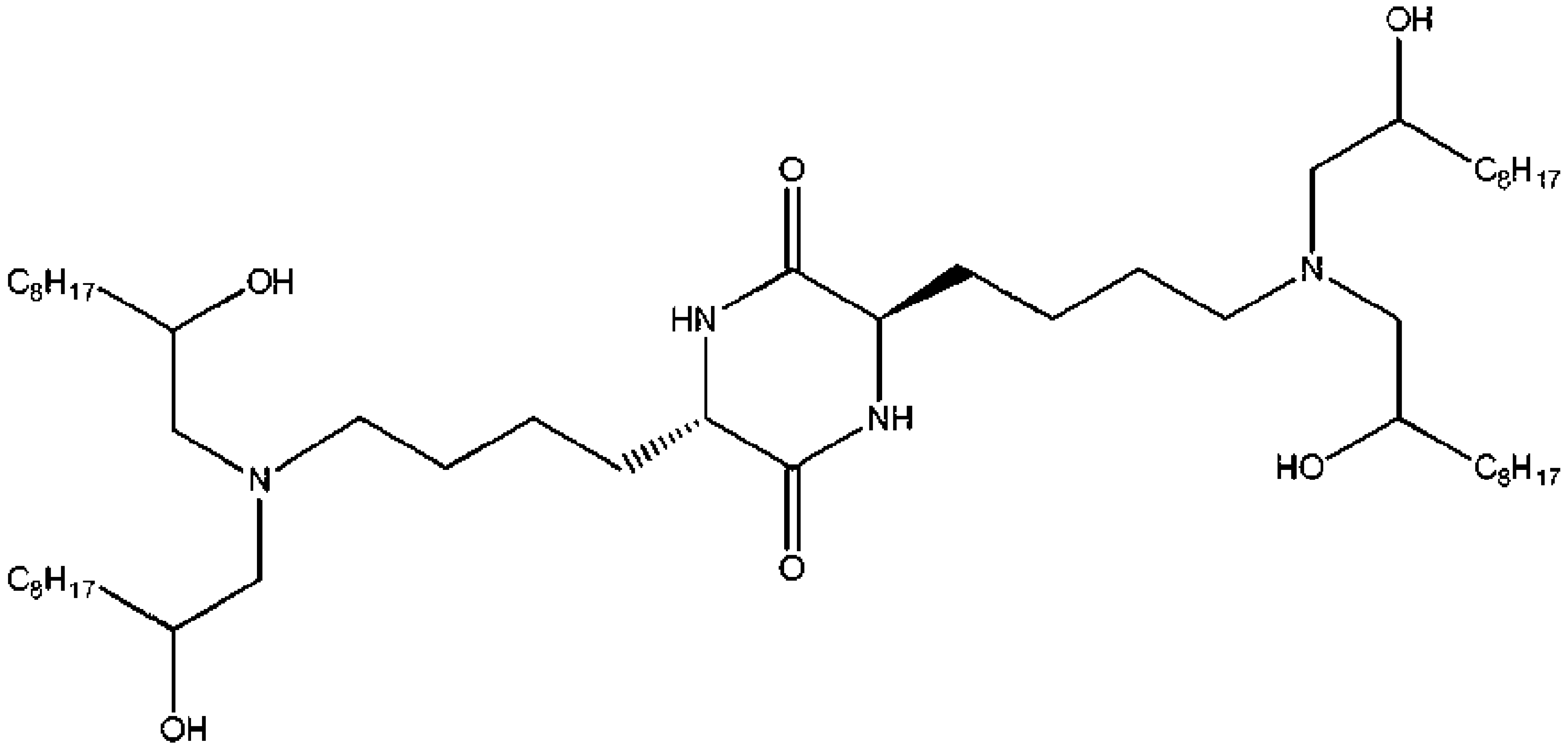
[0078] In some embodiments, the cationic lipid is OF-02:



Formula (I)

OF-02 is a non-degradable structural analog of OF-Deg-Lin. OF-Deg-Lin contains degradable ester linkages to attach the diketopiperazine core and the doubly-unsaturated tails, whereas OF-02 contains non-degradable 1,2-amino-alcohol linkages to attach the same diketopiperazine core and the doubly-unsaturated tails (Fenton et al., *Adv Mater.* (2016) 28:2939; U.S. Pat. 10,201,618). An exemplary LNP formulation herein, Lipid A, contains OF-2.

[0079] In some embodiments, the cationic lipid is cKK-E10 (Dong et al., *PNAS* (2014) 111(11):3955-60; U.S. Pat. 9,512,073):

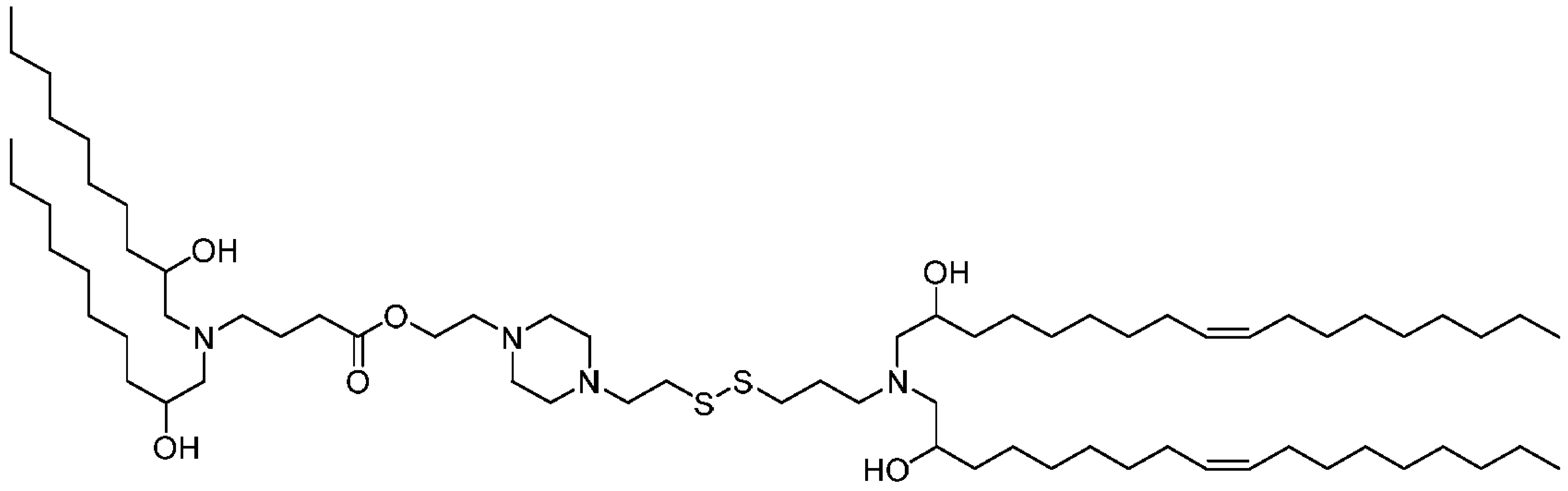


cKK-E10

Formula (II)

An exemplary LNP formulation herein, Lipid B, contains cKK-E10.

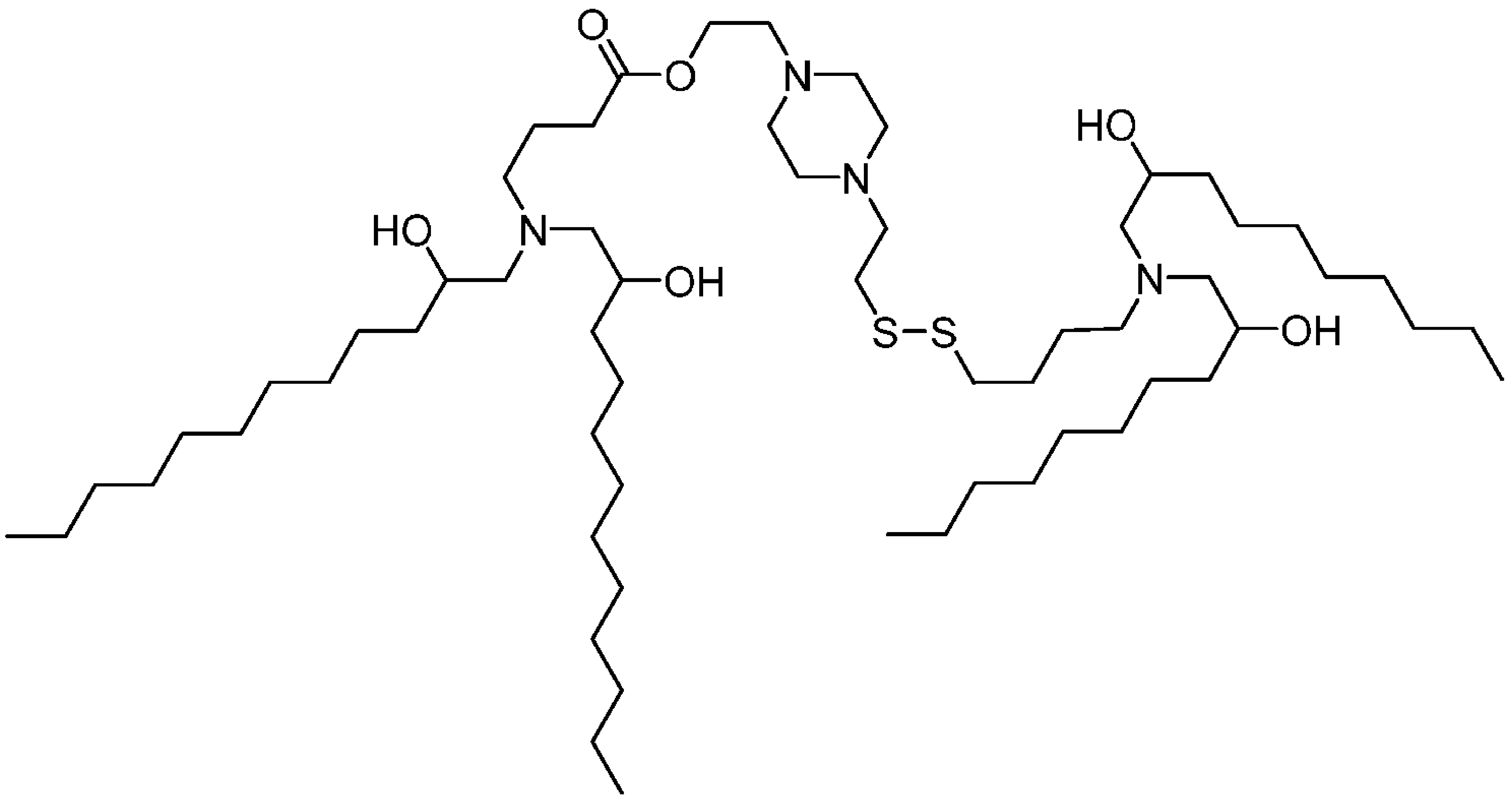
[0080] In some embodiments, the cationic lipid is GL-HEPES-E3-E10-DS-3-E18-1 (2-(4-(2-((3-(Bis((Z)-2-hydroxyoctadec-9-en-1-yl)amino)propyl)disulfaneyl)ethyl)piperazin-1-yl)ethyl 4-(bis(2-hydroxydecyl)amino)butanoate), which is a HEPES-based disulfide cationic lipid with a piperazine core, having the Formula III:



Formula (III)

An exemplary LNP formulation herein, Lipid C, contains GL-HEPES-E3-E10-DS-3-E18-1. Lipid C has the same composition as Lipid A or Lipid B but for the difference in the cationic lipid.

[0081] In some embodiments, the cationic lipid is GL-HEPES-E3-E12-DS-4-E10 (2-(4-(2-((3-(bis(2-hydroxydecyl)amino)butyl)disulfaneyl)ethyl)piperazin-1-yl)ethyl 4-(bis(2-hydroxydodecyl)amino)butanoate), which is a HEPES-based disulfide cationic lipid with a piperazine core, having the Formula IV:

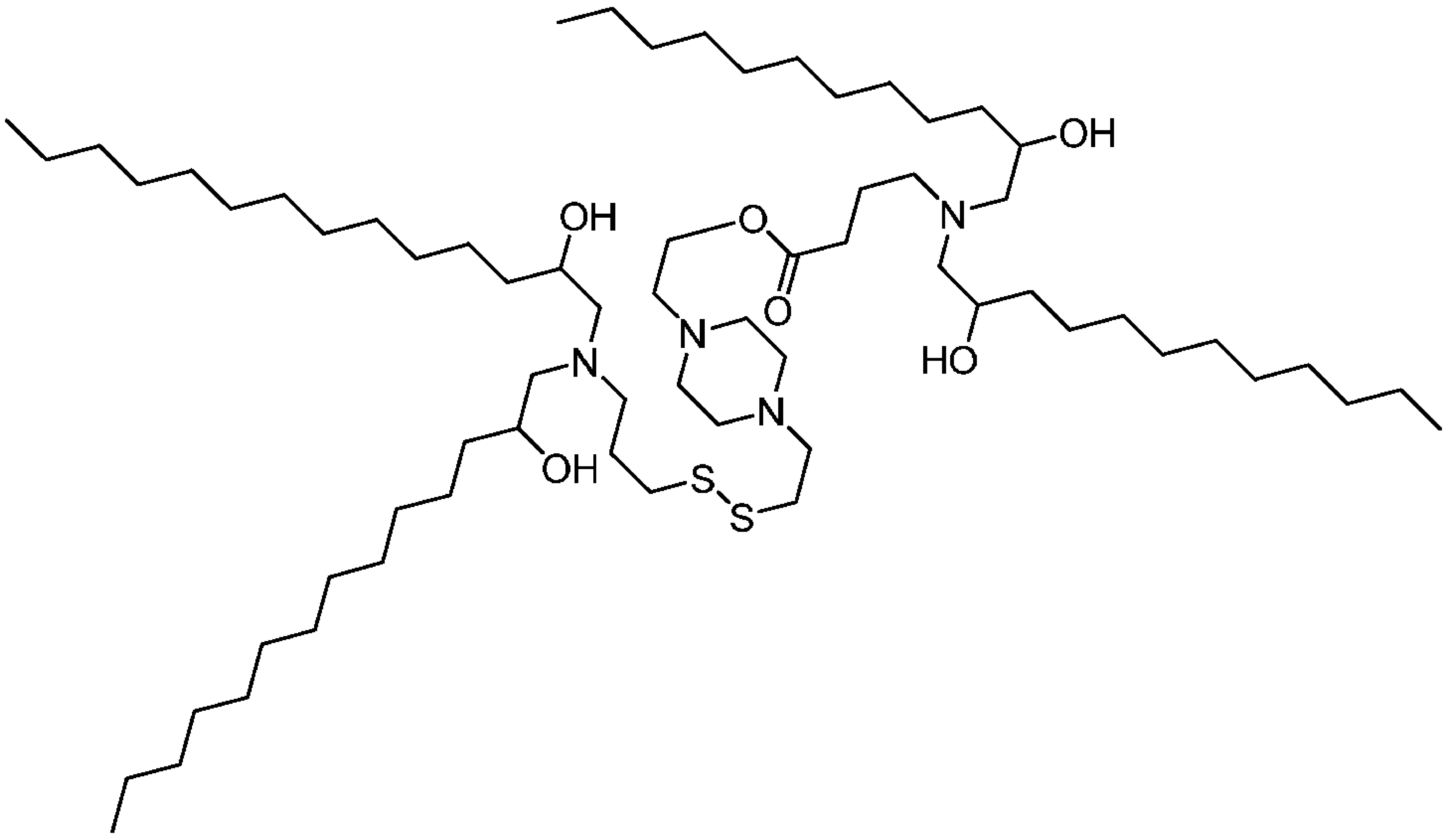


Formula (IV)

An exemplary LNP formulation herein, Lipid D, contains GL-HEPES-E3-E12-DS-4-E10. Lipid D has the same composition as Lipid A or Lipid B but for the difference in the cationic lipid.

[0082] In some embodiments, the cationic lipid is GL-HEPES-E3-E12-DS-3-E14 (2-(4-(2-((3-(Bis(2-hydroxytetradecyl)amino)propyl)disulfaneyl)ethyl)piperazin-1-yl)ethyl 4-(bis(2-

hydroxydodecyl)amino)butanoate), which is a HEPES-based disulfide cationic lipid with a piperazine core, having the Formula V:

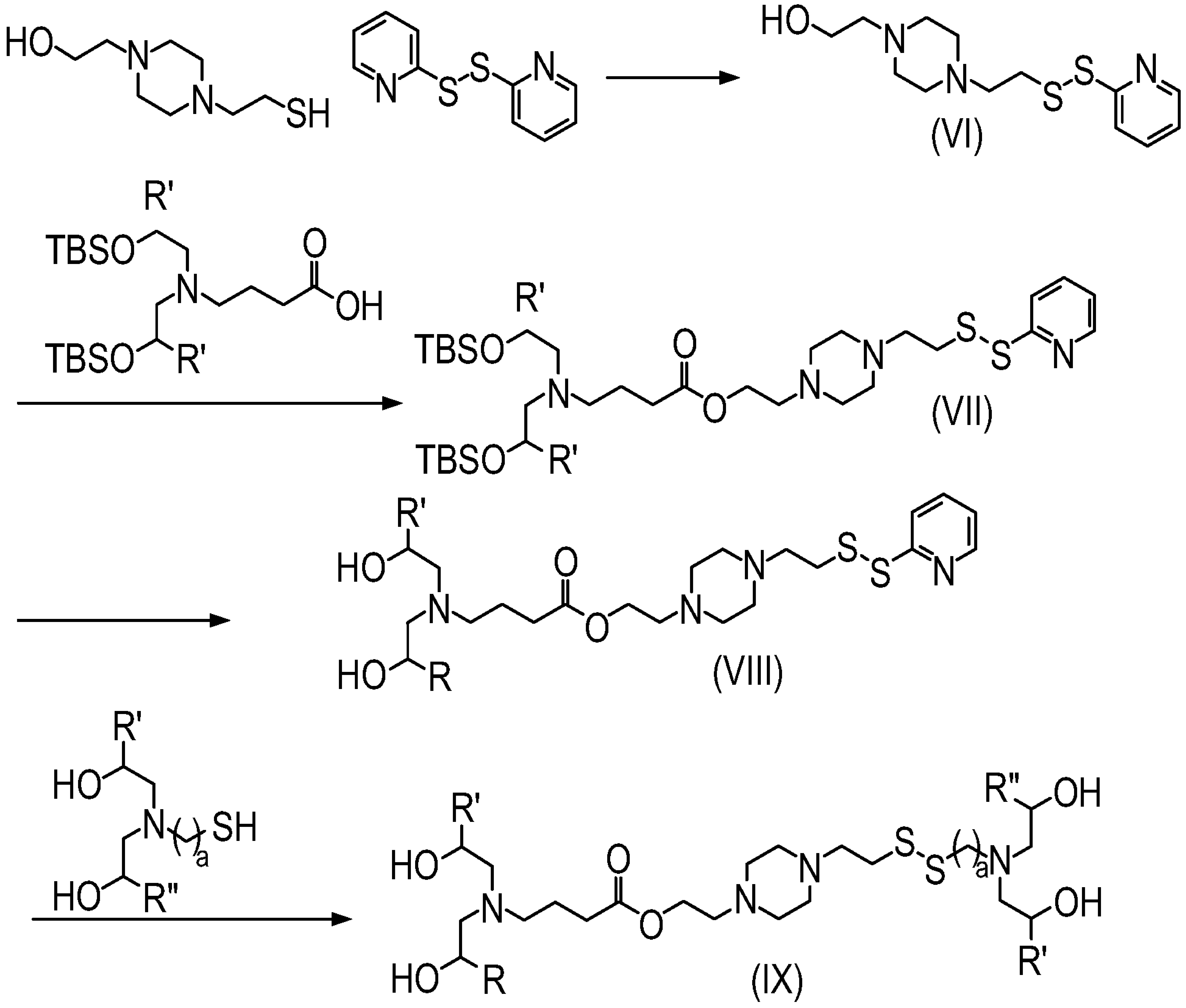


Formula (V)

An exemplary LNP formulation herein, Lipid E, contains GL-HEPES-E3-E12-DS-3-E14. Lipid E has the same composition as Lipid A or Lipid B but for the difference in the cationic lipid.

[0083] The cationic lipids GL-HEPES-E3-E10-DS-3-E18-1 (III), GL-HEPES-E3-E12-DS-4-E10 (IV), and GL-HEPES-E3-E12-DS-3-E14 (V) can be synthesized according to the general procedure set out in Scheme 1:

Scheme 1: General Synthetic Scheme for Lipids of Formulas (III), (IV), and (V)



[0084] Other cationic lipids that can be used include those described in Dong, *supra*; and U.S. Pat. 10,201,618.

B. PEGylated Lipids

[0085] The PEGylated lipid component provides control over particle size and stability of the nanoparticle. The addition of such components may prevent complex aggregation and provide a means for increasing circulation lifetime and increasing the delivery of the lipid-nucleic acid pharmaceutical composition to target tissues (Klibanov et al., *FEBS Letters* (1990) 268 (1):235-7). These components may be selected to rapidly exchange out of the pharmaceutical composition *in vivo* (*see, e.g.*, U.S. Pat. 5,885,613).

[0086] Contemplated PEGylated lipids include, but are not limited to, a polyethylene glycol (PEG) chain of up to 5 kDa in length covalently attached to a lipid with alkyl chain(s) of C_6-C_{20} (e.g., C_8 ,C_{10},C_{12},C_{14},C_{16}, or C_{18}) lenght, such as a derivatized ceramide (e.g., N-octanoyl-sphingosine-1-[succinyl(methoxypolyethylene glycol)] (C8 PEG ceramide)). In some embodiments, the PEGylated lipid is 1,2-dimyristoyl-rac-glycero-3-methoxypolyethylene glycol (DMG-PEG); 1,2-distearoyl-sn-glycero-3-phosphoethanolamine-polyethylene glycol (DSPE-PEG); 1,2-dilauroyl-sn-glycero-3-phosphoethanolamine-polyethylene glycol (DLPE-PEG); or 1,2-distearoyl-rac-glycero-polyethelene glycol (DSG-PEG).

[0087] In particularly exemplary embodiments, the PEG has a high molecular weight, e.g., 2000-2400 g/mol. In some embodiments, the PEG is PEG2000 (or PEG-2K). In particular embodiments, the PEGylated lipid herein is DMG-PEG2000, DSPE-PEG2000, DLPE-PEG2000, DSG-PEG2000, or C8 PEG2000.

C. Cholesterol-Based Lipids

[0088] The cholesterol component provides stability to the lipid bilayer structure within the nanoparticle. In some embodiments, the LNPs comprise one or more cholesterol-based lipids. Suitable cholesterol-based lipids include, for example: DC-Choi (N,N-dimethyl-N-ethylcarboxamidocholesterol), 1,4-bis(3-N-oleylamino-propyl)piperazine (Gao et al., *Biochem Biophys Res Comm.* (1991) 179:280; Wolf et al., *BioTechniques* (1997) 23:139; U.S. Pat. 5,744,335), imidazole cholesterol ester ("ICE"; WO 2011/068810), β-sitosterol, fucosterol, stigmasterol, and other modified forms of cholesterol. In some embodiments, the cholesterol-based lipid used in the LNPs is cholesterol.

D. Helper Lipids

[0089] A helper lipid enhances the structural stability of the LNP and helps the LNP in endosome escape. It improves uptake and release of the mRNA drug payload. In some embodiments, the helper lipid is a zwitterionic lipid, which has fusogenic properties for enhancing uptake and release of the drug payload. Examples of helper lipids are 1,2-dioleoyl-SN-glycero-3-phosphoethanolamine (DOPE); 1,2-distearoyl-sn-glycero-3-phosphocholine (DSPC); 1,2-dioleoyl-sn-glycero-3-phospho-L-serine (DOPS); 1,2-dielaidoyl-sn-glycero-3-phosphoethanolamine (DEPE); and 1,2-dioleoyl-sn-glycero-3-phosphocholine (DPOC), dipalmitoylphosphatidylcholine (DPPC), 1,2-dilauroyl-sn-glycero-3-phosphocholine (DLPC), 1,2-Distearoylphosphatidylethanolamine (DSPE), and 1,2-dilauroyl-sn-glycero-3-phosphoethanolamine (DLPE).

[0090] Other exemplary helper lipids are dioleoylphosphatidylcholine (DOPC), dioleoylphosphatidylglycerol (DOPG), dipalmitoylphosphatidylglycerol (DPPG), palmitoyloleoylphosphatidylcholine (POPC), palmitoyloleoyl-phosphatidylethanolamine

(POPE), dioleoyl-phosphatidylethanolamine 4-(N-maleimidomethyl)-cyclohexane-l-carboxylate (DOPE-mal), dipalmitoyl phosphatidyl ethanolamine (DPPE), dimyristoylphosphoethanolamine (DMPE), phosphatidylserine, sphingolipids, cerebrosides, gangliosides, 16-O-monomethyl PE, 16-O-dimethyl PE, 18-1-trans PE, l-stearoyl-2-oleoyl-phosphatidyethanolamine (SOPE), or a combination thereof.

[0091] In particular embodiments, the helper lipid is DOPE. In further embodiments, the present LNPs comprise (i) a cationic lipid selected from OF-02, cKK-E10, GL-HEPES-E3-E10-DS-3-E18-1, GL-HEPES-E3-E12-DS-4-E10, or GL-HEPES-E3-E12-DS-3-E14; (ii) DMG-PEG2000; (iii) cholesterol; and (iv) DOPE.

E. Molar Ratios of the Lipid Components

[0092] The inventors have discovered that specific molar ratios of the above components are important for the LNPs' effectiveness in delivering mRNA. The molar ratio of the cationic lipid, the PEGylated lipid, the cholesterol-based lipid, and the helper lipid is A: B: C: D, where A + B + C + D = 100%. In some embodiments, the molar ratio of the cationic lipid in the LNPs relative to the total lipids (i.e., A) is 35-45% (e.g., 38-42% such as 40%). In some embodiments, the molar ratio of the PEGylated lipid component relative to the total lipids (i.e., B) is 0.25-2.75% (e.g., 1-2% such as 1.5%). In some embodiments, the molar ratio of the cholesterol-based lipid relative to the total lipids (i.e., C) is 20-35% (e.g., 27-30% such as 28.5%). In some embodiments, the molar ratio of the helper lipid relative to the total lipids (i.e., D) is 25-35% (e.g., 28-32% such as 30%). In some embodiments, the (PEGylated lipid + cholesterol) components have the same molar amount as the helper lipid. In some embodiments, the LNPs contain a molar ratio of the cationic lipid to the helper lipid that is more than 1.

[0093] In particular embodiments, the LNPs contain a cationic lipid, a PEGylated lipid, a cholesterol-based lipid, and a helper lipid at a molar ratio of 40: 1.5: 28.5: 30. In further specific embodiments, the LNPs contain (i) OF-02, cKK-E10, GL-HEPES-E3-E10-DS-3-E18-1, GL-HEPES-E3-E12-DS-4-E10, or GL-HEPES-E3-E12-DS-3-E14; (ii) DMG-PEG2000; (iii) cholesterol; and (iv) DOPE at 40: 1.5: 28.5: 30.

[0094] To calculate the actual amount of each lipid to be put into an LNP formulation, the molar amount of the cationic lipid is first determined based on a desired N/P ratio, where N is the number of nitrogen atoms in the cationic lipid and P is the number of phosphate groups in the mRNA to be transported by the LNP. Next, the molar amount of each of the other lipids is calculated based on the molar amount of the cationic lipid and the molar ratio selected. These molar amounts are then converted to weights using the molecular weight of each lipid.

F. Active Ingredients of the LNPs

[0095] The active ingredient of the present LNP vaccine composition is an mRNA that encodes an antigen of interest. The antigen may be a polypeptide derived from a virus, for example, influenza virus, coronavirus (e.g., SARS-CoV-1, SARS-CoV-2, or MERS-related virus), Ebola virus, Dengue virus, human immunodeficiency virus (HIV), hepatitis A virus (HAV), hepatitis B virus (HBV), hepatitis C virus (HCV), herpes simplex virus (HSV), respiratory syncytial virus (RSV), rhinovirus, cytomegalovirus (CMV), zika virus, human papillomavirus (HPV), human metapneumovirus (hMPV), human parainfluenza virus type 3 (PIV3), Epstein-Barr virus (EBV), chikungunya virus, or respiratory syncytial virus (RSV).

[0096] The antigen also may be derived from a bacterium, for example, *Staphylococcus aureus*, *Moraxella* (e.g., *Moraxella catarrhalis*; causing otitis, respiratory infections, and/or sinusitis), *Chlamydia trachomatis* (causing chlamydia), borrelia (e.g., *Borrelia burgdorferi* causing Lyme Disease), *Bacillus anthracis* (causing anthrax), *Salmonella typhi* (causing typhoid fever), *Mycobacterium tuberculosis* (causing tuberculosis), *Propionibacterium acnes* (causing acne), or non-typeable *Haemophilus influenzae.*

[0097] Where desired, the LNP or the LNP formulation may be multi-valent. In some embodiments, the LNP may carry mRNAs that encode more than one antigen, such as two, three, four, five, six, seven, eight, nine, ten, or more antigens, from the same or different pathogens. For example, the LNP may carry multiple mRNA molecules, each encoding a different antigen; or carry a polycistronic mRNA that can be translated into more than one antigen (e.g., each antigen-coding sequence is separated by a nucleotide linker encoding a self-cleaving peptide such as a 2A peptide). An LNP carrying different mRNA molecules typically comprises (encapsulate) multiple copies of each mRNA molecule. For example, an LNP carrying or encapsulating two different mRNA molecules typically carries multiple copies of each of the two different mRNA molecules.

[0098] In some embodiments, a single LNP formulation may comprise multiple kinds (e.g., two, three, four, five, six, seven, eight, nine, ten, or more) of LNPs, each kind carrying a different mRNA.

[0099] Examples of multi-valent LNP vaccines are those containing mRNAs encoding two or more antigens from the above-listed pathogens, such as LNP vaccines comprising mRNAs encoding polypeptides derived from influenza virus. In some embodiments, the multi-valent LNP vaccines contain mRNA molecules encoding polypeptides derived from two or more (e.g., three, four, five, six, seven, eight, nine, or ten) influenza viral proteins selected from hemagglutinin (e.g., hemagglutinin 1 (HA1) and hemagglutinin 2 (HA2)), neuraminidase (NA), nucleoprotein (NP), matrix protein 1 (M1), matrix protein 2 (M2), nonstructural protein 1 (NS1), and non-structural protein 2 (NS2). In further embodiments, the multi-valent LNP vaccines containing two or more (e.g., three, four five, six, seven, eight, or more) mRNA molecules encoding antigenic polypeptides derived from an HA protein, from an NA protein, and from both HA and NA proteins. In some embodiments, the mRNA molecules encoding antigenic polypeptides are derived from different influenza strains.

[00100] In certain embodiments, the composition may comprise one or more mRNA molecules encoding antigens of influenza A, B and C viruses. In one embodiment, the composition may comprise one or more mRNA molecules encoding HA and/or NA antigens of influenza A and influenza B viruses. In one embodiment, the HA antigens of influenza A viruses are selected from subtypes H1, H2, H3, H4, H5, H6, H7, H8, H9, H10, H11, H12, H13, H14, H15, H16, H17, and H18. In one embodiment, the NA antigens of influenza A viruses are selected from subtypes N1, N2, N3, N4, N5, N6, N7, N8, N9, N10, and N11. In one embodiment, the HA and NA antigens of Influenza B viruses are from the Influenza B/Yamagata lineage. In one embodiment, the HA and NA antigens of Influenza B viruses are from the Influenza B/Victoria lineage. In some embodiments, the one or more HA and NA antigens are from influenza virus strains recommended by the World Health Organization (WHO) in their annual recommendation for influenza vaccine formulations.

[00101] In certain embodiments, at least one of the one or more influenza virus proteins comprises an influenza virus HA protein and/or an influenza virus NA protein having a molecular sequence identified or designed from a machine learning model, and in certain embodiments, at least one of the one or more ribonucleic acid molecules encode one or more influenza virus proteins having a molecular sequence identified or designed from a machine learning model.

[00102] In certain embodiments, the composition comprises two, three, four, five, six, seven, eight, nine, or more mRNA molecules encoding (i) one or more HA antigens, (ii) one or more NA antigens, or (iii) a combination of one or more HA antigens and NA antigens.

[00103] In one embodiment, the composition comprises two, three, four, five, six, seven, eight, nine, or more mRNA molecules encoding (i) one or more HA antigens, (ii) one or more NA antigens, or (iii) a combination of one or more HA antigens and NA antigens, selected from H1N1, H3N2, H2N2, H5N1, H7N9, H7N7, H1N2, H9N2, H7N2, H7N3, H5N2, and H10N7 subtypes and/or B/Yamagata and B/Victoria lineages.

[00104] In one embodiment, the composition comprises one mRNA molecule encoding an H3 HA antigen, one mRNA molecule encoding an H1 HA antigen, one mRNA molecule encoding an HA antigen from the Influenza B/Yamagata lineage, and one mRNA molecule encoding an HA antigen from the Influenza B/Victoria lineage.

[00105] In one embodiment, the composition comprises one mRNA molecule encoding an H3 HA antigen, one mRNA molecule encoding an N2 NA antigen, one mRNA molecule encoding an H1 HA antigen, one mRNA molecule encoding an N1 NA antigen, one mRNA molecule encoding an HA antigen from the Influenza B/Yamagata lineage, one mRNA molecule encoding an NA antigen from the Influenza B/Yamagata lineage, one mRNA molecule encoding an HA antigen from the Influenza B/Victoria lineage, and one mRNA molecule encoding an NA antigen from the Influenza B/Victoria lineage.

[00106] In an embodiment, the composition comprises further comprise one or more mRNA molecules encoding a machine learning influenza virus HA having a molecular sequence identified or designed from a machine learning model, wherein the one or more machine learning influenza virus HA may be selected from an H1 HA, an H3 HA, an HA from a B/Victoria lineage, an HA from a B/Yamagata lineage, or a combination thereof.

[00107] When selecting one or more machine learning influenza virus HAs, any machine learning algorithm may be used. For example, envisioned herein are any of the machine learning algorithms and methods disclosed in PCT Application Nos. WO 2021/080990 A1, entitled Systems and Methods for Designing Vaccines, and WO 2021/080999 A1, entitled Systems and Methods for Predicting Biological Responses, both of which are incorporated by reference in their entireties herein.

[00108] The mRNA molecule may be unmodified (i.e., containing only natural ribonucleotides A, U, C, and/or G linked by phosphodiester bonds), or chemically modified (e.g., including nucleotide analogs such as pseudouridines (e.g., N-1-methyl pseudouridine), 2’-fluoro ribonucleotides, and 2'-methoxy ribonucleotides, and/or phosphorothioate bonds). The mRNA molecule may comprise a 5' cap and a polyA tail.

[00109] RSV F Protein:

[00110] Respiratory syncytial virus (RSV) is a negative-sense, single-stranded RNA virus belonging to the *Pneumoviridae* family. RSV can cause infection of the respiratory tract. RSV is an enveloped virus with a glycoprotein (G protein), small hydrophobic protein (SH protein), and a fusion protein (F protein) on the surface.

[00111] The RSV F protein is responsible for fusion of viral and host cell membranes and takes on at least three conformations (pre-fusion, intermediate, and post-fusion conformations). In the pre-fusion conformation (pre-fusion, Pre-F), the F protein exists in a trimeric form with the major antigenic site Ø exposed. Site Ø serves as a primary target of neutralizing antibodies produced by RSV-infected subjects (see, Coultas et al., Thorax. 74: 986-993. 2019; McLellan et al., Science. 340(6136): 1113-7. 2013). After binding to its target on the host cell surface, Pre-F undergoes a conformational change during which site Ø is no longer exposed. Pre-F transitions into a transient intermediate conformation, enabling the F protein to insert into the host cell membrane, leading to fusion of the viral and host cell membranes. A final conformational shift results in a more stable and elongated form of the protein (post-fusion, Post-F). Site II and Site IV of the F protein are specific to Post-F, while Site I is present in both the Pre-F and Post-F conformations (McLellan et al., J. Virol. 85(15): 7788-7796. 2011).

[00112] As used herein, the term "F protein" or "RSV F protein" refers to the protein of RSV responsible for driving fusion of the viral envelope with host cell membrane during viral entry.

[00113] As used herein, the term "RSV F polypeptide" or "F polypeptide" refers to a polypeptide comprising at least one epitope of F protein.

[00114] As used herein, the term "post-fusion" with respect to RSV F refers to a stable conformation of RSV F that occurs after merging of the virus and cell membranes.

[00115] As used herein, the term "pre-fusion" with respect to RSV F refers to a conformation of RSV F that is adopted before virus-cell interaction.

[00116] Provided herein are mRNA molecules that encode for antigenic RSV F polypeptides.

[00117] In some embodiments, the mRNA molecule comprises an open reading frame (ORF) encoding a respiratory syncytial virus (RSV) F protein antigen.

[00118] In some embodiments, the RSV F protein antigen comprises a sequence having at least 85%, 90%, 95%, 97%, 98%, 99%, or 99.5% identity to an amino acid sequence set forth in SEQ ID NO: 16.

[00119] In some embodiments, the RSV F protein antigen comprises an amino acid sequence with at least 98% identity to SEQ ID NO: 16 or consists of an amino acid sequence of SEQ ID NO: 16.

[00120] In some embodiments, the mRNA comprises a nucleic acid sequence with at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity to the nucleic acid sequence set forth in SEQ ID NO: 17.

[00121] In some embodiments, the mRNA comprises a nucleic acid sequence with at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identity to the nucleic acid sequence set forth in SEQ ID NO: 21.

[00122] In some embodiments, the RSV F protein antigen is a pre-fusion protein.

[00123] In some embodiments, wherein the ORF is codon optimized.

[00124] In some embodiments, wherein the mRNA molecule comprises at least one 5' untranslated region (5' UTR), at least one 3' untranslated region (3' UTR), and at least one polyadenylation (poly(A)) sequence.

[00125] In some embodiments, the mRNA comprises at least one chemical modification.

[00126] In some embodiments, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of the uracil nucleotides in the mRNA are chemically modified.

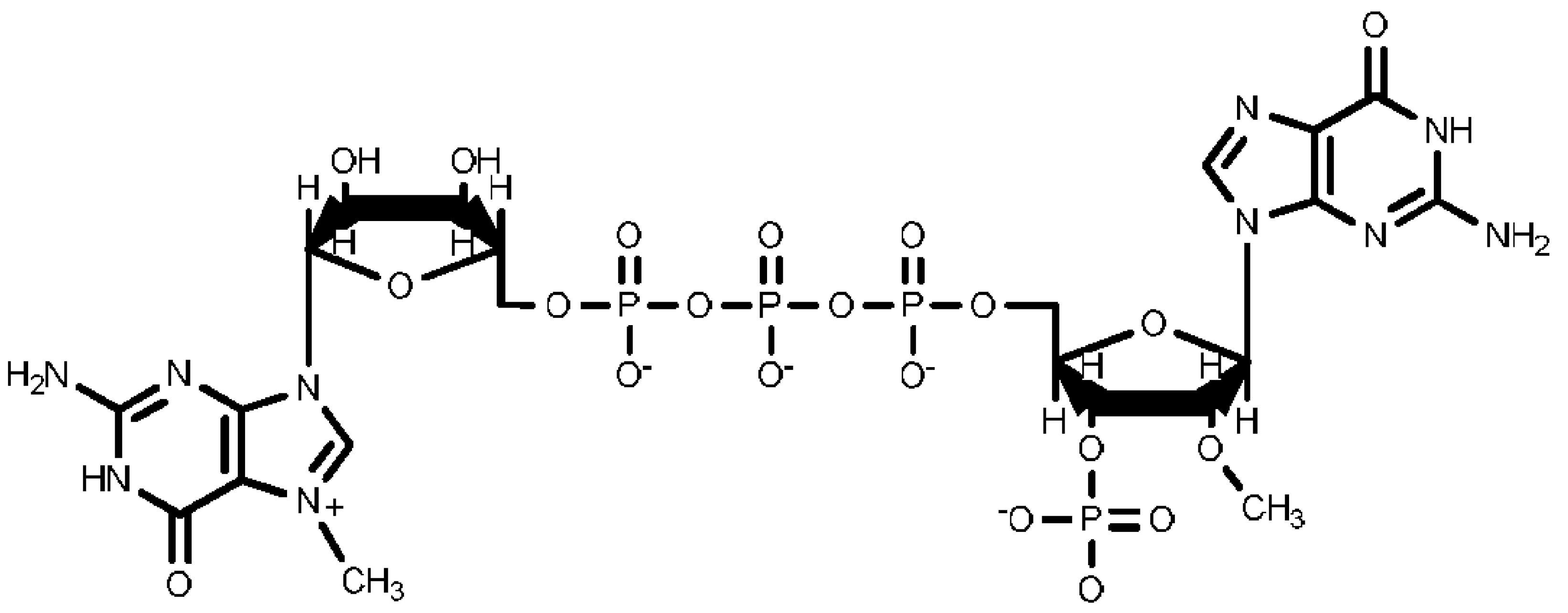
[00127] In some embodiments, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of the uracil nucleotides in the ORF are chemically modified.

[00128] In some embodiments, the chemical modification is selected from the group consisting of pseudouridine, N1-methylpseudouridine, 2-thiouridine, 4'-thiouridine, 5-methylcytosine, 2-thio-l-methyl-1-deaza-pseudouridine, 2-thio-l-methyl-pseudouridine, 2-thio-5-aza-uridine, 2-thio-dihydropseudouridine, 2-thio-dihydrouridine, 2-thio-pseudouridine, 4-methoxy-2-thio-pseudouridine, 4-methoxy-pseudouridine, 4-thio-l-methyl-pseudouridine, 4-thio-pseudouridine, 5-aza-uridine, dihydropseudouridine, 5-methyluridine, 5-methyluridine, 5-methoxyuridine, and 2'-O-methyl uridine.

[00129] In some embodiments, the chemical modification is selected from the group consisting of pseudouridine, N1-methylpseudouridine, 5-methylcytosine, 5-methoxyuridine, and a combination thereof. In some embodiments, the chemical modification is N1-methylpseudouridine.

[00130] In some embodiments, the mRNA comprises of the following structural elements:

(i) a 5' cap with the following structure:



;

(ii) a 5′ untranslated region (5' UTR) having the nucleic acid sequence of SEQ ID NO: 19;

(iii) a protein coding region having the nucleic acid sequence of SEQ ID NO: 17;

(iv) a 3' untranslated region (3' UTR) having the nucleic acid sequence of SEQ ID NO: 20; and

(v) a poly(A) tail.

G. Buffer and Other Components

[00131] To stabilize the nucleic acid and/or LNPs (e.g., to prolong the shelf-life of the vaccine product), to facilitate administration of the LNP pharmaceutical composition, and/or to enhance *in vivo* expression of the nucleic acid, the nucleic acid and/or LNP can be formulated in combination with one or more carriers, targeting ligands, stabilizing reagents (e.g., preservatives and antioxidants), and/or other pharmaceutically acceptable excipients. Examples of such excipients are parabens, thimerosal, thiomersal, chlorobutanol, bezalkonium chloride, chelators (e.g., EDTA) and the like.

[00132] The LNP compositions of the present disclosure can be provided as a frozen liquid form or a lyophilized form. A variety of cryoprotectants may be used, including, without limitations, sucrose, trehalose, glucose, mannitol, mannose, dextrose, and the like. The cryoprotectant may constitute 5-30% (w/v) of the LNP composition. In some embodiments, the LNP composition comprises trehalose, e.g., at 5-30% (e.g., 10%) (w/v). Once formulated with the cryoprotectant, the LNP compositions may be frozen (or lyophilized and cryopreserved) at -20°C to -80°C.

[00133] The LNP compositions may be provided to a patient in an aqueous buffered solution – thawed if previously frozen, or if previously lyophilized, reconstituted in an aqueous buffered solution at bedside. In particularly exemplary embodiments, the buffered solutionis isotonic and suitable for e.g., intramuscular or intradermal injection. In some embodiments, the buffered solution is a phosphate-buffered saline (PBS).

II. RNA

[00134] The present LNP vaccine compositions of the disclosure may comprise an RNA molecule (e.g., mRNA) that encodes an antigen of interest. The RNA molecule of the present disclosure may comprise at least one ribonucleic acid (RNA) comprising an ORF encoding an antigen of interest. In certain embodiments, the RNA is a messenger RNA (mRNA) comprising an ORF encoding an antigen of interest. In certain embodiments, the RNA (e.g., mRNA) further comprises at least one 5’ UTR, 3’ UTR, a poly(A) tail, and/or a 5’ cap.

II. A. 5’ Cap

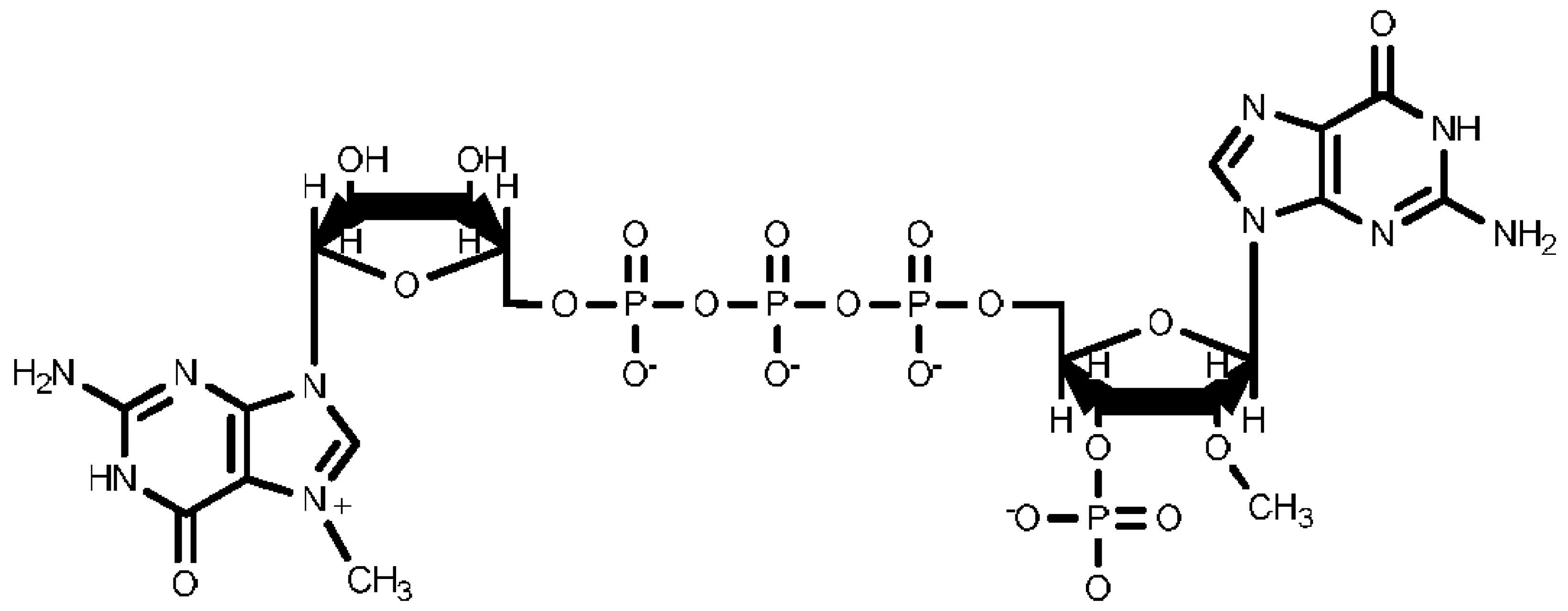
[00135] An mRNA 5’ cap can provide resistance to nucleases found in most eukaryotic cells and promote translation efficiency. Several types of 5’ caps are known. A 7-methylguanosine cap (also referred to as “m^{7}G” or “Cap-0”), comprises a guanosine that is linked through a 5’ – 5’ - triphosphate bond to the first transcribed nucleotide.

[00136] A 5' cap is typically added as follows: first, an RNA terminal phosphatase removes one of the terminal phosphate groups from the 5’ nucleotide, leaving two terminal phosphates; guanosine triphosphate (GTP) is then added to the terminal phosphates via a guanylyl transferase, producing a 5 ‘5 ‘5 triphosphate linkage; and the 7-nitrogen of guanine is then methylated by a methyltransferase. Examples of cap structures include, but are not limited to, m7G(5')ppp, (5'(A,G(5')ppp(5')A, and G(5')ppp(5')G. Additional cap structures are described in U.S. Publication No. US 2016/0032356 and U.S. Publication No. US 2018/0125989, which are incorporated herein by reference.

[00137] 5'-capping of polynucleotides may be completed concomitantly during the *in vitro*-transcription reaction using the following chemical RNA cap analogs to generate the 5'-guanosine cap structure according to manufacturer protocols: 3'-O-Me-m7G(5')ppp(5')G (the ARCA cap); G(5')ppp(5')A; G(5')ppp(5')G; m7G(5')ppp(5')A; m7G(5')ppp(5')G; m7G(5')ppp(5')(2'OMeA)pG; m7G(5')ppp(5')(2'OMeA)pU; m7G(5')ppp(5')(2'OMeG)pG (New England BioLabs, Ipswich, MA; TriLink Biotechnologies). 5'-capping of modified RNA may be completed post-transcriptionally using a vaccinia virus capping enzyme to generate the Cap 0 structure: m7G(5')ppp(5')G. Cap 1 structure may be generated using both vaccinia virus capping enzyme and a 2'-O methyl-transferase to generate: m7G(5')ppp(5')G-2'-O-methyl. Cap 2 structure may be generated from the Cap 1 structure followed by the 2'-O-methylation of the 5'-antepenultimate nucleotide using a 2'-O methyl-transferase. Cap 3 structure may be generated from the Cap 2 structure followed by the 2'-O-methylation of the 5'-preantepenultimate nucleotide using a 2'-O methyl-transferase.

[00138] In certain embodiments, the mRNA of the disclosure comprises a 5' cap selected from the group consisting of 3'-O-Me-m7G(5')ppp(5')G (the ARCA cap), G(5')ppp(5')A, G(5')ppp(5')G, m7G(5')ppp(5')A, m7G(5')ppp(5')G, m7G(5')ppp(5')(2'OMeA)pG, m7G(5')ppp(5')(2'OMeA)pU, and m7G(5')ppp(5')(2'OMeG)pG.

[00139] In certain embodiments, the mRNA of the disclosure comprises a 5' cap of:



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II. B. Untranslated Region (UTR)

[00140] In some embodiments, the mRNA of the disclosure includes a 5' and/or 3' untranslated region (UTR). In mRNA, the 5' UTR starts at the transcription start site and continues to the start codon but does not include the start codon. The 3' UTR starts immediately following the stop codon and continues until the transcriptional termination signal.

[00141] In some embodiments, the mRNA disclosed herein may comprise a 5' UTR that includes one or more elements that affect an mRNA's stability or translation. In some embodiments, a 5' UTR may be about 10 to 5,000 nucleotides in length. In some embodiments, a 5' UTR may be about 50 to 500 nucleotides in length. In some embodiments, the 5' UTR is at least about 10 nucleotides in length, about 20 nucleotides in length, about 30 nucleotides in length, about 40 nucleotides in length, about 50 nucleotides in length, about 100 nucleotides in length, about 150 nucleotides in length, about 200 nucleotides in length, about 250 nucleotides in length, about 300 nucleotides in length, about 350 nucleotides in length, about 400 nucleotides in length, about 450 nucleotides in length, about 500 nucleotides in length, about 550 nucleotides in length, about 600 nucleotides in length, about 650 nucleotides in length, about 700 nucleotides in length, about 750 nucleotides in length, about 800 nucleotides in length, about 850 nucleotides in length, about 900 nucleotides in length, about 950 nucleotides in length, about 1,000 nucleotides in length, about 1,500 nucleotides in length, about 2,000 nucleotides in length, about 2,500 nucleotides in length, about 3,000 nucleotides in length, about 3,500 nucleotides in length, about 4,000 nucleotides in length, about 4,500 nucleotides in length or about 5,000 nucleotides in length.

[00142] In some embodiments, the mRNA disclosed herein may comprise a 3' UTR comprising one or more of a polyadenylation signal, a binding site for proteins that affect an mRNA's stability of location in a cell, or one or more binding sites for miRNAs. In some embodiments, a 3' UTR may be 50 to 5,000 nucleotides in length or longer. In some embodiments, a 3' UTR may be 50 to 1,000 nucleotides in length or longer. In some embodiments, the 3' UTR is at least about 50 nucleotides in length, about 100 nucleotides in length, about 150 nucleotides in length, about 200 nucleotides in length, about 250 nucleotides in length, about 300 nucleotides in length, about 350 nucleotides in length, about 400 nucleotides in length, about 450 nucleotides in length, about 500 nucleotides in length, about 550 nucleotides in length, about 600 nucleotides in length, about 650 nucleotides in length, about 700 nucleotides in length, about 750 nucleotides in length, about 800 nucleotides in length, about 850 nucleotides in length, about 900 nucleotides in length, about 950 nucleotides in length, about 1,000 nucleotides in length, about 1,500 nucleotides in length, about 2,000 nucleotides in length, about 2,500 nucleotides in length, about 3,000 nucleotides in length, about 3,500 nucleotides in length, about 4,000 nucleotides in length, about 4,500 nucleotides in length, or about 5,000 nucleotides in length.

[00143] In some embodiments, the mRNA disclosed herein may comprise a 5' or 3' UTR that is derived from a gene distinct from the one encoded by the mRNA transcript (i.e., the UTR is a heterologous UTR).

[00144] In certain embodiments, the 5' and/or 3' UTR sequences can be derived from mRNA which are stable (e.g., globin, actin, GAPDH, tubulin, histone, or citric acid cycle enzymes) to increase the stability of the mRNA. For example, a 5' UTR sequence may include a partial sequence of a CMV immediate-early 1 (IE1) gene, or a fragment thereof, to improve the nuclease resistance and/or improve the half-life of the mRNA. Also contemplated is the inclusion of a sequence encoding human growth hormone (hGH), or a fragment thereof, to the 3' end or untranslated region of the mRNA. Generally, these modifications improve the stability and/or pharmacokinetic properties (e.g., half-life) of the mRNA relative to their unmodified counterparts, and include, for example, modifications made to improve such mRNA resistance to *in vivo* nuclease digestion.

[00145] Exemplary 5' UTRs include a sequence derived from a CMV immediate-early 1 (IE1) gene (U.S. Publication Nos. 2014/0206753 and 2015/0157565, each of which is incorporated herein by reference), or the sequence GGGAUCCUACC (SEQ ID NO: 22) (U.S. Publication No. 2016/0151409, incorporated herein by reference).

[00146] In various embodiments, the 5' UTR may be derived from the 5' UTR of a TOP gene. TOP genes are typically characterized by the presence of a 5'-terminal oligopyrimidine (TOP) tract. Furthermore, most TOP genes are characterized by growth-associated translational regulation. However, TOP genes with a tissue specific translational regulation are also known. In certain embodiments, the 5' UTR derived from the 5' UTR of a TOP gene lacks the 5' TOP motif (the oligopyrimidine tract) (e.g., U.S. Publication Nos. 2017/0029847, 2016/0304883, 2016/0235864, and 2016/0166710, each of which is incorporated herein by reference).

[00147] In certain embodiments, the 5' UTR is derived from a ribosomal protein Large 32 (L32) gene (U.S. Publication No. 2017/0029847, *supra*).

[00148] In certain embodiments, the 5' UTR is derived from the 5' UTR of an hydroxysteroid (17-b) dehydrogenase 4 gene (HSD17B4) (U.S. Publication No. 2016/0166710, *supra*).

[00149] In certain embodiments, the 5' UTR is derived from the 5' UTR of an ATP5A1 gene (U.S. Publication No. 2016/0166710, *supra*).

[00150] In some embodiments, an internal ribosome entry site (IRES) is used instead of a 5' UTR.

[00151] In some embodiments, the 5'UTR comprises a nucleic acid sequence set forth in SEQ ID NO: 19. In some embodiments, the 3'UTR comprises a nucleic acid sequence set forth in SEQ ID NO: 20. The 5' UTR and 3'UTR are described in further detail in WO2012/075040, incorporated herein by reference.

II. C. Polyadenylated Tail

[00152] As used herein, the terms "poly(A) sequence," "poly(A) tail," and "poly(A) region" refer to a sequence of adenosine nucleotides at the 3' end of the mRNA molecule. The poly(A) tail may confer stability to the mRNA and protect it from exonuclease degradation. The poly(A) tail may enhance translation. In some embodiments, the poly(A) tail is essentially homopolymeric. For example, a poly(A) tail of 100 adenosine nucleotides may have essentially a length of 100 nucleotides. In certain embodiments, the poly(A) tail may be interrupted by at least one nucleotide different from an adenosine nucleotide (e.g., a nucleotide that is not an adenosine nucleotide). For example, a poly(A) tail of 100 adenosine nucleotides may have a length of more than 100 nucleotides (comprising 100 adenosine nucleotides and at least one nucleotide, or a stretch of nucleotides, that are different from an adenosine nucleotide). In certain embodiments, the poly(A) tail comprises the sequence AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCAUAUGACUAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO: 23).

[00153] The "poly(A) tail," as used herein, typically relates to RNA. However, in the context of the disclosure, the term likewise relates to corresponding sequences in a DNA molecule (e.g., a "poly(T) sequence").

[00154] The poly(A) tail may comprise about 10 to about 500 adenosine nucleotides, about 10 to about 200 adenosine nucleotides, about 40 to about 200 adenosine nucleotides, or about 40 to about 150 adenosine nucleotides. The length of the poly(A) tail may be at least about 10, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, or 500 adenosine nucleotides.

[00155] In some embodiments where the nucleic acid is an RNA, the poly(A) tail of the nucleic acid is obtained from a DNA template during RNA *in vitro* transcription. In certain embodiments, the poly(A) tail is obtained *in vitro* by common methods of chemical synthesis without being transcribed from a DNA template. In various embodiments, poly(A) tails are generated by enzymatic polyadenylation of the RNA (after RNA *in vitro* transcription) using commercially available polyadenylation kits and corresponding protocols, or alternatively, by using immobilized poly(A)polymerases, e.g., using methods and means as described in WO2016/174271.

[00156] The nucleic acid may comprise a poly(A) tail obtained by enzymatic polyadenylation, wherein the majority of nucleic acid molecules comprise about 100 (+/-20) to about 500 (+/-50) or about 250 (+/-20) adenosine nucleotides.

[00157] In some embodiments, the nucleic acid may comprise a poly(A) tail derived from a template DNA and may additionally comprise at least one additional poly(A) tail generated by enzymatic polyadenylation, e.g., as described in WO2016/091391, incorporated herein by reference.

[00158] In certain embodiments, the nucleic acid comprises at least one polyadenylation signal.

[00159] In various embodiments, the nucleic acid may comprise at least one poly(C) sequence.

[00160] The term "poly(C) sequence," as used herein, is intended to be a sequence of cytosine nucleotides of up to about 200 cytosine nucleotides. In some embodiments, the poly(C) sequence comprises about 10 to about 200 cytosine nucleotides, about 10 to about 100 cytosine nucleotides, about 20 to about 70 cytosine nucleotides, about 20 to about 60 cytosine nucleotides, or about 10 to about 40 cytosine nucleotides. In some embodiments, the poly(C) sequence comprises about 30 cytosine nucleotides.

II. D. Chemical Modification

[00161] The mRNA disclosed herein may be modified or unmodified. In some embodiments, the mRNA may comprise at least one chemical modification. In some embodiments, the mRNA disclosed herein may contain one or more modifications that typically enhance RNA stability. Exemplary modifications can include backbone modifications, sugar modifications, or base modifications. In some embodiments, the disclosed mRNA may be synthesized from naturally occurring nucleotides and/or nucleotide analogues (modified nucleotides) including, but not limited to, purines (adenine (A) and guanine (G)) or pyrimidines (thymine (T), cytosine (C), and uracil (U)). In certain embodiments, the disclosed mRNA may be synthesized from modified nucleotide analogues or derivatives of purines and pyrimidines, such as, e.g., 1-methyl-adenine, 2-methyl-adenine, 2-methylthio-N-6-isopentenyl-adenine, N6-methyl-adenine, N6-isopentenyl-adenine, 2-thio-cytosine, 3-methyl-cytosine, 4-acetyl-cytosine, 5-methyl-cytosine, 2,6-diaminopurine, 1-methyl-guanine, 2-methyl-guanine, 2,2-dimethyl-guanine, 7-methyl-guanine, inosine, 1-methyl-inosine, pseudouracil (5-uracil), dihydro-uracil, 2-thio-uracil, 4-thio-uracil, 5-carboxymethylaminomethyl-2-thio-uracil, 5-(carboxyhydroxymethyl)-uracil, 5-fluoro-uracil, 5-bromo-uracil, 5-carboxymethylaminomethyl-uracil, 5-methyl-2-thio-uracil, 5-methyl-uracil, N-uracil-5-oxy acetic acid methyl ester, 5-methylaminomethyl-uracil, 5-methoxyaminomethyl-2-thio-uracil, 5'-methoxycarbonylmethyl-uracil, 5-methoxy-uracil, uracil-5-oxyacetic acid methyl ester, uracil-5-oxyacetic acid (v), 1-methyl-pseudouracil, queosine, β-D-mannosyl-queosine, phosphoramidates, phosphorothioates, peptide nucleotides, methylphosphonates, 7-deazaguanosine, 5-methylcytosine, and inosine.

[00162] In some embodiments, the disclosed mRNA may comprise at least one chemical modification including, but not limited to, pseudouridine, N1-methylpseudouridine, 2-thiouridine, 4'-thiouridine, 5-methylcytosine, 2-thio-l-methyl-1-deaza-pseudouridine, 2-thio-l-methyl-pseudouridine, 2-thio-5-aza-uridine, 2-thio-dihydropseudouridine, 2-thio-dihydrouridine, 2-thio-pseudouridine, 4-methoxy-2-thio-pseudouridine, 4-methoxy-pseudouridine, 4-thio-l-methyl-pseudouridine, 4-thio-pseudouridine, 5-aza-uridine, dihydropseudouridine, 5-methyluridine, 5-methyluridine, 5-methoxyuridine, and 2'-O-methyl uridine.

[00163] In some embodiments, the chemical modification is selected from the group consisting of pseudouridine, N1-methylpseudouridine, 5-methylcytosine, 5-methoxyuridine, and a combination thereof.

[00164] In some embodiments, the chemical modification comprises N1-methylpseudouridine.

[00165] In some embodiments, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of the uracil nucleotides in the mRNA are chemically modified.

[00166] In some embodiments, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of the uracil nucleotides in the ORF are chemically modified.

[00167] The preparation of such analogues is described, e.g., in U.S. Pat. No. 4,373,071, U.S. Pat. No. 4,401,796, U.S. Pat. No. 4,415,732, U.S. Pat. No. 4,458,066, U.S. Pat. No. 4,500,707, U.S. Pat. No. 4,668,777, U.S. Pat. No. 4,973,679, U.S. Pat. No. 5,047,524, U.S. Pat. No. 5,132,418, U.S. Pat. No. 5,153,319, U.S. Pat. No. 5,262,530, and U.S. Pat. No. 5,700,642.

II. E. mRNA Synthesis

[00168] The mRNAs disclosed herein may be synthesized according to any of a variety of methods. For example, mRNAs according to the present disclosure may be synthesized via *in vitro* transcription (IVT). Some methods for *in vitro* transcription are described, e.g., in Geall et al. (2013) Semin. Immunol. 25(2): 152-159; Brunelle et al. (2013) Methods Enzymol. 530:101-14. Briefly, IVT is typically performed with a linear or circular DNA template containing a promoter, a pool of ribonucleotide triphosphates, a buffer system that may include DTT and magnesium ions, an appropriate RNA polymerase (e.g., T3, T7, or SP6 RNA polymerase), DNase I, pyrophosphatase, and/or RNase inhibitor. The exact conditions may vary according to the specific application. The presence of these reagents is generally undesirable in a final mRNA product and these reagents can be considered impurities or contaminants which can be purified or removed to provide a clean and/or homogeneous mRNA that is suitable for therapeutic use. While mRNA provided from *in vitro* transcription reactions may be desirable in some embodiments, other sources of mRNA can be used according to the instant disclosure including wild-type mRNA produced from bacteria, fungi, plants, and/or animals.

III. Processes for Making the Present LNP Vaccines

[00169] The present LNPs can be prepared by various techniques presently known in the art. For example, multilamellar vesicles (MLV) may be prepared according to conventional techniques, such as by depositing a selected lipid on the inside wall of a suitable container or vessel by dissolving the lipid in an appropriate solvent, and then evaporating the solvent to leave a thin film on the inside of the vessel or by spray drying. An aqueous phase may then be added to the vessel with a vortexing motion that results in the formation of MLVs. Unilamellar vesicles (ULV) can then be formed by homogenization, sonication or extrusion of the multilamellar vesicles. In addition, unilamellar vesicles can be formed by detergent removal techniques.

[00170] Various methods are described in US 2011/0244026, US 2016/0038432, US 2018/0153822, US 2018/0125989, and PCT/US2020/043223 (filed July 23, 2020) and can be used to practice the present invention. One exemplary process entails encapsulating mRNA by mixing it with a mixture of lipids, without first pre-forming the lipids into lipid nanoparticles, as described in US 2016/0038432. Another exemplary process entails encapsulating mRNA by mixing pre-formed LNPs with mRNA, as described in US 2018/0153822.

[00171] In some embodiments, the process of preparing mRNA-loaded LNPs includes a step of heating one or more of the solutions to a temperature greater than ambient temperature, the one or more solutions being the solution comprising the pre-formed lipid nanoparticles, the solution comprising the mRNA and the mixed solution comprising the LNP-encapsulated mRNA. In some embodiments, the process includes the step of heating one or both of the mRNA solution and the pre-formed LNP solution, prior to the mixing step. In some embodiments, the process includes heating one or more of the solutions comprising the pre-formed LNPs, the solution comprising the mRNA and the solution comprising the LNP-encapsulated mRNA, during the mixing step. In some embodiments, the process includes the step of heating the LNP- encapsulated mRNA, after the mixing step. In some embodiments, the temperature to which one or more of the solutions is heated is or is greater than about 30°C, 37°C, 40°C, 45°C, 50°C, 55°C, 60°C, 65°C, or 70°C. In some embodiments, the temperature to which one or more of the solutions is heated ranges from about 25-70°C, about 30-70°C, about 35-70°C, about 40-70°C, about 45-70°C, about 50-70°C, or about 60-70°C. In some embodiments, the temperature is about 65°C.

[00172] Various methods may be used to prepare an mRNA solution suitable for the present invention. In some embodiments, mRNA may be directly dissolved in a buffer solution described herein. In some embodiments, an mRNA solution may be generated by mixing an mRNA stock solution with a buffer solution prior to mixing with a lipid solution for encapsulation. In some embodiments, an mRNA solution may be generated by mixing an mRNA stock solution with a buffer solution immediately before mixing with a lipid solution for encapsulation. In some embodiments, a suitable mRNA stock solution may contain mRNA in water or a buffer at a concentration at or greater than about 0.2 mg/ml, 0.4 mg/ml, 0.5 mg/ml, 0.6 mg/ml, 0.8 mg/ml, 1.0 mg/ml, 1.2 mg/ml, 1.4 mg/ml, 1.5 mg/ml, or 1.6 mg/ml, 2.0 mg/ml, 2.5 mg/ml, 3.0 mg/ml, 3.5 mg/ml, 4.0 mg/ml, 4.5 mg/ml, or 5.0 mg/ml.

[00173] In some embodiments, an mRNA stock solution is mixed with a buffer solution using a pump. Exemplary pumps include but are not limited to gear pumps, peristaltic pumps and centrifugal pumps. Typically, the buffer solution is mixed at a rate greater than that of the mRNA stock solution. For example, the buffer solution may be mixed at a rate at least 1x, 2x, 3x, 4x, 5x, 6x, 7x, 8x, 9x, 10x, 15x, or 20x greater than the rate of the mRNA stock solution. In some embodiments, a buffer solution is mixed at a flow rate ranging between about 100-6000 ml/minute (e.g., about 100-300 ml/minute, 300-600 ml/minute, 600-1200 ml/minute, 1200-2400 ml/minute, 2400-3600 ml/minute, 3600-4800 ml/minute, 4800-6000 ml/minute, or 60-420 ml/minute). In some embodiments, a buffer solution is mixed at a flow rate of, or greater than, about 60 ml/minute, 100 ml/minute, 140 ml/minute, 180 ml/minute, 220 ml/minute, 260 ml/minute, 300 ml/minute, 340 ml/minute, 380 ml/minute, 420 ml/minute, 480 ml/minute, 540 ml/minute, 600 ml/minute, 1200 ml/minute, 2400 ml/minute, 3600 ml/minute, 4800 ml/minute, or 6000 ml/minute.

[00174] In some embodiments, an mRNA stock solution is mixed at a flow rate ranging between about 10-600 ml/minute (e.g., about 5-50 ml/minute, about 10-30 ml/minute, about 30-60 ml/minute, about 60-120 ml/minute, about 120-240 ml/minute, about 240-360 ml/minute, about 360-480 ml/minute, or about 480-600 ml/minute). In some embodiments, an mRNA stock solution is mixed at a flow rate of or greater than about 5 ml/minute, 10 ml/minute, 15 ml/minute, 20 ml/minute, 25 ml/minute, 30 ml/minute, 35 ml/minute, 40 ml/minute, 45 ml/minute, 50 ml/minute, 60 ml/minute, 80 ml/minute, 100 ml/minute, 200 ml/minute, 300 ml/minute, 400 ml/minute, 500 ml/minute, or 600 ml/minute.

[00175] The process of incorporation of a desired mRNA into a lipid nanoparticle is referred to as “loading.” Exemplary methods are described in Lasic et al., *FEBS Lett.* (1992) 312:255-8. The LNP-incorporated nucleic acids may be completely or partially located in the interior space of the lipid nanoparticle, within the bilayer membrane of the lipid nanoparticle, or associated with the exterior surface of the lipid nanoparticle membrane. The incorporation of an mRNA into lipid nanoparticles is also referred to herein as “encapsulation” wherein the nucleic acid is entirely or substantially contained within the interior space of the lipid nanoparticle.

[00176] Suitable LNPs may be made in various sizes. In some embodiments, decreased size of lipid nanoparticles is associated with more efficient delivery of an mRNA. Selection of an appropriate LNP size may take into consideration the site of the target cell or tissue and to some extent the application for which the lipid nanoparticle is being made.

[00177] A variety of methods known in the art are available for sizing of a population of lipid nanoparticles. Particularly exemplary methods herein utilize Zetasizer Nano ZS (Malvern Panalytical) to measure LNP particle size. In one protocol, 10 µl of an LNP sample are mixed with 990 µl of 10% trehalose. This solution is loaded into a cuvette and then put into the Zetasizer machine. The z-average diameter (nm), or cumulants mean, is regarded as the average size for the LNPs in the sample. The Zetasizer machine can also be used to measure the polydispersity index (PDI) by using dynamic light scattering (DLS) and cumulant analysis of the autocorrelation function. Average LNP diameter may be reduced by sonication of formed LNP. Intermittent sonication cycles may be alternated with quasi-elastic light scattering (QELS) assessment to guide efficient lipid nanoparticle synthesis.

[00178] In some embodiments, the majority of purified LNPs, i.e., greater than about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the LNPs, have a size of about 70-150 nm (e.g., about 145 nm, about 140 nm, about 135 nm, about 130 nm, about 125 nm, about 120 nm, about 115 nm, about 110 nm, about 105 nm, about 100 nm, about 95 nm, about 90 nm, about 85 nm, or about 80 nm). In some embodiments, substantially all (e.g., greater than 80 or 90%) of the purified lipid nanoparticles have a size of about 70-150 nm (*e.g.*, about 145 nm, about 140 nm, about 135 nm, about 130 nm, about 125 nm, about 120 nm, about 115 nm, about 110 nm, about 105 nm, about 100 nm, about 95 nm, about 90 nm, about 85 nm, or about 80 nm).

[00179] In some embodiments, the LNPs in the present composition have an average size of less than 150 nm, less than 120 nm, less than 100 nm, less than 90 nm, less than 80 nm, less than 70 nm, less than 60 nm, less than 50 nm, less than 30 nm, or less than 20 nm.

[00180] In some embodiments, greater than about 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% of the LNPs in the present composition have a size ranging from about 40-90 nm (*e.g.*, about 45-85 nm, about 50-80 nm, about 55-75 nm, about 60-70 nm) or about 50-70 nm (*e.g.*, 55-65 nm) are particular suitable for pulmonary delivery via nebulization.

[00181] In some embodiments, the dispersity, or measure of heterogeneity in size of molecules (PDI), of LNPs in a pharmaceutical composition provided by the present invention is less than about 0.5. In some embodiments, an LNP has a PDI of less than about 0.5, less than about 0.4, less than about 0.3, less than about 0.28, less than about 0.25, less than about 0.23, less than about 0.20, less than about 0.18, less than about 0.16, less than about 0.14, less than about 0.12, less than about 0.10, or less than about 0.08. The PDI may be measured by a Zetasizer machine as described above.

[00182] In some embodiments, greater than about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the purified LNPs in a pharmaceutical composition provided herein encapsulate an mRNA within each individual particle. In some embodiments, substantially all (e.g., greater than 80% or 90%) of the purified lipid nanoparticles in a pharmaceutical composition encapsulate an mRNA within each individual particle. In some embodiments, a lipid nanoparticle has an encapsulation efficiency of between 50% and 99%; or greater than about 60, 65, 70, 75, 80, 85, 90, 92, 95, 98, or 99%. Typically, lipid nanoparticles for use herein have an encapsulation efficiency of at least 90% (e.g., at least 91, 92, 93, 94, or 95%).

[00183] In some embodiments, an LNP has a N/P ratio of between 1 and 10. In some embodiments, a lipid nanoparticle has a N/P ratio above 1, about 1, about 2, about 3, about 4, about 5, about 6, about 7, or about 8. In further embodiments, a typical LNP herein has an N/P ratio of 4.

[00184] In some embodiments, a pharmaceutical composition according to the present invention contains at least about 0.5 μg, 1 μg, 5 μg, 10 μg, 100 μg, 500 μg, or 1000 μg of encapsulated mRNA. In some embodiments, a pharmaceutical composition contains about 0.1 μg to 1000 μg, at least about 0.5 μg, at least about 0.8 μg, at least about 1 μg, at least about 5 μg, at least about 8 μg, at least about 10 μg, at least about 50 μg, at least about 100 μg, at least about 500 μg, or at least about 1000 μg of encapsulated mRNA.

[00185] In some embodiments, mRNA can be made by chemical synthesis or by *in vitro* transcription (IVT) of a DNA template. An exemplary process for making and purifying mRNA is described in Example 1. In this process, in an IVT process, a cDNA template is used to produce an mRNA transcript and the DNA template is degraded by a DNase. The transcript is purified by depth filtration and tangential flow filtration (TFF). The purified transcript is further modified by adding a cap and a tail, and the modified RNA is purified again by depth filtration and TFF.

[00186] The mRNA is then prepared in an aqueous buffer and mixed with an amphiphilic solution containing the lipid components of the LNPs. An amphiphilic solution for dissolving the four lipid components of the LNPs may be an alcohol solution. In some embodiments, the alcohol is ethanol. The aqueous buffer may be, for example, a citrate, phosphate, acetate, or succinate buffer and may have a pH of about 3.0-7.0, e.g., about 3.5, about 4.0, about 4.5, about 5.0, about 5.5, about 6.0, or about 6.5. The buffer may contain other components such as a salt (e.g., sodium, potassium, and/or calcium salts). In particular embodiments, the aqueous buffer has 1 mM citrate, 150 mM NaCl, pH 4.5.

[00187] An exemplary, nonlimiting process for making an mRNA-LNP composition is described in Example 1. The process involves mixing of a buffered mRNA solution with a solution of lipids in ethanol in a controlled homogeneous manner, where the ratio of lipids:mRNA is maintained throughout the mixing process. In this illustrative example, the mRNA is presented in an aqueous buffer containing citric acid monohydrate, tri-sodium citrate dihydrate, and sodium chloride. The mRNA solution is added to the solution (1 mM citrate buffer, 150 mM NaCl, pH 4.5). The lipid mixture of four lipids (e.g., a cationic lipid, a PEGylated lipid, a cholesterol-based lipid, and a helper lipid) is dissolved in ethanol. The aqueous mRNA solution and the ethanol lipid solution are mixed at a volume ratio of 4:1 in a “T” mixer with a near “pulseless” pump system. The resultant mixture is then subjected for downstream purification and buffer exchange. The buffer exchange may be achieved using dialysis cassettes or a TFF system. TFF may be used to concentrate and buffer-exchange the resulting nascent LNP immediately after formation via the T-mix process. The diafiltration process is a continuous operation, keeping the volume constant by adding appropriate buffer at the same rate as the permeate flow.

IV. Packaging and Use of the mRNA-LNP Vaccines

[00188] The mRNA-LNP vaccines can be packaged for parenteral (e.g., intramuscular, intradermal or subcutaneous) administration or nasopharyngeal (e.g., intranasal) administration. The vaccine compositions may be in the form of an extemporaneous formulation, where the LNP composition is lyophilized and reconstituted with a physiological buffer (e.g., PBS) just before use. The vaccine compositions also may be shipped and provided in the form of an aqueous solution or a frozen aqueous solution and can be directly administered to subjects without reconstitution (after thawing, if previously frozen).

[00189] Accordingly, the present disclosure provides an article of manufacture, such as a kit, that provides the mRNA-LNP vaccine in a single container, or provides the mRNA-LNP vaccine in one container and a physiological buffer for reconstitution in another container. The container(s) may contain a single-use dosage or multi-use dosage. The containers may be pre-treated glass vials or ampules. The article of manufacture may include instructions for use as well.

[00190] In particular embodiments, the mRNA-LNP vaccine is provided for use in intramuscular (IM) injection. The vaccine can be injected to a subject at, e.g., his/her deltoid muscle in the upper arm. In some embodiments, the vaccine is provided in a pre-filled syringe or injector (e.g., single-chambered or multi-chambered). In some embodiments, the vaccine is provided for use in inhalation and is provided in a pre-filled pump, aerosolizer, or inhaler.

[00191] The mRNA-LNP vaccines are administered to subjects in need thereof in a prophylactically effective amount, i.e., an amount that provides sufficient immune protection against a target pathogen for a sufficient amount of time (e.g., one year, two years, five years, ten years, or life-time). Sufficient immune protection may be, for example, prevention or alleviation of symptoms associated with infections by the pathogen. In some embodiments, multiple doses (e.g., two doses) of the vaccine are injected to subjects in need thereof to achieve the desired prophylactic effects. The doses (e.g., prime and booster doses) may be separated by an interval of e.g., 1 week, 2 weeks, 3 weeks, 4 weeks, one month, two months, three months, four months, five months, six months, one year, two years, five years, or ten years.

[00192] In some embodiments, a single dose of the mRNA-LNP vaccine contains 1-50 µg of mRNA (e.g., monovalent or multivalent). For example, a single dose may contain about 2.5 µg, about 5 µg, about 7.5 µg, about 10 µg, about 12.5 µg, or about 15 µg of the mRNA for intramuscular (IM) injection. In further embodiments, a multi-valent single dose of an LNP vaccine contains multiple (e.g., 2, 3, or 4) kinds of LNPs, each for a different antigen, and each kind of LNP has an mRNA amount of, e.g., 2.5 µg, about 5 µg, about 7.5 µg, about 10 µg, about 12.5 µg, or about 15 µg.

[00193] In another aspect, the present invention provides methods of immunizing a subject against one or more influenza viruses. The present invention further provides methods of eliciting an immune response against one or more influenza viruses in a subject. In some embodiments, the present methods comprise administering to the subject an effective amount of a composition described herein to a subject.

[00194] In various embodiments, the methods of immunizing provided herein elicit a broadly protective immune response against multiple epitopes within one or more influenza viruses. In various embodiments, the methods of immunizing provided herein elicit a broadly neutralizing immune response against one or more influenza viruses. In some embodiments, the immune response comprises an antibody response. Accordingly, in various embodiments, the composition described herein can offer broad cross-protection against different types of influenza viruses. In some embodiments, the composition offers cross-protectionagainst avian, swine, seasonal, and/or pandemic influenza viruses. In some embodiments, the composition offers cross-protection against one or more influenza A, B, or C subtypes. In some embodiments, the composition offers cross-protection against multiple strains of influenza A H1-subtype viruses (e.g., H1N1), influenza A H3-subtype viruses (e.g., H3N2), influenza A H5-subtype viruses (e.g., H5N1), and/or influenza B viruses (e.g., Yamagata lineage, Victoria lineage).

[00195] In some embodiments, the methods of the invention are capable of eliciting an improved immune response against one or more seasonal influenza strains. Exemplary seasonal strains include, without limitation, A/Puerto Rico/8/1934, A/Fort Monmouth/1/1947, A/Chile/1/1983, A/Texas/36/1991, A/Singapore/6/1986, A/Beijing/32/1992, A/New Caledonia/20/1999, A/Solomon Islands/03/2006, A/Brisbane/59/2007, A(H3N2) virus antigenically like the cell-propagated prototype virus A/Victoria/361/2011, A/Beijing/262/95 (H1N1)-like virus, A/Brisbane/02/2018 (H1N1)pdm09-like virus, A/Brisbane/10/2007 (H3N2)-like virus, A/California/7/2004 (H3N2)-like virus, A/California/7/2009 (H1N1)-like virus, A/California/7/2009 (H1N1)pdm09-like virus, A/Cambodia/e0826360/2020 (H3N2)-like virus, A/Fujian/411/2002 (H3N2) - like virus, A/Fujian/411/2002 (H3N2)-like virus, A/Guangdong-Maonan/SWL1536/2019 (H1N1)pdm09-like virus-like virus, A/Hawaii/70/2019 (H1N1)pdm09-like virus-like virus, A/Hong Kong/2671/2019 (H3N2)-like virus, A/Hong Kong/45/2019 (H3N2)-like virus, A/Hong Kong/4801/2014 (H3N2)-like virus, A/Kansas/14/2017 (H3N2)-like virus, A/Michigan/45/2015 (H1N1)pdm09-like virus, A/Moscow/10/99 (H3N2)-like virus, A/New Caledonia/20/99 (H1N1)-like virus, A/Perth/16/2009 (H3N2)-like virus, A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus, A/Solomon Islands/3/2006 (H1N1)-like virus, A/South Australia/34/2019 (H3N2)-like virus, A/Switzerland/8060/2017 (H3N2)-like virus, A/Switzerland/9715293/2013 (H3N2)-like virus, A/Sydney/5/97 (H3N2)-like virus, A/Texas/50/2012 (H3N2)-like virus, A/Victoria/2570/2019 (H1N1)pdm09-like virus, A/Victoria/2570/2019 (H1N1)pdm09-like virus -like virus, A/Victoria/361/2011 (H3N2)-like virus, A/Wellington/1/2004 (H3N2)-like virus, A/Wisconsin/588/2019 (H1N1)pdm09-like virus, A/Wisconsin/588/2019 (H1N1)pdm09-like virus-like virus, A/Wisconsin/67/2005 (H3N2)-like virus, B/Beijing/184/93-like virus, B/Brisbane/60/2008-like virus, B/Colorado/06/2017-like virus (B/Victoria/2/87 lineage), B/Florida/4/2006-like virus, B/Hong Kong/330/2001-like virus, B/Malaysia/2506/2004-like virus, B/Massachusetts/2/2012-like virus, B/Phuket/3073/2013 (B/Yamagata lineage)-like virus, B/Phuket/3073/2013-like virus, B/Phuket/3073/2013-like virus (B/Yamagata/16/88 lineage), B/Shangdong/7/97-like virus, B/Shanghai/361/2002-like virus, B/Sichuan/379/99-like virus, B/Washington/02/2019 (B/Victoria lineage)-like virus, B/Washington/02/2019-like (B/Victoria lineage) virus, and B/Wisconsin/1/2010-like virus. In some embodiments, the methods of the invention are capable of eliciting an improved immune response against one or more pandemic influenza strains. Exemplary pandemic strains include, without limitation, A/California/07/2009, A/California/04/2009, A/Belgium/145/2009, A/South Carolina/01/1918, and A/New Jersey/1976. Pandemic subtypes include, in particular, the H1N1, H5N1, H2N2, H3N2, H9N2, H7N7, H7N3, H7N9 and H10N7 subtypes. In some embodiments, the methods of the invention are capable of eliciting an improved immune response against one or more swine influenza strains. Exemplary swine strains include, without limitation, A/New Jersey/1976 isolates and A/California/07/2009. In some embodiments, the methods of the invention are capable of eliciting an improved immune response against one or more avian influenza strains. Exemplary avian strains include, without limitation, H5N1, H7N3, H7N7, H7N9, and H9N2. Additional influenza pandemic, seasonal, avian and/or swine strains are known in the art.

[00196] In some embodiments, the present invention provides methods of preventing or treating influenza infections by administering the composition of the invention to a subject in need thereof. In some embodiments, the subject is suffering from or susceptible to an influenza infection. In some embodiments, a subject is considered to be suffering from an influenza infection if the subject is displaying one or more symptoms commonly associated with influenza infection. In some embodiments, the subject is known or believed to have been exposed to the influenza virus. In some embodiments, a subject is considered to be susceptible to an influenza infection if the subject is known or believed to have been exposed to the influenza virus. In some embodiments, a subject is known or believed to have been exposed to the influenza virus if the subject has been in contact with other individuals known or suspected to have been infected with the influenza virus and/or if the subject is or has been present in a location in which influenza infection is known or thought to be prevalent.

[00197] In various embodiments, the composition as described herein may be administered prior to or after development of one or more symptoms of influenza infection. In some embodiments, the composition is administered as a prophylactic. In such embodiments, the methods of the invention are effective in preventing or protecting a subject from influenza virus infection. In some embodiments, the composition of the present invention is used as a component of a seasonal and/or pandemic influenza vaccine or as part of an influenza vaccination regimen intended to confer long-lasting (multi-season) protection. In some embodiments, the composition of the presenting invention is used to treat the symptoms of influenza infection.

[00198] In some embodiments, the subject is a non-human mammal. In some embodiments, the subject is a farm animal or a pet (*e.g.*, a dog, a cat, a sheep, cattle, and/or a pig). In some embodiments, the subject is a non-human primate. In some embodiments, the subject is an avian (e.g., a chicken, a duck, a goose and/or a turkey).

[00199] In some embodiments, the subject is a human. In certain embodiments, the subject is an adult, an adolescent, or an infant. In some embodiments, the human subject is younger than 6 months of age. In some embodiments, the human subject is 6 months of age or older, is 6 months through 35 months of age, is 36 months through 8 years of age, or is 9 years of age or older. In some embodiments, the human subject is an elderly aged 55 years or older, such as 60 years of age or older, or 65 years of age or older. Also contemplated by the present invention are the administration of the composition and/or performance of the methods of treatment in utero.

[00200] Unless otherwise defined herein, scientific and technical terms used in connection with the present invention shall have the meanings that are commonly understood by those of ordinary skill in the art. Exemplary methods and materials are described below, although methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present invention. In case of conflict, the present specification, including definitions, will control. Generally, nomenclature used in connection with, and techniques of, cell and tissue culture, molecular biology, virology, immunology, microbiology, genetics, analytical chemistry, synthetic organic chemistry, medicinal and pharmaceutical chemistry, and protein and nucleic acid chemistry and hybridization described herein are those well-known and commonly used in the art. Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. Throughout this specification and embodiments, the words "have" and "comprise," or variations such as "has," "having," "comprises," or "comprising," will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers. All publications and other references mentioned herein are incorporated by reference in their entirety. Although a number of documents are cited herein, this citation does not constitute an admission that any of these documents forms part of the common general knowledge in the art. As used herein, the term “approximately” or “about” as applied to one or more values of interest refers to a value that is similar to a stated reference value. In certain embodiments, the term refers to a range of values that fall within 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, or less in either direction (greater than or less than) of the stated reference value unless otherwise stated or otherwise evident from the context.

[00201] In order that this invention may be better understood, the following examples are set forth. These examples are for purposes of illustration only and are not to be construed as limiting the scope of the invention in any manner.

EXAMPLES

Example 1: Optimization of LNP Formulations

[00202] This Example describes a study in which a series of LNP formulations for mRNA vaccines was prepared from combinatorial libraries of various components. Rationally designed novel cationic lipids were synthesized. Altogether, more than 150 lipids and more than 430 formulations were tested. Human erythropoietin (hEPO) mRNA was used as a test mRNA. In the lead formulations described below, the mRNA was formulated into LNP using combinations of the cationic lipids and the three other lipids – helper lipids; cholesterol-based lipids; and PEGylated lipids – in various permutations of combinations.

[00203] The LNP formulations consisted of four lipid components – ionizable lipid, helper lipid DOPE, cholesterol, and PEGylated lipid DMG-PEG-2K. The PEGylated lipid molar fraction was held constant at 1.5%, while the ionizable lipid and the different helper lipids and their molar ratios were evaluated to identify the optimized ratios based on the hEPO screening studies.

[00204] Citrate buffer (1 mM citrate, 150 mM NaCl, pH 4.5) was used in the preparation of LNP formulation. mRNA solution added to the citrate buffer was mixed with the lipids in ethanol solution during the formulation process. The pH and the concentration of the buffer were selected to achieve the high rate of mRNA encapsulation in the LNP formulation.

[00205] The LNP formulation process included mixing the lipid ethanol solution and the mRNA citrate solution in a ‘T’ mixer using a pump system. The resultant solution was then subjected to buffer exchange using TFF/ dialysis tubes. The concentration of the final formulation in 10% (w/v) trehalose was adjusted based on dosing needs.

[00206] Mouse *in vivo* expression of hEPO protein was used as a surrogate to measure the potency of the LNPs to delivery mRNA in *vivo*. In this study, a single dose of hEPO mRNA (0.1 µg) formulated in LNPs derived from various combinations of the components was injected into mice intramuscularly (IM). Serum collected at 6 hours and 24 hours after administration was tested for hEPO levels using ELISA. MC3 formulation, an industry benchmark, was used a reference for the calculation of fold-increase in hEPO expression (Angew, *Chem Int Ed.* (2012) 51:8529-33).

[00207] The level of hEPO expression seen for each LNP formulation indicated the formulation’s ability to deliver mRNA into cells. The initial formulations included 2-dioleoyl-sn-glycero-3-phosphoethanolamine (DOPE; helper lipid), DMG-PEG2000, and cholesterol at the molar ratio of cationic lipid: DMG-PEG2000: cholesterol: DOPE at 40:1.5:28.5:30. These formulations were found to have robust potency when compared to MC3 formulations.

[00208] Further formulations were tested. Optimized formulations Lipid A LNP and Lipid B LNP are shown in **Table 1**. The mRNA in these formulations can be modified or unmodified and may encode an antigen derived from a virus such as influenza or SARS-CoV-2.

Table 1. Composition of Exemplary LNP Formulations

Components		**Function**	**Description**
mRNA		Active substance	mRNA Construct
lipid nanoparticle (LNP)	Cationic Lipid OF-02 (A) or cKK-E10 (B)	Delivery	Ionizable lipid, facilitates mRNA encapsulation
	DOPE		Zwitterionic lipid, enhances uptake and release of drug payload
	Cholesterol		Provides stability to lipid bilayer
	DMG-PEG-2K		Provides control and stability to the lipid bilayer
Trehalose		Excipient	Cryoprotectant
Water for Injection (WFI)		Diluent	N/A

[00209] In **Table 1**, the final dosing for a human vaccine would be dilution of the above final bulk product in phosphate-buffered saline (PBS) based on the intended single human dose. The WFI amount is calculated based upon nominal of final drug product. Trehalose content in the formulation corresponds to 10% (100 mg/mL) trehalose dihydrate, converted to an anhydrous basis using the ratio of the molecular weight values of anhydrous trehalose and trehalose dihydrate.

[00210] The molar ratios of lipid components in two optimized formulations – Lipid A and Lipid B LNP formulations – are shown in **Table 2** (CL: cationic lipid).

Table 2. Molar Ratios of Lipid Components in Exemplary LNPs

CL	LNP Code	Molar Ratios of CL: DMG-PEG2000: Cholesterol: DOPE
OF-02	Lipid A	40: 1.5: 28.5: 30
cKK-E10	Lipid B	40: 1.5: 28.5: 30

[00211] As shown in **Table 3** and **FIG. 1A**, the fold increase of hEPO expression for Lipid A and Lipid B compared to MC3 indicates the superiority of these LNPs over MC3 for the delivery of mRNA. In the table below, "P2" means PEG2000; "Times MC3" means the fold of increase over MC3; and "Std Dev" means standard deviation.

Table 3. *In vivo* Delivery of hEPO mRNA in Mice

Study #	Cationic lipid	Formulation Composition	Times MC3	Std Dev
1	OF-02 (P2 low DOPE)	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:3:27:30	1.74	0.97
	OF-02 (P2 w/ DSPC)	Cationic lipid: DMG-PEG2000: cholesterol: DSPC 50:1.5:38.5:10	0.18	0.17
2	OF-02	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	5.04	1.79
3	OF-02 (high DOPE)	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:13.5:45	7.35	3.90
4	OF-02	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	16.19	7.86
5	OF-02	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	12.13	6.56
6	cKK-E10	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	5.41	3.46
7	cKK-E10 (DEPE)	Cationic lipid: DMG-PEG2000: cholesterol: DEPE 40:1.5:28.5:30	5.77	2.09

Study #	Cationic lipid	Formulation Composition	Times MC3	Std Dev
8	OF-02 (177 nm)	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	6.59	2.50
	OF-02 (161 nm)	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	4.94	1.75
	OF-02 (153 nm)	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	7.40	3.54
	OF-02 (133 nm)	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	7.15	3.86
	OF-02 (115 nm)	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	5.91	2.79
	OF-02 (118 nm)	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	10.54	4.38
9	OF-02 (DSPC)	Cationic lipid: DMG-PEG2000: cholesterol: DSPC 40:5:25:30	0.00	0.00
	OF-02 (DSPC)	Cationic lipid: DMG-PEG2000: cholesterol: DSPC 40:3.5:26.5:30	0.00	0.00
	OF-02 (DSPC)	Cationic lipid: DMG-PEG2000: cholesterol: DSPC 40:2:28:30	0.00	0.00
	OF-02 (DSPC)	Cationic lipid: DMG-PEG2000: cholesterol: DSPC 40:2:53:5	0.99	0.70
10	OF-02 (DOPS)	Cationic lipid: DMG-PEG2000: cholesterol: DOPS 40:1.5:28.5:30	3.26	1.97
	OF-02 (DEPE)	Cationic lipid: DMG-PEG2000: cholesterol: DEPE 40:1.5:28.5:30	11.83	6.89
	OF-02 (DOPC)	Cationic lipid: DMG-PEG2000: cholesterol: DOPC 40:1.5:28.5:30	3.32	1.20
	OF-02	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	7.14	3.37
11	cKK-E10	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	5.58	2.01
	OF-02 (PD lot)	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	8.81	3.22
	cKK-E10	Cationic lipid: DMG-PEG2000: cholesterol: DOPE 40:1.5:28.5:30	5.16	3.25

[00212] **FIG. 1B** shows hEPO expression in mice and non-human primates (NHPs) using LNPs Lipid A and Lipid B. A single dose of hEPO mRNA (0.1 µg for mice and 10 µg for NHPs) formulated with Lipid A or Lipid B was injected intramuscularly. Serum hEPO levels were quantified at 6, 24, 48, and 72 hours after administration using ELISA. The data show prolonged hEPO protein expression *in vivo* even beyond 4 days in mice and NHPs.

[00213] One of the key process parameters identified during optimization was the flow rate during initial mixing step. Formulations with different final LNP sizes (ranging from 108-177 nm) were prepared by changing these flow rates during mixing, allowing additional control on process and product attributes. The higher the flow rate, the smaller the particle size. When the flow rate reached 375 ml/min, producing an average LNP size of 108 nM, there was a markedly increased potency. The impact of size on potency of LNP was noted as a measure of fold increase in hEPO expression over MC3 as **Table 4**.

Table 4. LNP Size Optimization

Formulation Lot#	Total Flow rate (ml/min)	Size (nm)	PDI	Encapsulation (%)	Cationic Lipid	Times MC3
1	250	108	0.077	99	MC3	1.00
2	62.5	177	0.086	94	OF-02	6.59
3	75	161	0.075	95	OF-02	4.94
2-88	87.5	152	0.116	97	OF-02	7.40
2-89	125	133	0.089	97	OF-02	7.15
2-90	250	115	0.076	98	OF-02	5.91
2-91	375	108	0.042	98	OF-02	10.54

*PDI: polydispersity index.

[00214] The above screening data show that helper lipid DOPE was effective in promoting protein expression. The data also led to determination of the promising molar composition of the four lipids (OF-02 or cKK-E10: DMG-PEG-2K: cholesterol: DOPE = 40:1.5:28.5:30). LNP formulations in 10% trehalose were characterized for all parameters including particle size, PDI, mRNA encapsulation, and mRNA integrity. All the tested batches showed the desired characteristics and stability in freeze/thaw cycling. The long-term stability of the formulation at -80°C in 10% (w/v) trehalose was assessed. Lipid A and Lipid B formulations were shown to be highly stable.

Example 2: Influenza H1N1 LNP Vaccine Formulations

[00215] Influenza pandemics can occur when a novel influenza virus emerges in the human population. Such pandemics remain a major threat to public health, requiring vigilant attention and preparedness with countermeasures to be used in the event of sustained human-to-human spread of the virus. In the experiments described in this Example, hemagglutinin (HA) from a highly pathogenic H1N1 strain A/California/7/2009 (CA09), the cause of the 2009 flu pandemic, was used as a prototype antigen to evaluate the potency of mRNA vaccines prepared with LNP formulations of Lipid A and Lipid B.

[00216] The HA mRNA was prepared as described above. Citrate buffer (1 mM citrate, 150 mM NaCl, pH 4.5) was used in the preparation of the LNP compositions. A citrate buffer containing the mRNA was mixed with the lipids in ethanol solution during the formulation process. The pH and the concentration of the buffer were selected to achieve the high encapsulation rate of mRNA in the LNP formulations. The two solutions (mRNA in citrate buffer and lipids in ethanol solution) were mixed in a "T" mixer using a pump system, resulting in a homogeneous pulseless flow, wherein the lipids and the mRNA were mixed at a constant ratio throughout the process. This was critical to achieve a homogeneous formulation with the desired size and a low PDI, an indicator of a more homogeneous size distribution. This process resulted in high mRNA encapsulation, which is critical for achieving high potency. The resultant solution was then subjected to buffer exchange using TFF/dialysis tubes.

[00217] In a mouse study, efficacy of Lipid A and Lipid B CA09 HA formulations were assessed in a head-to-head comparison to MC3 LNP formulation as well as recombinant HA (rHA). CA09 (H1) HA mRNA (0.4 μg) formulated with different cationic lipids was injected intramuscularly into Balb/C mice (n=8) on day 0 (D0) and day 28 (D28). Immunogenicity of the vaccines, as indicated by HA inhibition (HAI) titers, is shown in **FIG. 2A**. The data show that two immunizations of Lipid A or Lipid B on day 0 (D0) and day 28 (D28) elicited high HAI titers and allowed complete protection of animals from homologous viral challenge (Belgium09 H1N1 virus) (**FIG. 2B**). During 14 days of post challenge observation, no obvious signs of morbidity (weight loss) were observed within the Lipid A and Lipid B treated groups, while a small number of animals within the recombinant protein control group demonstrated morbidity (**FIG. 2B**).

[00218] Similarly, mRNA encoding neuraminidase (NA) from the Mich15 influenza strain (Mich15 N1) was formulated with Lipid A and evaluated for its potency. Two doses (0.4 or 0.016 μg) of NA mRNA formulated with Lipid A were injected intramuscularly into Balb/c mice (n=8). The control groups (n=8) were injected with 0.6 μg of hEPO mRNA or with diluent. Half of the mice received only one injection (1 dose) on study day 0, while the other half received two injections (2 doses) given at study day 0 and day 28. The data show that this N1 Lipid A formulation elicited robust immune response, as indicated by NA inhibition (NAI) titers (**FIG. 3A**). The data further show that the mice treated with either one dose or two doses of the vaccine were protected from lethal viral challenge by Belgium09 H1N1 (**FIG. 3B**). The level of protection correlated with the NAI titers of vaccine treatment groups versus the negative control groups (hEPO and diluent).

[00219] The CA09 H1 mRNA formulated with the present LNPs was also tested in an NHP model. The mRNA (10 µg) was formulated with Lipid A and Lipid B, and injected intramuscularly into cynomolgus macaque monkeys (n=6) on study days 0 and 28. Detectable HAI priming by day 14 and a significant boost in HAI titer by day 28 for all LNPs were observed (**FIG. 4**, right panel). ELISA data also demonstrated significant priming over baseline by day 14 for all doses tested with a robust boost detected two weeks after the boost (**FIG. 4**, left panel). The results show that the present H1 mRNA formulations resulted in robust immune responses as indicated by HAI and endpoint ELISA titers.

Example 3: Influenza H3N2 LNP Vaccine Formulation

[00220] This Example describes experiments in which mRNA-LNP vaccine formulations for influenza strain Sing16 (H3N2) were evaluated for potency. One of the mRNAs used in these experiments is MRT1400. MRT1400 is a biosynthetic codon-optimized HA-H3 (influenza virus hemagglutinin, H3 subtype) messenger RNA (CO-HA-H3 mRNA) manufactured by *in vitro* transcription.

[00221] The protein sequence for influenza virus hemagglutinin, H3 subtype, is shown below:

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MKTIIALSYI LCLVFAQKIP GNDNSTATLC LGHHAVPNGT IVKTITNDRI
EVTNATELVQ NSSIGEICDS PHQILDGENC TLIDALLGDP QCDGFQNKKW
DLFVERSKAY SNCYPYDVPD YASLRSLVAS SGTLEFKNES FNWTGVTQNG
TSSACIRGSS SSFFSRLNWL THLNYTYPAL NVTMPNKEQF DKLYIWGVHH
PGTDKDQIFL YAQSSGRITV STKRSQQAVI PNIGSRPRIR DIPSRISIYW
TIVKPGDILL INSTGNLIAP RGYFKIRSGK SSIMRSDAPI GKCKSECITP
NGSIPNDKPF QNVNRITYGA CPRYVKHSTL KLATGMRNVP EKQTRGIFGA
IAGFIENGWE GMVDGWYGFR HQNSEGRGQA ADLKSTQAAI DQINGKLNRL
IGKTNEKFHQ IEKEFSEVEG RVQDLEKYVE DTKIDLWSYN AELLVALENQ
HTIDLTDSEM NKLFEKTKKQ LRENAEDMGN GCFKIYHKCD NACIESIRNE
TYDHNVYRDE ALNNRFQIKG VELKSGYKDW ILWISFAISC FLLCVALLGF
IMWACQKGNI RCNICI* (SEQ ID NO:1)
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[00222] The coding sequence for this protein was codon-optimized. The codon-optimized sequence encoding the protein is shown in **FIG. 5A** (SEQ ID NO:2), where the wildtype sequence is shown as SEQ ID NO:3. The mRNA structure and sequence are shown in **FIGs. 5B** and **5C**, respectively. As shown in the figures, the HA-H3 mRNA coding sequence is flanked by 5' and 3' untranslated regions (UTRs) of 140 and 100 nucleotides, respectively. The biosynthetic HA-H3 mRNA also contains a 5’ cap structure consisting of a 7-methyl guanosine (m^7G) residue linked via an inverted 5’-5’ triphosphate bridge to the first nucleoside of the 5’ UTR, which is itself modified by 2’-O-ribose methylation. The 5’ cap is essential for initiation of translation by the ribosome. The entire linear structure is terminated at the 3’ end by a tract of approximately 100 to 500 adenosine nucleosides (polyA). The polyA region confers stability to the mRNA and is also thought to enhance translation. All of these structural elements are naturally occurring components used to promote the efficient translation of the HA-H3 mRNA.

[00223] A DNA plasmid was constructed for producing the codon-optimized mRNA sequence by *in vitro* transcription. *In vitro* transcription (IVT) reaction was carried out using RNA polymerase. The reaction mixes were precipitated. The precipitated RNA samples were loaded onto individual depth filtration cassette, washed with 80% ethanol and re-dissolved with recirculating water. A second aliquot of water was pumped through in a manner similar to the first step. This step was repeated one more time. The pooled eluates were subjected to ultrafiltration/diafiltration using a 50 kD hollow fiber TFF cassette. Each IVT TFF pool was then diluted in preparation for cap and tail reactions. Cap-tail reactions were precipitated and the RNA from the reaction was purified and collected as described above. The filtered mRNA was stored at -20°C until use.

[00224] In these experiments, mRNA encoding Sing16 NA (N2) or Sing16 HA (H3; MRT1400 mRNA) antigens was formulated with Lipid A or Lipid B LNPs and injected intramuscularly into Balb/c mice (n=8) on D0 and D28 at 0.4 μg of mRNA per dose. For comparison, 1 μg of recombinant Sing16 H3 or Sing16 N2 protein with an oil-in-water emulsion adjuvant (AF03) was injected by the intramuscular route into Balb/c mice (n=8). Immune responses were measured by NAI and HAI assays.

[00225] The data show that animals immunized with NA (N2) mRNA demonstrated detectable NAI priming by day 14 and a significant boost in NAI titer by day 28 (**FIG. 6**, right panel). The data also show that HA Sing16 Lipid A and Lipid B formulations elicited robust HAI responses after boosting on day 28 (**FIG. 6**, left panel).

[00226] Similarly, the Sing16 HA mRNA Lipid A and Lipid B vaccines were evaluated in non-human primates (NHPs), cynomolgus macaque monkeys (n=6). The HA Sing 16 mRNA (50 μg) formulated with Lipid A or Lipid B was injected by the intramuscular route into the monkeys. The first injection was given at study day 0 and the second injection was given at study day 28. The data show that the vaccines elicited robust immune functional responses boosted on day 28 (**FIG. 7A**).

[00227] In addition, four dose levels of HA Sing16 mRNA formulated in Lipid A (i.e., MRT5400 vaccine) – 15, 45, 135 and 250 µg – were evaluated in NHPs. The first immunization was given at study day 0 second immunization at study day 28. All NHPs demonstrated IgG binding and HAI titers for all doses tested with no differences in immune response between the various doses tested at two weeks after the second injection at D42 (**FIGs. 7B** and **7C**).

[00228] The Sing16 HA mRNA Lipid A vaccine was also evaluated for a T cell response in NHPs after the second vaccination. Peripheral blood mononuclear cells (PBMCs) were collected at day 42 and incubated overnight with either the Sing16 H3 recombinant protein or the peptide pools representing the entire HA open reading frame. Cytokines induced by the re-stimulation were assessed in ELISPOT assays. The frequencies of PBMC secreting IFN-γ, a Th1 cytokine (**FIG. 8A**), or IL-13, a Th2 cytokine (**FIG. 8B**) were calculated as spot-forming cells (SFC) per million PBMC. The majority of animals in the three dose level groups tested (250 µg, 135 µg, and 45 µg) demonstrated the presence of high frequency of IFN-γ secreting cells, with over 100 SFCs per million PBMCs (**FIG. 8A**). A dose-response was not observed, as the animals in the lower and higher dose level groups showed comparable frequencies of IFN-γ secreting cells. In contrast, the presence of IL-13 cytokine secreting cells was not detected in any of the groups tested and at any dose level (**FIG. 8B**). These data presented clear evidence for a Th1-biased cellular response and a lack of Th2 response to the HA antigen following vaccination in NHPs.

Example 4: Influenza LNP Vaccine Formulations with Modified mRNA

[00229] This Example describes experiments comparing the potency of vaccines containing unmodified (unmodified non-replicating or "UNR") and modified (modified non-replicating or "MNR") mRNA. UNR CA09 HA mRNA and MNR CA09 HA mRNA were prepared by *in vitro* transcription. In MNR, all uridines were replaced by pseudouridines.

[00230] Five different doses (0.016, 0.08, 0.4, 2, and 10 µg) of CA09 HA mRNA (either modified or unmodified) formulated with Lipid A were injected by the intramuscular route into Balb/c mice (n=15). The data show that the LNP formulations increased the stability and delivery efficiency of naked mRNA (UNR), for the potency between UNR and MNR mRNA was comparable as indicated by HAI titers (**FIG. 9A**). ELISA data for Balb/c mice also demonstrated significant priming over baseline by day 14 for all doses tested (both UNR and MNR mRNAs), with a robust boost detected two weeks after the boost. The data also show that UNR and MNR mRNAs were comparable in eliciting ELISA titers (**FIG. 9B**).

[00231] In conclusion, the present dose titration study demonstrated that unmodified and modified CA09 HA mRNA formulated with Lipid A elicited statistically indistinguishable immune responses in Balb/c mice, as indicated by either HAI or by endpoint ELISA assay. Balb/c mice immunized with the four higher doses of UNR and MNR mRNA demonstrate detectable HAI priming by day 14 and a significant boost in HAI titer by day 42 for all doses. These day-14 priming titers represent both a dose effect and dose sparing potential for generating detectable titers over a 125-fold range. The second injection titers at the same dose range confirms the robustness of the immune response to this mRNA-LNP formulation. Similar results were also observed in non-human primates.

Example 5: Multi-Valent Influenza Vaccine LNP Formulation

[00232] This Example describes a study using a Lipid A-based LNP vaccine containing mRNA encoding CA09 HA (as described in Example 2) and mRNA encoding Sing16 HA (as described in Example 3).

[00233] More specifically, CA09 HA mRNA and Sing16 HA mRNA co-encapsulated in Lipid A were evaluated in Balb/c mice (n=8). mRNA-LNP was administered as two mRNAs co-encapsulated or dosed separately as singly encapsulated mRNAs. For both approaches, a total of 0.4 μg LNP formulation was injected into mice by intramuscular injection. The first injection was given at study day 0 and the second injection was given at study day 28. The data show that the vaccines elicited robust immune functional responses. There did not appear to be any difference between the two administration approaches. These data show that co-encapsulation did not cause hindrance or interference between the two mRNAs.

Example 6: Further Studies on Multi-Valent Influenza Vaccine LNP Formulations

[00234] A panel of unmodified mRNAs encoding CA09 HA, Sing16 HA, Sing16 NA, Mich15 NA, A/Perth/16/2009 Influenza virus (Perth09 NA), and reporter antigens of firefly luciferase (FF) and hEPO were prepared. LNP formulations for HA and NA mRNA-LNP preparation were then tested for expression *in vitro*, the immune responses in animals, and for potency in preclinical models. For the studies in this Example, all of the LNP formulations were the Lipid A formulation.

Materials and Methods

mRNA-LNP Preparations

[00235] mRNA transcripts encoding for hEPO, FF, CA09 HA, Sing16 HA, Mich15 NA, and Sing16 NA were synthesized by *in vitro* transcription employing RNA polymerase with a plasmid DNA template encoding the desired gene using unmodified nucleotides. The resulting purified precursor mRNA was reacted further via enzymatic addition of a 5' cap structure (Cap 1) and a 3' poly(A) tail of approximately 200 nucleotides in length as determined by gel electrophoresis and purified. All mRNA preparations were analyzed for purity, integrity, and percentage of Cap 1 before storage at -20°C. Preparation of mRNA/lipid nanoparticle (LNP) formulations was described above. Briefly, an ethanolic solution of a mixture of lipids (ionizable lipid, phosphatidylethanolamine, cholesterol and polyethylene glycol-lipid) at a fixed lipid and mRNA ratio were combined with an aqueous buffered solution of target mRNA at an acidic pH under controlled conditions to yield a suspension of uniform LNPs. Upon ultrafiltration and diafiltration into a suitable diluent system, the resulting nanoparticle suspensions were diluted to final concentration, filtered, and stored frozen at -80°C until use. The mRNA-LNP formulations were characterized for size by dynamic light scattering, percentage encapsulation and were stored at -80°C at 1mg/mL until further use by dilution with suitable buffer. hEPO-LNPs and FF-LNPs were utilized to check level of expression of target protein *in vivo*.

Visualization of S-Proteins Expressed in HeLa cells

[00236] Immunocytochemistry-immunofluorescence analysis of influenza NA and HA-proteins was performed in HeLa cells transfected with bivalent H3N2 (Sing16 HA and Perth09 NA) mRNAs LNPs) using method described previously (Kalnin et al., *npj Vaccines* (2021) 6:61). Cells were fixed in 4% paraformaldehyde and subjected antibody staining for HA (GeneTex GTX40258), NA, and ER marker Calnexin (Abcam ab22595) was performed. Images were captured on confocal microscope followed by image analysis for quantification of HA and NA colocalization to the ER, mean signal intensity, and percent of cell area.

Flow Cytometry

[00237] Human skeletal muscle cells (HskMCs, Lonza) were cultured in M199 (Life Technologies) supplemented with GlutaMAX (Life Technologies), streptomycin, penicillin

(Gibco), and 20% heat inactivated FBS (VWR) at 37°C with 5% CO_2. The cells were harvested by trypsinization, washed with PBS, and electroporated using human primary muscle cell transfection kit on Nucleofector 2b (Lonza) with 12 mg of mRNA per 10^6 cells following manufacturer's electroporation program D-033. Post 24 hour harvested cells were fixed, permeabilized with Cytofix™/Perm (BD) and stained with CA09 HA (Immune Tech), Sing16 HA (30-2F11-F7-A5, GeneTex), Mich15 NA (6G6, Immune Tech) and Sing16 NA (40017-RP01, Sino Biologicals) specific Ab followed by PE conjugated goat anti-mouse IgG secondary Ab (Southern Biotech) or AF647 conjugated goat anti-rabbit IgG (Life Technologies). Then the antibody-labeled cells were acquired by Fortessa (BD) and the expression of each protein was analyzed by FlowJo™ (TreeStar).

Cryogenic Transmission Electron Microscopy

[00238] A PELCO easiGlow™ device was used to plasma-clean the grids prior to LNP sample application, and a Vitrobot Mark IV System (ThermoFisher) with the chamber held at 100% humidity and 18°C was used for plunge freezing. A 3.0 μl droplet of LNP sample was dispensed onto 300 mesh R2/1 QUANTIFOIL® grids with carbon film and gold bars. Grids were blotted for 4 seconds, held in place for 10 seconds, and then immediately plunge frozen in liquid ethane for storage and transfer to a Krios microscope. Exposures were collected using a Titan Krios transmission electron microscope (ThermoFisher) equipped with a BioQuantum energy filter and K3 direct electron detector (Gatan) operating in counting mode. Calibrated physical pixel size at the detector was 1.38 Å, corresponding to 64,000x magnification. A total of 3,141 69-frame movie exposures were collected at a dose per frame of 1.045 e/Å2 with defocus between -0.5 to -1.7 μm. For each movie exposure, patch-based motion correction, binning of super-resolution pixels, and frame dose-weighting was performed using RELION-3.1.34. From corrected images, over 700 candidate particle coordinates were extracted. Subsequent data analysis was done with MATLAB R2019a with image processing toolbox.

Immunization of Mice and NHPs for Expression Studies

[00239] Groups of four cynomolgus macaques (NHPs) (male and female) and four to eight male BALB/c mice were administered intramuscularly either dose of 10 μg (NHP) or 1, 0.5, 0.1, and 0.05 μg (mice) with hEPO-LNP prepared in the same ratio as the one intended to be used for HA/NA mRNA-LNP formulations. Blood samples were taken pre-administration, and at 6h, 24h, 48h, 72h, and 96h post administration to monitor for serum hEPO expression via an ELISA using

R and D Systems, Quantikine® IVD® ELISA, Human Erythropoietin Immunoassay kit as per manufacturers protocol, and reported as final values of mIU/ml and ng/ml. Briefly, microplate wells, precoated with a mouse monoclonal antibody specific for EPO were incubated with specimen or standard. After removing excess specimen or standard, wells were incubated with a rabbit anti-EPO polyclonal antibody conjugated to horseradish peroxidase. During the second incubation, the antibody-enzyme conjugate bound to the immobilized EPO. Excess conjugate was removed by washing. A chromogen was added to the wells and was oxidized by the enzyme reaction to form a blue colored complex. The reaction was stopped by the addition of acid, which turned the blue to yellow. The amount of color generated was directly proportional to the amount of conjugate bound to the EPO antibody complex, which, in turn, was directly proportional to the amount of EPO in the specimen or standard. The absorbance of this complex was measured, and a standard curve was generated by plotting absorbance versus the concentration of the EPO standards. The EPO concentration of the unknown specimen was determined by comparing the optical density of the specimen to the standard curve. The standards used in this assay were recombinant hEPO calibrated against the Second International Reference Preparation (67/343), a urine-derived form of human erythropoietin.

Immunization of Mice and NHPs for Immunogenicity Studies

[00240] Groups of Balb/c mice (*Mus musculus*) as per the treatment group were immunized under isoflurane anesthesia with a dose of 0.05 mL of designated vaccine preparation or diluent via the IM route in the quadriceps, on day 0 in one hind leg and day 28 in the contralateral leg. Mice that lost more than 20% of their initial body weight and displayed severe clinical signs were euthanized after the veterinarian's assessment of the animal's health prior to the study termination.

[00241] Naïve male and female Mauritius origin Cynomolgus macaques (*Macaca fascicularis*) were selected for the study. Animals weighed > 2kg and were >2 years of age at the start of the study. Animals selected for the study underwent comprehensive physical examinations prior to assignment to the study. The pre-assignment assessment of health status included a hands-on veterinarian examination and blood sample collections for CBC analysis as applicable per NIRC SOPs. Animals were generally housed in pairs and acclimated for at least 3 days prior to the start of the study. Groups consisted of up to 6 animals per treatment group. All animals were immunized under ketamine HCl (10 mg/kg, IM) or telazol (4-8 mg/kg, IM) sedation with a dose of 0.5 ml of their respected vaccine preparation or diluent via the IM route in one forelimb of each animal, targeting the deltoid, on Study Day 0. Twenty-eight days after the first immunization took place, a second immunization was given to the animals in the contralateral limb.

Immunization of Mice and NHPs for Challenge Studies

[00242] Mice were inoculated with the challenge strain approximately 9-12 weeks after the last immunization. Vials of stock virus were thawed and diluted to the appropriate concentration in ice-cold sterile PBS. All mice were challenged with a total volume of 50 µl containing 105.54 $TCID_{50}$ of Belgium09 virus in PBS which equated to $4LD_{50}$. Virus challenge was performed inside the biosafety cabinet in an enhanced ABSL2 laboratory. Mice were first anesthetized with an IP injection of a Ketamine/Xylazine solution (50 mg/kg Ketamine and 5 mg/kg Xylazine), and then challenged IN (dropwise into both nostrils; 25 µl per nostril) with a total volume of 50 µl of influenza virus using a micropipette. Following the challenge procedure, mice were placed in dorsal recumbency and observed until recovery from anesthesia. Daily body weights were taken following H1N1 challenge. Any individual animal with a single observation > 20% body weight loss was euthanized. The weight measurements were either recorded daily post challenge until euthanasia in the online database, Pristima® (Version 7.5.0 Build 8), or written on study specific working sheets.

Blood Collection

[00243] For mice, blood was collected via submandibular or orbital sinus bleeds (in-life bleed, pre-study and on study days 14, 28, and 42 approximately 200 µl) and cardiac puncture (terminal bleed, day 56) from all animals under sedation. Mice were bled on pre-study to obtain a base-line pre-immune serum sample and for pre-screening purposes. Processing of the serum, blood samples were collected into SST tubes and allowed to clot for 30 minutes to 1 hour at room temperature. The samples were then centrifuged 1000 – 1300 g for 5-10 minutes with brakes off. Serum was collected using a P200 pipettor, divided into two 0.5 ml cryovials, and stored at -20°C. All bleeds were documented on specimen collection and processing logs, indicating the time of sample collection and the technician responsible for performing the procedure. A portion of the serum samples were evaluated in the HAI or ELLA and ELISA assays for antibody titers.

[00244] NHPs were bled for serum isolation while under anesthesia administered intramuscularly using10 mg/kg ketamine/1 mg/kg acepromazine (days -4, 2, 7, 14, 28, 30, 35, 42, 56, 90, and 180). The volume of blood withdrawn did not exceed established guidelines with respect to percentage of body weight and animal’s physical condition. Blood was withdrawn from anesthetized NHPs using femoral venipuncture using a Vacutainer 21 ga x 1" blood collection needle or Abbott Butterfly 23 ga x ¾" tubing attached to BD Vacutainer® SST™ gel tubes. Serum was isolated by spinning the tubes at room temperature at a speed of 1200 x g for 10 minutes. Serum was then aliquoted into labeled cryovials (1 ml/vial) and stored at ≤ -20°C. A portion of the serum samples were evaluated in the HAI or ELLA and ELISA assays for antibody titers. For PBMCs, NHPs were pre-bled before vaccination and again approximately 42-63 days after the first injection. For this purpose, blood was collected into BD Vacutainer® tubes containing heparin anticoagulant. Briefly, anticoagulated blood samples were diluted in PBS and subjected to gradient density centrifugation for 30 minutes at 400 x g using Histopaque® separation solution (Sigma). The opaque interface containing mononuclear cells was then collected, washed three times in PBS using a low speed (250 x g) centrifugation for the last centrifugation to reduce the number of platelets. The live vs. dead PBMC were enumerated using a Nexcelom Cellometer K2. The PBMC were cryopreserved in FBS with 10% DMSO using Mr. Frosty® freezing boxes. The boxes were placed immediately into a -80°C freezer for 24 hours and then transferred for storage in a liquid nitrogen tank.

ELISA

[00245] The antibody ELISAs were performed using recombinantly produced Sing16 NA protein, Sing16 HA protein, or CA09 HA protein. The proteins were captured on 96 well high binding polystyrene plates at a concentration of 2μg/ml in carbonate-bicarbonate buffer. The plates were covered and incubated overnight (16 ± 4 hours) at 2-8°C. After overnight incubation, the antigen coated plates were washed 5 times with a washing buffer (PBS, 0.5% Tween20) and blocked with a blocking solution (10% BSA in PBS) for 60±30 minutes at room temperature. Test samples, naïve control, and the reference sample were diluted in a sample diluent (PBS 10% BSA 0.5% Tween 20) and added to wells in duplicates followed by incubation at room temperature for 90 minutes. Plates were washed 5 times with the washing buffer, and goat anti-mouse HRP for mouse sera or goat anti-monkey HRP for NHP sera was added at a dilution of 1:10,000. The plates were then incubated 30 minutes at room temperature and the excess HRP-IgG was washed with the washing buffer. Sure-Blue TMB substrate was added to each plate and the reaction was stopped after about 10 minutes with TMB stop solution. The plates were then read at 450 nm with a Thermo Labsystems Multiskan™ spectrophotometer. The anti-antigen (HA or NA) specific antibody titers were expressed as a reciprocal of the highest serum dilution with an absorbance value >0.3.

HAI Assay

[00246] HAI assays were performed using the Sing16 H3N2 and the CA09 H1N1 virus stocks (BIOQUAL, Inc.). Sera were treated with receptor-destroying enzyme (RDE) by diluting one-part serum with three parts enzyme and incubated overnight in a 37°C water bath. Enzyme was inactivated by a 30-minute incubation period at 56°C followed by addition of six parts PBS for a final dilution of 1/10. HAI assays were performed in V-bottom 96-well plates using four hemagglutinating units (HAU) of virus and 0.5% turkey RBC. The reference serum for each strain was included as a positive control on every assay plate. Each plate also included a back-titration to confirm the antigen dose (4 HAU/25µl) as well as a negative control sample (PBS or naïve control serum). The HAI titer was determined as the highest dilution of serum resulting in complete inhibition of hemagglutination. Results were only valid for plates with the appropriate back-titration result (verifying 4 HAU/25 µl added) and a reference serum titer within 2-fold of the expected titer.

NAI Assay

[00247] The method for the enzyme-linked lectin assay (ELLA) assay was used to determine neuraminidase-inhibiting (NAI) antibody titers. The source of antigen (virus NA) was titrated, and a standard amount was selected for incubation with serial dilutions of serum. Titration of sera was performed with serial dilutions of sera (heat inactivated at 56°C for 1 hour) and a standard amount of virus was added to duplicate wells of a fetuin-coated plate. This mixture was then incubated overnight (16-18 hours); the next day, HRP-conjugated peanut agglutinin PNA (diluted to 2.5 µg/ml) was added to the washed plate and incubated for 2 hours at room temperature. Substrate (ODP in sodium citrate) was added and incubated for 10 minutes to develop the color. And then stop buffer (1N sulfuric acid) was added to stop the reaction. Plates were scanned for absorbance at OD 490 nm. The reduction or absence of color relative to a viral control indicated inhibition of NA activity due to the presence of NA-specific antibodies. NAI titers (IC_{50} values) were calculated from the OD readings and the results were graphed in GraphPad Prism. If ELLA titration curves did not allow a good fit to determine a reliable IC50 value, the samples were retested using a different dilution scheme to reach the 50% endpoint.

T cell ELISPOT Assay

[00248] Complete medium (DMEM1640 + 10% heat-inactivated FCS) was prewarmed in a 37°C water bath. PBMCs were quickly thawed in a 37°C water bath and transferred dropwise to conical tubes with the prewarmed medium. The tubes were centrifuged at 1,500 rpm for 5 mins and the cells were resuspended and counted using a Guava cell counter. Monkey IFN-γ ELISPOT kit (Mabtech 3421M-4APW) and IL-13 ELISPOT kit (Mabtech 3470M-4APW) were used. Precoated plates provided by the kits were washed four times with sterile PBS and blocked with 200 μl of complete medium in 37°C incubator for at least 30 minutes. Sing16 H3 peptides pool (Genscript Custom Order) (at 1 μg/ml of each peptide) were used as recall antigens in the assay. Two μg/ml of ConA (Sigma CAT#C5275) was used as a positive control. Fifty μl of recall antigens and 300,000 of PBMCs in 50 μl were added to each well for stimulation. The plates were placed in a 37°C, 5% CO_2 humidified incubator for 48 hours.

[00249] After the incubation, cells were removed, plates were washed 5 times with PBS, and 100μl of 1 μg/ml biotinylated anti-IFN-γ or anti-IL-13 detection antibodies were added to each well in the plates. After a 2 hour incubation, the plates were washed 5 times with PBS and incubated with 100 μl of a 1:1000 dilution of streptavidin in each well for one hour at room temperature. Plates were developed with 100 μl of BCIP/NBT substrate solution until the spots emerged. Plates were rinsed by tap water, air-dried and scanned and counted using CTL ImmunoSpot® Reader (Cellular Technology Ltd.). The data was reported as spots forming cells (SFC) per million PBMCs.

Memory B cell (MBC) ELISPOT Assay

[00250] Human IgG Single-Color memory B cell ELISPOT kit (CAT# NC1911372, CTL) was used per manufacturer's instruction to measure Sing16 H3-specific and total IgG^+ antibody-secreting cells (ASCs). Differentiation of MBCs into ASCs was performed in PBMC using a stimulation cocktail provided by the kit. Briefly, frozen PBMCs were quickly thawed in a 37°C water bath, mixed with DNase I (CAT# 90083, Fisher Scientific) and transferred into the tube containing pre-warmed complete culture medium (CM) (RPMI 1640, (CAT# 22400-089, Gibco) containing 10% FCS (CAT # SH30073.03, HyClone™), and 1% penicillin/streptomycin (CAT# P4333, Sigma) and centrifuged at 1,500 rpm for 5 minutes. Cell pellet was re-suspended in 5 ml of complete medium at $2x10^6$ cells per ml and transferred to a T25 flask for 1 hour in 5% CO_2 incubator at 37°C. The volume of cell suspension was then adjusted to 6 ml and B-Poly-S was added at 1:1000 dilution. Cells were left in the CO_2 incubator for stimulation for 4 days. PVDF microplates supplied by the kit were pre-wetted with 70% ethanol, rinsed and coated overnight with 80 µl/well of either anti-human IgG capture Ab provided by the kit or Sing16/H3 recombinant protein at 4 µg/ml.

[00251] Cells were harvested after 4 days of stimulation, washed, and counted and adjusted to the designated concentration in the CM. Coated microplates were washed with PBS, blocked for 1 hour with the CM and emptied out. Cell suspension at 100 µl/well was added to the plates and incubated in CO_2 incubator at 37C for 18hrs. After washing, 80 µl/well of 1:400 diluted anti-human IgG biotin detection antibody was added to the plate and incubated at room temperature for 2 hours. Following washing, Streptavidin-AP at 1:1000 dilution was added to the plate at 80 µl/well for 1 hour. Freshly prepared Substrate solution was added and incubated at RT for 18 min. Plates were rinsed by tap water, air-dried and scanned and counted using CTL ImmunoSpot® Reader (Cellular Technology Ltd). For each individual animal the number of IgG^+ and number of Sing16/H3-specific ASCs was calculated per million of PBMCs. The frequency of antigen-specific ASCs was calculated as % of antigen-specific ASCs to the total IgG^+ ASCs. To assess assay background the negative control wells on every plate were coated with PBS (no background was detected).

Statistical Analysis

[00252] For estimating the T_{max} of Radiance, a non-parametric method was used to estimate the T_{max} of individual subject based on observed data. For estimating the half-life of Radiance, assuming exponential decay model for radiance after reaching the maximum value, a linear model was fitted to log transformed data per subject during the time course from the maximum radiance to decay to baseline (we estimate the baseline using the average of radiance in saline group). The half-life was estimated as the time point when the log radiance had reached the middle point between maximum and baseline values. For analysis of different readouts with results summarized as geometric mean, SE model based geometric means and SEs were estimated from a mixed effect model for repeated measures where the response was the log transformed readouts, vaccination was fixed effect and time was repeated measure; log-based means and SE estimates from the model were then back transformed to get geometric means and SEs. For weight change, over descriptive statistical analysis was used. Medians and ranges of each group of the maximum % body weight loss from baseline (Day 0) over time were reported to evaluate the worse scenarios; medians and ranges of each group of the % body weight change from baseline at the last observation were reported to evaluate the body weight recovery.

Antigen Sequences

[00253] The sequence of the Perth09 N2 antigen used here is:

MNPNQKIITIGSVSLTISTICFFMQIAILITTVTLHFKQYEFNSPPNNQVMLCEPTIIE
RNITEIVYLTNTTIEKEICPKLAEYRNWSKPQCDITGFAPFSKDNSIRLSAGGDIWVTR
EPYVSCDPDKCYQFALGQGTTLNNVHSNNTVRDRTPYRTLLMNELGVPFHLGTKQVCIA
WSSSSCHDGKAWLHVCITGDDKNATASFIYNGRLVDSVVSWSKEILRTQESECVCINGT
CTVVMTDGSASGKADTKILFIEEGKIVHTSTLSGSAQHVEECSCYPRYPGVRCVCRDNW
KGSNRPIVDINIKDHSIVSSYVCSGLVGDTPRKNDSSSSSHCLDPNNEEGGHGVKGWAF
DDGNDVWMGRTISEKSRLGYETFKVIEGWSNPKSKLQINRQVIVDRGNRSGYSGIFSVE
GKSCINRCFYVELIRGRKEETEVLWTSNSIVVFCGTSGTYGTGSWPDGADINLMPI*
(SEQ ID NO:4)

[00254] The sequence of the Mich15 N1 antigen used here is:

MNPNQKIITIGSICMTIGMANLILQIGNIISIWVSHSIQIGNQSQIETCNQSVITYENN
TWVNQTYVNISNTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIR
EPFISCSPLECRTFFLTQGALLNDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESV
AWSASACHDGINWLTIGISGPDSGAVAVLKYNGIITDTIKSWRNNILRTQESECACVNG
SCFTIMTDGPSDGQASYKIFRIEKGKIIKSVEMKAPNYHYEECSCYPDSSEITCVCRDN
WHGSNRPWVSFNQNLEYQMGYICSGVFGDNPRPNDKTGSCGPVSSNGANGVKGFSFKYG
NGVWIGRTKSISSRKGFEMIWDPNGWTGTDNKFSIKQDIVGINEWSGYSGSFVQHPELT
GLDCIRPCFWVELIRGRPEENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK*
(SEQ ID NO:5)

[00255] The sequence of the Sing16 H3 antigen used here is:

MKTIIALSYILCLVFAQKIPGNDNSTATLCLGHHAVPNGTIVKTITNDRIEVTNATELV
QNSSIGEICDSPHQILDGENCTLIDALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDV
PDYASLRSLVASSGTLEFKNESFNWTGVTQNGTSSACIRGSSSSFFSRLNWLTHLNYTY
PALNVTMPNKEQFDKLYIWGVHHPGTDKDQIFLYAQSSGRITVSTKRSQQAVIPNIGSR
PRIRDIPSRISIYWTIVKPGDILLINSTGNLIAPRGYFKIRSGKSSIMRSDAPIGKCKS
ECITPNGSIPNDKPFQNVNRITYGACPRYVKHSTLKLATGMRNVPEKQTRGIFGAIAGF
IENGWEGMVDGWYGFRHQNSEGRGQAADLKSTQAAIDQINGKLNRLIGKTNEKFHQIEK
EFSEVEGRVQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTKKQLR
ENAEDMGNGCFKIYHKCDNACIESIRNETYDHNVYRDEALNNRFQIKGVELKSGYKDWI
LWISFAISCFLLCVALLGFIMWACQKGNIRCNICI* (SEQ ID NO:6)

[00256] The sequence of the Sing16 N2 antigen used here is:

MNPNQKIITIGSVSLTISTICFFMQIAILITTVTLHFKQYEFNSPPNNQVMLCEPTIIE
RNITEIVYLTNTTIEKEICPKPAEYRNWSKPQCGITGFAPFSKDNSIRLSAGGDIWVTR
EPYVSCDPDKCYQFALGQGTTLNNVHSNNTVRDRTPYRTLLMNELGVPFHLGTKQVCIA
WSSSSCHDGKAWLHVCITGDDKNATASFIYNGRLIDSVVSWSKDILRTQESECVCINGT

CTVVMTDGNATGKADTKILFIEEGKIVHTSKLSGSAQHVEECSCYPRYPGVRCVCRDNW
KGSNRPIVDINIKDHSIVSSYVCSGLVGDTPRKNDSSSSHCLNPNNEEGGHGVKGWAF
DDGNDVWMGRTINETSRLGYETFKVVEGWSNPKSKLQINRQVIVDRGDRSGYSGIFSVE
GKSCINRCFYVELIRGRKEETEVLWTSNSIVVFCGTSGTYGTGSWPDGADLNLMHI*
(SEQ ID NO:7)

[00257] The sequence of the CA09 H1 antigen used here is:

MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDKHNGKLC
KLRGVAPLHLGKCNIAGWILGNPECESLSTASSWSYIVETPSSDNGTCYPGDFIDYEEL
REQLSSVSSFERFEIFPKTSSWPNHDSNKGVTAACPHAGAKSFYKNLIWLVKKGNSYPK
LSKSYINDKGKEVLVLWGIHHPSTSADQQSLYQNADAYVFVGSSRYSKKFKPEIAIRPK
VRDREGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGSGIIISDTPVHDCNTT
CQTPKGAINTSLPFQNIHPITIGKCPKYVKSTKLRLATGLRNIPSIQSRGLFGAIAGFI
EGGWTGMVDGWYGYHHQNEQGSGYAADLKSTQNAIDEITNKVNSVIEKMNTQFTAVGKE
FNHLEKRIENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKN
NAKEIGNGCFEFYHKCDNTCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQIL
AIYSTVASSLVLVVSLGAISFWMCSNGSLQCRICI* (SEQ ID NO: 24)

[00258] The sequence of the HA strain A/California/7/2009 (H1N1) (CA09) antigen mRNA open reading frame (ORF) used here is:

AUGAAAGCUAUCCUGGUCGUCUUGCUGUAUACUUUCGCCACUGCCAACGCCGACA
CCCUGUGUAUCGGUUACCACGCGAACAACUCCACCGACACUGUGGACACCGUGCU
CGAAAAGAACGUGACCGUGACUCAUUCUGUGAAUCUGCUCGAGGACAAGCACAAC
GGAAAGUUGUGCAAGCUGCGCGGAGUGGCACCGCUGCACCUUGGAAAGUGCAAC
AUUGCCGGAUGGAUCCUGGGAAACCCGGAGUGCGAAAGCCUGAGCACCGCGUCCU
CAUGGUCCUACAUCGUGGAAACCCCGUCCUCUGACAACGGCACCUGUUACCCCGG
CGAUUUCAUCGACUACGAAGAACUGCGGGAGCAGCUGUCCUCCGUGUCCUCGUUU
GAACGCUUCGAGAUUUUCCCUAAGACCUCCAGCUGGCCUAAUCACGAUAGCAACA
AGGGCGUGACGGCAGCCUGCCCGCACGCCGGAGCAAAGUCAUUCUACAAGAAUCU
GAUUUGGCUCGUGAAGAAAGGGAACUCAUACCCCAAGCUGUCCAAGUCGUACAUC
AACGACAAGGGAAAGGAAGUGCUCGUGCUCUGGGGGAUCCACCACCCAUCCACCU
CCGCCGACCAGCAGAGCCUGUACCAGAACGCCGAUGCUUACGUGUUUGUGGGUUC
CAGCCGGUACUCCAAGAAGUUCAAGCCUGAAAUCGCGAUCAGGCCUAAAGUCCGG
GACCGCGAGGGCCGCAUGAACUACUACUGGACUCUCGUGGAGCCUGGAGACAAGA
UCACCUUCGAGGCCACCGGAAAUCUCGUGGUGCCACGCUACGCUUUCGCCAUGGA
ACGGAACGCCGGAAGCGGCAUCAUCAUUAGCGAUACUCCUGUGCAUGACUGUAAC
ACCACGUGCCAGACACCCAAGGGCGCCAUCAACACCAGCCUGCCGUUUCAAAACA
UCCAUCCCAUUACCAUUGGGAAGUGCCCCAAAUACGUCAAGUCCACCAAGCUGAG
GCUGGCGACCGGACUGCGGAACAUUCCGAGCAUCCAGUCGAGAGGCCUGUUCGGU
GCCAUCGCGGGAUUCAUCGAGGGCGGCUGGACUGGAAUGGUGGACGGUUGGUAC
GGGUAUCACCACCAAAACGAACAGGGAUCAGGCUACGCGGCCGAUUUGAAGUCCA
CCCAGAACGCCAUUGAUGAAAUCACCAACAAGGUCAACUCCGUGAUUGAGAAGAU
GAAUACUCAAUUCACCGCCGUGGGCAAAGAAUUCAAUCACCUGGAGAAGAGAAU
AGAGAACCUGAACAAGAAGGUCGACGACGGGUUCCUCGACAUCUGGACCUAUAAC

GCCGAGUUGCUCGUGCUGCUGGAAAACGAACGGACCCUGGACUAUCACGACUCGA
ACGUGAAGAACCUGUACGAGAAAGUCCGCUCGCAACUGAAGAACAACGCCAAGGA
AAUCGGAAAUGGUUGCUUCGAGUUCUACCAUAAGUGCGACAACACUUGCAUGGA
GUCCGUGAAGAACGGCACUUACGAUUACCCCAAGUACUCCGAAGAGGCUAAACUU
AACCGGGAAGAGAUCGAUGGCGUGAAGCUCGAGUCCACCAGAAUCUACCAGAUUC
UCGCCAUCUACUCGACUGUGGCAUCGAGCCUCGUCCUUGUCGUGUCCCUGGGGGC
CAUUUCAUUCUGGAUGUGCUCCAACGGGUCCCUGCAGUGCCGGAUUUGCAUCUAA
(SEQ ID NO: 8)

[00259] The sequence of the A/Michigan/45/2015 (Mich15) neuraminidase (NA) antigen mRNA open reading frame (ORF) used here is:

AUGAACCCAAACCAGAAAAUCAUCACGAUUGGCUCGAUUUGCAUGACCAUUGGA
AUGGCGAACCUUAUCCUCCAAAUUGGCAACAUUAUCUCGAUCUGGGUCAGCCACU
CGAUCCAGAUCGGCAACCAAUCCCAGAUUGAAACUUGCAACCAGAGCGUGAUUAC
UUACGAAAACAACACGUGGGUGAACCAGACUUACGUCAAUAUUAGCAACACUAA
CUUCGCCGCUGGGCAGAGCGUCGUCAGCGUGAAGCUCGCCGGAAAUUCCUCGCUC
UGCCCCGUGUCCGGCUGGGCGAUCUACAGCAAGGAUAACAGCGUCCGGAUUGGUA
GCAAGGGCGACGUUUUCGUGAUCCGCGAACCCUUCAUAUCAUGCUCCCCGCUCGA
AUGUCGCACGUUCUUCCUGACCCAAGGCGCCCUGCUGAACGACAAGCACUCCAAU
GGCACUAUCAAGGAUCGGAGCCCUUACCGGACCUUGAUGUCCUGCCCUAUUGGAG
AAGUGCCUUCACCAUAUAACUCGCGCUUUGAAAGCGUGGCUUGGUCAGCCUCCGC
CUGCCAUGACGGGAUUAACUGGCUGACCAUUGGCAUAAGCGGCCCCGAUUCCGGC
GCCGUGGCCGUCCUGAAGUACAACGGGAUCAUCACCGACACCAUUAAGUCCUGGC
GCAACAACAUCCUGAGGACCCAGGAGUCCGAGUGCGCGUGCGUGAACGGGUCCUG
CUUUACCAUCAUGACCGACGGACCGUCCGACGGUCAAGCCUCGUACAAGAUCUUC
CGGAUCGAGAAAGGAAAGAUCAUCAAGAGCGUGGAGAUGAAGGCCCCGAACUAC
CACUACGAGGAAUGUUCAUGCUAUCCCGACUCGUCCGAGAUUACUUGCGUGUGCC
GCGACAAUUGGCACGGAUCCAACAGGCCGUGGGUCAGCUUCAACCAGAACCUUGA
AUACCAGAUGGGAUACAUUUGCAGCGGAGUGUUCGGGGACAACCCUCGCCCGAAC
GACAAGACCGGAUCGUGUGGGCCCGUGUCCUCCAACGGCGCAAACGGCGUCAAGG
GAUUUUCCUUCAAAUACGGGAACGGGGUCUGGAUCGGACGGACCAAGAGCAUUU
CAAGCAGAAAGGGAUUCGAGAUGAUUUGGGACCCGAACGGCUGGACUGGUACCG
AUAACAAAUUCAGCAUCAAGCAGGACAUCGUGGGAAUUAACGAGUGGUCCGGUU
ACUCCGGGAGCUUCGUGCAGCAUCCCGAACUCACUGGACUGGACUGCAUUCGGCC
GUGCUUUUGGGUGGAAUUGAUCCGGGGCAGACCUGAGGAGAACACGAUUUGGAC
CUCCGGCUCCUCGAUCUCGUUCUGCGGAGUGAACUCCGACACCGUGGGAUGGUCC
UGGCCCGACGGUGCAGAGCUGCCCUUCACCAUUGAUAAGUAA (SEQ ID NO: 9)

[00260] The sequence of the A/Singapore.INFIMH160019/2016 (Sing16; H3N2) HA hemagglutinin antigen mRNA open reading frame (ORF) used here is:

AUGAAAACCAUAAUCGCGCUCUCAUACAUACUUUGCCUGGUCUUUGCCCAAAAGA
UCCCUGGCAACGACAACUCAACCGCGACCCUUUGCCUCGGCCAUCACGCCGUGCC
GAACGGCACUAUCGUCAAGACCAUCACAAACGACCGCAUCGAAGUGACCAACGCG

ACUGAGCUAGUGCAGAACUCCAGCAUUGGAGAGAUUUGCGAUUCUCCACACCAAA
UCCUGGACGGAGAGAAUUGUACCUUGAUCGACGCGCUGCUGGGGGAUCCGCAGU
GCGACGGAUUCCAGAACAAGAAAUGGGACCUUUUCGUGGAACGGAGCAAGGCAU
ACUCGAAUUGCUACCCCUACGAUGUGCCCGACUACGCCUCGCUGCGGUCCUUGGU
CGCUUCCUCCGGGACCCUGGAAUUCAAAAACGAGAGCUUUAAUUGGACCGGAGUG
ACCCAGAAUGGCACCUCGAGCGCCUGCAUUCGGGGCUCCUCCUCGAGCUUCUUCA
GCCGCCUGAACUGGCUCACUCACCUCAACUACACCUACCCGGCACUGAACGUGAC
CAUGCCGAACAAGGAACAAUUCGACAAGCUCUACAUUUGGGGGGUGCAUCACCCG
GGUACCGAUAAGGACCAGAUCUUCCUCUACGCCCAAUCCUCGGGCCGGAUCACCG
UGUCCACUAAGCGCUCGCAGCAGGCCGUGAUCCCGAACAUUGGAAGCAGACCCCG
CAUUCGCGACAUUCCAUCGAGGAUCUCGAUCUACUGGACGAUUGUCAAGCCUGGC
GACAUCCUCCUCAUUAACUCCACCGGGAACCUCAUCGCCCCUCGGGGUUAUUUCA
AGAUCCGCAGCGGGAAGUCCUCCAUCAUGAGAAGCGAUGCCCCCAUUGGAAAGUG
CAAGUCCGAGUGUAUCACACCUAACGGAAGCAUUCCCAAUGACAAGCCAUUCCAG
AACGUGAACAGAAUUACCUACGGAGCUUGCCCUCGCUACGUCAAACAUUCGACCC
UCAAGUUGGCGACUGGAAUGCGCAACGUGCCGGAGAAGCAAACCCGGGGGAUCU
UCGGGGCUAUCGCGGGAUUCAUCGAAAAUGGAUGGGAAGGAAUGGUCGAUGGUU
GGUACGGUUUCAGACACCAGAACUCCGAGGGGCGGGGCCAGGCCGCAGACCUGAA
GUCCACUCAGGCCGCGAUUGACCAGAUCAACGGAAAGCUCAACAGACUCAUUGGA
AAGACCAACGAAAAGUUCCACCAAAUCGAAAAGGAAUUCUCCGAAGUGGAGGGC
CGGGUGCAAGACCUGGAGAAGUACGUGGAGGACACUAAGAUCGACCUUUGGAGC
UAUAACGCAGAACUCCUUGUGGCCCUGGAAAACCAGCACACCAUCGACCUGACCG
AUUCAGAGAUGAACAAGCUCUUUGAGAAAACUAAGAAGCAACUCCGGGAAAACG
CUGAGGACAUGGGAAAUGGAUGCUUUAAGAUCUACCACAAGUGCGACAACGCCU
GCAUUGAGUCCAUACGGAACGAAACUUACGACCAUAACGUCUACCGGGAUGAAGC
CCUGAACAACAGAUUCCAGAUCAAGGGCGUGGAGCUGAAGUCCGGCUACAAAGA
UUGGAUCCUGUGGAUUUCCUUCGCGAUUUCAUGCUUCUUGCUCUGCGUGGCCCUC
CUGGGAUUCAUAAUGUGGGCCUGUCAGAAGGGCAACAUUAGGUGCAACAUAUGC
AUAUAA (SEQ ID NO: 10)

[00261] The sequence of the Perth/16/2009 (H3N2) NA antigen mRNA open reading frame (ORF) used here is:

AUGAACCCUAACCAGAAGAUCAUCACAAUUGGAAGCGUGUCCCUGACCAUUUCGA
CGAUUUGCUUCUUCAUGCAAAUCGCGAUCUUGAUUACCACCGUCACCCUGCAUUU
CAAGCAAUACGAAUUCAACUCCCCGCCAAACAACCAAGUCAUGCUCUGCGAGCCC
ACCAUCAUCGAACGCAACAUCACCGAGAUCGUGUACCUUACCAACACUACCAUCG
AAAAGGAGAUUUGCCCCAAGUUGGCCGAAUACCGGAACUGGAGCAAGCCCCAGUG
UGACAUCACGGGAUUUGCGCCAUUCAGCAAGGAUAACUCGAUCAGACUUUCCGCC
GGGGGCGACAUUUGGGUCACUCGGGAGCCUUACGUGAGCUGCGACCCGGACAAGU
GCUACCAAUUCGCACUCGGACAGGGUACCACCCUGAACAACGUCCAUAGCAACAA
CACCGUGCGCGAUAGAACCCCGUACCGCACCCUCCUCAUGAACGAACUGGGAGUG
CCGUUCCACUUGGGAACCAAACAAGUCUGCAUUGCAUGGUCCUCCUCCUCCUGCC
ACGACGGCAAAGCCUGGCUUCACGUUUGCAUCACCGGCGACGACAAGAAUGCGAC
GGCCUCCUUCAUAUACAAUGGUAGACUCGUGGAUAGCGUGGUGUCAUGGUCCAA
GGAAAUUCUCAGGACUCAGGAGUCAGAGUGCGUGUGCAUCAACGGGACUUGCAC

UGUCGUGAUGACCGACGGAUCGGCCUCCGGAAAGGCCGACACUAAGAUCCUCUUC
AUCGAGGAGGGAAAGAUCGUGCACACUUCUACCCUGAGCGGCUCGGCUCAGCAUG
UCGAAGAGUGCUCGUGCUACCCCCGGUAUCCCGGGGUCCGCUGCGUGUGCCGGGA
CAAUUGGAAAGGCUCAAACCGCCCCAUCGUGGACAUUAACAUCAAGGACCACUCC
AUCGUGAGCUCCUACGUAUGCAGCGGGCUGGUCGGGGAUACCCCGCGGAAGAACG
AUUCCUCGUCCUCCUCCCACUGCCUGGACCCUAACAACGAAGAGGGAGGCCACGG
AGUGAAGGGAUGGGCUUUUGACGAUGGCAACGACGUGUGGAUGGGCAGGACUAU
UUCCGAAAAGUCCCGGCUGGGAUACGAAACCUUCAAGGUCAUCGAGGGCUGGUCC
AACCCGAAGUCAAAGCUCCAGAUCAACCGCCAGGUCAUCGUGGAUAGGGGCAAUA
GAUCCGGCUACUCCGGGAUCUUCAGCGUGGAAGGGAAGUCCUGCAUUAACCGAUG
CUUCUACGUGGAACUCAUUCGGGGUCGGAAGGAGGAAACCGAAGUGCUGUGGAC
UUCGAACUCAAUCGUGGUGUUUUGUGGGACCUCCGGAACUUACGGAACUGGGUC
CUGGCCUGACGGUGCCGACAUCAACCUUAUGCCGAUCUAA (SEQ ID NO: 11)

[00262] The sequence of the A/Wisconsin/588/2019 antigen mRNA open reading frame (ORF) used here is:

AUGAAAGCCAUCCUUGUUGUCAUGCUGUACACAUUCACCACCGCAAAUGCGGAUA
CCCUGUGUAUCGGCUACCACGCAAAUAAUUCCACCGACACCGUUGAUACCGUCCU
GGAAAAGAACGUGACAGUGACUCACAGCGUCAAUCUCCUUGAGGAUAAACAUAA
UGGCAAGCUGUGCAAGCUGAGAGGCGUGGCUCCCCUGCAUCUGGGAAAGUGCAAC
AUCGCUGGUUGGAUCCUCGGGAACCCAGAGUGUGAGUCCCUCUCAACCGCACGGU
CUUGGUCAUACAUCGUGGAGACUAGCAAUUCAGACAACGGCACAUGCUACCCCGG
UGACUUCAUUAACUACGAGGAGCUGAGAGAACAGCUGAGUUCCGUGUCAUCCUU
CGAGAGAUUCGAAAUCUUCCCCAAAACCUCCUCCUGGCCCAAUCAUGACUCCGAC
AAUGGAGUGACAGCCGCUUGUCCCCACGCCGGUGCCAAGAGUUUCUAUAAGAACC
UCAUCUGGCUGGUGAAAAAGGGCAAGUCCUAUCCCAAAAUUAACCAGACCUACAU
UAACGAUAAGGGGAAAGAAGUCCUGGUCCUGUGGGGAUACACCACCCCCCUACC
AUCGCCGACCAGCAGUCUCUGUAUCAGAACGCCGACGCCUACGUGUUCGUGGGUA
CCAGCCGUUAUAGUAAAAAGUUCAAGCCAGAAAUUGCCACCAGACCUAAGGUGCG
CGACCAGGAGGGCCGCAUGAACUACUACUGGACCCUGGUGGAACCUGGCGACAAG
AUUACAUUCGAGGCCACUGGGAACCUGGUGGCACCCAGAUACGCCUUUACAAUGG
AACGGGAUGCUGGGAGCGGAAUCAUUAUCUCCGAUACCCCUGUCCACGACUGCAA
UACUACCUGUCAGACCCCAGAAGGCGCUAUCAAUACCUCUCUGCCUUUCCAAAAC
GUGCACCCUAUCACUAUCGGGAAAUGUCCCAAGUAUGUGAAAAGCACCAAACUGC
GCCUGGCAACCGGUCUGAGAAAUGUGCCCUCCAUCCAGUCCCGCGGCUUGUUCGG
UGCAAUCGCUGGCUUUAUCGAGGGUGGCUGGACUGGAAUGGUCGAUGGCUGGUA
CGGCUACCAUCACCAGAACGAGCAGGGGUCCGGGUAUGCUGCCGACCUGAAAAGC
ACUCAGAACGCCAUCGAUAAAAUCACUAACAAGGUGAACUCCGUGAUCGAAAAG
AUGAAUACACAGUUCACAGCAGUUGGCAAGGAGUUCAACCACCUGGAAAAACGG
AUAGAGAACCUGAAUAAGAAAGUCGAUGAUGGCUUUCUGGACAUCUGGACUUAC
AAUGCCGAGCUGCUGGUGCUCCUGGAAAACGAGCGGACACUGGAUUAUCACGACU
CAAACGUGAAGAACCUGUAUGAAAAGGUGCGUAACCAGCUGAAAAACAACGCCA
AGGAAAUCGGCAAUGGCUGUUUCGAAUUUACCACAAGUGUGAUAAUACCUGUA
UGGAGAGCGUUAAGAACGGGACUUACGACUACCCAAAAUACAGCGAGGAGGCCA
AGCUGAACCGGGAGAAGAUCGACGGCGUCAAACUCGACUCCACUAGAAUAUACCA

GAUUCUCGCCAUCUAUAGCACAGUGGCAUCAAGUCUCGUCCUGGUGGUGUCACUG
GGAGCCAUCAGCUUUUGGAUGUGCAGCAAUGGAUCCCUCCAGUGUAGGAUCUGC
AUCUAA (SEQ ID NO: 12)

[00263] The sequence of the A/Tasmania/503/2020 antigen mRNA open reading frame (ORF) used here is:

AUGAAGACCAUCAUCGCUCUGUCCUACAUCCUGUGCCUGGUGUUUGCUCAGAAAA
UCCCCGGGAAUGACAAUUCCACUGCCACUCUCUGCCUGGGCCAUCAUGCCGUGCC
AAAUGGAACCAUUGUCAAGACUAUAACAAAUGACCGCAUCGAAGUGACCAACGC
UACCGAGCUGGUUCAGAACAGCAGUAUUGGAGAAAUCUGCGAUUCCCCACACCAG
AUACUGGAUGGCGGCAACUGCACCCUGAUCGACGCACUGCUGGGUGACCCUCAGU
GCGACGGAUUUCAGAAUAAGGAGUGGGACCUUUUCGUUGAGCGCAGCAGAGCCA
AUAGCAACUGCUACCCGUACGACGUGCCGGAUUACGCCAGUCUUCGAAGCCUGGU
CGCAUCCAGCGGGACACUGGAGUUUAAGAAUGAGUCCUUUAAUUGGACAGGCGU
GAAGCAGAACGGGACUAGCAGCGCAUGCAUUCGGGGCAGUAGCUCAUCCUUCUUU
AGCCGACUGAACUGGCUGACCCACCUCAACUACACAUACCCCGCACUGAAUGUGA
CUAUGCCAAACAAAGAACAGUUUGACAAACUGUACAUCUGGGGAGUGCACCAUCC
UAGCACAGACAAGGACCAGAUCAGCCUGUUUGCCCAGCCCAGCGGCAGGAUUACC
GUGUCCACAAAACGGUCACAGCAAGCCGUGAUCCCUAAUAUUGGAUCCCGCCCCC
GGAUAAGGGACAUCCCUAGUCGCAUCAGUAUCUACUGGACCAUCGUGAAGCCCGG
AGAUAUCUUGCUCAUCAAUAGCACUGGCAACCUCAUUGCCCCCAGGGGCUAUUUU
AAGAUCAGAAGCGGCAAGUCCAGCAUUAUGCGCAGCGACGCACCCAUUGGCAAGU
GCAAGUCCGAGUGCAUCACUCCUAAUGGGUCCAUCCCAAACGACAAGCCAUUCCA
AAAUGUCAACAGAAUCACCUACGGGGCUUGCCCCCGCUACGUGAAGCAGAGUACA
CUGAAACUGGCCACCGGGAUGCGCAACGUGCCCGAGAAGCAAACUAGAGGCAUCU
UUGGAGCUAUCGCUGGCUUCAUUGAGAAUGGCUGGGAGGGUAUGGUGGACGGCU
GGUACGGAUUCCGCCACCAGAAUAGCGAAGGCAGAGGCCAGGCAGCAGACUUGAA
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CGCGUGCAGGAUCUGGAAAAGUACGUUGAAGACACCAAGAUCGACCUGUGGUCA
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ACUCCGAAAUGAAUAAGCUCUUUGAAAAGACCAAGAAGCAGCUGCGCGAGAACG
CCGAGGAUAUGGGGAACGGUUGUUUUAAGAUCUACCACAAGUGUGACAACGCCU
GCAUUGGGUCCAUCCGAAAUGAAACAUACGACCACAACGUGUAUAGAGAUGAGG
CCCUGAACAACCGAUUCCAGAUUAAGGGAGUCGAGCUGAAGAGUGGCUAUAAGG
ACUGGAUCCUGUGGAUCUCAUUCGCCAUGUCAUGCUUCCUUCUGUGUAUUGCUCU
GCUCGGCUUCAUCAUGUGGGCUUGCCAGAAAGGCAAUAUCCGGUGCAACAUCUGC
AUCUAA (SEQ ID NO: 13)

[00264] The sequence of the B/Washington/02/2019 antigen mRNA open reading frame (ORF) used here is:

AUGAAAGCAAUCAUAGUGCUGCUGAUGGUGGUGACUAGCAAUGCCGAUCGGAUC
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GCGAGGUGAACGUGACCGGAGUGAUUCCACUGACAACUACACCAACGAAGAGUCA
CUUCGCCAACCUGAAGGGCACCGAAACACGAGGCAAGCUCUGCCCCAAGUGUCUG
AAUUGCACCGACCUGGACGUCGCUUUGGGCCGCCCUAAAUGUACCGGCAAAAUAC
CUUCCGCCAGAGUGUCCAUCCUGCACGAGGUGCGCCCCGUGACCUCCGGGUGUUU
UCCCAUAAUGCACGACCGCACUAAAAUCCGCCAGCUGCCCAAUCUUCUGAGGGGG
UACGAACAUGUCAGGCUGUCCACUCACAACGUGAUCAACGCAGAAGACGCCCCCG
GAAGGCCUUAUGAGAUUGGAACCAGUGGGUCCUGCCCAAACAUUACCAACGGCAA
CGGCUUCUUCGCCACUAUGGCCUGGGCCGUGCCAAAGAACAAGACCGCCACCAAC
CCCCUGACAAUUGAAGUCCCUUACAUCUGCACAGAGGGAGAGGAUCAGAUCACCG
UGUGGGGGUUUCACUCUGAUAACGAAACUCAGAUGGCCAAGCUGUACGGGGAUU
CUAAACCCCAGAAGUUCACCAGUAGCGCUAACGGGGUGACCACCCAUUAUGUGUC
UCAGAUCGGAGGUUUCCCAAAUCAGACCGAGGACGGCGGACUGCCCCAGUCUGGA
AGGAUCGUAGUGGACUAUAUGGUGCAGAAGAGUGGAAAAACCGGCACCAUUACC
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GUACGGCGGACUGAAUAAGAGCAAACCCUACUACACCGGAGAACACGCUAAGGCA
AUUGGGAAUUGUCCGAUCUGGGUGAAGACGCCCCUGAAACUGGCCAAUGGCACA
AAAUACCGGCCCCCCGCUAAGCUGCUGAAGGAACGGGGGUUCUUCGGCGCCAUAG
CCGGCUUUCUGGAGGGAGGCUGGGAGGGCAUGAUAGCCGGGUGGCACGGCUACA
CUUCCCAUGGGGCUCACGGGGUGGCUGUGGCCGCCGACCUGAAGUCUACGCAGGA
AGCUAUCAACAAAAUCACUAAGAACCUGAACAGCCUGUCGGAAUUGGAGGUCAA
GAAUCUGCAGCGGCUGAGCGGCGCCAUGGAUGAGCUGCACAAUGAGAUCCUGGA
GCUUGACGAGAAGGUCGAUGAUCUUCGGGCCGAUACAAUUAGUAGCCAAAUUGA
GUUGGCCGUGCUGCUCAGCAACGAAGGCAUAAUCAACAGCGAGGACGAGCACCUC
CUGGCUCUGGAGAGAAAGCUGAAGAAGAUGCUCGGCCCUAGCGCAGUUGAGAUC
GGAAACGGCUGCUUCGAAACCAAGCACAAGUGCAACCAGACCUGCCUGGACAGGA
UCGCGGCAGGAACAUUCGACGCUGGGGAAUUCAGCCUCCCCACCUUCGACAGCCU
GAACAUCACAGCCGCCAGUCUGAAUGAUGACGGACUGGAUAACCAUACCAUCCUG
CUGUACUACUCUACCGCUGCUUCCUCCCUGGCCGUGACAUUGAUGAUCGCAAUCU
UUGUGGUUUAUAUGGUGAGCCGAGACAACGUCAGUUGCAGUAUCUGCCUUUAA
(SEQ ID NO: 14)

[00265] The sequence of the B/Phuket/3073/2013 antigen mRNA open reading frame (ORF) used here is:

AUGAAAGCCAUCAUUGUGCUGCUGAUGGUUGUUACAAGCAACGCCGACCGCAUCU
GCACCGGGAUUACAAGCAGCAAUAGCCCUCACGUGGUGAAGACAGCAACACAGGG
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UUUGCAAACCUGAAAGGGACACGGACCAGAGGAAAGCUGUGCCCUGAUUGCCUG
AAUUGCACAGACCUGGACGUGGCCCUGGGCAGACCAAUGUGCGUGGGCACUACAC
CAAGCGCCAAGGCCUCCAUCCUCCAUGAGGUGCGGCCCGUGACUUCUGGAUGUUU
CCCCAUUAUGCACGACAGAACCAAGAUUAGACAGCUGCCAAACCUGCUCCGCGGC
UACGAGAAAAUUCGCCUGUCUACACAGAAUGUGAUCGACGCCGAGAAGGCUCCAG
GAGGACCAUACAGACUGGGGACUUCUGGCAGCUGCCCUAACGCCACCUCUAAGAU
CGGGUUCUUCGCAACCAUGGCUUGGGCCGUGCCUAAAGACAAUUACAAGAAUGCC
ACCAAUCCACUGACUGUCGAGGUGCCAUAUAUUUGCACAGAGGGGGAGGACCAG

AUCACUGUGUGGGGCUUUCAUAGCGAUAAUAAGACUCAGAUGAAGUCUCUCUAC
GGCGACUCUAACCCUCAGAAGUUCACCUCCUCUGCCAACGGGGUGACAACACACU
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GUCUGGACGCAUCGUGGUGGACUAUAUGAUGCAGAAGCCUGGGAAGACCGGCAC
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CAUGAAGAGUAUGGAGGGCUGAACAAGUCCAAGCCAUACUAUACAGGAAAGCAC
GCAAAAGCCAUCGGCAACUGUCCCAUCUGGGUCAAAACUCCUCUGAAGCUGGCCA
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CGCCAUUGCAGGGUUUCUGGAAGGAGGCUGGGAGGGCAUGAUUGCUGGAUGGCA
CGGAUAUACCUCUCACGGCGCUCACGGGGUGGCCGUGGCCGCCGAUCUGAAGUCC
ACACAGGAGGCAAUUAACAAGAUCACCAAGAAUCUGAAUUCACUGUCCGAGCUCG
AAGUGAAAAACCUGCAGCGCCUGUCCGGCGCCAUGGACGAGCUGCACAAUGAAAU
CCUGGAGCUGGACGAGAAGGUGGACGACCUGCGGGCUGACACUAUCAGCAGCCAG
AUCGAGCUGGCAGUGCUGCUGAGCAAUGAGGGCAUCAUCAACUCAGAAGACGAA
CACCUCCUGGCACUGGAAAGGAAACUCAAGAAGAUGCUGGGCCCCUCCGCAGUGG
ACAUUGGGAACGGCUGUUUCGAAACCAAGCAUAAGUGUAACCAGACUUGUCUGG
AUAGGAUCGCAGCAGGAACCUUCAACGCCGGCGAAUUUUCUCUGCCAACAUUUGA
CUCCCUGAACAUCACAGCUGCAUCCCUGAACGACGACGGACUGGACAAUCACACC
AUCCUGCUGUACUACUCUACUGCCGCUAGCUCCCUGGCCGUGACCCUGAUGCUGG
CCAUCUUCAUCGUGUACAUGGUUUCCAGGGAUAACGUGUCUUGUAGCAUUUGCC
UGUAA (SEQ ID NO: 15)

Results

mRNA Antigen Preparation, Characterization, and Expression

[00266] mRNAs coding for the full-length codon-optimized HA and NA for the various influenza strains were synthesized enzymatically using unmodified ribonucleotides. All mRNA preparations had > 95% of 5' Cap1 and showed a single homogenous peak on capillary electrophoresis. mRNA-LNP formulations were prepared by mixing the various lipid components with mRNA under controlled conditions and at fixed ratios. All mRNA-LNPs exhibited >95% encapsulation with uniform hydrodynamic radius ranging from 95-105nm and a poly dispersity index (PDI) of 0.060-0.136 as shown in **Table 5**.

Table 5. Attributes of LNP Formulations Used in Mouse Preclinical Testing

LNP	Size (nm)	PDI	% Encapsulation
CA09 HA	97.54	0.117	95.2
Sing16 HA	103.2	0.068	97.3
Sing16 NA	105.8	0.128	96.5
Mich15 NA	103.3	0.136	97.4

[00267] Cryo-electron microscopy (Cryo-TEM) of the CA09 HA mRNA-LNP images showed uniform spherical particles with a multi-lamellar inner core structure. The lamellarity of the solid core structure analyzed further with Fourier Transform, indicated a 3.7 nm periodicity between layers. The uniform morphology of the particles seen in the micrographs are indicative of homogenous LNP preparations with proper assembly of the LNPs.

[00268] Antigen expression was confirmed with flow cytometry by transiently transfecting human skeletal muscle cells (HskMCs) with the unencapsulated mRNA constructs of CA09 HA, Sing16 HA, Sing16 NA, or Mich15 NA, and stained with protein-specific antibodies for analysis. High levels of HA and NA expression from HskMCs were observed, confirming proper assembly and trafficking of native form HA trimers and NA tetramers upon expression in muscle cells. To study the subcellular localization of expressed HA and NA proteins, HeLa cells were transfected with bivalent H3N2 LNP and proteins were visualized by immunostaining and confocal microscopy. While NA signal indicated strong colocalization in ER (about 90%), HA was found to colocalize moderately (25%) with ER when permeabilized cells were stained with antibodies for corresponding proteins and calnexin, an endoplasmic reticulum (ER) marker. This is consistent with the understanding that nascent NA and HA proteins are translocated to ER for assembly (Dou et al., *Front Immunol.* (2018) 9:1581).

[00269] The efficiency of delivery of mRNA by LNPs and selection of optimal formulation parameters was evaluated using reporter mRNA expression (Thess et al., *Molecular Therapy* (2015) 23(1):S55). A single dose of either 0.05, 0.1, 1, 5, µg of unmodified FF-LNP formulations was administered intramuscularly (IM) in mice. Luciferase activity, measured by average bioluminescence, indicated sustained expression from mRNA construct which peaked at 6 hours post injection and detectable beyond 72 hours at all doses (**FIG. 11, panel (a)**). The high-level mRNA-mediated protein expression was further verified with hEPO at a single 0.1 µg dose in mice and 10 µg in non-human primate (NHP). The study was intended to compare LNP, using standard LNP Dlin-MC3-DMA25 formulation as a control. Serum hEPO quantified by ELISA demonstrated maximum expression at 6 h with approximately 12-fold higher erythropoietin expressed with hEPO-LNP compared to hEPO-MC3 (**FIG. 11, panel (c)**). Both hEPO-LNP and hEPO-MC3 showed similar expression kinetics in NHPs, detectable from 6 hours to 72 hours

(**FIG. 11, panel (d)**). The results confirmed the utility of the present LNP formulation for efficient delivery of mRNA for expression both *in vitro* and *in vivo*.

Immunogenicity of HA (H1, H3) and NA (N1, N2) mRNA-LNP in Mice

[00270] Natural history and vaccine studies have shown that antibodies to influenza HA and NA have antiviral function and both antigens are considered important for effective influenza vaccines (Krammer et al., *Nat Rev Immunol.* (2019) 19(6):383-97). Unmodified CA09 HA-LNP and Sing16 HA-LNP mRNA vaccines were evaluated in BALB/c mice (n=8) in a two-dose regimen at 2, 0.4, 0.08, or 0.016 µg mRNA-LNP administered at 4-week apart schedule. Recombinant HA (rHA) antigens of the same strain were used to evaluate the total IgG responses in ELISAs. HA-specific antibodies were detected in all groups after a single dose, but the titers peaked at day 42 after the second dose (**FIG. 12**). To measure functional antibodies, hemagglutination inhibition (HAI) response was evaluated against the homologous strains, CA09 and Sing16. Although the HAI titers after a first dose could be observed for the 2 µg dose of CA09-LNP and Sing16-LNP treatment groups with GMTs of 160 and GMT 70 at day 28 respectively, a more profound increase in HAI titers were observed after second dose. At day 42 GMT titers were 80 and 2200 for the 0.016 µg and 0.4 µg groups respectively in the CA09 -HA-LNP and 14 and 100 for the 0.016 µg and 0.4 µg groups respectively in the Sing 16 HA-LNP groups (**FIG. 13**).

[00271] Similarly, for testing anti-NA responses, mice were immunized with 2, 0.4, 0.08, or 0.016 µg of Sing16 NA-LNP or Mich15 NA-LNP. ELISA with recombinant NA antigens were conducted to assess the total IgG responses induced by either Mich15 NA-LNP or Sing16 NA-LNP formulations. Animals developed high antibody binding responses after a single dose, with a marked increase in NA binding antibodies post second dose at day 42 (**FIG. 14**). Enzyme-linked lectin assay (ELLA) was used as a surrogate for functional antibody titers for Neuraminidase inhibition (NAI) activity against H6N1 or H6N2 chimeric viruses. Although two doses of the vaccine substantially increased the functional antibody response as compared to a single dose, encouraging NAI titers with GMTs 800 and GMT 60 were recorded at day 28 after a single dose even with low dose of 0.016 µg of Mich15 NA-LNP and Sing16 NA-LNP, respectively. At day 42, the GMT titers between the 0.4 µg and 0.016 µg, were 900 and 10200 respectively in the Sing16 NA-LNP group indicating a dose-dependent response with titers reaching above ULOQ in case of Mich15 NA-LNP (**FIG. 15**).

Protection from Viral Challenge in Mice

[00272] To test the efficacy of the mRNA vaccine in mouse influenza virus challenge model, we inoculated BALB/c mice with 0.4 μg of CA09 HA-LNP IM at week 0 and 4, along with a negative control group with two doses of LNP diluent buffer. HAI titers for vaccine group serum samples at study days 0, 14, 28, 42, 56, 92, and 107 demonstrated robust immune response with GMT of 1660 and 1:830 at day 56 and day 92 respectively (**FIG. 16A**). At day 93, all mice were challenged intranasally with Belgium09 virus, homologous to CA09, at four times the dose which can cause 50% lethal outcome (4xLD$_{50}$). All mice in the vaccine group survived the challenge with no mortality, and some mild morbidity marked by transient weight loss of less than 5% (**FIG. 16B**). However, those in the diluent control group suffered significant and rapid weight loss which led to high mortality rate (90%) by day 9. These results demonstrated high efficacy of HA-based MRT formulations in a lethal mouse influenza challenge model.

[00273] To assess protective efficacy of NA-based MRT vaccines, we conducted an analogous challenge experiment in BALB/c mice. Since the Mich15 NA-LNP vaccine elicited robust NAI titers after a single immunization in naïve mice (**FIG. 16A**), we evaluated one or two dosing regimens with administrations of 0.4 or 0.016 μg of Mich15 NA-LNPs over a 4-week interval. The control groups were vaccinated at the same regimens, receiving either 0.6 μg hEPO-LNP or diluent buffer. Robust NAI titers were observed after a single administration with GMTs of 14,000 NAI for 0.4 μg and 1,800 NAI for 0.016 μg of Mich15 NA-LNP recorded at day 28 (**FIG. 17A**). After the second immunization at day 42, NAI titers rose to 108,000 NAI for 0.4 μg and 37,000 NAI for 0.016 μg groups. After more than 12 weeks post vaccination regimens, all groups were challenged with 4xLD$_{50}$ of Belgium09 H1N1 virus. Individual weight changes from baseline over time by treatment groups are graphed in **FIG. 17B**. All mice in the two control groups suffered significant morbidity, and all animals had to be euthanized due to >20% weight loss by day 8 post-infection. Remarkably, all animals except one in the vaccine groups survived the challenge in the single dose 0.016 μg group, indicating high protective efficacy against death even after a single dose of as low as 0.016 μg of Mich15 NA-LNP. The higher dose (0.4 μg) demonstrated overall higher protection, however, in contrast to HA-immunization, NA vaccination was not sufficient to protect against weight loss as vaccinated animals demonstrated median weight loss of 10 % of initial body weight, consistent with observations reported for other NA vaccines. Body weight recoveries were observed for vaccinated groups resulting in an average final weight change of

2.7% at the low dose and 4.8% weight gain for the higher dose, as compared to baseline. Overall, the results demonstrated that a single low-dose MRT NA-LNP vaccination can elicit functional antibodies measurable for blocking influenza NA activity and sufficient to confer protection against lethal challenge in mice.

Immunogenicity of HA (H3) mRNA-LNP in NHP

[00274] To evaluate immunogenicity of the mRNA-LNP in NHP, a dose range study covering 15, 45, 135, and 250 µg of Sing16 HA-LNP was performed in NHPs. After the first immunization, all vaccinated NHPs developed antibodies reactive to recombinant HA protein as noted in ELISA (**FIG. 18**). Further boosting of titers was observed post second dose. Surprisingly, the 15 µg dose induced only 1.8-fold lower ELISA titers than the 135 µg dose level (95% CI 1.0, 3.6), suggesting a dose saturation close to 15 µg level. Robust HAI antibodies were induced in all dose groups on day 42 and GMTs recorded were 400 for 15 µg, 700 for 45 µg, 900 for 135 µg and 570 for 250 µg. At day 42, the fold increase in GMT titers with 95% CI was 2.2-fold (1.0; 5.0) between the 135 µg and 15 µg and was 1.3-fold (0.6; 2.8) between the 135 µg and 45 µg treatment groups indicating that despite the observed trend towards higher titers with increasing dose, the difference between groups was minimal (**FIG. 19A**). The neutralization potency assessed by microneutralization (MN) assay (**FIG. 19B**) showed a better trend for dose effect with GMTs on D28 of 40 for 15 µg, 180 for 45 µg, 300 and for 135 µg.

[00275] Since T cells have been shown effective in reducing viral load and limiting disease severity in animal models (Rimmelzwaan et al., *Vaccine* (2008) 26(4):D41–D44; Sridhar et al., *Nat Med.* (2013) 19(10):1305-12; Sridhar et al., *Front Immunol.* (2016) 7:195), we evaluated recall T cells in the NHPs vaccinated with 45, 135, 250 µg of Sing16 HA-LNP or with 45 µg of recombinant HA. PBMCs collected at day 42 were evaluated in IFN-γ (Th1 cytokine) and IL-13 (Th2 cytokine) ELISPOT assay with recall stimulation with pooled overlapping peptides spanning the entire sequence of the Sing16 HA. All vaccinated animals except one in 250 µg group developed IFN-γ secreting cells, ranging from 28 to 1328 spot-forming cells (SFC) per million PBMCs (**FIG. 20A**). Notably, a dose-response was not observed, and the lower and higher dose level groups of animals showed comparable frequencies of IFN-γ secreting cells. In contrast, all animals in the control group immunized with the recombinant Sing16 HA protein demonstrated absence of IFN-γ producing cells. The presence of IL-13 cytokine secreting cells was either not detected or very low in all the groups tested (**FIG. 20B**). The data suggest that Sing16 HA-LNP induced strong Th1-biased cellular responses in NHPs, comparable to that seen with MRT5500 (Kalnin et al., *supra*), a SARS-CoV-2 vaccine currently under development.

[00276] To investigate frequency of memory B cells (MBCs) in NHPs after immunization with Sing16 HA-LNP, an ELISPOT assay was developed to quantify antigen-specific MBCs as a readout of humoral immune memory. On day 180, PBMCs were collected from the NHPs immunized with 45 µg or 15 µg of the Sing16 HA mRNA-LNP formulations or with a recombinant HA as a comparator at a 45 µg dose. A 4-day polyclonal stimulation of PBMCs that is optimized to drive memory B cells to antibody secreting cells (ASC) was performed, and the stimulated PBMCs were plated in an antigen-specific ELISPOT where the frequency of antigen-specific ASCs could be determined. Antigen-specific memory B cells were then quantified as a percentage of total IgG+ memory B cells. Antigen-specific memory B cells were detected in all animals and their frequency was ranging from 1 to 5% for the 45 ug dose group and 0.3 to 1.5% for the 15 µg dose group. In the rHA immunized animals, the memory B cell responses appeared to be markedly lower as antigen-specific memory B cells were undetectable in five out of six animals (**FIG. 21**). It was concluded that Sing16 HA-LNP, like other mRNA vaccines, elicits a population of anti-HA specific memory B cells that promise to prolong immunity (Lindgren et al., *Front Immunol.* (2019) 10:614).

Multivalent Influenza Virus Antigens

[00277] An advantage of mRNA-LNP platform is the flexibility of LNP encapsulation for multiple mRNA antigen constructs. However, this potential needs to be tested to address the concern of antigenic interference. To explore the combinations of influenza antigens, co-encapsulated HA and NA mRNA were formulated in LNPs as bivalent formulations containing 0.2 µg each of mRNA in an H3H1, H3N2, or N1N2 combination or with the monovalent containing 0.2 µg of each corresponding antigen. These formulations were administered in mice to determine any antigenic interference on immunogenicity by comparing the functional titers of the individual antigen in bivalent vs. monovalent formulations (**FIG. 22, panels (a)-(c)** and **Table 6**).

Table 6. Frequency of Antigen-Specific Memory B Cells in NHPs Vaccinated with H3 mRNA-LNP Vaccine

Animal group	**Animal ID**	**PBMCs/ well of Ag-Specific IgG**	**Spot # of Ag-Specific IgG/million PBMCs**	**PBMCs/ Well of Total IgG**	**Spot # of Total IgG/million PBMCs**	**% of Ag-Specific IgG to Total IgG**
H3 mRNA-LNP (45 μg)	1	3×10^5	1082	5×10^3	21700	5.0
	2	3×10^5	232	5×10^3	6100	3.8
	3	3×10^5	282	5×10^3	11700	2.4
	4	3×10^5	2	5×10^3	100	2.0
	5	3×10^5	283	5×10^3	8700	3.3
	6	3×10^5	225	5×10^3	22800	1.0
H3 mRNA-LNP (15 μg)	1	3×10^5	63	5×10^3	21600	0.3
	2	3×10^5	58	5×10^3	11300	0.5
	3	3×10^5	253	5×10^3	17300	1.5
	4	3×10^5	173	5×10^3	17300	1.0
	5	3×10^5	63	5×10^3	9300	0.7
	6	3×10^5	107	5×10^3	19300	0.6
rHA (45 μg)	1	3×10^5	2	5×10^3	19800	0.0
	2	3×10^5	28	5×10^3	14300	0.2
	3	3×10^5	2	5×10^3	17000	0.0
	4	3×10^5	0	5×10^3	7900	0.0
	5	3×10^5	0	5×10^3	21600	0.0
	6	3×10^5	0	5×10^3	14600	0.0
Diluent	1	3×10^5	0	5×10^3	30900	0.0
	2	3×10^5	0	5×10^3	7100	0.0

[00278] In the H1H3 combo, between the co-encapsulated and separately administered vaccines, no statistically significant difference (p= 0.2584) irrespective of the time points was observed for HAI titers and no significant difference (p=0.8389) at D42 was observed for H3 titers. In the case of H3N2 combo, the NA component of the vaccine elicited high neutralizing antibodies in combination with the HA component, demonstrating lack of HA dominance. Between the co-encapsulated and separately administered vaccines, no statistically significant difference (p=0.2960), irrespective of the time points, was observed for H3 titers, and no significant difference (p=0.0904) at D42 was observed for N2 titers. Likewise, the N1N2 combo was not statistically significantly different (p=0.3899) for N2. N1 titers at day 42 for co-encapsulated and separately administered vaccines were above limit of quantification. Combination of N2N1, H3H1, or H3N2 thus generated antibody titers equivalent to individual LNPs separately formulated.

[00279] Quadrivalent formulations of co-encapsulated H1, N1, H3, and/or N2 mRNA were further explored. These formulations were tested in NHPs in total 10 μg composed of 2.5 μg each of influenza antigen mRNA and filling amount of noncoding mRNA (nc mRNA) if needed in combinations, resulting in quadrivalent (H1N1H3N2), bivalent (H1N1 or H3N2), or monovalent (H1, H3, N1, or N2) LNPs (**Table 7**).

Table 7. Bivalent Combination of Influenza Virus in Mouse Study

Group	N	mRNA1	mRNA2	LNP	mRNA dose (μg)	Description	CA09 HAI	Sing16 HAI	Mich15 NAI	Perth09 NAI
1	8	Sing16 H3	Perth09 N2	Yes	0.2, 0.2	Coformulated		x		x
2	8					Separate		x		x
3	8	CA09 H1	Sing16 H3			Coformulated	x	x		
4	8					Separate	x	x		
5	8	Mich15 N1	Perth09 N2			Coformulated			x	x
6	8					Separate			x	x
7	8	Diluent	-	-	0	single	x	x	x	x

[00280] HAI titers to H1 or H3, or NAI titers to N1 or N2 were compared between the monovalent formulations vs. bivalent or quadrivalent formulations (**FIG. 23**). On day 42, the HAI titers to H1 of the quadrivalent group were comparable when analyzed with that of the H1 monovalent group (p=0.9054, t-test, unpaired, two-tailed) or H1N1 bivalent group (p=0.8002). Similarly, the H3 HAI titers of the quadrivalent group was comparable when analyzed with that of the H3 monovalent group (p=0.2504) or H3N2 bivalent group (p=0.5894). The NAI titers to N1 were almost identical in groups of animals vaccinated with N1 monovalent mRNA or H1N1 bivalent mRNA or the quadrivalent H1N1H3N2 mRNA formulations. Likewise, there was no difference in N2 NAI titers between the N2 monovalent mRNA (p=0.8485) or H3N2 bivalent mRNA (0.4545) with the quadrivalent H1N1H3N2 mRNA formulations.

[00281] Overall, these findings indicate that co-encapsulated or combination multivalent vaccines of HA/NA mRNA-LNPs at this dose level could efficiently deliver all four antigens without any concern for antigenic interference and all antigens were as immunogenic as in the formulation when these antigens were delivered singularly.

Example 7: Additional LNP Formulations

[00282] Additional LNP formulations for mRNA vaccines were prepared, designated Lipid C (containing cationic lipid GL-HEPES-E3-E10-DS-3-E18-1), Lipid D (containing cationic lipid GL-HEPES-E3-E12-DS-4-E10), and Lipid E (containing cationic lipid GL-HEPES-E3-E12-DS-3-E14). Human erythropoietin (hEPO) mRNA was used as a test mRNA. Expression of hEPO was measured by ELISA from samples taken from mice injected with the LNPs. Samples were taken 6 hours, 24 hours, 48 hours, and 72 hours after injection. As show in **FIG. 24**, hEPO expression was consistently higher at all time points with LNP formulations Lipid A, Lipid B, Lipid C, Lipid D, and Lipid E, compared to a control LNP formulation containing cationic lipid MC3.

[00283] **Table 8** below summarizes the results relative to a control LNP containing the MC3 cationic lipid.

[00284] **Table 8**. Levels of hEPO from LNP formulations Lipid A-E relative to MC3.

LNP Formulation	Fold higher hEPO at 6 hours (compared to MC3)	STDEV
Lipid A	10.35	4.15
Lipid B	5.62	1.34
Lipid D	7.78	2.79
Lipid E	6.17	1.57

[00285] The same hEPO mRNA-LNP formulations were next tested in non-human primates (NHPs). Samples were taken at 6 hours, 48 hours, and 96 hours after injection. As shown in **FIG. 25**, each LNP formulation produced levels of hEPO comparable to the MC3 control formulation.

[00286] Influenza HA-encoding mRNA-LNP formulations were also tested in NHPs. NHPs were administered the LNP formulations at 10 µg via intramuscular injection and samples were taken at say 28 and day 42 post injection. HAI titers were measured as described above. As shown in

FIG. 26, each LNP formulation produced HAI titers comparable to or higher than the MC3 control formulation.

[00287] The same experiment as shown in **FIG. 26** was performed while measuring HAI titers with the Cal09 H1 influenza antigen. As shown in **FIG. 27**, each LNP formulation produced HAI titers comparable to or higher than the MC3 control formulation.

[00288] As shown in FIG. 28, HAI titers with the Sing16 H3 antigen were elevated for LNP formulations Lipid C and Lipid D.

Example 8: Respiratory Syncytial Virus (RSV) F Protein-Encoding mRNA LNP Formulations

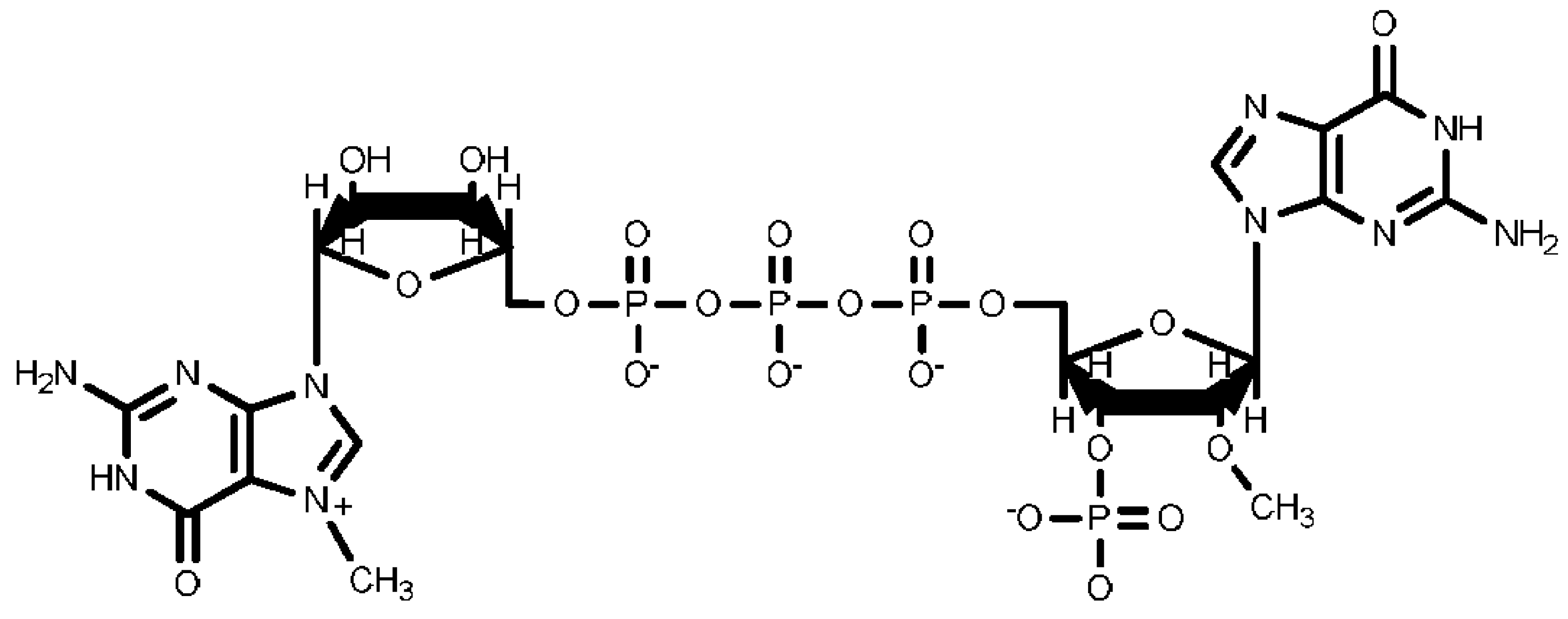
[00289] The effect of different cationic lipids in the LNP were tested for the LNP-encapsulated RSV F protein mRNA. Lipid formulations of Lipid A, Lipid B, Lipid C, Lipid D, and Lipid E were tested. Each LNP was composed of 40% of one of the five cationic lipids, 30% phospholipid DOPE, 1.5% PEGylated lipid DMG-PEG2000, and 28.5% cholesterol. An LNP with the cationic lipid MC3 was also used, considered an industry benchmark (Jayaraman et al. Angew Chem Int Ed. 51:8529-33. 2012).

[00290] The F protein tested was designated FD3, and corresponds to a pre-fusion RSV F protein. The amino acid sequence for FD3 is recited below.

[00291] FD3:

MELLILKANAITTILTAVTFCFASGQNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELS
NIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMGSGNVGLGGAIASGVAVSKVLHL
EGEVNKIKSALLSTNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNPETVI
EFQQKNNRLLEITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIV
RQQSYSIMSIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKNGSNICLTRTDRGW
YCDNAGNVSFFPQAETCKVQSNRVFCDTMNSRTLPSEVNLCNVDIFNPKYDCKIMTSKT
DVSSSVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYV
NKQEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNELINQSLAFINQSDELLHNVNAGK
STTNIMITTIIIVIIVILLSLIAVGLLLYCKARSTPVTLSKDQLSGINNIAFSN (SEQ ID NO: 16)

[00292] The mRNA molecule described herein comprises an open reading frame (ORF) encoding an RSV F protein antigen, at least one 5' untranslated region (5' UTR), at least one 3' untranslated region (3' UTR), and at least one polyadenylation (poly(A)) sequence. The mRNA further comprises a 5' cap with the following structure:



[00293] The nucleic acid sequence for the mRNA open reading frame (ORF) encoding the RSV F protein is recited below.

[00294] FD3 mRNA ORF:

AUGGAACUGCUGAUCCUCAAAGCCAACGCAAUCACCACCAUUCUCACCGCUGUGA
CCUUCUGCUUCGCAUCGGGGCAGAACAUCACUGAAGAGUUUUACCAGAGCACUUG
CAGCGCGGUGUCAAAGGGUUACCUUUCCGCACUGCGGACCGGAUGGUACACUUCC
GUGAUCACCAUUGAGCUCAGCAACAUCAAGGAAAACAAGUGCAAUGGCACCGACG
CCAAGGUCAAGCUGAUCAAACAAGAACUGGACAAGUACAAGAACGCCGUGACAG
AAUUGCAGCUCCUGAUGGGAUCCGGAAACGUCGGUCUGGGCGGAGCCAUCGCGAG
UGGAGUGGCUGUGUCCAAGGUCUUGCACCUCGAGGGAGAAGUGAACAAGAUCAA
GUCCGCGCUGCUGUCAACGAACAAGGCCGUGGUGUCCCUGUCUAACGGCGUCAGC
GUGCUGACGUUCAAGGUCCUGGACCUGAAGAAUUACAUUGACAAGCAGCUGCUG
CCCAUCCUCAACAAGCAAUCCUGCUCCAUCUCCAACCCCGAAACCGUGAUCGAGU
UCCAGCAGAAGAACAACCGCCUGCUGGAAAUUACUCGCGAGUUCUCUGUGAAUGC
CGGCGUGACCACCCCUGUGUCCACCUACAUGCUGACCAACUCCGAGCUUCUCUCC
CUUAUCAAUGACAUGCCUAUCACGAACGACCAGAAGAAGCUGAUGUCGAACAACG
UGCAGAUUGUGCGGCAGCAGUCAUACAGCAUCAUGUCGAUCAUCAAGGAAGAAG
UGCUGGCGUACGUGGUGCAACUCCCGCUGUACGGCGUCAUCGAUACCCCGUGCUG
GAAGCUGCACACCUCGCCUUUGUGUACCACCAACACCAAGAACGGAUCCAACAUC
UGCUUAACCCGGACUGAUCGGGGUUGGUACUGCGACAACGCCGGGAAUGUUUCG
UUCUUCCCACAAGCCGAGACUUGUAAAGUGCAGUCAAACAGAGUGUUCUGUGAC

ACCAUGAACUCGAGAACCCUGCCCAGCGAAGUGAACCUGUGUAACGUCGACAUCUUUAACCCAAAAUACGAUUGCAAGAUUAUGACCAGCAAAACCGACGUGUCCUCCUCCGUGAUAACAAGCCUGGGGGCGAUUGUGUCAUGCUACGGAAAGACUAAGUGCACCGCCUCGAACAAGAACCGCGGCAUCAUUAAGACUUUCUCGAAUGGUUGCGACUAUGUGUCCAACAAGGGCGUGGAUACUGUGUCAGUCGGGAAUACUCUUUACUACGUGAACAAGCAGGAGGGAAAAGCCUCUACGUGAAGGGAGAGCCUAUUAUCAACUUUUACGAUCCGCUGGUGUUCCCGUCCGACGAAUUCGACGCCAGCAUCAGCCAAGUCAACGAGCUGAUUAACCAGUCCCUCGCCUUCAUCAACCAAUCCGACGAGCUCCUGCAUAACGUGAACGCCGGAAAGUCCACCACCAACAUCAUGAUCACUACUAUUAUCAUCGUGAUCAUCGUCAUCCUGCUGAGCCUGAUUGCUGUGGGCCUGUUGCUGUAUUGCAAAGCCAGGUCCACCCCGGUCACCCUGUCGAAGGAUCAGCUGUCCGGAAUCAACAACAUUGCCUUCUCCAACUAA (SEQ ID NO: 17)

[00295] The nucleic acid sequences for the DNA template encoding the RSV F protein is recited below.

[00296] FD3 DNA:

ATGGAACTGCTGATCCTCAAAGCCAACGCAATCACCACCATTCTCACCGCTGTGACCTTCTGCTTCGCATCGGGGCAGAACATCACTGAAGAGTTTTACCAGAGCACTTGCAGCGCGGTGTCAAAGGGTTACCTTTCCGCACTGCGGACCGGATGGTACACTTCCGTGATCACCATTGAGCTCAGCAACATCAAGGAAAACAAGTGCAATGGCACCGACGCCAAGGTCAAGCTGATCAAACAAGAACTGGACAAGTACAAGAACGCCGTGACAGAATTGCAGCTCCTGATGGGATCCGGAAACGTCGGTCTGGGCGGAGCCATCGCGAGTGGAGTGGCTGTGTCCAAGGTCTTGCACCTCGAGGGAGAAGTGAACAAGATCAAGTCCGCGCTGCTGTCAACGAACAAGGCCGTGGTGTCCCTGTCTAACGGCGTCAGCGTGCTGACGTTCAAGGTCCTGGACCTGAAGAATTACATTGACAAGCAGCTGCTGCCCATCCTCAACAAGCAATCCTGCTCCATCTCCAACCCCGAAACCGTGATCGAGTTCCAGCAGAAGAACAACCGCCTGCTGGAAATTACTCGCGAGTTCTCTGTGAATGCCGGCGTGACCACCCCTGTGTCCACCTACATGCTGACCAACTCCGAGCTTCTCTCCCTTATCAATGACATGCCTATCACGAACGACCAGAAGAAGCTGATGTCGAACAACGTGCAGATTGTGCGGCAGCAGTCATACAGCATCATGTCGATCATCAAGGAAGAAGTGCTGGCGTACGTGGTGCAACTCCCGCTGTACGGCGTCATCGATACCCCGTGCTGGAAGCTGCACACCTCGCCTTTGTGTAC

CACCAACACCAAGAACGGATCCAACATCTGCTTAACCCGGACTGATCGGGGTTGGTACTGCGACAACGCCGGGAATGTTTCGTTCTTCCCACAAGCCGAGACTTGTAAAGTGCAGTCAAACAGAGTGTTCTGTGACACCATGAACTCGAGAACCCTGCCCAGCGAAGTGAACCTGTGTAACGTCGACATCTTTAACCCAAAATACGATTGCAAGATTATGACCAGCAAAACCGACGTGTCCTCCTCCGTGATAACAAGCCTGGGGGCGATTGTGTCATGCTACGGAAAGACTAAGTGCACCGCCTCGAACAAGAACCGCGGCATCATTAAGACTTTCTCGAATGGTTGCGACTATGTGTCCAACAAGGGCGTGGATACTGTGTCAGTCGGGAATACTCTTTACTACGTGAACAAGCAGGAGGGGAAAAGCCTCTACGTGAAGGGAGAGCCTATTATCAACTTTTACGATCCGCTGGTGTTCCCGTCCGACGAATTCGACGCCAGCATCAGCCAAGTCAACGAGCTGATTAACCAGTCCCTCGCCTTCATCAACCAATCCGACGAGCTCCTGCATAACGTGAACGCCGGAAAGTCCACCACCAACATCATGATCACTACTATTATCATCGTGATCATCGTCATCCTGCTGAGCCTGATTGCTGTGGGCCTGTTGCTGTATTGCAAAGCCAGGTCCACCCCGGTCACCCTGTCGAAGGATCAGCTGTCCGGAATCAACAACATTGCCTTCTCCAACTAA (SEQ ID NO: 18)

[00297] The nucleic acid sequences for the 5’UTR and 3’UTR are recited below.

[00298] 5’UTR:

GGACAGAUCGCCUGGAGACGCCAUCCACGCUGUUUUGACCUCCAUAGAAGACACCGGGACCGAUCCAGCCUCCGCGGCCGGGAACGGUGCAUUGGAACGCGGAUUCCCCGUGCCAAGAGUGACUCACCGUCCUUGACACG (SEQ ID NO: 19)

[00299] 3’UTR:

CGGGUGGCAUCCCUGUGACCCCUCCCCAGUGCCUCUCCUGGCCCUGGAAGUUGCCACUCCAGUGCCCACCAGCCUUGUCCUAAUAAAAUUAAGUUGCAUC (SEQ ID NO: 20)

[00300] The nucleic acid sequences for the full-length mRNA encoding the RSV F protein is recited below.

[00301] FD3 mRNA:

GGACAGAUCGCCUGGAGACGCCAUCCACGCUGUUUUGACCUCCAUAGAAGACACCGGGACCGAUCCAGCCUCCGCGGCCGGGAACGGUGCAUUGGAACGCGGAUUCCCCGUGCCAAGAGUGACUCACCGUCCUUGACACGAUGGAACUGCUGAUCCUCAAAGCCAACGCAAUCACCACCAUUCUCACCGCUGUGACCUUCUGCUUCGCAUCGGGGCAGAA

CAUCACUGAAGAGUUUUACCAGAGCACUUGCAGCGCGGUGUCAAAGGGUUACCUUUCCGCACUGCGGACCGGAUGGUACACUUCCGUGAUCACCAUUGAGCUCAGCAACAUCAAGGAAAACAAGUGCAAUGGCACCGACGCCAAGGUCAAGCUGAUCAAACAAGAACUGGACAAGUACAAGAACGCCGUGACAGAAUUGCAGCUCCUGAUGGGAUCCGGAAACGUCGGUCUGGGCGGAGCCAUCGCGAGUGGAGUGGCUGUGUCCAAGGUCUUGCACCUCGAGGGAGAAGUGAACAAGAUCAAGUCCGCGCUGCUGUCAACGAACAAGGCCGUGGUGUCCCUGUCUAACGGCGUCAGCGUGCUGACGUUCAAGGUCCUGGACCUGAAGAAUUACAUUGACAAGCAGCUGCUGCCCAUCCUCAACAAGCAAUCCUGCUCCAUCUCCAACCCCGAAACCGUGAUCGAGUUCCAGCAGAAGAACAACCGCCUGCUGGAAAUUACUCGCGAGUUCUCUGUGAAUGCCGGCGUGACCACCCCUGUGUCCACCUACAUGCUGACCAACUCCGAGCUUCUCUCCCUUAUCAAUGACAUGCCUAUCACGAACGACCAGAAGAAGCUGAUGUCGAACAACGUGCAGAUUGUGCGGCAGCAGUCAUACAGCAUCAUGUCGAUCAUCAAGGAAGAAGUGCUGGCGUACGUGGUGCAACUCCCGCUGUACGGCGUCAUCGAUACCCCGUGCUGGAAGCUGCACACCUCGCCUUUGUGUACCACCAACACCAAGAACGGAUCCAACAUCUGCUUAACCCGGACUGAUCGGGGUUGGUACUGCGACAACGCCGGGAAUGUUUCGUUCUUCCCACAAGCCGAGACUUGUAAAGUGCAGUCAAACAGAGUGUUCUGUGACACCAUGAACUCGAGAACCCUGCCCAGCGAAGUGAACCUGUGUAACGUCGACAUCUUUAACCCAAAAUACGAUUGCAAGAUUAUGACCAGCAAAACCGACGUGUCCUCCUCCGUGAUAACAAGCCUGGGGGCGAUUGUGUCAUGCUACGGAAAGACUAAGUGCACCGCCUCGAACAAGAACCGCGGCAUCAUUAAGACUUUCUCGAAUGGUUGCGACUAUGUGUCCAACAAGGGCGUGGAUACUGUGUCAGUCGGGAAUACUCUUUACUACGUGAACAAGCAGGAGGGGAAAAGCCUCUACGUGAAGGGAGAGCCUAUUAUCAACUUUUACGAUCCGCUGGUGUUCCCGUCCGACGAAUUCGACGCCAGCAUCAGCCAAGUCAACGAGCUGAUUAACCAGUCCCUCGCCUUCAUCAACCAAUCCGACGAGCUCCUGCAUAACGUGAACGCCGGAAAGUCCACCACCAACAUCAUGAUCACUACUAUUAUCAUCGUGAUCAUCGUCAUCCUGCUGAGCCUGAUUGCUGUGGGCCUGUUGCUGUAUUGCAAAGCCAGGUCCACCCCGGUCACCCUGUCGAAGGAUCAGCUGUCCGGAAUCAACAACAUUGCCUUCUCCAACUAACGGGUGGCAUCCCUGUGACCCCUCCCCAGUGCCUCUCCUGGCCCUGGAAGUUGCACUCCAGUGCCCACCAGCCUUGUCCUAAUAAAAUUAAGUUGCAUC (SEQ ID NO: 21)

[00302] LNP-RSV FD3 mRNA compositions were administered to NHPs. Groups of 6 cynomolgus macaques were administered a 5 µg dose of mRNA encapsulated with the above LNPs, or a 10 µg dose of an RSV Pre-F NP subunit control vaccine adjuvanted with $Al(OH)_3$, by intramuscular (IM) injection on D0 and D21. Monkeys were bled prior to each vaccine administration as well as at two weeks post-last vaccination (D35). As shown in **FIG. 29**, all tested cationic lipids effectively induced the production of anti-RSV F protein antibodies to a similar level as a Pre-F NP with an aluminum adjuvant.

[00303] As shown in **FIG. 30**, all tested cationic lipids generated effective RSV neutralization titers to a similar level as a Pre-F NP with an aluminum adjuvant.

[00304] The cumulative results of **FIG. 29** and **FIG. 30** are shown below in **Table 9** and **Table 10**.

Table 9. Magnitude of immune response

LNP Formulation	Neutralization Titer	Fold vs. MC3
LIPID A	9.86	23.43
LIPID B	10.03	26.35
LIPID C	8.509	9.18
LIPID E	6.929	3.07
LIPID D	8.894	11.99
MC3	5.308	1.00
Pre-F NP	10.97	50.56

Table 10. Quality of immune response

Cationic Lipid	Antibody Titer	Neutralization Titer	Antibody Titer / Neutralization Titer ratio
LIPID A	15.58	9.86	52.71
LIPID B	15.56	10.03	46.21
LIPID C	14.67	8.51	71.51
LIPID E	13.27	6.93	81.01
LIPID D	14.71	8.89	56.49
MC3	11.3	5.31	63.56

Pre-F NP	17.59	10.97	98.36

[00305] A better quality of an immune response is demonstrated with a lower value for the antibody titer / neutralization titer ratio. Here, the LNP formulation Lipid B demonstrated the best quality of immune response, while all LNP formulations demonstrated a superior quality of immune response compared to the non-mRNA vaccine, Pre-F NP, and several were better than the industry benchmark LNP formulation of MC3.

Example 9: SARS-CoV-2 Spike (S) protein-encoding mRNA LNP Formulations

[00306] <u>LNP Formulations with SARS-CoV-2 Spike (S) protein-encoding mRNA:</u>

[00307] An LNP formulation containing a SARS-CoV-2 S protein-encoding mRNA was administered to human subjects. The subjects were administered an LNP of formulation Lipid B. The unmodified mRNA encoded a SARS-CoV-2 S protein mutated to remove the furin cleavage site and to mutate residues 986 and 987 to proline. The subjects were administered the LNP-SARS-CoV-2 vaccine under clinical trial protocol for NCT04798027, described below.

[00308] This was a sequential group prevention study consisting of a sentinel cohort followed by the Full Enrollment Cohort. There were 3 dose levels (up to 25 participants 18-49 years of age for each dose level) in the Sentinel Cohort, which was done in an open-label fashion with stepwise safety evaluation for each dose level and each vaccination. All sentinel participants received 2 vaccinations, 21 days apart. For the Full Enrollment Cohort, participants were stratified into 2 age groups based on age at enrollment: the younger adult age group (140 participants 18-49 years of age) and the older adult age group (168 participants ≥ 50 years of age). The Full Enrollment Cohort 1 (Groups 1 to 4) received a single injection of study intervention while participants in Cohort 2 (Groups 5 to 8) received 2 vaccinations (to be given 21 days apart). The route of administration for all groups was intramuscular (IM).

[00309] Experimental: Group 1 – 1 injection of SARS-CoV-2 mRNA vaccine formulation 1 at Day 1.

[00310] Experimental: Group 2 – 1 injection of SARS-CoV-2 mRNA vaccine formulation 2 at Day 1.

[00311] Experimental: Group 3 – 1 injection of SARS-CoV-2 mRNA vaccine formulation 3 at Day 1.

[00312] Placebo Comparator: Group 4 – 1 injection of placebo (0.9% normal saline) at Day 1.

[00313] Experimental: Group 5 – 2 injections of SARS-CoV-2 mRNA vaccine formulation 1 at Day 1 and Day 22.

[00314] Experimental: Group 6 – 2 injections of SARS-CoV-2 mRNA vaccine formulation 2 at Day 1 and Day 22.

[00315] Experimental: Group 7 – 2 injections of SARS-CoV-2 mRNA vaccine formulation 3 at Day 1 and Day 22.

[00316] Placebo Comparator: Group 8 – 2 injections of placebo (0.9% normal saline) at Day 1 and Day 22.

[00317] Results from the study showed neutralizing antibody seroconversion (defined as 4-fold increase vs baseline) in 91% to 100% of study participants, two weeks after a second injection, across all 3 dosages tested. No safety concern has been observed and the tolerability profile is comparable to that of other unmodified mRNA SARS-CoV-2 vaccines.

Example 10: Further Studies on Quadrivalent or Octavalent Influenza Vaccine LNP Formulations

[00318] HAI titers and NAI titers were measured from mice administered various multivalent LNP-influenza mRNA vaccines. HAI titers were measured against influenza strains A/Michigan/45/2015, A/SINGAPORE/INFIMH160019/2016, B/Maryland/15/2016 BX69A, and B/Phuket/3073/2013. NAI titers were measured against influenza strains A/Michigan/45/2015, A/SINGAPORE/INFIMH160019/2016, B/Colorado/06/201, and B/Phuket/3073/2013.

[00319] The HAI titers and NAI titers were compared against mice receiving mono- or quadrivalent HA or NA mRNA vaccines.

[00320] Mice were injected with a prime vaccine on day 0 and a booster vaccine of the same dosage on Day 21. Blood was collected on days 1, 20, 22, and 35. For monovalent compositions containing mRNA encoding HA or NA antigens, mRNA encoding each of the following individually was used: H1, H3, HA from a B/Victoria lineage, and HA from a B/Yamagata lineage (specifically from strains A/Michigan/45/2015; A/Singapore/Infimh160019/2016; B/Maryland/15/2016; and B/Phuket/3037/2013). Quadrivalent vaccine compositions containing mRNA encoding each of N1, N2, NA from a B/Victoria lineage and NA from a B/Yamagata lineage, and each of H1, H3, HA from a B/Victoria lineage and HA from a B/Yamagata lineage (specifically from strains A/Michigan/45/2015; A/Singapore/Infimh160019/2016; B/Colorado/06/2017; and B/Phuket/3037/2013) were also prepared. Finally, an octavalent vaccine composition containing mRNA encoding each of H1, H3, HA from a B/Victoria lineage, HA from a B/Yamagata lineage, each of N1, N2, NA from a B/Victoria lineage and NA from a B/Yamagata lineage (specifically from strains A/Michigan/45/2015; A/Singapore/Infimh160019/2016; B/Colorado/06/2017; and B/Phuket/3037/2013) was prepared and administered as an octavalent vaccine. Each mRNA for all compositions was added in an amount of 0.4 μg/strain. For each group, n=6 mice.

[00321] An overview of each experimental group is recited below in **Table 11**.

Table 11. Overview of experimental groups for multivalent influenza vaccines in mice

Group #	N	Prime (D0)/boost (D21) - NA mRNA	Dose mRNA NA (μg per strain)	Prime (D0)/boost (D21) - HA (together with NA)	Dose rHA (μg per strain)	Adjuvant (rHA)
1	6	LNP diluent	-	-	-	-
3	6	NA mRNA-LNP (N2 Perth)	0.4	-	-	-
4	6	NA mRNA-LNP (N1)	0.4	-	-	-
5	6	NA mRNA-LNP (N2)	0.4	-	-	-
6	6	NA mRNA-LNP (NV)	0.4	-	-	-
7	6	NA mRNA-LNP (NY)	0.4	-	-	-
8	6	NA mRNA-LNP (N1, N2, BV, BY)	0.4	-	-	-
9	6	-	-	HA mRNA-LNP (H1)	0.4	-
10	6	-	-	HA mRNA-LNP (H3)	0.4	-
11	6	-	-	HA mRNA-LNP (BV)	0.4	-
12	6	-	-	HA mRNA-LNP (BY)	0.4	-
13	6	-	-	HA mRNA-LNP (H1, H3, BV, BY)	0.4	-
14	6	NA mRNA-LNP (N1, N2, BV, BY)	0.4	HA mRNA-LNP (H1, H3, BV, BY)	0.4	-

[00322] As shown in **FIG. 31**, octavalent mRNA-LNP formulations led to HAI titers within 4-fold of the quadrivalent for 3 out of 4 influenza strains.

[00323] An overview of the NAI titer results for each of the groups above is shown in **FIG. 33**. The octavalent mRNA-LNP formulations led to NAI titers comparable to the quadrivalent mRNA-LNP formulations.

[00324] Thus, the data demonstrate that an octavalent vaccine was capable of inducing robust HA and NA immune responses and that the presence of the immunodominant HA from four different influenza strains does not appear to suppress or interfere with the anti-NA immune response.

[00325] High content imaging-based neutralization test (HINT) titers for HA and NAI titers were additionally measured from ferrets administered various multivalent LNP-influenza mRNA vaccines. The HINT assay is described in further detail in Jorquera et al. (Scientific Reports. 9: 2676. 2019), incorporated herein by reference. HINT titers were measured against influenza strains A/Michigan/45/2015, A/SINGAPORE/INFIMH160019/2016, B/IOWA/06/2017, and B/Phuket/3073/2013. NAI titers were measured against influenza strains A/Michigan/45/2015, A/SINGAPORE/INFIMH160019/2016, B/Colorado/06/201, and B/Phuket/3073/2013.

[00326] Ferrets used to assess multivalent vaccine immunogenicity were vaccinated twice 21 days apart with (1) a mixture of four mRNAs encoding NA antigens (N1, N2, BvNA, and ByNA), (2) a mixture of four mRNAs encoding HA antigens (H1, H3, BvHA, and ByHA), or (3) a mixture of four mRNAs encoding NA antigens (N1, N2, BvNA, and ByNA) and four mRNAs encoding HA antigens (H1, H3, BvHA, and ByHA), as shown below in Table 12. Each HA includes HA from one of the following four strains: A/Michigan/45/2015 (H1); A/Singapore/Infimh-16-0019/2016 (H3); B/Iowa/06/2017 (B/Victoria lineage); and B/Phuket/3073/2013 (B/Yamagata lineage). All antigens were administered at a 1:1 ratio.

[00327] An overview of each experimental group is recited below in **Table 12**.

[00328] All ferrets were bled under sedation (isoflurane) at baseline, one day before or just before booster, at booster vaccination, and two weeks after challenge as required. Sera samples (stored at –20°C until required) were tested by ELLA to assess NAI activity. Additionally, the hemagglutinin inhibition assay (HAI) was undertaken to assess antibody responses to hemagglutinin antigens following multivalent vaccination.

Table 12. Overview of experimental groups for multivalent influenza vaccines in ferrets

Group #	N	Prime (D0)/boost (D21) - NA	Prime (D0)/boost (D21) - HA	Dose (µg per strain)	Adjuvant
1	6	PBS	PBS	0	-
11	6	NA mRNA-LNP (N1, N2, BV, BY)	-	1	-
12	6	NA mRNA-LNP (N1, N2, BV, BY)	-	15	-
13	6	-	HA mRNA-LNP (H1, H3, BV, BY)	1	-
14	6	-	HA mRNA-LNP (H1, H3, BV, BY)	15	-
15	6	NA mRNA-LNP (N1, N2, BV, BY)	HA mRNA-LNP (H1, H3, BV, BY)	1	-
16	6	NA mRNA-LNP (N1, N2, BV, BY)	HA mRNA-LNP (H1, H3, BV, BY)	15	-

[00329] An overview of the HINT results for each of the groups above is shown in **FIG. 32**. The octavalent mRNA-LNP formulations led to HINT titers comparable to the quadrivalent mRNA-LNP formulations.

[00330] An overview of the NAI titer results for each of the groups above is shown in **FIG. 34** (day 20) and **FIG. 35** (day 42). The octavalent mRNA-LNP formulations led to NAI titers comparable to the quadrivalent mRNA-LNP formulations. This was true from the day 20 and day 42 samples.

Example 11: Functional antibody titers to influenza heterologous subtype strains recorded with mRNA in Lipid A or Lipid B LNP Formulations:

[00331] To evaluate immunogenicity of the mRNA-LNP in NHP, 0, 15, 45, µg of Sing16 HA-encoding mRNA encapsulated in either Lipid A or Lipid B LNP formulation (encoding for HA A/Singapore/INFIMH-16-0019/2016) were immunized. Naïve male and female Mauritius origin Cynomolgus macaques (*Macaca fascicularis*) were used. Animals weighed >2kg and were >2 years of age at the start of the studies. Groups consisted of up to 6 animals per treatment group and were vaccinated in 0.5 mL of their respected vaccine dose or diluent via the IM route in one forelimb of each animal, targeting the deltoid, on Study Day 0. Twenty-eight days after the first immunization took place, a second immunization was given to the animals in the contralateral limb. A quadrivalent egg-derived inactivated influenza vaccine (IIV) containing the A/Singapore/INFIMH-16-0019/2016 (H3N2) strain was used as a comparator.

[00332] Influenza assays were performed using the A/Singapore/INFIMH-16-0019/2016 (H3N2) virus stocks from BIOQUAL, Inc. Additional breadth testing by HAI was performed using the following H3N1 virus stocks: A/Shandoglaicheng/1763/2016, A/Louisiana/13/2017, A/Kenya/105/2017, A/Victoria/746/2017, and A/Michigan/84/2016, A/Aksaray/4048/2016. These include strains from both 3c.2a and 3c.3a clades, as well as a very distant swine-like H3 sequence (A/Michigan/84/2016) based on bioinformatics analysis to select a set of maximally diverse H3N2 sequences from the same timeframe as A/Singapore/INFIMH-16-0019/2016.

[00333] For microneutralization (MN) assays, sera samples were diluted in receptor-destroying enzyme (Denka Seiken, 370013) and incubated overnight in a 37°C water bath. Samples were heat-inactivated for 30-minutes at 56°C then two-fold serial dilutions were run in duplicate in 96-well plates. An equal volume of virus at 100TCID$_{50}$ was added to the plates followed by a 1-hour incubation at 37°C. One-hundred microliters of sample/virus mixture was transferred to 96-well flat-bottom plates of MDCK cells (ATCC#CCL-34) containing TPCK-treated media and incubated for 48-hours at 37°C with 5% CO$_2$. Plates were fixed with cold acetone then stained with biotin-conjugated anti-Influenza A NP (Millipore, MAB8258B) followed by incubation with DELFIA Europium-labeled streptavidin in Delfia assay buffer. Fluorescence was measured and endpoint titers reported.

[00334] At day 43, after the second immunization, NHPs vaccinated with Sing16HA-CL-059 and Sing16HA-CL017 developed neutralizing antibodies to homologous virus, A/Singapore/INFIMH-16-0019/2016 (H3N2), as noted in MN assay (**FIG. 36** and **FIG. 37**). Further, in this model, MN titers were observed to hetero subtype viral panel including A/Shandoglaicheng/1763/2016, A/Louisiana/13/2017, A/Kenya/105/2017, A/Victoria/746/2017, and A/Aksaray/4048/2016 contrary to the IIV vaccine. The data indicates the said mRNA formulations have potential to provide greater breadth than IIV covering for hetero subtype strains of influenza.

CLAIMS

1. A pharmaceutical composition comprising a nucleic acid molecule encapsulated in a lipid nanoparticle (LNP), wherein the LNP comprises:

a cationic lipid at a molar ratio between 35% and 45%,

a polyethylene glycol (PEG) conjugated (PEGylated) lipid at a molar ratio between 0.25% and 2.75%,

a cholesterol-based lipid at a molar ratio between 20% and 35%, and

a helper lipid at a molar ratio of between 25% and 35%,

wherein all the molar ratios are relative to the total lipid content of the LNP.

2. The composition of claim 1, wherein the LNP comprises:

a cationic lipid at a molar ratio of 40%,

a PEGylated lipid at a molar ratio of 1.5%,

a cholesterol-based lipid at a molar ratio of 28.5%, and

a helper lipid at a molar ratio of 30%.

3. The composition of claim 1 or 2, wherein the cationic lipid is OF-02, cKK-E10, GL-HEPES-E3-E10-DS-3-E18-1, GL-HEPES-E3-E12-DS-4-E10, or GL-HEPES-E3-E12-DS-3-E14.

4. The composition of any one of the preceding claims, wherein the PEGylated lipid is dimyristoyl-PEG2000 (DMG-PEG2000).

5. The composition of any one of the preceding claims, wherein the cholesterol-based lipid is cholesterol.

6. The composition of any one of the preceding claims, wherein the helper lipid is 1,2-dioleoyl-SN-glycero-3-phosphoethanolamine (DOPE).

7. The composition of claim 1, wherein the LNP comprises:

OF-02 at a molar ratio of 40%,

DMG-PEG2000 at a molar ratio of 1.5%,
cholesterol at a molar ratio of 28.5%, and
DOPE at a molar ratio of 30%.

8. The composition of claim 1, wherein the LNP comprises:
cKK-E10 at a molar ratio of 40%,
DMG-PEG2000 at a molar ratio of 1.5%,
cholesterol at a molar ratio of 28.5%, and
DOPE at a molar ratio of 30%.

9. The composition of claim 1, wherein the LNP comprises:
GL-HEPES-E3-E10-DS-3-E18-1 at a molar ratio of 40%,
DMG-PEG2000 at a molar ratio of 1.5%,
cholesterol at a molar ratio of 28.5%, and
DOPE at a molar ratio of 30%.

10. The composition of claim 1, wherein the LNP comprises:
GL-HEPES-E3-E12-DS-4-E10 at a molar ratio of 40%,
DMG-PEG2000 at a molar ratio of 1.5%,
cholesterol at a molar ratio of 28.5%, and
DOPE at a molar ratio of 30%.

11. The composition of claim 1, wherein the LNP comprises:
GL-HEPES-E3-E12-DS-3-E14 at a molar ratio of 40%,
DMG-PEG2000 at a molar ratio of 1.5%,
cholesterol at a molar ratio of 28.5%, and
DOPE at a molar ratio of 30%.

12. The composition of any one of the preceding claims, wherein the LNP has an average diameter of 30-200 nm.

13. The composition of claim 12, wherein the LNP has an average diameter of 80-150 nm.

14. The composition of any one of the preceding claims, wherein the composition comprises 1-10, optionally 1, mg/mL of the LNP.

15. The composition of any one of the preceding claims, wherein the LNP comprises 1-20, optionally 5-10 or 6-8, nucleic acid molecules.

16. The composition of any one of the preceding claims, wherein the nucleic acid molecule(s) is an mRNA molecule comprising an open reading frame (ORF).

17. The composition of claim 16, wherein the mRNA molecule encodes an antigen, optionally a viral antigen or a bacterial antigen.

18. The composition of claim 17, wherein the antigen is derived from influenza virus.

19. The composition of claim 17 or 18, wherein the LNP comprises two or more mRNA molecules, wherein each mRNA molecule encodes a different antigen, optionally wherein the different antigens are from the same pathogen or from different pathogens.

20. The composition of claim 17 or 18, wherein the composition comprises two or more LNPs, wherein each LNP comprises an mRNA encoding a different antigen, optionally wherein the different antigens are from the same pathogen or from different pathogens.

21. The composition of claim 19 or 20, wherein the composition comprises two, three, four, five, six, seven, eight, nine, or more mRNA molecules encoding (i) one or more hemagglutinin (HA) antigens, (ii) one or more neuraminidase (NA) antigens, or (iii) at least one HA antigen and at least one NA antigen.

22. The composition of any one of claims 18-21, wherein the composition comprises one or more mRNA molecules encoding antigens of influenza A, B and/or C viruses, optionally wherein the antigens are HA and/or NA antigens of influenza A and influenza B viruses.

23. The composition of claim 22, wherein the HA antigens of influenza A viruses are selected from subtypes H1, H2, H3, H4, H5, H6, H7, H8, H9, H10, H11, H12, H13, H14, H15, H16, H17, and H18; and/or the NA antigens of influenza A viruses are selected from subtypes N1, N2, N3, N4, N5, N6, N7, N8, N9, N10, and N11.

24. The composition of claim 22 or 23, wherein the HA and NA antigens of Influenza B viruses are from the Influenza B/Yamagata lineage or the Influenza B/Victoria lineage.

25. The composition of any one of claims 22-24, wherein the composition comprises two, three, four, five, six, seven, eight, nine, or more mRNA molecules encoding (i) one or more HA antigens, (ii) one or more NA antigens, or (iii) a combination of one or more HA antigens and NA antigens selected from H1N1, H3N2, H2N2, H5N1, H7N9, H7N7, H1N2, H9N2, H7N2, H7N3, H5N2, and H10N7 subtypes and/or B/Yamagata and B/Victoria lineages.

26. The composition of any one of claim 22-25, wherein the composition comprises one mRNA molecule encoding an H3 HA antigen, one mRNA molecule encoding an H1 HA antigen, one mRNA molecule encoding an HA antigen from the Influenza B/Yamagata lineage, and one mRNA molecule encoding an HA antigen from the Influenza B/Victoria lineage.

27. The composition of any one of claims 22-26, wherein the composition comprises one mRNA molecule encoding an H3 HA antigen, one mRNA molecule encoding an N2 NA antigen, one mRNA molecule encoding an H1 HA antigen, one mRNA molecule encoding an N1 NA antigen, one mRNA molecule encoding an HA antigen from the Influenza B/Yamagata lineage, one mRNA molecule encoding an NA antigen from the Influenza B/Yamagata lineage, one mRNA molecule encoding an HA antigen from the Influenza B/Victoria lineage, and one mRNA molecule encoding an NA antigen from the Influenza B/Victoria lineage.

28. The composition of claim 16, wherein the mRNA molecule comprises an open reading frame (ORF) encoding a respiratory syncytial virus (RSV) F protein antigen.

29. The composition of claim 28, wherein the RSV F protein antigen comprises an amino acid sequence with at least 98% identity to SEQ ID NO: 16 or consists of an amino acid sequence of SEQ ID NO: 16.

30. The composition of claim 28 or 29, wherein the RSV F protein antigen is a pre-fusion protein.

31. The composition of any one of claims 16-30, wherein the ORF is codon optimized.

32. The composition of any one of claims 16-31, wherein the mRNA molecule comprises at least one 5' untranslated region (5' UTR), at least one 3' untranslated region (3' UTR), and at least one polyadenylation (poly(A)) sequence.

33. The composition of any one of claims 16-32, wherein the mRNA comprises at least one chemical modification.

34. The composition of any one of claims 16-33, wherein at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of the uracil nucleotides in the mRNA are chemically modified.

35. The composition of any one of claims 16-33, wherein at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of the uracil nucleotides in the ORF are chemically modified.

36. The composition of any one of claims 33-35, wherein the chemical modification is selected from the group consisting of pseudouridine, N1-methylpseudouridine, 2-thiouridine, 4'-thiouridine, 5-methylcytosine, 2-thio-l-methyl-1-deaza-pseudouridine, 2-thio-l-methyl-pseudouridine, 2-thio-5-aza-uridine, 2-thio-dihydropseudouridine, 2-thio-dihydrouridine, 2-thio-

pseudouridine, 4-methoxy-2-thio-pseudouridine, 4-methoxy-pseudouridine, 4-thio-1-methyl-pseudouridine, 4-thio-pseudouridine, 5-aza-uridine, dihydropseudouridine, 5-methyluridine, 5-methyluridine, 5-methoxyuridine, and 2’-O-methyl uridine.

37. The composition of claim 36, wherein the chemical modification is selected from the group consisting of pseudouridine, N1-methylpseudouridine, 5-methylcytosine, 5-methoxyuridine, and a combination thereof.

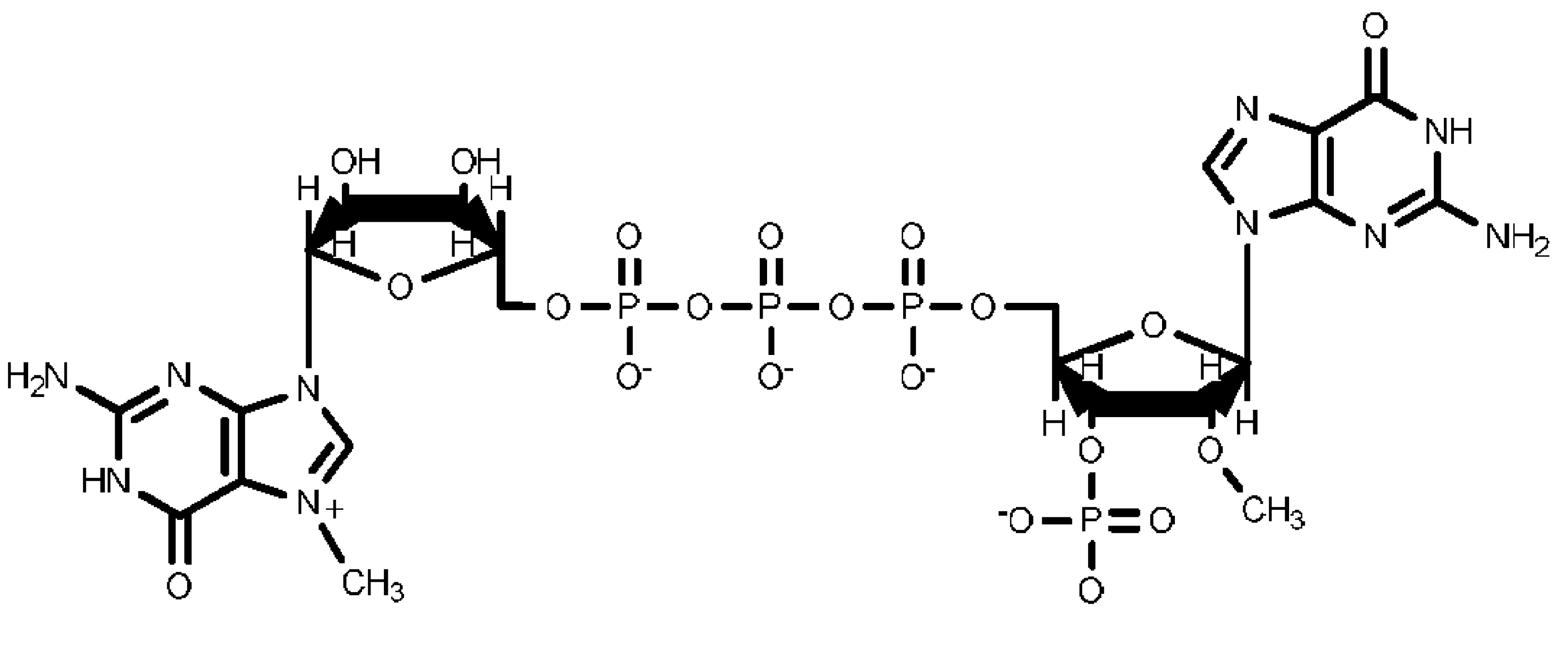
38. The composition of claim 36, wherein the chemical modification is N1-methylpseudouridine.

39. The composition of any one of claims 28-38, wherein the mRNA comprises a nucleic acid sequence with at least 80% identity to a nucleic acid sequence set forth in SEQ ID NO: 17.

40. The composition of any one of claims 28-38, wherein the mRNA comprises a nucleic acid sequence with at least 80% identity to a nucleic acid sequence set forth in SEQ ID NO: 21.

41. The composition of any one of claims 28-38, wherein the mRNA comprises of the following structural elements:

(i) a 5’ cap with the following structure:



;

(ii) a 5′ untranslated region (5’ UTR) having the nucleic acid sequence of SEQ ID NO: 19;

(iii) a protein coding region having the nucleic acid sequence of SEQ ID NO: 17;

(iv) a 3’ untranslated region (3’ UTR) having the nucleic acid sequence of SEQ ID NO: 20; and

(v) a poly(A) tail.

42. The composition of any one of the preceding claims, wherein the composition is formulated for intramuscular injection.

43. The composition of claim 42, wherein the composition comprises a phosphate-buffer saline.

44. The composition of any one of the preceding claims, wherein the composition comprising trehalose, optionally at 10% (w/v) of the composition.

45. A method of preparing the composition of any one of the preceding claims, comprising

providing an aqueous buffered solution comprising the nucleic acid molecule,

providing an amphiphilic solution comprising the cationic lipid, the PEGylated lipid, the cholesterol-based lipid, and the helper lipid, and

mixing the aqueous buffered solution and the amphiphilic solution at a ratio of 5:1 to 3:1, optionally 4:1.

46. The method of claim 45, wherein the aqueous buffered solution is an acidic buffered solution, optionally comprising 1 mM citrate and 150 mM sodium chloride with a pH of about 4.5.

47. The method of claim 45 or 46, wherein the amphiphilic solution is an ethanol solution.

48. A method of eliciting an immune response in a subject in need thereof, comprising administering to the subject, optionally intramuscularly, intranasally, intravenously, subcutaneously, or intradermally, a prophylactically effective amount of the composition of any one of claims 1-47.

49. A method of preventing influenza infections or reducing one or more symptoms of influenza infections, comprising administering to the subject, optionally intramuscularly, intranasally, intravenously, subcutaneously, or intradermally, a prophylactically effective amount of the composition of any one of claims 18-27.

50. The method of claim 49, wherein the composition elicits an immune response against one or more seasonal and/or pandemic influenza strains.

51. The method of any one of claims 48-50, comprising administering to the subject one or more doses of the composition, each dose comprising 1-250, optionally 2.5., 5, 15, 45, or 135, µg of mRNA.

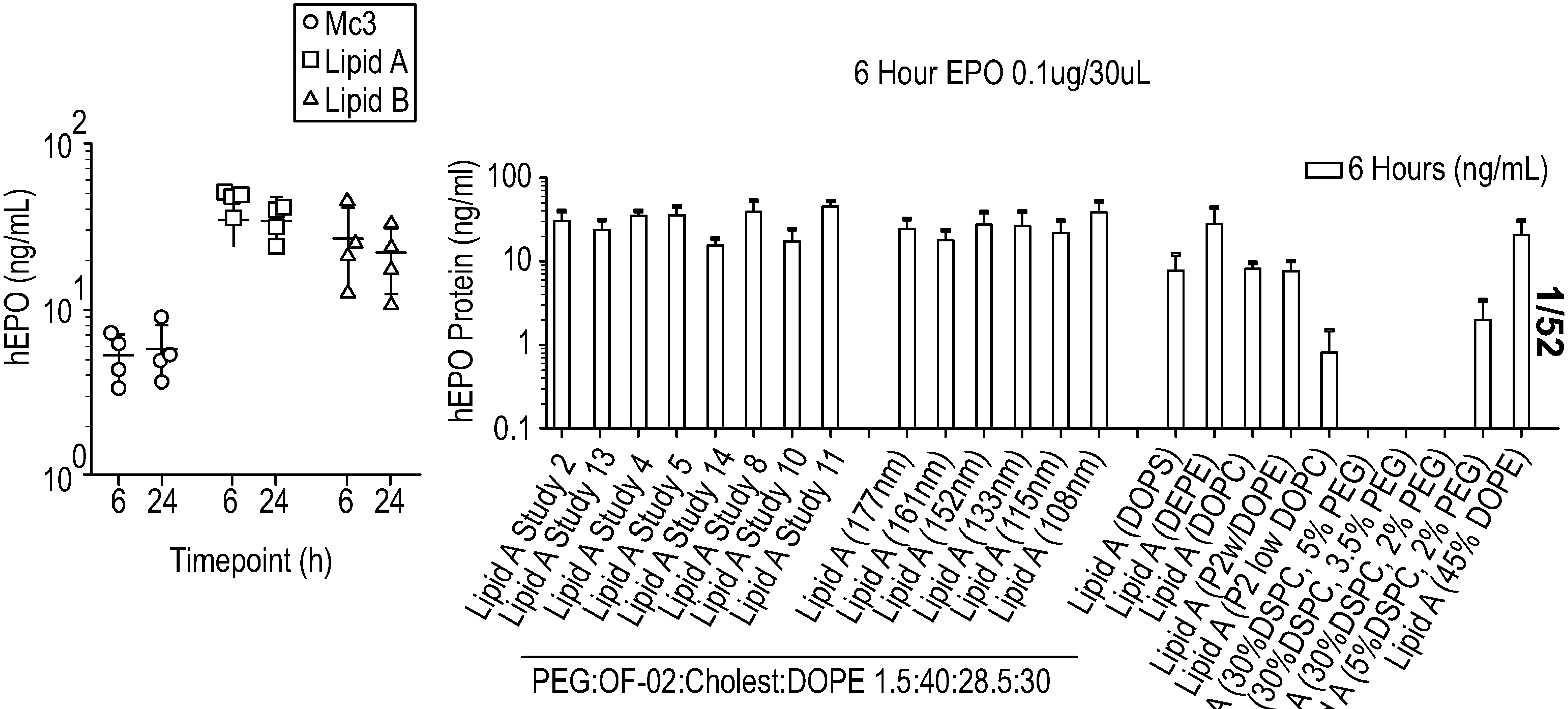
52. The method of any one of claims 48-51, comprising administering to the subject two doses of the composition with an interval of 2-6, optionally 4, weeks.

53. Use of the composition of any one of claims 1-44 for the manufacture of a medicament for use in treating a subject in need thereof, optionally in a method of any one of claims 48-52.

54. The composition of any one of claims 1-44 for use in treating a subject in need thereof, optionally in a method of any one of claims 48-52.

55. A kit comprising a container comprising a single-use or multi-use dosage of the composition of any one of claims 1-44, optionally wherein the container is a vial or a pre-filled syringe or injector.

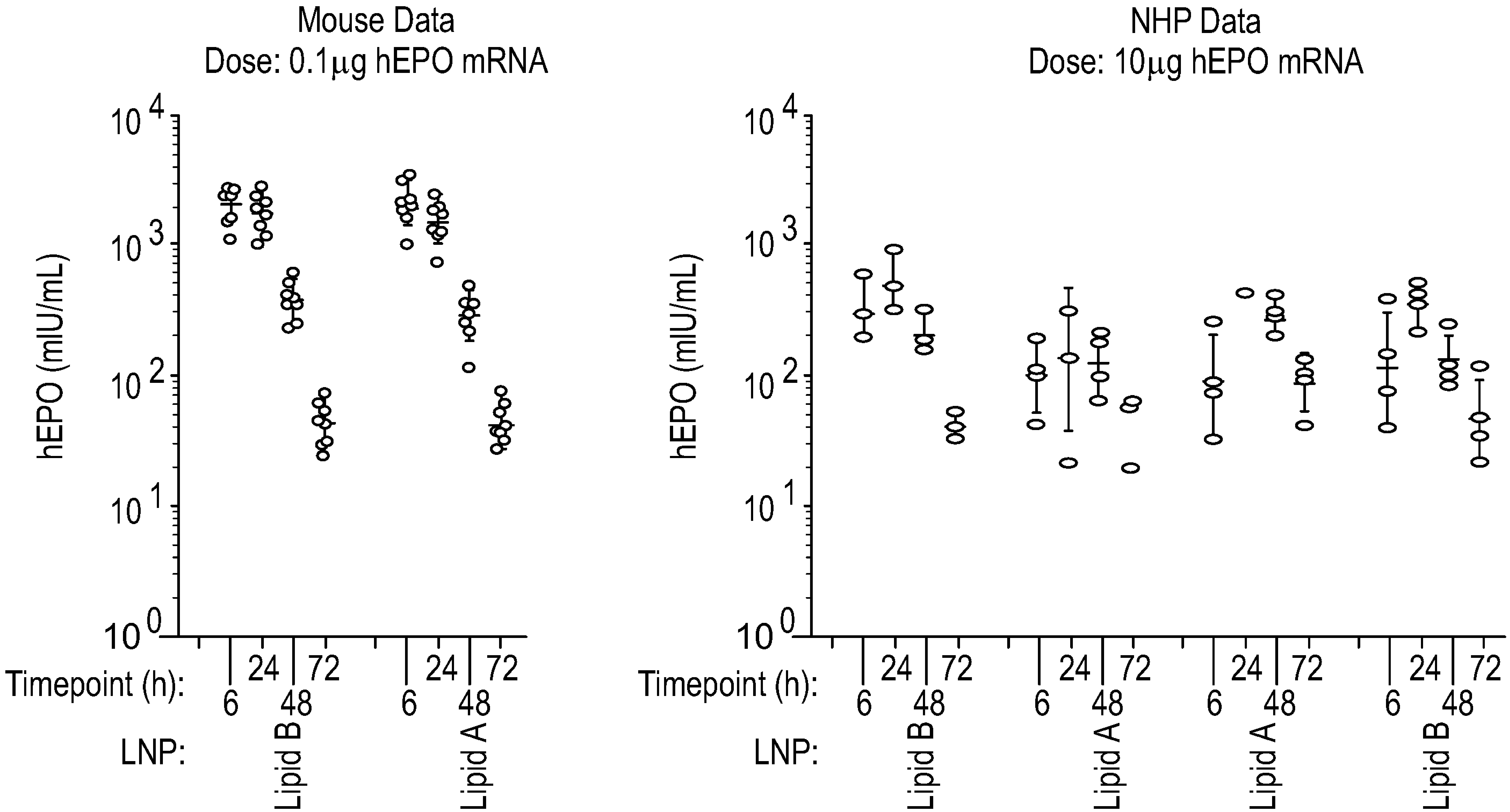
56. The composition according to any of claims 21-27, wherein the antigens comprise an influenza virus HA antigen and/or an influenza virus NA antigen having a molecular sequence identified or designed from a machine learning model.


Mc3
Lipid A
Lipid B
hEPO (ng/mL)
10^2
10^1
10^0
6
24
6
24
6
24
Timepoint (h)
6 Hour EPO 0.1ug/30uL
6 Hours (ng/mL)
hEPO Protein (ng/ml)
100
10
1
0.1
Lipid A Study 2
Lipid A Study 13
Lipid A Study 4
Lipid A Study 5
Lipid A Study 14
Lipid A Study 8
Lipid A Study 10
Lipid A Study 11
Lipid A (177nm)
Lipid A (161nm)
Lipid A (152nm)
Lipid A (133nm)
Lipid A (115nm)
Lipid A (108nm)
Lipid A (DOPS)
Lipid A (DEPE)
Lipid A (DOPC)
Lipid A (P2w/DOPE)
Lipid A (P2 low DOPC)
Lipid A (30%DSPC, 5% PEG)
Lipid A (30%DSPC, 3.5% PEG)
Lipid A (30%DSPC, 2% PEG)
Lipid A (5%DSPC, 2% PEG)
Lipid A (45% DOPE)
PEG:OF-02:Cholest:DOPE 1.5:40:28.5:30

a

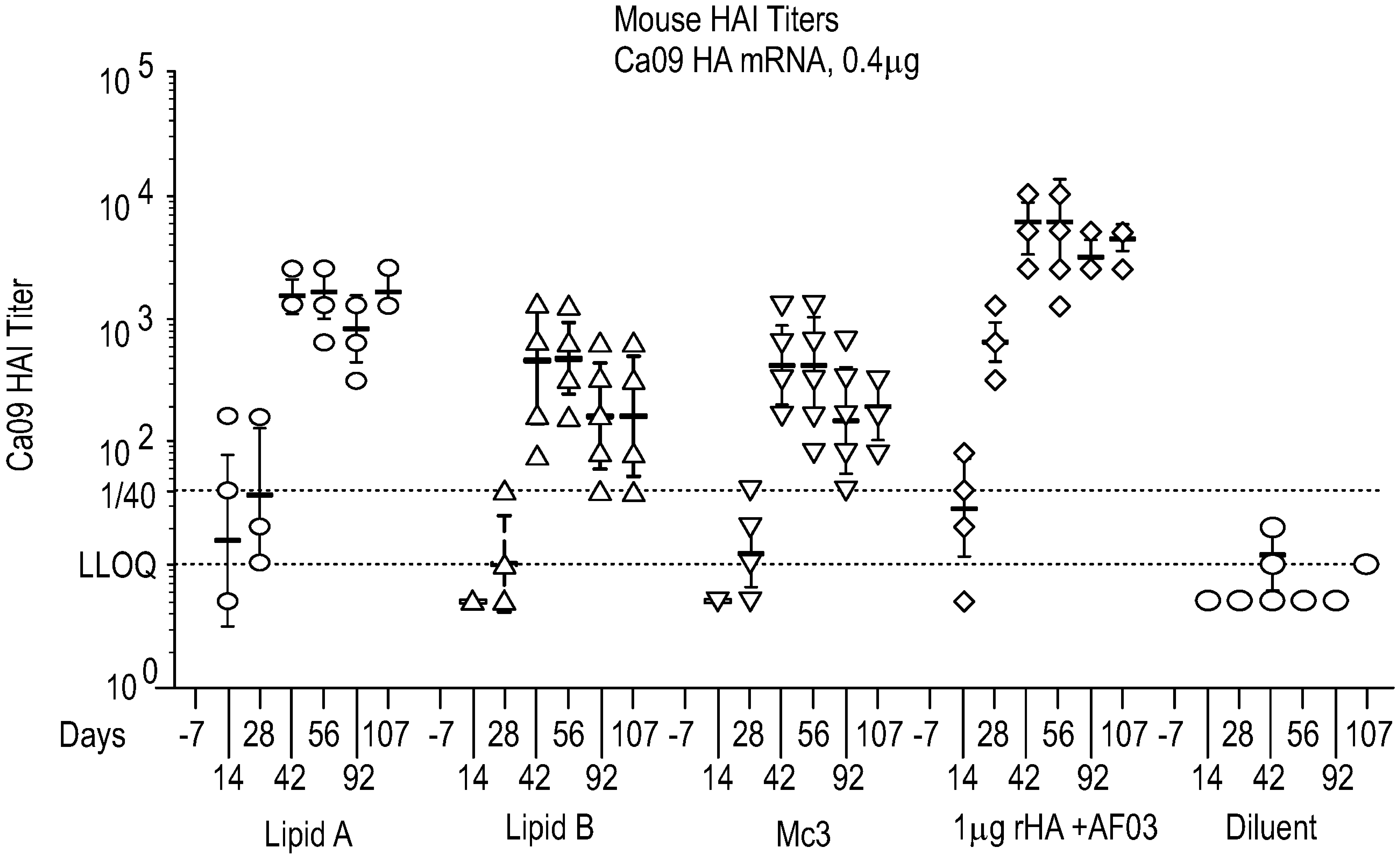
b

FIG. 1A



Lipid	Composition (Molar Ratio)
Lipid A	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30
Lipid B	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30

FIG. 1B



Lipid	Composition (Molar Ratio)
Lipid A	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30
Lipid B	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30

FIG. 2A

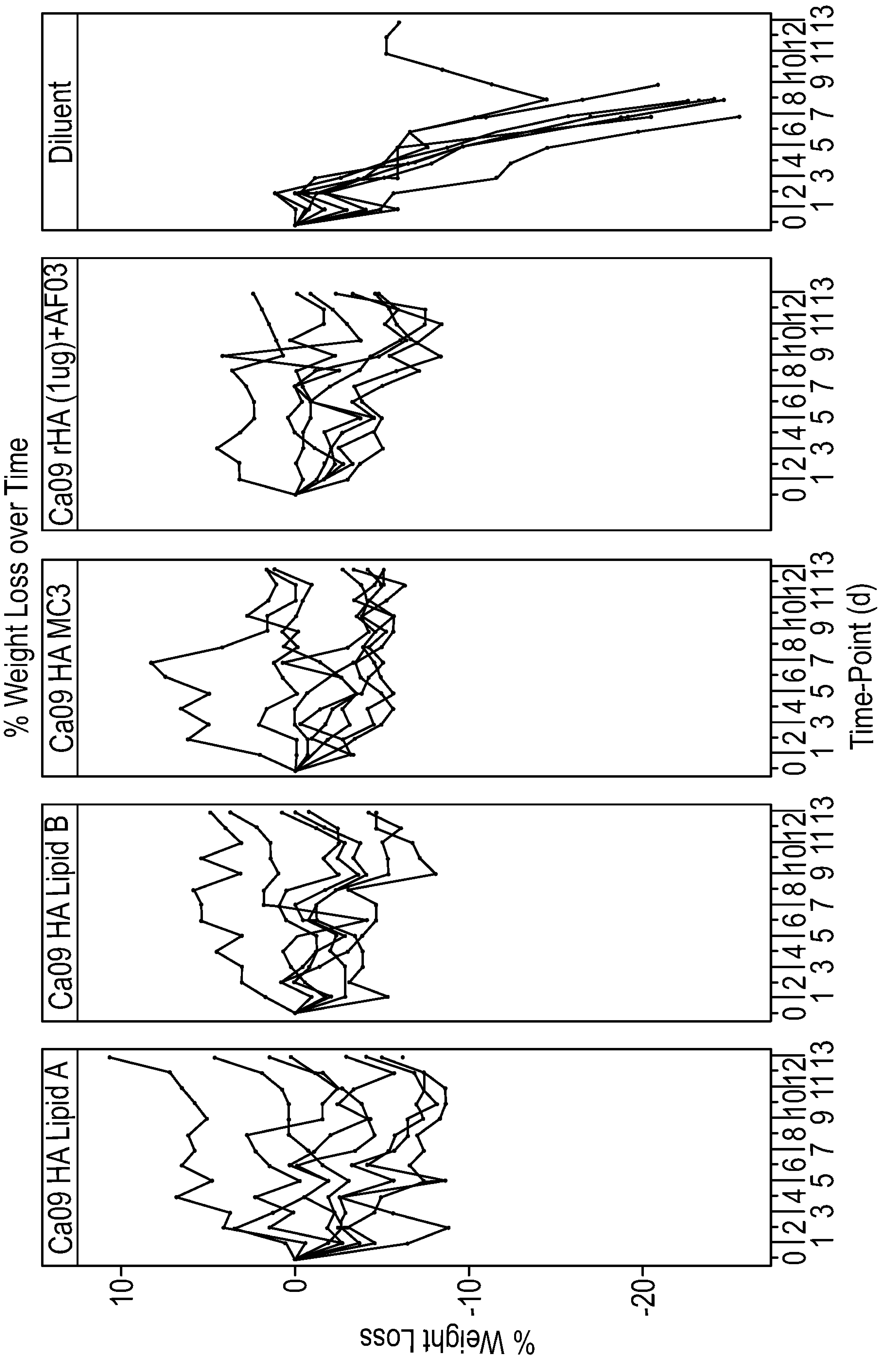
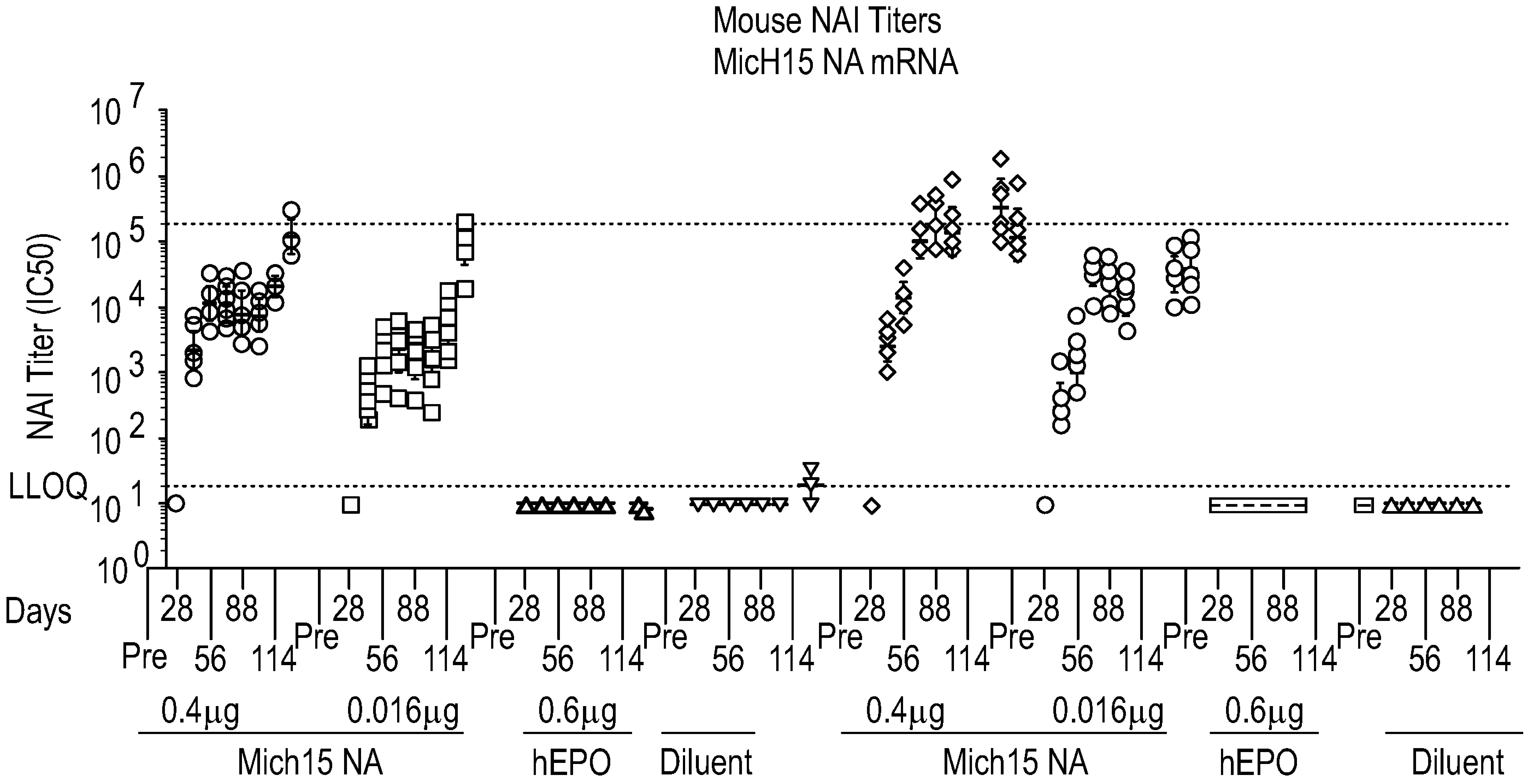

% Weight Loss over Time
Ca09 HA Lipid A
Ca09 HA Lipid B
Ca09 HA MC3
Ca09 rHA (1ug)+AF03
Diluent
% Weight Loss
10
0
-10
-20
0 1 2 3 4 5 6 7 8 9 10 11 12 13
Time-Point (d)

FIG. 2B



Lipid	Composition (Molar Ratio)
Lipid A	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40: 1.5:28.5:30

FIG. 3A

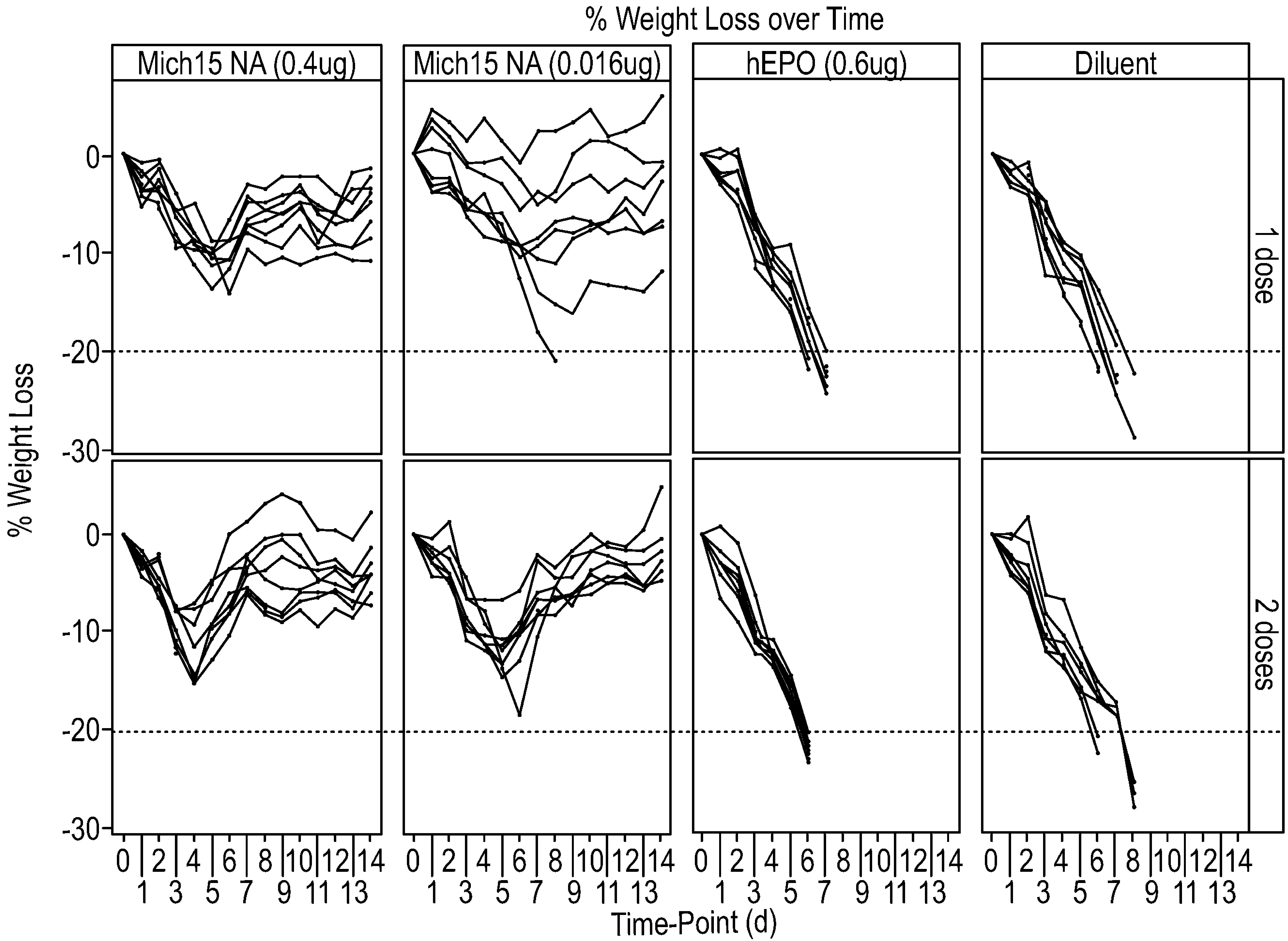
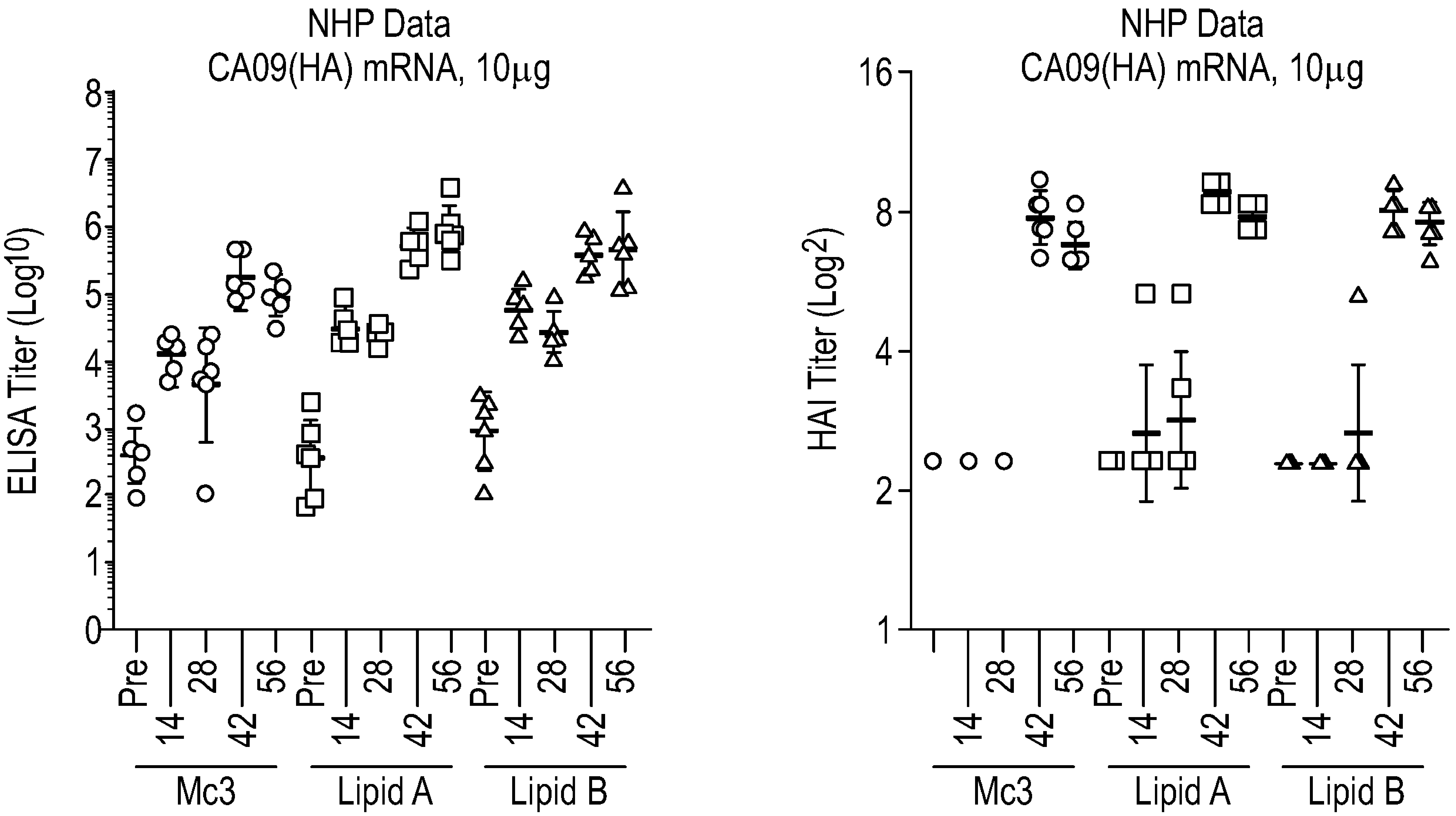

% Weight Loss over Time
Mich15 NA (0.4ug)
Mich15 NA (0.016ug)
hEPO (0.6ug)
Diluent
1 dose
2 doses
% Weight Loss
0
-10
-20
-30
0
-10
-20
-30
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Time-Point (d)

FIG. 3B



Lipid	Composition (Molar Ratio)
Lipid A	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30
Lipid B	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30

FIG. 4

```
ATGAAAACCATAATCGCGCTCTCATACATACTTTGCCTGGTCTTTGCCCAAAAGATCCCTGGCAACGACAA
CTCAACCGCGACCCTTTGCCTCGGCCATCACGCCGTGCCGAACGGCACTATCGTCAAGACCATCACAAACG
ACCGCATCGAAGTGACCAACGCGACTGAGCTAGTGCAGAACTCCAGCATTGGAGAGATTTGCGATTCTCCA
CACCAAATCCTGGACGGAGAGAATTGTACCTTGATCGACGCGCTGCTGGGGGATCCGCAGTGCGACGGATT
CCAGAACAAGAAATGGGACCTTTTCGTGGAACGGAGCAAGGCATACTCGAATTGCTACCCCTACGATGTGC
CCGACTACGCCTCGCTGCGGTCCTTGGTCGCTTCCTCCGGGACCCTGGAATTCAAAAACGAGAGCTTTAAT
TGGACCGGAGTGACCCAGAATGGCACCTCGAGCGCCTGCATTCGGGGCTCCTCCTCGAGCTTCTTCAGCCG
CCTGAACTGGCTCACTCACCTCAACTACACCTACCCGGCACTGAACGTGACCATGCCGAACAAGGAACAAT
TCGACAAGCTCTACATTTGGGGGGTGCATCACCCGGGTACCGATAAGGACCAGATCTTCCTCTACGCCCAA
TCCTCGGGCCGGATCACCGTGTCCACTAAGCGCTCGCAGCAGGCCGTGATCCCGAACATTGGAAGCAGACC
CCGCATTCGCGACATTCCATCGAGGATCTCGATCTACTGGACGATTGTCAAGCCTGGCGACATCCTCCTCA
TTAACTCCACCGGGAACCTCATCGCCCCTCGGGGTTATTTCAAGATCCGCAGCGGGAAGTCCTCCATCATG
AGAAGCGATGCCCCCATTGGAAAGTGCAAGTCCGAGTGTATCACACCTAACGGAAGCATTCCCAATGACAA
GCCATTCCAGAACGTGAACAGAATTACCTACGGAGCTTGCCCTCGCTACGTCAAACATTCGACCCTCAAGT
TGGCGACTGGAATGCGCAACGTGCCGGAGAAGCAAACCCGGGGGATCTTCGGGGCTATCGCGGGATTCATC
GAAAATGGATGGGAAGGAATGGTCGATGGTTGGTACGGTTTCAGACACCAGAACTCCGAGGGGCGGGGCCA
GGCCGCAGACCTGAAGTCCACTCAGGCCGCGATTGACCAGATCAACGGAAAGCTCAACAGACTCATTGGAA
AGACCAACGAAAAGTTCCACCAAATCGAAAAGGAATTCTCCGAAGTGGAGGGCCGGGTGCAAGACCTGGAG
AAGTACGTGGAGGACACTAAGATCGACCTTTGGAGCTATAACGCAGAACTCCTTGTGGCCCTGGAAAACCA
GCACACCATCGACCTGACCGATTCAGAGATGAACAAGCTCTTTGAGAAAACTAAGAAGCAACTCCGGGAAA
ACGCTGAGGACATGGGAAATGGATGCTTTAAGATCTACCACAAGTGCGACAACGCCTGCATTGAGTCCATA
CGGAACGAAACTTACGACCATAACGTCTACCGGGATGAAGCCCTGAACAACAGATTCCAGATCAAGGGCGT
GGAGCTGAAGTCCGGCTACAAAGATTGGATCCTGTGGATTTCCTTCGCGATTTCATGCTTCTTGCTCTGCG
TGGCCCTCCTGGGATTCATAATGTGGGCCTGTCAGAAGGGCAACATTAGGTGCAACATATGCATATAA
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MRT10279   ATGAAAACCATAATCGCGCTCTCATACATACTTTGCCTGGTCTTTGCCCAAAAGATCCCT
H3_WT      ATGAAGACTATCATTGCTTTGAGCTACATTCTATGTCTGGTTTTCGCTCAAAAAATTCCT
           ***** ** ** ** **  *    ***** ** ** ***** ** ** ***** ** ***

MRT10279   GGCAACGACAACTCAACCGCGACCCTTTGCCTCGGCCATCACGCCGTGCCGAACGGCACT
H3_WT      GGAAATGACAATAGCACGGCAACGCTGTGCCTTGGGCACCATGCAGTACCAAACGGAACG
           ** ** *****    ** ** ** ** ***** ** ** ** ** ** ** ***** **

MRT10279   ATCGTCAAGACCATCACAAACGACCGCATCGAAGTGACCAACGCGACTGAGCTAGTGCAG
H3_WT      ATAGTGAAAACAATCACAAATGACCGAATTGAAGTTACTAATGCTACTGAGTTGGTTCAG
           ** ** ** ** ******** ***** ** ***** ** ** ** ****** * ** ***

MRT10279   AACTCCAGCATTGGAGAGATTTGCGATTCTCCACACCAAATCCTGGACGGAGAGAATTGT
H3_WT      AATTCCTCAATAGGTGAAATATGCGACAGTCCTCATCAGATCCTTGATGGAGAGAACTGC
           ** ***   ** ** ** ** *****   *** ** ** ***** ** ******** **

MRT10279   ACCTTGATCGACGCGCTGCTGGGGGATCCGCAGTGCGACGGATTCCAGAACAAGAAATGG
H3_WT      ACACTAATAGATGCTCTATTGGGAGACCCTCAGTGTGATGGCTTTCAAAATAAGAAATGG
           **  * ** ** ** **  **** ** ** ***** ** ** ** ** ** *********

MRT10279   GACCTTTTCGTGGAACGGAGCAAGGCATACTCGAATTGCTACCCCTACGATGTGCCCGAC
H3_WT      GACCTTTTTGTTGAACGAAGCAAAGCCTACAGCAACTGTTACCCTTATGATGTGCCGGAT
           ******** ** ***** ***** ** ***   ** ** ***** ** ******** **

MRT10279   TACGCCTCGCTGCGGTCCTTGGTCGCTTCCTCCGGGACCCTGGAATTCAAAAACGAGAGC
H3_WT      TATGCCTCCCTTAGGTCACTAGTTGCCTCATCCGGCACACTGGAGTTTAAAAATGAAAGC
           ** ***** **  ****  * ** ** ** ***** ** ***** ** ***** ** ***

MRT10279   TTTAATTGGACCGGAGTGACCCAGAATGGCACCTCGAGCGCCTGCATTCGGGGCTCCTCC
H3_WT      TTCAATTGGACTGGAGTCACTCAAAACGGAACAAGTTCTGCTTGCATAAGGGGATCTAGT
           ** ******** ***** ** ** ** ** **       ** *****  **** **

MRT10279   TCGAGCTTCTTCAGCCGCCTGAACTGGCTCACTCACCTCAACTACACCTACCCGGCACTG
H3_WT      AGTAGTTTCTTTAGTAGATTAAATTGGTTGACCCACTTAAACTACACATATCCAGCATTG
           ** ***** **  *  * ** *** * ** *** * ******** ** ** *** **
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```
MRT10279    AACGTGACCATGCCGAACAAGGAACAATTCGACAAGCTCTACATTTGGGGGGTGCATCAC
H3_WT       AACGTGACTATGCCAAACAAGGAACAATTTGACAAATTGTACATTTGGGGGGTTCACCAC
            ******** ***** ************** *****  * ************** ** ***

MRT10279    CCGGGTACCGATAAGGACCAGATCTTCCTCTACGCCCAATCCTCGGGCCGGATCACCGTG
H3_WT       CCGGGTACGGACAAGGACCAAATCTTCCTGTATGCTCAATCATCAGGAAGAATCACAGTA
            ******** ** ******** ******** ** ** ***** ** **  * ***** **

MRT10279    TCCACTAAGCGCTCGCAGCAGGCCGTGATCCCGAACATTGGAAGCAGACCCCGCATTCGC
H3_WT       TCTACCAAAAGAAGCCAACAAGCTGTAATCCCAAATATCGGATCTAGACCCAGAATAAGG
            ** ** **  *    ** ** ** ** ***** ** ** ***   ****** * **  *

MRT10279    GACATTCCATCGAGGATCTCGATCTACTGGACGATTGTCAAGCCTGGCGACATCCTCCTC
H3_WT       GATATCCCTAGCAGAATAAGCATCTATTGGACAATAGTAAAACCGGGAGACATACTTTTG
            ** ** **    ** **    ***** ***** ** ** ** ** ** ***** **  *

MRT10279    ATTAACTCCACCGGGAACCTCATCGCCCCTCGGGGTTATTTCAAGATCCGCAGCGGGAAG
H3_WT       ATTAACAGCACAGGGAATCTAATTGCTCCTAGGGGTTACTTCAAAATACGAAGTGGGAAA
            ******  *** ***** ** ** ** *** ******* ***** ** ** ** *****

MRT10279    TCCTCCATCATGAGAAGCGATGCCCCCATTGGAAAGTGCAAGTCCGAGTGTATCACACCT
H3_WT       AGCTCAATAATGAGATCAGATGCACCCATTGGCAAATGCAAGTCTGAATGCATCACTCCA
              *** ** ******   ***** ******** ** ******** ** ** ***** **

MRT10279    AACGGAAGCATTCCCAATGACAAGCCATTCCAGAACGTGAACAGAATTACCTACGGAGCT
H3_WT       AATGGAAGCATTCCCAATGACAAACCATTCCAAAATGTAAACAGGATCACATACGGGGCC
            ** ******************** ******** ** ** ***** ** ** ***** **

MRT10279    TGCCCTCGCTACGTCAAACATTCGACCCTCAAGTTGGCGACTGGAATGCGCAACGTGCCG
H3_WT       TGTCCCAGATATGTTAAGCATAGCACTCTGAAATTGGCAACAGGAATGCGAAATGTACCA
            ** **  * ** ** ** ***   ** ** ** ***** ** ******** ** ** **

MRT10279    GAGAAGCAAACCCGGGGGATCTTCGGGGCTATCGCGGGATTCATCGAAAATGGATGGGAA
H3_WT       GAGAAACAAACTAGAGGCATATTTGGCGCAATAGCGGGTTTCATAGAAAATGGTTGGGAG
            ***** *****  * ** ** ** ** ** ** ***** ***** ******** *****
```

```
MRT10279  GGAATGGTCGATGGTTGGTACGGTTTCAGACACCAGAACTCCGAGGGGCGGGGCCAGGCC
H3_WT     GGAATGGTGGATGGTTGGTACGGTTTCAGGCATCAAAATTCTGAGGGAAGAGGACAAGCA
          ******** ******************** ** ** ** ** *****  * ** ** **

MRT10279  GCAGACCTGAAGTCCACTCAGGCCGCGATTGACCAGATCAACGGAAAGCTCAACAGACTC
H3_WT     GCAGATCTCAAAAGCACTCAAGCAGCAATCGATCAAATCAATGGGAAGCTGAATAGGTTG
          ***** ** **   ****** ** ** ** ** ** ***** ** ***** ** **  *

MRT10279  ATTGGAAAGACCAACGAAAAGTTCCACCAAATCGAAAAGGAATTCTCCGAAGTGGAGGGC
H3_WT     ATCGGAAAAACCAACGAGAAATTCCATCAGATTGAAAAAGAATTCTCAGAAGTAGAAGGA
          ** ***** ******** ** ***** ** ** ***** ******** ***** ** **

MRT10279  CGGGTGCAAGACCTGGAGAAGTACGTGGAGGACACTAAGATCGACCTTTGGAGCTATAAC
H3_WT     AGAGTTCAAGACCTTGAGAAATATGTTGAGGACACTAAAATAGATCTCTGGTCATACAAC
          * ** ******** ***** ** ** *********** ** ** ** ***   ** ***

MRT10279  GCAGAACTCCTTGTGGCCCTGGAAAACCAGCACACCATCGACCTGACCGATTCAGAGATG
H3_WT     GCGGAGCTTCTTGTTGCCCTGGAGAACCAACATACAATTGATCTAACTGACTCAGAAATG
          ** ** ** ***** ******** ***** ** ** ** ** ** ** ** ***** ***

MRT10279  AACAAGCTCTTTGAGAAAACTAAGAAGCAACTCCGGGAAAACGCTGAGGACATGGGAAAT
H3_WT     AACAAACTGTTTGAAAAAACAAAGAAGCAACTGAGGGAAAATGCTGAGGATATGGGAAAT
          ***** ** ***** ***** ***********  ******* ******** *********

MRT10279  GGATGCTTTAAGATCTACCACAAGTGCGACAACGCCTGCATTGAGTCCATACGGAACGAA
H3_WT     GGTTGTTTCAAAATATACCACAAATGTGACAATGCCTGCATAGAATCAATAAGAAATGAA
          ** ** ** ** ** ******** ** ***** ******** ** ** *** * ** ***

MRT10279  ACTTACGACCATAACGTCTACCGGGATGAAGCCCTGAACAACAGATTCCAGATCAAGGGC
H3_WT     ACTTATGACCACAATGTGTACAGGGATGAAGCATTGAACAACCGGTTCCAGATCAAGGGA
          ***** ***** ** ** *** **********  ******** * **************
```

```
MRT10279  GTGGAGCTGAAGTCCGGCTACAAAGATTGGATCCTGTGGATTTCCTTCGCGATTTCATGC
H3_WT     GTTGAGCTGAAGTCAGGATACAAAGATTGGATCCTATGGATTTCCTTTGCCATATCATGT
          ** *********** ** ***************** *********** ** ** *****

MRT10279  TTCTTGCTCTGCGTGGCCCTCCTGGGATTCATAATGTGGGCCTGTCAGAAGGGCAACATT
H3_WT     TTTTTGCTTTGTGTTGCTTTGTTGGGGTTCATCATGTGGGCCTGCCAAAAGGGCAACATT
          ** ***** ** ** **   *  **** ***** *********** ** ************

MRT10279  AGGTGCAACATATGCATATAA (SEQ ID NO:2)
H3_WT     AGATGCAACATTTGCATTTGA (SEQ ID NO:3)
          ** ******** ***** * *
```

FIG. 5A

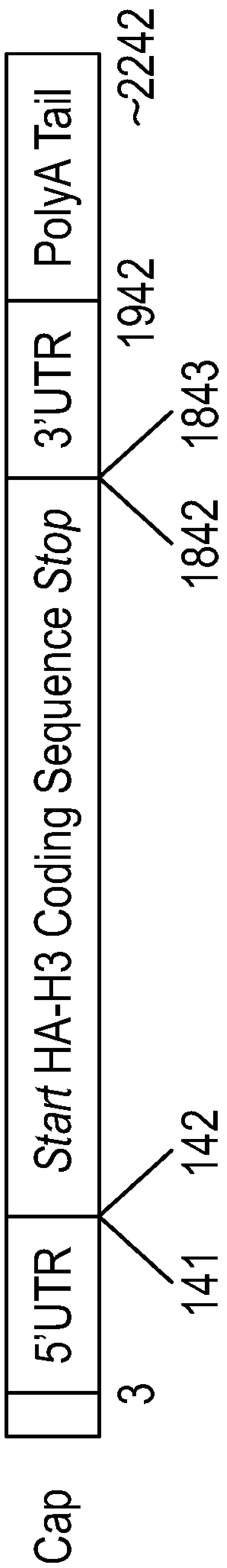

Cap
3
5'UTR
141
142
Start HA-H3 Coding Sequence *Stop*
1842
1843
3'UTR
1942
PolyA Tail
~2242

FIG. 5B

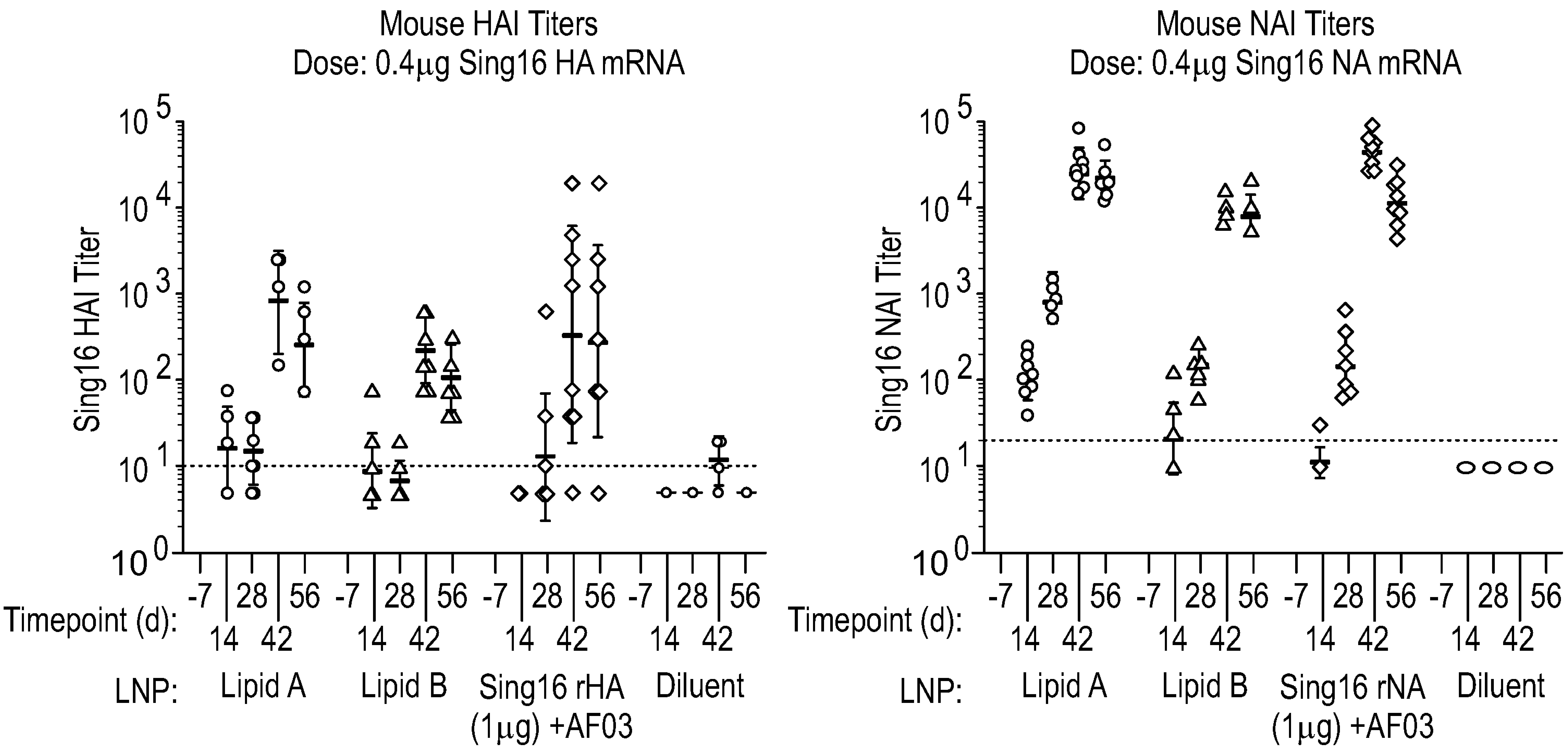
5'UTR
GGACAGAUCGCCUGGAGACGCCAUCCACGCUGUUUUGACCUCCAUAGAAGACACCGGGACCGAUCCAGCCUCCGCG
GCCGGGAACGGUGCAUUGGAACGCGGAUUCCCCGUGCCAAGAGUGACUCACCGUCCUUGACACG
CDS (coding Sequence)
AUGAAAACCAUAAUCGCGCUCUCAUACAUACUUUGCCUGGUCUUUGCCCAAAAGAUCCCUGGCAAC
GACAACUCAACCGCGACCCUUUGCCUCGGCCAUCACGCCGUGCCGAACGGCACUAUCGUCAAGACC
AUCACAAACGACCGCAUCGAAGUGACCAACGCGACUGAGCUAGUGCAGAACUCCAGCAUUGGAGAG
AUUUGCGAUUCUCCACACCAAAUCCUGGACGGAGAGAAUUGUACCUUGAUCGACGCGCUGCUGGGG
GAUCCGCAGUGCGACGGAUUCCAGAACAAGAAAUGGGACCUUUUCGUGGAACGGAGCAAGGCAUAC
UCGAAUUGCUACCCCUACGAUGUGCCCGACUACGCCUCGCUGCGGUCCUUGGUCGCUUCCUCCGGG
ACCCUGGAAUUCAAAAACGAGAGCUUUAAUUGGACCGGAGUGACCCAGAAUGGCACCUCGAGCGCC
UGCAUUCGGGGCUCCUCCUCGAGCUUCUUCAGCCGCCUGAACUGGCUCACUCACCUCAACUACACC
UACCCGGCACUGAACGUGACCAUGCCGAACAAGGAACAAUUCGACAAGCUCUACAUUUGGGGGGUG
CAUCACCCGGGUACCGAUAAGGACCAGAUCUUCCUCUACGCCCAAUCCUCGGGCCGGAUCACCGUG
UCCACUAAGCGCUCGCAGCAGGCCGUGAUCCCGAACAUUGGAAGCAGACCCCGCAUUCGCGACAUU
CCAUCGAGGAUCUCGAUCUACUGGACGAUUGUCAAGCCUGGCGACAUCCUCCUCAUUAACUCCACC
GGGAACCUCAUCGCCCCUCGGGGUUAUUUCAAGAUCCGCAGCGGGAAGUCCUCCAUCAUGAGAAGC
GAUGCCCCCAUUGGAAAGUGCAAGUCCGAGUGUAUCACACCUAACGGAAGCAUUCCCAAUGACAAG
CCAUUCCAGAACGUGAACAGAAUUACCUACGGAGCUUGCCCUCGCUACGUCAAACAUUCGACCCUC
AAGUUGGCGACUGGAAUGCGCAACGUGCCGGAGAAGCAAACCCGGGGGAUCUUCGGGGCUAUCGCG
GGAUUCAUCGAAAAUGGAUGGGAAGGAAUGGUCGAUGGUUGGUACGGUUUCAGACACCAGAACUCC
GAGGGGCGGGGCCAGGCCGCAGACCUGAAGUCCACUCAGGCCGCGAUUGACCAGAUCAACGGAAAG
CUCAACAGACUCAUUGGAAAGACCAACGAAAAGUUCCACCAAAUCGAAAAGGAAUUCUCCGAAGUG
GAGGGCCGGGUGCAAGACCUGGAGAAGUACGUGGAGGACACUAAGAUCGACCUUUGGAGCUAUAAC
GCAGAACUCCUUGUGGCCCUGGAAAACCAGCACACCAUCGACCUGACCGAUUCAGAGAUGAACAAG
CUCUUUGAGAAAACUAAGAAGCAACUCCGGGAAAACGCUGAGGACAUGGGAAAUGGAUGCUUUAAG
AUCUACCACAAGUGCGACAACGCCUGCAUUGAGUCCAUACGGAACGAAACUUACGACCAUAACGUC
UACCGGGAUGAAGCCCUGAACAACAGAUUCCAGAUCAAGGGCGUGGAGCUGAAGUCCGGCUACAAA
GAUUGGAUCCUGUGGAUUUCCUUCGCGAUUUCAUGCUUCUUGCUCUGCGUGGCCCUCCUGGGAUUC
AUAAUGUGGGCCUGUCAGAAGGGCAACAUUAGGUGCAACAUAUGCAUAUAA

3'UTR
CGGGUGGCAUCCCUGUGACCCCUCCCCAGUGCCUCUCCUGGCCCUGGAAGUUGCCACUCCAGUGCC
CACCAGCCUUGUCCUAAUAAAAUUAAGUUGCAUC

+ Poly A Tail

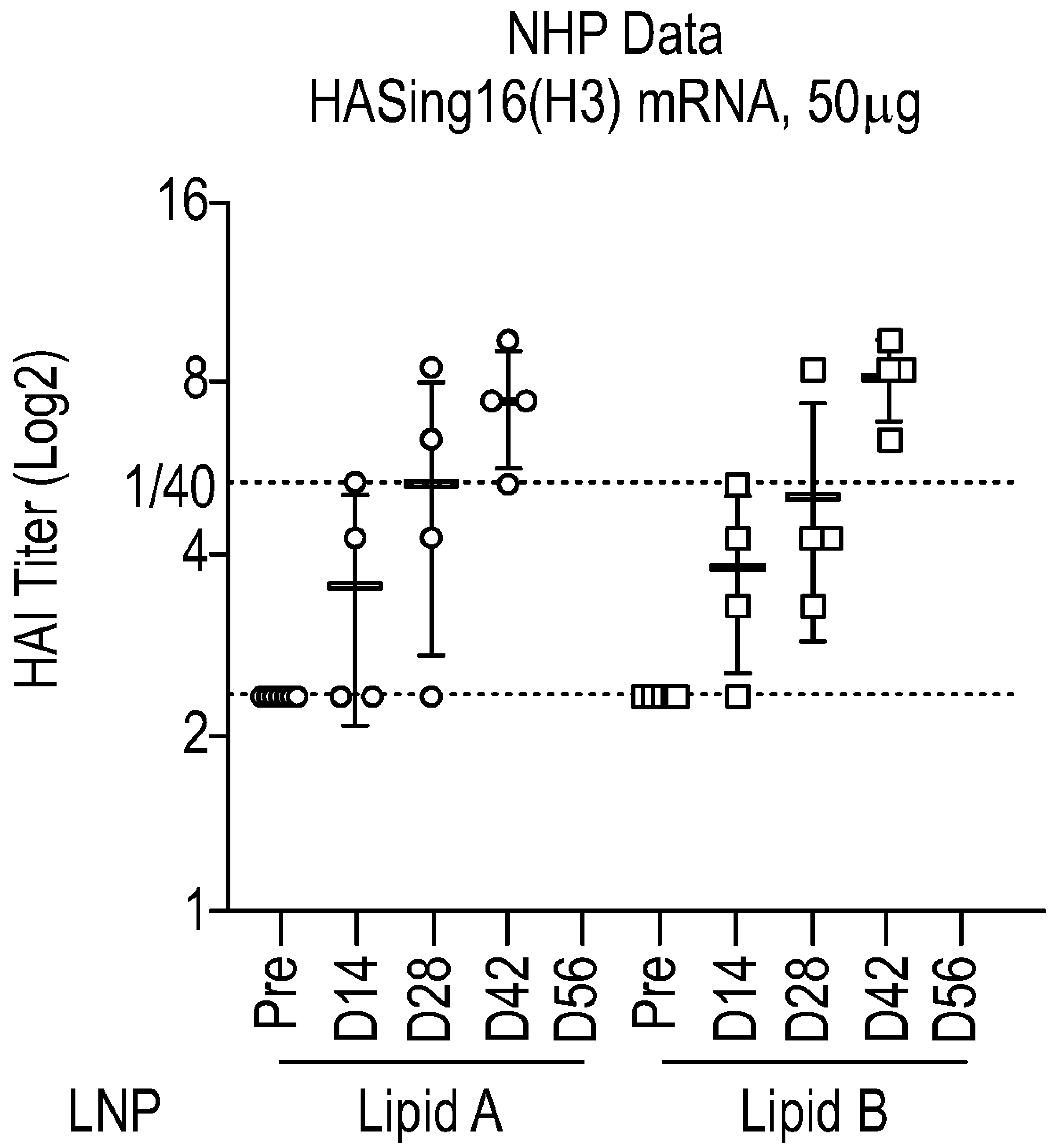
(SEQ ID N0:4)

FIG. 5C



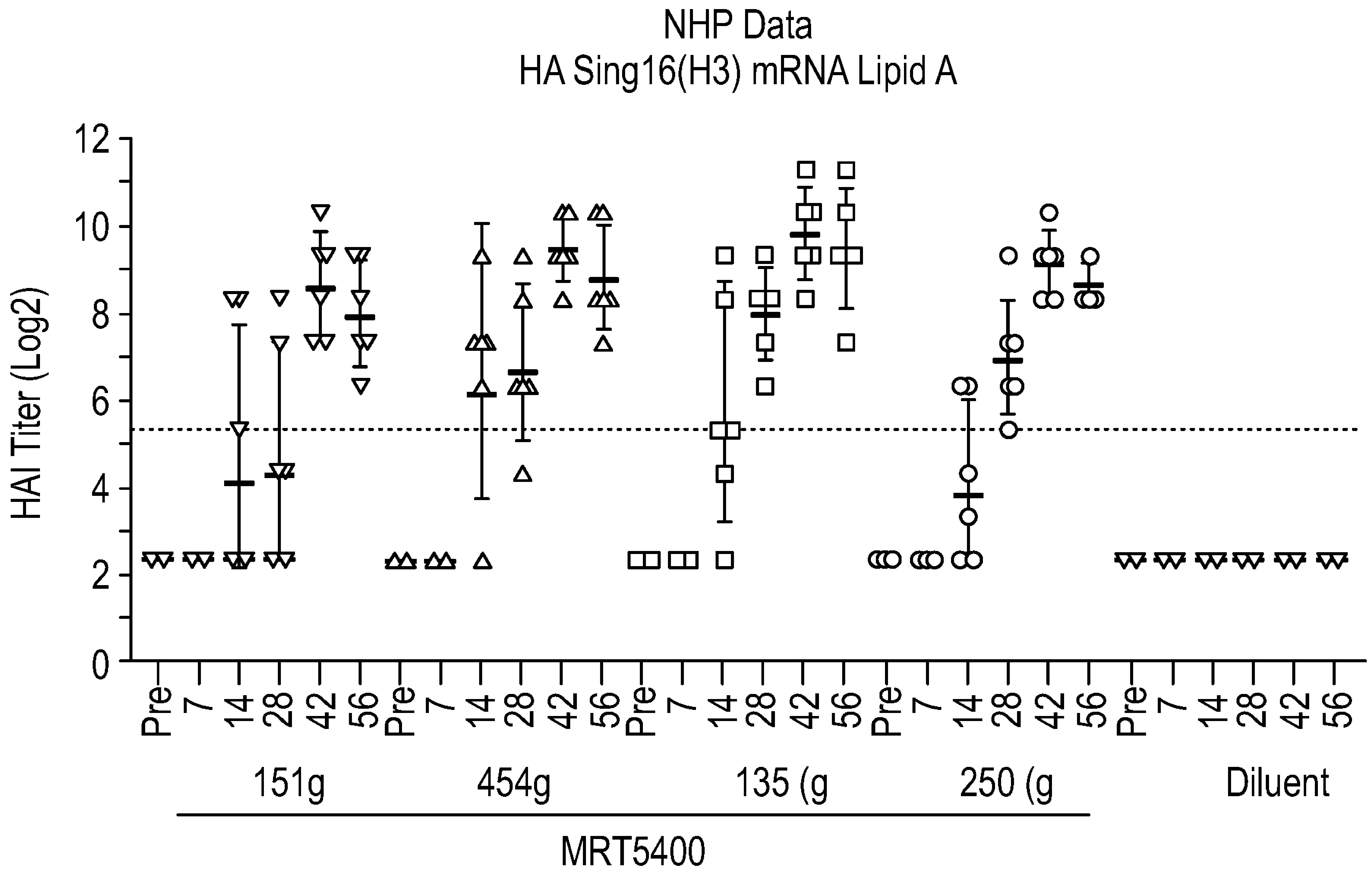
Lipid	Composition (Molar Ratio)
Lipid A	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30
Lipid B	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30

FIG. 6



Lipid	Composition (Molar Ratio)
Lipid A	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30
Lipid B	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30

FIG. 7A



Lipid	Composition (Molar Ratio)
Lipid A	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30

FIG. 7B

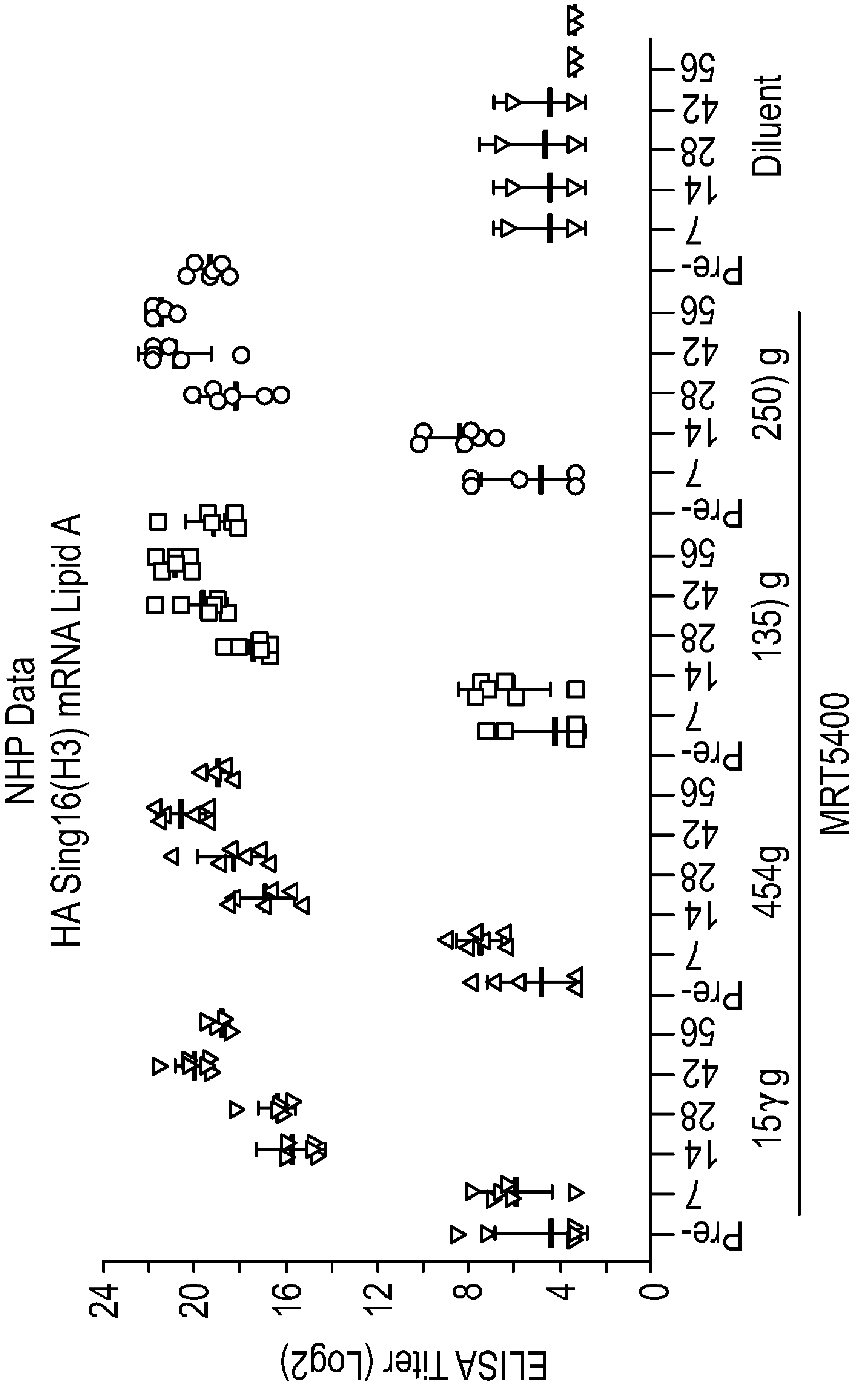
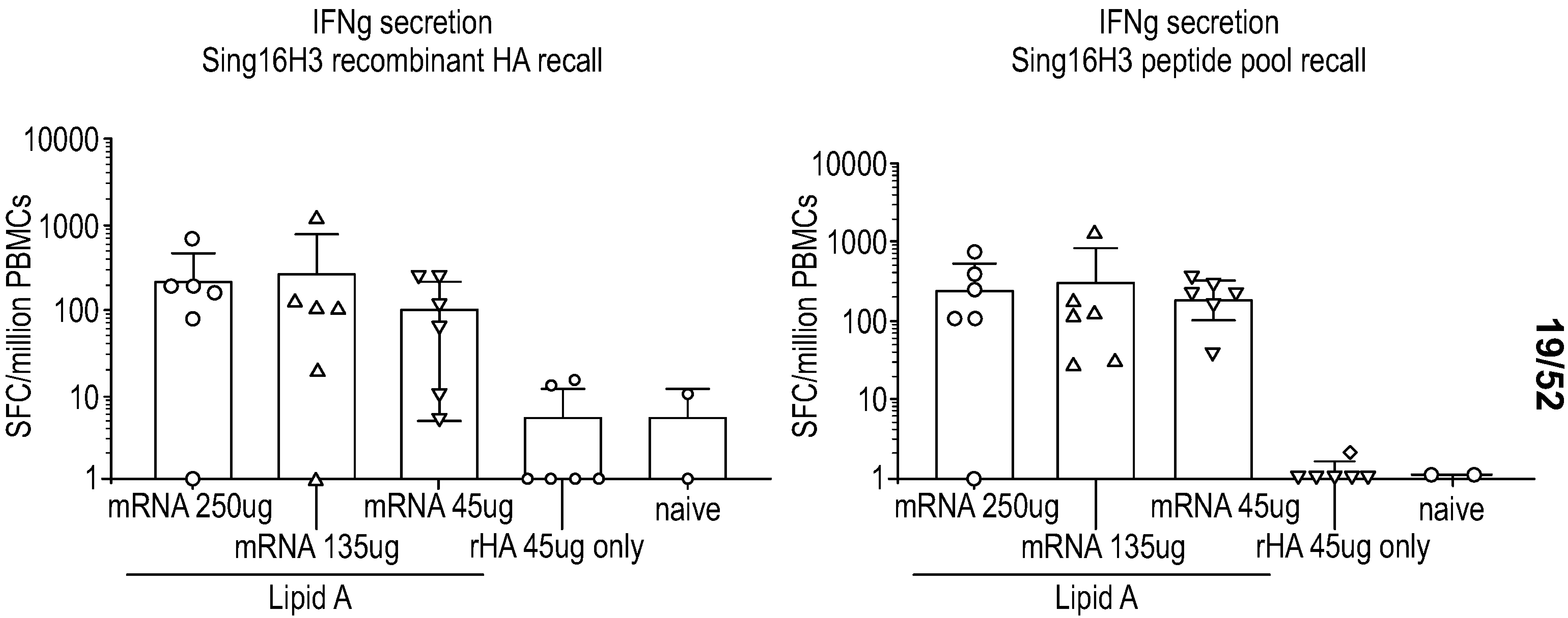
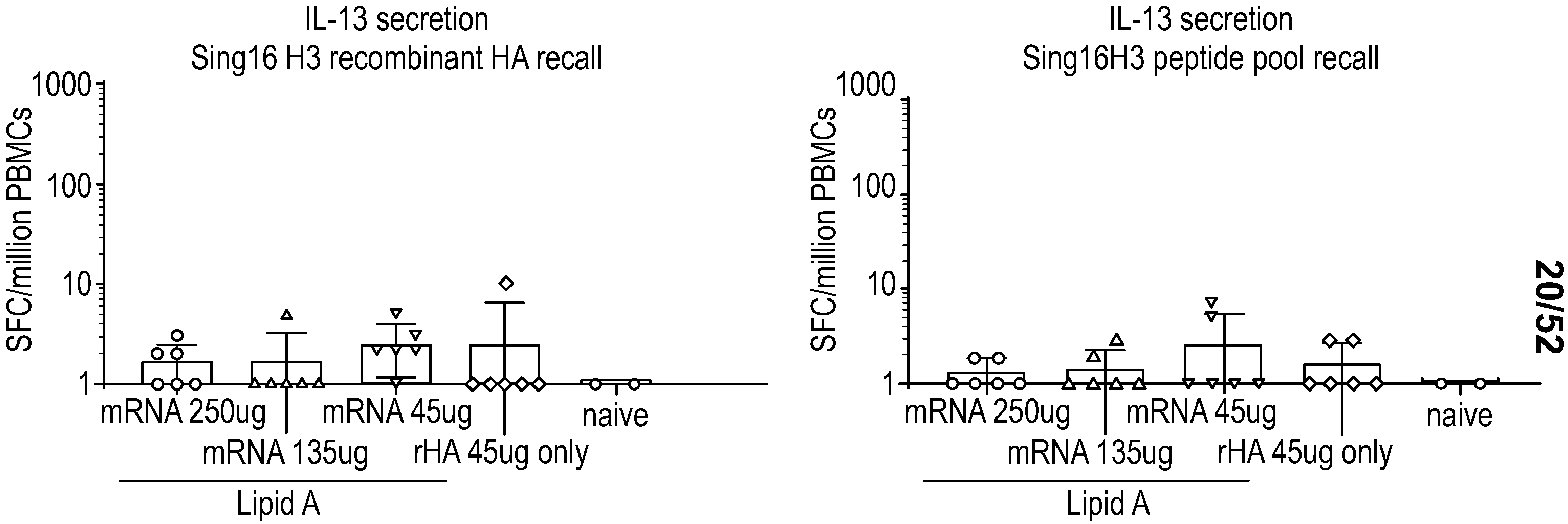

NHP Data
HA Sing16(H3) mRNA Lipid A
ELISA Titer (Log2)
0
4
8
12
16
20
24
Pre-
7
14
28
42
56
Pre-
7
14
28
42
56
Pre-
7
14
28
42
56
Pre-
7
14
28
42
56
Pre-
7
14
28
42
56
15γg
454g
135) g
250) g
Diluent
MRT5400

FIG. 7C



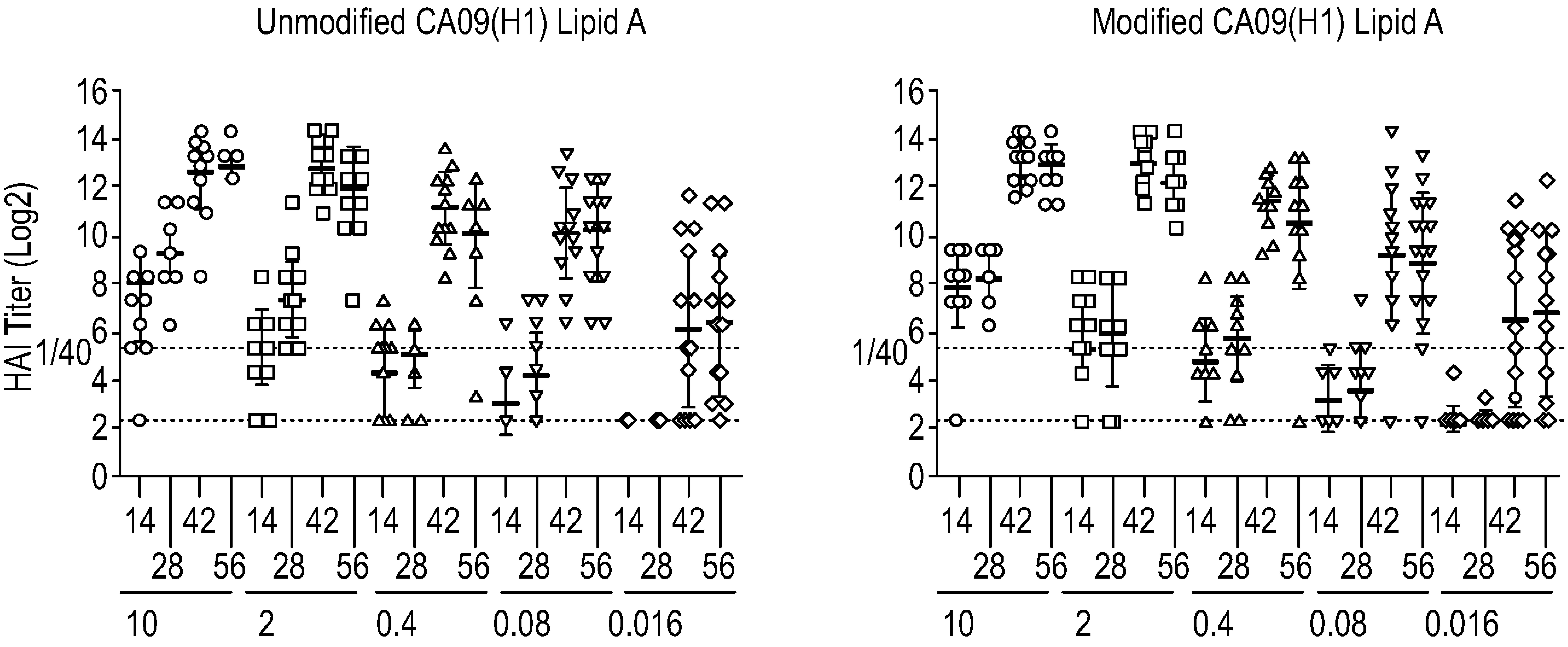
Lipid	Composition (Molar Ratio)
Lipid A	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30

FIG. 8A



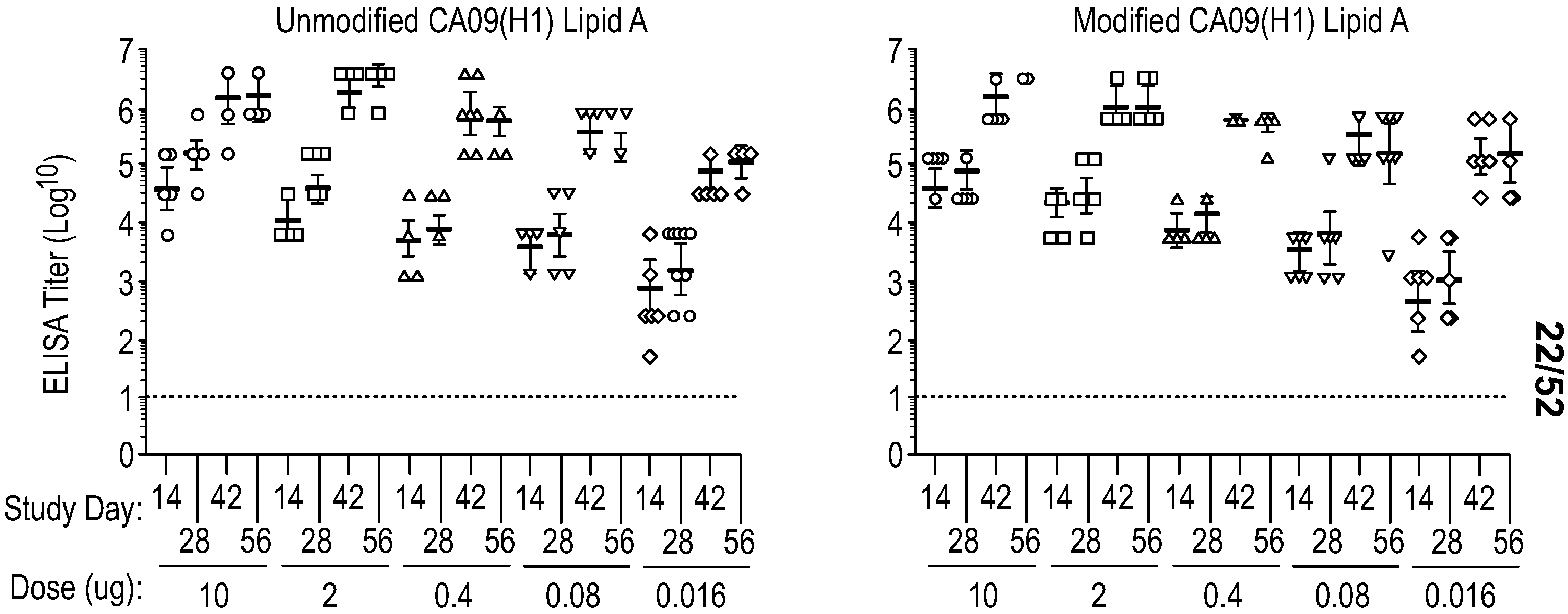
Lipid	Composition (Molar Ratio)
Lipid A	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30

FIG. 8B



Lipid	Composition (Molar Ratio)
Lipid A	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30

FIG. 9A



Unmodified CA09(H1) Lipid A

Modified CA09(H1) Lipid A

Lipid	Composition (Molar Ratio)
Lipid A	Cationic lipid : DMG-PEG2000: Cholestrol: DOPE 40:1.5:28.5:30

FIG. 9B

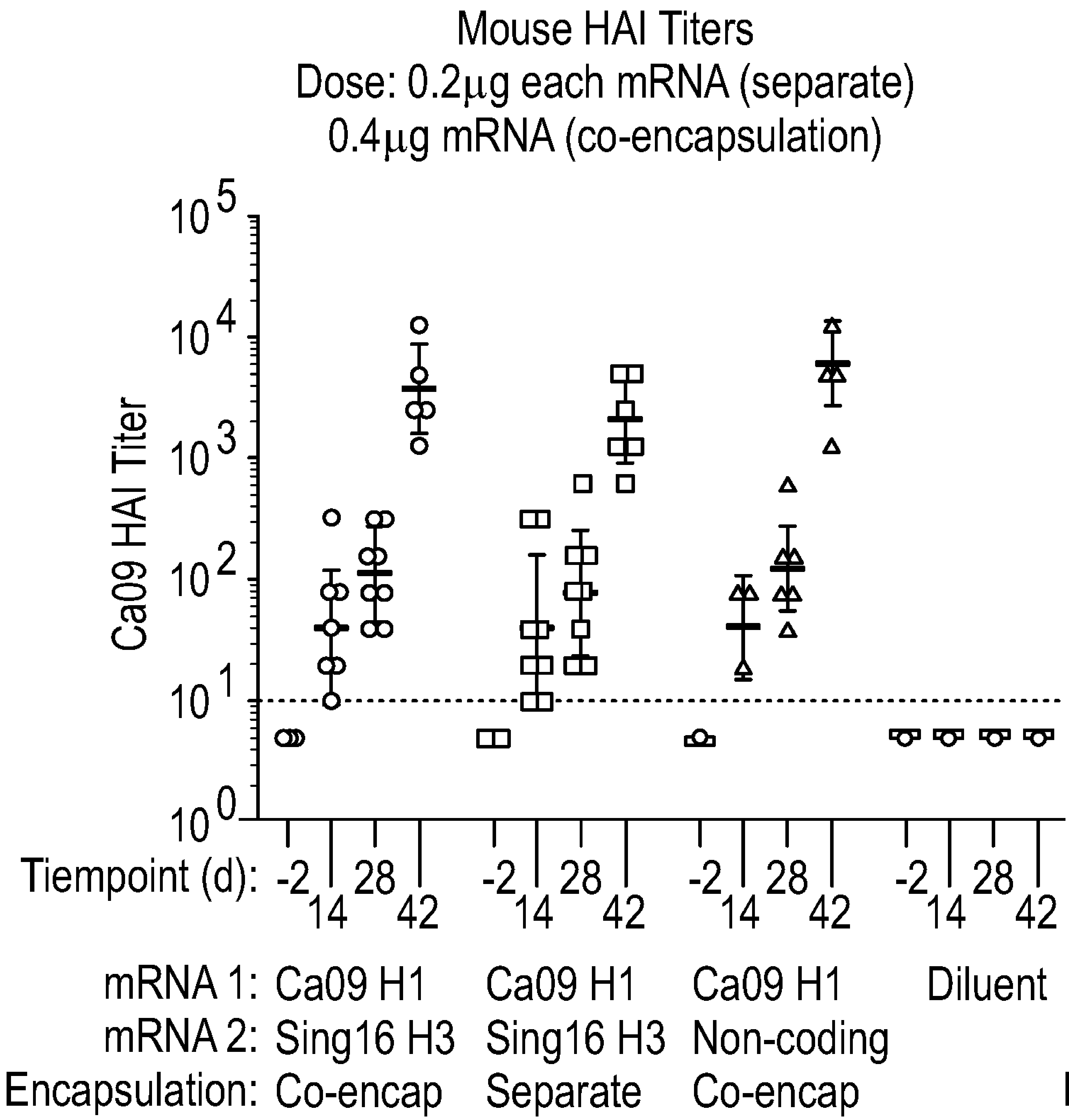


FIG. 10A

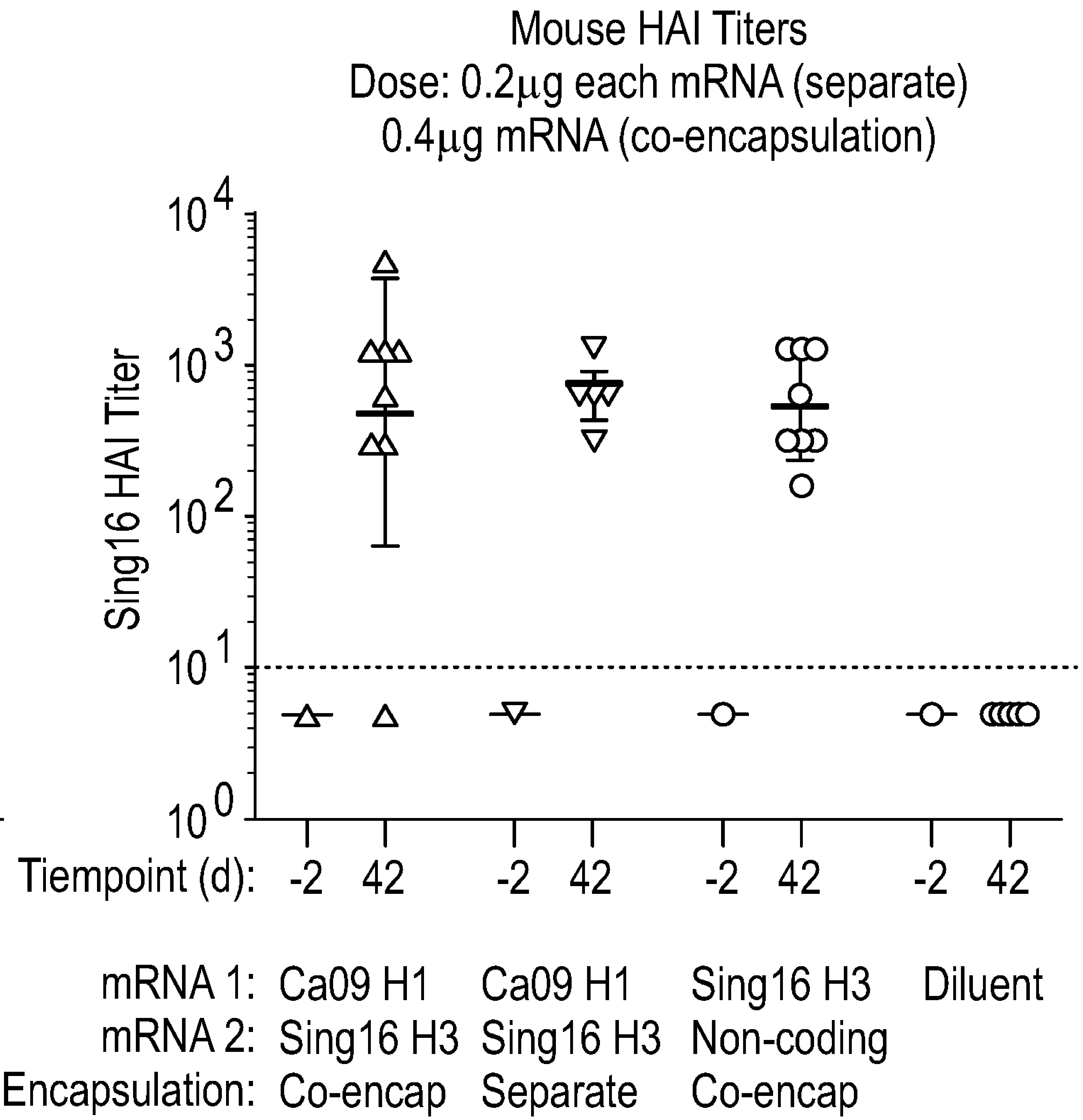


FIG. 10B

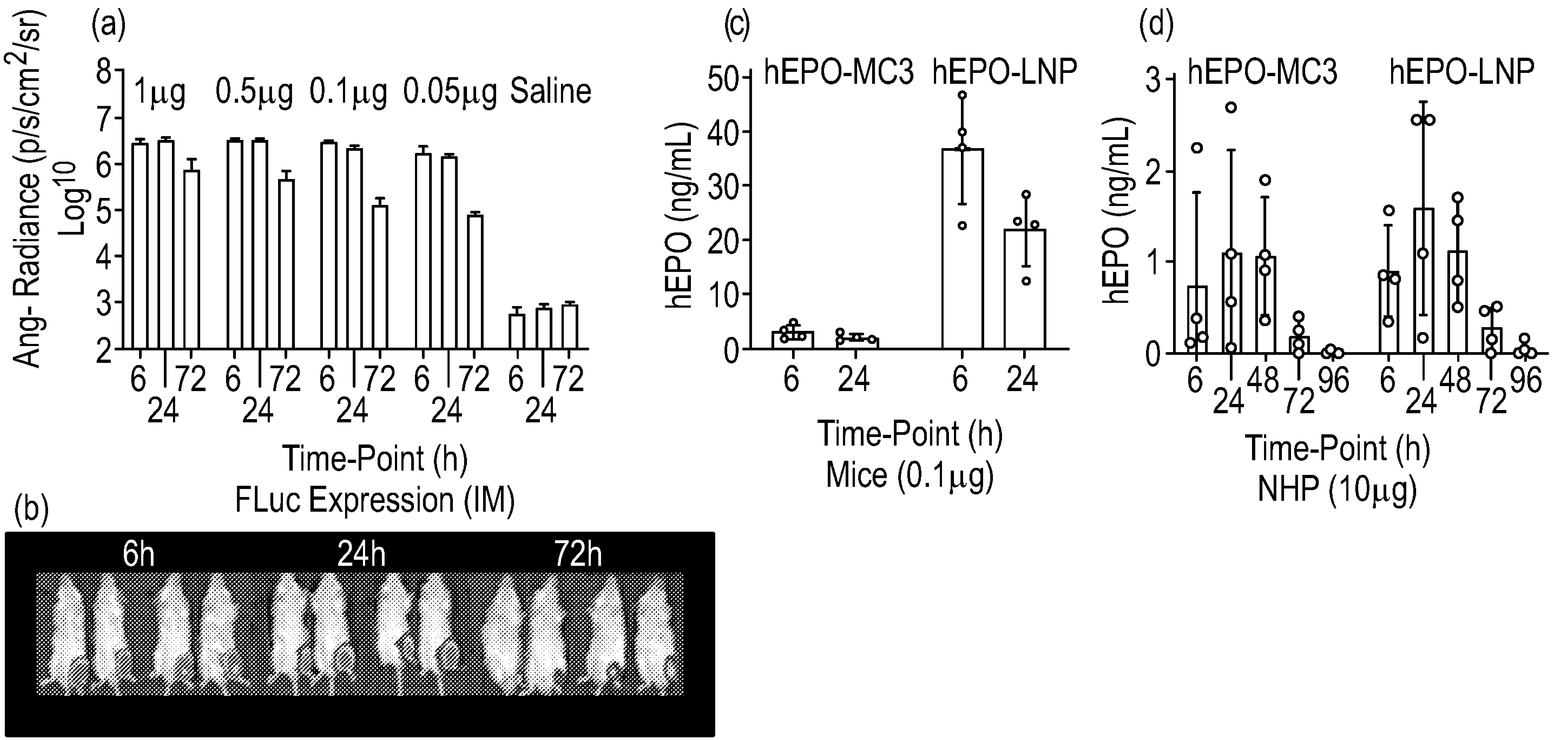

(a)
Ang- Radiance (p/s/cm2/sr) Log10
8
7
6
5
4
3
2
1μg
0.5μg
0.1μg
0.05μg
Saline
6
24
72
Time-Point (h)
FLuc Expression (IM)
(b)
6h
24h
72h
(c)
hEPO (ng/mL)
50
40
30
20
10
0
hEPO-MC3
hEPO-LNP
6
24
Time-Point (h)
Mice (0.1μg)
(d)
hEPO (ng/mL)
3
2
1
0
hEPO-MC3
hEPO-LNP
6
24
48
72
96
Time-Point (h)
NHP (10μg)

FIG. 11

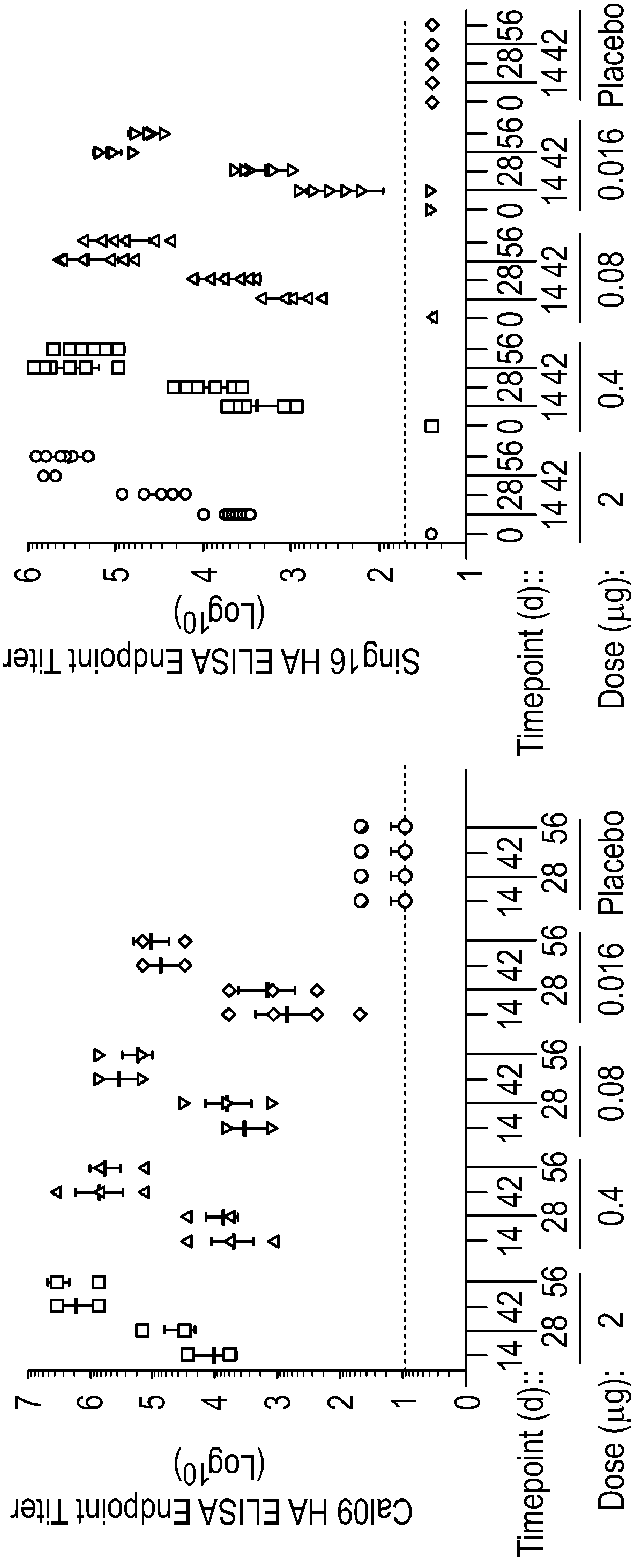

Sing16 HA ELISA Endpoint Titer
(Log10)
1
2
3
4
5
6
Timepoint (d)::
0
14
28
42
56
0
14
28
42
56
0
14
28
42
56
0
14
28
42
56
0
14
28
42
56
Dose (μg):
2
0.4
0.08
0.016
Placebo
Cal09 HA ELISA Endpoint Titer
(Log10)
0
1
2
3
4
5
6
7
Timepoint (d)::
14
28
42
56
14
28
42
56
14
28
42
56
14
28
42
56
14
28
42
56
Dose (μg):
2
0.4
0.08
0.016
Placebo

FIG. 12

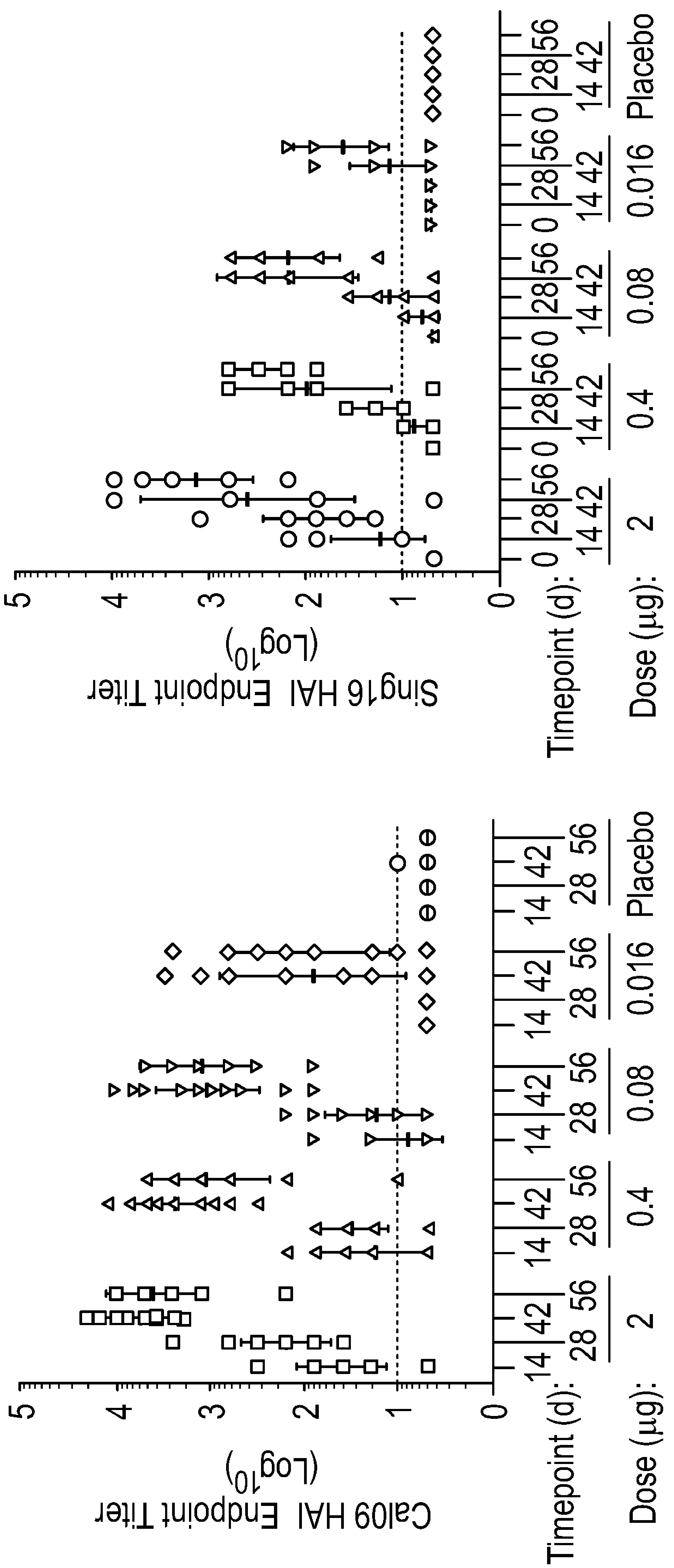

Cal09 HAI Endpoint Titer
(Log10)
0
1
2
3
4
5
Timepoint (d):
14
28
42
56
Dose (μg):
2
0.4
0.08
0.016
Placebo
Sing16 HAI Endpoint Titer
(Log10)
0
1
2
3
4
5
Timepoint (d):
0
14
28
42
56
Dose (μg):
2
0.4
0.08
0.016
Placebo

FIG. 13

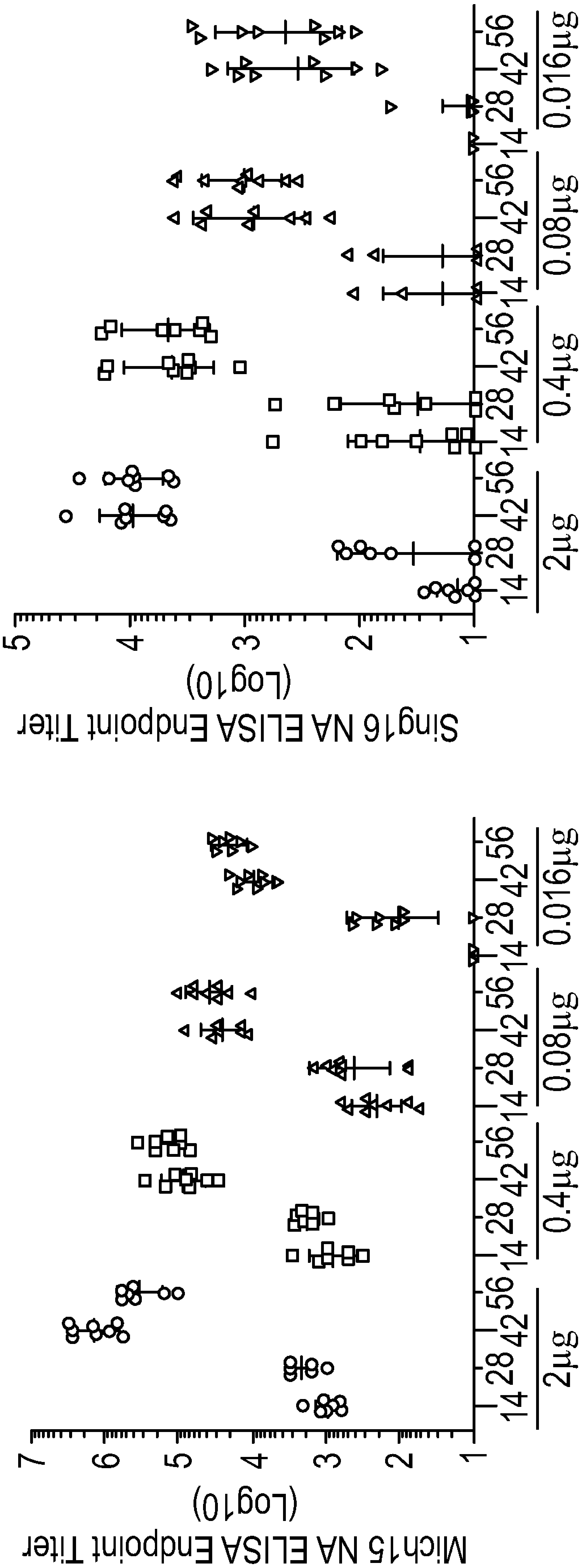

Sing16 NA ELISA Endpoint Titer (Log10)
1
2
3
4
5
14
28
42
56
2µg
0.4µg
0.08µg
0.016µg
Mich15 NA ELISA Endpoint Titer (Log10)
1
2
3
4
5
6
7

FIG. 14

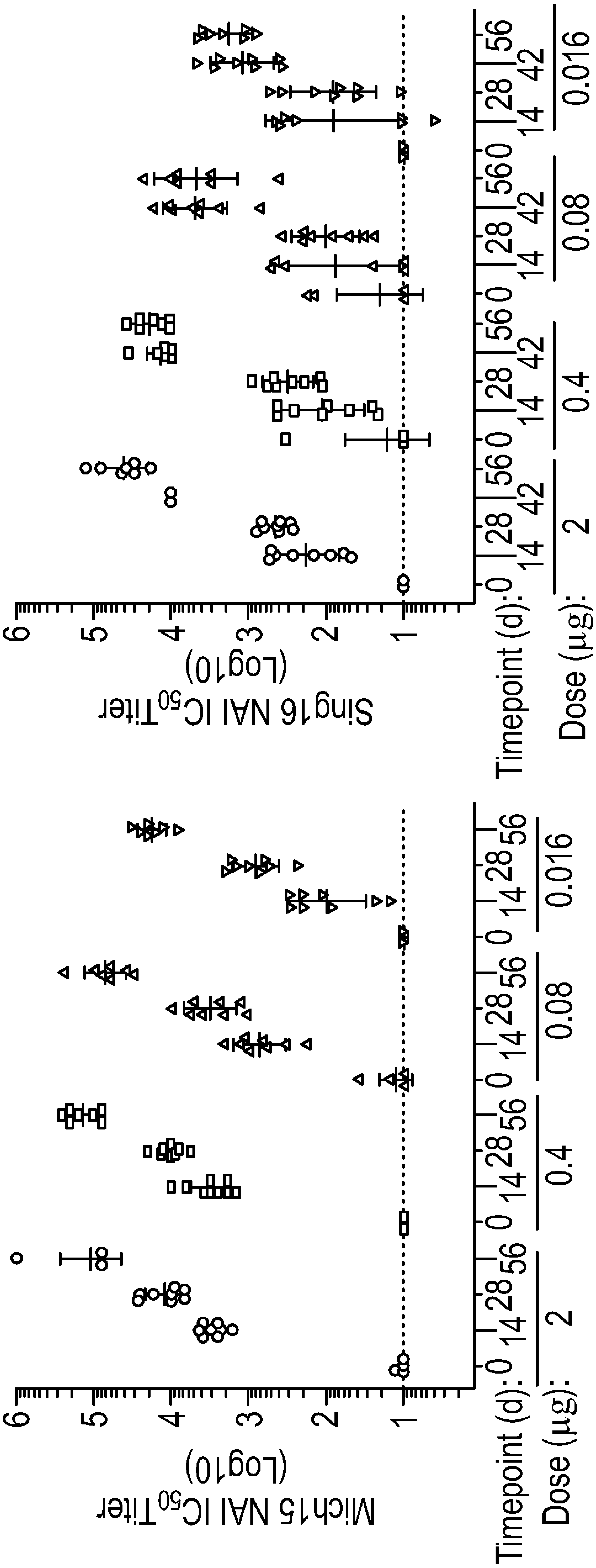

Sing16 NAI IC50 Titer (Log10)
6
5
4
3
2
1
Timepoint (d):
0
14
28
42
56
0
14
28
42
56
0
14
28
42
56
0
14
28
42
56
Dose (µg):
2
0.4
0.08
0.016
Mich15 NAI IC50 Titer (Log10)
6
5
4
3
2
1
Timepoint (d):
0
14
28
56
0
14
28
56
0
14
28
56
0
14
28
56
Dose (µg):
2
0.4
0.08
0.016

FIG. 15

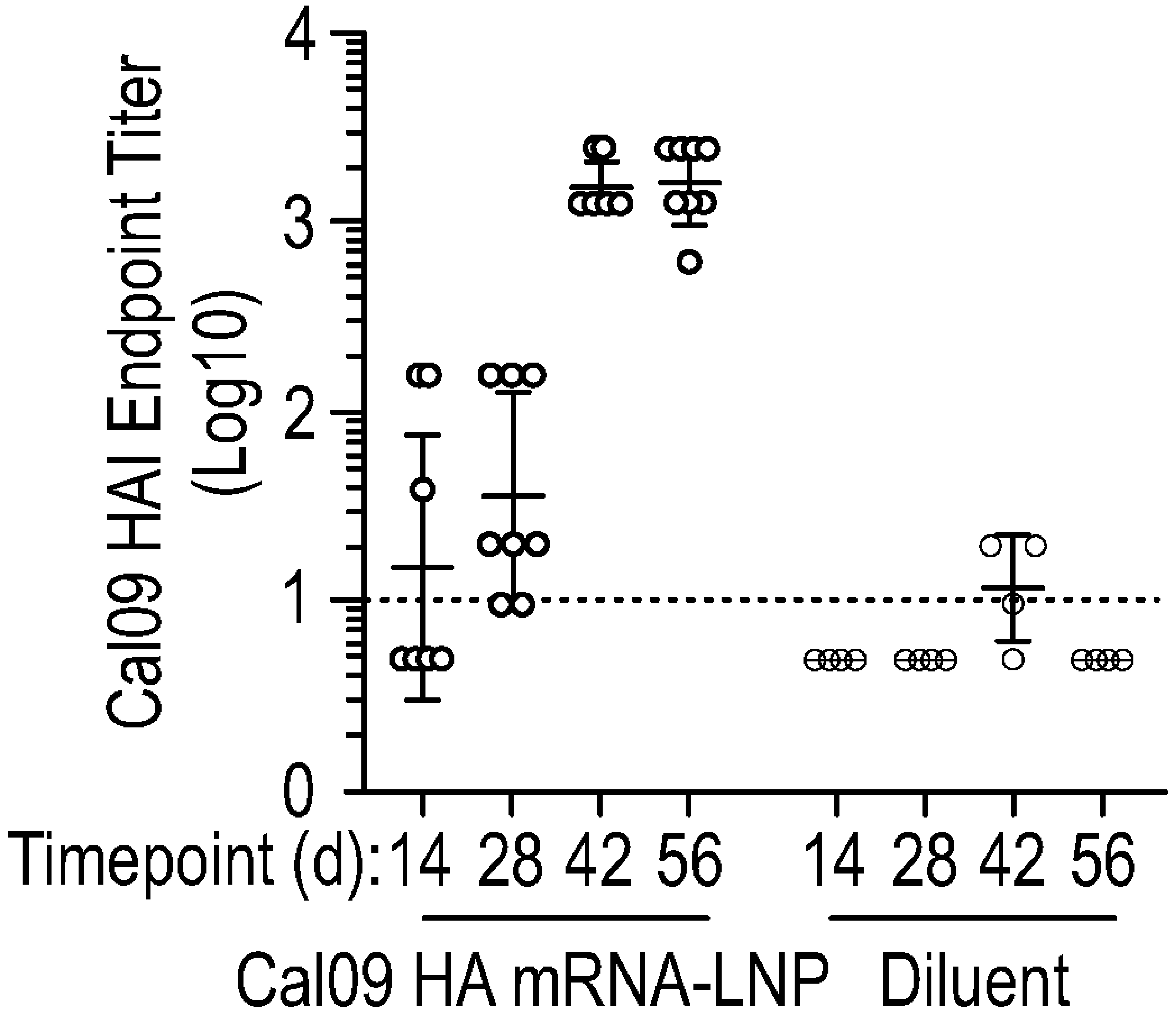


FIG. 16A

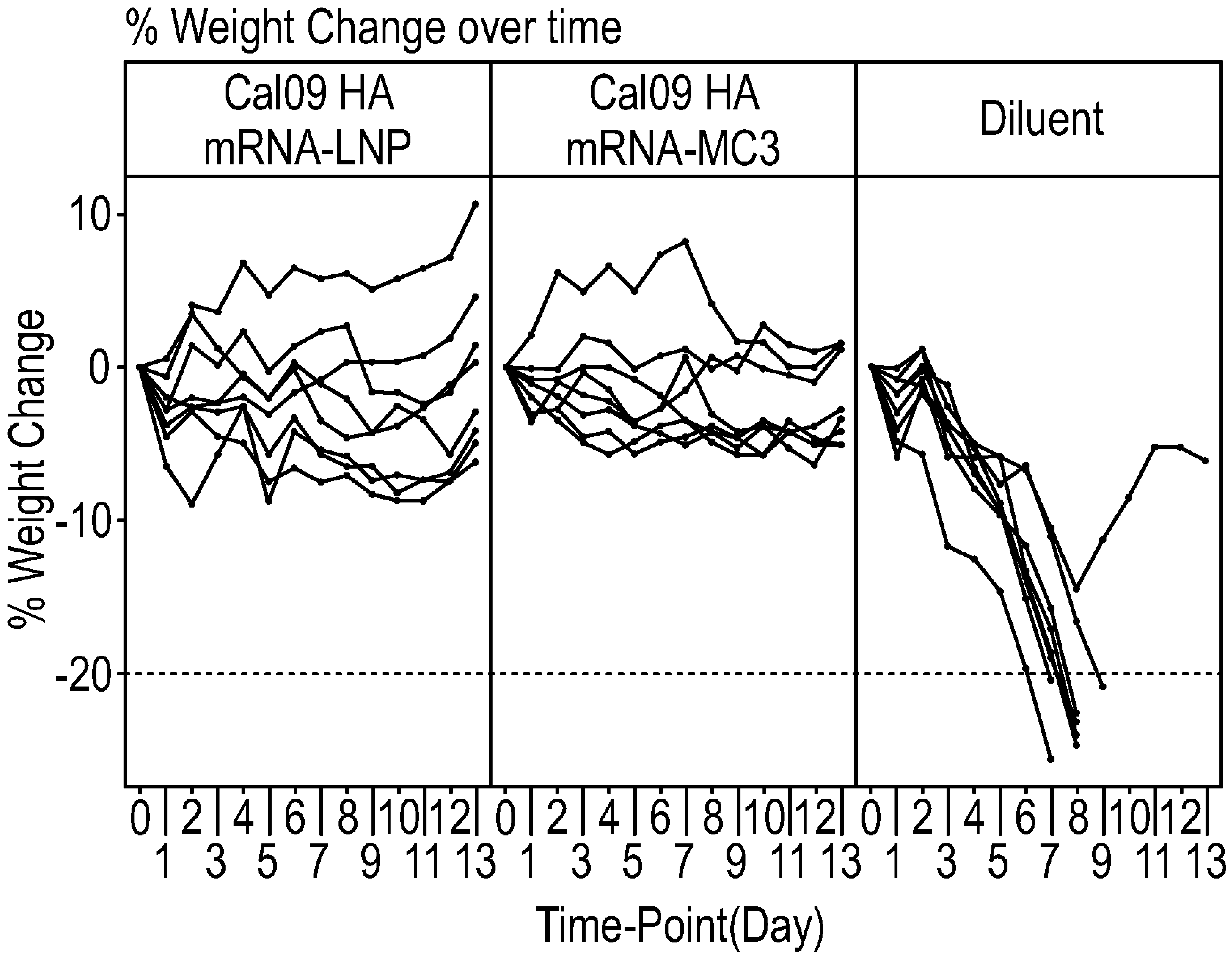


FIG. 16B

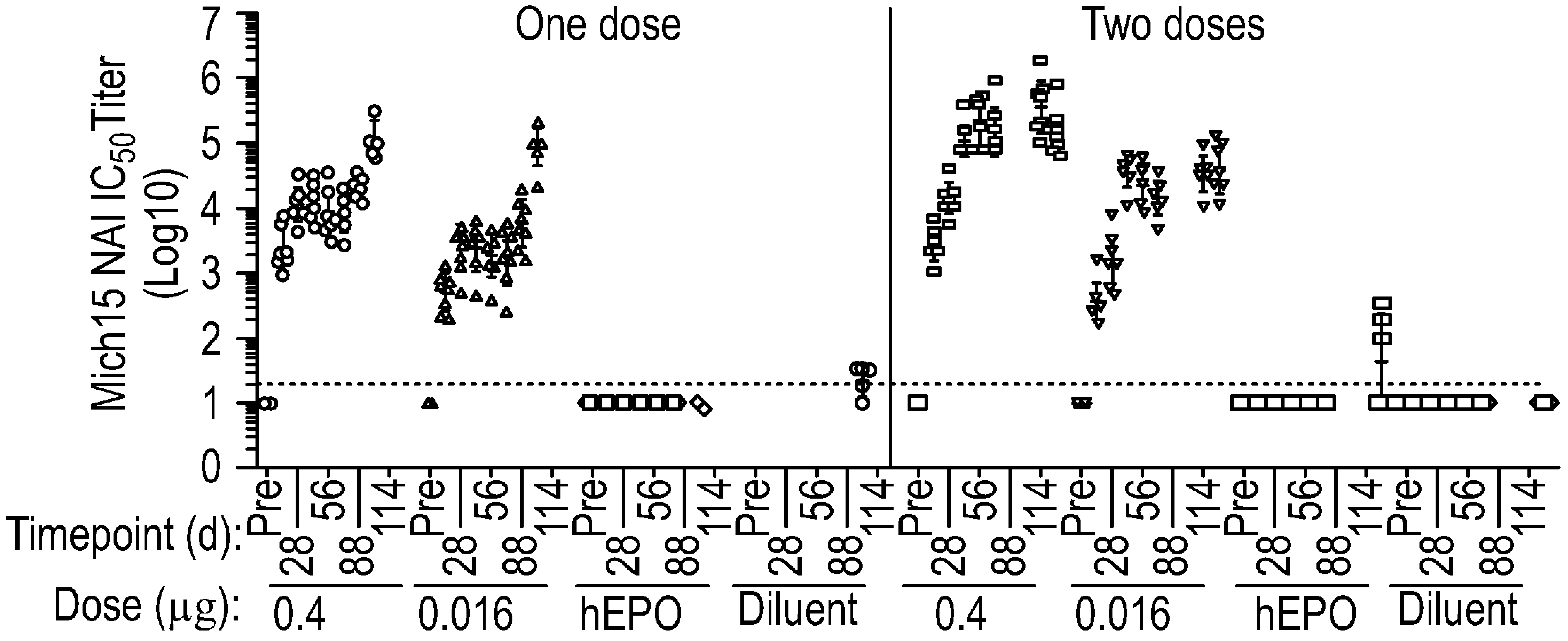

One dose
Two doses
Mich15 NAI IC_{50} Titer (Log10)
7
6
5
4
3
2
1
0
Timepoint (d):
Pre
28
56
88
114
Pre
28
56
88
114
Pre
28
56
88
114
Pre
28
56
88
114
Pre
28
56
88
114
Pre
28
56
88
114
Pre
28
56
88
114
Pre
28
56
88
114
Dose (μg):
0.4
0.016
hEPO
Diluent
0.4
0.016
hEPO
Diluent

FIG. 17A

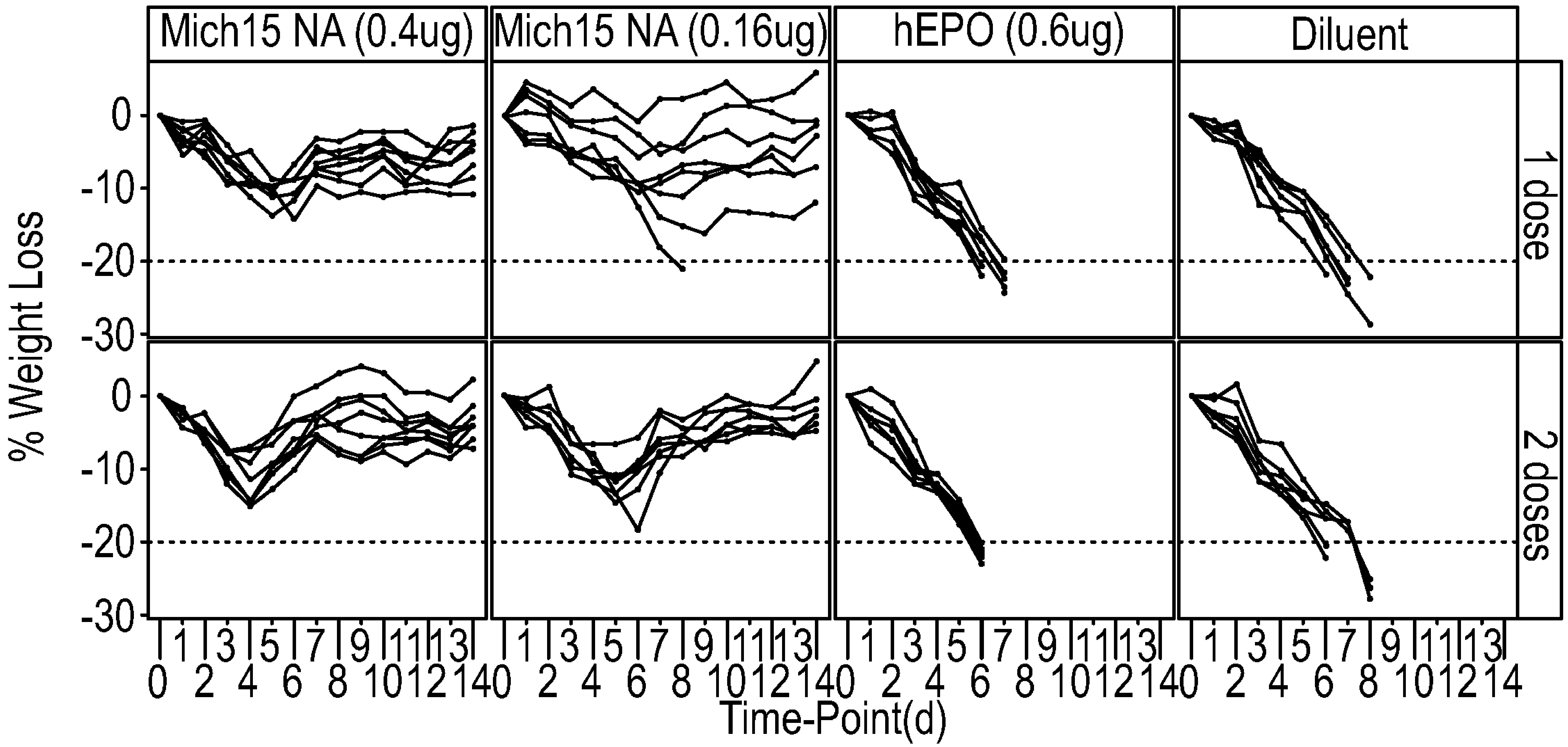

Mich15 NA (0.4ug)
Mich15 NA (0.16ug)
hEPO (0.6ug)
Diluent
1 dose
2 doses
% Weight Loss
0
-10
-20
-30
Time-Point(d)
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14

FIG. 17B

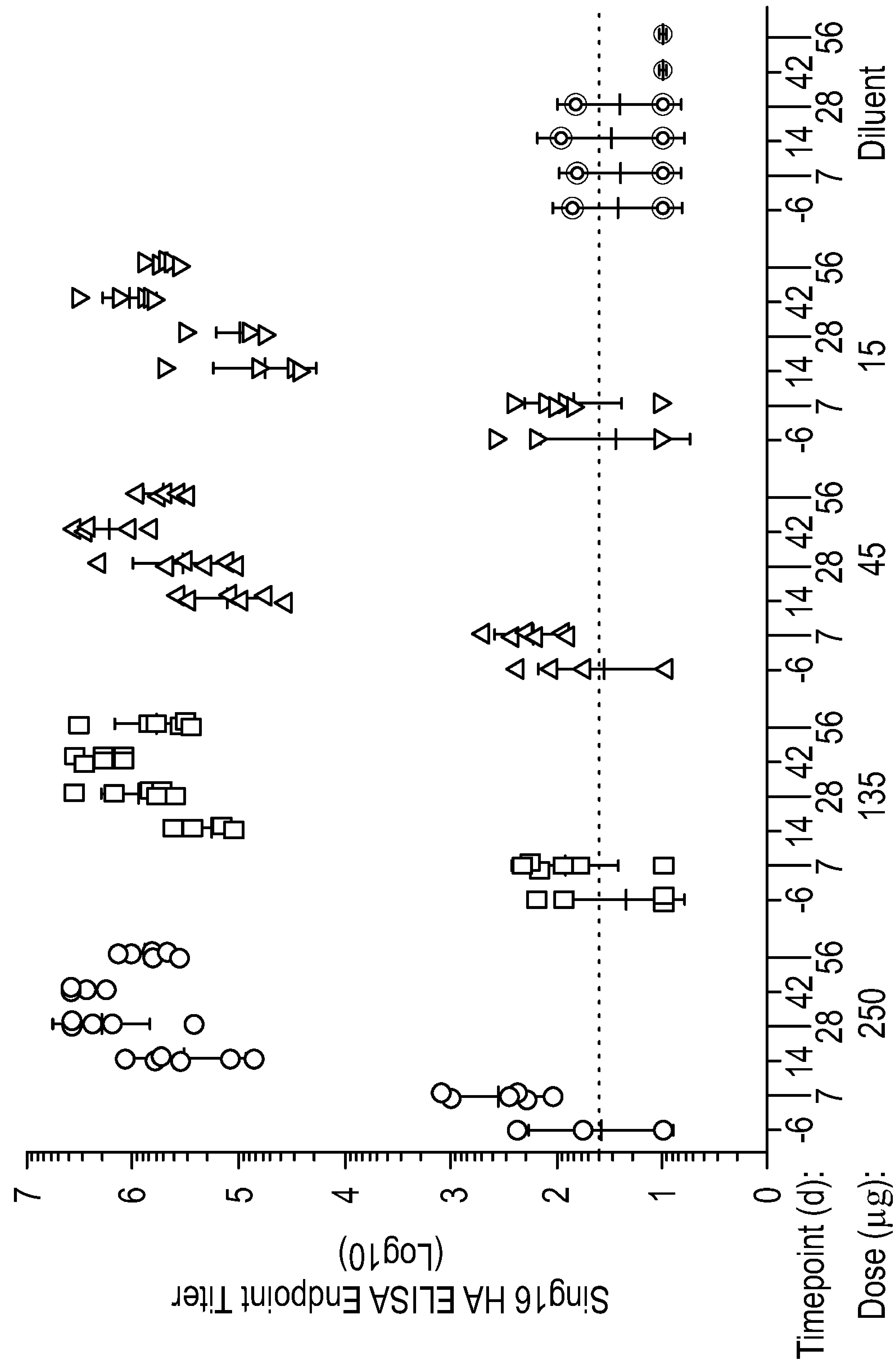

Sing16 HA ELISA Endpoint Titer
(Log10)
0
1
2
3
4
5
6
7
Timepoint (d):
Dose (μg):
-6
7
14
28
42
56
250
-6
7
14
28
42
56
135
-6
7
14
28
42
56
45
-6
7
14
28
42
56
15
-6
7
14
28
42
56
Diluent

FIG. 18

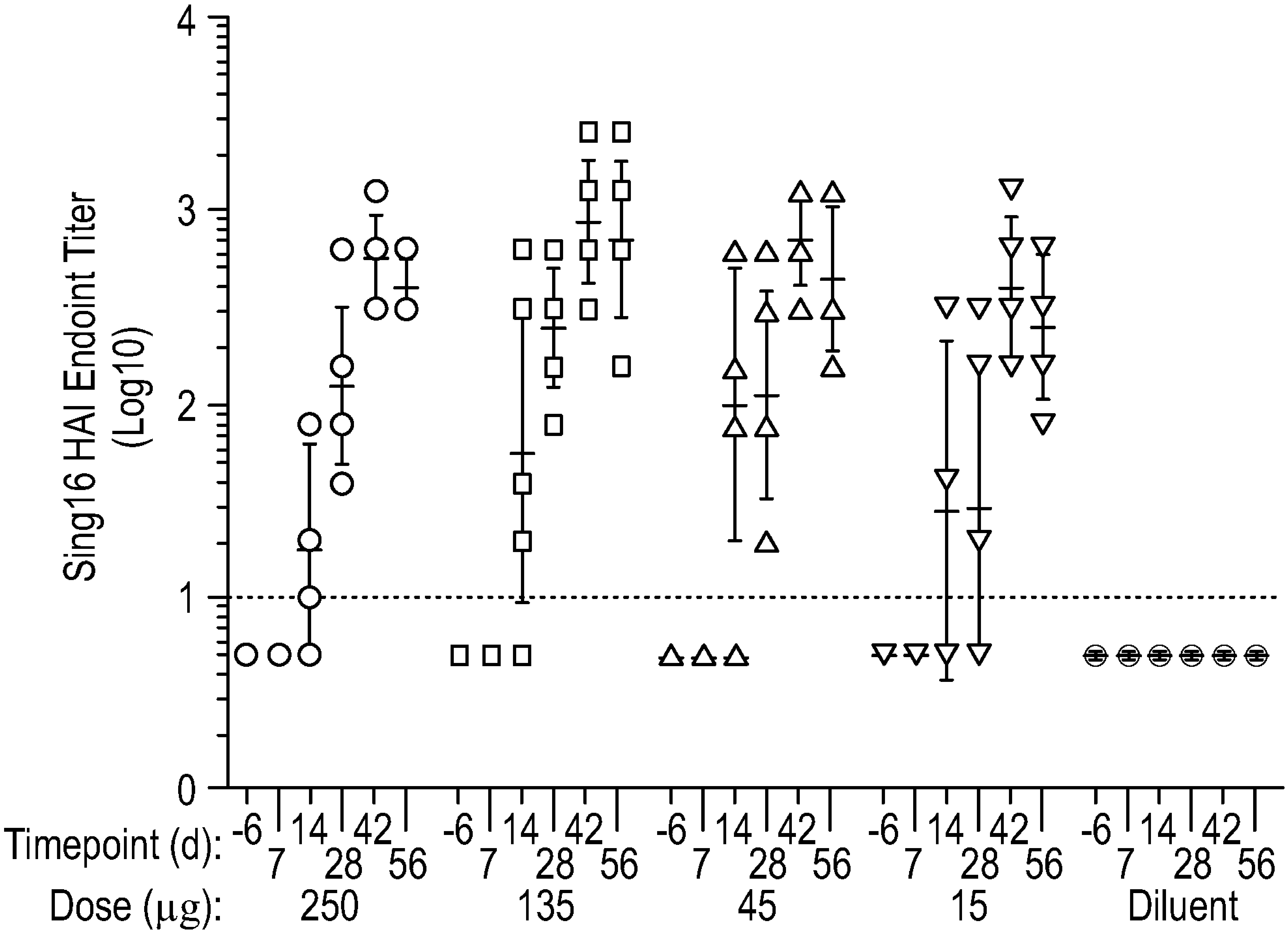


FIG. 19A

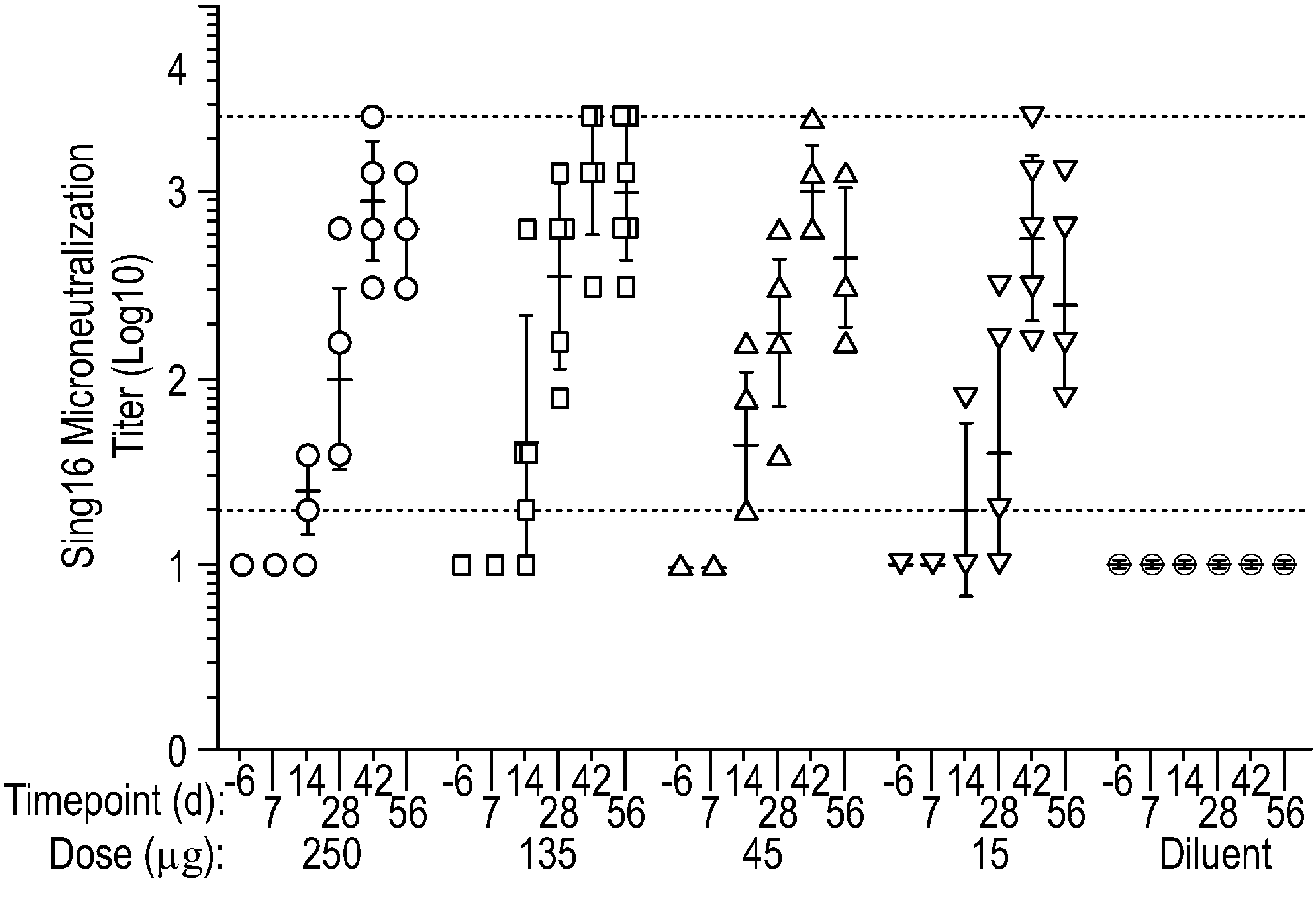


FIG. 19B

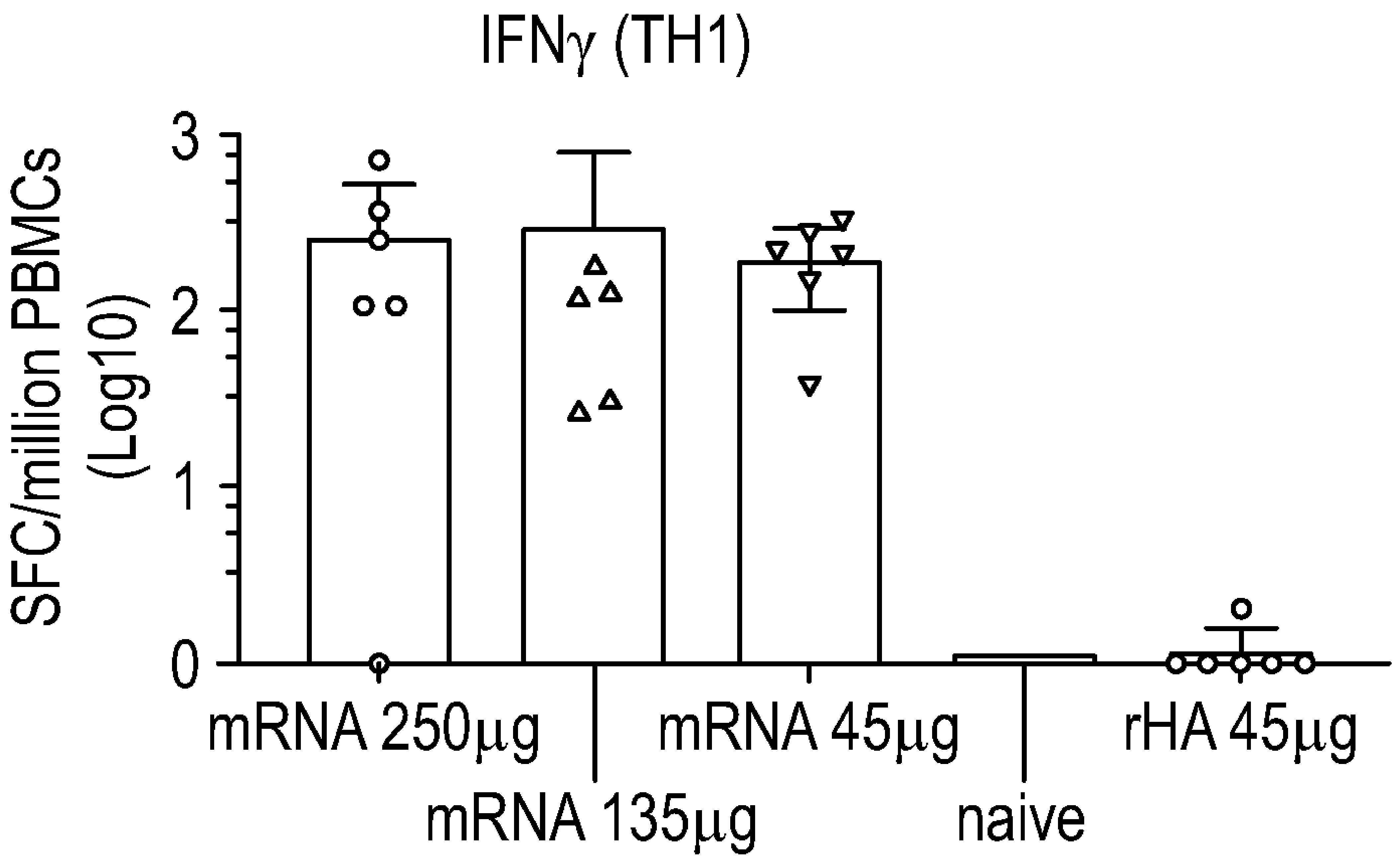


FIG. 20A

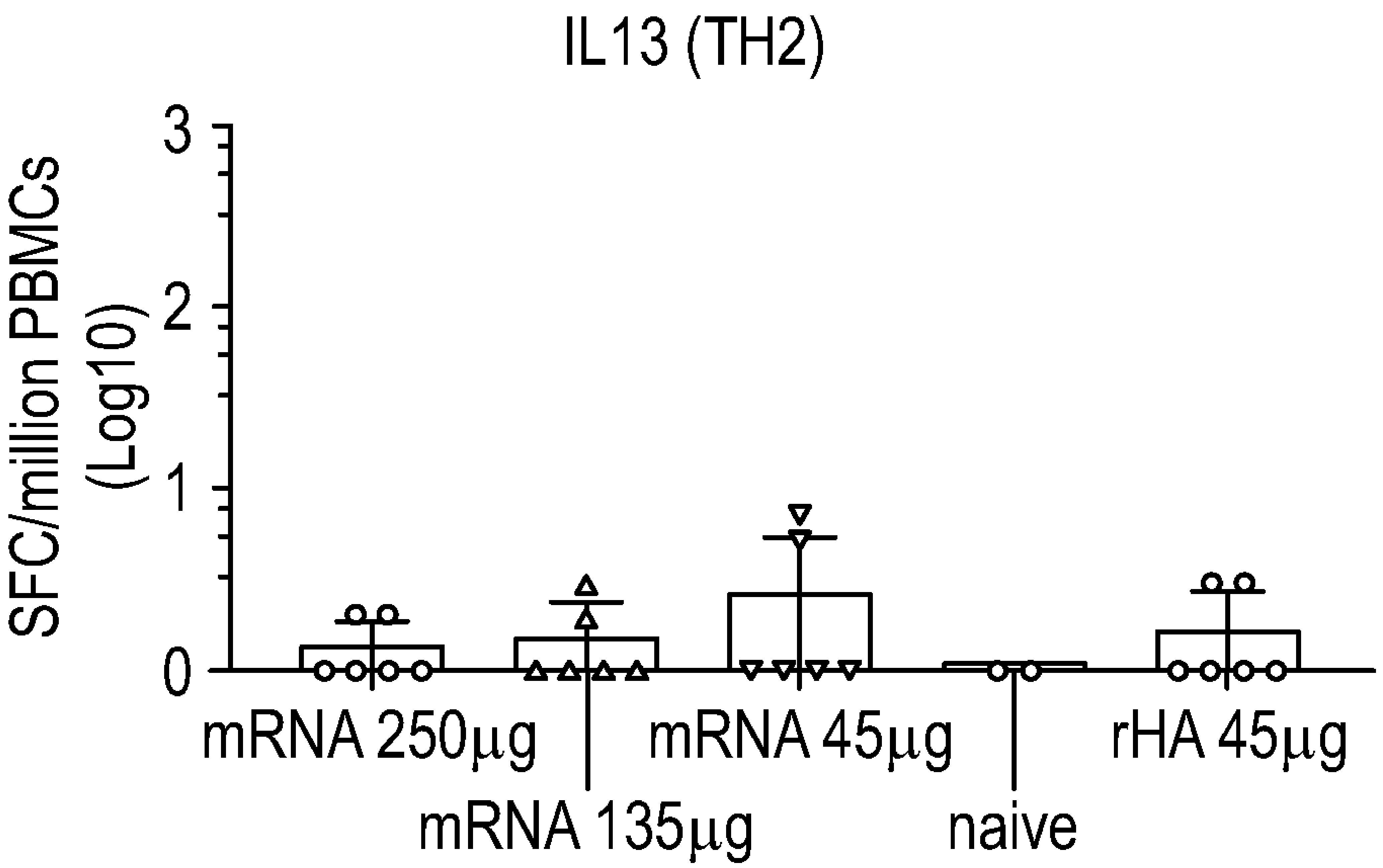


FIG. 20B

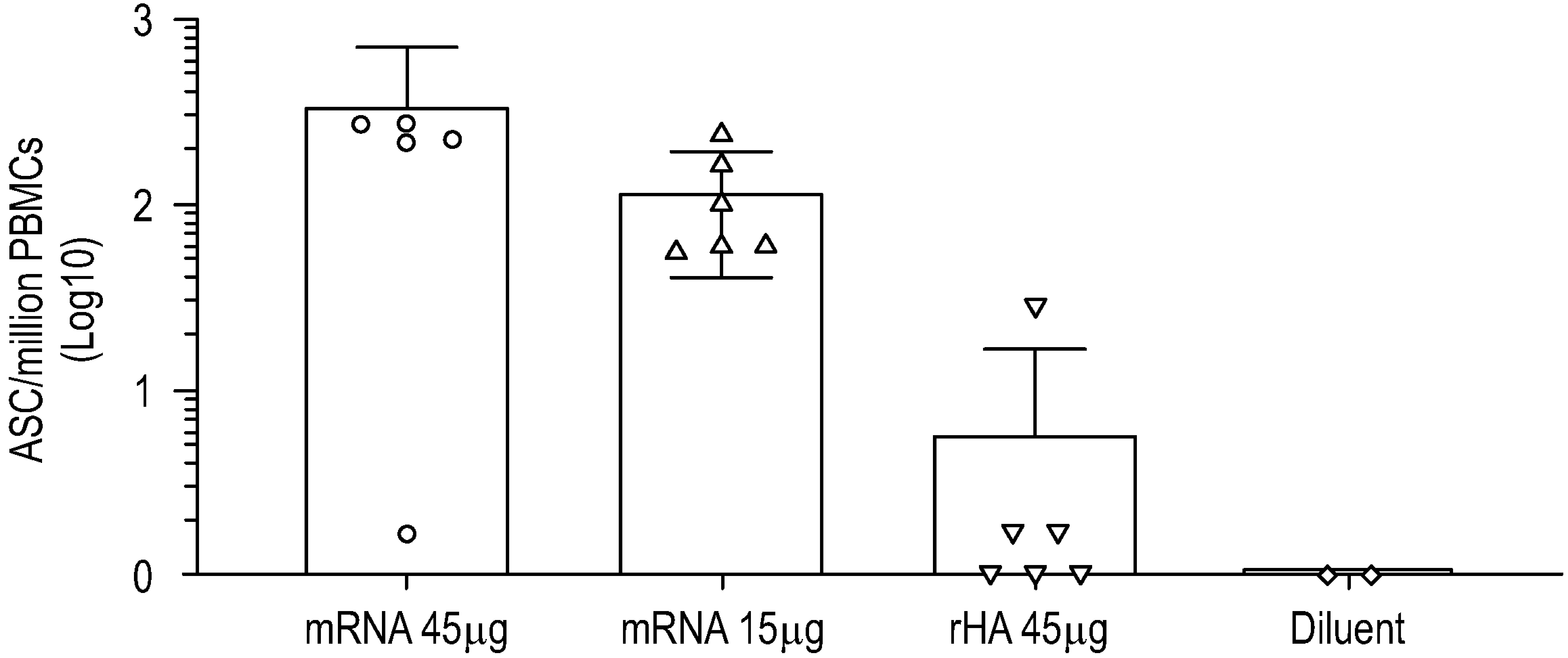

ASC/million PBMCs
(Log10)
3
2
1
0
mRNA 45μg
mRNA 15μg
rHA 45μg
Diluent

FIG. 21

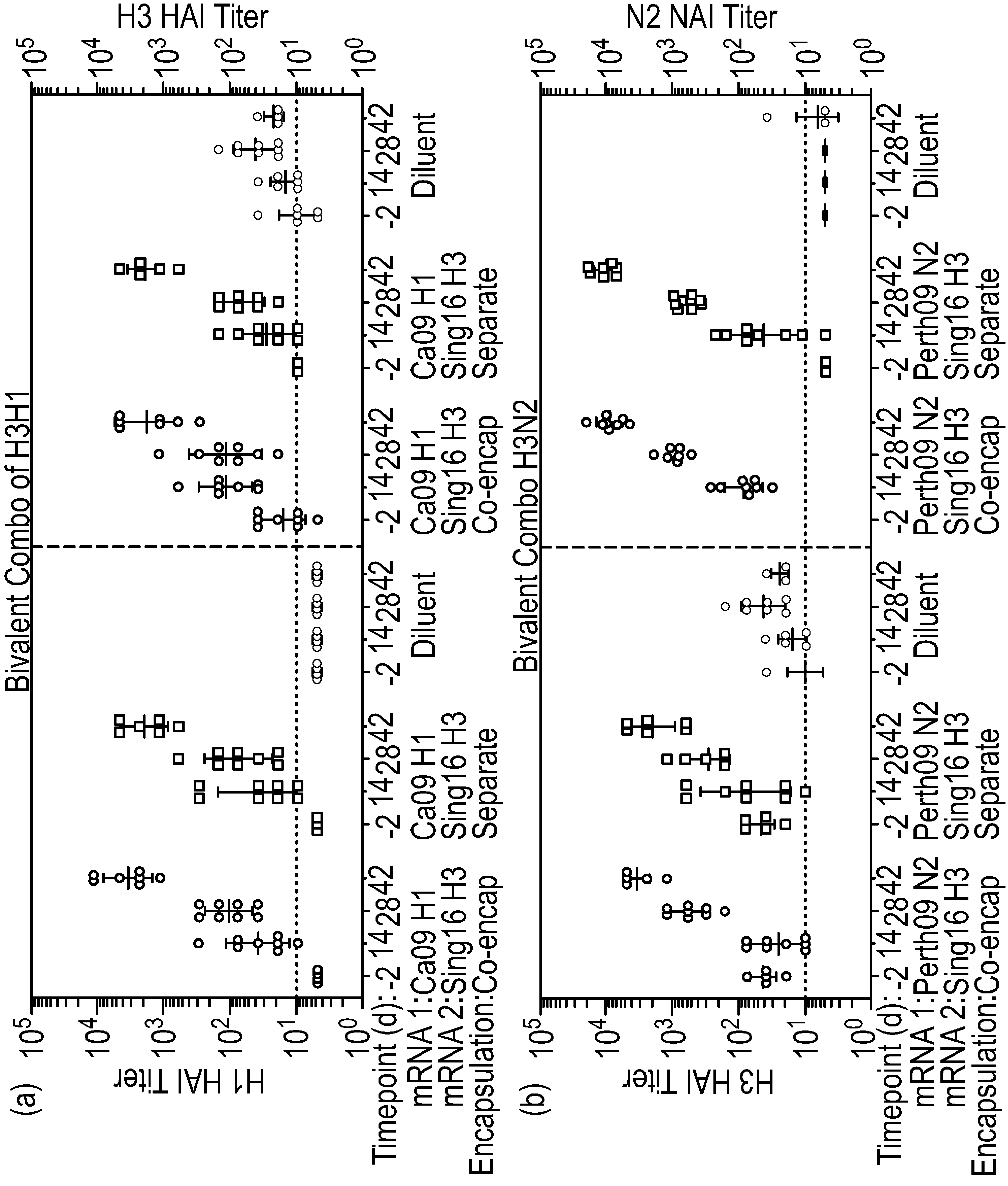

(a)
Bivalent Combo of H3H1
H1 HAI Titer
H3 HAI Titer
10^0
10^1
10^2
10^3
10^4
10^5
Timepoint (d): -2 14 28 42 -2 14 28 42 -2 14 28 42 -2 14 28 42 -2 14 28 42 -2 14 28 42
mRNA 1: Ca09 H1 Ca09 H1 Diluent Ca09 H1 Ca09 H1 Diluent
mRNA 2: Sing16 H3 Sing16 H3 Sing16 H3 Sing16 H3
Encapsulation: Co-encap Separate Co-encap Separate
(b)
Bivalent Combo H3N2
H3 HAI Titer
N2 NAI Titer
10^0
10^1
10^2
10^3
10^4
10^5
Timepoint (d): -2 14 28 42 -2 14 28 42 -2 14 28 42 -2 14 28 42 -2 14 28 42 -2 14 28 42
mRNA 1: Perth09 N2 Perth09 N2 Diluent Perth09 N2 Perth09 N2 Diluent
mRNA 2: Sing16 H3 Sing16 H3 Sing16 H3 Sing16 H3
Encapsulation: Co-encap Separate Co-encap Separate

FIG. 22

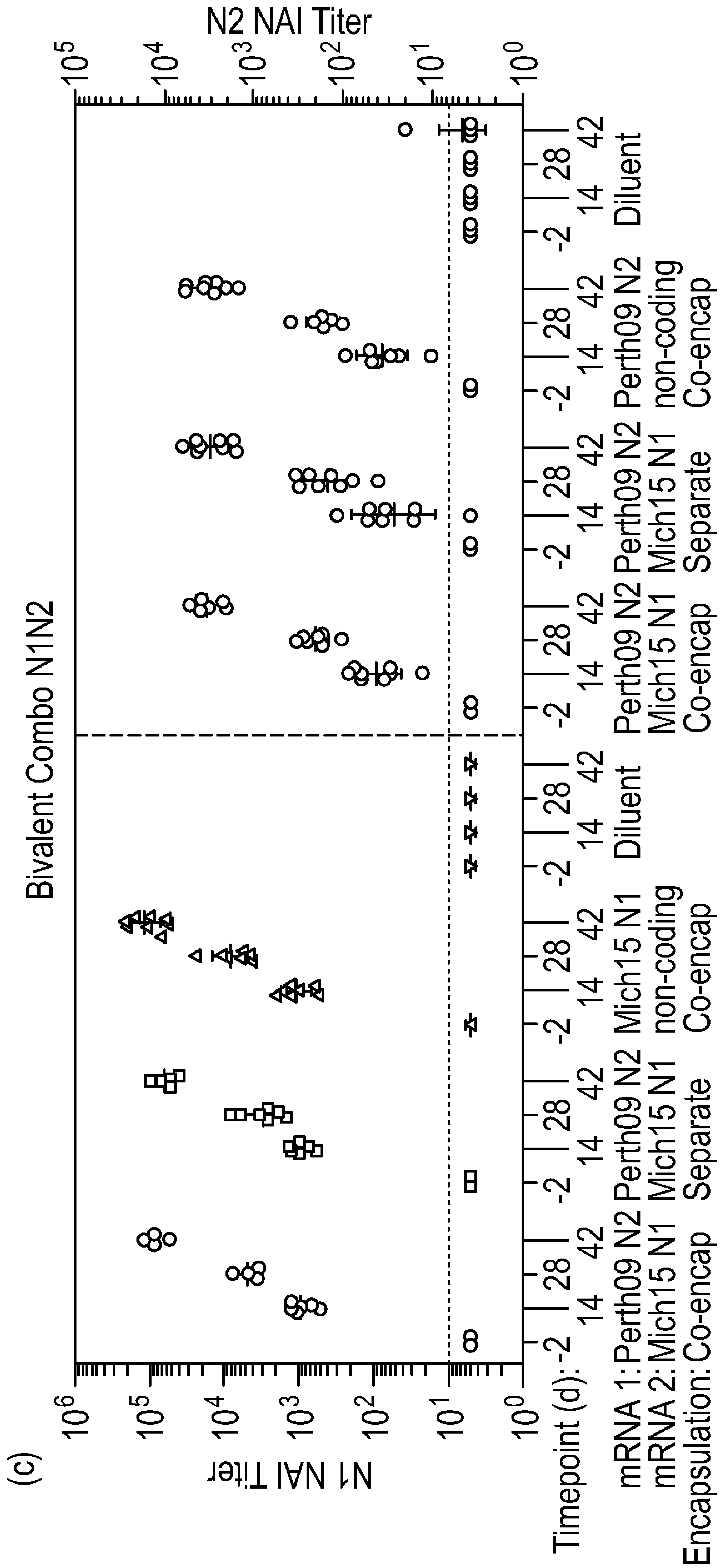

(c)
Bivalent Combo N1N2
N1 NAI Titer
10^0
10^1
10^2
10^3
10^4
10^5
10^6
N2 NAI Titer
10^0
10^1
10^2
10^3
10^4
10^5
Timepoint (d): -2 14 28 42 -2 14 28 42 -2 14 28 42 -2 14 28 42 -2 14 28 42 -2 14 28 42 -2 14 28 42 -2 14 28 42
mRNA 1: Perth09 N2 | Perth09 N2 | Mich15 N1 | Diluent | Perth09 N2 | Perth09 N2 | Perth09 N2 | Diluent
mRNA 2: Mich15 N1 | Mich15 N1 | non-coding | Mich15 N1 | Mich15 N1 | non-coding
Encapsulation: Co-encap | Separate | Co-encap | Co-encap | Separate | Co-encap

FIG. 22 (cont'd)

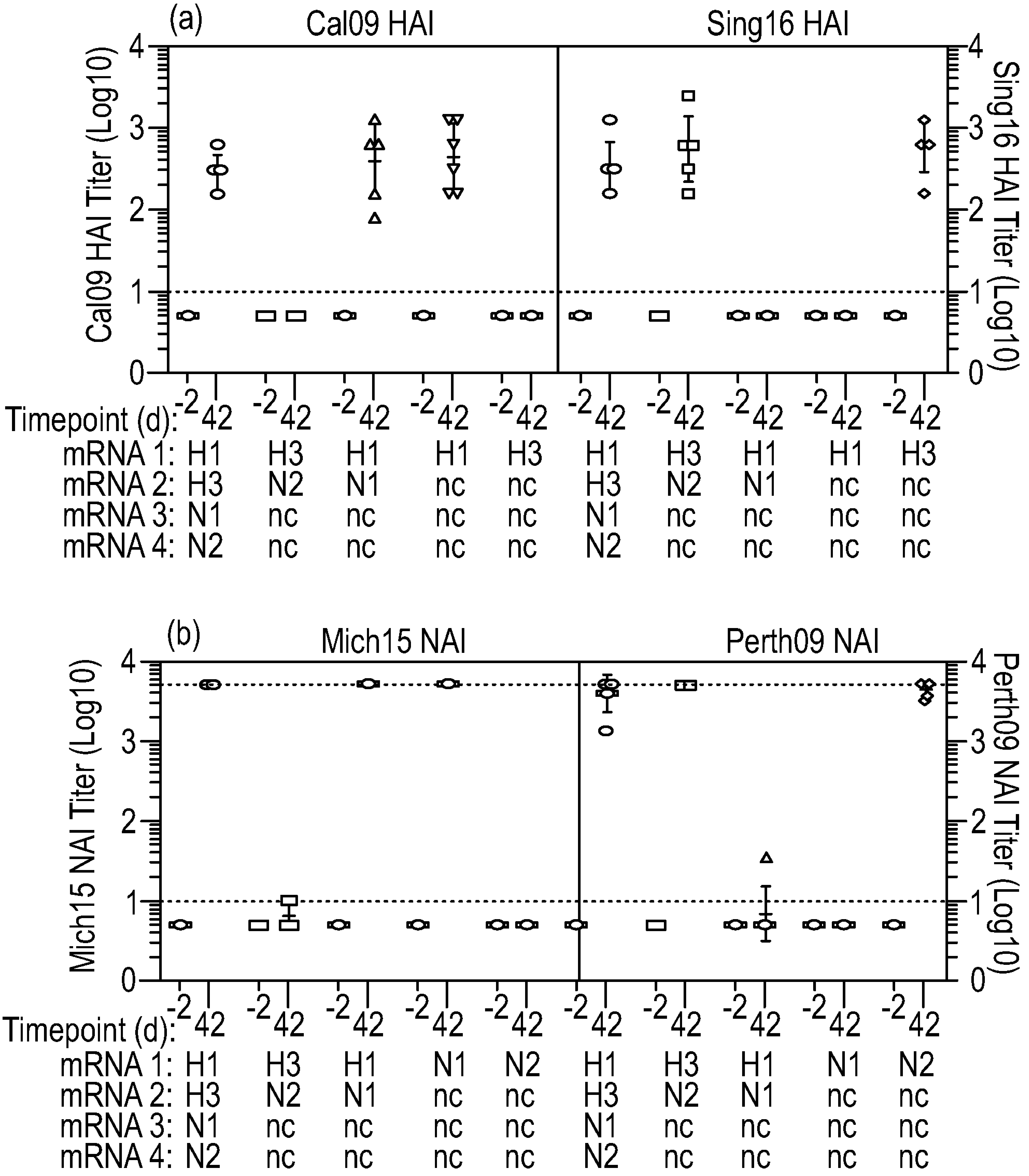

(a)
Cal09 HAI
Sing16 HAI
Cal09 HAI Titer (Log10)
Sing16 HAI Titer (Log10)
0
1
2
3
4
Timepoint (d): -2 42 -2 42 -2 42 -2 42 -2 42 -2 42 -2 42 -2 42 -2 42 -2 42
mRNA 1: H1 H3 H1 H1 H3 H1 H3 H1 H1 H3
mRNA 2: H3 N2 N1 nc nc H3 N2 N1 nc nc
mRNA 3: N1 nc nc nc nc N1 nc nc nc nc
mRNA 4: N2 nc nc nc nc N2 nc nc nc nc
(b)
Mich15 NAI
Perth09 NAI
Mich15 NAI Titer (Log10)
Perth09 NAI Titer (Log10)
0
1
2
3
4
Timepoint (d): -2 42 -2 42 -2 42 -2 42 -2 42 -2 42 -2 42 -2 42 -2 42 -2 42
mRNA 1: H1 H3 H1 N1 N2 H1 H3 H1 N1 N2
mRNA 2: H3 N2 N1 nc nc H3 N2 N1 nc nc
mRNA 3: N1 nc nc nc nc N1 nc nc nc nc
mRNA 4: N2 nc nc nc nc N2 nc nc nc nc

FIG. 23

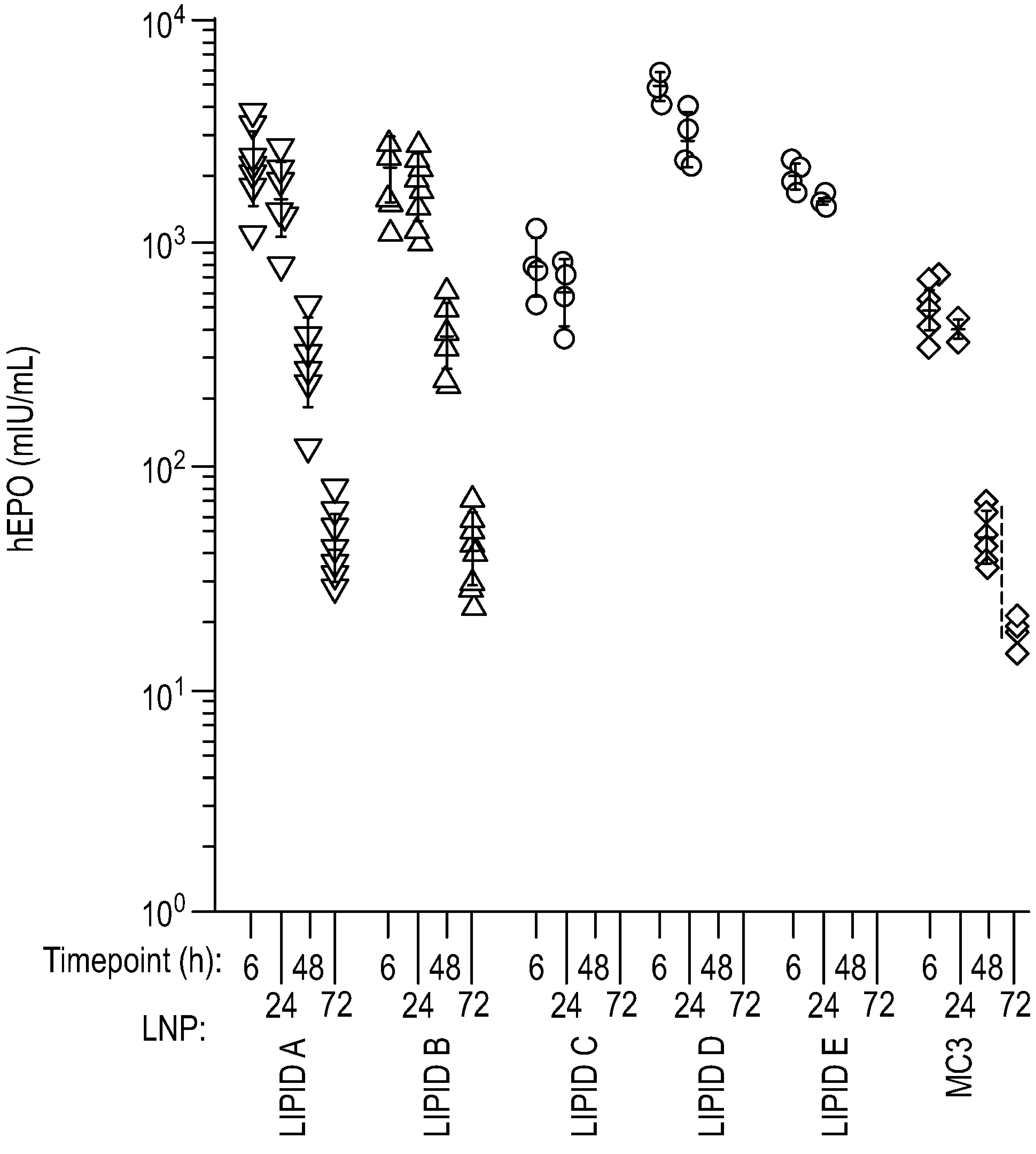

hEPO (mIU/mL)
10^4
10^3
10^2
10^1
10^0
Timepoint (h):
6
24
48
72
LNP:
LIPID A
LIPID B
LIPID C
LIPID D
LIPID E
MC3

FIG. 24

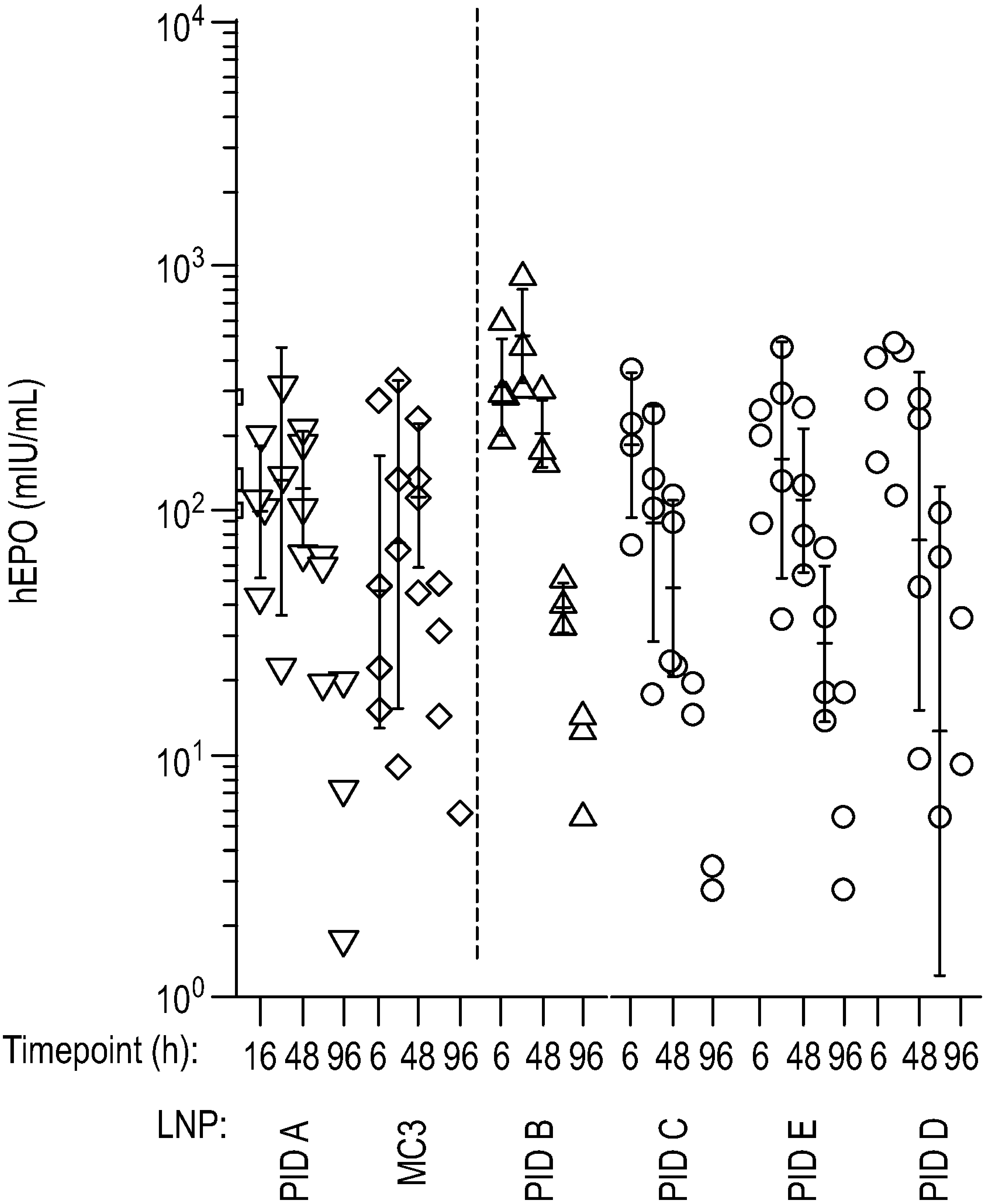

hEPO (mIU/mL)
10^4
10^3
10^2
10^1
10^0
Timepoint (h):
16
48
96
6
48
96
6
48
96
6
48
96
6
48
96
6
48
96
LNP:
LIPID A
MC3
LIPID B
LIPID C
LIPID E
LIPID D

FIG. 25

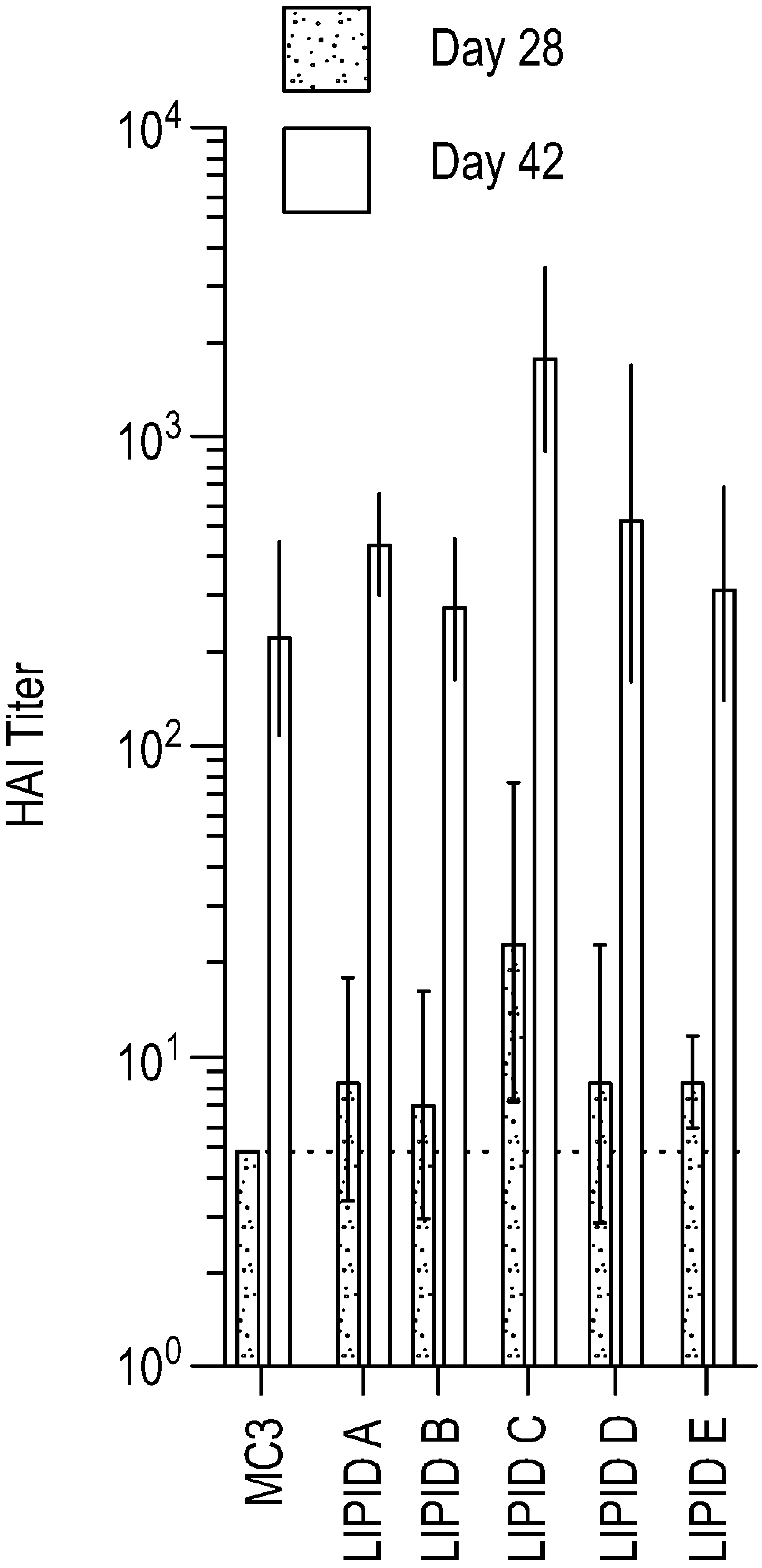

Day 28
Day 42
HAI Titer
10^4
10^3
10^2
10^1
10^0
MC3
LIPID A
LIPID B
LIPID C
LIPID D
LIPID E

FIG. 26

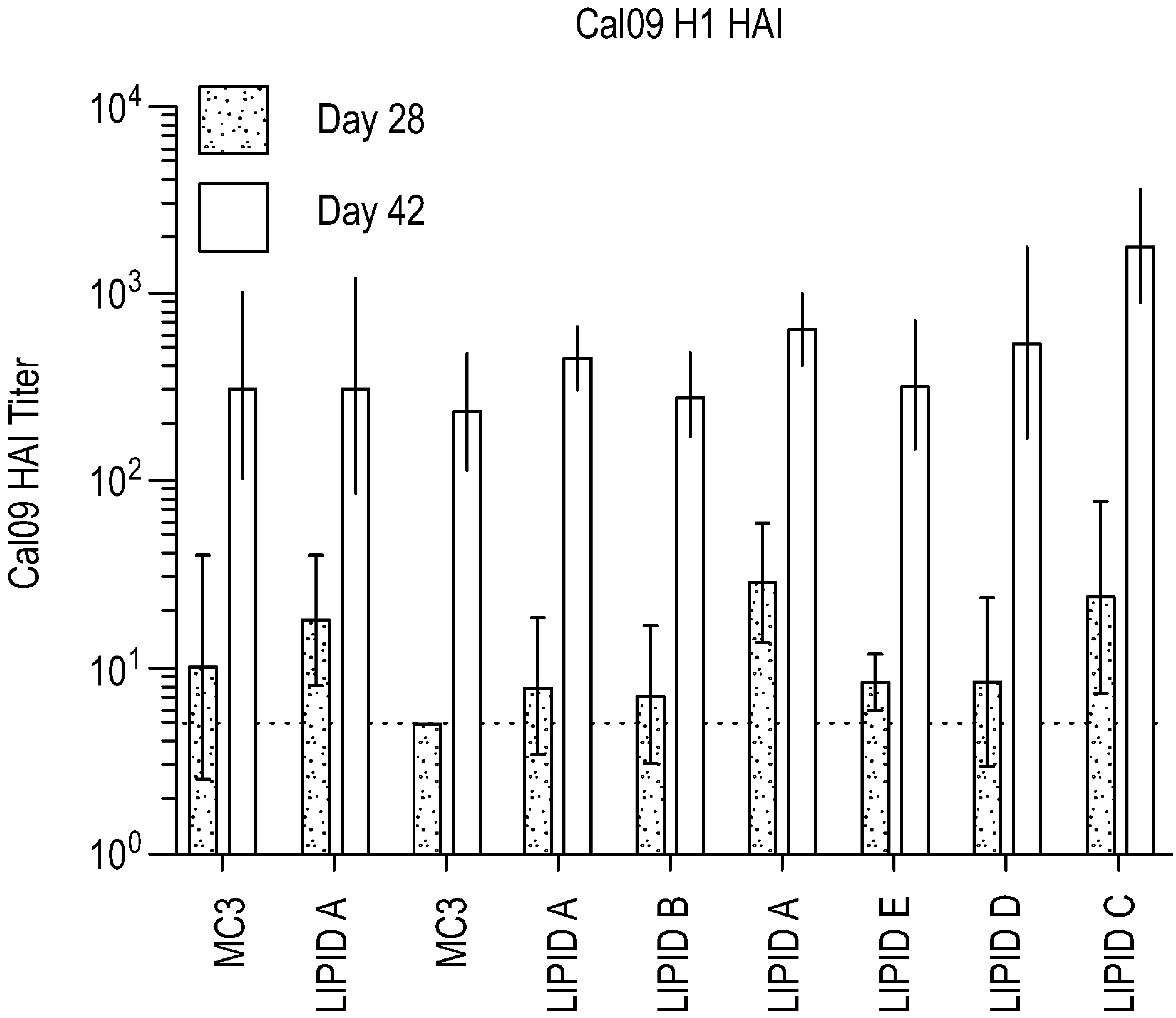

Cal09 H1 HAI
Cal09 HAI Titer
10^4
10^3
10^2
10^1
10^0
Day 28
Day 42
MC3
LIPID A
MC3
LIPID A
LIPID B
LIPID A
LIPID E
LIPID D
LIPID C

FIG. 27

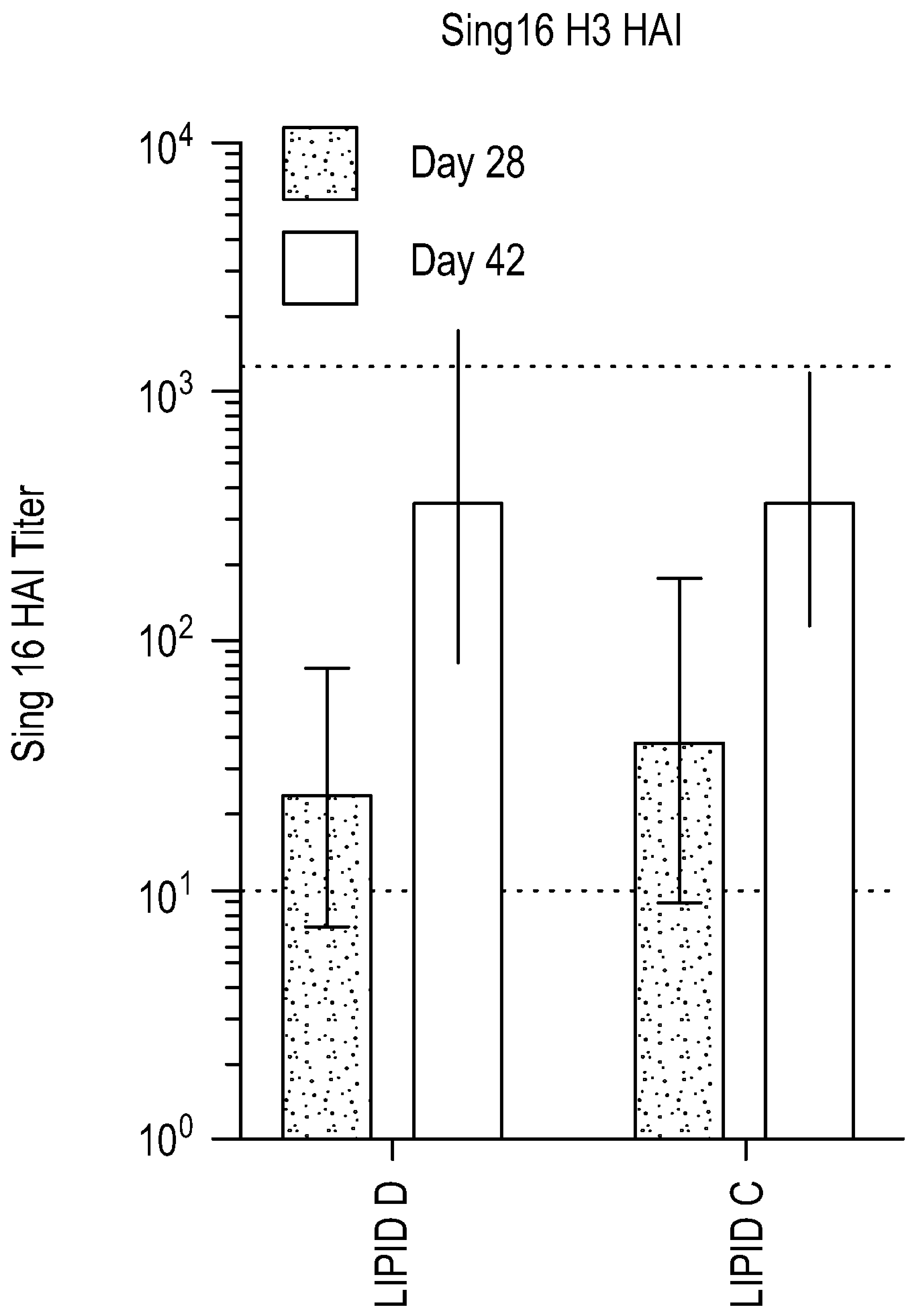

Sing16 H3 HAI
Day 28
Day 42
Sing 16 HAI Titer
10^4
10^3
10^2
10^1
10^0
LIPID D
LIPID C

FIG. 28

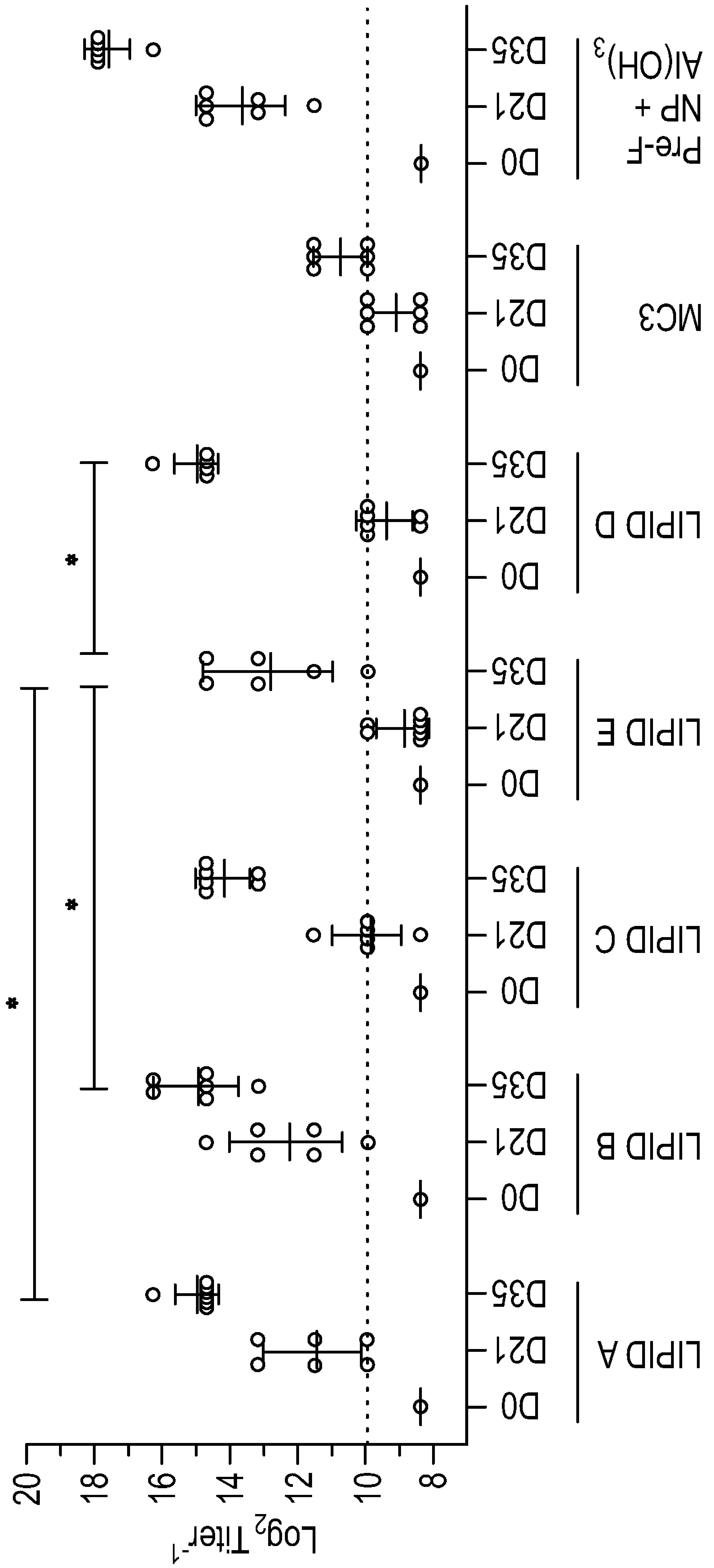
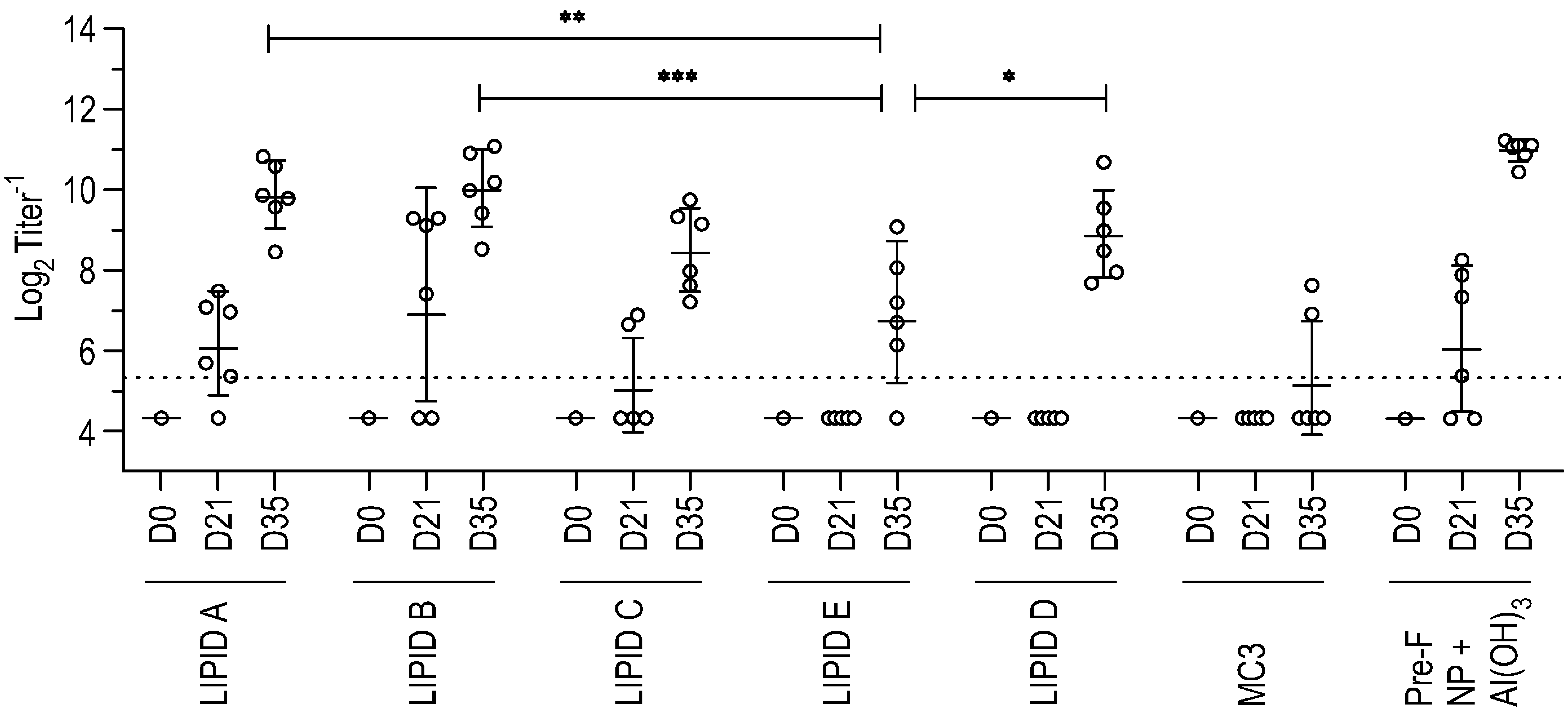

Log$_2$ Titer^{-1}
20
18
16
14
12
10
8
D0
D21
D35
LIPID A
LIPID B
LIPID C
LIPID E
LIPID D
MC3
Pre-F NP + Al(OH)$_3$
*
*
*
*

FIG. 29



Log$_2$ Titer^{-1}
14
12
10
8
6
4
**
***
*
D0
D21
D35
LIPID A
LIPID B
LIPID C
LIPID E
LIPID D
MC3
Pre-F NP + Al(OH)$_3$

FIG. 30

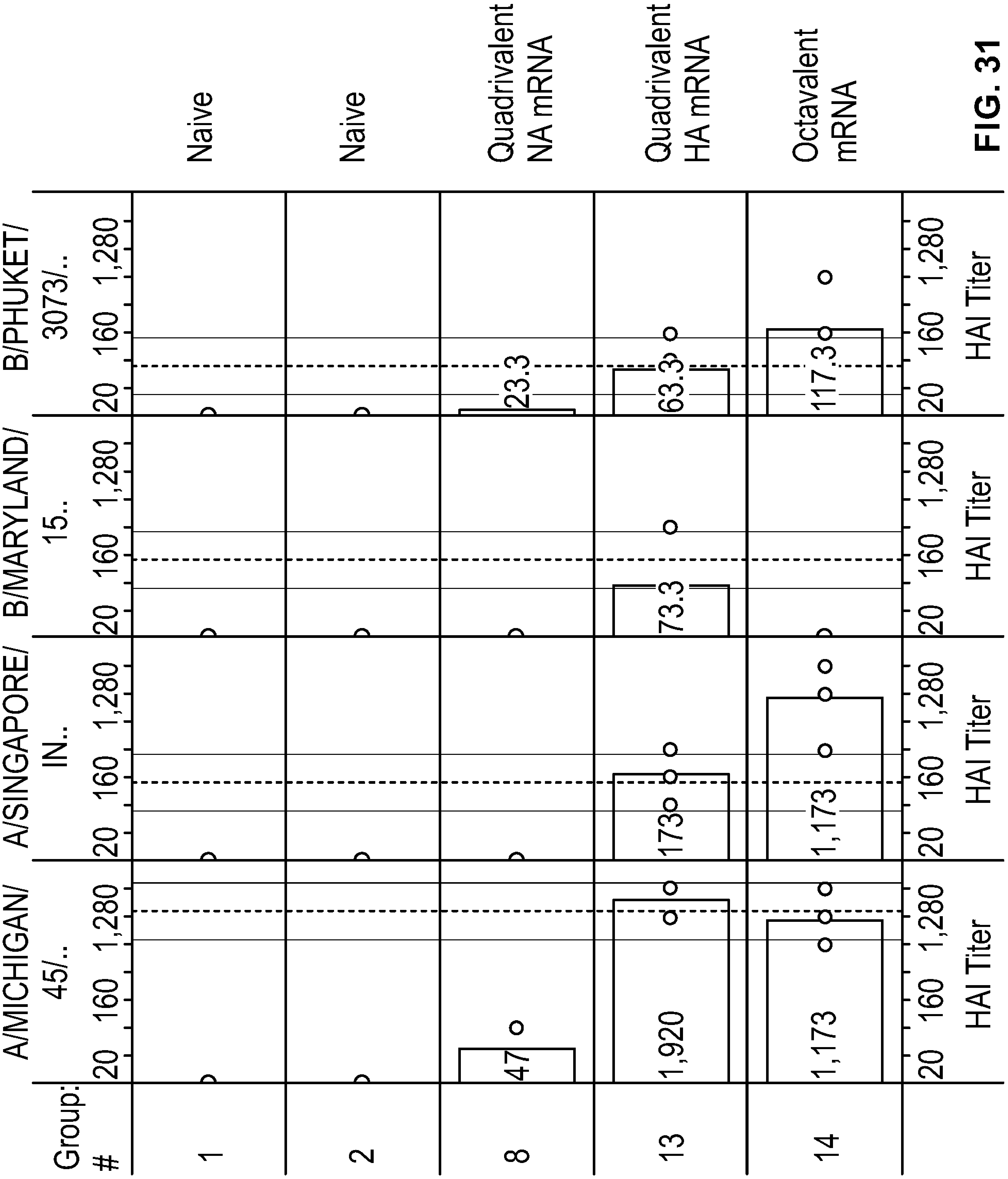

Group: #
1
2
8
13
14
Naive
Naive
Quadrivalent NA mRNA
Quadrivalent HA mRNA
Octavalent mRNA
A/MICHIGAN/ 45/..
A/SINGAPORE/ IN..
B/MARYLAND/ 15..
B/PHUKET/ 3073/..
20
160
1,280
HAI Titer
47
1,920
1,173
173
1,173
73.3
23.3
63.3
117.3

FIG. 31

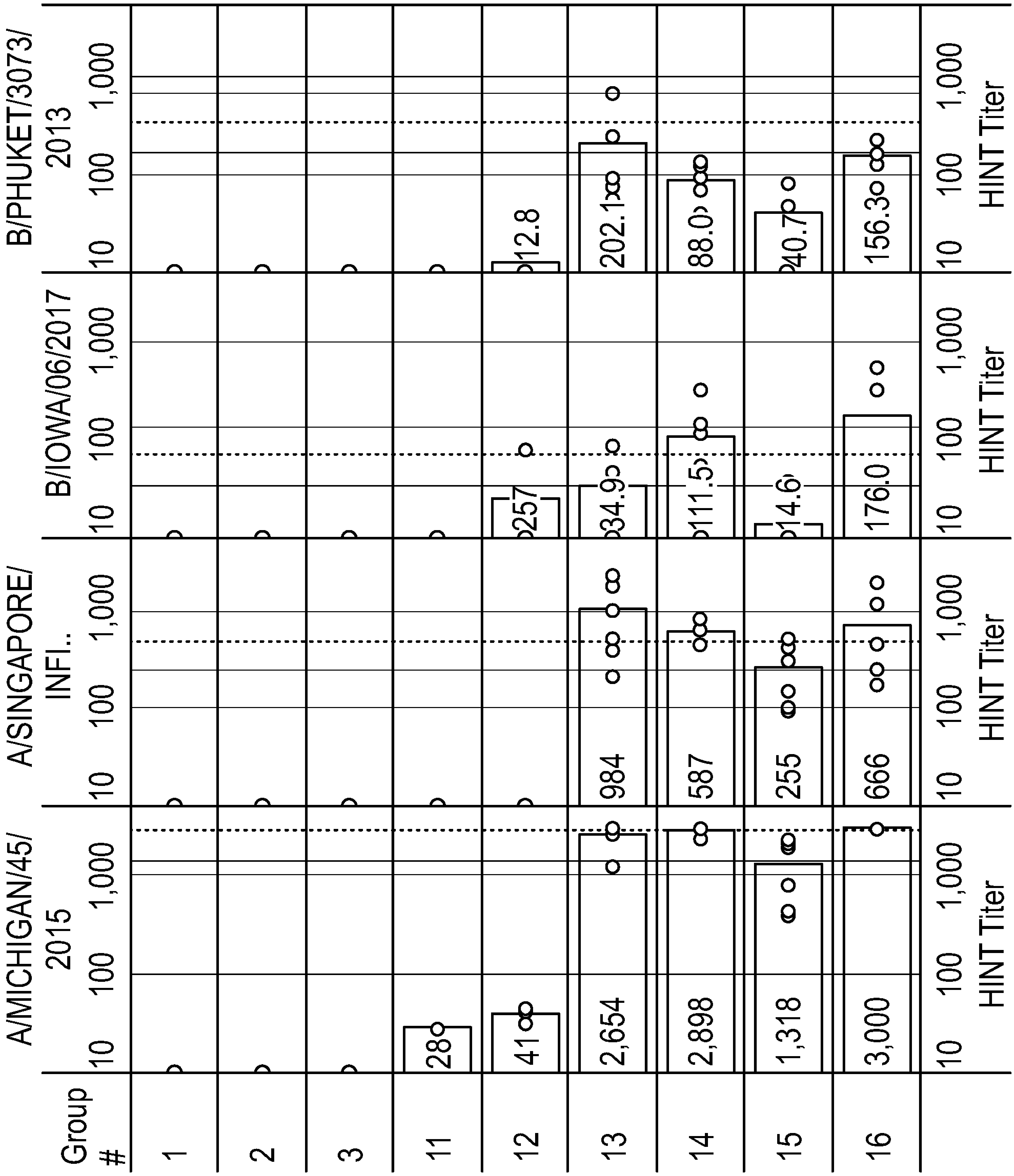

Group #
1
2
3
11
12
13
14
15
16
A/MICHIGAN/45/ 2015
28
41
2,654
2,898
1,318
3,000
A/SINGAPORE/ INFI..
984
587
255
666
B/IOWA/06/2017
257
34.9
111.5
14.6
176.0
B/PHUKET/3073/ 2013
12.8
202.1
88.0
40.7
156.3
10
100
1,000
HINT Titer

FIG. 32

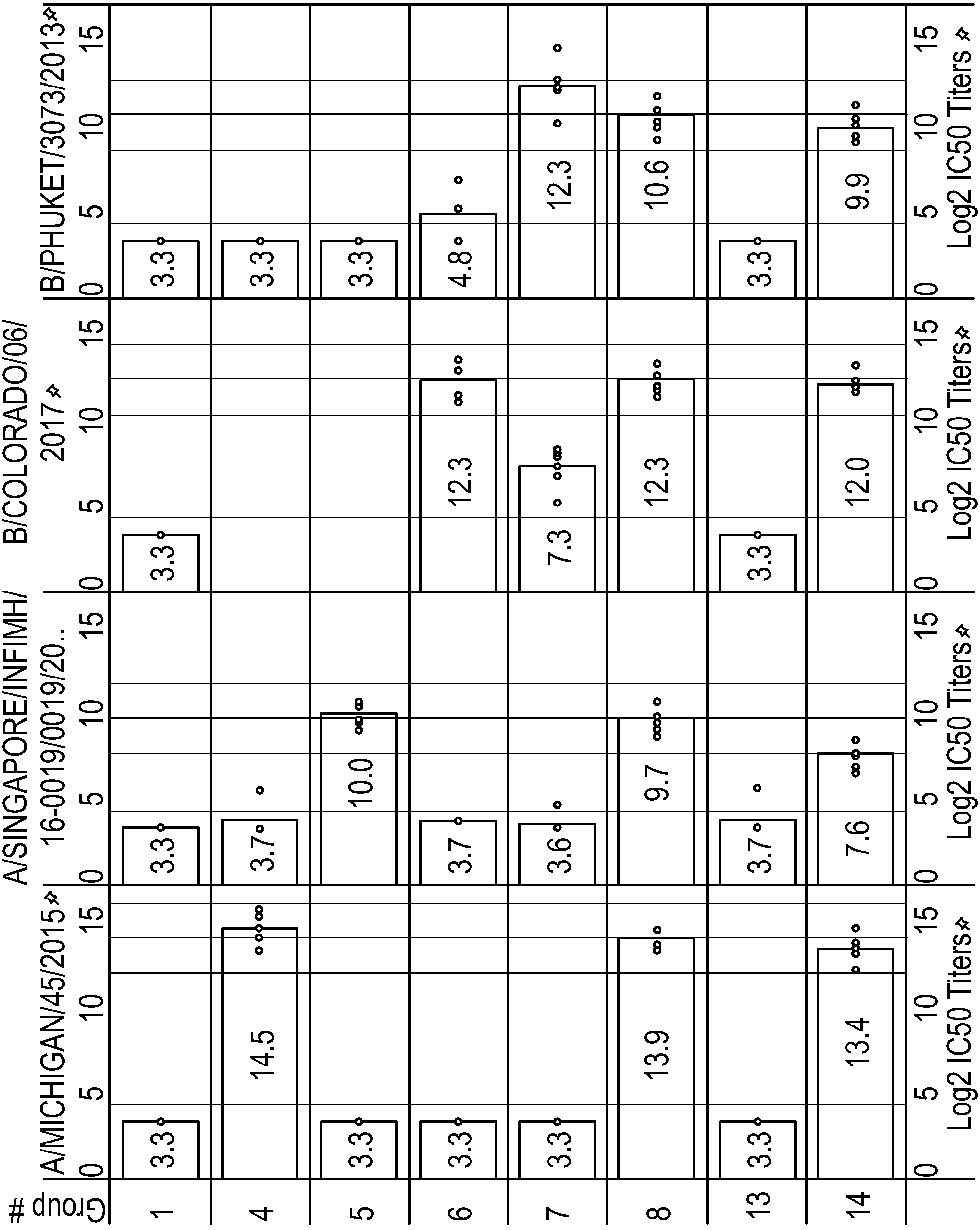

Group #
1
4
5
6
7
8
13
14
A/MICHIGAN/45/2015✩
A/SINGAPORE/INFIMH/16-0019/0019/20..
B/COLORADO/06/2017✩
B/PHUKET/3073/2013✩
0
5
10
15
Log2 IC50 Titers✩
3.3
14.5
3.3
3.3
3.3
13.9
3.3
13.4
3.3
3.7
10.0
3.7
3.6
9.7
3.7
7.6
3.3
12.3
7.3
12.3
3.3
12.0
3.3
3.3
3.3
4.8
12.3
10.6
3.3
9.9

FIG. 33

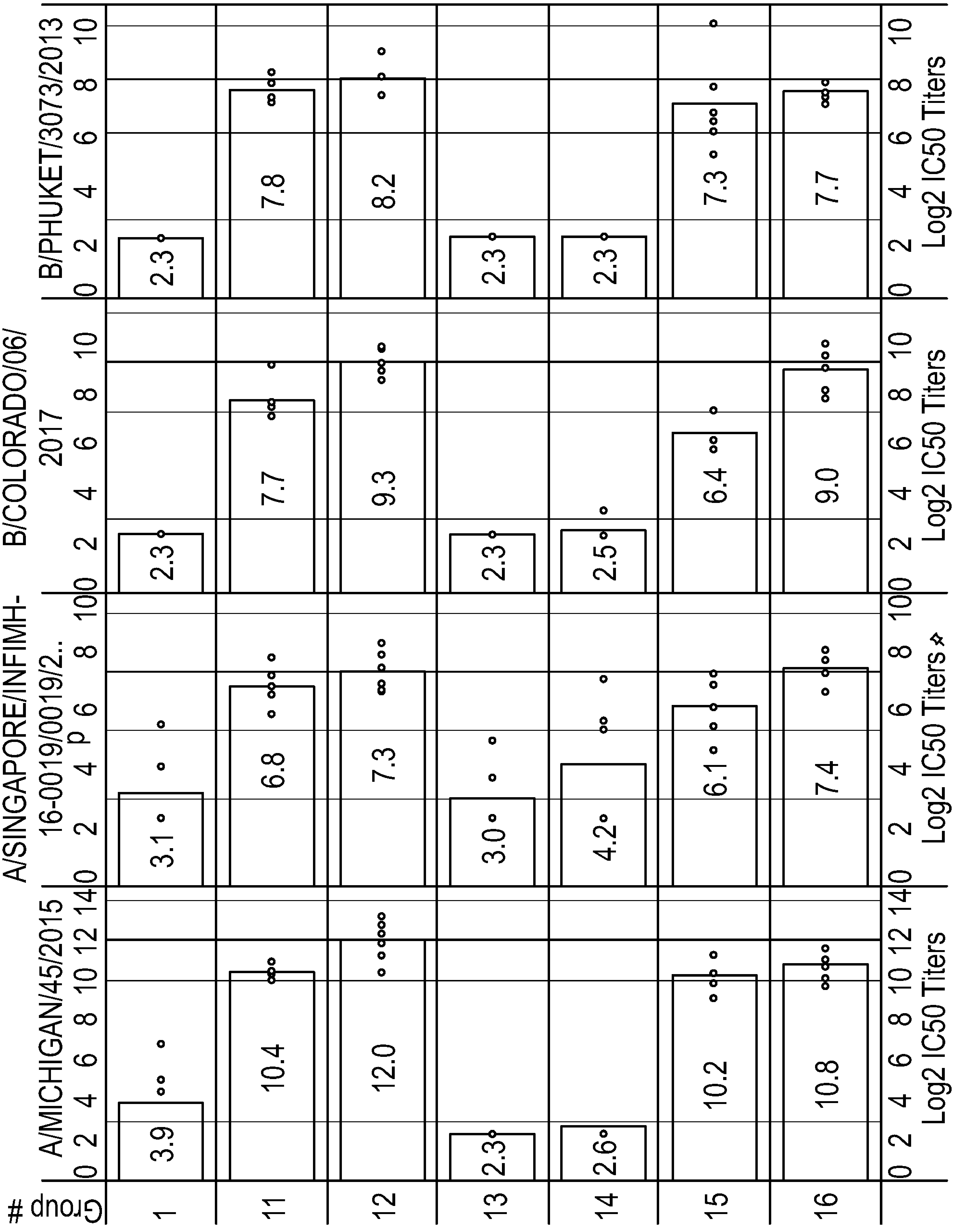

Group #
1
11
12
13
14
15
16
A/MICHIGAN/45/2015
3.9
10.4
12.0
2.3
2.6
10.2
10.8
0 2 4 6 8 10 12 14
Log2 IC50 Titers
A/SINGAPORE/INFIMH-16-0019/0019/2..
p
3.1
6.8
7.3
3.0
4.2
6.1
7.4
0 2 4 6 8 10
Log2 IC50 Titers
B/COLORADO/06/2017
2.3
7.7
9.3
2.3
2.5
6.4
9.0
0 2 4 6 8 10
Log2 IC50 Titers
B/PHUKET/3073/2013
2.3
7.8
8.2
2.3
2.3
7.3
7.7
0 2 4 6 8 10
Log2 IC50 Titers

FIG. 34

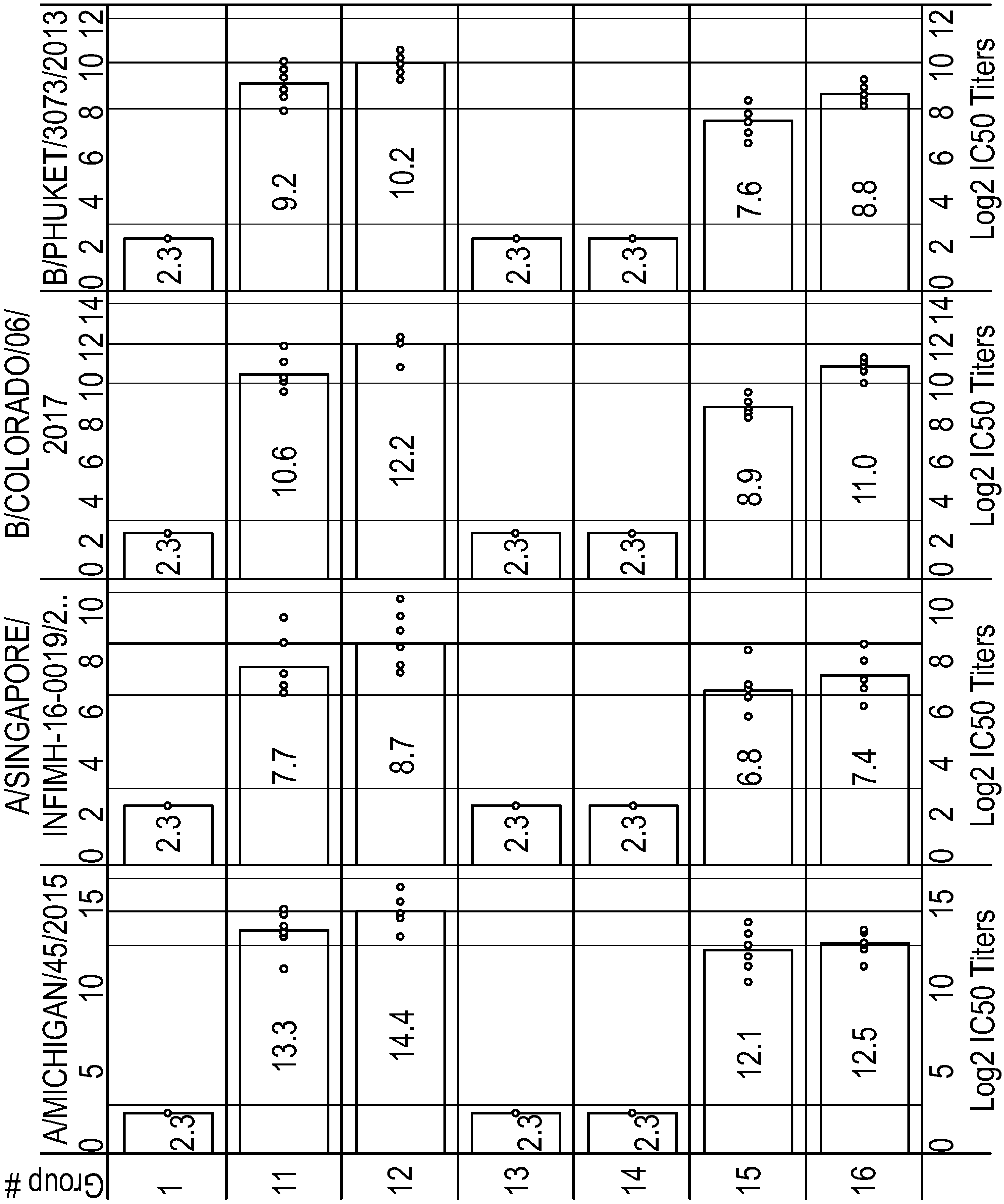

Group #
1
11
12
13
14
15
16
A/MICHIGAN/45/2015
0 5 10 15
2.3
13.3
14.4
2.3
2.3
12.1
12.5
Log2 IC50 Titers
A/SINGAPORE/
INFIMH-16-0019/2..
0 2 4 6 8 10
2.3
7.7
8.7
2.3
2.3
6.8
7.4
Log2 IC50 Titers
B/COLORADO/06/
2017
0 2 4 6 8 10 12 14
2.3
10.6
12.2
2.3
2.3
8.9
11.0
Log2 IC50 Titers
B/PHUKET/3073/2013
0 2 4 6 8 10 12
2.3
9.2
10.2
2.3
2.3
7.6
8.8
Log2 IC50 Titers

FIG. 35

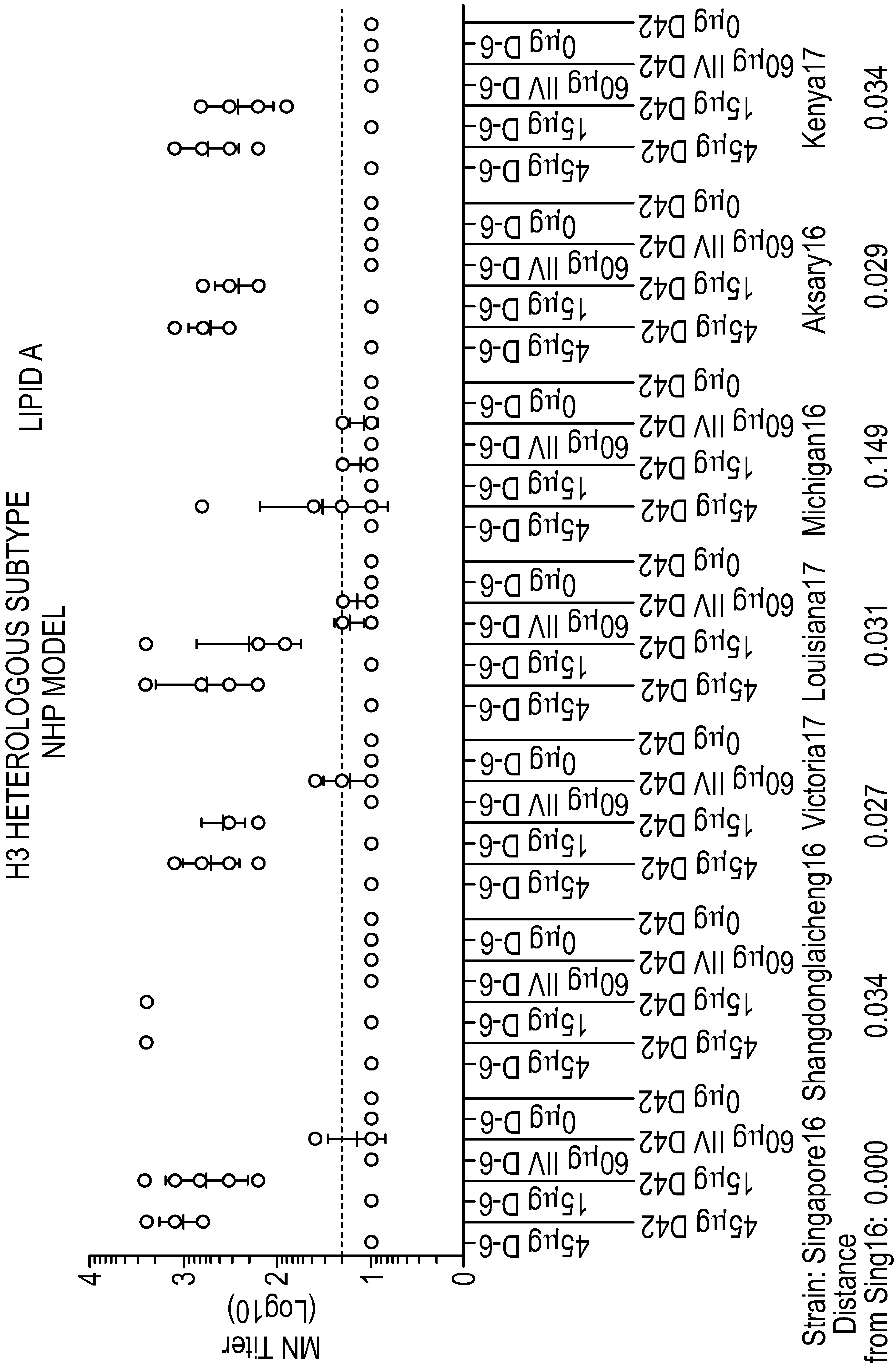

H3 HETEROLOGOUS SUBTYPE
NHP MODEL
LIPID A
MN Titer
(Log10)
0
1
2
3
4
45µg D-6
45µg D42
15µg D-6
15µg D42
60µg IIV D-6
60µg IIV D42
0µg D-6
0µg D42
Strain: Singapore16
Shangdonglaicheng16
Victoria17
Louisiana17
Michigan16
Aksary16
Kenya17
Distance
from Sing16: 0.000
0.034
0.027
0.031
0.149
0.029
0.034

FIG. 36

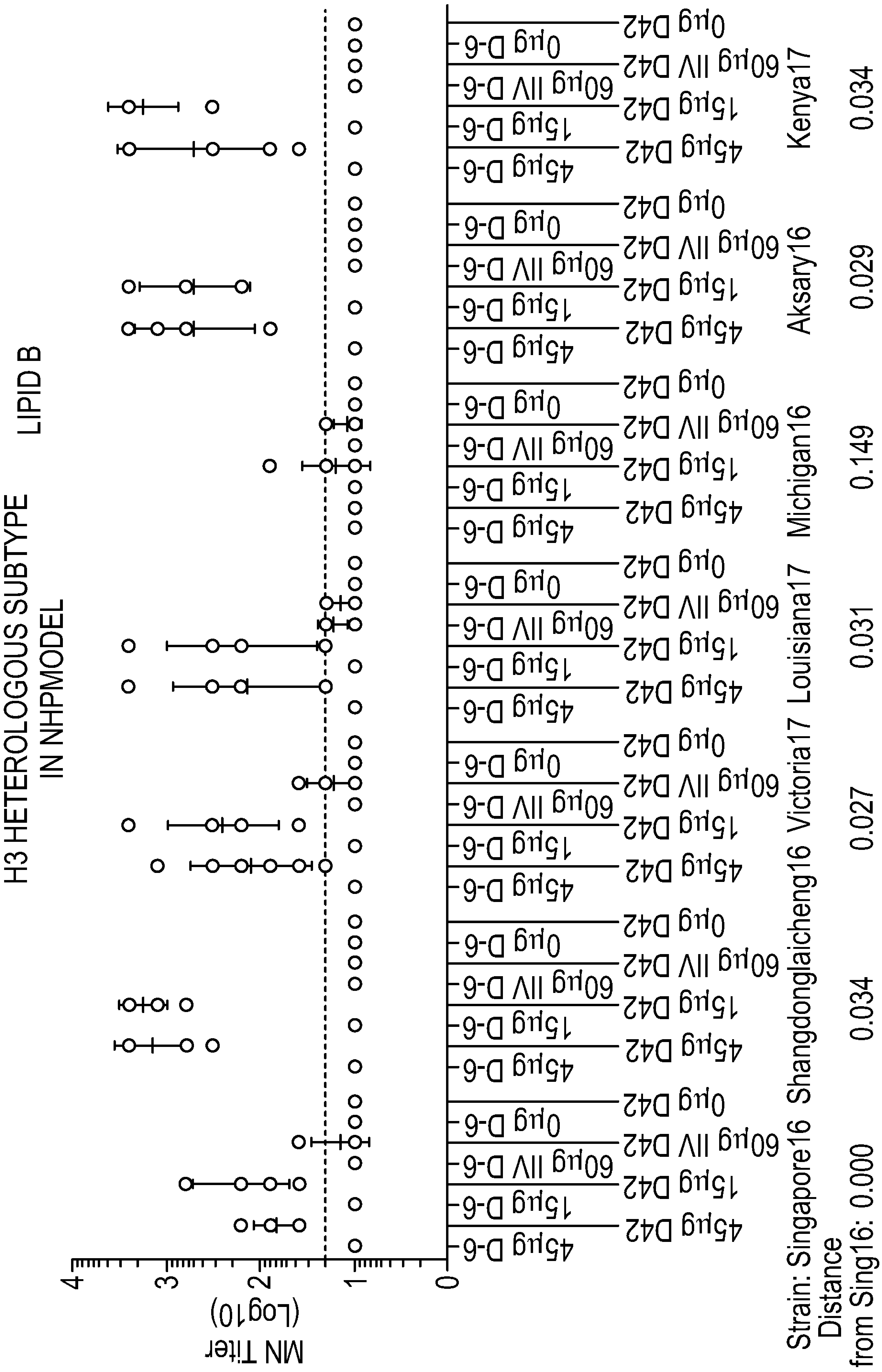

H3 HETEROLOGOUS SUBTYPE
IN NHPMODEL
LIPID B
MN Titer
(Log10)
0
1
2
3
4
45μg D-6
45μg D42
15μg D-6
15μg D42
60μg IIV D-6
60μg IIV D42
0μg D-6
0μg D42
Strain: Singapore16
Shangdonglaicheng16
Victoria17
Louisiana17
Michigan16
Aksary16
Kenya17
Distance
from Sing16: 0.000
0.034
0.027
0.031
0.149
0.029
0.034

FIG. 37