CLAIMS

1. A virus particle comprising a lymphocytic choriomeningitis virus (LCMV) glycoprotein (GP) and/or a nucleic acid encoding said GP, wherein the glycoprotein is a mutated LCMV strain WE glycoprotein which comprises in comparison with the wild type LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 at least one mutated amino acid residue selected from the group consisting of Lys 492→ Ile, Ser 102 → Asn, Phe 122 → Leu, Phe 129 → Ser, Lys 132 → Arg, His 136 → Gln, Asn 152 → Tyr, Ser 153 → Pro, Phe or Tyr, Asn 154 → Asp, His 155 → Leu or Tyr, Lys 156 → Glu, Thr 217 → Ile, Thr 218 → Ile, Lys 256 →Arg, Leu 260 → Ile, Tyr 284 → His, Ala 328 → Ser, Phe 332 → Leu, Val 342 → Ala, and Arg 358→ Lys, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises the wild type glycoprotein set forth in SEQ ID NO: 4.

2. The virus particle of claim 1, wherein the glycoprotein has at least 95% sequence identity to any one of SEQ ID NOs: 4 and 30-57.

3. The virus particle of claim 1 or 2, wherein the GP comprises the following set of mutated amino acid residues in comparison with the linear polypeptide sequence of the wild type LCMV strain WE glycoprotein set forth in SEQ ID NO: 4:
   (a) Lys 492→ Ile;
   (b) Ala 211→ Thr;
   (c) Lys 260→ Phe and Lys 492→ Ile;
   (d) Ser 153 → Pro and Lys 492→ Ile,;
   (e) Phe 122 → Leu, His 136 → Gln, and Ser 153 → Pro;
   (f) Phe 122 → Leu, and Lys 492→ Ile,;
   (g) Phe 122 → Leu, His 136 → Gln, Ser 153 → Pro, and Lys 492→ Ile,;
   (h) Glu 255 →Gly and Lys 492→ Ile,;
   (i) Ser 153 → Pro and Arg 358→ Lys;
   (j) Ser 153 → Pro, Lys 256 →Arg, Leu 260 → Phe and Lys 492→ Ile,;
   (k) Ser 153 → Phe, Glu 255 →Gly, and Leu 260 → Phe;
   (l) Lys 156 → Glu and Lys 492→ Ile,;
   (m) Ser 153 → Pro, Lys 256 →Arg, and Leu 260 → Phe;
   (n) Phe 122 → Leu, His 136 → Gln, Ser 153 → Pro, Lys 256 →Arg and Lys 492→ Ile; or
   (o) Glu 379 → Asn and Lys 492→ Ile.

4. An LCMV GP, wherein the glycoprotein comprises in comparison with the wild type LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 at least one mutated amino acid residue as defined in any one of claims 1-3.

5. A nucleic acid molecule encoding a LCMV GP of claim 4, wherein the nucleic acid molecule preferably comprises a sequence that has at least about 95%, preferably at least about 96%, preferably at least about 97%, preferably at least about 98% preferably at least about 99%, preferably at least about 99.1%, preferably at least about 99.2%, preferably at least about 99.3%, preferably at least about 99.4%, preferably at least about 99.5%, preferably at least about 99.6%, preferably at least about 99.7% sequence identity, or is preferably identical, to a sequence set forth in SEQ ID NOs: 58-85, or a respective complementary sequence.

6. A virus particle comprising a glycoprotein (GP) of an arenavirus and/or a nucleic acid encoding said GP, wherein the glycoprotein comprises at least one of the following amino acid residues:
   (a) at the position corresponding to Lys 492 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 an Ile residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Lys residue at said position;
   (b) at the position corresponding to Ser 102 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 an Asn residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Ser residue at said position;
   (c) at the position corresponding to Phe 122 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 a Leu residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Phe residue at said position;
   (d) at the position corresponding to Phe 129 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 a Ser residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Phe residue at said position;
   (e) at the position corresponding to His 136 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 a Gln residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a His residue at said position;
   (f) at the position corresponding to Asn 152 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 a Tyr residue, wherein the virus particle

has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Phe residue at said position;

(g) at the position corresponding to Ser 153 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 a Pro, Phe, or Tyr residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Ser residue at said position;

(h) at the position corresponding to Asn 154 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 an Asp residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Phe residue at said position;

(i) at the position corresponding to His 155 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 a Leu or Tyr residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Phe residue at said position;

(j) at the position corresponding to Lys 156 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 a Glu residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Lys residue at said position;

(l) at the position corresponding to Thr 217 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 an Ile residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Phe residue at said position;

(m) at the position corresponding to Thr 218 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 an Ile residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Phe residue at said position;

(n) at the position corresponding to Lys 256 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 an Arg residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Lys residue at said position;

(o) at the position corresponding to Leu 260 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 a Phe residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Leu residue at said position;

(p) at the position corresponding to Tyr 284 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 a His residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Tyr residue at said position;

(q) at the position corresponding to Ala 328 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 a Ser residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Ala residue at said position;

(r) at the position corresponding to Phe 332 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 a Leu residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Phe residue at said position;

(s) at the position corresponding to Val 342 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 an Ala residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Val residue at said position; and

(t) at the position corresponding to Arg 358 of the GP of LCMV strain WE glycoprotein set forth in SEQ ID NO: 4 a Lys residue, wherein the virus particle has an increased capacity to enter a tumor cell as compared to a reference virus particle that comprises a Arg residue at said position.

7. A host cell comprising the nucleic acid molecule of claim 5 or a cDNA of the genome of a virus particle of any one of claims 1-3 and 6.

8. A method of producing a virus particle of any one of claims 1-3 and 6 comprising cultivating the host cell of claim 7 under conditions suitable for virus particle formation.

9. A pharmaceutical composition comprising a virus particle of any one of claims 1-3, a GP of claim 4, a nucleic acid molecule of claim 5, or an arenavirus particle of claim 6.

10. A virus particle of any one of claims 1-3, a GP of claim 4, a nucleic acid molecule of claim 5, or an arenavirus particle of claim 6, for use in therapy, preferably in the treatment of cancer.

11. A use of a virus particle of any one of claims 1-3, a GP of claim 4, a nucleic acid molecule of claim 5, or an arenavirus particle of claim 6, for the manufacture of a medicament, wherein the medicament is preferably for the treatment of cancer.

12. A method of producing a virus particle having an increased capacity to enter a tumor cell, comprising:

(i) Providing a nucleic acid encoding a mutated LCMV strain WE glycoprotein which comprises in comparison with the wild type LCMV strain WE glycoprotein set

forth in SEQ ID NO: 4 at least one mutated amino acid residue at one or more positions comprised in

(a) Strand β1 N terminal defined by positions 59-89, wherein the at least one mutated amino acid residue is preferably at one or more positions selected from the group consisting of 59-78 and 81-87;

(b) Strands β3, β4, and/or β5 as defined by positions 90-113, wherein the at least one mutated amino acid residue is preferably at one or more positions selected from the group consisting of 90-93, 98-103, and 106-113;

(c) Helix α 1 and/or α 2 as defined by positions 114-147, wherein the at least one mutated amino acid residue is preferably at one or more positions selected from the group consisting of 126-130 and 136-147;

(d) Loop 1 as defined by positions 148-157, wherein the at least one mutated amino acid residue is preferably at one or more positions selected from the group consisting of 148-157;

(e) Helix α3 as defined by positions 187-199;

(f) Loop 3 as defined by positions 200-226;

(g) the α4, α5 domain as defined by positions 245-265, wherein the at least one mutated amino acid residue is preferably at one or more positions selected from the group consisting of 245-251 and 253-258;

(h) the N-Helix as defined by positions 313-373, wherein the at least one mutated amino acid residue is preferably at one or more positions selected from the group consisting of 313-349 and 353-365;

(i) the H1,H2 domain as defined by positions 1-58; and/or

(j) the TM cytoplasmic domain as defined by positions 439-498; and

(ii) Expressing the mutated LCMV strain WE glycoprotein and further viral proteins to produce a virus particle comprising said mutated LCMV strain WE glycoprotein; and

(iii) Assessing the capacity of a virus particle comprising said mutated LCMV strain WE glycoprotein to enter and/or infect a tumor cell, preferably comprising comparing the virus particle comprising said mutated LCMV strain WE glycoprotein to a value, wherein the reference value is preferably at least as high or higher than the value that is obtained for a virus particle that comprises the wild type glycoprotein set forth in SEQ ID NO: 4.

13. A method of producing a virus particle having an increased tropism for a tumor cell, comprising:

(i) Providing a nucleic acid encoding a mutated LCMV strain WE glycoprotein which comprises in comparison with the wild type LCMV strain WE glycoprotein set

forth in SEQ ID NO: 4 at least one mutated amino acid residue at one or more positions comprised in

(a) Strand β1 N terminal defined by positions 59-89, wherein the at least one mutated amino acid residue is preferably at one or more positions selected from the group consisting of 59-78 and 81-87;

(b) Strands β3, β4, and/or β5 as defined by positions 90-113, wherein the at least one mutated amino acid residue is preferably at one or more positions selected from the group consisting of 90-93, 98-103, and 106-113;

(c) Helix α 1 and/or α 2 as defined by positions 114-147, wherein the at least one mutated amino acid residue is preferably at one or more positions selected from the group consisting of 126-130 and 136-147;

(d) Loop 1 as defined by positions 148-157, wherein the at least one mutated amino acid residue is preferably at one or more positions selected from the group consisting of 148-157;

(e) Helix α3 as defined by positions 187-199;

(f) Loop 3 as defined by positions 200-226;

(g) the α4, α5 domain as defined by positions 245-265, wherein the at least one mutated amino acid residue is preferably at one or more positions selected from the group consisting of 245-251 and 253-258;

(h) the N-Helix as defined by positions 313-373, wherein the at least one mutated amino acid residue is preferably at one or more positions selected from the group consisting of 313-349 and 353-365;

(i) the H1,H2 domain as defined by positions 1-58; and/or

(j) the TM cytoplasmic domain as defined by positions 439-498; and

(ii) Expressing the mutated LCMV strain WE glycoprotein and further viral proteins to produce a virus particle comprising said mutated LCMV strain WE glycoprotein; and

(iii) Assessing the capacity of a virus particle comprising said mutated LCMV strain WE glycoprotein to enter and/or infect a tumor cell and/or a non-tumor cell, preferably comprising comparing the virus particle comprising said mutated LCMV strain WE glycoprotein to a reference value, wherein the reference value is preferably at least as high or higher than the value that is obtained for a virus particle that comprises the wild type glycoprotein set forth in SEQ ID NO: 4.

14. The method of claim 12 or 13, wherein the virus particle has increased capacity to enter or an increased tropism for at least one of the following tumor cells: lung tumor cells, such as H1975 or A549, LLC, TC-1, gastrointestinal tumor cells, such as Gist-T1, melanoma cells, such as MaMel86a, MaMel51, A375, B16F10, or RPMI-7951,

pancreatic tumor cells, such as 511950, 60590, 511950R, or 60590R, thyroid tumor cells, such as 8305C or C643, sarcoma cells, such as Gist-T1, breast tumor cells, such as HCC1954, cervical tumor cells, such as HeLa, liver tumor cells, such as HepG2, colon tumor cells, such as MC38, Sw620, or Sw480, neuroblastoma cells, such as SK-N-BE(2), and/or prostate tumor cells, such as TrampC2.

15. A virus particle having an increased capacity to enter a tumor cell or having an increased tropism for a tumor cell obtainable by the method of claim 12 or 13.