

CLAIMS

1. A method for *in vitro* determining if an individual having a renal cell cancer (RCC) is likely to respond to a treatment with an immune checkpoint inhibitor (ICI)-based therapy, comprising the following steps:

- 5 (i) from a fecal sample of said individual, obtaining an abundances pattern based on the relative abundances of a set of bacterial species comprising at least 8 bacterial species selected from the group consisting of:

CAG number	Bacterial species
CAG00008	<i>Clostridium bolteae</i> ATCC BAA 613
CAG00013	<i>Clostridiales bacterium</i> 1_7_47FAA
CAG00037	<i>Bacteroides faecis</i> MAJ27
CAG00048_1	<i>Clostridium</i> sp_CAG 226
CAG00063	<i>Barnesiella viscericola</i> DSM 18177
CAG00122	<i>Coprococcus catus</i> GD 7
CAG00140	<i>Subdoligranulum</i> sp_4_3_54A2FAA
CAG00142	<i>Bacteroides stercoris</i> ATCC 43183
CAG00211	<i>Firmicutes bacterium</i> CAG 227
CAG00218	<i>Bacteroides</i> sp_CAG 20
CAG00243	<i>Lachnospiraceae bacterium</i> 1_1_57FAA
CAG00300	<i>Prevotella</i> sp_CAG 891
CAG00317	<i>Clostridium</i> sp_CAG 230
CAG00327	<i>Faecalibacterium</i> sp_CAG 74
CAG00341	<i>Eubacterium</i> sp_CAG 115
CAG00346	<i>Eubacterium rectale</i> M104_1
CAG00357	<i>Bacteroides ovatus</i> V975
CAG00413	<i>Bacteroides</i> sp_CAG 144
CAG00473	<i>Prevotella</i> sp_CAG 617
CAG00474	<i>Sutterella wadsworthensis</i> 2_1_59BFAA
CAG00487	<i>Prevotella</i> sp_CAG 279
CAG00508	<i>Alistipes obesi</i>
CAG00530	<i>Prevotella</i> sp_CAG 617
CAG00557	<i>Ruminococcus callidus</i> ATCC 27760
CAG00580	<i>Clostridium</i> sp_CAG 62
CAG00601	uncultured <i>Faecalibacterium</i> sp_
CAG00607	<i>Eubacterium</i> sp_CAG 251
CAG00610	<i>Hungatella hathewayi</i> 12489931
CAG00624	<i>Firmicutes bacterium</i> CAG 552
CAG00646	<i>Alistipes</i> sp_CAG 268
CAG00650	<i>Dorea formicigenerans</i> ATCC 27755
CAG00668	<i>Azospirillum</i> sp_CAG 239
CAG00669	<i>Firmicutes bacterium</i> CAG 103
CAG00676	<i>Firmicutes bacterium</i> CAG 176
CAG00698	<i>Ruminococcus</i> sp_CAG 177
CAG00713	<i>Firmicutes bacterium</i> CAG 270
CAG00720	<i>Anaerotruncus colihominis</i> DSM 17241

CAG00727	Eggerthella lenta DSM 2243
CAG00766	Firmicutes bacterium CAG 176
CAG00771	Clostridium sp CAG 413
CAG00782	Eubacterium rectale CAG 36
CAG00861	Oscillibacter sp CAG 241
CAG00873	Butyricimonas virosa DSM 23226
CAG00880	Subdoligranulum sp CAG 314
CAG00886	Sutterella sp CAG 351
CAG00889	Megasphaera elsdenii 14 14
CAG00897	Firmicutes bacterium CAG 83
CAG00919	Clostridium methylpentosum DSM 5476
CAG00928	Acidiphilium sp CAG 727
CAG00937	Clostridium sp CAG 7
CAG00963	Clostridium sp CAG 524
CAG01039	Faecalibacterium cf prausnitzii KLE1255
CAG01141	Holdemanella biformis DSM 3989
CAG01144	Lactobacillus vaginalis DSM 5837 ATCC 49540
CAG01158	Pseudoflavonifractor capillosus ATCC 29799
CAG01197	Dialister succinatiphilus YIT 11850
CAG01208	Coprococcus catus GD 7
CAG01263	Clostridium clostridioforme 2 1 49FAA
CAG01321	Faecalibacterium prausnitzii SL3 3

- (ii) using one or several pre-defined equations each corresponding to a model obtained for at least 8 bacterial species from said set of bacterial species, calculating the probability that said individual responds to the treatment (P_R) or the probability that said individual resists to the treatment (P_{NR}) with an ICI-based therapy.

wherein:

(a) when the individual's antibiotic regimen exposure during the last two months is unknown, one or more equations are used, selected from the group consisting of the equations described below for models 1.2, 2.2, 3.2, 7.2, 8.2 and 9.2, in which the equations for calculating the probability that said individual resists (P_{NR}) or responds (P_R) to the treatment are as follows:

$$[A] \ P_{NR} = 1 / [1 + \exp^{-(\sum_{j=1}^8 \beta_j X_j)}] \text{ for models 7.2, 8.2 and 9.2}$$

$$[B] \ P_R = 1 / [1 + \exp^{-(\sum_{j=1}^8 \beta_j X_j)}] \text{ for models 1.2, 2.2 and 3.2}$$

wherein X_j ($j = 1$ to 8) are the relative abundances of the bacterial species identified in the following table by their CAG numbers, measured in the individual's sample and β_j ($j = 1$ to 8) are the following regression coefficients:

Model 1.2		Model 2.2		Model 3.2	
<u>bacterial species</u>	<u>R coefficients</u>	<u>bacterial species</u>	<u>R coefficients</u>	<u>bacterial species</u>	<u>R coefficients</u>
<u>CAG00008</u>	<u>-1.0323</u>	<u>CAG00727</u>	<u>-1.0791</u>	<u>CAG00243</u>	<u>-1.1735</u>
<u>CAG01039</u>	<u>-1.084</u>	<u>CAG01141</u>	<u>-1.1164</u>	<u>CAG00473</u>	<u>-1.027</u>
<u>CAG00473</u>	<u>-0.9723</u>	<u>CAG00650</u>	<u>-1.2839</u>	<u>CAG00327</u>	<u>-0.9968</u>
<u>CAG00140</u>	<u>-0.9907</u>	<u>CAG00928</u>	<u>-1.1156</u>	<u>CAG01039</u>	<u>-1.0043</u>
<u>CAG00610</u>	<u>-0.6234</u>	<u>CAG00473</u>	<u>-1.014</u>	<u>CAG00140</u>	<u>-0.7456</u>
<u>CAG01141</u>	<u>-0.8468</u>	<u>CAG00122</u>	<u>-0.9394</u>	<u>CAG01263</u>	<u>-0.8736</u>
<u>CAG00413</u>	<u>0.8994</u>	<u>CAG01144</u>	<u>-0.8085</u>	<u>CAG00037</u>	<u>0.7032</u>
<u>CAG00317</u>	<u>0.6041</u>	<u>CAG00063</u>	<u>-0.7679</u>	<u>CAG00357</u>	<u>-0.6073</u>
Model 7.2		Model 8.2		Model 9.2	
<u>bacterial species</u>	<u>NR coefficients</u>	<u>bacterial species</u>	<u>NR coefficients</u>	<u>bacterial species</u>	<u>NR coefficients</u>
<u>CAG00782</u>	<u>-0.2034</u>	<u>CAG00211</u>	<u>0.6422</u>	<u>CAG00557</u>	<u>0.9341</u>
<u>CAG00013</u>	<u>0.4092</u>	<u>CAG00474</u>	<u>-1.0581</u>	<u>CAG00601</u>	<u>0.8927</u>
<u>CAG00873</u>	<u>0.2708</u>	<u>CAG00624</u>	<u>-0.8984</u>	<u>CAG00607</u>	<u>0.7108</u>
<u>CAG01141</u>	<u>0.7665</u>	<u>CAG00650</u>	<u>1.3189</u>	<u>CAG00669</u>	<u>-1.2341</u>
<u>CAG00668</u>	<u>-0.5899</u>	<u>CAG00676</u>	<u>-0.7324</u>	<u>CAG00861</u>	<u>1.0379</u>
<u>CAG00669</u>	<u>-0.5181</u>	<u>CAG00771</u>	<u>-0.6623</u>	<u>CAG00880</u>	<u>-1.0016</u>
<u>CAG00886</u>	<u>-0.8415</u>	<u>CAG01197</u>	<u>-1.1372</u>	<u>CAG00937</u>	<u>-0.872</u>
<u>CAG00889</u>	<u>-0.7339</u>	<u>CAG01321</u>	<u>-0.8525</u>	<u>CAG01321</u>	<u>-0.8362</u>

(b) when the individual did not take any antibiotic during the last two months, one or more equations are used, selected from the group consisting of the equations described below for models 4.2, 5.2, 6.2, 8.2, 9.2 and 10.2, in which the equations for calculating the probability that said individual resists (P_{NR}) or responds (P_R) to the treatment are as follows:

$$[A] \ P_{NR} = 1 / [1 + \exp^{-\left(\sum_{j=1}^8 \beta_j X_j\right)}] \text{ for models 4.2, 5.2 and 12.2}$$

$$[B] \ P_R = 1 / [1 + \exp^{-\left(\sum_{j=1}^8 \beta_j X_j\right)}] \text{ for models 6.2, 10.2 and 11.2}$$

wherein X_j ($j = 1$ to 8) are the relative abundances of the bacterial species identified in the following table by their CAG numbers, measured in the individual's sample and β_j ($j = 1$ to 8) are the following regression coefficients:

Model 4.2		Model 5.2		Model 6.2	
<u>bacterial species</u>	<u>NR coefficients</u>	<u>bacterial species</u>	<u>NR coefficients</u>	<u>bacterial species</u>	<u>R coefficients</u>
<u>CAG00008</u>	<u>0.955</u>	<u>CAG00048 1</u>	<u>0.7112</u>	<u>CAG00243</u>	<u>-1.2907</u>
<u>CAG01039</u>	<u>0.8761</u>	<u>CAG00300</u>	<u>0.8931</u>	<u>CAG00008</u>	<u>-0.8848</u>
<u>CAG00473</u>	<u>0.9951</u>	<u>CAG00473</u>	<u>1.0042</u>	<u>CAG00698</u>	<u>-0.9776</u>
<u>CAG00487</u>	<u>0.7609</u>	<u>CAG00650</u>	<u>1.1282</u>	<u>CAG00473</u>	<u>-0.9997</u>
<u>CAG00140</u>	<u>1.1107</u>	<u>CAG00720</u>	<u>1.2569</u>	<u>CAG00327</u>	<u>-1.0697</u>
<u>CAG01141</u>	<u>0.9402</u>	<u>CAG00727</u>	<u>1.2397</u>	<u>CAG01039</u>	<u>-0.7806</u>

<u>CAG01208</u>	<u>0.7187</u>	<u>CAG00963</u>	<u>0.7595</u>	<u>CAG00897</u>	<u>-0.8376</u>
<u>CAG00413</u>	<u>-0.5812</u>	<u>CAG01141</u>	<u>1.0235</u>	<u>CAG00766</u>	<u>-0.7459</u>
Model 7.2		Model 8.2		Model 9.2	
<u>bacterial species</u>	<u>NR coefficients</u>	<u>bacterial species</u>	<u>NR coefficients</u>	<u>bacterial species</u>	<u>NR coefficients</u>
<u>CAG00782</u>	<u>-0.2034</u>	<u>CAG00211</u>	<u>0.6422</u>	<u>CAG00557</u>	<u>0.9341</u>
<u>CAG00013</u>	<u>0.4092</u>	<u>CAG00474</u>	<u>-1.0581</u>	<u>CAG00601</u>	<u>0.8927</u>
<u>CAG00873</u>	<u>0.2708</u>	<u>CAG00624</u>	<u>-0.8984</u>	<u>CAG00607</u>	<u>0.7108</u>
<u>CAG01141</u>	<u>0.7665</u>	<u>CAG00650</u>	<u>1.3189</u>	<u>CAG00669</u>	<u>-1.2341</u>
<u>CAG00668</u>	<u>-0.5899</u>	<u>CAG00676</u>	<u>-0.7324</u>	<u>CAG00861</u>	<u>1.0379</u>
<u>CAG00669</u>	<u>-0.5181</u>	<u>CAG00771</u>	<u>-0.6623</u>	<u>CAG00880</u>	<u>-1.0016</u>
<u>CAG00886</u>	<u>-0.8415</u>	<u>CAG01197</u>	<u>-1.1372</u>	<u>CAG00937</u>	<u>-0.872</u>
<u>CAG00889</u>	<u>-0.7339</u>	<u>CAG01321</u>	<u>-0.8525</u>	<u>CAG01321</u>	<u>-0.8362</u>

2. The method of claim 1, wherein in step (ii), at least one equation corresponds to a model for a set of at least 8 bacterial species which are present in the fecal sample of said individual.

3. The method of claim 1 or claim 2, wherein the model(s) used in step (ii) lead to an individual probability percentage of at least 75% and/or to a predictability of at least 65% and a success rate of at least 70%.

4. The method of any of claims 1 to 3, which further comprises a step (iii) of assessing, in an animal model, whether the individual is likely to be a good responder to the treatment with an ICI-based therapy, wherein step (iii) comprises (iiia) performing a fecal microbial transplantation (FMT) of feces from the individual into a germ free (GF) model animal; (iiib) at least 7 to 14 days after step (iiia), inoculating said animal with a transplantable tumor model; (iiic) treating the inoculated animal with the ICI-based therapy; and (iiid) measuring the tumor size in the treated animals, wherein the results of step (iiid) are illustrative of the response that can be expected for said individual to said treatment.

~~5. The method of any of claims 1 to 4, wherein the individual's antibiotic regimen exposure during the last two months is unknown and wherein, in step (i), the set of bacterial species comprises at least 8 bacterial species selected from the group consisting of:~~

~~CAG-number~~	~~Bacterial species~~
~~CAG00008~~	~~Clostridium bolteae ATCC BAA_613~~
~~CAG00037~~	~~Bacteroides faecis MAJ27~~
~~CAG00063~~	~~Barnesiella viscericola DSM_18177~~

CAG00122	Coprococcus_catus_GD_7
CAG00140	Subdoligranulum_sp_4_3_54A2FAA-----NR
CAG00243	Lachnospiraceae_bacterium_1_1_57FAA
CAG00317	Clostridium_sp_CAG_230-----NR
CAG00327	Faecalibacterium_sp_CAG_74-----R
CAG00357	Bacteroides_ovatus_V975
CAG00413	Bacteroides_sp_CAG_144-----R
CAG00473	Prevotella_sp_CAG_617
CAG00610	Hungatella_hathewayi_12489931
CAG00650	Dorea_formicigenerans_ATCC_27755
CAG00727	Eggerthella_lenta_DSM_2243
CAG00928	Acidiphilium_sp_CAG_727
CAG01039	Faecalibacterium_cf_prausnitzii_KLE1255-----R
CAG01141	Holdemanella_biformis_DSM_3989
CAG01144	Lactobacillus_vaginalis_DSM_5837_ATCC_49540
CAG01263	Clostridium_clostridioforme_2_1_49FAA

6. The method of claim 5, wherein in step (ii), one, two or three equations are used, which correspond to models obtained for the following sets of bacterial species, identified by their CAG numbers:

set for model 1.2	set for model 2.2	set for model 3.2
CAG00008	CAG00727	CAG00243
CAG01039	CAG01141	CAG00473
CAG00473	CAG00650	CAG00327
CAG00140	CAG00928	CAG01039
CAG00610	CAG00473	CAG00140
CAG01141	CAG00122	CAG01263
CAG00413	CAG01144	CAG00037
CAG00317	CAG00063	CAG00357

and wherein preferably at least one equation used corresponds to a model obtained with a set of bacteria which are all present in the individual's sample.

7. The method of claim 6, wherein the equations for calculating the probability that said individual responds to the treatment (P_R) are as follows:

$$[B] \quad P_R = 1 / [1 + \exp^{-(\sum_{j=1}^8 \beta_j X_j)}]$$

wherein X_j ($j = 1$ to 8) are the relative abundances of the bacterial species measured in the individual's sample and β_j ($j = 1$ to 8) are the following regression coefficients:

Model 1.2		Model 2.2		Model 3.2	
bacterial species	R coefficients	bacterial species	R coefficients	bacterial species	R coefficients
CAG00008	-1.0323	CAG00727	-1.0791	CAG00243	-1.1735
CAG01039	-1.084	CAG01141	-1.1164	CAG00473	-1.027
CAG00473	-0.9723	CAG00650	-1.2839	CAG00327	-0.9968

CAG00140	-0.9907	CAG00928	-1.1156	CAG01039	-1.0043
CAG00610	-0.6234	CAG00473	-1.014	CAG00140	-0.7456
CAG01141	-0.8468	CAG00122	-0.9394	CAG01263	-0.8736
CAG00413	0.8994	CAG01144	-0.8085	CAG00037	0.7032
CAG00317	0.6041	CAG00063	-0.7679	CAG00357	-0.6073

8. The method of any of claims 1 to 4, wherein the individual did not take any antibiotic during the last two months and wherein, in step (i), the set of bacterial species comprises at least 8 bacterial species selected from the group consisting of:

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CAG-number	Bacterial species
CAG00008	Clostridium bolteae ATCC BAA 613
CAG00048_1	Clostridium sp CAG 226-----R
CAG00140	Subdoligranulum sp 4_3_54A2FAA-----NR
CAG00243	Lachnospiraceae bacterium 1_1_57FAA
CAG00300	Prevotella sp CAG 891-----R
CAG00327	Faecalibacterium sp CAG 74-----R
CAG00413	Bacteroides sp CAG 144-----R
CAG00473	Prevotella sp CAG 617
CAG00487	Prevotella sp CAG 279
CAG00650	Dorea formicigenerans ATCC 27755
CAG00698	Ruminococcus sp CAG 177-----R
CAG00720	Anaerotruncus colihominis DSM 17241
CAG00727	Eggerthella lenta DSM 2243
CAG00766	Firmicutes bacterium CAG 176-----R
CAG00897	Firmicutes bacterium CAG 83
CAG00963	Clostridium sp CAG 524
CAG01039	Faecalibacterium cf prausnitzii KLE1255-----R
CAG01141	Holdemanella biformis DSM 3989
CAG01208	Coprococcus catus GD 7

9. The method of claim 8, wherein in step (ii), one, two or three equations are used, which correspond to models obtained for the following sets of bacterial species, identified by their CAG numbers:

set for model 4.2	set for model 5.2	set for model 6.2
CAG00008	CAG00048_1	CAG00243
CAG01039	CAG00300	CAG00008
CAG00473	CAG00473	CAG00698
CAG00487	CAG00650	CAG00473
CAG00140	CAG00720	CAG00327
CAG01141	CAG00727	CAG01039
CAG01208	CAG00963	CAG00897
CAG00413	CAG01141	CAG00766

and wherein preferably at least one equation used corresponds to a model obtained with a set of bacteria which are all present in the individual's sample.

10. The method of claim 9, wherein the equations for calculating the probability that said individual resists (P_{NR}) or responds (P_R) to the treatment are as follows:

$$[A] \ P_{NR} = 1 / [1 + \exp^{\left(-\sum_{j=1}^8 \beta_j X_j\right)}] \text{ for models 4.2 and 5.2}$$

$$[B] \ P_R = 1 / [1 + \exp^{\left(-\sum_{j=1}^8 \beta_j X_j\right)}] \text{ for model 6.2}$$

wherein X_j ($j = 1$ to 8) are the relative abundances of the bacterial species measured in the individual's sample and β_j ($j = 1$ to 8) are the following regression coefficients:

Model 4.2		Model 5.2		Model 6.2	
bacterial species	NR coefficients	bacterial species	NR coefficients	bacterial species	R coefficients
CAG00008	0.955	CAG00048_1	0.7112	CAG00243	-1.2907
CAG01039	0.8761	CAG00300	0.8931	CAG00008	-0.8848
CAG00473	0.9951	CAG00473	1.0042	CAG00698	-0.9776
CAG00487	0.7609	CAG00650	1.1282	CAG00473	-0.9997
CAG00140	1.1107	CAG00720	1.2569	CAG00327	-1.0697
CAG01141	0.9402	CAG00727	1.2397	CAG01039	-0.7806
CAG01208	0.7187	CAG00963	0.7595	CAG00897	-0.8376
CAG00413	-0.5812	CAG01141	1.0235	CAG00766	-0.7459

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115. The method of any of claims 1 to 4, wherein the individual's antibiotic regimen exposure during the last two months is unknown and wherein one, two or three equations corresponding to models selected from the group consisting of models 7.2, 8.2 and 9.2 are used in step (ii) for determining if the individual is likely to have a long-term benefit

- 15 from a treatment with an ICI-based therapy, wherein the individual's antibiotic regimen exposure during the last two months is unknown and wherein, in step (i), the set of bacterial species comprises at least 8 bacterial species selected from the group consisting of:

CAG number	Bacterial species
CAG00013	Clostridiales_bacterium_1_7_47FAA
CAG00211	Firmicutes_bacterium_CAG_227
CAG00474	Sutterella_wadsworthensis_2_1_59BFAA
CAG00557	Ruminococcus_callidus_ATCC_27760
CAG00601	uncultured_Faecalibacterium_sp_
CAG00607	Eubacterium_sp_CAG_251
CAG00624	Firmicutes_bacterium_CAG_552
CAG00650	Dorea_formicigenerans_ATCC_27755
CAG00668	Azospirillum_sp_CAG_239

CAG00669	Firmicutes_bacterium_CAG_103
CAG00676	Firmicutes_bacterium_CAG_176
CAG00771	Clostridium_sp_CAG_413
CAG00782	Eubacterium_rectale_CAG_36
CAG00861	Oscillibacter_sp_CAG_241
CAG00873	Butyricimonas_virosa_DSM_23226
CAG00880	Subdoligranulum_sp_CAG_314
CAG00886	Sutterella_sp_CAG_351
CAG00889	Megasphaera_elsdenii_14_14
CAG00937	Clostridium_sp_CAG_7
CAG01141	Holdemanella_biformis_DSM_3989
CAG01197	Dialister_succinatiphilus_YIT_11850
CAG01321	Faecalibacterium_prausnitzii_SL3_3

12. The method of claim 11, wherein in step (ii), one, two or three equations are used, which correspond to models obtained for the following sets of bacterial species, identified by their CAG numbers:

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set for model 7.2	set for model 8.2	set for model 9.2
CAG00782	CAG00211	CAG00557
CAG00013	CAG00474	CAG00601
CAG00873	CAG00624	CAG00607
CAG01141	CAG00650	CAG00669
CAG00668	CAG00676	CAG00861
CAG00669	CAG00771	CAG00880
CAG00886	CAG01197	CAG00937
CAG00889	CAG01321	CAG01321

and wherein preferably at least one equation used corresponds to a model obtained with a set of bacteria which are all present in the individual's sample.

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13. The method of claim 12, wherein the equations for calculating the probability that said individual resists (P_{NR}) to the treatment are as follows:

$$[A] \ P_{NR} = 1 / [1 + \exp^{\left(\sum_{j=1}^8 \beta_j X_j \right)}]$$

wherein X_j ($j = 1$ to 8) are the relative abundances of the bacterial species measured in the individual's sample and β_j ($j = 1$ to 8) are the following regression coefficients:

Model 7.2		Model 8.2		Model 9.2	
bacterial species	NR coefficients	bacterial species	NR coefficients	bacterial species	NR coefficients
CAG00782	-0.2034	CAG00211	0.6422	CAG00557	0.9341
CAG00013	0.4092	CAG00474	-1.0581	CAG00601	0.8927
CAG00873	0.2708	CAG00624	-0.8984	CAG00607	0.7108
CAG01141	0.7665	CAG00650	1.3189	CAG00669	-1.2341
CAG00668	-0.5899	CAG00676	-0.7324	CAG00861	1.0379
CAG00669	-0.5181	CAG00771	-0.6623	CAG00880	-1.0016

CAG00886	-0.8415	CAG01197	-1.1372	CAG00937	-0.872
CAG00889	-0.7339	CAG01321	-0.8525	CAG01321	-0.8362

146. The method of any of claims 1 to 4, wherein the individual did not take any antibiotic during the last two months and wherein one, two or three equations corresponding to models selected from the group consisting of models 10.2, 11.2 and 12.2 are used in step (ii) for determining if the individual is likely to have a long-term benefit from a treatment with an ICI-based therapy, wherein the individual did not take any antibiotic during the last two months and wherein, in step (i), the set of bacterial species comprises at least 8 bacterial species selected from the group consisting of:

CAG number	Bacterial species
CAG00013	Clostridiales_bacterium_1_7_47FAA
CAG00142	Bacteroides_stercoris_ATCC_43183
CAG00218	Bacteroides_sp_CAG_20
CAG00341	Eubacterium_sp_CAG_115
CAG00346	Eubacterium_rectale_M104_1
CAG00474	Sutterella_wadsworthensis_2_1_59BFAA
CAG00508	Alistipes_obesi
CAG00530	Prevotella_sp_CAG_617
CAG00580	Clostridium_sp_CAG_62
CAG00601	uncultured_Faecalibacterium_sp_
CAG00607	Eubacterium_sp_CAG_251
CAG00646	Alistipes_sp_CAG_268
CAG00668	Azospirillum_sp_CAG_239
CAG00669	Firmicutes_bacterium_CAG_103
CAG00713	Firmicutes_bacterium_CAG_270
CAG00873	Butyricimonas_virosa_DSM_23226
CAG00880	Subdoligranulum_sp_CAG_314
CAG00886	Sutterella_sp_CAG_351
CAG00889	Megasphaera_elsdenii_14_14
CAG00919	Clostridium_methylpentosum_DSM_5476
CAG01141	Holdemanella_biformis_DSM_3989
CAG01158	Pseudoflavonifractor_capillosus_ATCC_29799
CAG01263	Clostridium_clostridioforme_2_1_49FAA
CAG01321	Faecalibacterium_prausnitzii_SL3_3

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15. The method of claim 14, wherein in step (ii), one, two or three equations are used, which correspond to models obtained for the following sets of bacterial species, identified by their CAG numbers:

set for model 10.2	set for model 11.2	set for model 12.2
CAG00580	CAG00346	CAG00142
CAG00013	CAG00530	CAG00218
CAG00873	CAG00601	CAG00341
CAG01141	CAG00607	CAG00474
CAG00668	CAG00646	CAG00508

CAG00669	CAG00713	CAG00880
CAG00886	CAG00919	CAG01263
CAG00889	CAG01158	CAG01321

and wherein preferably at least one equation used corresponds to a model obtained with a set of bacteria which are all present in the individual's sample.

- 5 ~~16.~~ The method of claim 15, wherein the equations for calculating the probability that said individual resists to the treatment (P_{NR}) or responds (P_R) are as follows:

$$[A] \ P_{NR} = 1 / [1 + \exp^{\left(-\sum_{j=1}^8 \beta_j X_j\right)}] \text{ for model 12.2}$$

$$[B] \ P_R = 1 / [1 + \exp^{\left(-\sum_{j=1}^8 \beta_j X_j\right)}] \text{ for models 10.2 and 11.2}$$

wherein X_j ($j = 1$ to 8) are the relative abundances of the bacterial species measured in the individual's sample and β_j ($j = 1$ to 8) are the following regression coefficients:

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Model 10.2		Model 11.2		Model 12.2	
bacterial species	R coefficients	bacterial species	R coefficients	bacterial species	NR coefficients
CAG00580	-0.1456	CAG00346	-0.8463	CAG00142	1.138
CAG00013	-0.5496	CAG00530	1.13	CAG00218	1.1396
CAG00873	-0.4646	CAG00601	-1.183	CAG00341	-1.0166
CAG01141	-0.5496	CAG00607	-0.9544	CAG00474	-0.8403
CAG00668	0.5684	CAG00646	0.8929	CAG00508	-0.7067
CAG00669	0.5129	CAG00713	1.0919	CAG00880	-1.185
CAG00886	0.6623	CAG00919	0.4881	CAG01263	0.8466
CAG00889	0.7102	CAG01158	1.1606	CAG01321	-0.8895

~~17.~~ The method of any of claims 1 to ~~16~~, wherein the fecal sample is obtained before the first administration of ICI.

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~~18.~~ The method of any of claims 1 to ~~17~~, wherein the ICI-based therapy is a treatment with an anti-PD1 antibody, an anti-PD-L1 antibody and/or an anti-PD-L2 antibody.

~~19.~~ The method of claim ~~18~~, wherein the ICI-based therapy is a treatment with an anti-PD1 antibody.

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~~2010.~~ A theranostic method for determining if a cancer patient needs a bacterial compensation before administration of an ICI-based therapy and/or during such a therapy, comprising assessing, by a method according to any of claims 1 to ~~19~~, whether

the patient is likely to be a good responder to such a therapy, wherein if the patient is not identified as likely to be a good responder, the patient needs a bacterial compensation.

5 ~~21. A nucleic acid microarray designed to perform the method according to any of claims 1 to 19, characterized in that it comprises nucleic acid probes specific for each of the microorganism species to be detected in said method.~~

10 ~~22. A set of primers for performing the method according to any of claims 1 to 19, characterized in that it comprises primer pairs for amplifying sequences specific for each of the microorganism species to be detected in said method.~~