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(54) Title: HUMANIZED EBOLA ANTIBODIES AND USES THEREOF

(57) Abstract: The present disclosure relates to an antibody or antigen-binding portion thereof that binds to *Ebolavirus*. The antibody or antigen-binding portion thereof may have one or more murine CDRs and one or more human framework regions. Also provided herein are compositions comprising the antibody or antigen-binding portion thereof, methods of producing the antibody or antigen-binding portion thereof and methods of using the antibody or antigen- binding portion thereof.

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HUMANIZED EBOLA ANTIBODIES AND USES THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

[1001] This application claims priority to U.S. Provisional Application No. 62/118,430, filed February 19, 2015, which is hereby incorporated by reference in its entirety for all purposes.

FIELD OF THE DISCLOSURE

[1002] The present disclosure relates to an antibody or antigen-binding portion thereof that binds to *Ebolavirus* (EBOV), compositions comprising the antibody or antigen-binding portion thereof, methods of producing the antibody or antigen-binding portion thereof and methods of using the antibody or antigen-binding portion thereof.

DESCRIPTION OF THE TEXT FILE SUBMITTED ELECTRONCIALLY

[1003] The content of the text file submitted electronically herewith is incorporated herein by reference in its entirety: A computer readable format copy of the Sequence Listing (filename: EMER_050_01WO_SeqList_ST25.txt; date recorded: February 19, 2016; file size 133 KB).

BACKGROUND

[1004] The *Ebolavirus* (EBOV) is a pleiomorphic filamentous virus in the *Filoviridae* family. Infection with EBOV usually causes a severe hemorrhagic fever, with 50-90% lethality. The outbreak frequency of EBOV has also increased recently. Five different species of EBOV have been identified: Zaire, Sudan, Cote d'Ivoire, Reston and Bundibugyo, each named after the location in which the species was first described. All species are believed to be lethal to humans, with the possible exception of the rare Cote d'Ivoire species and the Reston species. Of these species, the Zaire species of ebolavirus (ZEBOV) is believed to be the most common and the most lethal.

[1005] The negative-stranded RNA genome of EBOV encodes seven genes. The fourth gene, GP, actually encodes two unique proteins: a non-structural, dimeric and secreted glycoprotein (called sGP), and a trimeric, virion-attached, membrane embedded envelope glycoprotein, termed GP. These glycoproteins share the first 295 amino acids, but have unique C termini as a result of transcriptional editing. The unique C termini result in different patterns of disulfide bonding and different structures as well as different roles in pathogenesis. In EBOV, about 80% of the mRNA transcripts direct synthesis of sGP, which is secreted abundantly early in infection. The remaining 20% of the mRNA transcripts direct synthesis of GP. The unique C-terminus of GP encodes a heavily glycosylated mucin-like domain, a transmembrane region and a short cytoplasmic tail.

[1006] Natural survival from EBOV infection is rare and not clearly understood. There are currently no approved vaccines or therapeutics for EBOV infection. Development of neutralizing antibodies in the context of natural infection is believed to be difficult. Accordingly, there is a need for the development of vaccines and therapeutics for EBOV infection. The present disclosure addresses these needs and provides related advantages.

SUMMARY OF THE DISCLOSURE

[1007] The present disclosure provides an antibody or antigen-binding portion thereof that binds to *Ebolavirus* (EBOV). In some embodiments, the antibody or antigen-binding portion thereof that binds to *Ebolavirus*, is an isolated antibody or antigen-binding portion thereof comprising: (a) a light chain CDR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 6, 30, 54, 78, 102, 126, 150, 174 or 198; (b) a light chain CDR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 7, 31, 55, 79, 103, 127, 151, 175, or 199; (c) a light chain CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 8, 32, 56, 80, 104, 128, 152, 176, or 200; (d) a heavy chain CDR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 18, 42, 66, 90, 114, 138, 162, 186, 210, 345, 357, or 369; (e) a heavy chain CDR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 19, 43, 67, 91, 115, 139, 163, 187, 211, 346, 358, or 370; (f) a heavy chain CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 20, 44, 68, 92, 116, 140, 164, 188, 212, 347, 359, or 371; (g) a light chain FR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence e comprising SEQ ID NO: 268, 276, 284, 292, 300, 308, 316, 324, or 332; (h) a light chain FR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 269, 277, 285, 293, 301, 309, 317, 325, or 333; (i) a light chain FR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 270, 278, 286, 294, 302, 310, 318, 326, or 334; (j) a light chain FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 271, 279, 287, 295, 303, 311, 319, 327, or 335; (k) a heavy chain FR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 272, 280, 288, 296, 304, 312, 320, 328 336, 376, 380, or 384; (l) a heavy chain FR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 273, 281, 289, 297, 305, 313, 321, 329 337, 377, 381, or 385; (m) a heavy chain FR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 274, 282, 290, 298, 306, 314, 322, 330, 338, 378, 382, or 386; and, (n) a heavy chain FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 275, 283, 291, 299, 307, 315, 323, 331, 339, 379, 383, or 387.

[1008] In another embodiment, the isolated antibody or antigen-binding portion thereof comprises: (a) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 6, 7 and 8, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 18, 19 and 20, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 268, 269, 270, and 271, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 272, 273, 274 and 275, respectively; (b) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 30, 31, and 32, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 42, 43, and 44, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence e comprising SEQ ID NOs: 276, 277, 278, and 279, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 280, 281, 282, and 283, respectively; (c) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 54, 55, and 56, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 66, 67, and 68, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 284, 285, 286, and 287, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 288, 289, 290, and 291, respectively; (d) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 78, 79 and 80, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 90, 91 and 92, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 292, 293, 294 and 295, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 296, 297, 298, and 299, respectively; (e) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs:102, 103, and 104, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 114, 115, and 116, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 300, 301, 302 and 303, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 304, 305, 306 and 307, respectively; (f) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 126, 127, and 128, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 138, 139, and 140, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 308, 309, 310 and 311, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 312, 313, 314, and 315, respectively; (g) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 150, 151, and 152, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 162, 163, and 164, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 316, 317, 318 and 319, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 320, 321, 322, and 323, respectively; (h) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 174, 175, and 176, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 186, 187, and 188, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 324, 325, 326 and 327, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 328, 329, 330 and 331, respectively; (i) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 198, 199 and 200, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 210, 211, and 212, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 332, 333, 334 and 335, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 336, 337, 338, and 339, respectively; (j) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 78, 79 and 80, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 345, 346, and 347, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 292, 293, 294 and 295, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 376, 377, 378, and 379, respectively; (k) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 78, 79 and 80, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 357, 358, and 359, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 292, 293, 294 and 295, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 380, 381, 382, and 383, respectively; or (l) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 78, 79 and 80, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 369, 370, and 371, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 292, 293, 294 and 295, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 384, 385, 386, and 387, respectively.

[1009] In some embodiments, the antibody or antigen-binding portion thereof that binds to *Ebolavirus*, is an isolated antibody or antigen-binding portion thereof comprising: (a) a light chain CDR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 3, 27, 51, 75, 99, 123, 147, 171 or 195; (b) a light chain CDR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 4, 28, 52, 76, 100, 124, 148, 172, or 196; (c) a light chain CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 5, 29, 53, 77, 101, 125, 149, 173, or 197; (d) a heavy chain CDR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 15, 39, 63, 87, 111, 135, 159, 183, 207, 342, 354, or 366; (e) a heavy chain CDR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 16, 40, 64, 88, 112, 136, 160, 184, 208, 343, 355, or 367; (f) a heavy chain CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 17, 41, 65, 89, 113, 137, 161, 185 209, 344, 356, or 368; (g) a light chain FR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 9, 33, 57, 81, 105, 129, 153, 177, or 201; (h) a light chain FR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 10, 34, 58, 82, 106, 130, 154, 178, or 202; (i) a light chain FR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 11, 35, 59, 83, 107 131, 155, 179 or 203; (j) a light chain FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 12, 36, 60, 84, 108, 132, 156, 180 or 204; (k) a heavy chain FR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 21, 45, 69, 93, 117, 141, 165, 189, 213, 348, 360, or 372; (l) a heavy chain FR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 22, 46, 70, 94, 118, 142, 166, 190, 214, 349, 361, or 373; (m) a heavy chain FR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 23, 47, 71, 95, 119, 143, 167, 191, 215, 350, 362, or 374; and (n) a heavy chain FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 24, 48, 72, 96, 120, 144, 168, 192, 216, 351, 363, or 375.

[1010] In some embodiments, the isolated antibody or antigen-binding portion thereof comprises: (a) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 3, 4, and 5, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 15, 16, and 17, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 9, 10, 11, and 12, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 21, 22, 23, and 24, respectively; (b) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 27, 28, and 29, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 39, 40, and 41, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 33, 34, 35, and 36, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 45, 46, 47 and 48, respectively; (c) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 51, 52, and 53, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 63, 64, and 65, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 57, 58, 59 and 60, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 69, 70, 71, and 72, respectively; (d) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 75, 76, and 77, respectively; a heavy chain CDR1, CDR2, and

CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 87, 88, and 89, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 81, 82, 83, and 84, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 93, 94, 95, and 96, respectively; (e) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 99, 100, and 101, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 111, 112, and 113, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 105, 106, 107, and 108, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 117, 118, 119, and 120, respectively; (f) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 123, 124 and 125, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 135, 136, and 137, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 129, 130, 131, 132, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 141, 142, 143, and 144, respectively; (g) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 147, 148 and 149, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 159, 160, and 161, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 153, 154, 155, and 156, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 165, 166, 167, and 168, respectively; (h) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 171, 172, and 173, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 183, 184, and 185, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 177, 178, 179 and 180, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 189, 190, 191, and 192, respectively; (i) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 195, 196 and 197, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 207, 208, and 209, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 201, 202, 203 and 204, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 213, 214, 215 and 216, respectively; (j) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 75, 76, and 77, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 342, 343, and 344, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%

sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 81, 82, 83, and 84, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 348, 349, 350, and 351, respectively; (k) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 75, 76, and 77, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 354, 355, and 356, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 81, 82, 83, and 84, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 360, 361, 362, and 363, respectively; or (l) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 75, 76, and 77, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 366, 367, and 368, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 81, 82, 83, and 84, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 372, 373, 374, and 375, respectively.

[1011] In some embodiments, the antibody or antigen-binding portion thereof comprises: (a) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 13, 37, 61, 85, 109, 133, 157, 181, 205, 340, 352, or 364; and (b) a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 1, 25, 49, 73, 97, 121, 145, 169, or 193. In some embodiments, the antibody or antigen-binding portion thereof comprises: (a) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 13 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 1; (b) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 37 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 25; (c) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 61 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 49; (d) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 85 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 73; (e) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 109 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 97; (f) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 133 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 121; (g) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 157 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 145; (h) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 181 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 169; (i) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 205 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 193; (j) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 340 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 73; (k) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 352 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 73; or (l) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 364 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 73.

[1012] In some embodiments, the isolated antibody or antigen-binding portion thereof that binds to *Ebolavirus* comprises: (a) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 14, 38, 62, 86, 110, 134, 158, 182, 206, 341, 353, or 365; and (b) a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 2, 26, 50, 74, 98, 122, 146, 170 or 194. In some embodiments, the isolated antibody or antigen-binding portion thereof comprises: (a) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 14 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 2; (b) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 38 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 26; (c) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 62 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 50; (d) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 86 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 74; (e) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 110 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 98; (f) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 134 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 122; (g) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 158 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 146; (h) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 182 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 170; (i) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 206 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 194; (j) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 341 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 74; (k) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 353 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 74; or (l) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 365 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 74.

[1013] In yet other embodiments, the isolated antibody or antigen-binding portion thereof comprises: (a) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 14 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 2; (b) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 38 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 26; (c) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 62 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 50; (d) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 86 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 74; (e) a variable heavy chain comprising an amino acid sequence comprising SEQ ID

NO: 110 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 98; (f) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 134 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 122; (g) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 158 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 146; (h) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 182 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 170; (i) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 206 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 194; (j) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 341 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 74; (k) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 353 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 74; or (l) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 365 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 74.

[1014] The isolated antibody or antigen-binding portion thereof disclosed herein can be a whole immunoglobulin, an scFv, a Fab fragment, an F(ab')2, or a disulfide linked Fv.

[1015] In some embodiments, the isolated antibody of antigen-binding portion thereof binds to the GP subunit of the *Ebolavirus*. In some embodiments, the antibody or antigen-binding portion thereof binds to the mucin domain of the GP subunit of the *Ebolavirus*. The *Ebolavirus* can be *Zaire ebolavirus, Sudan ebolavirus, Reston ebolavirus, Tai Forest ebolavirus,* or *Bundibugyo ebolavirus*. In some embodiments, the *Ebolavirus* is *Cote d'Ivoire ebolavirus*.

[1016] Also provided herein is a nucleic acid sequence encoding an antibody or antigen-binding portion thereof disclosed herein. The present disclosure also provides an expression vector comprising a promoter operably linked to a nucleotide sequence disclosed herein, such as a nucleic acid sequence encoding an antibody or antigen-binding portion thereof disclosed herein. In some embodiments, the expression vector comprises a nucleotide sequence with the following sequences: (a) SEQ ID NOs: 3, 4, 5, 9, 10, 11, 12, 15, 16, 17, 21, 22, 23, and 24; (b) SEQ ID NOs: 27, 28, 29, 33, 34, 35, 36, 39, 40, 41, 45, 46, 47, and 48; (c) SEQ ID NOs: 51, 52, 53, 57, 58, 59, 60, 63, 64, ,65, 69, 70, 71, and 72; (d) SEQ ID NOs: 75, 76, 77, 81, 82, 83, 84, 87, 88, 89, 93, 94, 95, and 96; (e) SEQ ID NOs: 99, 100, 101, 105, 106, 107, 108, 111, 112, 113, 117, 118, 119, and 120, (f) SEQ ID NOs: 123, 124, 125, 129, 130, 131, 132, 135, 136, 137, 141, 142, 143, and 144; (g) SEQ ID NOs: 147, 148, 149, 153, 154, 155, 156, 159, 160, 161, 165, 166, 167, and 168; (h) SEQ ID NOs: 171, 172, 173, 177, 178, 179, 180, 183, 184, 185, 189, 190, 191, and 192; (i) SEQ ID NOs: 195, 196, 197, 201, 202, 203, 204, 207, 208, 209, 213, 214, 215 and 216; (j) SEQ ID NOs: 75, 76, 77, 81, 82, 83, 84, 342, 343, 344, 348, 349, 350, and 351; (k) SEQ ID NOs: 75, 76, 77, 81, 82, 83, 84, 354, 355, 356, 360, 361, 362, and 363; or (l) SEQ ID NOs: 75, 76, 77, 81, 82, 83, 84, 366, 367, 368, 372, 373, 374, and 375. In some embodiments, the expression vector comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1, 13, 25, 37, 49, 61, 73, 85, 97, 109, 121, 133, 145, 157, 169, 181, 193, 205, 340, 352, and 364. In some embodiments, the expression vector comprises a nucleotide sequence according to SEQ ID NO: 1, 25, 49, 73, 97, 121, 145, 169, or 193. In some embodiments, the expression vector comprises a nucleotide sequence according to SEQ ID NO: 13, 37, 61, 85, 109, 133, 157, 181, 205, 340, 352, or 364. In other embodiments, the expression vector comprises nucleotide sequences with the following sequences: (a) SEQ ID NOs: 1 and 13; (b) SEQ ID NOs: 25 and 37; (c) SEQ ID NOs: 49 and 61; (d) SEQ ID NOs: 73 and 85; (e) SEQ ID NOs: 97 and 109; (f) SEQ ID NOs: 121 and 133; (g) SEQ ID NOs: 145 and 157; (h) SEQ ID NOs: 169 and 181; (i) SEQ ID NOs: 193 and 205; (j) SEQ ID NOs: 73 and 340; (k) SEQ ID NOs: 73 and 352; or (l) SEQ ID NOs: 73 and 364.

[1017] Also provided herein is a host cell comprising an expression vector disclosed herein. In some embodiments, the cell is a bacterial, eukaryotic or mammalian cell. The cell can be a COS-1, COS-7, HEK293, BHK21, CHO, BSC-1, HepG2, SP2/0, HeLa, myeloma or lymphoma cell.

[1018] The present disclosure also provides a method of producing an antibody or antigen-binding portion thereof that binds to *Ebolavirus* disclosed herein. In some embodiments, the method comprises culturing a host cell, such as one disclosed herein, and recovering the antibody or antigen-binding portion thereof.

[1019] The present disclosure also provides compositions comprising an antibody or antigen-binding portion thereof disclosed herein. In some embodiments, the composition is a pharmaceutical composition comprising an antibody or antigen-binding portion thereof. The pharmaceutical composition can further comprise a pharmaceutically acceptable carrier.

[1020] In some embodiments, the composition comprises an antibody or antigen-binding portion thereof disclosed herein and one or more other antibodies or antigen-binding portions thereof. In some embodiments, the one or more other antibodies or antigen-binding portions thereof can bind a protein produced by a virus in the *Filoviridae* family. In some embodiments, the protein is a glycoprotein. The virus can be *Ebolavirus* or *Marburgvirus*. In some embodiments, the virus is *Zaire ebolavirus, Sudan ebolavirus, Reston ebolavirus, Tai Forest ebolavirus, Cote d'Ivoire ebolavirus, Bundibugyo ebolavirus,* Marburg virus or Ravn virus. The composition can further comprise a pharmaceutically acceptable carrier.

[1021] Also provided herein are methods comprising administering an antibody or antigen-binding portion disclosed herein. In one embodiment, a method for reducing, treating or preventing an *Ebolavirus* infection in a subject in need thereof comprising administering to the subject a therapeutically effective amount of the antibody or antigen-binding portion thereof disclosed herein is provided. In some embodiments, a method for reducing, treating or preventing an *Ebolavirus* infection in a subject in need thereof comprises administering to the subject a therapeutically effective amount of a composition disclosed herein. In some embodiments, the subject is a human.

[1022] Methods for detecting *Ebolavirus* in a sample is also provided herein. In some embodiments, the method comprises contacting the sample with an antibody or antigen-binding portion thereof disclosed herein. In some embodiments, the sample is a cell, tissue, or biological fluid from a subject suspected of having or at risk of a filovirus infection.

DETAILED DESCRIPTION

[1023] The present disclosure relates to an antibody or antigen-binding portion thereof that binds to *Ebolavirus* (EBOV), compositions comprising the antibody or antigen-binding portion thereof, methods of producing the antibody or antigen-binding portion thereof and methods of using the antibody or antigen-binding portion thereof, which are described in further detail below.

[1024] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All documents, or portions of documents, cited herein, including but not limited to patents, patent applications, articles, books, and treatises, are hereby expressly incorporated by reference in their entirety for any purpose. In the event that one or more of the incorporated documents or portions of documents define a term that contradicts that term's definition in the application, the definition that appears in this application controls. However, mention of any reference, article, publication, patent, patent publication, and patent application cited herein is not, and should not be taken as an acknowledgment, or any form of suggestion, that they constitute valid prior art or form part of the common general knowledge in any country in the world.

[1025] In the present description, any concentration range, percentage range, ratio range, or integer range is to be understood to include the value of any integer within the recited range and, when appropriate, fractions thereof (such as one tenth and one hundredth of an integer), unless otherwise indicated. As used herein, "about" means ± 20% of the indicated range, value, or structure, unless otherwise indicated. It should be understood that the terms "a" and "an" as used herein refer to "one or more" of the enumerated components unless otherwise indicated. The use of the alternative (*e.g.*, "or") should be understood to mean either one, both, or any combination thereof of the alternatives. As used herein, the terms "include" and "comprise" are used synonymously.

[1026] As used herein, "an antibody that binds to *Ebolavirus* (EBOV)" is used interchangeably with "an anti-EBOV antibody." An anti-EBOV antibody refers to a monoclonal or recombinant antibody or antibody fragment that binds to EBOV with specificity. The antibody can be human, humanized or chimeric. An anti-EBOV antibody or antigen-binding portion thereof includes any antibody or substance having a binding domain with the required specificity. Thus, an anti-EBOV antibody or antigen-binding portion thereof includes antibody fragments, derivatives, functional equivalents and homologues of antibodies, humanized antibodies, including any polypeptide comprising an immunoglobulin binding domain, whether natural or wholly or partially synthetic. Chimeric molecules comprising an immunoglobulin binding domain, or equivalent, fused to another polypeptide are also included. A humanized antibody may be a modified antibody having the variable regions of a non-human, *e.g.*, murine, antibody and the constant region of a human antibody. A humanized antibody may also be a modified antibody having the variable regions of a non-human, *e.g.*, murine, antibody and the framework region(s) of a human antibody.

[1027] As used herein, the term "humanized" refers to a process of making an antibody or immunoglobulin binding proteins and polypeptides derived from a non-human species (*e.g.*, mouse or rat) less immunogenic to humans, while still retaining antigen-binding properties of the original antibody, using genetic engineering techniques. In some embodiments, the binding domain(s) of an antibody or immunoglobulin binding proteins and polypeptides (*e.g.*, light and heavy chain variable regions, Fab, scFv) are humanized. If derived from a non-human source, other regions of the antibody or immunoglobulin binding proteins and polypeptides, such as the hinge region and constant region domains, can also be humanized.

[1028] The terms “light chain variable region” (also referred to as “light chain variable domain” or “VL” or V_L) and “heavy chain variable region” (also referred to as “heavy chain variable domain” or “VH” or V_H) refer to the variable binding region from an antibody light and heavy chain, respectively. The variable binding regions are made up of discrete, well-defined sub-regions known as “complementarity determining regions” (CDRs) and “framework regions” (FRs). In one embodiment, the FRs are humanized. The term “CL” refers to an “immunoglobulin light chain constant region” or a “light chain constant region,” i.e., a constant region from an antibody light chain. The term “CH” refers to an “immunoglobulin heavy chain constant region” or a “heavy chain constant region,” which is further divisible, depending on the antibody isotype into CH1, CH2, and CH3 (IgA, IgD, IgG), or CH1, CH2, CH3, and CH4 domains (IgE, IgM). A "Fab" (fragment antigen binding) is the part of an antibody that binds to antigens and includes the variable region and CH1 domain of the heavy chain linked to the light chain via an inter-chain disulfide bond.

[1029] The six “complementarity determining regions” or “CDRs” present in an antibody antigen-binding domain are short, non-contiguous sequences of amino acids that are specifically positioned to form the binding domain as the antibody assumes its three dimensional configuration in an aqueous environment. The remainder of the amino acids in the binding domain, referred to as "framework" regions, show less inter-molecular variability. The framework regions largely adopt a β-sheet conformation and the CDRs form loops which connect, and in some cases form part of, the β-sheet structure. Thus, framework regions act to form a scaffold that provides for positioning the CDRs in correct orientation by inter-chain, non-covalent interactions. The binding domain formed by the positioned CDRs defines a surface complementary to the epitope on the immunoreactive antigen. This complementary surface promotes the non-covalent binding of the antibody to its cognate epitope. The amino acids that make up the CDRs and the framework regions, respectively, can be readily identified for any given heavy or light chain variable region by one of ordinary skill in the art, since they have been defined in various different ways (see, "Sequences of Proteins of Immunological Interest," Kabat, E., et al., U.S. Department of Health and Human Services, (1983); and Chothia and Lesk, J. Mol. Biol., 196:901-917 (1987), which are incorporated herein by reference in their entireties). In some embodiments, an antibody, or antigen-binding fragment thereof, contains at least one heavy chain variable region and/or at least one light chain variable region. The heavy chain variable region (or light chain variable region) typically contains three CDRs and four framework regions (FRs), arranged from amino-terminus to carboxyl-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.

[1030] In the case where there are two or more definitions of a term which is used and/or accepted within the art, the definition of the term as used herein is intended to include all such meanings unless explicitly stated to the contrary. A specific example is the use of the term "complementarity determining region" ("CDR") to describe the non-contiguous antigen combining sites found within the variable region of both heavy and light chain polypeptides. These particular regions have been described, for example, by Kabat et al., U.S. Dept. of Health and Human Services, "Sequences of Proteins of Immunological Interest" (1983) and by Chothia et al., J. Mol. Biol. 196:901-917 (1987), which are incorporated herein by reference. The Kabat and Chothia definitions include overlapping or subsets of amino acids when compared against each other. Nevertheless, application of either definition (or other definitions known to those of ordinary skill in the art) to refer to a CDR of an antibody or variant thereof is intended to be within the scope of the term as defined and used herein, unless otherwise indicated. The appropriate amino acids which encompass the CDRs as defined by each of the above cited references are set forth below in Table 1 as a comparison. The exact amino acid numbers which encompass a particular CDR will vary depending on the sequence and size of the CDR. Those skilled in the art can routinely determine which amino acids comprise a particular CDR given the variable region amino acid sequence of the antibody.

Table 1: CDR Definitions*

	Kabat	Chothia
VH CDR1	31-35	26-32
VH CDR2	50-65	52-58
VH CDR3	95-102	95-102
VL CDR1	24-34	26-32
VL CDR2	50-56	50-52
VL CDR3	89-97	91-96

[1031] *Numbering of all CDR definitions in Table 1 is according to the numbering conventions set forth by Kabat et al. (see below).

[1032] CDRs can also be determined using IMGT® (the international ImMunoGeneTics information system®) numbering. H: heavy chain; K: kappa or L: light chain. Kabat et al.

also defined a numbering system for variable domain sequences that is applicable to any antibody. One of ordinary skill in the art can unambiguously assign this system of "Kabat numbering" to any variable domain sequence, without reliance on any experimental data beyond the sequence itself. As used herein, "Kabat numbering" refers to the numbering system set forth by Kabat et al., U.S. Dept. of Health and Human Services, "Sequence of Proteins of Immunological Interest" (1983). Unless use of the Kabat numbering system is explicitly noted, however, consecutive numbering is used for all amino acid sequences in this disclosure.

[1033] As used herein, the term "antigen-binding portion," "antigen-binding region" "or antigen-binding domain" refers to the domain, region, portion, or site of a protein, polypeptide, oligopeptide, or peptide or antibody or binding domain derived from an antibody that possesses the ability to specifically recognize and bind to an antigen. Exemplary binding antigen-binding portions include single-chain antibody variable regions (*e.g.*, domain antibodies, sFv, scFv, scFab). In certain embodiments, the binding domain comprises or consists of an antigen binding site (*e.g.*, comprising a variable heavy chain sequence and variable light chain sequence or three light chain complementary determining regions (CDRs) and three heavy chain CDRs from an antibody placed into alternative framework regions (FRs) (*e.g.*, human FRs optionally comprising one or more amino acid substitutions). A variety of assays are known for identifying binding domains of the present disclosure that specifically bind a particular target, including Western blot, ELISA, phage display library screening, and BIACORE® interaction analysis.

[1034] An antibody or antigen-binding portion "specifically binds" an antigen if it binds the antigen with an affinity or K_a (*i.e.*, an equilibrium association constant of a particular binding interaction with units of 1/M) equal to or greater than 10^5 M^{-1}, while not significantly binding other components present in a test sample. The antibody or antigen-binding portion can be classified as "high affinity" or "low affinity." "High affinity" refer to those antibodies or antigen-binding portions with a K_a of at least about 10^7 M^{-1}, at least about 10^8 M^{-1}, at least about 10^9 M^{-1}, at least about 10^{10} M^{-1}, at least about 10^{11} M^{-1}, at least about 10^{12} M^{-1}, or at least about 10^{13} M^{-1}. "Low affinity" r refer to those antibodies or antigen-binding portions with a K_a of up to 10^7 M^{-1}, up to 10^6 M^{-1}, up to 10^5 M^{-1}. Alternatively, affinity can be defined as an equilibrium dissociation constant (K_d) of a particular binding interaction with units of M (*e.g.*, 10^{-5} M to 10^{-13} M). Affinities of refer to those antibodies or antigen-binding portions according to the present disclosure can be readily determined using conventional techniques (*see, e.g.*, Scatchard et al. (1949) Ann. N.Y. Acad. Sci. 51:660; and U.S. Patent Nos. 5,283,173, 5,468,614, or the equivalent).

[1035] As used herein, “reference antibody” refers to an antibody that is known in the art and which serves the basis for a humanized, chimeric or recombinant antibody. The reference antibody may be a non-human, (*e.g.*, murine), human, humanized, chimeric and / or recombinant antibody or antibody-like polypeptide.

[1036] “Treatment” or “treating” refers to either a therapeutic treatment or prophylactic/preventative treatment. A therapeutic treatment may improve at least one symptom of disease in an individual receiving treatment or may delay worsening of a progressive disease in an individual, or prevent onset of additional associated diseases.

[1037] Ameliorating or reducing or reduction of infection, as used herein, can include but is not limited to delaying the onset of the infection, attenuating the symptoms of the infection, shortening the duration of the infection, reducing the viral titer in a patient (eg. in the blood), or slowing the progression of the infection. Filovirus infections encompassed by the present application include, but are not limited to, *Marburgvirus* and *Ebolavirus*.

[1038] A “therapeutically effective amount,” “therapeutically effective dose” or “effective dose” refers to that amount of the antibody or compound sufficient to result in amelioration of one or more symptoms of the disease being treated. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered serially or simultaneously. One or more specific therapeutic molecules may be administered according to methods of the invention, each in an effective dose. The effective dose can be determined empirically through dose studies. The term “therapeutically effective amount” is used interchangeably with “prophylactically effective amount” herein, and refers to an amount that prevents infection with EBOV, prevents disease associated with EBOV infection, reduces the number and/or severity of symptoms of an EBOV infection, stops or limits the spread of EBOV, and/or shortens the duration of an EBOV infection.

[1039] As used herein, the term "pharmaceutically acceptable" refers to molecular entities and compositions that do not generally produce allergic or other serious adverse reactions when administered using routes well known in the art. Molecular entities and compositions approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans are considered to be “pharmaceutically acceptable.”

[1040] As used herein, the terms "nucleic acid," "nucleic acid molecule," or "polynucleotide" refer to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. Unless specifically limited, the terms encompass nucleic acids containing analogues of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions) and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions can be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al.* (1991) *Nucleic Acid Res.* 19:5081; Ohtsuka *et al.* (1985) *J. Biol. Chem.* 260:2605-2608; Cassol *et al.* (1992); Rossolini *et al.* (1994) *Mol. Cell. Probes* 8:91-98). The term nucleic acid is used interchangeably with gene, cDNA, and mRNA encoded by a gene. As used herein, the terms "nucleic acid," "nucleic acid molecule," or "polynucleotide" are intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof.

[1041] The term “expression vector,” as used herein, refers to a nucleic acid molecule, linear or circular, comprising one or more expression units. In addition to one or more expression units, an expression vector can also include additional nucleic acid segments such as, for example, one or more origins of replication or one or more selectable markers. Expression vectors are generally derived from plasmid or viral DNA, or can contain elements of both.

[1042] As used herein, the term “sequence identity” refers to a relationship between two or more polynucleotide sequences or between two or more polypeptide sequences. When a position in one sequence is occupied by the same nucleic acid base or amino acid residue in the corresponding position of the comparator sequence, the sequences are said to be “identical” at that position. The percentage “sequence identity” is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of “identical” positions. The number of “identical” positions is then divided by the total number of positions in the comparison window and multiplied by 100 to yield the percentage of “sequence identity.” Percentage of “sequence identity” is determined by comparing two optimally aligned sequences over a comparison window. The comparison window for nucleic acid sequences can be, for instance, at least about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 300, 400, 500, 600, 700, 800, 900 or 1000 or more nucleic acids in length. The comparison window for polypeptide sequences can be, for instance, at least about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 300 or more amino acids in length. In order to optimally align sequences for comparison, the portion of a polynucleotide or polypeptide sequence in the comparison window can comprise additions or deletions termed gaps while the reference sequence is kept constant. An optimal alignment is that alignment which, even with gaps, produces the greatest possible number of "identical" positions between the reference and comparator sequences. Percentage "sequence identity" between two sequences can be determined using the version of the program "BLAST 2 Sequences" which was available from the National Center for Biotechnology Information as of September 1, 2004, which program incorporates the programs BLASTN (for nucleotide sequence comparison) and BLASTP (for polypeptide sequence comparison), which programs are based on the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90(12):5873-5877, 1993). When utilizing "BLAST 2 Sequences," parameters that were default parameters as of September 1, 2004, can be used for word size (3), open gap penalty (11), extension gap penalty (1), gap dropoff (50), expect value (10) and any other required parameter including but not limited to matrix option. Two nucleotide or amino acid sequences are considered to have "substantially similar sequence identity" or "substantial sequence identity" if the two sequences have at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% sequence identity relative to each other.

[1043] The present disclosure relates to an antibody or antigen-binding portion thereof that binds to *Ebolavirus* (EBOV), compositions comprising the antibody or antigen-binding portion thereof, methods of producing the antibody or antigen-binding portion thereof and methods of using the antibody or antigen-binding portion thereof.

[1044] The terms "antibody that binds to *Ebolavirus* (EBOV)," and "anti-EBOV antibody" are used interchangeably herein. Examples of an anti-EBOV antibody or antigen-binding portion thereof, include, but are not limited to, (i) the Fab fragment consisting of VL, VH, CL and CH domains; (ii) the Fd fragment consisting of the VH and CH domains; (iii) the Fv fragment consisting of the VL and VH domains of a single antibody (e.g., linked by a disulfide bond); (iv) the dAb fragment (Ward, E. S. et al., Nature 341: 544-546 (1989)) which consists of a VH domain; (v) isolated CDR regions; (vi) F(ab')$_2$ a bivalent fragment comprising two linked Fab fragments; (vii) single chain Fv molecules (scFv), wherein a VH domain and a VL domain are linked by a peptide linker which allows the two domains to associate to form an antigen binding site (Bird et al., Science 242: 423-426 (1988); Huston et al., PNAS USA 85: 5879-5883 (1988)); (viii) bispecific single chain Fv dimers (PCT/US92/09965); (ix) "diabodies", multivalent or multispecific fragments constructed by gene fusion (WO94/13804; P. Hollinger et al., Proc. Natl. Acad. Sci. USA 90: 6444-6448 (1993)); and (x) whole immunoglobulin.

[1045] In one embodiment, an "anti-EBOV antibody" is a recombinant anti-EBOV antibody or polypeptide. Recombinant anti-EBOV antibodies and polypeptides include, for instance, Fc fusions, toxin fusions, fusions to enzymatic activities, minibodies, diabodies, linear antibodies, single chain antibodies, bispecific antibody fragments, scFv and Fab fragments. A recombinant anti-EBOV antibody includes a molecule or polypeptide that incorporates an amino acid sequence derived from an anti-EBOV antibody and which is capable of binding EBOV with specificity. Recombinant anti-EBOV antibodies include molecules that are optimized, for instance, for stability, solubility, *in vitro* and *in vivo* binding.

[1046] In one embodiment, an anti-EBOV antibody is a diabody. Diabodies are multimers of polypeptides, each polypeptide comprising a first domain comprising a binding region of an immunoglobulin light chain and a second domain comprising a binding region of an immunoglobulin heavy chain, the two domains being linked (*e.g.*, by a peptide linker) but unable to associated with each other to form an antigen binding site: antigen binding sites are formed by the association of the first domain of one polypeptide within the multimer with the second domain of another polypeptide within the multimer. See WO94/13804 which is incorporated by reference in its entirety.

[1047] In one embodiment, an anti-EBOV antibody is a scFv. A scFv is constructed by joining a variable heavy chain and a variable light chain with a linker using recombinant methods. The linker that enables the V_H and V_L regions to be made as a single chain protein. See, for instance, Bird *et al.*, 1988, *Science* 242:423-426 and Huston *et al.*, 1988, *Proc. Natl. Acad. Sci. USA* 85:5879-5883. In one embodiment, the scFv comprises V_H and V_L regions that are identical or derived from a reference anti-EBOV antibody.

[1048] In one embodiment, an anti-EBOV antibody or antigen-binding portion thereof is an Fv. An Fv is an antibody fragment which contains a complete antigen-recognition and binding site. This region consists of a dimer of one heavy and one light chain variable domain in tight, non-covalent or covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L

dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site. In one embodiment, the Fv comprises V_H and V_L regions that are identical or derived from a reference anti-EBOV antibody.

[1049] In one embodiment of the invention, an anti-EBOV antibody is a single chain polypeptide comprising, from amino to carboxyl terminus, a binding domain (*e.g.*, scFv), an immunoglobulin hinge region and an immunoglobulin constant region. In this embodiment, also known as a small modular immunopharmaceutical (SMIP), the single chain polypeptide forms a dimer in solution.

[1050] The anti-EBOV antibody or antigen-binding portion thereof can be a recombinant polypeptide, fusion protein or immunoconjugate that binds EBOV and comprise an antibody fragment or are derived in part from a monoclonal or polyclonal anti-EBOV antibody. In some embodiments, an anti-EBOV antibody or antigen-binding portion thereof is a molecule or polypeptide that is derived from a reference anti-EBOV antibody and is capable of binding with specificity to the same epitope as the reference anti-EBOV antibody. In some embodiments, the epitope is on the GP subunit of EBOV. Thus, in one embodiment, the anti-EBOV antibody or antigen-binding portion thereof binds to the GP subunit of the *Ebolavirus*. In some embodiments, the mucin domain of the GP subunit of the *Ebolavirus*. The GP subunit can be of the *Zaire ebolavirus, Sudan ebolavirus, Reston ebolavirus, Tai Forest ebolavirus,* or *Bundibugyo ebolavirus.*

[1051] An anti-EBOV derived from a reference anti-EBOV antibody can include a molecule or polypeptide comprising at least about 10 contiguous amino acids, at least about 20 contiguous amino acids or at least about 50 or more contiguous amino acids as the reference anti-EBOV antibody.

[1052] In one embodiment, an anti-EBOV antibody or antigen-binding portion thereof comprises a heavy chain CDR1, heavy chain CDR2, heavy chain CDR3, light chain CDR1, light chain CDR2, and/or light chain CDR3 with the same amino acid sequence as a reference anti-EBOV antibody. In another embodiment, an anti-EBOV antibody or antigen-binding portion thereof comprises a heavy chain CDR1, heavy chain CDR2, heavy chain CDR3, light chain CDR1, light chain CDR2, and/or light chain CDR3 that has an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence of the respective heavy chain CDR1, heavy chain CDR2, heavy chain CDR3, light chain CDR1, light chain CDR2, and/or light chain CDR3 of a reference anti-EBOV antibody.

[1053] In another embodiment, an anti-EBOV antibody or antigen-binding portion thereof comprises a VH and/or VL with the same amino acid sequence as a reference anti-EBOV molecule. In another embodiment, an anti-EBOV antibody or antigen-binding portion thereof comprises a VH and/or VL that has an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence of the respective VH and/or VL of a reference anti-EBOV molecule.

[1054] In some embodiments, the reference anti-EBOV molecule is a murine anti-EBOV antibody. In one embodiment, the reference anti-EBOV molecule is the murine anti-EBOV antibody CAN7G1. In another embodiment, the reference anti-EBOV molecule is the murine anti-EBOV antibody CAN8G1. In yet another embodiment, the reference anti-EBOV molecule is the murine anti-EBOV antibody CAN9G1. The CDRs, VHs and VLs of these murine antibodies are provided in Table 2.

__Table 2__

Name	Chain, Region	Origin	Sequence	SEQ ID NO
huCAN7G1	K, Variable region	Artificial sequence	atggctcagatcgtgctgtcccagtcccccgccatcctgtccctgtcccccggcgagcgcgccaccctgtcctgccgcgcctcctcctccgtgtcctacatgcactggtaccaccagaaccccggctcctcccccaagccctggatctacgccacctccaacctggccaccggcatccccgcccgcttctccggctccggctccggcaccgactacaccctgaccatctcctccctggagcccgaggacttcgccgtgtactactgccagcagtggtcctccaacccccccaccttcggcggcggcaccaaggtggagatcaagc	**1**
huCAN7G1	K, Variable region	Artificial sequence	MAQIVLSQSPAILSLSPGERATLSCRASSSVSYMHWYHQNPGSSPKPWIYATSNLATGIPARFSGSGSGTDYTLTISSLEPEDFAVYYCQQWSSNPPTFGGGTKVEIK	**2**
huCAN7G1	K, CDR1	Artificial sequence	gcctcctcctccgtgtcctac	**3**
huCAN7G1	K, CDR2	Artificial sequence	gccacctcc	**4**
huCAN7G1	K, CDR3	Artificial sequence	cagcagtggtcctccaacccccccacc	**5**
huCAN7G1	K, CDR1	Artificial sequence	ASSSVSY	**6**
huCAN7G1	K, CDR2	Artificial sequence	ATS	**7**
huCAN7G1	K, CDR3	Artificial sequence	QQWSSNPPT	**8**
huCAN7G1	K, FR1	Artificial sequence	atggctcagatcgtgctgtcccagtcccccgccatcctgtccctgtcccccggcgagcgcgccaccctgtcctgccgc	**9**
huCAN7G1	K, FR2	Artificial sequence	atgcactggtaccaccagaaccccggctcctcccccaagccctggatctac	**10**
huCAN7G1	K, FR3	Artificial	aacctggccaccggcatccccgcccgcttctccggctccggctccggcaccga	**11**

		sequence	ctacaccctgaccatctcctccctggagcccgaggacttcgccgtgtactactgc	
huCAN7G1	K, FR4	Artificial sequence	ttcggcggcggcaccaaggtggagatcaagc	**12**
huCAN7G1	H, Variable region	Artificial sequence	gaggtgcagctgcagcagtccggccccgagctggtgaagcccggcgcctccgtgaaggtgtcctgcaaggcctccggctacaccttcacctcctacgtgatgcactgggtgcgccaggcccccggccagggcctggagtggatcggctacatcaacccctacaacgacggccccaagtacaacgagaagttcaagggccgcgtgaccctgacctccgacacctccgcccgcaccgcctacatggagctgtcctccctgcgctccgaggacaccgccgtgttctactgcgcccgcggccgcggcgacgcctacttctacgtgctggactactggggccagggcaccctggtgaccgtgtcctccg	**13**
huCAN7G1	H, Variable region	Artificial sequence	EVQLQQSGPELVKPGASVKVSCKASGYTFTSYVMHWVRQAPGQGLEWIGYINPYNDGPKYNEKFKGRVTLTSDTSARTAYMELSSLRSEDTAVFYCARGRGDAYFYVLDYWGQGTLVTVSS	**14**
huCAN7G1	H, CDR1	Artificial sequence	ggctacaccttcacctcctacgtg	**15**
huCAN7G1	H, CDR2	Artificial sequence	atcaacccctacaacgacggcccc	**16**
huCAN7G1	H, CDR3	Artificial sequence	gcccgcggccgcggcgacgcctacttctacgtgctggactac	**17**
huCAN7G1	H, CDR1	Artificial sequence	GYTFTSYV	**18**
huCAN7G1	H, CDR2	Artificial sequence	INPYNDGP	**19**
huCAN7G1	H, CDR3	Artificial sequence	ARGRGDAYFYVLDY	**20**
huCAN7G1	H, FR1	Artificial sequence	gaggtgcagctgcagcagtccggccccgagctggtgaagcccggcgcctccgtgaaggtgtcctgcaaggcctcc	**21**
huCAN7G1	H, FR2	Artificial sequence	atgcactgggtgcgccaggcccccggccagggcctggagtggatcggctac	**22**
huCAN7G1	H, FR3	Artificial sequence	aagtacaacgagaagttcaagggccgcgtgaccctgacctccgacacctccgcccgcaccgcctacatggagctgtcctccctgcgctccgaggacaccgccgtgttctactgc	**23**
huCAN7G1	H, FR4	Artificial sequence	tggggccagggcaccctggtgaccgtgtcctccg	**24**
rehuCAN7G1	K, Variable region	Artificial sequence	cagatcgtgctgtcccagtcccccgccatcctgtccgcctcccccggcgagcgcgtgaccatgtcctgccgcgcctcctcctccgtgtcctacatgcactggtaccaccagaacccggctcctcccccaagccctggatctacgccacctccaacctggccaccggcgtgcccgcccgcttctccggctccggctccggcaccgactactccctgaccatctcctccgtggagcccgaggacttcgccacctactactgccagcagtggtcctccaacccccccaccttcggcggcggcaccaagctggagatcaag	**25**
rehuCAN7G1	K, variable region	Artificial sequence	QIVLSQSPAILSASPGERVTMSCRASSSVSYMHWYHQNPGSSPKPWIYATSNLATGVPARFSGSGSGTDYSLTISSVEPEDFATYYCQQWSSNPPTFGGGTKLEIK	**26**
rehuCAN7G1	K, CDR1	Artificial sequence	gcctcctcctccgtgtcctac	**27**
rehuCAN7G1	K, CDR2	Artificial sequence	gccacctcc	**28**
rehuCAN7G1	K, CDR3	Artificial sequence	cagcagtggtcctccaacccccccacc	**29**
rehuCAN7G1	K, CDR1	Artificial sequence	ASSSVSY	**30**
rehuCAN7G1	K, CDR2	Artificial sequence	ATS	**31**
rehuCAN7G1	K, CDR3	Artificial sequence	QQWSSNPPT	**32**
rehuCAN7G1	K, FR1	Artificial	cagatcgtgctgtcccagtcccccgccatcctgtccgcctcccccggcgagcgc	**33**

		sequence	gtgaccatgtcctgccgc	
rehuCAN7G1	K, FR2	Artificial sequence	atgcactggtaccaccagaaccccggctcctcccccaagccctggatctac	**34**
rehuCAN7G1	K, FR3	Artificial sequence	aacctggccaccggcgtgcccgcccgcttctccggctccggctccggcaccgactactccctgaccatctcctccgtggagcccgaggacttcgccacctactactgc	**35**
rehuCAN7G1	K, FR4	Artificial sequence	ttcggcggcggcaccaagctggagatcaag	**36**
rehuCAN7G1	H, Variable region	Artificial sequence	gaggtgcagctgcagcagtccggccccgagctggtgaagcccggcgcctccgtgaagatgtcctgcaaggcctccggctacaccttcacctcctacgtgatgcactgggtgaagcaggcccccggccagggcctggagtggatcggctacatcaacccctacaacgacggccccaagtacaacgagaagttcaagggccgcgccaccctgacctccgacacctccgcccgcaccgcctacatggagctgtcctccctgcgctccgaggacaccgccgtgttctactgcgcccgcggccgcggcgacgcctacttctacgtgctggactactggggccagggcaccctggtgaccgtgtcctcc	**37**
rehuCAN7G1	H, variable region	Artificial sequence	EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQAPGQGLEWIGYINPYNDGPKYNEKFKGRATLTSDTSARTAYMELSSLRSEDTAVFYCARGRGDAYFYVLDYWGQGTLVTVSS	**38**
rehuCAN7G1	H, CDR1	Artificial sequence	ggctacaccttcacctcctacgtg	**39**
rehuCAN7G1	H, CDR2	Artificial sequence	atcaacccctacaacgacggcccc	**40**
rehuCAN7G1	H, CDR3	Artificial sequence	gcccgcggccgcggcgacgcctacttctacgtgctggactac	**41**
rehuCAN7G1	H, CDR1	Artificial sequence	GYTFTSYV	**42**
rehuCAN7G1	H, CDR2	Artificial sequence	INPYNDGP	**43**
rehuCAN7G1	H, CDR3	Artificial sequence	ARGRGDAYFYVLDY	**44**
rehuCAN7G1	H, FR1	Artificial sequence	gaggtgcagctgcagcagtccggccccgagctggtgaagcccggcgcctccgtgaagatgtcctgcaaggcctcc	**45**
rehuCAN7G1	H, FR2	Artificial sequence	atgcactgggtgaagcaggcccccggccagggcctggagtggatcggctac	**46**
rehuCAN7G1	H, FR3	Artificial sequence	aagtacaacgagaagttcaagggccgcgccaccctgacctccgacacctccgcccgcaccgcctacatggagctgtcctccctgcgctccgaggacaccgccgtgttctactgc	**47**
rehuCAN7G1	H, FR4	Artificial sequence	tggggccagggcaccctggtgaccgtgtcctcc	**48**
cdrCAN7G1	K, Variable region	Artificial sequence	gagatcgtgctgacccagtcccccgccaccctgtccctgtcccccggcgagcgcgccaccctgtcctgccgcgcctcctcctccgtgtcctacctggcctggtaccagcagaagcccggccaggcccccgcctgctgatctacgccacctccaaccgcgccaccggcatccccgcccgcttctccggctccggctccggcaccgacttcaccctgaccatctcctccctggagcccgaggacttcgccgtgtactactgccagcagtggtcctccaacccccccaccttcggcggcggcaccaaggtggagatcaag	**49**
cdrCAN7G1	K, variable region	Artificial sequence	EIVLTQSPATLSLSPGERATLSCRASSSVSYLAWYQQKPGQAPRLLIYATSNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQWSSNPPTFGGGTKVEIK	**50**
cdrCAN7G1	K, CDR1	Artificial sequence	gcctcctcctccgtgtcctac	**51**
cdrCAN7G1	K, CDR2	Artificial sequence	gccacctcc	**52**
cdrCAN7G1	K, CDR3	Artificial sequence	cagcagtggtcctccaacccccccacc	**53**
cdrCAN7G1	K,	Artificial	ASSSVSY	**54**

	CDR1	sequence		
cdrCAN7G1	K, CDR2	Artificial sequence	ATS	**55**
cdrCAN7G1	K, CDR3	Artificial sequence	QQWSSNPPT	**56**
cdrCAN7G1	K, FR1	Artificial sequence	gagatcgtgctgacccagtcccccgccaccctgtccctgtcccccggcgagcgcgccaccctgtcctgccgc	**57**
cdrCAN7G1	K, FR2	Artificial sequence	ctggcctggtaccagcagaagcccggccaggcccccgcctgctgatctac	**58**
cdrCAN7G1	K, FR3	Artificial sequence	aaccgcgccaccggcatccccgcccgcttctccggctccggctccggcaccgacttcaccctgaccatctcctccctggagcccgaggacttcgccgtgtactactgc	**59**
cdrCAN7G1	K, FR4	Artificial sequence	ttcggcggcggcaccaaggtggagatcaag	**60**
cdrCAN7G1	H, Variable region	Artificial sequence	caggtgcagctggtgcagtccggcgccgaggtgaagaagcccggcgcctccgtgaaggtgtcctgcaaggcctccggctacaccttcacctcctacgtgatgcactgggtgcgccaggcccccggccagcgcctggagtggatgggctggatcaacccctacaacgacggccccaagtactcccagaagttccagggccgcgtgaccatcacccgcgacacctccgcctccaccgcctacatggagctgtcctccctgcgctccgaggacaccgccgtgtactactgcgcccgcggccgcggcgacgcctacttctacgtgctggactactggggccagggcaccctggtgaccgtgtcctcc	**61**
cdrCAN7G1	H, variable region	Artificial sequence	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYVMHWVRQAPGQRLEWMGWINPYNDGPKYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARGRGDAYFYVLDYWGQGTLVTVSS	**62**
cdrCAN7G1	H, CDR1	Artificial sequence	ggctacaccttcacctcctacgtg	**63**
cdrCAN7G1	H, CDR2	Artificial sequence	atcaacccctacaacgacggcccc	**64**
cdrCAN7G1	H, CDR3	Artificial sequence	gcccgcggccgcggcgacgcctacttctacgtgctggactac	**65**
cdrCAN7G1	H, CDR1	Artificial sequence	GYTFTSYV	**66**
cdrCAN7G1	H, CDR2	Artificial sequence	INPYNDGP	**67**
cdrCAN7G1	H, CDR3	Artificial sequence	ARGRGDAYFYVLDY	**68**
cdrCAN7G1	H, FR1	Artificial sequence	caggtgcagctggtgcagtccggcgccgaggtgaagaagcccggcgcctccgtgaaggtgtcctgcaaggcctcc	**69**
cdrCAN7G1	H, FR2	Artificial sequence	atgcactgggtgcgccaggcccccggccagcgcctggagtggatgggctgg	**70**
cdrCAN7G1	H, FR3	Artificial sequence	aagtactcccagaagttccagggccgcgtgaccatcacccgcgacacctccgcctccaccgcctacatggagctgtcctccctgcgctccgaggacaccgccgtgtactactgc	**71**
cdrCAN7G1	H, FR4	Artificial sequence	tggggccagggcaccctggtgaccgtgtcctcc	**72**
huCAN8G1	K, Variable region	Artificial sequence	gagatcgtgctgacccagtcccccgccaccctgtccgtgtcccccggcgagcgcgccaccatctcctgctccgtgtcctcctccatctcctcctccaacctgcactggtaccagcagaagcccggcacctcccccaagccctggatctacggcacctccaacctggccaccggcgtgcccgcccgcttctccggctccggctccggcaccgacttcaccctgaccatctcctccctgcagtccgaggacttcgccctgtactactgccaccagtacctgtcctcctggaccttcggcggcggcaccaaggtggagatcaag	**73**
huCAN8G1	K, variable region	Artificial sequence	EIVLTQSPATLSVSPGERATISCSVSSSISSSNLHWYQQKPGTSPKPWIYGTSNLATGVPARFSGSGSGTDFTLTISSLQSEDFALYYCHQYLSSWTFGGGTKVEIK	**74**
huCAN8G1	K, CDR1	Artificial sequence	tcctccatctcctcctccaac	**75**
huCAN8G1	K, CDR2	Artificial sequence	ggcacctcc	**76**

huCAN8G1	K, CDR3	Artificial sequence	caccagtacctgtcctcctggacc	**77**
huCAN8G1	K, CDR1	Artificial sequence	SSISSSN	**78**
huCAN8G1	K, CDR2	Artificial sequence	GTS	**79**
huCAN8G1	K, CDR3	Artificial sequence	HQYLSSWT	**80**
huCAN8G1	K, FR1	Artificial sequence	gagatcgtgctgacccagtcccccgccaccctgtccgtgtcccccggcgagcgcgccaccatctcctgctccgtgtcc	**81**
huCAN8G1	K, FR2	Artificial sequence	ctgcactggtaccagcagaagcccggcacctcccccaagccctggatctac	**82**
huCAN8G1	K, FR3	Artificial sequence	aacctggccaccggcgtgcccgcccgcttctccggctccggctccggcaccgacttcaccctgaccatctcctccctgcagtccgaggacttcgccctgtactactgc	**83**
huCAN8G1	K, FR4	Artificial sequence	ttcggcggcggcaccaaggtggagatcaag	**84**
huCAN8G1	H, Variable region	Artificial sequence	caggtgaccctgaaggagtccggccccggcatcctgcagccctcccagaccctgtccctgacctgcaccttctccggcttctccctgtccacctccggcatgtccgtgggctggttccgccagcccccggcaagggcctggagtggctggcccacatctggtggaccgacgacaagtactacaaccccgccctgaagtcccgcctgaccatctccaaggacacctccaacaaccaggtggtgctgaccatgaccaacatggaccccgtggacaccgccacctactactgcgcccgcatcggctacgacggcccccccgactactggggccagggcaccctggtgaccgtgtcctcc	**85**
huCAN8G1	H, variable region	Artificial sequence	QVTLKESGPGILQPSQTLSLTCTFSGFSLSTSGMSVGWFRQPPGKGLEWLAHIWWTDDKYYNPALKSRLTISKDTSNNQVVLTMTNMDPVDTATYYCARIGYDGPPDYWGQGTLVTVSS	**86**
huCAN8G1	H, CDR1	Artificial sequence	ggcttctccctgtccacctccggcatgtcc	**87**
huCAN8G1	H, CDR2	Artificial sequence	atctggtggaccgacgacaag	**88**
huCAN8G1	H, CDR3	Artificial sequence	gcccgcatcggctacgacggcccccccgactac	**89**
huCAN8G1	H, CDR1	Artificial sequence	GFSLSTSGMS	**90**
huCAN8G1	H, CDR2	Artificial sequence	IWWTDDK	**91**
huCAN8G1	H, CDR3	Artificial sequence	ARIGYDGPPDY	**92**
huCAN8G1	H, FR1	Artificial sequence	caggtgaccctgaaggagtccggccccggcatcctgcagccctcccagaccctgtccctgacctgcaccttctcc	**93**
huCAN8G1	H, FR2	Artificial sequence	gtgggctggttccgccagcccccggcaagggcctggagtggctggcccac	**94**
huCAN8G1	H, FR3	Artificial sequence	tactacaaccccgccctgaagtcccgcctgaccatctccaaggacacctccaacaaccaggtggtgctgaccatgaccaacatggaccccgtggacaccgccacctactactgc	**95**
huCAN8G1	H, FR4	Artificial sequence	tggggccagggcaccctggtgaccgtgtcctcc	**96**
rehuCAN8G1	K, Variable region	Artificial sequence	gagatcgtgctgacccagtcccccgccaccatgtccgcctcccccggcgagcgcgtgaccatctcctgctccgtgtcctcctccatctcctcctccaacctgcactggtaccagcagaagcccggcacctcccccaagccctggatctacggcacctccaacctggccaccggcgtgcccgcccgcttctccggctccggctccggcaccgacttcaccctgaccatctcctccgtgcagtccgaggacttcaccctgtactactgccaccagtacctgtcctcctggaccttcggcggcggcaccaagctggagatcaag	**97**
rehuCAN8G1	K, variable region	Artificial sequence	EIVLTQSPATMSASPGERVTISCSVSSSISSSNLHWYQQKPGTSPKPWIYGTSNLATGVPARFSGSGSGTDFTLTISSVQSEDFTLYYCHQYLSSWTFGGGTKLEIK	**98**
rehuCAN8G1	K, CDR1	Artificial sequence	tcctccatctcctcctccaac	**99**

rehuCAN8G1	K, CDR2	Artificial sequence	ggcacctcc	**100**
rehuCAN8G1	K, CDR3	Artificial sequence	caccagtacctgtcctcctggacc	**101**
rehuCAN8G1	K, CDR1	Artificial sequence	SSISSSN	**102**
rehuCAN8G1	K, CDR2	Artificial sequence	GTS	**103**
rehuCAN8G1	K, CDR3	Artificial sequence	HQYLSSWT	**104**
rehuCAN8G1	K, FR1	Artificial sequence	gagatcgtgctgacccagtcccccgccaccatgtccgcctcccccggcgagcgcgtgaccatctcctgctccgtgtcc	**105**
rehuCAN8G1	K, FR2	Artificial sequence	ctgcactggtaccagcagaagcccggcacctcccccaagccctggatctac	**106**
rehuCAN8G1	K, FR3	Artificial sequence	aacctggccaccggcgtgcccgcccgcttctccggctccggctccggcaccgacttcaccctgaccatctcctccgtgcagtccgaggacttcaccctgtactactgc	**107**
rehuCAN8G1	K, FR4	Artificial sequence	ttcggcggcggcaccaagctggagatcaag	**108**
rehuCAN8G1	H, Variable region	Artificial sequence	caggtgaccctgaaggagtccggccccggcatcctgcagccctcccagaccctgaccctgacctgctccttctccggcttctccctgtccacctccggcatgtccgtgggctggttccgccagcccccccggcaagggcctggagtggctggcccacatctggtggaccgacgacaagtactacaaccccgccctgaagtcccgcctgaccatctccaaggacacctccaacaaccaggtggtgctgaccatcaccaacgtggaccccgtggagaccgccacctactactgcgcccgcatcggctacgacggcccccccgactactggggccagggcaccctgttcaccgtgtcctcc	**109**
rehuCAN8G1	H, variable region	Artificial sequence	QVTLKESGPGILQPSQTLTLTCSFSGFSLSTSGMSVGWFRQPPGKGLEWLAHIWWTDDKYYNPALKSRLTISKDTSNNQVVLTITNVDPVETATYYCARIGYDGPPDYWGQGTLFTVSS	**110**
rehuCAN8G1	H, CDR1	Artificial sequence	ggcttctccctgtccacctccggcatgtcc	**111**
rehuCAN8G1	H, CDR2	Artificial sequence	atctggtggaccgacgacaag	**112**
rehuCAN8G1	H, CDR3	Artificial sequence	gcccgcatcggctacgacggcccccccgactac	**113**
rehuCAN8G1	H, CDR1	Artificial sequence	GFSLSTSGMS	**114**
rehuCAN8G1	H, CDR2	Artificial sequence	IWWTDDK	**115**
rehuCAN8G1	H, CDR3	Artificial sequence	ARIGYDGPPDY	**116**
rehuCAN8G1	H, FR1	Artificial sequence	caggtgaccctgaaggagtccggccccggcatcctgcagccctcccagaccctgaccctgacctgctccttctcc	**117**
rehuCAN8G1	H, FR2	Artificial sequence	gtgggctggttccgccagcccccccggcaagggcctggagtggctggcccac	**118**
rehuCAN8G1	H, FR3	Artificial sequence	tactacaaccccgccctgaagtcccgcctgaccatctccaaggacacctccaacaaccaggtggtgctgaccatcaccaacgtggaccccgtggagaccgccacctactactgc	**119**
rehuCAN8G1	H, FR4	Artificial sequence	tggggccagggcaccctgttcaccgtgtcctcc	**120**
cdrCAN8G1	K, Variable region	Artificial sequence	gagatcgtgatgacccagtcccccgccaccctgtccgtgtcccccggcgagcgcgccaccctgtcctgccgcgcctcctcctccatctcctcctccaacctggcctggtaccagcagaagcccggccaggcccccccgcctgctgatctacggcacctccacccgcgccaccggcatccccgcccgcttctccggctccggctccggcaccgagttcaccctgaccatctcctccctgcagtccgaggacttcgccgtgtactactgccaccagtacctgtcctcctggaccttcggcggcggcaccaaggtggagatcaag	**121**
cdrCAN8G1	K, variable region	Artificial sequence	EIVMTQSPATLSVSPGERATLSCRASSSISSSNLAWYQQKPGQAPRLLIYGTSTRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCHQYLSSWTFGGGTKVEIK	**122**

cdrCAN8G1	K, CDR1	Artificial sequence	tcctccatctcctcctccaac	**123**
cdrCAN8G1	K, CDR2	Artificial sequence	ggcacctcc	**124**
cdrCAN8G1	K, CDR3	Artificial sequence	caccagtacctgtcctcctggacc	**125**
cdrCAN8G1	K, CDR1	Artificial sequence	SSISSSN	**126**
cdrCAN8G1	K, CDR2	Artificial sequence	GTS	**127**
cdrCAN8G1	K, CDR3	Artificial sequence	HQYLSSWT	**128**
cdrCAN8G1	K, FR1	Artificial sequence	gagatcgtgatgacccagtcccccgccaccctgtccgtgtcccccggcgagcgcgccaccctgtcctgccgcgcctcc	**129**
cdrCAN8G1	K, FR2	Artificial sequence	ctggcctggtaccagcagaagcccggccaggcccccgcctgctgatctac	**130**
cdrCAN8G1	K, FR3	Artificial sequence	acccgcgccaccggcatccccgcccgcttctccggctccggctccggcaccgagttcaccctgaccatctcctccctgcagtccgaggacttcgccgtgtactactgc	**131**
cdrCAN8G1	K, FR4	Artificial sequence	ttcggcggcggcaccaaggtggagatcaag	**132**
cdrCAN8G1	H, Variable region	Artificial sequence	caggtgaccctgaaggagtccggccccgccctggtgaagcccacccagaccctgaccctgacctgcaccttctccggcttctccctgtccacctccggcatgtccgtgtcctggatccgccagcccccggcaaggccctggagtggctggccctgatctggtggaccgacgacaagcgctactcccccctccctgaagtcccgcctgaccatcaccaaggacacctccaagaaccaggtggtgctgaccatgaccaacatggaccccgtggacaccgccacctactactgcgcccgcatcggctacgacggcccccccgactactggggccagggcaccctggtgaccgtgtcctcc	**133**
cdrCAN8G1	H, variable region	Artificial sequence	QVTLKESGPALVKPTQTLTLTCTFSGFSLSTSGMSVSWIRQPPGKALEWLALIWWTDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCARIGYDGPPDYWGQGTLVTVSS	**134**
cdrCAN8G1	H, CDR1	Artificial sequence	ggcttctccctgtccacctccggcatgtcc	**135**
cdrCAN8G1	H, CDR2	Artificial sequence	atctggtggaccgacgacaag	**136**
cdrCAN8G1	H, CDR3	Artificial sequence	gcccgcatcggctacgacggcccccccgactac	**137**
cdrCAN8G1	H, CDR1	Artificial sequence	GFSLSTSGMS	**138**
cdrCAN8G1	H, CDR2	Artificial sequence	IWWTDDK	**139**
cdrCAN8G1	H, CDR3	Artificial sequence	ARIGYDGPPDY	**140**
cdrCAN8G1	H, FR1	Artificial sequence	caggtgaccctgaaggagtccggccccgccctggtgaagcccacccagaccctgaccctgacctgcaccttctcc	**141**
cdrCAN8G1	H, FR2	Artificial sequence	gtgtcctggatccgccagcccccggcaaggccctggagtggctggccctg	**142**
cdrCAN8G1	H, FR3	Artificial sequence	cgctactcccccctccctgaagtcccgcctgaccatcaccaaggacacctccaagaaccaggtggtgctgaccatgaccaacatggaccccgtggacaccgccacctactactgc	**143**
cdrCAN8G1	H, FR4	Artificial sequence	tggggccagggcaccctggtgaccgtgtcctcc	**144**
huCAN9G1	L, Variable region	Artificial sequence	cagctggtgctgacccagtcctcctccgcctccgcctccctgggcgcctccgtgaagctgacctgcaccctgtcctcccagcactccaccttcaccatcgagtggtaccagcagcagcccctgaaggcccccaagtacgtgatggagctgaagaaggacggctcccactccaccggcgacggcatccccgaccgcttctccggctcctcctccggcgccgagcgctacctgaccatctcctccctgcagtccgaggacgaggccatgtacatctgcggcgtgggcgacaccatcaaggagcagttcgtgtacgtgttcggcggcggcaccaaggtgaccgtgctgg	**145**

huCAN9G1	L, variable region	Artificial sequence	QLVLTQSSSASASLGASVKLTCTLSSQHSTFTIEWYQQQPLKAPKYVMELKKDGSHSTGDGIPDRFSGSSSGAERYLTISSLQSEDEAMYICGVGDTIKEQFVYVFGGGTKVTVL	**146**
huCAN9G1	L, CDR1	Artificial sequence	tcccagcactccaccttcacc	**147**
huCAN9G1	L, CDR2	Artificial sequence	ctgaagaaggacggctcccac	**148**
huCAN9G1	L, CDR3	Artificial sequence	ggcgtgggcgacaccatcaaggagcagttcgtgtacgtg	**149**
huCAN9G1	L, CDR1	Artificial sequence	SQHSTFT	**150**
huCAN9G1	L, CDR2	Artificial sequence	LKKDGSH	**151**
huCAN9G1	L, CDR3	Artificial sequence	GVGDTIKEQFVYV	**152**
huCAN9G1	L, FR1	Artificial sequence	cagctggtgctgacccagtcctcctccgcctccgcctccctgggcgcctccgtgaagctgacctgcaccctgtcc	**153**
huCAN9G1	L, FR2	Artificial sequence	atcgagtggtaccagcagcagcccctgaaggcccccaagtacgtgatggag	**154**
huCAN9G1	L, FR3	Artificial sequence	tccaccggcgacggcatccccgaccgcttctccggctcctcctccggcgccgagcgctacctgaccatctcctccctgcagtccgaggacgaggccatgtacatctgc	**155**
huCAN9G1	L, FR4	Artificial sequence	ttcggcggcggcaccaaggtgaccgtgctgg	**156**
huCAN9G1	H, Variable region	Artificial sequence	gagcgccagctggtggagtccggcggcggcgtggtgcagcccggccgctccctgcgcctgtcctgcgccgcctccggcttcgccttctcctcctacgacatgtcctgggtgcgccaggcccccggcaagggcctggagtgggtggcctactcctcccgcggcggcggcttcacctactaccccgactccgtgaagggccgcttcaccatctcccgcgacaactccaagaacaccctgtacctgcagatgtcctccctgcgcgccgaggacaccgccgtgtactactgcgccacccactactacggccccctgtacgccatggactactggggccagggcaccctggtgaccgtgtcctccg	**157**
huCAN9G1	H, variable region	Artificial sequence	ERQLVESGGGVVQPGRSLRLSCAASGFAFSSYDMSWVRQAPGKGLEWVAYSSRGGGFTYYPDSVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYCATHYYGPLYAMDYWGQGTLVTVSS	**158**
huCAN9G1	H, CDR1	Artificial sequence	ggcttcgccttctcctcctacgac	**159**
huCAN9G1	H, CDR2	Artificial sequence	tcctcccgcggcggcggcttcacc	**160**
huCAN9G1	H, CDR3	Artificial sequence	gccacccactactacggccccctgtacgccatggactac	**161**
huCAN9G1	H, CDR1	Artificial sequence	GFAFSSYD	**162**
huCAN9G1	H, CDR2	Artificial sequence	SSRGGGFT	**163**
huCAN9G1	H, CDR3	Artificial sequence	ATHYYGPLYAMDY	**164**
huCAN9G1	H, FR1	Artificial sequence	gagcgccagctggtggagtccggcggcggcgtggtgcagcccggccgctccctgcgcctgtcctgcgccgcctcc	**165**
huCAN9G1	H, FR2	Artificial sequence	atgtcctgggtgcgccaggcccccggcaagggcctggagtgggtggcctac	**166**
huCAN9G1	H, FR3	Artificial sequence	tactaccccgactccgtgaagggccgcttcaccatctcccgcgacaactccaagaacaccctgtacctgcagatgtcctccctgcgcgccgaggacaccgccgtgtactactgc	**167**
huCAN9G1	H, FR4	Artificial	tggggccagggcaccctggtgaccgtgtcctccg	**168**

		sequence		
rehuCAN9G1	L, Variable region	Artificial sequence	cagctggtgctgacccagtcctcctccgcctccttctccctgggcgcctccgccaagctgacctgcaccctgtcctcccagcactccaccttcaccatcgagtggtaccagcagcagcccctgaaggcccccaagtacgtgatggagctgaagaaggacggctcccactccaccggcgacggcatccccgaccgcttctccggctcctcctccggcgccgagcgctacctgaccatctcctccatccagtccgaggacgaggccatgtacatctgcggcgtgggcgacaccatcaaggagcagttcgtgtacgtgttcggcggcggcaccaaggtgaccgtgctg	**169**
rehuCAN9G1	L, variable region	Artificial sequence	QLVLTQSSSASFSLGASAKLTCTLSSQHSTFTIEWYQQQPLKAPKYVMELKKDGSHSTGDGIPDRFSGSSSGAERYLTISSIQSEDEAMYICGVGDTIKEQFVYVFGGGTKVTVL	**170**
rehuCAN9G1	L, CDR1	Artificial sequence	tcccagcactccaccttcacc	**171**
rehuCAN9G1	L, CDR2	Artificial sequence	ctgaagaaggacggctcccac	**172**
rehuCAN9G1	L, CDR3	Artificial sequence	ggcgtgggcgacaccatcaaggagcagttcgtgtacgtg	**173**
rehuCAN9G1	L, CDR1	Artificial sequence	SQHSTFT	**174**
rehuCAN9G1	L, CDR2	Artificial sequence	LKKDGSH	**175**
rehuCAN9G1	L, CDR3	Artificial sequence	GVGDTIKEQFVYV	**176**
rehuCAN9G1	L, FR1	Artificial sequence	cagctggtgctgacccagtcctcctccgcctccttctccctgggcgcctccgccaagctgacctgcaccctgtcc	**177**
rehuCAN9G1	L, FR2	Artificial sequence	atcgagtggtaccagcagcagcccctgaaggcccccaagtacgtgatggag	**178**
rehuCAN9G1	L, FR3	Artificial sequence	tccaccggcgacggcatccccgaccgcttctccggctcctcctccggcgccgagcgctacctgaccatctcctccatccagtccgaggacgaggccatgtacatctgc	**179**
rehuCAN9G1	L, FR4	Artificial sequence	ttcggcggcggcaccaaggtgaccgtgctg	**180**
rehuCAN9G1	H, Variable region	Artificial sequence	gagcgccagctggtggagtccggcggcggcgtggtgcagcccggccgctccctgcgcctgtcctgcgccgcctccggcttcgccttctcctcctacgacatgtcctgggtgcgccagacccccggcaagggcctggagtgggtggcctactcctcccgcggcggcggcttcacctactaccccgactccgtgaagggccgcttcaccatcgcccgcgacaactccaagaacaccctgcacctgcagatgtcctccctgcgcgccgaggacaccgccgtgtactactgcgccacccactactacggcccccctgtacgccatggactactggggccagggcaccctggtgaccgtgtcctcc	**181**
rehuCAN9G1	H, Variable region	Artificial sequence	ERQLVESGGGVVQPGRSLRLSCAASGFAFSSYDMSWVRQTPGKGLEWVAYSSRGGGFTYYPDSVKGRFTIARDNSKNTLHLQMSSLRAEDTAVYYCATHYYGPLYAMDYWGQGTLVTVSS	**182**
rehuCAN9G1	H, CDR1	Artificial sequence	ggcttcgccttctcctcctacgac	**183**
rehuCAN9G1	H, CDR2	Artificial sequence	tcctcccgcggcggcggcttcacc	**184**
rehuCAN9G1	H, CDR3	Artificial sequence	gccacccactactacggcccccctgtacgccatggactac	**185**
rehuCAN9G1	H, CDR1	Artificial sequence	GFAFSSYD	**186**
rehuCAN9G1	H, CDR2	Artificial sequence	SSRGGGFT	**187**
rehuCAN9G1	H, CDR3	Artificial sequence	ATHYYGPLYAMDY	**188**
rehuCAN9G1	H, FR1	Artificial sequence	gagcgccagctggtggagtccggcggcggcgtggtgcagcccggccgctccctgcgcctgtcctgcgccgcctcc	**189**
rehuCAN9G1	H, FR2	Artificial sequence	atgtcctgggtgcgccagacccccggcaagggcctggagtgggtggcctac	**190**

rehuCAN9G1	H, FR3	Artificial sequence	tactaccccgactccgtgaagggccgcttcaccatcgcccgcgacaactccaagaacaccctgcacctgcagatgtcctccctgcgcgccgaggacaccgccgtgtactactgc	191
rehuCAN9G1	H, FR4	Artificial sequence	tggggccagggcaccctggtgaccgtgtcctcc	192
cdrCAN9G1	L, Variable region	Artificial sequence	cagctggtgctgacccagtcccccctccgcctccgcctccctgggcgcctccgtgaagctgacctgcaccctgtcctcccagcactccaccttcaccatcgcctggcaccagcagcagcccgagaagggcccccgctacctgatgaagctgaagaaggacggctcccactccaagggcgacggcatccccgaccgcttctccggctcctcctccggcgccgagcgctacctgaccatctcctccctgcagtccgaggacgaggccgactactactgcggcgtgggcgacaccatcaaggagcagttcgtgtacgtgttcggcaccggcaccaaggtgaccgtgctg	193
cdrCAN9G1	L, variable region	Artificial sequence	QLVLTQSPSASASLGASVKLTCTLSSQHSTFTIAWHQQQPEKGPRYLMKLKKDGSHSKGDGIPDRFSGSSSGAERYLTISSLQSEDEADYYCGVGDTIKEQFVYVFGTGTKVTVL	194
cdrCAN9G1	L, CDR1	Artificial sequence	tcccagcactccaccttcacc	195
cdrCAN9G1	L, CDR2	Artificial sequence	ctgaagaaggacggctcccac	196
cdrCAN9G1	L, CDR3	Artificial sequence	ggcgtgggcgacaccatcaaggagcagttcgtgtacgtg	197
cdrCAN9G1	L, CDR1	Artificial sequence	SQHSTFT	198
cdrCAN9G1	L, CDR2	Artificial sequence	LKKDGSH	199
cdrCAN9G1	L, CDR3	Artificial sequence	GVGDTIKEQFVYV	200
cdrCAN9G1	L, FR1	Artificial sequence	cagctggtgctgacccagtcccccctccgcctccgcctccctgggcgcctccgtgaagctgacctgcaccctgtcc	201
cdrCAN9G1	L, FR2	Artificial sequence	atcgcctggcaccagcagcagcccgagaagggcccccgctacctgatgaag	202
cdrCAN9G1	L, FR3	Artificial sequence	tccaagggcgacggcatccccgaccgcttctccggctcctcctccggcgccgagcgctacctgaccatctcctccctgcagtccgaggacgaggccgactactactgc	203
cdrCAN9G1	L, FR4	Artificial sequence	ttcggcaccggcaccaaggtgaccgtgctg	204
cdrCAN9G1	H, Variable region	Artificial sequence	caggtgcagctggtggagtccggcggcggcgtggtgcagcccggccgctccctgcgcctgtcctgcgccgcctccggcttcgccttctcctcctacgacatgcactgggtgcgccaggcccccggcaagggcctggagtgggtggccgtgtcctcccgcggcggcggcttcacctactacgccgactccgtgaagggccgcttcaccatctcccgcgacaactccaagaacaccctgtacctgcagatgtcctccctgcgcgccgaggacaccgccgtgtactactgcgccacccactactacggcccccctgtacgccatggactactggggccagggcaccctggtgaccgtgtcctcc	205
cdrCAN9G1	H, variable region	Artificial sequence	QVQLVESGGGVVQPGRSLRLSCAASGFAFSSYDMHWVRQAPGKGLEWVAVSSRGGGFTYYADSVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYCATHYYGPLYAMDYWGQGTLVTVSS	206
cdrCAN9G1	H, CDR1	Artificial sequence	ggcttcgccttctcctcctacgac	207
cdrCAN9G1	H, CDR2	Artificial sequence	tcctcccgcggcggcggcttcacc	208
cdrCAN9G1	H, CDR3	Artificial sequence	gccacccactactacggcccccctgtacgccatggactac	209
cdrCAN9G1	H, CDR1	Artificial sequence	GFAFSSYD	210
cdrCAN9G1	H, CDR2	Artificial sequence	SSRGGGFT	211

cdrCAN9G1	H, CDR3	Artificial sequence	ATHYYGPLYAMDY	**212**
cdrCAN9G1	H, FR1	Artificial sequence	caggtgcagctggtggagtccggcggcggcgtggtgcagcccggccgctccctgcgcctgtcctgcgccgcctcc	**213**
cdrCAN9G1	H, FR2	Artificial sequence	atgcactgggtgcgccaggcccccggcaagggcctggagtgggtggccgtg	**214**
cdrCAN9G1	H, FR3	Artificial sequence	tactacgccgactccgtgaagggccgcttcaccatctcccgcgacaactccaagaacaccctgtacctgcagatgtcctccctgcgcgccgaggacaccgccgtgtactactgc	**215**
cdrCAN9G1	H, FR4	Artificial sequence	tggggccagggcaccctggtgaccgtgtcctcc	**216**
CAN7G1	K, Variable region	Murine sequence	caaattgttctctcccagtctccagcaatcctgtctgcatctccaggggagaaggtcacaatgacttgcagggccagctcaagtgtaagttacatgcactggtaccatcagaacccaggatcctcccccaaaccctggatttatgccacttccaacctggcttctggagtccctgctcgcttcagtggcagtgggtctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgccacttattactgccagcaatggagtagtaacccacccacgttcggaggggggaccaagctggcaataaaac	**217**
CAN7G1	K, variable region	Murine sequence	QIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWYHQNPGSSPKPWIYATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTKLAIK	**218**
CAN7G1	K, CDR1	Murine sequence	gccagctcaagtgtaagttac	**219**
CAN7G1	K, CDR2	Murine sequence	gccacttcc	**220**
CAN7G1	K, CDR3	Murine sequence	cagcaatggagtagtaacccacccacg	**221**
CAN7G1	K, CDR1	Murine sequence	ASSSVSY	**222**
CAN7G1	K, CDR2	Murine sequence	ATS	**223**
CAN7G1	K, CDR3	Murine sequence	QQWSSNPPT	**224**
CAN7G1	H, Variable region	Murine sequence	gaggtccagctgcagcagtctggacctgagctggtaaagcctggggcttcagtgaagatgtcctgcaaggcttctggatacacattcactagctatgttatgcactgggtgaagcagaagcctgggcagggccttgagtggattggatatattaatccttacaatgatggtcctaagtacaatgagaagttcaaaggcaaggccacactgacttcagacaaatcctcccgcacagcctatatggagctcagcagcctgaccactgaggactctgcggtcttttactgtgcaagagggcggggtgacgcttatttctatgttctggactactggggtcaaggaacctcagtcaccgtctcctcag	**225**
CAN7G1	H, variable region	Murine sequence	EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGPKYNEKFKGKATLTSDKSSRTAYMELSSLTTEDSAVFYCARGRGDAYFYVLDYWGQGTSVTVSS	**226**
CAN7G1	H, CDR1	Murine sequence	ggatacacattcactagctatgtt	**227**
CAN7G1	H, CDR2	Murine sequence	attaatccttacaatgatggtcct	**228**
CAN7G1	H, CDR3	Murine sequence	gcaagagggcggggtgacgcttatttctatgttctggactac	**229**
CAN7G1	H, CDR1	Murine sequence	GYTFTSYV	**230**
CAN7G1	H, CDR2	Murine sequence	INPYNDGP	**231**
CAN7G1	H, CDR3	Murine sequence	ARGRGDAYFYVLDY	**232**
CAN8G1	K,	Murine	gaaattgtgctcacccagtctccagcactcatggctgcatctccaggggagaag	**233**

	Variable region	sequence	gtcaccatcacctgcagtgtcagctcaagtataagttccagcaacttgcactggtaccagcagaagtcagaaacctcccccaaaccctggatttatggcacatccaacctggcttctggagtccctgatcgcttcacaggcagcggatctgggacagattttactcttaccatcagcagtgtacaagctgaagacctgacactttattactgtcatcaatacctctcctcgtggacgttcggtggaggcaccaagctggaaatcaaac	
CAN8G1	K, variable region	Murine sequence	EIVLTQSPALMAASPGEKVTITCSVSSSISSSNLHWYQQKSETSPKPWIYGTSNLASGVPDRFTGSGSGTDFTLTISSVQAEDLTLYYCHQYLSSWTFGGGTKLEIK	**234**
CAN8G1	K, CDR1	Murine sequence	tcaagtataagttccagcaac	**235**
CAN8G1	K, CDR2	Murine sequence	ggcacatcc	**236**
CAN8G1	K, CDR3	Murine sequence	catcaatacctctcctcgtggacg	**237**
CAN8G1	K, CDR1	Murine sequence	SSISSSN	**238**
CAN8G1	K, CDR2	Murine sequence	GTS	**239**
CAN8G1	K, CDR3	Murine sequence	HQYLSSWT	**240**
CAN8G1	H, Variable region	Murine sequence	caggttactctgaaagagtctggccctgggatattgcagccctcccagaccctcagtctgacttgttctttctctgggttttcactgagtacttctggtatgagtgtaggctggtttcgtcagccttcagggaagggtctggagtggctggcacacatttggtggactgatgataagtattataatccagccctgaaaagccgtctcacaatctccaaggatacctccaacaaccaggtattcctcaagatcgccagtgtggtcactgcagagagtgccacatactactgtgctcgaataggctatgatggtccccctgactattggggccaaggcaccattttcacagtctcctcag	**241**
CAN8G1	H, variable region	Murine sequence	QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMSVGWFRQPSGKGLEWLAHIWWTDDKYYNPALKSRLTISKDTSNNQVFLKIASVVTAESATYYCARIGYDGPPDYWGQGTIFTVSS	**242**
CAN8G1	H, CDR1	Murine sequence	gggttttcactgagtacttctggtatgagt	**243**
CAN8G1	H, CDR2	Murine sequence	atttggtggactgatgataag	**244**
CAN8G1	H, CDR3	Murine sequence	gctcgaataggctatgatggtccccctgactat	**245**
CAN8G1	H, CDR1	Murine sequence	GFSLSTSGMS	**246**
CAN8G1	H, CDR2	Murine sequence	IWWTDDK	**247**
CAN8G1	H, CDR3	Murine sequence	ARIGYDGPPDY	**248**
CAN9G1	L, Variable region	Murine sequence	caacttgtgctcactcagtcatcttcagcctctttctccctgggagcctcagcaaaactcacgtgcaccttgagtagtcagcacagtacgttcaccattgaatggtatcagcaacagccactcaaggctcctaagtatgtgatggagcttaagaaagatggaagccacagcacaggtgatgggattcctgatcgcttctctggatccagctctggtgctgatcgctacctttggatttccaacatccagcctgaagatgaagcaatgtacatctgtggtgtgggtgatacaattaaggaacaatttgtgtatgttttcggcggtggaaccaaggtcactgtcctag	**249**
CAN9G1	L, variable region	Murine sequence	QLVLTQSSSASFSLGASAKLTCTLSSQHSTFTIEWYQQQPLKAPKYVMELKKDGSHSTGDGIPDRFSGSSSGADRYLWISNIQPEDEAMYICGVGDTIKEQFVYVFGGGTKVTVL	**250**
CAN9G1	L, CDR1	Murine sequence	agtcagcacagtacgttcacc	**251**
CAN9G1	L, CDR2	Murine sequence	cttaagaaagatggaagccac	**252**
CAN9G1	L,	Murine	ggtgtgggtgatacaattaaggaacaatttgtgtatgtt	**253**

	CDR3	sequence		
CAN9G1	L, CDR1	Murine sequence	SQHSTFT	**254**
CAN9G1	L, CDR2	Murine sequence	LKKDGSH	**255**
CAN9G1	L, CDR3	Murine sequence	GVGDTIKEQFVYV	**256**
CAN9G1	H, Variable region	Murine sequence	gaacggcagctggtggagtctgggggaggcgtagtgaagcctggagagtccctgaaactctcctgtgcagcctctggattcgctttcagtagttatgacatgtcttgggttcgccagactccggagaagaggctggagtgggtcgcatacagtagtcgtggtggtggttttacctactatccagacactgtgaagggccggttcaccatcgccagagacaatgccaagaataccctgcacctgcaaatgagcagtctgaagtctgaggacacagccatgtattactgtgcaacccattactacggcccccctctatgctatggactactggggtcaaggaacctcagtcaccgtctcctcag	**257**
CAN9G1	H, variable region	Murine sequence	ERQLVESGGGVVKPGESLKLSCAASGFAFSSYDMSWVRQTPEKRLEWVAYSSRGGGFTYYPDTVKGRFTIARDNAKNTLHLQMSSLKSEDTAMYYCATHYYGPLYAMDYWGQGTSVTVSS	**258**
CAN9G1	H, CDR1	Murine sequence	ggattcgctttcagtagttatgac	**259**
CAN9G1	H, CDR2	Murine sequence	agtagtcgtggtggtggttttacc	**260**
CAN9G1	H, CDR3	Murine sequence	gcaacccattactacggcccccctctatgctatggactac	**261**
CAN9G1	H, CDR1	Murine sequence	GFAFSSYD	**262**
CAN9G1	H, CDR2	Murine sequence	SSRGGGFT	**263**
CAN9G1	H, CDR3	Murine sequence	ATHYYGPLYAMDY	**264**
Zaire Ebola glycoprotein (1976 strain; Yambuku-Mayinga)	GPΔmucΔtm	Synthetic Ebolavirus GP	MGVTGILQLP RDRFKRTSFF LWVIILFQRT FSIPLGVIHN STLQVSDVDK LVCRDKLSST NQLRPVGLNL EGNGVATDVP SATKRWGFRS GVPPKVVNYE AGEWAENCYN LEIKKPDGSE CLPAAPDGIR GFPRCRYVHK VSGTGPCAGD FAFHKEGAFF LYDRLASTVI YRGTTFAEGV VAFLILPQAK KDFFSSHPLR EPVNATEDPS SGYYSTTIRY QATGFGTNET EYLFEVDNLT YVQLEPRFTP QFLLQLNETI YTSGKRSNTT GKLIWKVNPE IDTTIGEWAF WETKKNLTRK IRSEELSFTV VSNTHHQDTG EESASSGKLG LITNTIAGVA GLITGGRRTR REAIVNAQPK CNPNLHYWTT QDEGAAIGLA WIPYFGPAAE GIYTEGLMHN QDGLICGLRQ LANETTQALQ LFLRATTELR TFSILNRKAI DFLLQRWGGT CHILGPDCCI EPHDWTKNIT DKIDQIIHDF VDKTLPD	**265**
Sudan Ebola glycoprotein	GPΔmucΔtm	Synthetic Ebolavirus GP	MGGLSLLQLP RDKFRKSSFF VWVIILFQKA FSMPLGVVTN STLEVTEIDQ LVCKDHLAST DQLKSVGLNL EGSGVSTDIP SATKRWGFRS GVPPKVVSYE AGEWAENCYN LEIKKPDGSE CLPPPPDGVR GFPRCRYVHK AQGTGPCPGD YAFHKDGAFF LYDRLASTVI YRGVNFAEGV IAFLILAKPK ETFLQSPPIR EAVNYTENTS SYYATSYLEY EIENFGAQHS TTLFKIDNNT FVRLDRPHTP QFLFQLNDTI HLHQQLSNTT GRLIWTLDAN INADIGEWAF WENKKNLSEQ LRGEELSFEA LSNITTAVKT VLPQESTSNG LITSTVTGIL GSLGLRKRSR RQTNTKATGK CNPNLHYWTA QEQHNAAGIA WIPYFGPGAE	**266**

			GIYTEGLMHN QNALVCGLRQ LANETTQALQ LFLRATTELR TYTILNRKAI DFLLRRWGGT CRILGPDCCI EPHDWTKNIT DKINQIIHDF IDNPLPN	
Zaire Ebola glycoprotein (1995 strain; Kikwit)	GPΔmucΔtm	Synthetic Ebolavirus GP	MGVTGILQLP RDRFKRTSFF LWVIILFQRT FSIPLGVIHN STLQVSEVDK LVCRDKLSST NQLRSVGLNL EGNGVATDVP SATKRWGFRS GVPPKVVNYE AGEWAENCYN LEIKKPDGSE CLPAAPDGIR GFPRCRYVHK VSGTGPCAGD FAFHKEGAFF LYDRLASTVI YRGTTFAEGV VAFLILPQAK KDFFSSHPLR EPVNATEDPS SGYYSTTIRY QATGFGTNET EYLFEVDNLT YVQLESRFTP QFLLQLNETI YTSGKRSNTT GKLIWKVNPE IDTTIGEWAF WETKKNLTRK IRSEELSFTA VSNTHHQDTG EESASSGKLG LITNTIAGVA GLITGGRRAR REAIVNAQPK CNPNLHYWTT QDEGAAIGLA WIPYFGPAAE GIYTEGLMHN QDGLICGLRQ LANETTQALQ LFLRATTELR TFSILNRKAI DFLLQRWGGT CHILGPDCCI EPHDWTKNIT DKIDQIIHDF VDKTLPD	**267**
huCAN7G1	K, FR1	Artificial sequence	MAQIVLSQSPAILSLSPGERATLSCR	**268**
huCAN7G1	K, FR2	Artificial sequence	MHWYHQNPGSSPKPWIY	**269**
huCAN7G1	K, FR3	Artificial sequence	NLATGIPARFSGSGSGTDYTLTISSLEPEDFAVYYC	**270**
huCAN7G1	K, FR4	Artificial sequence	FGGGTKVEIK	**271**
huCAN7G1	H, FR1	Artificial sequence	EVQLQQSGPELVKPGASVKVSCKAS	**272**
huCAN7G1	H, FR2	Artificial sequence	MHWVRQAPGQGLEWIGY	**273**
huCAN7G1	H, FR3	Artificial sequence	KYNEKFKGRVTLTSDTSARTAYMELSSLRSEDTAVFYC	**274**
huCAN7G1	H, FR4	Artificial sequence	WGQGTLVTVSS	**275**
rehuCAN7G1	K, FR1	Artificial sequence	QIVLSQSPAILSASPGERVTMSCR	**276**
rehuCAN7G1	K, FR2	Artificial sequence	MHWYHQNPGSSPKPWIY	**277**
rehuCAN7G1	K, FR3	Artificial sequence	NLATGVPARFSGSGSGTDYSLTISSVEPEDFATYYC	**278**
rehuCAN7G1	K, FR4	Artificial sequence	FGGGTKLEIK	**279**
rehuCAN7G1	H, FR1	Artificial sequence	EVQLQQSGPELVKPGASVKMSCKAS	**280**
rehuCAN7G1	H, FR2	Artificial sequence	MHWVKQAPGQGLEWIGY	**281**
rehuCAN7G1	H, FR3	Artificial sequence	KYNEKFKGRATLTSDTSARTAYMELSSLRSEDTAVFYC	**282**
rehuCAN7G1	H, FR4	Artificial sequence	WGQGTLVTVSS	**283**
cdrCAN7G1	K, FR1	Artificial sequence	EIVLTQSPATLSLSPGERATLSCR	**284**
cdrCAN7G1	K, FR2	Artificial sequence	LAWYQQKPGQAPRLLIY	**285**
cdrCAN7G1	K, FR3	Artificial sequence	NRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	**286**

cdrCAN7G1	K, FR4	Artificial sequence	FGGGTKVEIK	**287**
cdrCAN7G1	H, FR1	Artificial sequence	QVQLVQSGAEVKKPGASVKVSCKAS	**288**
cdrCAN7G1	H, FR2	Artificial sequence	MHWVRQAPGQRLEWMGW	**289**
cdrCAN7G1	H, FR3	Artificial sequence	KYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYC	**290**
cdrCAN7G1	H, FR4	Artificial sequence	WGQGTLVTVSS	**291**
huCAN8G1	K, FR1	Artificial sequence	EIVLTQSPATLSVSPGERATISCSVS	**292**
huCAN8G1	K, FR2	Artificial sequence	LHWYQQKPGTSPKPWIY	**293**
huCAN8G1	K, FR3	Artificial sequence	NLATGVPARFSGSGSGTDFTLTISSLQSEDFALYYC	**294**
huCAN8G1	K, FR4	Artificial sequence	FGGGTKVEIK	**295**
huCAN8G1	H, FR1	Artificial sequence	QVTLKESGPGILQPSQTLSLTCTFS	**296**
huCAN8G1	H, FR2	Artificial sequence	VGWFRQPPGKGLEWLAH	**297**
huCAN8G1	H, FR3	Artificial sequence	YYNPALKSRLTISKDTSNNQVVLTMTNMDPVDTATYYC	**298**
huCAN8G1	H, FR4	Artificial sequence	WGQGTLVTVSS	**299**
rehuCAN8G1	K, FR1	Artificial sequence	EIVLTQSPATMSASPGERVTISCSVS	**300**
rehuCAN8G1	K, FR2	Artificial sequence	LHWYQQKPGTSPKPWIY	**301**
rehuCAN8G1	K, FR3	Artificial sequence	NLATGVPARFSGSGSGTDFTLTISSVQSEDFTLYYC	**302**
rehuCAN8G1	K, FR4	Artificial sequence	FGGGTKLEIK	**303**
rehuCAN8G1	H, FR1	Artificial sequence	QVTLKESGPGILQPSQTLTLTCSFS	**304**
rehuCAN8G1	H, FR2	Artificial sequence	VGWFRQPPGKGLEWLAH	**305**
rehuCAN8G1	H, FR3	Artificial sequence	YYNPALKSRLTISKDTSNNQVVLTITNVDPVETATYYC	**306**
rehuCAN8G1	H, FR4	Artificial sequence	WGQGTLFTVSS	**307**
cdrCAN8G1	K, FR1	Artificial sequence	EIVMTQSPATLSVSPGERATLSCRAS	**308**
cdrCAN8G1	K, FR2	Artificial sequence	LAWYQQKPGQAPRLLIY	**309**
cdrCAN8G1	K, FR3	Artificial sequence	TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	**310**
cdrCAN8G1	K, FR4	Artificial sequence	FGGGTKVEIK	**311**
cdrCAN8G1	H, FR1	Artificial sequence	QVTLKESGPALVKPTQTLTLTCTFS	**312**
cdrCAN8G1	H, FR2	Artificial sequence	VSWIRQPPGKALEWLAL	**313**
cdrCAN8G1	H, FR3	Artificial sequence	RYSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYC	**314**
cdrCAN8G1	H, FR4	Artificial sequence	WGQGTLVTVSS	**315**

huCAN9G1	K, FR1	Artificial sequence	QLVLTQSSSASASLGASVKLTCTLS	**316**
huCAN9G1	K, FR2	Artificial sequence	IEWYQQQPLKAPKYVME	**317**
huCAN9G1	K, FR3	Artificial sequence	STGDGIPDRFSGSSSGAERYLTISSLQSEDEAMYIC	**318**
huCAN9G1	K, FR4	Artificial sequence	FGGGTKVTVL	**319**
huCAN9G1	H, FR1	Artificial sequence	ERQLVESGGGVVQPGRSLRLSCAAS	**320**
huCAN9G1	H, FR2	Artificial sequence	MSWVRQAPGKGLEWVAY	**321**
huCAN9G1	H, FR3	Artificial sequence	YYPDSVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYC	**322**
huCAN9G1	H, FR4	Artificial sequence	WGQGTLVTVSS	**323**
rehuCAN9G1	K, FR1	Artificial sequence	QLVLTQSSSASFSLGASAKLTCTLS	**324**
rehuCAN9G1	K, FR2	Artificial sequence	IEWYQQQPLKAPKYVME	**325**
rehuCAN9G1	K, FR3	Artificial sequence	STGDGIPDRFSGSSSGAERYLTISSIQSEDEAMYIC	**326**
rehuCAN9G1	K, FR4	Artificial sequence	FGGGTKVTVL	**327**
rehuCAN9G1	H, FR1	Artificial sequence	ERQLVESGGGVVQPGRSLRLSCAAS	**328**
rehuCAN9G1	H, FR2	Artificial sequence	MSWVRQTPGKGLEWVAY	**329**
rehuCAN9G1	H, FR3	Artificial sequence	YYPDSVKGRFTIARDNSKNTLHLQMSSLRAEDTAVYYC	**330**
rehuCAN9G1	H, FR4	Artificial sequence	WGQGTLVTVSS	**331**
cdrCAN9G1	K, FR1	Artificial sequence	QLVLTQSPSASASLGASVKLTCTLS	**332**
cdrCAN9G1	K, FR2	Artificial sequence	IAWHQQQPEKGPRYLMK	**333**
cdrCAN9G1	K, FR3	Artificial sequence	SKGDGIPDRFSGSSSGAERYLTISSLQSEDEADYYC	**334**
cdrCAN9G1	K, FR4	Artificial sequence	FGTGTKVTVL	**335**
cdrCAN9G1	H, FR1	Artificial sequence	QVQLVESGGGVVQPGRSLRLSCAAS	**336**
cdrCAN9G1	H, FR2	Artificial sequence	MHWVRQAPGKGLEWVAV	**337**
cdrCAN9G1	H, FR3	Artificial sequence	YYADSVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYC	**338**
cdrCAN9G1	H, FR4	Artificial sequence	WGQGTLVTVSS	**339**
huCAN8G1-IF	H, Variable region	Artificial sequence	caggtgaccctgaaggagtccggccccggcatcctgcagccctcccagaccctgtccctgacctgcaccttctccggcttctccctgtccacctccggcatgtccgtgggctggttccgccagcccccccggcaagggcctggagtggctggcccacatctggtggaccgacgacaagtactacaaccccgccctgaagtcccgcctgaccatctccaaggacacctccaacaaccaggtggtgctgaccatgaccaacatggaccccgtggacaccgccacctactactgcgcccgcatcggctacgacggcccccccgactactggggccagggcacc**atcttc**accgtgtcctcc	**340**
huCAN8G1-IF	H, Variable region	Artificial sequence	QVTLKESGPGILQPSQTLSLTCTFSGFSLSTSGMSVGWFRQPPGKGLEWLAHIWWTDDKYYNPALKSRLTISKDTSNNQVVLTMTNMDPVDTATYYCARIGYDGPPDYWGQGT**IF**TVSS	**341**

huCAN8G1-IF	H, CDR1	Artificial sequence	ggcttctccctgtccacctccggcatgtcc	**342**
huCAN8G1-IF	H, CDR2	Artificial sequence	atctggtggaccgacgacaag	**343**
huCAN8G1-IF	H, CDR3	Artificial sequence	gcccgcatcggctacgacggcccccccgactac	**344**
huCAN8G1-IF	H, CDR1	Artificial sequence	GFSLSTSGMS	**345**
huCAN8G1-IF	H, CDR2	Artificial sequence	IWWTDDK	**346**
huCAN8G1-IF	H, CDR3	Artificial sequence	ARIGYDGPPDY	**347**
huCAN8G1-IF	H, FR1	Artificial sequence	caggtgaccctgaaggagtccggccccggcatcctgcagccctcccagaccctgtccctgacctgcaccttctcc	**348**
huCAN8G1-IF	H, FR2	Artificial sequence	gtgggctggttccgccagccccccggcaagggcctggagtggctggcccac	**349**
huCAN8G1-IF	H, FR3	Artificial sequence	tactacaaccccgccctgaagtcccgcctgaccatctccaaggacacctccaacaaccaggtggtgctgaccatgaccaacatggaccccgtggacaccgccacctactactgc	**350**
huCAN8G1-IF	H, FR4	Artificial sequence	tggggccagggcacc**atcttc**accgtgtcctcc	**351**
huCAN8G1-LF	H, Variable region	Artificial sequence	caggtgaccctgaaggagtccggccccggcatcctgcagccctcccagaccctgtccctgacctgcaccttctccggcttctccctgtccacctccggcatgtccgtgggctggttccgccagccccccggcaagggcctggagtggctggcccacatctggtggaccgacgacaagtactacaaccccgccctgaagtcccgcctgaccatctccaaggacacctccaacaaccaggtggtgctgaccatgaccaacatggaccccgtggacaccgccacctactactgcgcccgcatcggctacgacggcccccccgactactggggccagggcacc**ctgttc**accgtgtcctcc	**352**
huCAN8G1-LF	H, Variable region	Artificial sequence	QVTLKESGPGILQPSQTLSLTCTFSGFSLSTSGMSVGWFRQPPGKGLEWLAHIWWTDDKYYNPALKSRLTISKDTSNNQVVLTMTNMDPVDTATYYCARIGYDGPPDYWGQGT**LF**TVSS	**353**
huCAN8G1-LF	H, CDR1	Artificial sequence	ggcttctccctgtccacctccggcatgtcc	**354**
huCAN8G1-LF	H, CDR2	Artificial sequence	atctggtggaccgacgacaag	**355**
huCAN8G1-LF	H, CDR3	Artificial sequence	gcccgcatcggctacgacggcccccccgactac	**356**
huCAN8G1-LF	H, CDR1	Artificial sequence	GFSLSTSGMS	**357**
huCAN8G1-LF	H, CDR2	Artificial sequence	IWWTDDK	**358**
huCAN8G1-LF	H, CDR3	Artificial sequence	ARIGYDGPPDY	**359**
huCAN8G1-LF	H, FR1	Artificial sequence	caggtgaccctgaaggagtccggccccggcatcctgcagccctcccagaccctgtccctgacctgcaccttctcc	**360**
huCAN8G1-LF	H, FR2	Artificial sequence	gtgggctggttccgccagccccccggcaagggcctggagtggctggcccac	**361**
huCAN8G1-LF	H, FR3	Artificial sequence	tactacaaccccgccctgaagtcccgcctgaccatctccaaggacacctccaacaaccaggtggtgctgaccatgaccaacatggaccccgtggacaccgccacctactactgc	**362**
huCAN8G1-LF	H, FR4	Artificial sequence	tggggccagggcacc**ctgttc**accgtgtcctcc	**363**
huCAN8G1-IV	H, Variable	Artificial sequence	caggtgaccctgaaggagtccggccccggcatcctgcagccctcccagaccctgtccctgacctgcaccttctccggcttctccctgtccacctccggcatgtccgtgg	**364**

	region		gctggttccgccagcccccggcaagggcctggagtggctggcccacatctggtggaccgacgacaagtactacaaccccgccctgaagtcccgcctgaccatctccaaggacacctccaacaaccaggtggtgctgaccatgaccaacatggaccccgtggacaccgccacctactactgcgcccgcatcggctacgacggcccccccgactactggggccagggcacc**atcgtg**accgtgtcctcc	
huCAN8G1-IV	H, Variable region	Artificial sequence	QVTLKESGPGILQPSQTLSLTCTFSGFSLSTSGMSVGWFRQPPGKGLEWLAHIWWTDDKYYNPALKSRLTISKDTSNNQVVLTMTNMDPVDTATYYCARIGYDGPPDYWGQGT**IV**TVSS	**365**
huCAN8G1-IV	H, CDR1	Artificial sequence	ggcttctccctgtccacctccggcatgtcc	**366**
huCAN8G1-IV	H, CDR2	Artificial sequence	atctggtggaccgacgacaag	**367**
huCAN8G1-IV	H, CDR3	Artificial sequence	gcccgcatcggctacgacggcccccccgactac	**368**
huCAN8G1-IV	H, CDR1	Artificial sequence	GFSLSTSGMS	**369**
huCAN8G1-IV	H, CDR2	Artificial sequence	IWWTDDK	**370**
huCAN8G1-IV	H, CDR3	Artificial sequence	ARIGYDGPPDY	**371**
huCAN8G1-IV	H, FR1	Artificial sequence	caggtgaccctgaaggagtccggccccggcatcctgcagccctcccagaccctgtccctgacctgcaccttctcc	**372**
huCAN8G1-IV	H, FR2	Artificial sequence	gtgggctggttccgccagcccccggcaagggcctggagtggctggcccac	**373**
huCAN8G1-IV	H, FR3	Artificial sequence	tactacaaccccgccctgaagtcccgcctgaccatctccaaggacacctccaacaaccaggtggtgctgaccatgaccaacatggaccccgtggacaccgccacctactactgc	**374**
huCAN8G1-IV	H, FR4	Artificial sequence	tggggccagggcaccatcgtgaccgtgtcctcc	**375**
huCAN8G1-IF	H, FR1	Artificial sequence	QVTLKESGPGILQPSQTLSLTCTFS	**376**
huCAN8G1-IF	H, FR2	Artificial sequence	VGWFRQPPGKGLEWLAH	**377**
huCAN8G1-IF	H, FR3	Artificial sequence	YYNPALKSRLTISKDTSNNQVVLTMTNMDPVDTATYYC	**378**
huCAN8G1-IF	H, FR4	Artificial sequence	WGQGT**IF**TVSS	**379**
huCAN8G1-LF	H, FR1	Artificial sequence	QVTLKESGPGILQPSQTLSLTCTFS	**380**
huCAN8G1-LF	H, FR2	Artificial sequence	VGWFRQPPGKGLEWLAH	**381**
huCAN8G1-LF	H, FR3	Artificial sequence	YYNPALKSRLTISKDTSNNQVVLTMTNMDPVDTATYYC	**382**
huCAN8G1-LF	H, FR4	Artificial sequence	WGQGT**LF**TVSS	**383**
huCAN8G1-IV	H, FR1	Artificial sequence	QVTLKESGPGILQPSQTLSLTCTFS	**384**
huCAN8G1-IV	H, FR2	Artificial sequence	VGWFRQPPGKGLEWLAH	**385**
huCAN8G1-IV	H, FR3	Artificial sequence	YYNPALKSRLTISKDTSNNQVVLTMTNMDPVDTATYYC	**386**
huCAN8G1-IV	H, FR4	Artificial sequence	WGQGT**IV**TVSS	**387**

[1055] In one embodiment, an anti-EBOV antibody or antigen-binding portion thereof is a humanized antibody of a murine anti-EBOV antibody. The humanized anti-EBOV antibody or antigen-binding fragment thereof can comprise one or more CDRs of a murine anti-EBOV antibody and one or more human FRs. In one embodiment, the humanized anti-EBOV antibody or antigen-binding fragment thereof comprises one or more CDRs of the murine anti-EBOV antibody CAN7G1, CAN8G1, or CAN9G1. In one embodiment, the humanized anti-EBOV antibody or antigen-binding fragment thereof comprises one or more human FRs from Table 2.

[1056] In one embodiment, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a light chain CDR1 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 6, 30, 54, 78, 102, 126, 150, 174 or 198; a light chain CDR2 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 7, 31, 55, 79, 103, 127, 151, 175, or 199; a light chain CDR3 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 8, 32, 56, 80, 104, 128, 152, 176, or 200; a heavy chain CDR1 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 18, 42, 66, 90, 114, 138, 162, 186, 210, 345, 357, or 369; a heavy chain CDR2 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 19, 43, 67, 91, 115, 139, 163, 187, 211, 346, 358, or 370; and/or a heavy chain CDR3 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 20, 44, 68, 92, 116, 140, 164, 188, 212, 347, 359, or 371.

[1057] In one embodiment, a humanized anti-EBOV antibody or antigen-binding portion thereof further comprises a light chain FR1 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 268, 276, 284, 292, 300, 308, 316, 324, or 332; a light chain FR2 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 269, 277, 285, 293, 301, 309, 317, 325, or 333; a light chain FR3 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 270, 278, 286, 294, 302, 310, 318, 326, or 334; a light chain FR4 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 271, 279, 287, 295, 303, 311, 319, 327, or 335; a heavy chain FR1 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NOs: 272, 280, 288, 296, 304, 312, 320, 328, 336, 376, 380, or 384; a heavy chain FR2 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 273, 281, 289, 297, 305, 313, 321, 329, 377, 381, or 385; a heavy chain FR3 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 274, 282, 290, 298, 306, 314, 322, 330, 338, 378, 382, or 386; and/or a heavy chain FR4 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence of SEQ ID NO: 275, 283, 291, 299, 307, 315, 323, 331, 339, 379, 383, or 387.

[1058] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises: a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 6, 7 and 8, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 18, 19 and 20, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 268, 269, 270, and 271, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 272, 273, 274 and 275, respectively.

[1059] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 30, 31, and 32, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 42, 43, and 44, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence e comprising SEQ ID NOs: 276, 277, 278, and 279, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 280, 281, 282, and 283, respectively.

[1060] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 54, 55, and 56, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 66, 67, and 68, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 284, 285, 286, and 287, respectively; and a heavy chain

FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 288, 289, 290, and 291, respectively.

[1061] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 78, 79 and 80, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 90, 91 and 92, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 292, 293, 294 and 295, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 296, 297, 298, and 299, respectively.

[1062] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs:102, 103, and 104, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 114, 115, and 116, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 300, 301, 302 and 303, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 304, 305, 306 and 307, respectively.

[1063] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 126, 127, and 128, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 138, 139, and 140, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 308, 309, 310 and 311, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 312, 313, 314, and 315, respectively;

[1064] In another embodiment, the humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 150, 151, and 152, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 162, 163, and 164, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 316, 317, 318 and 319, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 320, 321, 322, and 323, respectively.

[1065] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 174, 175, and

176, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 186, 187, and 188, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 324, 325, 326 and 327, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 328, 329, 330 and 331, respectively.

[1066] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 198, 199 and 200, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 210, 211, and 212, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 332, 333, 334 and 335, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 336, 337, 338, and 339, respectively.

[1067] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 78, 79, and 80, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 345, 346, and 347, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 292, 293, 294 and 295, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 376, 377, 378, and 379, respectively.

[1068] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 78, 79, and 80, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 357, 358, and 359, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 292, 293, 294 and 295, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 380, 381, 382, and 383, respectively.

[1069] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 78, 79, and 80, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 369, 370, and 371, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 292, 293, 294 and 295, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence comprising SEQ ID NOs: 384, 385, 386, and 387, respectively.

[1070] In another embodiment, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 14, 38, 62, 86, 110, 134, 158, 182, 206, 341, 353, or 365; and/or a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 2, 26, 50, 74, 98, 122, 146, 170 or 194.

[1071] A humanized anti-EBOV antibody or antigen-binding portion thereof can comprise a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 14 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 2.

[1072] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 38 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 26.

[1073] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 62 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 50.

[1074] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 86 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 74.

[1075] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 110 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 98.

[1076] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 134 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 122.

[1077] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 158 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 146.

[1078] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 182 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 170.

[1079] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 206 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 194.

[1080] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 341 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 74.

[1081] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 353 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 74.

[1082] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 365 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 74.

[1083] In one embodiment, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a light chain CDR1 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 3, 27, 51, 75, 99, 123, 147, 171 or 195; a light chain CDR2 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 4, 28, 52, 76, 100, 124, 148, 172, or 196; a light chain CDR3 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 5, 29, 53, 77, 101, 125, 149, 173, or 197; a heavy chain CDR1 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 15, 39, 63, 87, 111, 135, 159, 183, 207, 342, 354, or 366; a heavy chain CDR2 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 16, 40, 64, 88, 112, 136, 160, 184, 208, 343, 355, or 367; and/or a heavy chain CDR3 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 17, 41, 65, 89, 113, 137, 161, 185 209, 344, 356, or 368.

[1084] In one embodiment, a humanized anti-EBOV antibody or antigen-binding portion thereof further comprises a light chain FR1 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 9, 33, 57, 81, 105, 129, 153, 177, or 201; a light chain FR2 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 10, 34, 58, 82, 106, 130, 154, 178, or 202; a light chain FR3 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 11, 35, 59, 83, 107 131, 155, 179 or 203; a light chain FR4 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 12, 36, 60, 84, 108, 132, 156, 180 or 204; a heavy chain FR1 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 21, 45, 69, 93, 117, 141, 165, 189, 213, 348, 360, or 372; a heavy chain FR2 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 22, 46, 70, 94, 118, 142, 166, 190, 214, 349, 361, or 373; a heavy chain FR3 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 23, 47, 71, 95, 119, 143, 167, 191, 215, 350, 362, or 374; and/or a heavy chain FR4 comprising an amino acid sequence comprising a sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 24, 48, 72, 96, 120, 144, 168, 192, 216, 351, 363, or 375.

[1085] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises: a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 3, 4, and 5, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 15, 16, and 17, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 9, 10, 11, and 12, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 21, 22, 23, and 24, respectively.

[1086] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 27, 28, and 29, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 39, 40, and 41, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 33, 34, 35, and 36, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%

sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 45, 46, 47 and 48, respectively.

[1087] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 51, 52, and 53, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 63, 64, and 65, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 57, 58, 59 and 60, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 69, 70, 71, and 72, respectively.

[1088] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 75, 76, and 77, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 87, 88, and 89, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 81, 82, 83, and 84, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 93, 94, 95, and 96, respectively.

[1089] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 99, 100, and 101, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 111, 112, and 113, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 105, 106, 107, and 108, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 117, 118, 119, and 120, respectively.

[1090] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 123, 124 and 125,, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 135, 136, and 137, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 129, 130, 131, and 132, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 141, 142, 143, and 144, respectively.

[1091] In another embodiment, the humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about

85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 147, 148 and 149, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 159, 160, and 161, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 153, 154, 155, and 156, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 165, 166, 167, and 168, respectively.

[1092] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 171, 172, and 173, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 183, 184, and 185, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 177, 178, 179 and 180, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 189, 190, 191, and 192, respectively.

[1093] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ

ID NOs: 195, 196 and 197, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 207, 208, and 209, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 201, 202, 203 and 204, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 213, 214, 215 and 216, respectively.

[1094] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 75, 76, and 77, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 342, 343, and 344, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 81, 82, 83, and 84, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 348, 349, 350, and 351, respectively.

[1095] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 75, 76, and 77, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 354, 355, and 356, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 81, 82, 83, and 84, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 360, 361, 362, and 363, respectively.

[1096] In another embodiment, a humanized anti-EBOV antibody comprises a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 75, 76, and 77, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 366, 367, and 368, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 81, 82, 83, and 84, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NOs: 372, 373, 374, and 375, respectively

[1097] In another embodiment, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 13, 37, 61, 85, 109, 133, 157, 181, 205, 340, 352, or 364; and/or a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 1, 25, 49, 73, 97, 121, 145, 169, or 193.

[1098] A humanized anti-EBOV antibody or antigen-binding portion thereof can comprise a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 13 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 1.

[1099] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 37 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 25.

[1100] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 61 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 49.

[1101] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 85 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 73.

[1102] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 109 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 97.

[1103] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 133 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 121.

[1104] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 157 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 145.

[1105] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 181 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 169.

[1106] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about

85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 205 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 193.

[1107] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 340 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 73.

[1108] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 352 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 73.

[1109] In some embodiments, a humanized anti-EBOV antibody or antigen-binding portion thereof comprises a VH comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 364 and a VL comprising an amino acid sequence that has at least about 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 73

[1110] Another aspect of the present disclosure is a multispecific molecule comprising a humanized anti-EBOV antibody or antigen-binding portion thereof disclosed herein. A multispecific molecule has specificity for at least two different antigens or epitopes. While such a molecule generally binds to two antigens (*i.e.*, bispecific molecule or antibody), the term "multispecific molecule" in the present invention encompasses an anti-EBOV antibody having specificity for two or more (such as three) antigens. A multispecific molecule comprising an anti-EBOV antibody or antigen-binding portion thereof binds at least one epitope of EBOV.

[1111] A multispecific molecule may comprise a full length antibody or a fragment of such an antibody. In one embodiment, the anti-EBOV antibody is a scFv dimer or diabody rather than whole antibody. Diabodies and scFv can be constructed without an Fc region, using only variable domains. Diabodies are bivalent, bispecific antibodies in which V_H and V_L domains are expressed on a single polypeptide chain, but using a linker that is too short to allow for pairing between the two domains on the same chain, thereby forcing the domains to pair with complementary domains of another chain and creating two antigen binding sites.

[1112] In one embodiment, the multivalent or multispecific anti-EBOV antibody comprises two dimerized single chain polypeptides. For instance, in one embodiment, each single chain polypeptide comprises, from amino to carboxyl terminus, a first binding domain (*e.g.*, scFv), an immunoglobulin hinge region, an immunoglobulin constant region (with or without a CH1 region), a c-terminus linker, and a second binding domain. The c-terminus linker may comprise, for instance, an amino acid linker derived from an amino acid sequence of an immunoglobulin hinge region (*e.g.*, an immunoglobulin "core" hinge region) or an amino acid sequence derived from a stalk region of a type II C lectin (*e.g.*, NKG2A, NKG2D). In one embodiment, the c-terminus linker comprises an amino acid sequence such as $(A_4S)^3$ or $(G_4S)^3$. The single chain polypeptide may also comprise a heterodimerization domain so that each single chain polypeptide dimerizes with a different single chain polypeptide such that a heterodimer is formed with up to four different binding domains.

[1113] The disclosure also includes nucleic acids (*e.g.*, DNA or RNA) encoding an anti-EBOV antibody or antigen-binding portion thereof described herein. Nucleic acids of the disclosure include nucleic acids having a region that is substantially identical to a polynucleotide as listed in Table 2. Nucleic acids of the disclosure also include complementary nucleic acids. The nucleic acid sequences provided herein can be exploited using codon optimization, degenerate sequence, silent mutations, and other DNA techniques to optimize expression in a particular host, and the present disclosure encompasses such sequence modifications.

[1114] Nucleic acids encoding an anti-EBOV antibody or antigen-binding portion thereof described herein can be propagated by placing the nucleic acids in a vector. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially. A nucleic acid encoding an antibody or antigen-binding portion thereof disclosed herein, a nucleic acid molecule encoding the polypeptide, operably linked to regulatory sequences that control transcriptional expression in an expression vector, is introduced into a host cell. In addition to transcriptional regulatory sequences, such as promoters and enhancers, expression vectors can include translational regulatory sequences and a marker gene which is suitable for selection of cells that carry the expression vector. The gene product encoded by a polynucleotide of the disclosure is expressed in any convenient expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems.

[1115] The disclosure includes an expression vector comprising a nucleic acid segment, wherein the nucleic acid segment may comprise a nucleotide sequence with the following sequences: (a) SEQ ID NOs: 3, 4, 5, 9, 10, 11, 12, 15, 16, 17, 21, 22, 23, and 24; (b) SEQ ID NOs: 27, 28, 29, 33, 34, 35, 36, 39, 40, 41, 45, 46, 47, and 48; (c) SEQ ID NOs: 51, 52, 53, 57, 58, 59, 60, 63, 64, 65, 69, 70, 71, and 72; (d) SEQ ID NOs: 75, 76, 77, 81, 82, 83, 84, 87, 88, 89, 93, 94, 95, and 96; (e) SEQ ID NOs: 99, 100, 101, 105, 106, 107, 108, 111, 112, 113, 117, 118, 119, and 120; (f) SEQ ID NOs: 123, 124, 125, 129, 130, 131, 132, 135, 136, 137, 141, 142, 143, and 144; (g) SEQ ID NOs: 147, 148, 149, 153, 154, 155, 156, 159, 160, 161, 165, 166, 167, and 168; (h) SEQ ID NOs: 171, 172, 173, 177, 178, 179, 180, 183, 184, 185, 189, 190, 191, and 192; (i) SEQ ID NOs: 195, 196, 197, 201, 202, 203, 204, 207, 208, 209, 213, 214, 215 and 216; (j) SEQ ID NOs: 75, 76, 77, 81, 82, 83, 84, 342, 343, 344, 348, 349, 350, and 351; (k) SEQ ID NOs: 75, 76, 77, 81, 82, 83, 84, 354, 355, 356, 360, 361, 362, and 363; (l) SEQ ID NOs: 75, 76, 77, 81, 82, 83, 84, 366, 367, 368, 372, 373, 374, and 375; a nucleotide sequence that has at least about 70%, 75%, 80%, 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to one of the nucleotide sequences of (a)-(l); or a nucleotide sequence encoding the same amino acids as one of the nucleotide sequences of (a)-(l).

[1116] In some embodiments, an expression vector comprises a nucleotide sequence with the following sequences: (a) SEQ ID NOs: 1 and 13; (b) SEQ ID NOs: 25 and 37; (c) SEQ ID NOs: 49 and 61; (d) SEQ ID NOs: 73 and 85; (e) SEQ ID NOs: 97 and 109; (f) SEQ ID NOs: 121 and 133; (g) SEQ ID NOs: 145 and 157; (h) SEQ ID NOs: 169 and 181; (i) SEQ ID NOs: 193 and 205; (j) SEQ ID NOs: 73 and 340; (k) SEQ ID NOs: 73 and 352; (l) SEQ ID NOs: 73 and 364; a nucleotide sequence that has at least about 70%, 75%, 80%, 85%, 86%, 87%, 88%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%

sequence identity to one of the nucleotide sequences of (a)-(l); or a nucleotide sequence encoding the same amino acids as one of the nucleotide sequences of (a)-(l).

[1117] Also provided herein is a host cell comprising an expression vector disclosed herein. Accordingly, antibodies and antigen-binding portions thereof disclosed herein can be produced in genetically engineered host cells according to conventional techniques. Suitable host cells are those cell types that can be transformed or transfected with exogenous DNA and grown in culture, and include bacterial, eukaryotic or mammalian cells, such as cultured higher eukaryotic cells (including cultured cells of multicellular organisms), particularly cultured mammalian cells. Cultured mammalian cells are suitable hosts for production of recombinant proteins for use within the present disclosure. Examples of suitable mammalian host cells include COS-1, COS-7, HEK293, BHK21, CHO, BSC-1, HepG2, SP2/0, HeLa, myeloma or lymphoma cell. Other mammalian host cells include African green monkey kidney cells (Vero; ATCC CRL 1587), human embryonic kidney cells (293-HEK; ATCC CRL 1573), baby hamster kidney cells (BHK-21, BHK-570; ATCC CRL 8544, ATCC CRL 10314), canine kidney cells (MDCK; ATCC CCL 34), Chinese hamster ovary cells (CHO-K1; ATCC CCL61; CHO DG44; CHO DXB11 (Hyclone, Logan, UT); *see also, e.g.*, Chasin *et al., Som. Cell. Molec. Genet.* 12:555, 1986)), rat pituitary cells (GH1; ATCC CCL82), HeLa S3 cells (ATCC CCL2.2), rat hepatoma cells (H-4-II-E; ATCC CRL 1548) SV40-transformed monkey kidney cells (COS-1; ATCC CRL 1650) and murine embryonic cells (NIH-3T3; ATCC CRL 1658). Additional suitable cell lines are known in the art and available from public depositories such as the American Type Culture Collection, Manassas, Virginia.

[1118] The present disclosure also provides a composition comprising an anti-EBOV antibody or antigen-binding portion thereof and one or more other antibodies or antigen-binding portions thereof, wherein the one or more other antibodies or antigen-binding portions thereof binds a protein produced by a virus in the *Filoviridae* family. The one or more other antibodies or antigen-binding portions thereof can bind a glycoprotein, such as GP. In some embodiments, the one or more other antibodies or antigen-binding portions thereof binds *Ebolavirus* or *Marburgvirus*, such as *Zaire ebolavirus, Sudan ebolavirus, Reston ebolavirus, Tai Forest ebolavirus, Bundibugyo ebolavirus*, *Cote d'Ivoire ebolavirus*, Marburg virus or Ravn virus. In some embodiments, the composition further comprises a pharmaceutically acceptable carrier.

[1119] In some embodiments, a composition comprising an anti-EBOV antibody or antigen-binding portion thereof disclosed herein with another antibody or antigen-binding portion thereof act synergistically when administered to a subject in need. As used herein, “synergy” or a “synergistic” response refers to an activity or improvement (e.g., prevents infection with EBOV, prevents disease associated with EBOV infection, reduces the number and/or severity of symptoms of an EBOV infection, stops or limits the spread of EBOV, and/or shortens the duration of an EBOV infection at a rate) that is greater than the sum of the effect of each therapy as a monotherapy. As can be appreciated by a skilled artisan, synergy can be shown *in vitro*, *ex vivo* and *in vivo*.

[1120] As will be appreciated by one of skill in the art, the antibody or antigen-binding portion thereof may be used in the preparation of a medicament or pharmaceutical composition for administration (either therapeutic or prophylactic) to a subject in need of such treatment. In these embodiments, the medicament or pharmaceutical composition is prepared by mixing the antibody or antigen-binding portion thereof with a pharmaceutically acceptable carrier. The resulting composition is pharmacologically acceptable if its administration can be tolerated by a recipient patient. Accordingly, another aspect of the present disclosure is a pharmaceutical composition comprising an anti-EBOV antibody or antigen-binding portion thereof disclosed herein and a pharmaceutically acceptable carrier. The pharmaceutical composition can comprise a pharmaceutically acceptable carrier, diluent, excipient, and/or other additives, such as water, a pharmaceutical acceptable organic solvent, collagen, polyvinyl alcohol, polyvinylpyrrolidone, a carboxyvinyl polymer, carboxymethylcellulose sodium, polyacrylic sodium, sodium alginate, water-soluble dextran, carboxymethyl starch sodium, pectin, methyl cellulose, ethyl cellulose, xanthan gum, gum Arabic, casein, gelatin, agar, diglycerin, glycerin, propylene glycol, polyethylene glycol, Vaseline, paraffin, stearyl alcohol, stearic acid, human serum albumin (HSA), mannitol, sorbitol, lactose, a pharmaceutically acceptable surfactant and the like. Additives used are chosen from, but not limited to, the above or combinations thereof, as appropriate, depending on the dosage form of the present invention.

[1121] Formulation of the composition will vary according to the route of administration selected (*e.g.*, solution, emulsion). An appropriate composition comprising the active agent to be administered can be prepared in a physiologically acceptable vehicle or carrier. For solutions or emulsions, suitable carriers include, for example, aqueous or alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles can include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's or fixed oils. Intravenous vehicles can include various additives, preservatives, or fluid, nutrient or electrolyte replenishers

[1122] The pharmaceutical compositions may be in the form of a sterile injectable aqueous, oleaginous suspension, dispersions or sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. The suspension may be formulated according to the known art using those suitable dispersing or wetting agents and suspending agents which have been mentioned above. The sterile injectable preparation may also be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example as a solution in 1,3-butane diol. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, vegetable oils, Ringer's solution and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono- or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables.

[1123] In all cases the form should be sterile and must be fluid to the extent that easy syringability exists. The proper fluidity can be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be desirable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

[1124] Compositions useful for administration may be formulated with uptake or absorption enhancers to increase their efficacy. Such enhancers include for example, salicylate, glycocholate/linoleate, glycholate, aprotinin, bacitracin, SDS, caprate and the like. See, *e.g.*, Fix (*J. Pharm. Sci.*, 85:1282-1285, 1996) and Oliyai and Stella (*Ann. Rev. Pharmacol. Toxicol.*, 32:521-544, 1993).

[1125] In some embodiments, the present disclosure provides methods for reducing, preventing, or treating an EBOV infection in a subject in need thereof. In some embodiments, a subject in need thereof includes a subject that has been infected with EBOV, is showing symptoms consistent with an EBOV infection, is exhibiting an EBOV infection, is suspected of having an EBOV infection, or is at risk of developing an EBOV infection. Thus, in some embodiments, provided herein is a method of treating an EBOV infection or outbreak comprising administering a therapeutically or prophylactically effective amount of an anti-EBOV antibody or antigen-binding portion thereof to an individual in need of such treatment.

[1126] In one aspect, the antibodies or antigen-binding portion thereof may be formulated into a pharmaceutical product for providing treatment for individuals for EBOV infection, comprising a therapeutically effective amount of said antibody or antigen-binding portion. In some embodiments, an effective amount of the antibody or antigen-binding portion thereof may be formulated into a pharmaceutical product for treating an individual who has been exposed to or infected with EBOV, who is at risk of EBOV infection, or who is displaying symptoms of an EBOV infection. A therapeutically effective amount can be determined by the skilled person. The therapeutically effective dosage of the pharmaceutical composition can be determined readily by the skilled artisan, for example, from animal studies. In addition, human clinical studies can be performed to determine the preferred effective dose for humans by a skilled artisan. The precise dose to be employed will also depend on the route of administration.

[1127] In some embodiments, the antibodies and antigen-binding portions provided herein may be administered via enteral (including without limitation oral administration and rectal administration) or parenteral (including without limitation intravenous administration, intramuscular administration, and aerosol delivery) administration. Additional exemplary appropriate methods for administration of the antibodies and antigen-binding fragments provided herein include nasal, buccal, vaginal, ophthalmic, subcutaneous, intraperitoneal, intraarterial, spinal, intrathecal, intra-articular, intra-arterial, sub-arachnoid, sublingual, oral mucosal, bronchial, lymphatic, intra-uterine, integrated on an implantable device such as a suture or in an implantable device such as an implantable polymer, intradural, intracortical, or dermal. Such compositions would normally be administered as pharmaceutically acceptable compositions as described herein. In some embodiments, the antibodies or antigen-binding portions thereof may be administered to the subject once per day, or in multiple doses per day. In one embodiment, the antibodies or antigen-binding portions thereof are administered to the subject until symptoms improve or resolve and/or until the subject is no longer at risk of EBOV infection.

[1128] As used herein, the term "subject" or "patient" refers to any member of the subphylum cordata, including, without limitation, humans and other primates, including non-human primates such as chimpanzees and other apes and monkey species. Farm animals such as cattle, sheep, pigs, goats and horses; domestic mammals such as dogs and cats;

laboratory animals including rodents such as mice, rats (including cotton rats) and guinea pigs; birds, including domestic, wild and game birds such as chickens, turkeys and other gallinaceous birds, ducks, geese, and the like are also non-limiting examples. The terms "mammals" and "animals" are included in this definition. Both adult and newborn individuals are intended to be covered. In particular, the methods and compositions provided herein are methods and compositions for treating EBOV infections in human subjects.

[1129] In general, it is desirable to provide the recipient with a dosage of antibody which is in the range of from about 1 μg/kg body weight of individual to 1 g/kg body weight. It is of note that many factors are involved in determining what is a therapeutically effective dose or effective amount such as, for example but by no means limited to, the patient's age, weight, sex and general condition. Effective amounts may also vary according to the quality of the preparation and the severity of the infection or outbreak. Accordingly, it is noted that one of skill in the art will be able to determine what constitutes an "effective amount" based on a particular set of circumstances without undue experimentation.

[1130] In some embodiments, the antibody or antigen-binding portion thereof is "protective" or "neutralizing" and accordingly on administration will hinder the spread of the virus. In some embodiments, the antibodies and antigen-binding portions thereof provided herein interfere either with viral attachment, entry and/or unpackaging once inside the cell. Accordingly, in some embodiments, administering an effective amount to an individual in need of such treatment will result in at least one of the following: reduced viral load, reduction in severity of symptoms associated with the EBOV infection, and reduced or slowed viral reproduction.

[1131] In other embodiments of the invention, the antibody or antigen-binding portion thereof described herein may be used in a method for detecting EBOV in a sample suspected of containing EBOV. In other embodiments, the antibody or antigen-binding portion thereof described herein may be used in a method for diagnosing a filovirus infection. Such methods are well known in the art and a wide variety of suitable methods will be readily apparent to one of skill in the art. Such methods may involve contacting the sample to be investigated with the antibody or antigen-binding fragment thereof under conditions suitable for binding, and then detecting the bound antibody or fragment. The sample may be, for example, a biological sample, such as cells, tissue, biological fluid or the like or may be an environmental sample such as a soil or water sample or a food sample such as canned goods, meats and the like. Other suitable samples will be readily apparent to one of skill in the art.

[1132] As will be appreciated by one of skill in the art, detection antibodies must show high specificity and avidity for their antigenic target. As such, showing that a monoclonal antibody or antigen-binding fragment thereof reacts with the antigenic target derived from a highly purified or in vitro prepared sample does not guarantee that the antibody has sufficient specificity for use with biological sample. That is, the antibody must have sufficient specificity that it will not produce false positives or react with antigens from related, viruses. Examples of suitable tests for determining utility as a diagnostic or as a neutralizing mAb include but are by no means limited to negative neutralization and/or negative detection of a non-EBOV, or C-ELISA data showing competition of binding with the mouse mAbs that is being detected thereby showing that the mAbs can be used to show that an immune response to EBOV has occurred in patient/animal sera, meaning that they were exposed/infected (abrogation of binding by human antibodies). Alternatively, biological material such as blood, mucus or stool with could be spiked or enriched with the virus and the monoclonal antibodies used to detect added virus in the sample, which would in turn determine limits of detection as well as other parameters of the monoclonal antibodies. Biological samples from experimentally infected animals could also be used to determine the utility of the mAbs at different stages of the infection cycle.

[1133] In some embodiments, at least one of the detection antibodies is mixed with a biological sample under suitable conditions to promote binding of the at least one detection antibody with the antigenic target if the antigenic target is present in the biological sample. Binding of the detection antibody to an antigenic target within the sample is then detected using means known in the art, for example, by use of a labelled secondary antibody or other means discussed herein and/or known in the art. In some embodiments, the detection antibody (e.g., an anti-EBOV antibody disclosed herein) is labelled.

[1134] While various embodiments have been described above, it should be understood that they have been presented by way of example, and not limitation. Where methods described above indicate certain events occurring in certain order, the ordering of certain events can be modified. Additionally, certain of the events may be performed concurrently in a parallel process when possible, as well as performed sequentially as described above.

[1135] All publications, patents and patent applications discussed and cited herein are incorporated herein by reference in their entireties. It is understood that the disclosed invention is not limited to the particular methodology, protocols and materials described as these can vary. It is also understood that the terminology used herein is for the purposes of describing particular embodiments only and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

EXAMPLES

[1136] The invention will be further clarified by the following examples, which are intended to be purely exemplary of the invention and in no way limiting.

Example 1: V Gene Sequencing

[1137] V gene sequencing for CAN9G1 was performed by first isolating RNA from the CAN9G1 parental hybridoma clonal cell line using the RNAeasy Mini Kit. A panel of specific primers for each variable gene group was used to amplify the cDNA in a single step RT-PCR reaction to generate cDNA encoding the heavy and light chain variable domains (VH and VL) of CAN9G1. The cDNAs were cloned and sequenced using standard techniques. After sequencing and identification of the variable gene, subgroup specific leader primers were designed to remove potential mutations from degenerate primers in the original primer panel to ensure sequence identity of the full variable gene sequence. The cDNA sequences encoding the VL and VH of CAN9G1 are presented as SEQ ID NO: 249 and SEQ ID NO: 257, respectively, and the amino acid sequences are shown as SEQ ID NO: 250 and SEQ ID NO: 258, respectively. The amino acid sequences of the three light chain complementarity determining regions LCDR1, LCDR2, and LCDR3 are presented as SEQ ID NO: 254, SEQ ID NO: 255, and SEQ ID NO: 256, respectively, and the HCDR1, HCDR2, and HCDR3 regions are presented as SEQ ID NO: 262, SEQ ID NO: 263, and SEQ ID NO: 264, respectively.

[1138] V gene sequencing for the CAN8G1 parental hybridoma clonal cell line follows the same procedure as described above for CAN9G1. The cDNA sequences encoding the VL and VH of CAN8G1 are presented as SEQ ID NO: 233 and SEQ ID NO: 241, respectively, and the amino acid sequences are shown as SEQ ID NO: 234 and SEQ ID NO: 242, respectively. The amino acid sequences of the three light chain complementarity determining regions LCDR1, LCDR2, and LCDR3 are presented as SEQ ID NO: 238, SEQ ID NO: 239, and SEQ ID NO: 240, respectively, and the HCDR1, HCDR2, and HCDR3 regions are presented as SEQ ID NO: 246, SEQ ID NO: 247, and SEQ ID NO: 248, respectively.

[1139] V gene sequencing for the CAN7G1 parental hybridoma clonal cell line follows the same procedure as described above for CAN9G1. The cDNA sequences encoding the VL and VH of CAN7G1 are presented as SEQ ID NO: 217 and SEQ ID NO: 225, respectively, and the amino acid sequences are shown as SEQ ID NO: 218 and SEQ ID NO: 226, respectively. The amino acid sequences of the three light chain complementarity determining regions LCDR1, LCDR2, and LCDR3 are presented as SEQ ID NO: 222, SEQ ID NO: 223, and SEQ ID NO: 224, respectively, and the HCDR1, HCDR2, and HCDR3 regions are presented as SEQ ID NO: 230, SEQ ID NO: 231, and SEQ ID NO: 232, respectively.

Example 2: Humanization of Murine Ebola mAb

[1140] Humanization of CAN9G1

[1141] Human germline heavy and light chain variable domains with maximum identity alignment with the murine sequences were identified in the NCBI databases for use as identify acceptor frameworks. The human germline alleles selected were IGHV3-30-15/ IGHJ4-01 (VH chain) and IGLV4-69-01/ IGLJ1-01 (VK chain). These human germline alleles were identified as best matching and used as an acceptor framework for grafting the CDRs. All 6 CDRs (SEQ ID NOs: 259-261 and 251-253) corresponding to heavy and light chains were inserted into the human framework regions to encode complementarity determining regions for heavy and light chains (SEQ ID NOs: 254-256 and 262-264). The cdrCAN9G1 VL and VH regions are presented as SEQ ID NOs: 193 and 194 (nucleotide and amino acid sequences of cdrCAN9G1 VL) and SEQ ID NOs: 205 and 206 (nucleotide and amino acid sequences of cdrCAN9G1 VH).

[1142] Surface exposure and/or involvement in folding or interchain contacts were determined and residues were changed or maintained based on these determinations. Antibodies huCAN9G1 and rehuCAN9G1 “Human engineered” were generated by identifying the closest human germline allele for CAN9G1 mAbs VH and Vk, individually. These were then designed for use as acceptor frameworks, resulting in the VH and VL sequences of huCAN9G1. These sequences are presented as SEQ ID NOs: 145 and 146 (nucleotide and amino acid sequences of huCAN9G1 VL, respectively) and SEQ ID NOs: 157 and 158 (nucleotide and amino acid sequences of huCAN9G1 VH, respectively). The rehuCAN9G1 mAb was further resurfaced by substitution(s) made on surface exposed amino acids to correspond to the adopted human frameworks without disruption of the CDRs. These sequences are presented as SEQ ID NOs: 169 and 170 (nucleotide and amino acid sequences of rehuCAN9G1 VL) and SEQ ID NOs: 181 and 182 (nucleotide and amino acid sequences of rehuCAN9G1 VH).

[1143] Humanization of CAN8G1

[1144] The humanized IgG/k versions of the CAN8G1 murine mAb were created as above for CAN9G1. The human germline alleles selected were hIGHV2-5-08/hIGHJ4-01(VH chain) and hIGKV3-15-01/hIGKJ4-02(VK chain). All 6 CDRs (SEQ ID NOs: 135-137 and 123-125) corresponding to heavy and light chains were inserted into the human framework regions to encode complementarity determining regions for heavy and light chains (SEQ ID NOs: 138-140 and 126-128). The cdrCAN8G1 VL and VH regions are presented as SEQ ID NOs: 121 and 122 (nucleotide and amino acid sequences of cdrCAN8G1 VL) and SEQ ID NOs: 133 and 134 (nucleotide and amino acid sequences of cdrCAN8G1 VH). The huCAN8G1 sequences are presented as SEQ ID NOs: 73 and 74 (nucleotide and amino acid sequences of huCAN8G1 VL) and SEQ ID NOs: 85 and 86 (nucleotide and amino acid sequences of huCAN8G1 VH). The rehuCAN8G1 sequences are presented as SEQ ID NOs 97 and 98 (nucleotide and amino acid sequences of rehuCAN8G1 VL) and SEQ ID NOs 109 and 110 (nucleotide and amino acid sequences of rehuCAN8G1 VH).

[1145] Humanization of CAN7G1

[1146] The humanized IgG/k versions of the CAN8G1 murine mAb were created as above for CAN9G1. The human germline alleles selected were IGHV1-3-01/ IGHJ4-01 (VH chain) and IGKV3-11-01/ IGKJ4-01 (VK chain). All 6 CDRs (SEQ ID NOs: 63-65 and 51-53) corresponding to heavy and light chains were inserted into the human framework regions to encode complementarity determining regions for heavy and light chains (SEQ ID NOs: 66-68 and 54-56). The cdrCAN7G1 VL and VH regions are presented as SEQ ID NOs: 49 and 50 (nucleotide and amino acid sequences of cdrCAN7G1 VL) and SEQ ID NOs: 61 and 62 (nucleotide and amino acid sequences of cdrCAN7G1 VH). The huCAN7G1 sequences are presented as SEQ ID NOs: 1 and 2 (nucleotide and amino acid sequences of huCAN7G1 VL) and SEQ ID NOs: 13 and 14 (nucleotide and amino acid sequences of huCAN7G1 VH). The rehuCAN7G1 sequences are presented as SEQ ID NOs: 25 and 26 (nucleotide and amino acid sequences of rehuCAN7G1 VL) and SEQ ID NOs: 37 and 38 (nucleotide and amino acid sequences of rehuCAN7G1 VH).

Example 3: Transient Expression and Purification of Humanized Ebola mAbs

[1147] The VH and VL regions for the humanized Ebola mAbs described in Example 2 (cdrCAN9G1, huCAN9G1, rehuCAN9G1, cdrCAN8G1, huCAN8G1, rehuCAN8G1, cdrCAN7G1, huCAN7G1, and rehuCAN7G1) are cloned into vectors for expression as full-sized humanized antibodies having human IgG constant regions. The VH and VL regions of the parent murine antibody (CAN9G1, CAN8G1, and CAN7G1) are also cloned into human constant region vectors for expression as mouse-human chimeric antibodies.

[1148] Humanized Ebola mAbs were produced by transient transfections in 293F, CHO-S or CHOK1S-V cells. One day prior to transfection, 293F, CHO-S or CHOK1S-V cells were counted using a Haemocytometer in the presence of Trypan Blue, then passaged into transfection medium (293F cells remain in FreeStyle 293 Expression medium; CHO cells are transferred into DMEM/F12 supplemented with 10% FBS and L-Glutamine) at a concentration of 6-8x10^5 cells/ml and incubated 24 hours at 37°C, 8% CO_2 and in a shaking incubator at 100 rpm. Freestyle Max Transfection Agentwas diluted 1/16 in Optimem before being added to 312.5 μg of the appropriate DNA also diluted in Optimem. DNA/Freestyle Max Transfection Agent mix is incubated at room temperature for 20 minutes and added to 250 x 10^6 cells in FreeStyle 293 Expression Medium (no DMSO) for 293F cells or DMEM/F12 + 10% FBS + 5 mM L-Glutamine that had been treated for 3 hours with 1% DMSO for CHO cells.

[1149] The culture was harvested after incubation at 37°C/5% CO_2/125 rpm in a shaking incubator by centrifuging the culture at 2500 rpm for 30 minutes, removing the supernatant and filtering it through a 0.22 μM bottle top filter. The supernatant was concentrated by spin cell concentrator equipped with a 50 kDa membrane to a final volume of ~100 mL. The concentrated supernatant was purified by Protein G purification on the FPLC or by using Protein G GraviTrap columns (manual purification system). The purified sample was buffer exchanged by spin-cell concentrator equipped with a 50 kDa membrane into D-PBS and concentrated down to a final volume of 1-2 mL. The final protein concentration was determined by BCA using the Pierce BCA Kit.

Example 4: Screening of Humanized Ebola mAbs

[1150] An ELISA was performed to test the binding of the humanized Ebola mAbs described in Example 3 against multiple strains of Ebola GP or derivatives thereof (GPe, GP ectodomain; GPeΔmuc, GPe with mucin domain removed; GPeΔmucΔtm, GPe with both mucin and transmembrane domains removed) and to determine if they are cross-reactive to various strains of Marburg virus (MARV) GP or derivatives thereof (GPe, GPeΔmuc, GPeΔmucΔtm). The ELISA plate was coated with 200ng/well of antigen. The wells were blocked with 5% skim milk then probed with 60 μl serially diluted humanized mAbs (starting at 17.0ug/mL to 2.1ug/mL). After washing plates, binding was detected with commercial goat anti-human HRP conjugate antibody. Where appropriate, development and detection were carried out with anti-murine HRP-conjugated secondary Ab at the appropriate dilution for positive controls, murine mAbs, and negative (IgG Control mAb) controls were also run. The plate was read at 405nm after minimum 10 minutes incubation with ABTS substrate.

[1151] Results: huCAN9G1 was tested, along with the murine versions (muCAN8G1 and muCAN9G1) for binding by ELISA to EBOV Zaire GPe and/or EBOV Sudan GPe. Table 3 lists the ELISA results in table form. The results show the binding of muCAN8G1, muCAN9G1 and huCAN9G1 binding to EBOV Zaire GPe, as well as muCAN8G1 binding to EBOV Sudan GPe.

[1152] Table 3: Summary of ELISA Results for anti-EBOV humanized and murine mAbs vs. EBOV Glycoproteins

Glycoprotein (GP)	mAb @ 2ug/mL	OD_{405} @ 30 min
EBOV Zaire	muCAN9G1	1.385
	huCAN9G1	3.349
	muCAN8G1	0.553
	IgG Neg Control (murine)	0.048
	IgG Neg Control (human)	0.051
EBOV Sudan	muCAN8G1	0.411
	IgG Neg Control (murine)	0.049

Example 5: Western Blots of Humanized Ebola mAbs

[1153] A 4-12% gradient SDS-PAGE gel is run for 1.5 hours at 200 volts with a combination of MARV and EBOV GP proteins. The gel is then transferred to a nitrocellulose membrane for a minimum of 1 hour at 45 volts. The membrane is blocked overnight at 4°C with 5% skim milk in 1xTBST. The next day the humanized Ebola mAbs (1°Ab) described in Example 3 are diluted in 2.5% skim milk in 1xTBST at concentrations ranging from 2 μg/mL to 5 μg/mL depending on the antibody and used to probe the membrane containing the transferred proteins for 2 hours at room temperature (RT). The membranes are then washed with 1xTBST to remove unbound 1°Ab and probed with anti-human IgG-HRP (2°Ab) at a dilution of 1:4000 to 1:5000 for 1.5 hours at RT. Where appropriate, development and detection are carried out with anti-murine HRP-conjugated secondary Abs at the appropriate dilution for controls.

Example 6: Pseudovirus Neutralization Assay

[1154] The humanized Ebola mAbs described in Example 3 are tested for neutralization of recombinant Vesicular stomatitis virus (VSV) pseudotyped with EBOV GP. VSV pseudovirions containing a GFP gene in place of the VSV G gene (VSVΔG) and bearing the glycoprotein of EBOV are generated as previously described (Takeda, A. et al. Proc Natl Acad Sci USA, 1997. 94(26): 14764-14769). Experiments are performed in triplicate with VSVΔG bearing either full-length EBOV GP (VSVΔG-GP) or mucin-deleted Δ257-425 GP (VSVΔG-GPΔmuc). Pseudovirions are incubated with anti-VSV G mAb for 1 hour at RT, then incubated with 2.5, 10 or 50 µg/mL of each humanized Ebola mAb in DMEM-10%FBS for an additional hour. Pseudovirion/mAb complexes are added to Vero cells at a multiplicity of infection (MOI) of 0.01. After 48 hours, infection was evaluated by counting GFP-expressing cells.

Example 7: Mouse in vivo Protection Experiments

[1155] All procedures with infectious ebolaviruses are performed in biosafety level 4 facilities under IACUC-approved protocols. One hour pre- or post-exposure, BALB/c mice are treated intraperitoneally (IP) with purified humanized Ebola mAbs described in Example 3, non-relevant IgG, or PBS alone. The mice are then challenged IP with 1000 plaque-forming units (p.f.u.) mouse-adapted EBOV. Mice are monitored for clinical signs of infections for 28 days post-exposure at which point the study ends and the mice are euthanized.

What is claimed is:

1. An isolated antibody or antigen-binding portion thereof that binds to *Ebolavirus*, wherein the antibody or antigen-binding portion thereof comprises:

   a) a light chain CDR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 6, 78, or 150;
   b) a light chain CDR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 7, 79, or 151;
   c) a light chain CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 8, 80, or 152;
   d) a heavy chain CDR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 18, 90, or 162;
   e) a heavy chain CDR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 19, 91, or 163;
   f) a heavy chain CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 20, 92, or 164;
   g) a light chain FR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence e comprising SEQ ID NO: 268, 276, 284, 292, 300, 308, 316, 324, or 332;
   h) a light chain FR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 269, 285, 293, 317, or 333;
   i) a light chain FR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 270, 278, 286, 294, 302, 310, 318, 326, or 334;
   j) a light chain FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 271, 279, 295, 319, or 335;
   k) a heavy chain FR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 272, 280, 288, 296, 304, 312, 320, or 336;
   l) a heavy chain FR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 273, 281, 289, 297, 313, 321, 329, or 337;

m) a heavy chain FR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 274, 282, 290, 298, 306, 314, 322, 330, or 338; and,

n) a heavy chain FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NO: 275, 299, 307, 323, 379, or 387.

2. The isolated antibody or antigen-binding portion thereof of claim 1, wherein the antibody or antigen-binding portion thereof comprises:

a) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 6, 7 and 8, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 18, 19 and 20, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 268, 269, 270, and 271, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 272, 273, 274 and 275, respectively;

b) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 30, 31, and 32, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 42, 43, and 44, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence e comprising SEQ ID NOs: 276, 277, 278, and 279, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 280, 281, 282, and 283, respectively;

c) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 54, 55, and 56, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 66, 67, and 68, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 284, 285, 286, and 287, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 288, 289, 290, and 291, respectively;

d) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 78, 79 and 80, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 90, 91 and 92, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 292, 293, 294 and 295, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 296, 297, 298, and 299, respectively;

e) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs:102, 103, and 104, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 114, 115, and 116, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 300, 301, 302 and 303, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 304, 305, 306 and 307, respectively;

f) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 126, 127, and 128, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 138, 139, and 140, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 308, 309, 310 and 311, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 312, 313, 314, and 315, respectively;

g) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 150, 151, and 152, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 162, 163, and 164, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 316, 317, 318 and 319, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 320, 321, 322, and 323, respectively;

h) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 174, 175, and 176, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 186, 187, and 188, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 324, 325, 326 and 327, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 328, 329, 330 and 331, respectively;

i) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 198, 199 and 200, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 210, 211, and 212, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 332, 333, 334 and 335, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 336, 337, 338, and 339, respectively;

j) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 78, 79 and 80, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 345, 346, and 347, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 292, 293, 294 and 295, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 376, 377, 378, and 379, respectively;

k) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 78, 79 and 80, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 357, 358, and 359, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 292, 293, 294 and 295, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 380, 381, 382, and 383, respectively; or

l) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 78, 79 and 80, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 369, 370, and 371, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID

NOs: 292, 293, 294 and 295, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence comprising SEQ ID NOs: 384, 385, 386, and 387, respectively.

3. An isolated antibody or antigen-binding portion thereof that binds to *Ebolavirus*, wherein the antibody or antigen-binding portion thereof comprises:

a) a light chain CDR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 3, 75, or 147;

b) a light chain CDR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 4, 76, or 148;

c) a light chain CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 5, 77, or 149;

d) a heavy chain CDR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 15, 87, or 159, 183;

e) a heavy chain CDR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 16, 88, or 160;

f) a heavy chain CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 17, 89, or 161;

g) a light chain FR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 9, 33, 57, 81, 105, 129, 153, 177, or 201;

h) a light chain FR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 10, 58, 82, 154, or 202;

i) a light chain FR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 11, 35, 59, 83, 107 131, 155, 179 or 203;

j) a light chain FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 12, 36, 156, or 204;

k) a heavy chain FR1 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 21, 45, 69, 93, 117, 141, 165, or 213;

l) a heavy chain FR2 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 22, 46, 70, 94, 142, 166, 190, or 214;

m) a heavy chain FR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 23, 47, 71, 95, 119, 143, 167, 191, or 215; and,

n) a heavy chain FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 24, 351, 363, or 375.

4. The isolated antibody or antigen-binding portion thereof of claim 3, wherein the antibody or antigen-binding portion thereof comprises:

a) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 3, 4, and 5, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 15, 16, and 17, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 9, 10, 11, and 12, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 21, 22, 23, and 24, respectively;

b) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 27, 28, and 29, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 39, 40, and 41, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 33, 34, 35, and 36, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 45, 46, 47 and 48, respectively;

c) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 51, 52, and 53, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 63, 64, and 65, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 57, 58, 59 and 60, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 69, 70, 71, and 72, respectively;

d) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 75, 76, and 77, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 87, 88, and 89, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 81, 82, 83, and 84, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 93, 94, 95, and 96, respectively;

e) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 99, 100, and 101, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 111, 112, and 113, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 105, 106, 107, and 108, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 117, 118, 119, and 120, respectively;

f) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 123, 124 and 125, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 135, 136, and 137, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 129, 130, 131, and 132, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 141, 142, 143, and 144, respectively;

g) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 147, 148 and 149, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 159, 160, and 161, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 153, 154, 155, and 156, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 165, 166, 167, and 168, respectively;

h) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 171, 172, and 173, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 183, 184, and 185, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 177, 178, 179 and 180, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 189, 190, 191, and 192, respectively;

i) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 195, 196 and 197, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 207, 208, and 209, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 201, 202, 203 and 204, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 213, 214, 215 and 216, respectively;

j) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 75, 76, and 77, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 342, 343, and 344, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 81, 82, 83, and 84, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85%

sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 348, 349, 350, and 351, respectively;

k) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 75, 76, and 77, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 354, 355, and 356, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 81, 82, 83, and 84, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 360, 361, 362, and 363, respectively; or

l) a light chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 75, 76, and 77, respectively; a heavy chain CDR1, CDR2, and CDR3 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 366, 367, and 368, respectively; a light chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 81, 82, 83, and 84, respectively; and a heavy chain FR1, FR2, FR3, and FR4 comprising an amino acid sequence that has at least about 85% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NOs: 372, 373, 374, and 375, respectively.

5. An isolated antibody or antigen-binding portion thereof that binds to *Ebolavirus*, wherein the antibody or antigen-binding portion thereof comprises:

a) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 13, 37, 61, 85, 109, 133, 157, 181, 205, 340, 352, or 364; and

b) a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 1, 25, 49, 73, 97, 121, 145, 169, or 193.

6. The antibody or antigen-binding portion thereof of claim 5, wherein the antibody or antigen-binding portion thereof comprises:

a) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 13 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 1;

b) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 37 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 25;

c) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 61 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 49;

d) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 85 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 73;

e) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 109 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 97;

f) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 133 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 121;

g) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 157 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 145;

h) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 181 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 169;

i) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 205 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 193;

j) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 340 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 73;

k) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 352 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 73; or

l) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 364 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to an amino acid sequence encoded by a nucleotide sequence comprising SEQ ID NO: 73.

7. An isolated antibody or antigen-binding portion thereof that binds to *Ebolavirus*, wherein the antibody or antigen-binding portion thereof comprises:

a) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 14, 38, 62, 86, 110, 134, 158, 182, 206, 341, 353, or 365; and

b) a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 2, 26, 50, 74, 98, 122, 146, 170 or 194.

8. The isolated antibody or antigen-binding portion of claim 7, wherein the antibody or antigen-binding portion thereof comprises:

a) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 14 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 2;

b) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 38 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 26;

c) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 62 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 50;

d) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 86 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 74;

e) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 110 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 98;

f) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 134 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 122;

g) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 158 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 146;

h) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 182 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 170;

i) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 206 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 194;
j) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 341 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 74;
k) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 353 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 74; or
l) a variable heavy chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 365 and a variable light chain comprising an amino acid sequence that has at least about 98% sequence identity to SEQ ID NO: 74.

9. The isolated antibody or antigen-binding portion of claim 8, wherein the antibody or antigen-binding portion thereof comprises:
a) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 14 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 2;
b) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 38 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 26;
c) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 62 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 50;
d) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 86 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 74;
e) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 110 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 98;
f) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 134 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 122;

g) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 158 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 146;

h) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 182 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 170;

i) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 206 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 194;

j) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 341 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 74;

k) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 353 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 74; or

l) a variable heavy chain comprising an amino acid sequence comprising SEQ ID NO: 365 and a variable light chain comprising an amino acid sequence comprising SEQ ID NO: 74.

10. The isolated antibody or antigen-binding portion thereof of any one of the preceding claims, wherein the antibody or antigen-binding portion is selected from the group consisting of: (i) a whole immunoglobulin; (ii) an scFv; (iii) a Fab fragment; (iv) an F(ab')2; and (v) a disulfide linked Fv.

11. The isolated antibody of antigen-binding portion thereof of any one of the preceding claims, wherein the antibody or antigen-binding portion thereof binds to the GP subunit of the *Ebolavirus*.

12. The isolated antibody or antigen-binding portion thereof of any one of the preceding claims, wherein the antibody or antigen-binding portion thereof binds to the mucin domain of the GP subunit of the *Ebolavirus*.

13. The isolated antibody of antigen-binding portion thereof of any one of the preceding claims, wherein the *Ebolavirus* is *Zaire ebolavirus, Sudan ebolavirus, Reston ebolavirus, Tai Forest ebolavirus, Cote d'Ivoire ebolavirus* or *Bundibugyo ebolavirus.*

14. A nucleic acid sequence encoding the antibody or antigen-binding portion thereof of any one of claims 1-13.

15. An expression vector comprising a promoter operably linked to a nucleotide sequence of claim 14.

16. An expression vector comprising a nucleotide sequence with the following sequences:
    a) SEQ ID NOs: 3, 4, 5, 9, 10, 11, 12, 15, 16, 17, 21, 22, 23, and 24;
    b) SEQ ID NOs: 27, 28, 29, 33, 34, 35, 36, 39, 40, 41, 45, 46, 47, and 48;
    c) SEQ ID NOs: 51, 52, 53, 57, 58, 59, 60, 63, 64, 65, 69, 70, 71, and 72;
    d) SEQ ID NOs: 75, 76, 77, 81, 82, 83, 84, 87, 88, 89, 93, 94, 95, and 96;
    e) SEQ ID NOs: 99, 100, 101, 105, 106, 107, 108, 111, 112, 113, 117, 118, 119, and 120,
    f) SEQ ID NOs: 123, 124, 125, 129, 130, 131, 132, 135, 136, 137, 141, 142, 143, and 144;
    g) SEQ ID NOs: 147, 148, 149, 153, 154, 155, 156, 159, 160, 161, 165, 166, 167, and 168;
    h) SEQ ID NOs: 171, 172, 173, 177, 178, 179, 180, 183, 184, 185, 189, 190, 191, and 192;
    i) SEQ ID NOs: 195, 196, 197, 201, 202, 203, 204, 207, 208, 209, 213, 214, 215 and 216;
    j) SEQ ID NOs: 75, 76, 77, 81, 82, 83, 84, 342, 343, 344, 348, 349, 350, and 351;
    k) SEQ ID NOs: 75, 76, 77, 81, 82, 83, 84, 354, 355, 356, 360, 361, 362, and 363; or
    l) SEQ ID NOs: 75, 76, 77, 81, 82, 83, 84, 366, 367, 368, 372, 373, 374, and 375.

17. An expression vector comprising nucleotide sequences having the following sequences:
    a) SEQ ID NOs: 1 and 13;
    b) SEQ ID NOs: 25 and 37;
    c) SEQ ID NOs: 49 and 61;
    d) SEQ ID NOs: 73 and 85;

e) SEQ ID NOs: 97 and 109;
f) SEQ ID NOs: 121 and 133;
g) SEQ ID NOs: 145 and 157;
h) SEQ ID NOs: 169 and 181;
i) SEQ ID NOs: 193 and 205;
j) SEQ ID NOs: 73 and 340;
k) SEQ ID NOs: 73 and 352; or
l) SEQ ID NOs: 73 and 364.

18. A host cell comprising the expression vector of any one of claims 15-17.

19. The host cell of claim 18, wherein the cell is a bacterial, eukaryotic or mammalian cell.

20. The host cell of claim 18 or 19, wherein the cell is COS-1, COS-7, HEK293, BHK21, CHO, BSC-1, HepG2, SP2/0, HeLa, myeloma or lymphoma cell.

21. A method of producing an antibody or antigen-binding portion thereof that binds to *Ebolavirus* comprising:
a) culturing a host cell of any one of claims 18-20; and
b) recovering the antibody or antigen-binding portion thereof.

22. A pharmaceutical composition comprising the antibody or antigen-binding portion thereof of any one of claims 1-13 and a pharmaceutically acceptable carrier.

23. A composition comprising the antibody or antigen-binding portion thereof of any one of claims 1-13 and one or more other antibodies or antigen-binding portions thereof, wherein the one or more other antibodies or antigen-binding portions thereof binds a protein produced by a virus in the *Filoviridae* family.

24. The composition of claim 23, wherein the protein is a glycoprotein.

25. The composition of claim 23 or 24, wherein the virus is *Ebolavirus* or *Marburgvirus*.

26. The composition of claim 25, wherein the virus is *Zaire ebolavirus, Sudan ebolavirus, Reston ebolavirus, Tai Forest ebolavirus, Bundibugyo ebolavirus, Cote d'Ivoire ebolavirus*, Marburg virus or Ravn virus.

27. The composition of any one of claims 23-26, further comprising a pharmaceutically acceptable carrier.

28. A method for ameliorating, treating or preventing an *Ebolavirus* infection in a subject in need thereof, the method comprising administering to the subject a therapeutically effective amount of the antibody or antigen-binding portion thereof of any one of claims 1-13.

29. A method for ameliorating, treating or preventing an *Ebolavirus* infection in a subject in need thereof, the method comprising administering to the subject a therapeutically effective amount of the composition of any one of claims 22-27.

30. The method of claim 28 or 29, wherein the subject is a human.

31. A method for detecting *Ebolavirus* in a sample, the method comprising contacting the sample with the antibody or antigen-binding portion thereof of any one of claims 1-13.

32. The method of claim 31, wherein the sample is a cell, tissue, or biological fluid from a subject suspected of having or at risk of a filovirus infection.

33. An expression vector comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1, 13, 25, 37, 49, 61, 73, 85, 97, 109, 121, 133, 145, 157, 169, 181, 193, 205, 340, 352, and 364.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CA2016/000061

A. CLASSIFICATION OF SUBJECT MATTER
IPC: ***C12N 15/13*** (2006.01), ***A61K 39/42*** (2006.01), ***A61P 31/12*** (2006.01), ***C07K 16/10*** (2006.01), ***C07K 16/46*** (2006.01), ***C12N 15/63*** (2006.01), ***C12N 5/10*** (2006.01), ***C12P 21/08*** (2006.01), ***G01N 33/569*** (2006.01)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
All IPCs

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic database(s) consulted during the international search (name of database(s) and, where practicable, search terms used)
Questel Orbit, Scopus, GenomeQuest, Keywords: ebola, antibody, monoclonal, Author: JOHNSTONE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO2004/018649 A2, HART, M.K. and WILSON, J.A., 4 March 2004 (04-03-2004). The whole document.	1-27 and 31-33
A	WO2009/094755 Al (JONES, S. et al.) 6 August 2009 (06-08-2009). The whole document.	1-27 and 31-33
P,X	WO2015/127136 A2 (BERRY, J. et al.) 27 August 2015 (27-08-2015). The whole document.	1-27 and 31-33

☐ Further documents are listed in the continuation of Box C.

☑ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier application or patent but published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

Date of mailing of the international search report
15 June 2016 (15-06-2016)

Name and mailing address of the ISA/CA
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Box No. I **Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)**

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

a. ☑ forming part of the international application as filed:

☐ in the form of an Annex C/ST.25 text file.

☑ on paper or in the form of an image file.

b. ☐ furnished together with the international application under PCT Rule 13*ter*.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

c. ☑ furnished subsequent to the international filing date for the purposes of international search only:

☑ in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

☐ on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. ☑ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT	International application No. **PCT/CA2016/000061**

Box No. II **Observations where certain claims were found unsearchable (Continuation of item 2 of the first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☑ Claim Nos.: 28-30
because they relate to subject matter not required to be searched by this Authority, namely:

Claims 28-30 are directed to a method for treatment of the human or animal body by surgery or therapy, which the International Searching Authority is not required to search under PCT Rule 39.1(iv). However, this Authority has carried out a search based on the alleged effect or purpose/use of the antibody or antigen-binding portion thereof of any one of claims 1-13 or a composition comprising said antibody or antigen-binding portion thereof.

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III **Observations where unity of invention is lacking (Continuation of item 3 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:
See extra sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☑ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claim Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claim Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

Continuation of Box III:

The claims are directed to a plurality of inventive concepts as follows:

Group A - Claims 1-33 (all partially) are directed to an antibody that specifically binds ebola virus and comprising the CDRs of antibody CAN7G1, a nucleic acid, a vector, a host cell, a pharmaceutical composition and methods, all relating to said antibody;

Group B - Claims 1-33 (all partially are directed to same subject matter of Group A but relating to the CDRs of antibody CAN8G1; and

Group C - Claims 1-33 (all partially) are directed to same subject matter of Group A but relating to the CDRs of antibody CAN9G1.

The only linking feature between the different groups is an antibody that specifically binds ebola virus. Said concept is known in the prior art (see D1 and D2). Thus, the claims must be limited to one inventive concept as set out in PCT Rule 13.

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/CA2016/000061

Patent Document Cited in Search Report	Publication Date	Patent Family Member(s)	Publication Date
WO2004018649A2	04 March 2004 (04-03-2004)	WO2004018649A2	04 March 2004 (04-03-2004)
		WO2004018649A3	17 June 2004 (17-06-2004)
		AU2003265883A1	11 March 2004 (11-03-2004)
		AU2003265883A8	11 March 2004 (11-03-2004)
		DE60317800D1	10 January 2008 (10-01-2008)
		EP1539238A2	15 June 2005 (15-06-2005)
		EP1539238A4	21 December 2005 (21-12-2005)
		EP1539238B1	28 November 2007 (28-11-2007)
		US2004053865A1	18 March 2004 (18-03-2004)
		US6875433B2	05 April 2005 (05-04-2005)
		US2007298042A1	27 December 2007 (27-12-2007)
		US7335356B2	26 February 2008 (26-02-2008)
WO2009094755A1	06 August 2009 (06-08-2009)	WO2009094755A1	06 August 2009 (06-08-2009)
		CA2712605A1	06 August 2009 (06-08-2009)
		EP2262832A1	22 December 2010 (22-12-2010)
		EP2262832A4	09 March 2011 (09-03-2011)
		US2012283414A1	08 November 2012 (08-11-2012)
		US8513391B2	20 August 2013 (20-08-2013)
		US2015232538A1	20 August 2015 (20-08-2015)
		US9145454B2	29 September 2015 (29-09-2015)
		US2015344546A1	03 December 2015 (03-12-2015)
		US9249214B2	02 February 2016 (02-02-2016)
WO2015127136A2	27 August 2015 (27-08-2015)	WO2015127136A2	27 August 2015 (27-08-2015)
		WO2015127136A3	01 October 2015 (01-10-2015)