WHAT CLAIMED IS:

1. A modified Zika virus in which expression of viral proteins is reduced compared to a parent virus, wherein the reduction in expression is the result of recoding the prM, or envelope (E) region, or the nonstructural protein 3 (NS3) region or both the E and NS3 regions.
2. The modified Zika virus of claim 1, wherein one or both of the E protein-encoding sequence and the NS3 protein-encoding sequence are recoded by reducing the codon pair bias or codon usage bias of the protein-encoding sequence.
3. The modified Zika virus of claim 2, wherein reducing the codon-pair bias comprises identifying a codon pair in the parent protein-encoding sequence having a codon-pair score that can be reduced, and reducing the codon-pair bias by substituting the codon pair with a codon pair that has a lower codon-pair score.
4. The modified Zika virus of claim 2, wherein reducing the codon-pair bias comprises rearranging the codons of a parent protein-encoding sequence.
5. The modified Zika virus of claim 1, wherein one or both of the E protein-encoding sequence and the NS3 protein-encoding sequence are recoded by increasing the number of CpG or UpA di-nucleotides compared to a parent virus.
6. The modified Zika virus of claim 1, wherein each of the recoded prM/E protein-encoding sequence and the recoded NS3 protein-encoding sequence have a codon pair bias less than, -0.05, −0.1, or less than −0.2, or less than −0.3, or less than −0.4.
7. The modified Zika virus of claim 1, wherein one or both of the E protein-encoding sequence and the NS3 protein-encoding sequence are recoded by replacing one or more codons with synonymous codons that are less frequent in the host.
8. A Zika vaccine composition for inducing a protective immune response in a subject, comprising a modified virus of any of claims 1-7.
9. A method of eliciting a protective immune response in a subject, comprising: administering to the subject a prophylactically or therapeutically effective dose of a vaccine composition comprising a modified virus of any of claims 1-7.
10. The method of claim 9, further comprising administering to the subject at least one adjuvant.
11. The method of claim 9, wherein the immune response is cross-protective against a heterologous Zika virus.
12. A method of making a modified Zika virus genome comprising:

obtaining the nucleotide sequence encoding the envelope protein of a Zika virus and the nucleotide sequence encoding the nonstructural 3 proteins of a Zika virus;

recoding the envelope encoding nucleotide sequence to reduce protein expression and recoding the nonstructural protein 3-encoding nucleotide sequence to reduce protein expression, and

substituting a nucleic acid having the recoded envelope-encoding nucleotide sequence and a nucleic acid having the recoded nonstructural protein 3-encoding nucleotide sequence into a parent Zika virus genome to make a modified Zika virus genome; whereby expression of the recoded envelope-encoding nucleotide sequence and expression of the recoded nonstructural protein 3-encoding nucleotide sequence is reduced compared to the parent virus.

13. A modified Flavivirus virus in which expression of viral proteins is reduced compared to a parent virus, wherein the reduction in expression is the result of recoding the prM, or envelope (E) region, or the nonstructural protein 3 (NS3) region or both the E and NS3 regions.

14. The modified Flavivirus virus of claim 13, wherein one or both of the E protein-encoding sequence and the NS3 protein-encoding sequence are recoded by reducing the codon pair bias or codon usage bias of the protein-encoding sequence.

15. The modified Flavivirus virus of claim 14, wherein reducing the codon-pair bias comprises identifying a codon pair in the parent protein-encoding sequence having a codon-pair score that can be reduced, and reducing the codon-pair bias by substituting the codon pair with a codon pair that has a lower codon-pair score.

16. The modified Flavivirus virus of claim 14, wherein reducing the codon-pair bias comprises rearranging the codons of a parent protein-encoding sequence.

17. The modified Flavivirus virus of claim 13, wherein one or both of the E protein-encoding sequence and the NS3 protein-encoding sequence are recoded by increasing the number of CpG or UpA di nucleotides compared to a parent virus.

18. The modified Flavivirus virus of claim 13, wherein each of the recoded prM/E protein-encoding sequence and the recoded NS3 protein-encoding sequence have a codon pair bias less than, -0.05, −0.1, or less than −0.2, or less than −0.3, or less than −0.4.

19. The modified Flavivirus virus of claim 13, wherein one or both of the E protein-encoding sequence and the NS3 protein-encoding sequence are recoded by replacing one or more codons with synonymous codons that are less frequent in the viral host.

20. The modified Flavivirus of claim 13, wherein the parent virus is a Flavivirus selected from the group consisting of dengue fever virus, West Nile virus, yellow fever virus, Japanese encephalitis virus, Spondweni virus, Saint Louis encephalitis virus, and Powassan virus.

21. The modified Flavivirus of claim 13, wherein the parent virus is a natural isolate.

22. The modified Flavivirus of claim 13, wherein the parent virus is a mutant of a natural isolate.

23. A Flavivirus vaccine composition for inducing a protective immune response in a subject, which comprises a modified virus of any of claims 13-22.

24. A method of eliciting a protective immune response in a subject comprising administering to the subject a prophylactically or therapeutically effective dose of a vaccine composition comprising a modified virus of any of claims 13-22.

25. The method of claim 24, further comprising administering to the subject at least one adjuvant.

26. The method of claim 24, wherein the immune response is cross-protective against a heterologous Flavivirus virus.

27. A method of making a modified Flavivirus virus genome comprising:

obtaining the nucleotide sequence encoding the envelope protein of a Flavivirus virus and the nucleotide sequence encoding the nonstructural 3 proteins of a Flavivirus virus;

recoding the envelope encoding nucleotide sequence to reduce protein expression and recoding the nonstructural protein 3-encoding nucleotide sequence to reduce protein expression, and

substituting a nucleic acid having the recoded envelope-encoding nucleotide sequence and a nucleic acid having the recoded nonstructural protein 3-encoding nucleotide sequence into a parent Flavivirus virus genome to make a modified Flavivirus virus genome; whereby expression of the recoded envelope-encoding nucleotide sequence and expression of the recoded nonstructural protein 3-encoding nucleotide sequence is reduced compared to the parent virus.

28. A method of eliciting an immune response in a subject in need thereof, comprising:

administering a prime dose of an attenuated Flavivirus produced by a method other than codon-pair deoptimization or a modified Flavivirus in which expression of viral proteins is reduced compared to a parent virus, wherein the reduction in expression is the result of recoding the prM, or envelope (E) region, or the nonstructural protein 3 (NS3) region or both the E and NS3 regions; and

administering one or more boost dose of the attenuated Flavivirus by methods other than codon-pair deoptimization or the modified Flavivirus to the subject in need thereof,

wherein at least the prime dose or the one or more boost dose is the modified virus.

29. The method of claim 28, wherein a first of the one or more boost dose is administered about 2 weeks after the prime dose.

30. The method of claim 28, wherein the Flavivirus is a Zika virus.

31. The method of claim 28, wherein the Flavivirus is selected from the group consisting of dengue fever virus, West Nile virus, yellow fever virus, Japanese encephalitis virus, Spondweni virus, Saint Louis encephalitis virus, and Powassan virus.

32. The method of claim 28, wherein one or both of the E protein-encoding sequence and the NS3 protein-encoding sequence are recoded by reducing the codon pair bias or codon usage bias of the protein-encoding sequence.

33. The method of claim 28, wherein one or both of the E protein-encoding sequence and the NS3 protein-encoding sequence are recoded by increasing the number of CpG or UpA di nucleotides compared to a parent virus.

34. The method of claim 28, wherein reducing the codon-pair bias comprises identifying a codon pair in the parent protein-encoding sequence having a codon-pair score that can be reduced, and reducing the codon-pair bias by substituting the codon pair with a codon pair that has a lower codon-pair score.

35. The method of claim 28, wherein reducing the codon-pair bias comprises rearranging the codons of a parent protein-encoding sequence.

36. The method of claim 28, wherein each of the recoded prM/E protein-encoding sequence and the recoded NS3 protein-encoding sequence have a codon pair bias less than, -0.05, −0.1, or less than −0.2, or less than −0.3, or less than −0.4.

37. The method of claim 28, wherein one or both of the E protein-encoding sequence and the NS3 protein-encoding sequence are recoded by replacing one or more codons with synonymous codons that are less frequent in the viral host.