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, and wherein said bacterial composition is to be administered in combination with an antineoplastic drug.

2. The use of claim 1, wherein said at least one bacterial strain expresses a fragment of at least 20 amino acids of the protein of SEQ ID No: 1, comprising at least one epitope selected from the group consisting of SEQ ID Nos: 13, 14, 53 to 188 and 209.

~~2.~~3. 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.~~4. 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.~~5. 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~~ amino acids 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.~~6. 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.~~7. 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.~~8. The method of claim ~~6~~7, 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.~~9. The method of claim ~~7~~8, 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.~~10. Use of a bacterial composition comprising an engineered bacterial strain which has been obtained by the method according to any of claims ~~6~~ 7 to ~~8~~9, in the manufacture of a medicament for the treatment of a cancer.

~~10.~~11. The use of claim ~~9~~10, wherein said bacterial strain is selected from the group consisting of *Escherichia coli*, *Enterococcus gallinarum, Enterococcus faecalis* and *Enterococcus hirae*.

~~11.~~12. The use of claim ~~9~~10, for the treatment of a cancer in a HLA-A*0201 patient.

~~12.~~13. 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~~ 6 and ~~9~~ 10 to ~~11~~12, in the manufacture of a medicament for the treatment of a cancer, wherein said bacterial composition is ~~used~~ to be administered 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.~~14. The use of claim ~~12~~13, wherein said bacterial composition is ~~used~~ to be administered in combination with a CDK4/6 inhibitor.

~~14.~~15. The use of claim ~~12~~ 13 or ~~13~~14, wherein said bacterial composition is ~~used~~ to be administered in combination with an immune checkpoint blocker.

~~15.~~16. 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.~~17. The use of claim ~~15~~16, 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.~~18. The use of claim ~~15~~16, 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.

19. ~~Use of a~~A cell composition comprising antigen presenting cells (APC) which have been pulsed *ex vivo* with a bacterial composition ~~as defined in~~ according to any of claims 1 to ~~5~~ 6 and ~~9~~ 10 to ~~12~~ 13 or with an immunogenic composition ~~as defined in~~according to any of claim ~~15~~ 16 to ~~17~~18~~, in the manufacture of a medicament for the treatment of cancer~~.

~~18.~~20. Use of a cell composition according to claim 19, in the manufacture of a medicament for treating cancer.

~~19.~~21. ~~Use of a~~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.~~22. The MHC multimer ~~use~~ of claim ~~19~~21, which~~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.~~23. Use of a bacteriophage composition in the manufacture of a medicament for treating a cancer, wherein said bacteriophage expresses a protein comprising at least one epitope selected from the group consisting of SEQ ID Nos: 13, 14, 53 to 188 and 209 and having at least 80, preferably at least 90 and more preferably at least 95% identity with the protein of SEQ ID No: 1.

~~22.~~24. The use of claim ~~20~~23, wherein ~~said~~ the bacteriophage present in said bacteriophage composition 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.

25. The use of any of claims ~~15~~ 16 to ~~22~~18, wherein said ~~medicament~~ vaccine is to be administered in combination with a drug blocking an immune checkpoint.

~~23.~~26. The use of any of claims 20, 23 and 24, wherein said medicament is to be administered in combination with a drug blocking an immune checkpoint.

~~24.~~27. The use of any of claims 1 to ~~5~~ 6 and ~~9~~ 10 to ~~12~~13, or the use of any of claims ~~15~~ 16 to ~~22~~18, 20, 23 and 24, wherein the ~~tumor~~ cancer expresses mRNA levels of GPD1L superior to levels expressed in paired normal tissues.

~~25.~~28. 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 by incubating different concentrations of the drug candidates with 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, and measuring the phage excision at several time points of incubation.

~~26.~~29. 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.~~30. The method of claim ~~26~~29, 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.~~31. 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~~ 21 or claim ~~20~~ 22 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.~~32. The method of claim ~~28~~31, wherein the patient is HLA-A*0201 and the MHC multimer is as defined in claim ~~20~~23.

~~30.~~33. The method of any of claims ~~26~~ 29 to ~~29~~32, 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.~~34. 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.~~35. The method of any of claims ~~26~~ 29 to ~~30~~33, 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~~ 6 and ~~9~~ 10 to ~~12~~ 13 or an immunogenic composition as defined in any of claims ~~15~~ 16 to ~~17~~ 18 is to be administered to the patient to increase his/her response to the treatment by chemotherapy or immune checkpoint blockade.