Marburg virus survivor immune responses are Th1-skewed with limited neutralizing antibody responses

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Abbreviations

MARV, Marburg virus; EBOV, Ebola virus; SUDV, Sudan virus; BDBV, Bundibugyo virus; CFR, case fatality rate; GP, glycoprotein; PRNT, plaque reduction/neutralization test; NP, nucleoprotein

Summary

Immune responses that develop in survivors of filovirus infection may indicate critical parameters that could inform rational vaccine development. Stonier et al. characterize immune responses in Marburg virus survivors and demonstrate robust CD4+ T cell responses but limited CD8+ T cell and neutralizing antibody responses.

Abstract

Until recently, immune responses in filovirus survivors remained poorly understood. Early studies revealed IgM and IgG responses to infection with various filoviruses but recent outbreaks have greatly expanded our understanding of filovirus immune responses. Immune responses in survivors of EBOV and SUDV infections have provided the most insight, with T cell responses as well as detailed antibody responses having been described. Immune responses to MARV, however, remain almost entirely uncharacterized. We report that immune responses in MARV survivors share characteristics with EBOV and SUDV infections but have some distinct differences. MARV survivors developed multivariate CD4+ T cell responses but limited CD8+ T cell responses, more in keeping with SUDV survivors than EBOV survivors. In stark contrast to SUDV survivors, rare neutralizing antibody responses in MARV survivors diminished rapidly after the outbreak. These results warrant serious consideration for any vaccine or therapeutic that seeks to be broadly protective as different filoviruses may require different immune responses to achieve immunity.

Introduction

The genera *Marburgvirus* and *Ebolavirus* comprise the family *Filoviridae*, which contains the etiological agents that cause Marburg virus (MARV) disease and Ebola virus (EBOV) disease, respectively. EBOV recently caused an outbreak of unprecedented scale, spanning two years and infecting more than 28,000 individuals. Previously, the largest filovirus outbreaks had numbered in the tens to hundreds. While EBOV is responsible for the greatest number of human filovirus infections, Marburg virus (MARV), Sudan virus (SUDV), and Bundibugyo virus (BDBV) have all caused outbreaks in humans that numbered over 100 cases – twice, in the cases of MARV and SUDV. EBOV may garner much of the attention, but it is only one of several filoviruses that could potentially kindle outbreaks of massive scale. To date, there have been 11 incidences of MARV transmission to the human population that spawned outbreaks of varying size. While many outbreaks have been of limited scale, afflicting fewer than 5 individuals per instance, two outbreaks alone account for 406 cases of MARV infections that had fatality rates of 83% and 90% (Bausch et al., 2006; Towner et al., 2006). Furthermore, a precedent already exists for the importation of MARV to other countries from travelers that visited MARV hotspots (Centers for Disease and Prevention, 2009; van Paassen et al., 2012), which was a concern during the 2013-2015 EBOV outbreak in Western Africa. Simple luck or coincidence has thus far prevented these MARV outbreaks from growing into larger problems.

In 2012 alone, four distinct filovirus outbreaks occurred in Africa. Three outbreaks occurred in Uganda (two of SUDV, one of MARV), with the fourth occurring in the Democratic Republic of Congo (BDBV) (Albarino et al., 2013). Sequencing of viral genomes isolated from two fatal cases of MARV in 2012 indicated a high similarity with the original MARV isolate (Albarino et al., 2013; Amman et al., 2012). MARV case fatality rates (CFRs) vary from 23-90% in cases where more than one individual was infected. The CFR for the MARV outbreak in 2012 was 27% (n=15 confirmed cases), in keeping with the outbreak that was caused by the MARV isolate bearing the greatest homology to the 2012 isolates (original MARV isolate in 1967; CFR 23%) (Albarino et al., 2013; Amman et al., 2012; Bukreyev et al., 1995; Slenczka and Klenk, 2007).

Profiles of immunity developed in filovirus survivors have begun to shed light on immune responses that had been understudied. Antibody responses to EBOV had previously been relatively well-characterized, with IgM responses being succeeded by IgG in survivors, whereas non-survivors fail to develop IgG responses (Baize et al., 1999; Ksiazek et al., 1999) Additionally, neutralizing antibody responses have been described in cases of EBOV, SUDV, BDBV and a single case of MARV infection (Bornholdt et al., 2016; Flyak et al., 2015; Flyak et al., 2016; Maruyama et al., 1999; Sobarzo et al., 2012). Recent studies have directly shown that EBOV survivors treated in the United States, either after exposure in Western Africa or after nosocomial infection in the U.S., developed IFNγ- and TNFα-positive CD4+ and CD8+ T cell responses to various EBOV proteins (McElroy et al., 2015). This was the first time antigen-specific responses in T cells had been directly demonstrated in human survivors of filovirus infection. A subset of EBOV-infected individuals also had elevated levels of serum IL-2, IFNγ, and IL-4 that were measured longitudinally during their treatment in the U.S. (McElroy et al., 2016). IL-2, IFNγ and TNFα were also found to be present in serum samples from survivors and non-survivors of an EBOV outbreak in DRC (Villinger et al., 1999), whereas TNFα was found to be decreased and IFNγ showed no statistical change in serum from BDBV-infected individuals (Gupta et al., 2012). Levels of these cytokines were not reported in a broad cytokine analysis of serum from the 2000-2001 SUDV

outbreak (McElroy et al., 2014) but previous studies of serum from that outbreak showed mixed results for TNFα and IFNγ by ELISA and quantitative PCR analyses (Hutchinson and Rollin, 2007; Sanchez et al., 2004). Later studies revealed the presence of CD4+ T cell responses in the same SUDV survivor pool, measured >10 years after the outbreak (Sobarzo et al., 2016). Taken together, these studies have provided a detailed description of adaptive immune responses in survivors of EBOV, SUDV and BDBV infection.

It is unknown if immune responses from MARV survivors will present similar profiles to those described for other filoviruses, or if there will be critical differences. Beyond IgG or IgM ELISAs performed for diagnostic purposes, virtually the entirety of the literature available regarding filovirus immune responses in humans comes from studies of survivors of EBOV, SUDV, and BDBV infection. In our studies we provide the first comprehensive immune profiling of responses in human MARV survivors. Identification of a consensus immune response elicited by filovirus infection would be highly valuable for the evaluation of vaccines and therapeutics against MARV disease and those that would seek to be broadly protective.

Results and Discussion

T cell cytokine responses.

Heparinized blood samples from 6 survivors of 2012 MARV outbreak in Uganda, as well as local individuals who had not been infected, were obtained approximately 9 months after the resolution of the outbreak. Our use of whole blood cultures to measure filovirus survivor immune responses has been described previously (Sobarzo et al., 2016). While many valuable phenotypic analyses on bulk T cell populations have been conducted on acute-phase samples from EBOV-infected individuals (Agrati et al., 2016; McElroy et al., 2015; Ruibal et al., 2016), we deemed a functional analysis of virus-specific immune responses to be more informative as the samples in our studies are far removed from the acute infection. Unfortunately, we were unable to procure acute-phase samples from the 2012 MARV outbreak; however, such phenotypic studies would be invaluable should samples be available in future outbreaks.

A representative set of flow cytometry plots for CD4+ and CD8+ T cell responses from a MARV survivor is shown in figure 1A. Plots are gated sequentially on lymphocytes, singlets, live cells, and CD3+, CD4+ or CD8+ events (Sobarzo et al., 2016). Resting, SUDV GP, MARV GP, and irradiated SUDV cultures elicited minimal to no cytokine secretion from either CD4+ or CD8+ T cells. Irradiated MARV stimulation elicited cytokine expression in survivor CD4+ T cells (upper panels), comprised of IFNγ and IL-2 double- and single-positive responses. Survivor CD8+ T cells (lower panel) displayed a more limited response, consisting almost exclusively of IFNγ production. Cells from uninfected control individuals showed no reactivity to irradiated MARV or SUDV, or the respective recombinant GP (data not shown).

Individual survivors' CD4+ T cell responses are depicted in figure 1B. IFNγ and IL-2 single- or double-positive responses to irradiated MARV stimulation are shown for each survivor. As only the irradiated MARV stimulation resulted in cytokine production, we focused further on that response to determine its composition. Resting values were subtracted to account for nonspecific responses. All but one survivor (S1) had IFNγ single-positive responses, whereas all survivors had IFNγ, IL-2 double-positive and IL-2 single-positive responses. The magnitude of each individual's response varied greatly, with some survivors having small but detectable responses (S1, S6), whereas others were very robust (S2, S5) (figure 1B). Levels of CD8+ T cell responses were low and did not permit a similar analysis (figure 1A and data not shown).

Secreted cytokine analysis

To complement the flow cytometry analysis, we performed a multiplex ELISA assay with the culture supernatants to analyze a broader range of secreted cytokines. We focused on five cytokines that are germane to adaptive immune responses: IL-2, IFNγ, TNFα, IL-4, and IL-5. Average resting and irradiated SUDV-stimulated expression levels of each cytokine were low for uninfected control and survivor samples. MARV stimulation elicited IL-2, IFNγ and TNFα expression that was significantly higher than resting and SUDV-stimulated cultures ($p<0.05$). IL-4 was not measured in any of the cultures and only a slight, insignificant increase in IL-5 expression was measured following irradiated MARV stimulation.

CD40L expression and cytokine responses

Whereas we demonstrated the utility of whole blood cultures to measure T cell responses in MARV survivors (figure 1), the use of PBMCs allows for the analysis of greater cell numbers. Additionally, purified PBMCs can better elaborate cytokine responses in comparison to whole blood cultures (Hoffmeister et al., 2003). We therefore developed an assay to use PBMCs instead of whole blood to attempt a more detailed and comprehensive analysis of T cell responses in MARV survivors. PBMCs were cultured with the specific antigens as before, with the exception that monensin (instead of brefeldin A) was added after 2hr of culture to begin trapping intracellular cytokines. Additionally, fluorescently-labeled antibodies against CD107a and CD40L were added at this time to enable detection of a degranulation phenotype (Betts et al., 2003) and CD4+ T cell activation (Chattopadhyay et al., 2006), respectively. Cultures were then incubated for a further 16hr. Cell viability gated on lymphocytes after culture (18hr total, 16hr with monensin) was measured by an amine-reactive dye and found to be 91 ± 5.8% inclusive of all survivors and culture conditions (data not shown).

With a combination of CD40L and IFNγ expression, we identified activated CD4+ T cells after stimulation with irradiated MARV antigen from 7 MARV survivors from the 2012 outbreak. In our previous collection we had only obtained samples from 6 survivors; however, in the intervening time, we gained access to an additional survivor sample for flow cytometry analysis. IFNγ expression was coordinately expressed with CD40L, which is consistent with the description of CD40L expression as an activation marker (figure 3a, upper panel) (Chattopadhyay et al., 2006). TNFα and IL-2 expression also followed the same pattern with regards to CD40L expression (data not shown). PBMCs from uninfected controls demonstrated no cytokine response to irradiated MARV antigen (figure 3a, middle panel). Representative IFNγ and TNFα staining, gated on CD40L+ CD4+ T cells, is depicted in figure 3a (lower panel) for all survivors after irradiated MARV antigen stimulation.

To measure the overall magnitude of the CD4+ T cell response, we used a Boolean gating strategy to determine the frequency of IFNγ, TNFα, or IL-2 positive events that were identified by CD40L expression after stimulation (figure 3b). CD40L expression has been shown to increase in a nonspecific manner during culture (Chattopadhyay et al., 2006) and this analysis enabled us to determine the frequency of only cytokine-expressing, CD40L+ CD4+ T cells to give a more accurate representation of the specific response. Resting, SUDV GP, and irradiated SUDV antigen cultures elicited negligible CD40L+ cytokine+ responses (figure 3b), reinforcing both the utility and specificity of the stimulation and analysis. Furthermore, PBMC samples from uninfected controls exhibited no coordinate expression of CD40L and IFNγ after stimulation with irradiated MARV, demonstrating that this response is specific to MARV survivors. MARV GP elicited responses of low magnitude, whereas the CD40L+ cytokine+ response to irradiated MARV was more robust in comparison (figure 3b). CD4+ T cell responses directed against MARV GP were low in magnitude compared to irradiated virus, as in figure 1, despite skewing the amount of antigen toward favoring GP-specific responses. The composition of each individual survivor's CD40L+ response to irradiated MARV stimulation in terms of IFNγ, TNFα, and IL-2 is depicted in figure 3c. Resting culture values were subtracted to account for any background cytokine expression. The most dominant response was found to be cells producing IFNγ, TNFα and IL-2, whereas the double- and single-positive responses for these cytokines varied to a greater extent amongst survivors (figure 3c).

We had measured CD8+ T cell responses in whole blood cultures previously (figure 1 and data not shown), but the IFNγ and IL-2 cytokine responses were low in magnitude. We considered it possible that perhaps these parameters were not capturing the totality of the CD8+ T cell response. Therefore, we incorporated CD107a staining into our analysis to detect any CD8+ T cells that had degranulated and/or produced cytokines in response to MARV antigens. To this end, we analyzed CD107a and IFNγ expression after MARV stimulation. Control CD8+ T cells demonstrated no detectable IFNγ expression in response to MARV stimulation, whereas CD107a expression was found in both resting and MARV-stimulated cultures. This apparently nonspecific CD107a expression was found in resting cultures for survivors' CD8+ T cells as well. CD107a expression in the context of IFNγ and TNFα (data not shown) demonstrated specificity with regards to MARV stimulation, and only in a subset of survivors (figure 4, right panels). These results confirm our earlier findings showing little to no CD8+ T cell responses in MARV survivors, and add the additional functional characteristic of apparent cytotoxic responses.

CD4+ T cell responses to MARV were readily detectable in many cases, either in whole blood samples or purified PBMCs (figures 1,3). In contrast, CD8+ T cell responses were far more rare (figures 1,4), regardless of the sample type. While the CD8+ T cell response to EBOV is relatively well-documented in survivors and non-survivors during infection or shortly after convalescence (Agrati et al., 2016; McElroy et al., 2015; Ruibal et al., 2016), still little is known about the long-term persistence of these responses. We demonstrate here that anti-MARV CD4+ T cell responses are present for at least two years after infection. Furthermore, SUDV survivors' CD4+ T cell responses have been shown to persist for more than a decade, whereas CD8+ T cell responses were far more rare (Sobarzo et al., 2016). Blood samples collected at the time of this SUDV outbreak demonstrated elevated CD8+ T cell counts in nonfatal cases (Sanchez et al., 2004), which suggests there was an active CD8+ T cell response that had diminished greatly over time. A similar phenomenon may have occurred with the MARV survivor immune responses we have reported here, albeit over a shorter timescale. Indeed, a study of immune response in smallpox vaccine recipients showed that CD8+ T cell responses measured longitudinally diminished greatly over time and were present at very low frequencies when measured two years post-vaccination (Miller et al., 2008). Alternatively, CD4+ T cell cytokine responses were found to be of relatively lower magnitude compared to CD8+ T cell cytokine responses in EBOV survivors when assayed between 28 and 144d post onset of symptoms (McElroy et al., 2015). MARV and SUDV survivor immune responses, on the other hand, appear to heavily favor CD4+ T cell responses, though these studies were conducted with samples collected months and years after convalescence. Despite the difference in timeframes, the MARV survivor CD4+ T cell cytokine responses we report in this study are of greater magnitude than those observed with EBOV survivors. These discordant immune responses among filovirus infection survivors may indicate that the composition of T cell responses to filovirus infection may vary significantly between MARV, EBOV and SUDV.

Antiviral antibody responses

To address the humoral immune response to MARV infection, we collected serum from uninfected control donors and survivors and analyzed these samples for IgG antibodies against irradiated MARV antigen. Serum samples were serially diluted to determine an end titer. All survivors developed IgG responses to irradiated MARV, reaching an end titer between 4.25 and 6 (LOG_{10} serum dilutions) (figure 5a). Cell lysates expressing various MARV proteins were employed to determine the individual protein specificity of the MARV IgG response. Responses to lysate-derived antigens were denoted as +/- based on a signal-to-noise ratio of cell lysates without MARV proteins (table S1). All survivors were found to have IgG responses against MARV nucleoprotein (NP) and GP, but not against VP35 or VP24 (table S1). Survivors 2-7 had IgG responses to VP40 and survivors 1-4 and 5-6 had responses to VP30. Control sera were also included in these analyses and found to be nonreactive against lysates bearing MARV proteins (data not shown). Antibody reactivity to MARV proteins is not likely to strictly be a consequence of relative protein abundance in the virion as VP30 and VP24 constitute a similar fraction of overall virion protein content (Kiley et al., 1988). MARV VP40 is roughly twice as abundant as VP35 in the MARV virion (Kiley et al., 1988), however, and both are described to be interferon antagonists (Guito et al., 2017; Valmas et al., 2010). Antibody reactivity in MARV survivor serum to VP40 and not VP35 may be reflective of either greater accessibility to VP40 due to its greater abundance or its association with the viral membrane. Though it is beyond the scope of our current studies, it would be intriguing to determine if antibodies to VP40 can inhibit its interferon antagonism and/or its role in virion assembly, which could impute novel roles for antibody function in filovirus infections.

In order to address one potential function of the MARV-specific serum antibodies, we used a plaque reduction/neutralization test (PRNT) to determine if survivor serum could neutralize live virus *in vitro*. Serum samples were serially diluted beginning at 1:10 and pre-incubated with MARV. This mixture was then used to inoculate Vero E6 cells and resulting plaques were counted. Serum from only two survivors, S2 and S3, neutralized MARV plaque formation by at least 50%, our pre-determined threshold (figure 4b). Uninfected control serum samples had very low neutralization values, illustrating the specificity of this response in MARV survivors. We evaluated serological responses longitudinally with serum samples collected every 6 months. For our purposes, we used a threshold of ≥50% neutralization of MARV ($PRNT_{50}$) to determine positive neutralization responses. For samples collected 9 and 15 months after the outbreak, 2/6 survivors had neutralizing antibody titers between 1:20 and 1:40 (figure 3b and table S2). Neutralizing responses to MARV began to diminish 21mo. after the outbreak and dropped below our threshold after 27mo. In contrast, antibody titers to irradiated MARV over this same timeframe remained consistent with no drop in antibody end titer (table S2).

Whereas our current knowledge of T cell responses to various filovirus infections suggests common themes, such as robust Th1-skewed CD4+ T cell responses, the antibody responses appear to be more divergent. MARV survivors generate IgG responses against GP, NP (all survivors), VP40 (S2-7), VP30 (S1-4,6,7) but not to VP35 or VP24 (table S1). These profiles of viral protein reactivity resemble the serological profile of SUDV survivors (Sobarzo et al., 2013). Neutralizing antibody responses in MARV survivors, however, appear to be more divergent from that seen in SUDV survivors. Analyses of survivors of the SUDV outbreak in Gulu, Uganda demonstrate long-lived neutralizing antibody titers (Sobarzo et al., 2013). Admittedly, this particular MARV cohort is small in number (n=8); however, in a similar sample size for a recent SUDV outbreak in Kibaale, Uganda (Albarino et al., 2013), 5/5 survivors had neutralizing serum responses (Sobarzo et al., 2015). Even more striking is the magnitude of neutralizing titers among recent SUDV survivors: 3/5 had $PRNT_{50}$ values at or above 1/80. Neutralizing antibody responses in a MARV survivor have been previously reported (Flyak et al., 2015) but our data is the first longitudinal analysis to demonstrate a decline in these responses, despite maintaining high antibody titers overall. Our first serum samples were obtained ~9 mo. after the outbreak so it remains possible that all survivors may have had neutralizing responses at time points more proximal to infection. What is clear, however, is that these responses are lower in magnitude than analogous SUDV survivors (Sobarzo et al., 2015).

Neutralizing antibody responses have been achieved through vaccination against MARV GP in mouse, guinea pig and cynomolgus macaques (Grant-Klein et al., 2015; Shedlock et al., 2013). Interestingly, cynomolgus macaques vaccinated against MARV GP showed diminishing neutralizing antibody titers over time (Mire et al., 2014), similar to our observations with human survivors of MARV infection. It would be interesting to see if a similar phenomenon would occur in any surviving naïve macaques that were experimentally infected with MARV. Whereas neutralizing antibodies elicited by vaccination against filoviruses is a coveted immune response, functions of non-neutralizing antibodies have been described in other viral immune responses. Non-neutralizing antibodies to HIV and LCMV glycoproteins inhibit infection of DCs and macrophages (Holl et al., 2006) and limit virus spread (Hangartner et al., 2006), respectively. Various non-neutralizing functions of antibodies elicited by vaccination against HIV have been described in great detail (Chung et al., 2014; Chung et al., 2015). Perhaps more intriguing is a report that non-neutralizing antibodies elicited by vaccination against influenza NP can play a role in aiding the T cell response in protecting mice against influenza infection (Carragher et al., 2008). Indeed, immunization with influenza-NP antibody complexes elicited IFNγ production from CD8+ and CD4+ T cells (Zheng et al., 2007), indicating a Th1-skewed immune response. As all the MARV survivors in this have antibodies recognizing MARV NP (table S1), these studies describing a role for NP-specific antibodies in T cell responses may provide a roadmap for the ontogeny of the MARV survivor immune responses described herein.

Our studies are the first to provide a detailed longitudinal analysis of immune responses among human MARV survivors. Our findings highlight that while CD4+ T cell responses may be common among human filovirus survivors, the neutralizing antibody response varies to a greater degree. The discord in neutralizing responses between MARV and SUDV survivors indicate that there is a critical knowledge gap regarding what can be considered a protective response to filovirus infection.

Materials and Methods

Study design

Subjects included confirmed survivors, according to patient PCR and ELISA results, from the MARV outbreak of 2012 in the Ibanda and Kabale districts of Uganda, as well as healthy local community members that were not infected. Based on records obtained from the CDC in Uganda, we identified a total of 10 survivors from this outbreak. We were able to collect from 8 of these survivors, with the others not being available or too young in age for collections. Whole blood stimulations were conducted with blood samples from 6 survivors and PBMC stimulations were conducted with samples from 7 survivors. Survivors in these studies ranged in age from 18-50 years old. Whole blood analyses involved two male and four female survivors, and PBMC analyses included three male and four female survivors. An additional survivor (S7, female) for whom we have serological data but not flow cytometry data is included in tables S1 and S2. Health questionnaires administered prior to sample collection indicated that the study subjects were relatively healthy with a few individuals reporting nonspecific malaise. One survivor was receiving medication for malaria.

Ethics statement

The study was approved by the Helsinki committees of the Uganda Virus Research Institute in Entebbe, Uganda (reference number GC/127/13/01/15), Soroka Hospital, Beer-sheva, Israel (protocol number 0263-13-SOR) and the Ugandan National Council for Science and Technology (UNCST) (registration number HS1332). Written informed consent as well as a personal health questionnaire was completed for each subject.

Flow cytometry assays

Whole blood cultures were established as previously reported (Sobarzo et al., 2016). Briefly, 0.25mL fresh whole blood was mixed with 0.75mL Roswell Park Memorial Institute medium-5% FBS and cultures were incubated with 50 μg MARV or SUDV glycoproteins or 10 μg noninfectious irradiated whole virus preparations of MARV (Marburg virus/H.sapiens-tc/DEU/1967/Hesse-Ci67) or SUDV (Sudan virus/H.sapiens-tc/UGA/2000/Gulu). The amount of antigen used for stimulation was titrated using survivor samples from an unrelated SUDV outbreak in 2000-2001. In these studies, cultures were supplemented after 18hrs with brefeldin A and incubated for a further 4hrs. After 22hrs total, cultures were vortexed, cells were pelleted, and the resultant supernatant was collected. Cells were subjected to two 5-minute incubations with a Tris-ammonium chloride solution to lyse red blood cells and subsequently stained for surface and intracellular antigens. This approach enabled a flow cytometry analysis of cytokine response with matched supernatants for an expanded cytokine analysis by ELISA. PBMCs were collected in Cell preparation tube (CPT) vacutainers (BD Biosciences) and isolated according to the manufacturer's protocol. Total cell yields were split between various culture conditions in Roswell Park Memorial Institute medium+5%FBS: no stimulation, 50 μg recombinant MARV or SUDV GP, 10 μg irradiated MARV or SUDV, or staphylococcus enterotoxin B (1 μg). Culture volume across all conditions was 1mL. After 2hrs, cultures were supplemented with monensin and antibodies against CD40L and CD107a. Total culture time was 18hrs. Following stimulation, cells were stained with the amine-reactive Aqua dye (Thermo Fisher) to detect dead cells, nonspecific staining was blocked with 1% mouse serum, and surface proteins stained with fluorescently-labeled antibodies. Following fixation and permeabilization, intracellular cytokines were detected. Samples were acquired on an LSRII (BD Biosciences) at the Uganda Virus Research Institute/Medical Research Council in Entebbe, Uganda. Flowjo (version X, Treestar) was used to analyze flow cytometry data. Antibodies used in these studies are as follows: CD3 (S4.1/Qdot 605 for whole blood, UCHT1/BV650 for PBMC), CD4 (S3.5/Qdot 655 for whole blood, RPA-T4/BV605 for PBMC), CD8 (3B5/Qdot 705 for whole blood, SK1/BV711 for PBMC), CD40L (TRAP1/PE), CD107a (eBioH4A3/eFluor660), IFNγ (4S.B3/APC-eFluor780), IL-2 (MQ1-17H12/PE-Cy7), and TNFα (MAb11/FITC).

Plaque reduction neutralization test

Plaque reduction neutralization tests (PRNT) were performed as previously described (Sobarzo et al., 2016). Neutralization titers were determined to be the last dilution of serum that reduced the number of plaques by 50% compared with control wells. Plaque reduction neutralization assays were performed in the BSL-4 lab of the United States Army Medical Research Institute of Infectious Diseases (Fort Detrick, Frederick, Maryland, USA).

Cytokine and chemokines detection using Q-Plex™ ELISA-based chemiluminescent assay

Levels of human cytokines were measured in whole blood culture supernatants using Q-Plex technology (Quansys Biosciences, Logan, Utah, USA) according to the manufacturer's instructions. Readouts were obtained with a Quansys Imager (Quansys Biosciences) and results analyzed using the Q-View Software program (Quansys Biosciences).

ELISA antigens

For ELISA assays, irradiated MARV (Ci67 isolate), recombinant MARV $GP_{1–649}$, and total 293T cell lysate that expressed a given recombinant MARV protein (NP, VP24, and VP35) were used as the capture antigens. Total IgG was detected with an anti-human IgG antibody conjugated to HRP. ABTS: 2,2′-Azino-bis(3-ethylbenzthiazoline-6-sulfonic acid) (KPL, Gaithersburg, MD) was used as the substrate for irradiated MARV end titer ELISAs and a chemiluminescent substrate was used in ELISAs for viral proteins.

Statistical analysis

Statistical analyses were performed using GraphPad Prism software 6.01 (GraphPad Software, Inc. LA Jolla, CA, USA). Correlation analysis was assessed by the Spearman nonparametric test. Differences in cytokine values between study groups were assessed by analysis of variants (ANOVA) and Wilcoxon rank sum test; p-values represent 2-sided p values, and p values < 0.05 were considered statistically significant.

Supplemental material

Table S1 shows MARV survivor serum reactivity to individual MARV proteins. Table S2 shows a longitudinal analysis of anti-MARV serum antibody responses by ELISA and PRNT.

Author Contributions

Experiments were designed by J. Lutwama, L. Lobel, J. Dye, S. Stonier and A. Herbert. S. Stonier, A. Herbert, A. Kuehne, A. Sobarzo, P. Habibulin, C. Abramovitch Dahan, J. Lutwama, L. Lobel, and J. Dye acquired and processed blood samples. S. Stonier, A. Herbert and M. Egesa performed flow cytometry experiments under the supervision of S. Cose. A. Kuehne, R. James, P. Habibulin, and C. Abramovitch Dahan performed serological assays. Supernatant cytokines were measured by A. Sobarzo. Data analysis was performed by S. Stonier (flow cytometry, ELISA, cytokines), R. James (ELISA), A. Kuehne (PRNT), A. Sobarzo (cytokines) and P. Habibulin and C. Abramovitch Dahan analyzed lysate ELISAs. The manuscript was written by S. Stonier and edited by A. Herbert, J. Dye and L. Lobel.

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Figure 1. Analysis of MARV survivor T cell responses in whole blood cultures. Heparinized whole blood samples were collected from MARV survivors (n=6) approximately 9 months after the 2012 MARV outbreak in Uganda. A) Representative IFNγ and IL-2 responses in CD4+ and CD8+ T cells to recombinant SUDV GP or MARV GP, irradiated SUDV or MARV, and SEB for 22hrs are shown. B) The frequency of IFNγ single-positive, IL-2 single-positive, or IFNγ and IL-2 double-positive responses among total CD4+ T cells are shown for six MARV survivors.

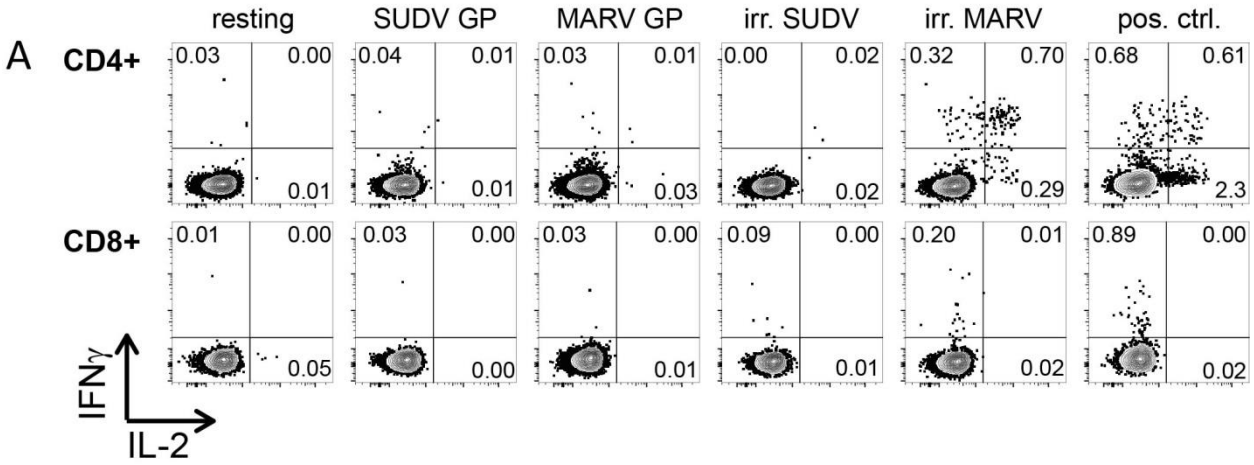
Figure 2. Multiplex ELISA for secreted cytokines. Supernatant was collected after 22hr stimulation of whole blood cultures from MARV survivors (n=6) and uninfected controls (n=5). Supernatants were analyzed in duplicate. Average values for the indicated cytokine secretion are reported among survivor and control populations. * indicates $p<0.05$ for irradiated MARV vs irradiated SUDV stimulations. # indicates $p<0.05$ for irradiated MARV stimulation vs resting cultures. n.s. indicates no significant difference.

Figure 3. Flow cytometry analysis of MARV survivor CD4+ T cell responses in PBMC cultures. Purified PBMCs from MARV survivors (n=7) and uninfected controls (n=3) were collected 27mo after the MARV outbreak and stimulated with antigens as before for a total of 18hrs. Monensin, CD40L antibody, and CD107a antibody were added after 2hrs. A) CD40L and IFNγ staining on CD4+ T cells after stimulation with irradiated MARV antigen. Upper panels depict responses seen in survivors and uninfected control responses are depicted in the middle panel. The lower panel demonstrates IFNγ and TNFα staining after gating on CD40L+ CD4+ T cells from survivors as identified in the upper panel. B) Bar graph shows the frequency of total cytokine+ CD40L+ CD4+ T cells after stimulation with the indicated MARV and SUDV antigens. C) Pie charts display the composition of the CD40L+ cytokine response in MARV survivors after stimulation with irradiated MARV.

Figure 4. MARV survivor CD8+ T cell responses. PBMCs from MARV survivors (n=4) and uninfected controls (n=2) were cultured as before. Plots depict IFNγ+ and CD107a+ CD8+ T cell responses after stimulation with irradiated MARV. Left panels depict staining of uninfected control samples. Right panels show representative staining of four MARV survivors with and without apparent CD8+ T cell responses. Positive CD8+ T cell responses are considered to be CD107a+ IFNγ+.

Figure 5. Antibody responses from MARV survivors. A) Irradiated MARV was coated on plates to capture MARV-specific antibodies from serum samples collected from MARV survivors (n=5) and uninfected controls (n=3). Total IgG was detected using an anti-human IgG-HRP antibody and ABTS substrate. End titer is reported as the antilog of the reciprocal of the last dilution of serum that exceeds a threshold based on naïve serum. The limit of detection is depicted by the dashed line. B) Beginning at 1:10, serial 1:2 dilutions of serum samples from MARV survivors (n=6) and uninfected controls (n=5) were incubated with MARV prior to inoculation of Vero E6 cells. The percentage of neutralization is reported at 1:10, 1:20, 1:40, and 1:80 dilutions based on the reduction of plaques relative to control MARV-infected Vero cells. Dashed line indicates 50% neutralization, or $PRNT_{50}$, which is used to define positive neutralizing responses. Serum samples used in ELISA and PRNT were analyzed in duplicate.

Figure 1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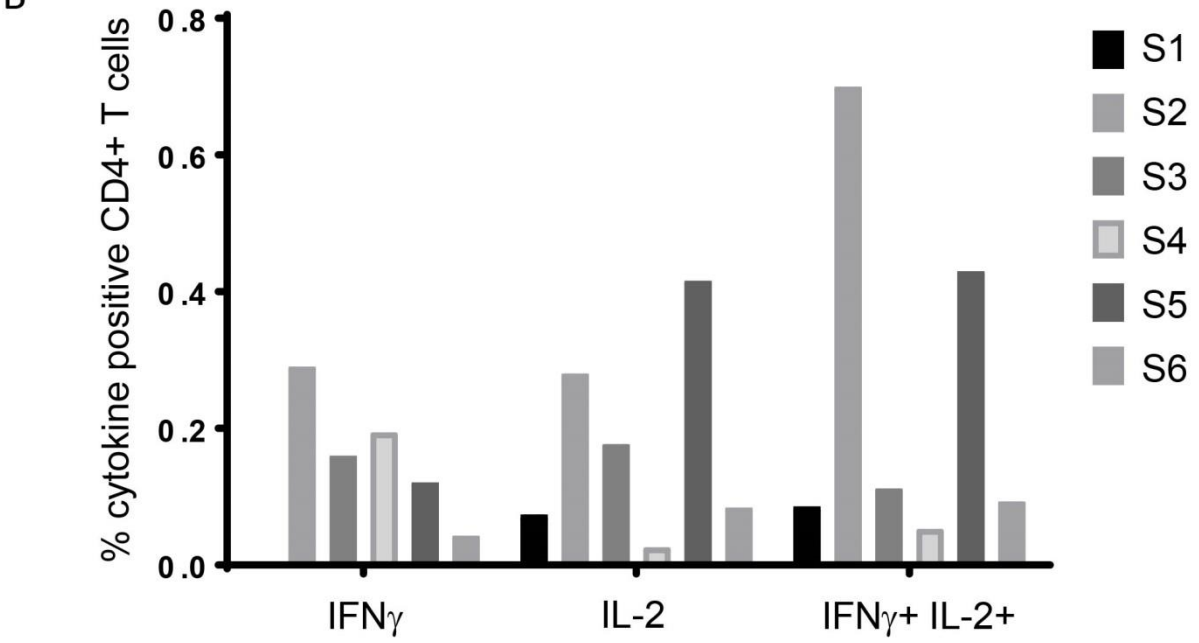
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Figure 2

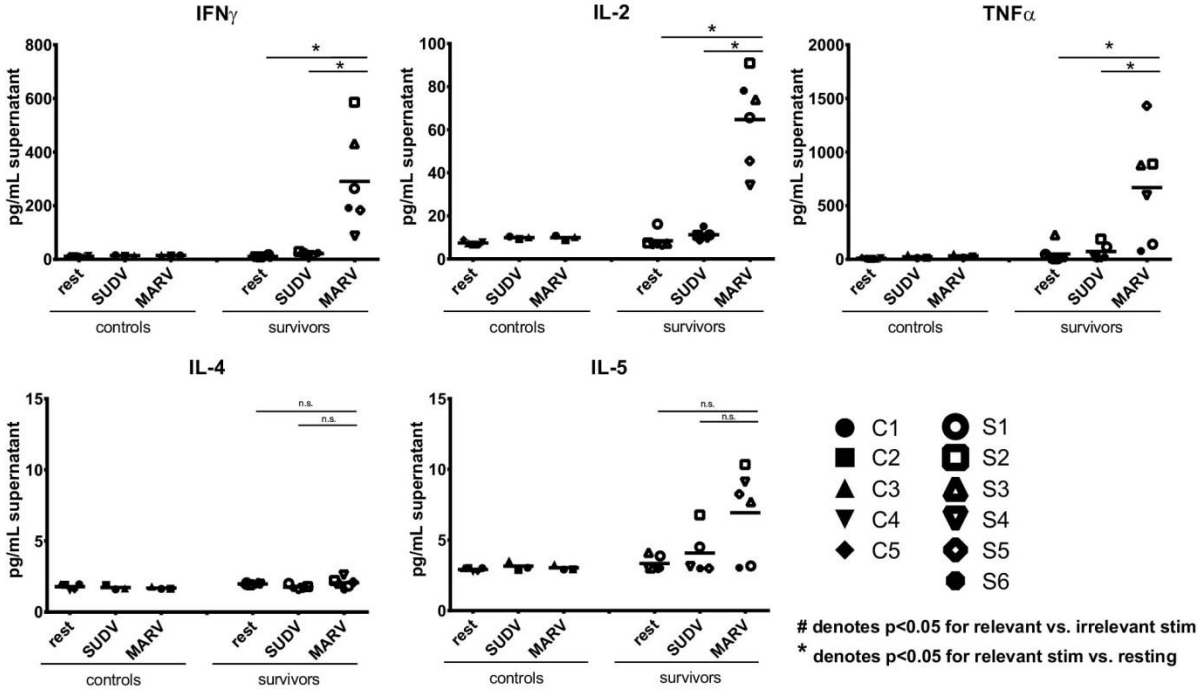
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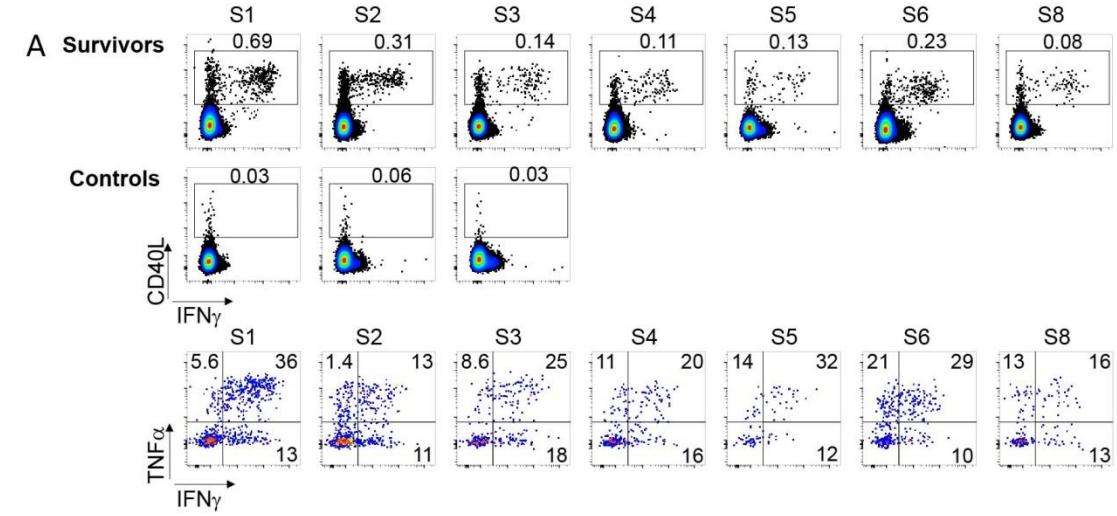
Figure 3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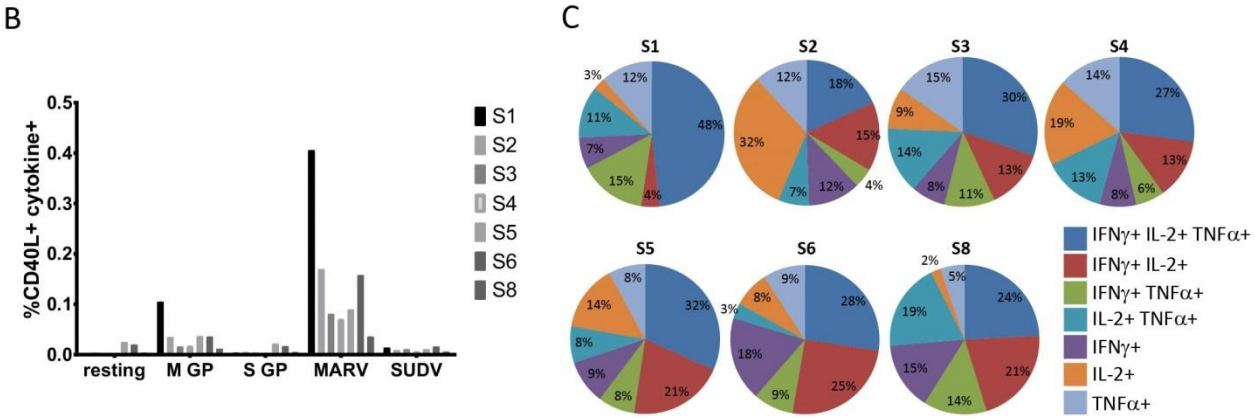
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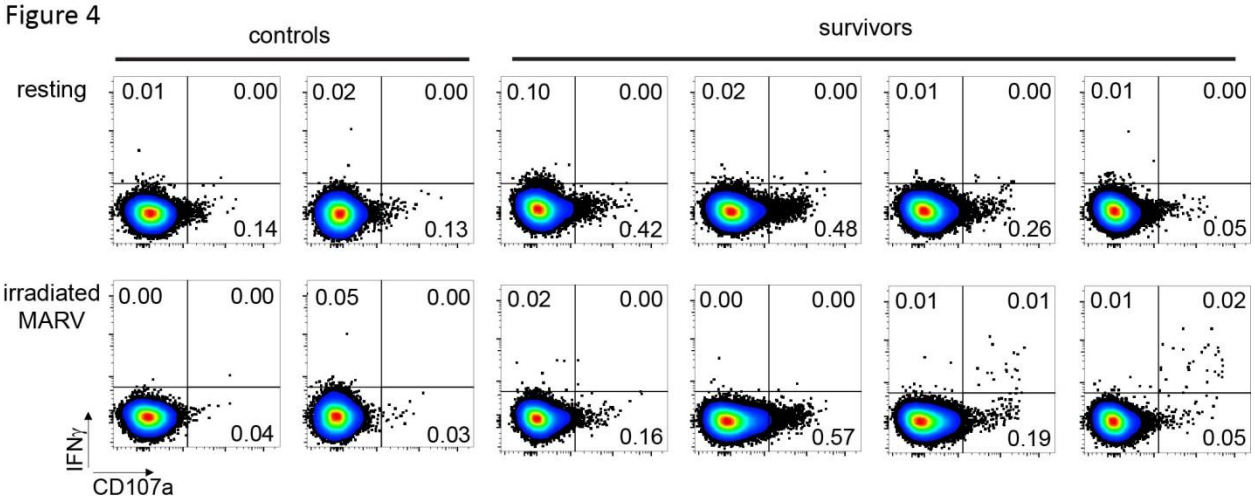
Figure 4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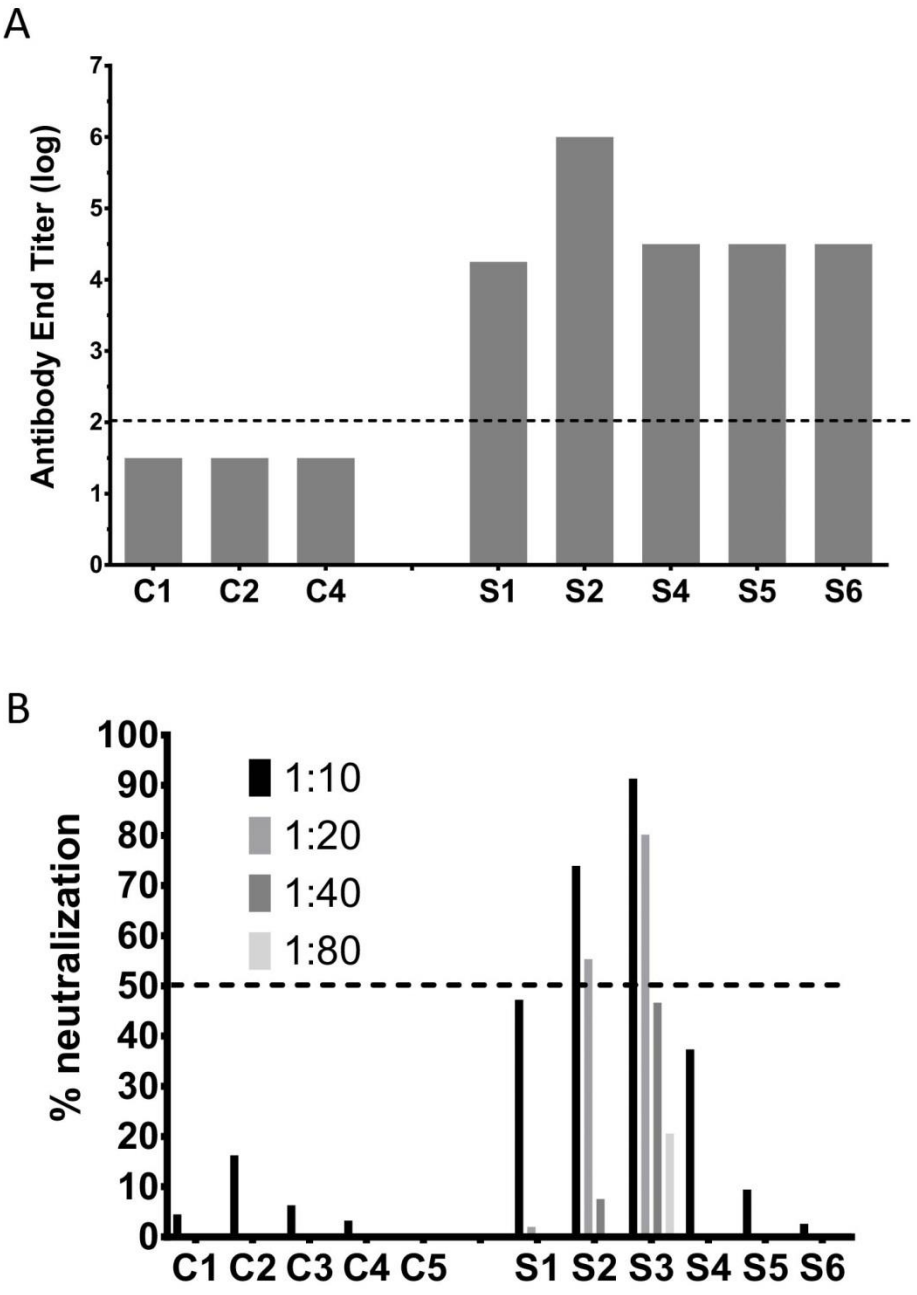
CD107a

Figure 5


A
Antibody End Titer (log)
0
1
2
3
4
5
6
7
C1
C2
C4
S1
S2
S4
S5
S6
B
% neutralization
0
10
20
30
40
50
60
70
80
90
100
1:10
1:20
1:40
1:80
C1 C2 C3 C4 C5
S1 S2 S3 S4 S5 S6

	GP	NP	VP35	VP24	VP40	VP30	Whole virus
S1	+	+	-	-	-	+	+
S2	+	+	-	-	+	+	+
S3	+	+	-	-	+	+	+
S4	+	+	-	-	+	+	+
S5	+	+	-	-	-	-	+
S6	+	+	-	-	+	+	+
S7	+	+	-	-	+	+	+
S8	+	+	-	-	+	-	+

Table S1. MARV survivor serum reactivity to individual virus proteins. MARV proteins were expressed in 293T cells and cell lysates were used as ELISA capture antigens. Antibody responses were scored as positive or negative based on the signal-to-noise ratio of MARV protein-transfected lysates and non-transfected lysates.

		Time of collection post-outbreak				
		9 mo.	15 mo.	21 mo.	27 mo.	33 mo.
S1	$PRNT_{50}$	<10	<10	<10	<10	<10
	End titer	4.25	4	4	3.75	4
S2	$PRNT_{50}$	20	20	10	<10	<10
	End titer	6	5.75	5.5	5.5	6
S3	$PRNT_{50}$	40	40	n.d.	<10	<10
	End titer	5.5	5.0	5.5	6	5.5
S4	$PRNT_{50}$	<10	10	<10	<10	<10
	End titer	4.5	4.5	4.25	4.0	4.5
S5	$PRNT_{50}$	<10	<10	<10	<10	<10
	End titer	4.5	4	4.5	4.5	4.5
S6	$PRNT_{50}$	<10	<10	<10	<10	<10
	End titer	4.5	4.5	4.75	5.5	6
S7	$PRNT_{50}$	n.d.	10	n.d.	n.d.	n.d.
	End titer	n.d.	4.5	n.d.	n.d.	n.d.
S8	$PRNT_{50}$	n.d.	<10	<10	<10	<10
	End titer	n.d.	4.5	n.d.	4.75	4.75

Table S2. Longitudinal analysis of antibody responses. Antibody end titer and $PRNT_{50}$ titers are shown at 6 month intervals beginning 9 months after the end of the 2012 MARV outbreak in Uganda. n.d. indicates that a value was not determined due to sample unavailability. All serum samples were analyzed in duplicate.