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## CLAIMS

An isolated hEbola virus comprising a nucleic acid molecule comprising a nucleotide
 sequence of:

a) a nucleotide sequence set forth in SEQ ID NOS: 1 or 10;

b) a nucleotide sequence hybridizing under stringent conditions to SEQ ID NOS: 1 or 10: or

c) a nucleotide sequence of at least 70%-99% identity to the SEQ ID NOS: 1 or 10.

2. An isolated hEbola virus having Centers for Disease Control Deposit Accession No.
 200706291.

3. The hEbola virus of any one of claims 1 or 2 which is killed.

4. The hEbola virus of claim 1 which is an attenuated hEbola virus.

The virus of claim 4 wherein at least one property of the attenuated hEbola virus is
 reduced from among infectivity, replication ability, protein synthesis ability, assembling ability or cytopathic effect.

6. An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS: 1 or 10 or a complement thereof.

20 7. An isolated nucleic acid molecule comprising a nucleotide sequence of between 4 and 4900 contiguous nucleotides of the nucleotide sequence of SEQ ID NOS: 1 or 10, or a complement thereof; with the proviso that said nucleotide sequence is not comprised by the nucleotide sequence set forth in SEQ ID NO: 20; or between 5500 and 6600 contiguous nucleotides of the nucleotide sequence of SEQ ID NOS: 1 or 10, or a complement thereof.

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8. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 2-9, 59, or SEQ ID NO: 11-19 or a complement of said nucleotide sequence.

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9. An isolated RNA or DNA nucleic acid molecule which hybridizes under stringent conditions to a nucleic acid molecule having the nucleotide sequence of SEQ ID NOS: 1 or 10 or a complement thereof.

10. An isolated polypeptide encoded by the nucleic acid molecule of any one of claims 7-5 9.

- 11. An isolated polypeptide comprising the amino acid of:
- a) an amino acid sequence set forth in any of SEQ ID NOS: 2-19, or 59; or
- b) an amino acid sequence that has 70% 99% homology to the amino acid sequence of

(a).

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12. An isolated polypeptide comprising the amino acid sequence having

5 to 250 contiguous amino acid residues of the amino acid sequence of SEQ ID NOS: 5 or 18 (VP24);

- 5 to 280 contiguous residues of the amino acid sequence of SEQ ID NOS: 6 or 17 (VP30);
- 5 to 320 contiguous residues of the amino acid sequence of SEQ ID NOS: 8 or 13 (VP40);
- 5 to 340 contiguous residues of the amino acid sequence of SEQ ID NOS: 7 or 12 (VP35);
- 5 to 370 contiguous residues of the amino acid sequence of SEQ ID NOS: 4 or 15 (SGP);
- 5 to 370 contiguous residues of the amino acid sequence of SEQ ID NOS: 59 or 16 (SSGP);
- 5 to 670 contiguous residues of the amino acid sequence of SEQ ID NOS: 9 or 14 (GP);
- 5 to 730 contiguous residues of the amino acid sequence of SEQ ID NOS: 3 or 11 (NP); or
  - 5 to 2200 contiguous residues of the amino acid sequence of SEQ ID NOS: 2 or 19 (L).
- 13. An isolated antibody or an antigen-binding fragment thereof which immunospecifically binds to the hEbola virus of any one of claims 1 or 2 or neutralizes the virus.
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14. An isolated antibody or an antigen-binding fragment thereof which immunospecifically binds to the polypeptide of any one of claims 11 or 12 or neutralizes an hEbola virus.

30 15. A method for detecting the presence of a the hEbola virus or a nucleic acid molecule derived therefrom of claim 1 in a biological sample, said method comprising:

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(a) contacting the sample with an agent that selectively binds to the virus or the nucleic acid molecule derived therefrom; and

(b) detecting whether the compound binds to the virus or the nucleic acid molecule derived therefrom in the sample.

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16. The method of claim 15, wherein the agent is an antibody.

17. The method of claim 15, wherein the agent is a nucleic acid molecule comprising a nucleotide sequence having between 4 and 6600 contiguous nucleotides of the nucleotide sequence of SEQ ID NOS: 1 or 10, or a complement thereof.

18. A method for detecting the presence of the polypeptide of claim 11 in a biologicalsample, said method comprising:

(a) contacting the biological sample with an agent that selectively binds to said polypeptide; and

(b) detecting whether the compound binds to said polypeptide in the sample.

15 19. The method of claim 18, wherein the agent is an antibody or an antigen-binding fragment thereof.

20. A formulation comprising the hEbola virus of any one of claims 3 or 4, and a pharmaceutically acceptable carrier.

21. A formulation comprising an amount of a protein extract of the hEbola virus of claim20 3 or 4 or a subunit thereof, and a pharmaceutically acceptable carrier.

22. A formulation comprising an amount of a nucleic acid molecule of the nucleotide sequence of SEQ ID NOS: 1 or 10 or a complement thereof, and a pharmaceutically acceptable carrier.

23. A formulation comprising an immunogenically effective amount of the nucleic acidmolecule of claim 9 or a complement thereof, and a pharmaceutically acceptable carrier.

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24. A vaccine formulation comprising a therapeutically or prophylactically effective amount of the hEbola virus of claim 3 or 4 or a protein extract therefrom, and a pharmaceutically acceptable carrier.

25. A vaccine formulation comprising a therapeutically or prophylactically effective
5 amount of a nucleic acid molecule SEQ ID NOS: 1 or 10 or a complement thereof, and a pharmaceutically acceptable carrier.

26. A vaccine formulation comprising a therapeutically or prophylactically effective amount of a nucleic acid molecule of claim 9 or a complement thereof, and a pharmaceutically acceptable carrier.

- 10 27. A pharmaceutical composition comprising a prophylactically or therapeutically effective amount of an anti-hEbola agent of an antibody or an antigen-binding fragment thereof which immunospecifically binds to the hEbola virus of Deposit Accession No. 200706291, or polypeptides or protein derived therefrom and optionally has the nucleotide sequence of SEQ ID NOS: 1 or 10, or a fragment thereof.
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28. A kit comprising a container containing the formulation of any one of claims 24-26.

29. A method for identifying a subject infected with the virus of claim 1 or 2, comprising:

(a) obtaining total RNA from a biological sample obtained from the subject;

(b) reverse transcribing the total RNA to obtain cDNA; and

(c) amplifying the cDNA using a set of primers derived from a nucleotide sequence ofthe virus of claim 1 or 2.

30. A primer that has the nucleotide sequence of one of SEQ ID NOS: 24-57.