Supporting Information for "Synthetic Antibodies with a Human Framework that Protect Mice from Lethal Sudan Ebolavirus Challenge"

Gang Chen,[1,#] Jayne F. Koellhoffer,[2,#] Samantha E. Zak,[3,#] Julia C. Frei,[2] Nina Liu,[2] Hua Long,[1] Wei Ye,[1] Kaajal Nagar,[1] Guohua Pan,[1] Kartik Chandran,[4] John M. Dye,[3,] Sachdev S. Sidhu,[1,]* and Jonathan R. Lai[2,]**

[1] Banting and Best Department of Medical Research, Terrence Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, 160 College Street, Toronto, ON, Canada M5S 3E1

[2] Department of Biochemistry, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY, USA 10461

[3] Virology Division, United States Army Medical Research Institute of Infectious Diseases, 1425 Porter Street, Fort Detrick, MD, USA 21702

[4] Department of Microbiology and Immunology, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY, USA 10461

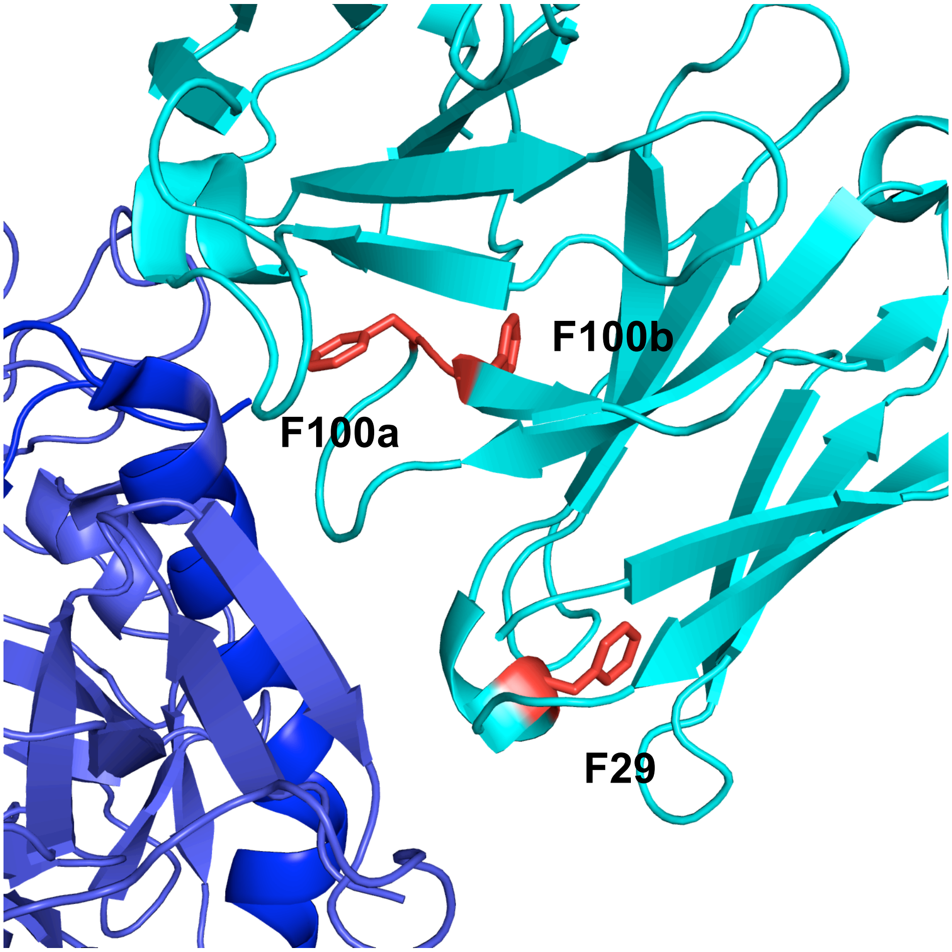

Figure S1 Potential Role of 16F6 residues F29, F100a, and F100b in supporting or direct interactions with SUDV GP. 16F6 shown in cyan and SUDV in blue. F29 and F100b point torward the domain core and likely support loop conformations required for interaction with SUDV GP. F100a points directly toward the antigen and is likely important for direct contacts.

Sequences of antibodies characterized for neutralization potential

Note: A spurious Asn->Lys mutation was observed at position 52 (CDR-H2) of F4. This was caused by a single nucleotide mutation at the wobble position (AAC->AAG). This position is underlined below.

```
HEAVY CHAIN SEQUENCES:
       1         11        21        31        41
16F6 : EVQLVESGGGLVTPGGSLKLSCAASGFAFNYYDMFWVRQNTEKRLE
YADS1:             Q     R        DIYDD IH    APG G
E10  :             Q     R              IH    APG G
F4   :             Q     R                    APG G
31C7 :             Q     R                    APG G
31E3 :             Q     R                    APG G
31F8 :             Q     R                    APG G
31G11:             Q     R                    APG G
34F5 :             Q     R                    APG G
35A1 :             Q     R                    APG G
35B5 :             Q     R                    APG G
41C6 :             Q     R               H    APG G
41F10:             Q     R              LH    APG G
42F2 :             Q     R                    APG G
51B6 :             Q     R              LY    APG G
51F7 :             Q     R                    APG G
52D11:             Q     R                    APG G
52F2 :             Q     R               H    APG G

            52       60        70        80  82b   87
16F6 : WVAYINSGGGNTYYPDTVKGRFTISRDNAKKTLFLQMSSLRSEDTA
YADS1:      APSY Y D A S        A TS N AY   N   A
E10  :       P       A S        A TS N AY   N   A
F4   :      KP       A S        A TS N AY   N   A
31C7 :       P       A S        A TS N AY   N   A
31E3 :       P         S        A TS N AY   N   A
31F8 :               A S        A TS N AY   N   A
31G11:       P         S        A TS N AY   N   A
34F5 :                 S        A TS N AY   N   A
35A1 :       P         S        A TS N AY   N   A
35B5 :                 S        A TS N AY   N   A
41C6 :       P       A S        A TS N AY   N   A
41F10:       P       A S        A TS N AY   N   A
42F2 :       P         S        A TS N AY   N   A
51B6 :       P         S        A TS N AY   N   A
51F7 :                 S        A TS N AY   N   A
52D11:       P         S        A TS N AY   N   A
52F2 :       P       A S        A TS N AY   N   A

               97  abcde
16F6 : MYYCARQLYGNS---FFDYWGQGTSLTV
YADS1: V   S SSDASYSYSAM       LV
E10  : V               M       LV
F4   : V                       LV
31C7 : V               L       LV
31E3 : V                       LV
31F8 : V                       LV
31G11: V                       LV
34F5 : V                       LV
35A1 : V                       LV
35B5 : V                       LV
41C6 : V                       LV
41F10: V                       LV
42F2 : V                       LV
51B6 : V                       LV
51F7 : V                       LV
52D11: V                       LV
52F2 : V               M       LV
```

LIGHT CHAIN SEQUENCES:

```
       1         11        21        31        41
16F6 : DIVMTQSHKFMSTSVGDRVTITCKASQDVTTAVAWYQQKPGHSPKL
YADS1:   Q    PSSL A          R   ASYSS          KA
E10  :   Q    PSSL A          R                  KA
F4   :   Q    PSSL A                             KA
31C7 :   Q    PSSL A                             KA
31E3 :   Q    PSSL A                             KA
31F8 :   Q    PSSL A                             KA
31G11:   Q    PSSL A                             KA
34F5 :   Q    PSSL A                             KA
35A1 :   Q    PSSL A          Q                  KA
35B5 :   Q    PSSL A                             KA
41C6 :   Q    PSSL A                             KA
41F10:   Q    PSSL A                             KA
42F2 :   Q    PSSL A                             KA
51B6 :   Q    PSSL A                             KA
51F7 :   Q    PSSL A                             KA
52D11:   Q    PSSL A                             KA
52F2 :   Q    PSSL A          Q                  KA

           51        61        71        81
16F6 : LIYWASTRHTGVPDRFTGSGSGTAFTLTLNSVQAEDLALYYCQQ
YADS1:    A  YLYS   S  S      D    IS L P  F T    -
E10  :       RLHN   S  S      D    IS L P  F T
F4   :              S  S      D    IS L P  F T
31C7 :       S YP   S  S      D    IS L P  F T
31E3 :       G YI   S  S      D    IS L P  F T
31F8 :              S  S      D    IS L P  F T
31G11:       S Y    S  S      D    IS L P  F T
34F5 :       A  R   S  S      D    IS L P  F T
35A1 :       SL F   S  S      D    IS L P  F T
35B5 :              S  S      D    IS L P  F T
41C6 :              S  S      D    IS L P  F T
41F10:              S  S      D    IS L P  F T
42F2 :              S  S      D    IS L P  F T
51B6 :              S  S      D    IS L P  F T
51F7 :              S  S      D    IS L P  F T
52D11:       FL R   S  S      D    IS L P  F T
52F2 :       G  K   S  S      D    IS L P  F T

       91        101
16F6 : HYSTPLTFGAGTKLFL
YADS1: SSAS A   Q   V I
E10  :          Q   VEI
F4   :          Q   VEI
31C7 :          Q   VEI
31E3 :          Q   VEI
31F8 :          Q   VEI
31G11:          Q   VEI
34F5 :          Q   VEI
35A1 :          Q   VEI
35B5 :          Q   VEI
41C6 :          Q   VEI
41F10:          Q   VEI
42F2 :          Q   VEI
51B6 :          Q   VEI
51F7 :          Q   VEI
52D11:          Q   VEI
52F2 :          Q   VEI
```