

CLAIMS:

1. A viral vector comprising:

- i) a henipavirus F protein molecule or biologically active portion thereof;
- ii) a henipavirus envelope glycoprotein G (G protein) or a biologically active portion thereof; and
- iii) at least one antibody or antigen binding fragment thereof that specifically binds CD8,

wherein the antibody or antigen binding fragment thereof is attached to the C-terminus of the G protein or the biologically active portion thereof,

wherein the antibody or antigen binding fragment thereof that specifically binds CD8 α or CD8 β , comprises a heavy chain variable region and/or a light chain variable region, wherein the heavy chain variable region comprises three heavy chain complementarity determining regions (HCDR1, HCDR2, and HCDR3), and the light chain variable region comprises three light chain complementarity determining regions (LCDR1, LCDR2, and LCDR3), wherein the HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3, respectively, comprise:

- a) SEQ ID NOS: 1, 70, 148, 240, 294, and 333, respectively;
- b) SEQ ID NOS: 2, 71, 149, 241, 294, and 334, respectively;
- c) SEQ ID NOS: 3, 72, 148, 240, 294, and 333, respectively;
- d) SEQ ID NOS: 4, 73, 649, 242, 295, and 335, respectively;
- e) SEQ ID NOS: 5, 74, 150, 242, 295, and 336, respectively;
- f) SEQ ID NOS: 6, 75, 151, 243, 296, and 337, respectively;
- g) SEQ ID NOS: 7, 76, 152, 242, 295, and 338, respectively;
- h) SEQ ID NOS: 8, 77, 153, 244, 297, and 339, respectively;
- i) SEQ ID NOS: 9, 77, 154, 245, 298, and 340, respectively;
- j) SEQ ID NOS: 10, 78, 650, 246, 297, and 341, respectively;
- k) SEQ ID NOS: 11, 79, 155, 247, 299, and 342, respectively;
- l) SEQ ID NOS: 12, 80, 156, 248, 300, and 343, respectively;

- m) SEQ ID NOs: 13, 81, 157, 249, 294, and 344, respectively;
- n) SEQ ID NOs: 14, 76, 158, 242, 295, and 345, respectively;
- o) SEQ ID NOs: 15, 76, 159, 250, 301, and 346, respectively;
- p) SEQ ID NOs: 11, 82, 160, 249, 294, and 347, respectively;
- q) SEQ ID NOs: 16, 83, 161, 251, 302, and 340, respectively;
- r) SEQ ID NOs: 17, 84, 162, 241, 303, and 348, respectively;
- s) SEQ ID NOs: 18, 85, 163, 252, 304, and 349, respectively;
- t) SEQ ID NOs: 19, 86, 164, 241, 305, and 350, respectively;
- u) SEQ ID NOs: 20, 87, 165, 253, 299, and 351, respectively;
- v) SEQ ID NOs: 4, 88, 166, 249, 299, and 352, respectively;
- w) SEQ ID NOs: 21, 89, 167, 242, 306, and 353, respectively;
- x) SEQ ID NOs: 22, 90, 168, 241, 307, and 354, respectively;
- y) SEQ ID NOs: 23, 91, 169, 241, 299, and 355, respectively;
- z) SEQ ID NOs: 24, 92, 170, 241, 299, and 356, respectively;
- aa) SEQ ID NOs: 25, 93, 171, 254, 308, and 344, respectively;
- bb) SEQ ID NOs: 26, 94, 172, 240, 294, and 333, respectively;
- cc) SEQ ID NOs: 617, 91, 173, 241, 299, and 357, respectively;
- dd) SEQ ID NOs: 1, 79, 174, 255, 294, and 358, respectively;
- ee) SEQ ID NOs: 28, 95, 175, 256, 294, and 359, respectively;
- ff) SEQ ID NOs: 29, 79, 176, 257, 309, and 360, respectively;
- gg) SEQ ID NOs: 1, 96, 177, 240, 294, and 333, respectively;
- hh) SEQ ID NOs: 20, 97, 149, 251, 299, and 361, respectively;
- ii) SEQ ID NOs: 30, 98, 178, 241, 310, and 362, respectively;
- jj) SEQ ID NOs: 31, 99, 179, 240, 311, and 363, respectively;
- kk) SEQ ID NOs: 32, 100, 180, 258, 312, and 364, respectively;
- ll) SEQ ID NOs: 19, 101, 181, 259, 313, and 333, respectively;
- mm) SEQ ID NOs: 33, 102, 182, 242, 314, and 365, respectively;
- nn) SEQ ID NOs: 34, 103, 183, 260, 315, and 366, respectively;
- oo) SEQ ID NOs: 35, 104, 184, 241, 302, and 367, respectively;

- pp) SEQ ID NOs: 36, 105, 185, 261, 316, and 368, respectively;
- qq) SEQ ID NOs: 37, 106, 186, 262, 294, and 369, respectively;
- rr) SEQ ID NOs: 38, 107, 187, 263, 294, and 344, respectively;
- ss) SEQ ID NOs: 39, 108, 188, 264, 317, and 344, respectively;
- tt) SEQ ID NOs: 40, 109, 189, 240, 294, and 370, respectively;
- uu) SEQ ID NOs: 8, 110, 190, 265, 299, and 371, respectively;
- vv) SEQ ID NOs: 41, 111, 191, 266, 299, and 346, respectively;
- ww) SEQ ID NOs: 19, 112, 192, 242, 318, and 372, respectively;
- xx) SEQ ID NOs: 4, 113, 193, 267, 309, and 373, respectively;
- yy) SEQ ID NOs: 4, 114, 194, 268, 302, 344, and 453, respectively;
- zz) SEQ ID NOs: 42, 115, 195, 269, 319, 374, and 454, respectively;
- aaa) SEQ ID NOs: 43, 77, 196, 270, 320, and 375, respectively;
- bbb) SEQ ID NOs: 44, 116, 197, 271, 299, and 376, respectively;
- ccc) SEQ ID NOs: 40, 117, 198, 272, 302, and 377, respectively;
- ddd) SEQ ID NOs: 40, 118, 199, 259, 302, and 378, respectively;
- eee) SEQ ID NOs: 45, 114, 200, 273, 321, and 379, respectively;
- fff) SEQ ID NOs: 46, 119, 201, 240, 322, and 380, respectively;
- ggg) SEQ ID NOs: 47, 120, 202, 274, 309, and 333, respectively;
- hhh) SEQ ID NOs: 48, 121, 203, 252, 302, and 333, respectively;
- iii) SEQ ID NOs: 49, 122, 204, 275, 311, and 381, respectively;
- jjj) SEQ ID NOs: 44, 123, 205, 276, 311, and 333, respectively;
- kkk) SEQ ID NOs: 50, 124, 206, 277, 299, and 382, respectively;
- lll) SEQ ID NOs: 51, 77, 207, 278, 294, and 383, respectively;
- mmm) SEQ ID NOs: 52, 125, 208, 240, 323, and 384, respectively;
- nnn) SEQ ID NOs: 34, 126, 209, 279, 324, and 385, respectively;
- ooo) SEQ ID NOs: 53, 127, 210, 280, 294, and 386, respectively;
- ppp) SEQ ID NOs: 54, 128, 211, 281, 294, and 387, respectively;
- qqq) SEQ ID NOs: 19, 129, 212, 282, 317, and 342, respectively;
- rrr) SEQ ID NOs: 19, 130, 213, 242, 295, and 388, respectively;

sss) SEQ ID NOs: 55, 77, 214, 240, 325, and 389, respectively;
ttt) SEQ ID NOs: 8, 77, 215, 241, 326, and 390, respectively;
uuu) SEQ ID NOs: 56, 131, 216, 283, 294, and 344, respectively;
vvv) SEQ ID NOs: 57, 132, 217, 249, 327, and 333, respectively;
www) SEQ ID NOs: 19, 133, 218, 284, 297, and 391, respectively;
xxx) SEQ ID NOs: 58, 79, 219, 240, 294, and 333, respectively;
yyy) SEQ ID NOs: 19, 95, 220, 285, 299, and 342, respectively;
zzz) SEQ ID NOs: 58, 134, 221, 286, 294, and 392, respectively;
aaaa) SEQ ID NOs: 40, 93, 222, 241, 309, and 393, respectively;
bbbb) SEQ ID NOs: 59, 135, 223, 275, 299, and 344, respectively;
cccc) SEQ ID NOs: 19, 136, 224, 287, 302, and 394, respectively;
dddd) SEQ ID NOs: 60, 137, 225, 288, 309, and 333, respectively;
eeee) SEQ ID NOs: 10, 138, 226, 289, 328, and 395, respectively;
ffff) SEQ ID NOs: 19, 139, 227, 241, 329, and 396, respectively;
gggg) SEQ ID NOs: 1, 140, 228, 241, 294, and 397, respectively;
hhhh) SEQ ID NOs: 61, 141, 229, 241, 328, and 395, respectively;
iiii) SEQ ID NOs: 62, 93, 230, 241, 316, and 362, respectively;
jjjj) SEQ ID NOs: 63, 142, 231, 249, 330, 361, and 490, respectively;
kkkk) SEQ ID NOs: 64, 143, 232, 290, 299, and 399, respectively;
llll) SEQ ID NOs: 65, 79, 233, 241, 331, and 400, respectively;
mmmm) SEQ ID NOs: 66, 79, 234, 241, 299, and 401, respectively;
nnnn) SEQ ID NOs: 19, 144, 235, 241, 332, and 371, respectively;
oooo) SEQ ID NOs: 67, 145, 236, 291, 330, and 402, respectively;
pppp) SEQ ID NOs: 19, 146, 237, 292, 294, and 344, respectively;
qqqq) SEQ ID NOs: 68, 147, 238, 241, 299, and 403, respectively;
rrrr) SEQ ID NOs: 69, 77, 239, 293, 299, and 404, respectively; and
ssss) SEQ ID NOs: 1061, 1062, and 1063, respectively.

2. The viral vector of claim 1, comprising a heavy chain variable region (VH) having an amino acid sequence with at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from SEQ ID NOs: 405-498 or 1060.
3. The viral vector of claim 1 or 2, comprising a light chain variable region (VL) having an amino acid sequence with at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from SEQ ID NOs: 499-591.
4. The viral vector of claim 2 or 3, comprising a VH having an amino acid sequence with at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from SEQ ID NOs: 405-498 and a VL having an amino acid sequence with at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from SEQ ID NOs: 499-591.
5. The viral vector of any one of claims 1-4, wherein the VH is selected from SEQ ID NOs: 405, 408, 448, 455, and 1060, and the VL is selected from 499, 503, 542, and 549.
6. The viral vector of claim 5, wherein the HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3, respectively, comprise:
 - a) SEQ ID NOs: 1, 70, 148, 240, 294, 333, respectively;
 - b) SEQ ID NOs: 5, 74, 150, 242, 295, 336, respectively;
 - c) SEQ ID NOs: 40, 109, 189, 240, 294, 370, respectively;
 - d) SEQ ID NOs: 43, 77, 196, 270, 320, 375, respectively;
7. The viral vector of any one of claims 1-6, which binds to human CD8 α or CD8 β .
8. The viral vector of any one of claims 4-10, wherein the antigen binding fragment is a Fab, Fab', F(ab')₂, Fd, scFv, (scFv)₂, scFv-Fc, sdAb, VHH, or Fv fragment.
9. The viral vector of claim 13, wherein the antigen binding fragment is a scFv.
10. The viral vector of any one of claims 1-9, wherein the F protein or the biologically active portion thereof is a wild-type Nipah virus F (NiV-F) protein or a functionally active variant or a biologically active portion thereof.
11. The viral vector of any one of claims 1-10, wherein the NiV-F-protein or the functionally active variant or biologically active portion thereof comprises the

amino acid sequence set forth in SEQ ID NO: 593, or an amino acid sequence having at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity to SEQ ID NO: 593 or 596.

12. The viral vector of any one of claims 1-11, wherein the NiV-F protein is a biologically active portion thereof that has a 20 amino acid truncation at or near the C-terminus of the wild-type NiV-F protein (SEQ ID NO: 593 or 596).
13. The viral vector of any one of claims 1-11, wherein the NiV-F protein is a biologically active portion thereof that has a 22 amino acid truncation at or near the C-terminus of the wild-type NiV-F protein (SEQ ID NO: 593 or 596), optionally wherein a point mutation on an N linked glycosylation site.
14. The viral vector of claim 13, wherein the NiV-F protein has an amino acid sequence that is encoded by a sequence of nucleotides encoding a sequence having at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity to SEQ ID NO: 599.
15. The viral vector of claim 14, wherein the NiV-F protein has an amino acid sequence having at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity to SEQ ID NO: 1092.
16. The viral vector of any one of claims 1-15, wherein the G protein or a biologically active portion thereof is a wild-type Nipah virus G glycoprotein (NiV-G) or a functionally active variant or a biologically active portion thereof.

17. The viral vector of any one of claims 1-16, wherein the NiV-G variant or biologically active portion thereof comprises an amino acid sequence having at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity to SEQ ID NO: 600, SEQ ID NO: 618, or SEQ ID NO: 628.
18. The viral vector of any one of claims 1-17, wherein the NiV-G protein is a biologically active portion that is truncated and lacks up to 40 contiguous amino acid residues at or near the N-terminus of the wild-type NiV-G protein SEQ ID NO: 600, SEQ ID NO: 618, or SEQ ID NO: 628.
19. The viral vector of any one of claims 1-17, wherein the NiV-G protein has a 5 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO: 600, SEQ ID NO: 618, or SEQ ID NO: 628), wherein the NiV-G protein has a 10 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO: 600, SEQ ID NO: 618, or SEQ ID NO: 628), wherein the NiV-G protein has a 15 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO: 600, SEQ ID NO: 618, or SEQ ID NO: 628), wherein the NiV-G protein has a 20 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO: 600, SEQ ID NO: 618, or SEQ ID NO: 628), , wherein the NiV-G protein has a 25 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO: 600, SEQ ID NO: 618, or SEQ ID NO: 628), wherein the NiV-G protein has a 30 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO: 600, SEQ ID NO: 618, or SEQ ID NO: 628), or wherein the NiV-G protein has a 34 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO: 600, SEQ ID NO: 618, or SEQ ID NO: 628).

20. The viral vector of any one of claims 1-19, wherein the NiV-G variant or biologically active portion thereof exhibits reduced binding to Ephrin B2 or Ephrin B3.
21. The viral vector of any one of claims 1-20, wherein the NiV-G variant or biologically active portion thereof comprises one or more amino acid substitutions corresponding to amino acid substitutions selected from E501A, W504A, Q530A and E533A with reference to the numbering set forth in SEQ ID NO: 618, optionally wherein the NiV-G variant or biologically active portion thereof comprises the amino acid substitutions corresponding to amino acid substitutions selected from E501A, W504A, Q530A and E533A with reference to the numbering set forth in SEQ ID NO: 618.
22. The viral vector of any one of claims 1-21, wherein the NiV-G variant or biologically active portion thereof comprises an amino acid sequence having at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity to SEQ ID NO: 607 or 635.
23. The viral vector of any one of claims 1-22, wherein the NiV-G protein has a 34 amino acid truncation at or near the N-terminus of the wild-type NiV-G protein (SEQ ID NO: 600, SEQ ID NO: 618, or SEQ ID NO: 628) and one or more amino acid substitutions corresponding to amino acid substitutions selected from E501A, W504A, Q530A and E533A with reference to the numbering set forth in SEQ ID NO: 618.
24. The viral vector of any one of claims 1-23, wherein the viral vector is a lentiviral vector.
25. The viral vector of any one of claims 1-24, wherein the viral vector comprises one or more viral components other than the F protein molecule and the G protein.

26. The viral vector of claim 25, wherein the one or more viral components comprises one or more endogenous nucleic acid sequences encoding a chimeric antigen receptor (CAR), optionally wherein the CAR targets a tumor antigen selected from CD19, CD20, CD22, or BCMA.
27. The viral vector of claim 26, wherein the CAR comprises an anti-CD19 scFv having an amino acid sequence comprising SEQ ID NO: 1075.
28. Use of a viral vector according to any one of claims 1-27 in the manufacture of a medicament for the treatment of cancer, wherein the viral vector further comprises an exogenous agent, wherein the exogenous agent encodes a therapeutic agent, wherein the therapeutic agent is a chimeric antigen receptor (CAR) or T-cell receptor (TCR), optionally, wherein the CAR targets a tumor antigen selected from CD19, CD20, CD22, or BCMA.
29. Use of a viral vector according to any one of claims 1-27 in the manufacture of a medicament for the treatment of a B cell malignancy selected from the group consisting of Non-Hodgkin lymphoma (NHL), acute lymphocytic leukemia (ALL), chronic lymphocytic leukemia (CLL), and multiple myeloma.