CLAIMS

1. Use of a bacterial composition comprising at least one naturally occurring or engineered bacterial strain in the manufacture of a medicament for the treatment of a cancer, in combination with an antineoplastic drug, wherein said at least one bacterial strain expresses the protein of SEQ ID No: 1 or a fragment thereof of at least 9, preferably at least 20 amino acids comprising at least one epitope selected from the group consisting of SEQ ID Nos: 13, 14, 53 to 188 and 209, with the proviso that said at least one bacterial strain is different from the *Enterococcus hirae* strain 13144 deposited on November 7, 2013 at the CNCM under the number I-4815.

2. The use of claim 1, wherein said composition comprises at least one bacterial strain containing a prophage genome encoding a protein with at least 80, preferably at least 90 and more preferably at least 95% identity with the protein of SEQ ID No: 1.

3. The use of claim 1, wherein said composition comprises at least one strain harbouring a prophage genome with at least 80 and preferably at least 95% identity with the prophage of SEQ ID No: 2, so that the phage encoded by this prophage can *in vivo* infect the other strains of the composition and/or commensal bacteria of the gut microbiota of a subject in need thereof.

4. The use of claim 1, wherein said composition comprises bacteria selected from the group consisting of:

(i) *Enterococcus hirae* strain IGR7 deposited on August 31, 2017 at the CNCM under the number I-5224,

(ii) *Enterococcus hirae* strain IGR11 deposited on November 27, 2017, at the CNCM under the number I-5261,

(iii) any other bacterial strain expressing a protein with at least 65, preferably at least 80 and more preferably at least 95% identity with a fragment of at least 20, preferably at least 30 and more preferably at least 40 nucleotides from the protein of SEQ ID No: 1, and

(iv) mixtures of at least two strains selected from the group consisting of the strains recited in (i) to (iii) and *Enterococcus hirae* strain CNCM I-4815, preferably a mixture of the strain I-4815 and the strains recited in (i).

5. The use of claim 1, wherein said composition further comprises *Enterococcus hirae* strain IGR4 deposited on November 27, 2017, at the CNCM under the number I-5260.

6. A method of increasing the immunogenicity of a bacterial strain, comprising *in vitro* introducing, into said strain, a nucleotide sequence encoding the protein of SEQ ID No: 1 or a fragment thereof comprising at least the peptides of SEQ ID Nos: 13 and 14, or a sequence encoding a peptide of at least 9, preferably at least 20 amino acids comprising at least one epitope selected from the group consisting of SEQ ID No: 53 to 187, or a sequence encoding a peptide of at least 9, preferably at least 20 amino acids comprising at least one epitope of SEQ ID No: 209.

7. The method of claim 6, comprising *in vitro* infecting bacteria of said strain with a bacteriophage encoding a protein with at least 80, preferably at least 90 and more preferably at least 95% identity with the protein of SEQ ID No: 1.

8. The method of claim 7, wherein said bacteriophage has a genome comprising a nucleotide sequence of SEQ ID NOs: 2 or a sequence having at least 90% or at least 95% identity thereto.

9. Use of a bacterial composition comprising an engineered bacterial strain which has been obtained by the method according to any of claims 6 to 8, in the manufacture of a medicament for the treatment of a cancer.

10. The use of claim 9, wherein said bacterial strain is selected from the group consisting of *Escherichia coli*, *Enterococcus gallinarum, Enterococcus faecalis* and *Enterococcus hirae*.

11. The use of claim 9, for the treatment of a cancer in a HLA-A*0201 patient.

12. Use of a bacterial composition selected from the group consisting of a bacterial composition comprising the *Enterococcus hirae* CNCM I-4815 and the bacterial composition as defined in claims 1 to 5 and 9 to 11, in the manufacture of a medicament for the treatment of a cancer, wherein said bacterial composition is used in combination with an antineoplastic drug capable of triggering the lytic cycle of a phage encoded by a prophage present in at least some bacteria of the composition.

13. The use of claim 12, wherein said bacterial composition is used in combination with a CDK4/6 inhibitor.

14. The use of claim 12 or 13, wherein said bacterial composition is used in combination with an immune checkpoint blocker.

15. Use of an immunogenic composition comprising a polypeptide comprising a sequence of at least 9 consecutive amino acids from the protein of SEQ ID No: 1 or a sequence of SEQ ID No: 209, or a polynucleotide encoding the same, in the manufacture of an anticancer vaccine.

16. The use of claim 15, wherein the sequence of at least 9 consecutive amino acids from the protein of SEQ ID No: 1 is selected from the group consisting of SEQ ID No: 53-187.

17. The use of claim 15, which comprises a peptide comprising sequence selected from the group consisting of SEQ ID No: 63, SEQ ID No: 188 and SEQ ID No: 209 or a polynucleotide encoding the same, wherein said anticancer vaccine is to be administered to a HLA-A*0201 patient.

18. Use of a cell composition comprising antigen presenting cells (APC) which have been pulsed *ex vivo* with a bacterial composition as defined in any of claims 1 to 5 and 9 to 12 or with an immunogenic composition as defined in any of claim 15 to 17, in the manufacture of a medicament for the treatment of cancer.

19. Use of an MHC multimer for isolating T-cells with high affinity for the protein of SEQ ID No: 1 in the manufacture of a medicament for treating cancer, characterized in that MHC molecules are bound to an epitope selected from the group consisting of SEQ ID No: 53-188 and SEQ ID No: 209.

20. The use of claim 19, wherein the MHC multimer is a HLA-A*0201 multimer loaded with an antigenic peptide comprising SEQ ID No: 63, SEQ ID No: 188 or another sequence of SEQ ID No: 209.

21. Use of a bacteriophage composition in the manufacture of a medicament for treating a cancer, wherein said bacteriophage expresses a protein having at least 80, preferably at least 90 and more preferably at least 95% identity with the protein of SEQ ID No: 1.

22. The use of claim 20, wherein said bacteriophage has a genome comprising a nucleotide sequence of SEQ ID No: 2 or a sequence having at least 90% or at least 95% identity thereto.

23. The use of any of claims 15 to 22, wherein said medicament is to be administered in combination with a drug blocking an immune checkpoint.

24. The use of any of claims 1 to 5 and 9 to 12, or the use of any of claims 15 to 22, wherein the tumor expresses mRNA levels of GPD1L superior to levels expressed in paired normal tissues.

25. A screening method for identifying antineoplastic drugs, comprising using bacteria from the strain CNCM I-4815 or any other bacterial strain harbouring a prophage genome with at least 80 and preferably at least 90% or 95% identity with the prophage of SEQ ID No: 2, for assessing the ability of drug candidates to trigger the lytic cycle of the phage comprising the protein of SEQ ID No: 1.

26. A method of determining if a patient having a cancer is likely to be a good responder to a treatment by chemotherapy or immune checkpoint blockade,

comprising assessing the presence, in a biological sample from said patient, of a sequence having at least 80% identity with the protein of SEQ ID No: 1, wherein if such a sequence is present in the sample, the patient is likely to respond to the treatment.

27. The method of claim 26, comprising the steps of

(i) cultivating a stool sample from said patient in aerobic conditions in a permissive medium to allow isolation of enterococci colonies,

(ii) performing a PCR in several cultivable isolated colonies with a pair of primers specific for a fragment of SEQ ID No: 1, and

(iii) detecting the amplified fragment.

28. A method of determining if a patient is likely to be a good responder to a treatment by chemotherapy or immune checkpoint blockade, comprising using the MHC multimer as defined in claim 19 or claim 20 to measure the levels of circulating $CCR9^+$ $CXCR3^+$ $CD8^+$ T cells specific to the protein of SEQ ID No: 1 at diagnosis and/or during said treatment, wherein if said level is above a predetermined threshold, the patient is likely to respond to the treatment.

29. The method of claim 28, wherein the patient is HLA-A*0201 and the MHC multimer is as defined in claim 20.

30. The method of any of claims 26 to 29, further comprising assessing the level of GPD1L mRNA or the level of GPD1L protein in the tumor, wherein if said level is above a predetermined threshold, the patient is likely to respond to the treatment.

31. A method of determining if a patient having a tumor is likely to be a good responder to a treatment by immune checkpoint blockade, comprising assessing the level of GPD1L mRNA or the level of GPD1L protein in the tumor, wherein if said level is above a predetermined threshold, the patient is likely to respond to the treatment, wherein if the patient is not identified as likely to be a good responder to a treatment by chemotherapy or immune checkpoint blockade, a bacterial composition as defined in any of claims 1 to 5 and 9 to 12 or an immunogenic composition as defined in any of claims 15 to 17 is to be administered to the patient to increase his/her response to the treatment by chemotherapy or immune checkpoint blockade.

32. The method of any of claims 26 to 30, wherein if the patient is not identified as likely to be a good responder to a treatment by chemotherapy or immune checkpoint blockade, a bacterial composition as defined in any of claims 1 to 5 and 9 to 12 or an immunogenic composition as defined in any of claims 15 to 17 is to be administered to the patient to increase his/her response to the treatment by chemotherapy or immune checkpoint blockade.