CLAIMS

What is claimed is:

1. A myxoma virus (MYXV) comprising a transgene that encodes a multi-specific immune cell engager.

2. The MYXV of claim 1, wherein the multi-specific immune cell engager comprises a Bi-specific Natural Killer and Neutrophil engager (BiKE), a Bi-specific T Cell Engager (BiTE), or a membrane-integrated T cell engager (MiTE).

3. The MYXV of claim 1 or claim 2, wherein the multi-specific immune cell engager binds to an antigen present on a hematologic cancer cell.

4. The MYXV of claim 3, wherein the hematologic cancer cell is a myeloma cell, a leukemia cell, or a lymphoma cell.

5. The MYXV of claim 2, wherein the BiKE binds to an antigen present on a natural killer cell or a neutrophil.

6. The MYXV of claim 2, wherein the BiTE binds to an antigen present on a T cell.

7. The MYXV of claim 2, wherein the MiTE binds to an antigen present on a T cell.

8. The MYXV of any one of claims 2-7, wherein the BiKE binds to CD16 or CD138.

9. The MYXV of any one of claims 2-8, wherein the BiKE binds to CD16 and CD138.

10. The MYXV of any one of claims 2-8, wherein the BiTE binds to CD3 or CD138.

11. The MYXV of any one of claims 2-8, wherein the BiTE binds to CD3 and CD138.

12. The MYXV of any one of claims 2-8, wherein MiTE binds to CD3 or CD138.

13. The MYXV of any one of claims 2-8, wherein MiTE binds to CD3 and CD138.

14. The MYXV of any one of claims 1-13, wherein the multi-specific immune cell engager comprises one or more single chain variable fragments (scFvs) derived from an anti-human CD antibody.

15. The MYXV of any one of claims 1-13, wherein the multi-specific immune cell engager comprises one or more humanized single chain variable fragments (scFvs).

16. The MYXV of any one of claims 2-15, wherein the BiKE comprises a sequence that is at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 98%, at least 99%, or 100% identical to any one of SEQ ID NOs: 4-21.

17. The MYXV of any one of claims 2-15, wherein the BiTE comprises a sequence that is at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 98%, at least 99%, or 100% identical to any one of SEQ ID NOs: 6, 7, 10-15, or 32-39.

18. The MYXV of any one of claims 2-15, wherein the MiTE comprises a sequence that is at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 98%, at least 99%, or 100% identical to any one of SEQ ID NOs: 6, 7, 10-15, or 32-39.

19. The MYXV of any one of claims 1-18, wherein the transgene is located between the M135 gene and M136 gene of the genome of the MYXV.

20. The MYXV of any one of claims 1-19, further comprising a reporter gene.