

Life Sciences Reporting Summary

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▶ Experimental design

1. Sample size

Describe how sample size was determined.

The antibodies in this study were previously isolated. The only real sample size calculations pertain to the animal studies. These mouse and guinea pig studies are constrained in that they require BSL-4 challenge facilities, which are a limited resource. We determined the group sizes that would show statistically and biologically meaningful differences based on many years of studies at UTMB on antivirals, antibodies and vaccines for ebolaviruses.

2. Data exclusions

Describe any data exclusions.

No data were excluded.

3. Replication

Describe the measures taken to verify the reproducibility of the experimental findings.

Findings presented were based on independent experiments or replicates, as stated in the figure legends. The number of samples was the minimum number required to obtain scientifically valid results. For in vivo experiments, we included justification for group size through a power analysis when possible. All attempts at replication in the stated conditions were successful.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

In Figure 2, mice and guinea pigs were allocated randomly into each treatment group.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

Five animals per experimental group were used, based on 100% mortality following infection with filoviruses, which allowed statistical assessment at the 95% confidence level (1-tailed Fisher exact test). The animals were randomly assigned for the experimental groups. UTMB Animal Resource Center veterinary staff was blinded for the antibodies' administration to experimental groups.

Note: all in vivo studies must report how sample size was determined and whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a Confirmed

- The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- A statement indicating how many times each experiment was replicated
- The statistical test(s) used and whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- Test values indicating whether an effect is present
Provide confidence intervals or give results of significance tests (e.g. P values) as exact values whenever appropriate and with effect sizes noted.
- A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- Clearly defined error bars in all relevant figure captions (with explicit mention of central tendency and variation)

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

Policy information about [availability of computer code](#)

7. Software

Describe the software used to analyze the data in this study.

Prism version 5 (GraphPad), Appion platform (Lander G. C., 2009), DoG Picker (Voss, N. R., 1009).

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). [Nature Methods guidance for providing algorithms and software for publication](#) provides further information on this topic.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a third party.

Antibodies described in this paper are available under MTA from Vanderbilt University Medical Center.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

Human antibodies used were generated as part of our study using previously described methods (Flyak AI, Cell 2016; 164: 392-405. PMC ID 4733404.)
The following secondary antibodies were used were validated in the previous study: goat anti-human IgG alkaline phosphatase conjugate (Meridian Life Science #W99008A) and anti-human Alexa Fluor 488-conjugate (Jackson ImmunoResearch Laboratories, Westgrove, PA).

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

Vero-E6 cell line was obtained from the American Type Culture Collection. FreeStyle 293F cell line was purchased from Thermo Fisher Scientific.

b. Describe the method of cell line authentication used.

STR testing.

c. Report whether the cell lines were tested for mycoplasma contamination.

All cell lines were tested on a monthly basis for Mycoplasma and found to be negative in all cases.

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

No commonly misidentified cell lines were used.

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide all relevant details on animals and/or animal-derived materials used in the study.

The animal protocols for testing of mAbs in mice and guinea pigs were approved by the Institutional Animal Care and Use Committee of the UTMB and performed in the ABSL-4 facility of the Galveston National Laboratory. The 7-8-week-old female BALB/c mice (Charles River Laboratories) at five animals per group were injected with 1,000 PFU of the mouse-adapted EBOV, strain Mayinga, by the intraperitoneal route. 24 hours later, animals were injected with individual mAbs at 100 µg per animal by the intraperitoneal route. Animals treated with the antibody specific to dengue virus 2D22 served as controls. Mice were monitored twice daily from day 0 to day 14 post challenge, followed by once daily monitoring from day 15 to the end of the study at day 28. The disease was scored using the following parameters: dyspnea (possible scores 0-5), recumbency (0-5), unresponsiveness (0-5), and bleeding/hemorrhage (0-5). All mice were euthanized at day 28 post EBOV challenge. To test the protective efficacy of mAbs in guinea pigs (strain Hartley), five- to six-week-old female guinea pigs at five animals per group were injected with 1,000 PFU of guinea pig-adapted EBOV, strain Mayinga, by the intraperitoneal route. 24 hours later, animals were injected with individual mAbs at 5 mg per animal by the intraperitoneal route. Animals were monitored and weighed daily for 28 days. After animals became symptomatic, they were examined no less than twice per day. The disease was scored using the same parameters as used for mice. All guinea pigs were euthanized at day 28 post EBOV challenge. Groups of 6-month-old male and female animals (*Mustela putorius furo*, Marshall BioResources) were challenged intramuscularly with 1,000 pfu of BDBV as described previously. Animals were treated with 20 mg of BDBV223 or control 2D22 antibody on day 3, and the same dose of the antibody on day 6 after challenge. The disease scores were assessed as follows: healthy, 1; developing clinical disease, 2; advanced disease, 3; moribund, 4. Ferrets were monitored for 28 days after infection and then euthanized.

Policy information about [studies involving human research participants](#)

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

None.