

# Targeting the Microbiome & Optimizing Immunotherapy in Cancer

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Center

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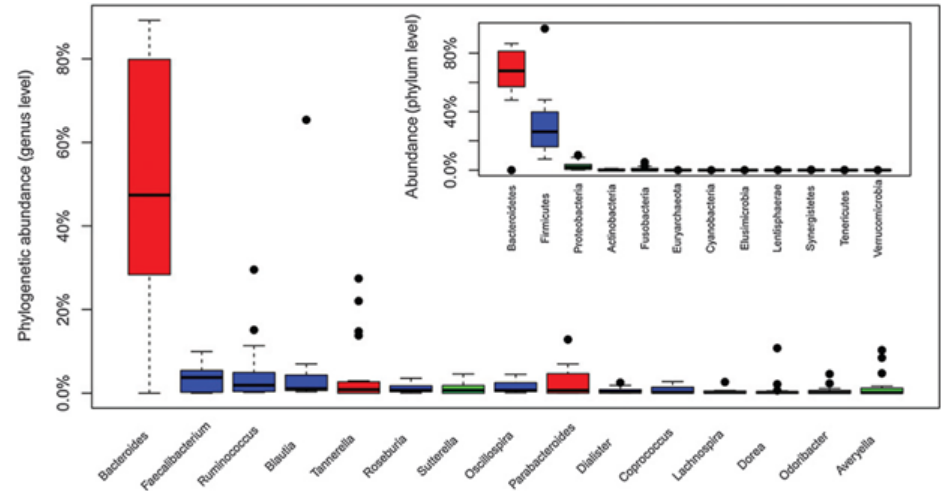
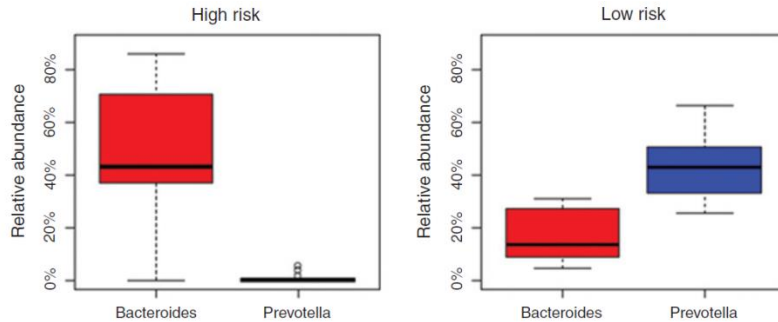


# Optimizing Sequencing: Targeting the Microbiome

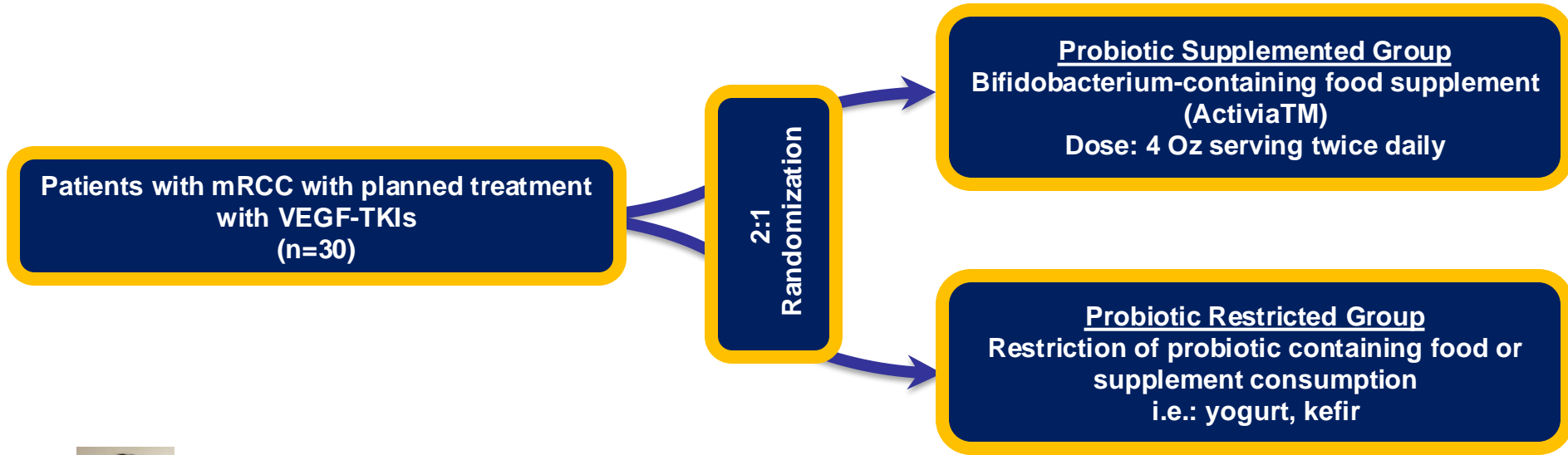


## Summary:

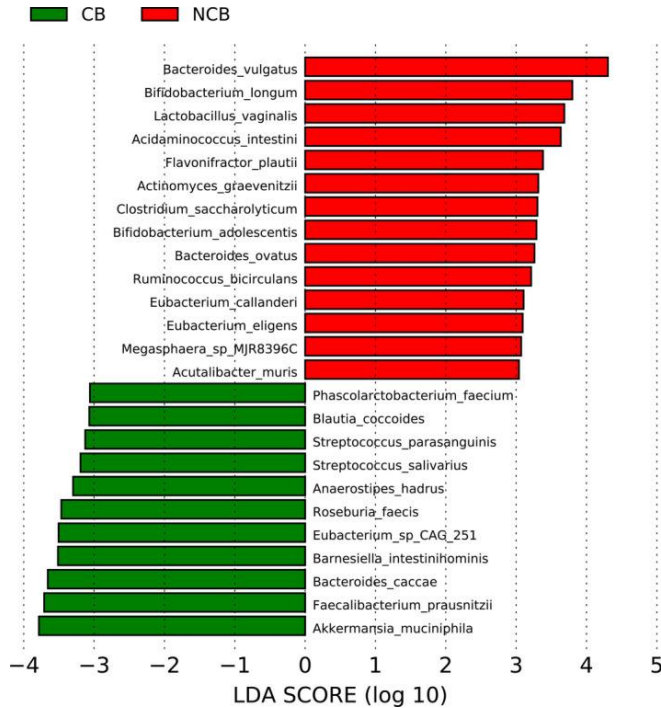
- 20 patients with mRCC
- Receiving VEGF-TKIs
- Median of 2 prior lines of therapy
- Objective: To determine association between bacteriomic profile and presence or absence of diarrhea



# Microbiome in Renal Cell Carcinoma

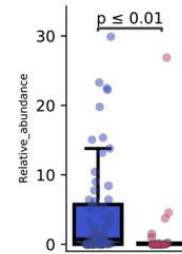


# Microbiome in Renal Cell Carcinoma

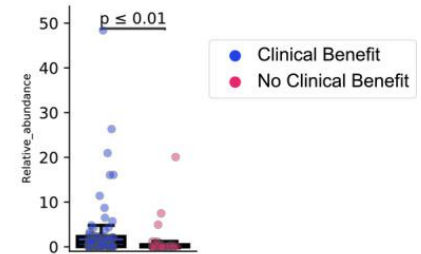


Dizman et al. Cancer Med 2020

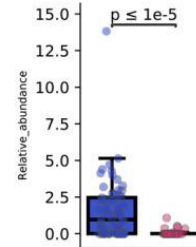
**Akkermansia\_muciniphila**



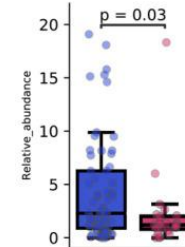
**Bacteroides\_caccae**



**Barnesiella\_intestinihominis**

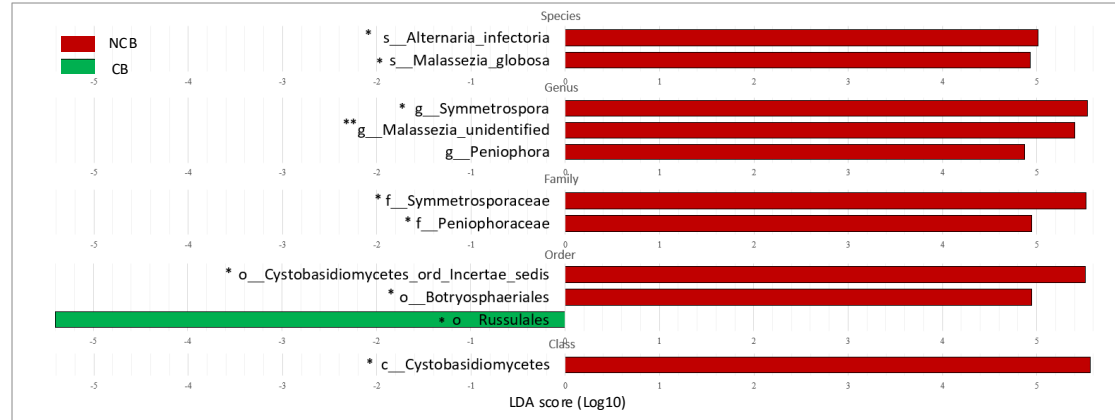
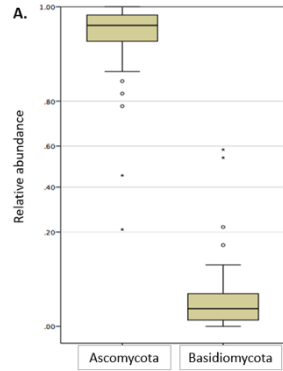


**Faecalibacterium\_prausnitzii**

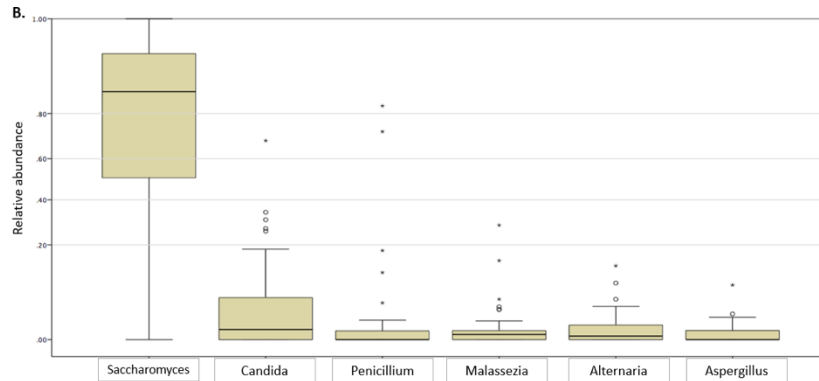


# Microbiome in Renal Cell Carcinoma

Fungal microbiome  
aka mycobiome  
in mRCC (n=24)



Dizman *et al.* ASCO GU Cancers Symposium 2020



# A Triumvirate of Key Papers in Science (January 2018)

RESEARCH

CANCER IMMUNOTHERAPY

## Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients

V. Gopalakrishnan,<sup>1,2,3</sup> C. N. Spencer,<sup>1,2,3</sup> L. Nish,<sup>2,3</sup> A. Redden,<sup>2,3</sup> M. C. Andrews,<sup>1</sup> E. V. Karjalainen,<sup>4</sup> P. A. Pielke,<sup>1</sup> D. Vignani,<sup>1</sup> K. Haffman,<sup>5</sup> S. C. Wei,<sup>1</sup> A. P. Coghill,<sup>1</sup> L. Zhao,<sup>6</sup> C. W. Hudgson,<sup>7</sup> D. S. Huhliksson,<sup>7</sup> T. Mizuno,<sup>8</sup> M. Petricola de Macedo,<sup>9</sup> F. Cotechiño,<sup>10</sup> F. Kassar,<sup>11</sup> W. S. Chen,<sup>12</sup> S. M. Reddy,<sup>13</sup> R. Sreerajapada Simons,<sup>14</sup> J. Galloway Pons,<sup>15</sup> H. Jiang,<sup>16</sup> P. L. Chen,<sup>17</sup> E. J. Shipton,<sup>18</sup> K. Rivard,<sup>19</sup> A. M. Alami,<sup>20</sup> E. F. Chomaly,<sup>21</sup> S. Skellern,<sup>22,23</sup> L. M. Young,<sup>24</sup> P. C. Okhoyen,<sup>25</sup> V. R. Jensen,<sup>26</sup> A. G. Swenson,<sup>27</sup> F. McAllister,<sup>28</sup> E. Marino Ripolles Sanchez,<sup>29</sup> Y. Zhang,<sup>30</sup> E. Le Chatelier,<sup>31</sup> L. Zitvogel,<sup>32</sup> N. Pons,<sup>33</sup> J. L. Austin Brimacombe,<sup>34</sup> L. E. Hayde,<sup>35</sup> E. M. Burton,<sup>36</sup> J. M. Gardner,<sup>37</sup> E. Srinivas,<sup>38</sup> J. He,<sup>39</sup> A. J. Lazar,<sup>40</sup> T. Tsujikawa,<sup>41</sup> A. Dlab,<sup>42</sup> H. Tanihi,<sup>43</sup> I. C. Gilboa,<sup>44</sup> W. J. Hwu,<sup>45</sup> S. P. Patel,<sup>46</sup> S. F. Woodman,<sup>47</sup> E. N. Amaral,<sup>48</sup> M. A. Davies,<sup>49</sup> J. E. Gordonswald,<sup>50</sup> P. Hwu,<sup>51</sup> J. E. Lee,<sup>52</sup> J. Zhang,<sup>53</sup> L. M. Commins,<sup>54</sup> K. A. Cooper,<sup>55</sup> P. A. Forstal,<sup>56</sup> C. R. DuHadway,<sup>57</sup> N. J. Ajami,<sup>58</sup> J. F. Petrosino,<sup>59</sup> M. T. Tetzlaff,<sup>60</sup> P. Sharma,<sup>61</sup> J. P. Allison,<sup>2</sup> E. B. Jang,<sup>3</sup> & J. A. Wargo<sup>1,2,3\*</sup>

Preclinical mouse models suggest that the gut microbiome modulates tumor response to checkpoint blockade immunotherapy. However, this has not been well characterized in human cancer patients. Here we examined the oral and gut microbiome of melanoma patients undergoing anti-programmed cell death 1 protein (PD-1) immunotherapy (n = 122). Significant differences were observed in the diversity and composition of the patient gut microbiome of responders versus nonresponders. Analysis of patient fecal microbiome samples (n = 43, 30 responders, 13 nonresponders) showed significantly higher alpha diversity (P < 0.01) and relative abundance of bacteria of the Luminococcaceae family (P < 0.01) in responding patients. Metagenomic studies revealed functional differences in gut bacteria in responders, including enrichment of antibiotic pathways. Immune profiling suggested enhanced systemic and antitumor immunity in responding patients with a favorable gut microbiome as well as in germ-free mice receiving fecal transplants from responding patients. Together, these data have important implications for the treatment of melanoma patients with immune checkpoint inhibitors.

RESEARCH

CANCER IMMUNOTHERAPY

## Gut microbiome influences efficacy of PD-1-based immunotherapy against epithelial tumors

Bertrand Routy,<sup>1,2,3</sup> Emmanuelle Le Chatelier,<sup>4</sup> Lisa Deroose,<sup>1,2,3</sup> Connie P. M. Duong,<sup>1,2,3</sup> Maryam Tadjali Alen,<sup>1,2,3</sup> Romain Ducloux,<sup>1,2,3</sup> Aurélie Fluckiger,<sup>1,2,3</sup> Mervien Mestanzano,<sup>1,2</sup> Conrad Rauben,<sup>1,2,3</sup> Maria F. Robert,<sup>1,2,3</sup> Marline Flahelle,<sup>1,2,3</sup> Caroline Flament,<sup>1,2,3</sup> Yichoua Polier-Colame,<sup>1,2,3</sup> Pauline Opolons,<sup>4</sup> Christophe Klein,<sup>5</sup> Kristina Iribarren,<sup>6,7,8,9,10,11</sup> Laura Monedragin,<sup>12,13,14</sup> Nicolas Jarquiel,<sup>1,2,3</sup> Bo Qiu,<sup>1,2,3</sup> Gladys Ferrere,<sup>1,2,3</sup> Céline Clémenson,<sup>1,2,3</sup> Laura Menquillo,<sup>1,2</sup> Jordi Remon Manó,<sup>1,2</sup> Charles Nabot,<sup>15</sup> Sofiane Brasseur,<sup>16</sup> Cécile Kaderofthal,<sup>17</sup> Corentin Richard,<sup>18</sup> Hira Rizvi,<sup>17</sup> Florence Lecomte,<sup>4</sup> Nathalie Galleron,<sup>4</sup> Benoît Quispel,<sup>4</sup> Nicolas Pons,<sup>19</sup> Bernhard Ryffel,<sup>20</sup> Véronique Minard-Colin,<sup>1,2</sup> Patrick Gosin,<sup>1,2</sup> Jean Charles Soria,<sup>1,2</sup> Eric Deutsch,<sup>1,2,3</sup> Yohann Lacroix,<sup>1,2</sup> François Ghiringhelli,<sup>21</sup> Gérard Zalcman,<sup>22</sup> François Gobet,<sup>23,24</sup> Bernard Escudier,<sup>1,2,3,25</sup> Matthew D. Hellmann,<sup>26,27</sup> Alexander Eggerston,<sup>1,2,3</sup> Didier Raouf,<sup>28</sup> Laurence Allibert,<sup>1,2,3</sup> Guido Kroemer,<sup>1,2,3,29,30,31,32,33</sup> Laurence Zitvogel<sup>1,2,3,34</sup>

Immune checkpoint inhibitors (ICIs) targeting the PD-1/PD-L1 axis induce sustained clinical responses in a sizable minority of cancer patients. We found that primary resistance to ICIs can be attributed to abnormal gut microbiome composition. Antibiotic inhibited the clinical benefit of ICIs in patients with advanced cancer. Fecal microbiota transplantation (FMT) from cancer patients who responded to ICIs into germ-free or antibiotic-treated mice ameliorated the antitumor effects of PD-1 blockade, whereas FMT from nonresponding patients failed to do so. Metagenomics of patient stool samples at diagnosis revealed correlations between clinical responses to ICIs and the relative abundance of *Akkermansia muciniphila*. Oral supplementation with *A. muciniphila* after FMT with nonresponding feces restored the efficacy of PD-1 blockade in an interleukin 12-dependent manner by increasing the recruitment of CCR9<sup>+</sup>CXCR3<sup>+</sup>CD4<sup>+</sup> T lymphocytes into mouse tumor beds.

RESEARCH

CANCER IMMUNOTHERAPY

## The commensal microbiome is associated with anti-PD-1 efficacy in metastatic melanoma patients

Vyara Matveev,<sup>1</sup> Jessica Froder,<sup>2</sup> Rhye Han,<sup>3,4</sup> Tara Chongswat,<sup>4</sup> Yueshan Zhu,<sup>4</sup> Maria Luisa Alegre,<sup>4</sup> Jason J. Luke,<sup>4</sup> Thomas F. Gajewski<sup>1,4,5</sup>

Anti-PD-1-based immunotherapy has had a major impact on cancer treatment but has only benefited a subset of patients. Among the variables that could contribute to interpatient heterogeneity is differential composition of the patients' microbiome, which has been shown to affect antitumor immunity and immunotherapy efficacy in preclinical murine models. We analyzed baseline stool samples from metastatic melanoma patients before immunotherapy treatment, through an integration of 16S ribosomal RNA gene sequencing, metagenomic shotgun sequencing, and quantitative polymerase chain reaction for selected bacteria. A significant association was observed between commensal microbial composition and clinical response. Bacterial species more abundant in responders included *Bifidobacterium longum*, *Collinsella aerofaciens*, and *Enterococcus faecium*. Reconstitution of germ-free mice with fecal material from responding patients could lead to improved tumor control, augmented T cell responses, and greater efficacy of anti-PD-1 therapy. Our results suggest that the commensal microbiome may have a mechanistic impact on antitumor immunity in human cancer patients.

Three papers linking gut microbiome to outcome with PD-1 inhibitors.

# A Triumvirate of Key Papers in Science (January 2018)

RESEARCH

CANCER IMMUNOTHERAPY

## Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients

V. Gopalakrishnan,<sup>1</sup> L. V. Reddy,<sup>1</sup> L. Zhao,<sup>1</sup> F. Collier,<sup>1</sup> J. Gallardo,<sup>1</sup> K. F. Chan,<sup>1</sup> A. G. Srinivasan,<sup>1</sup> E. Le Chatelier,<sup>1</sup> E. M. Bertram,<sup>1</sup> S. Dhillon,<sup>1</sup> R. N. Amaral,<sup>1</sup> M. N. Arora,<sup>1</sup> F. A. Fretwell,<sup>1</sup> C. R. Daniel,<sup>1</sup> N. J. Ajani,<sup>1</sup> I. F. Petrosini,<sup>1</sup> M. T. Tetzlaff,<sup>1</sup> P. Sharma,<sup>1</sup> J. P. Allison,<sup>1</sup> E. B. Jang,<sup>1</sup> J. A. Wargo<sup>1,2,3\*</sup>

**Disease Type:**  
Melanoma

**Bacteria implicated in response:**  
*Ruminococcaceae*

Preclinical mouse models suggest that the gut microbiome modulates tumor response to checkpoint blockade immunotherapy; however, this has not been well characterized in human cancer patients. Here we examined the oral and gut microbiome of melanoma patients undergoing anti-programmed cell death 1 protein (PD-1) immunotherapy (n = 122). Significant differences were observed in the diversity and composition of the patient gut microbiome of responders versus nonresponders. Analysis of patient fecal microbiome samples (n = 43, 30 responders, 13 nonresponders) showed significantly higher alpha diversity (P < 0.05) and relative abundance of bacteria of the Ruminococcaceae family (P < 0.05) in responding patients. Metagenomic studies revealed functional differences in gut bacteria in responders, including enrichment of antibiotic pathways. Immune profiling suggested enhanced systemic and antitumor immunity in responding patients with a favorable gut microbiome as well as in germ-free mice receiving fecal transplants from responding patients. Together, these data have important implications for the treatment of melanoma patients with immune checkpoint inhibitors.

RESEARCH

CANCER IMMUNOTHERAPY

## Microbiome Modulates the Efficacy of Immune Checkpoint Inhibitors in Lung and Kidney Cancer

Bertrand B. de Lencastre,<sup>1</sup> Connie P. V. de Bont,<sup>1</sup> Aurélie Fleury,<sup>1</sup> Marline Fidi,<sup>1</sup> Christophe L. M. de Boer,<sup>1</sup> Nicolas J. de Boer,<sup>1</sup> Laura M. de Boer,<sup>1</sup> Constanze K. de Boer,<sup>1</sup> Nathalie G. de Boer,<sup>1</sup> Vitorique Minard-Colin,<sup>1,2</sup> Patrick Goslé,<sup>1,2</sup> Jean-Charles Sorio,<sup>1,2</sup> Eric Deutsch,<sup>1,2</sup> Yohann Lécot,<sup>1,2,3</sup> François Ghiringhelli,<sup>4</sup> Gérard Zalcman,<sup>5</sup> François Goldwasser,<sup>6,7,8</sup> Bernard Escudier,<sup>1,2,9</sup> Matthew D. Hellmann,<sup>10,11</sup> Alexander Eggensmeier,<sup>12,13</sup> Didier Raouf,<sup>14</sup> Laurence Abigun,<sup>15,16</sup> Guido Kroemer,<sup>17,18,19,20,21</sup> Laurence Zitvogel<sup>22,23,24</sup>

**Disease Type:**  
Lung/Kidney Cancer

**Bacteria implicated in response:**  
*Akkermansia*

Immune checkpoint inhibitors (ICIs) targeting the PD-1/PD-L1 axis induce sustained clinical responses in a sizable minority of cancer patients. We found that primary resistance to ICIs can be attributed to abnormal gut microbiome composition. Antibiotic inhibition of the clinical benefit of ICIs in patients with advanced cancer. Fecal microbiota transplantation (FMT) from cancer patients who responded to ICIs into germ-free or antibiotic-treated mice ameliorated the antitumor effects of PD-1 blockade, whereas FMT from nonresponding patients failed to do so. Metagenomics of patient stool samples at diagnosis revealed correlations between clinical responses to ICIs and the relative abundance of *Akkermansia muciniphila*. Oral supplementation with *A. muciniphila* after FMT with nonresponder feces restored the efficacy of PD-1 blockade in an interleukin 12-dependent manner by increasing the recruitment of CCR9<sup>+</sup> CXCR3<sup>+</sup> CD4<sup>+</sup> T lymphocytes into mouse tumor beds.

RESEARCH

CANCER IMMUNOTHERAPY

## The composition of the gut microbiome is associated with response to anti-PD-1 immunotherapy in melanoma patients

Yiyan Ma,<sup>1</sup> Maria Laha,<sup>1</sup> ...

**Disease Type:**  
Melanoma

**Bacteria implicated in response:**  
*Bifidobacterium*

Anti-PD-1 immunotherapy has shown promising clinical outcomes in melanoma patients. However, the mechanism of response remains unclear. Here we performed a mechanistic study of the gut microbiome in melanoma patients before and after immunotherapy. We found that the gut microbiome composition is associated with response to anti-PD-1 immunotherapy. A significant association was observed between commensal microbial composition and clinical response. Bacterial species more abundant in responders included *Bifidobacterium longum*, *Collinsella aerofaciens*, and *Enterococcus faecium*. Reconstitution of germ-free mice with fecal material from responding patients could lead to improved tumor control, augmented T cell responses, and greater efficacy of anti-PD-1 therapy. Our results suggest that the commensal microbiome may have a mechanistic impact on antitumor immunity in human cancer patients.

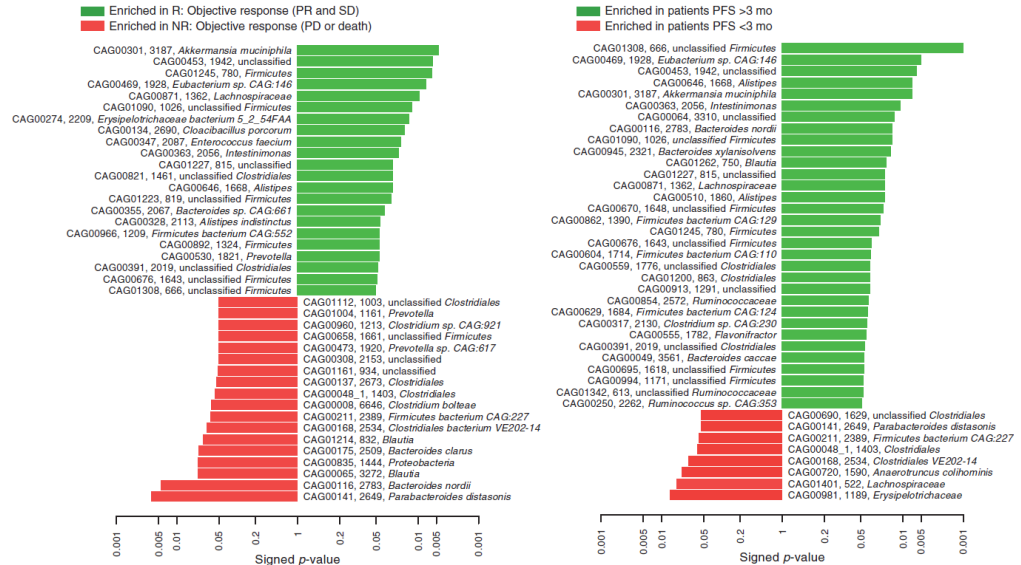
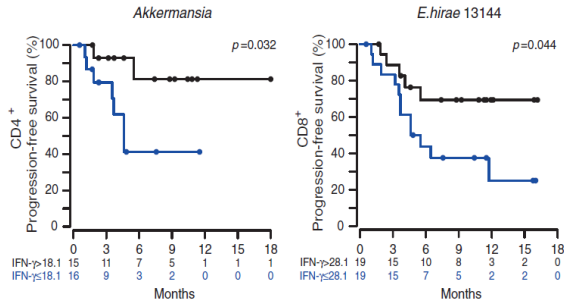
Three papers linking gut microbiome to outcome with PD-1 inhibitors.

# Microbiome in Renal Cell Carcinoma



## Summary:

- 60 pts with NSCLC
- 40 pts with RCC
- Baseline and serial stool collections after checkpoint inhibitor initiated
- Specific bacterial species associated with response



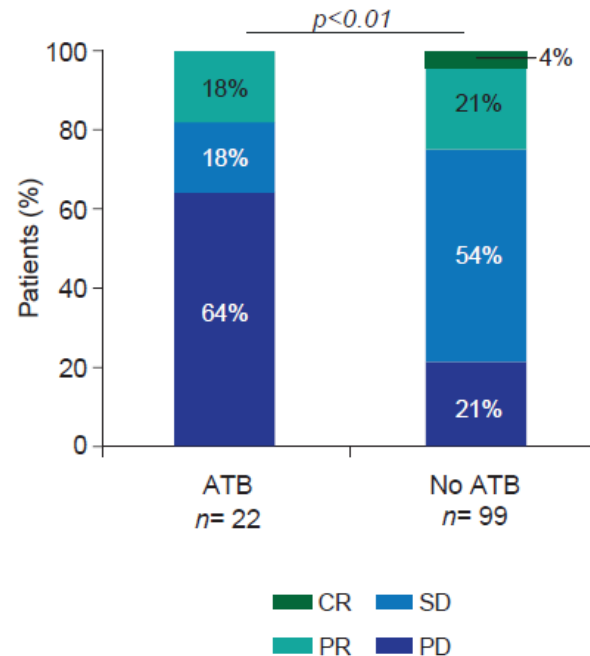
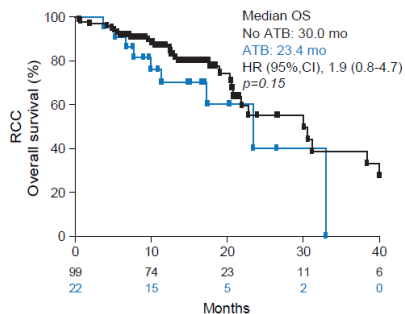
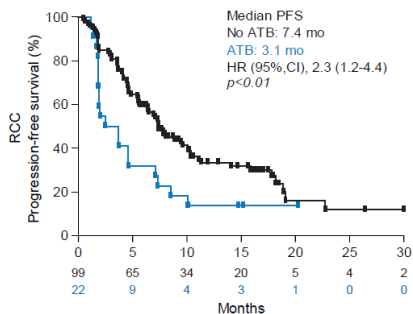


# Microbiome in Renal Cell Carcinoma

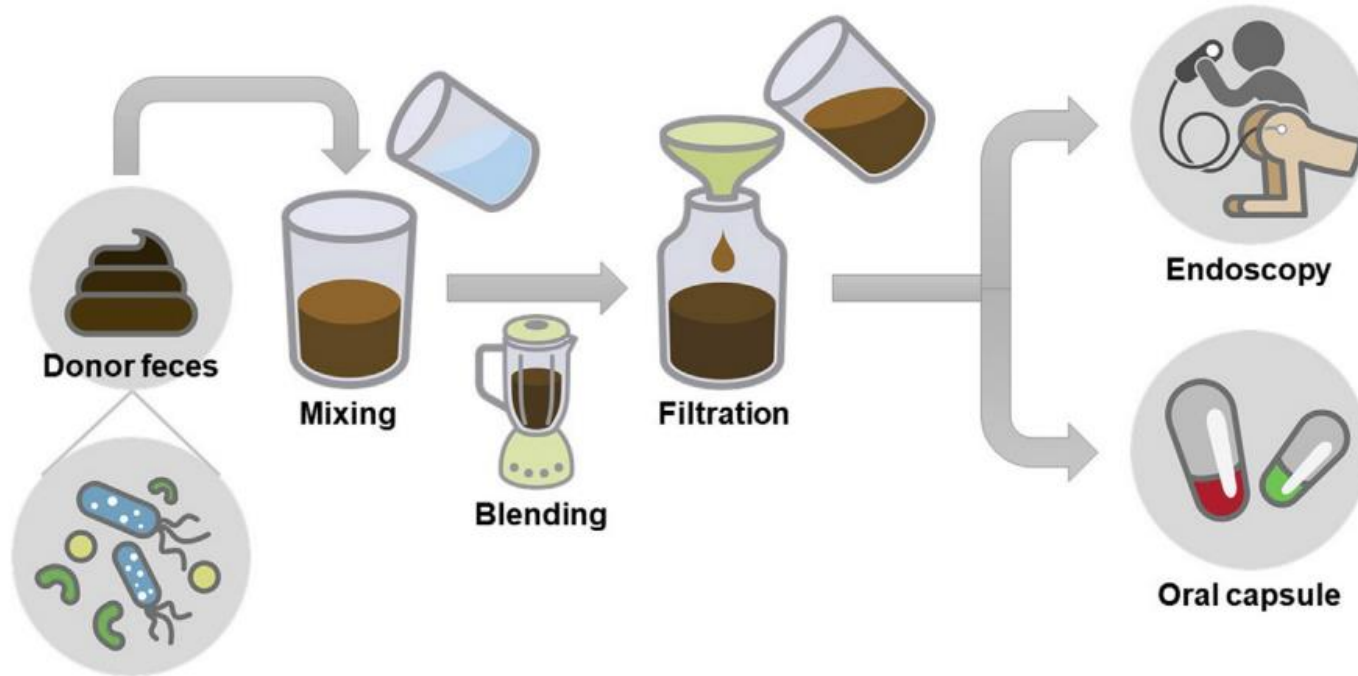


## Summary:

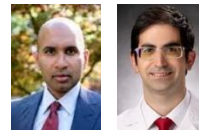
- 121 pts with RCC
- 239 pts with NSCLC
- Antibiotic use associated with inferior outcome in pts receiving checkpoint inhibitors
- Similar trends in NSCLC and RCC pts



# Modulating the Microbiome: Fecal Microbiome Transplant (FMT)



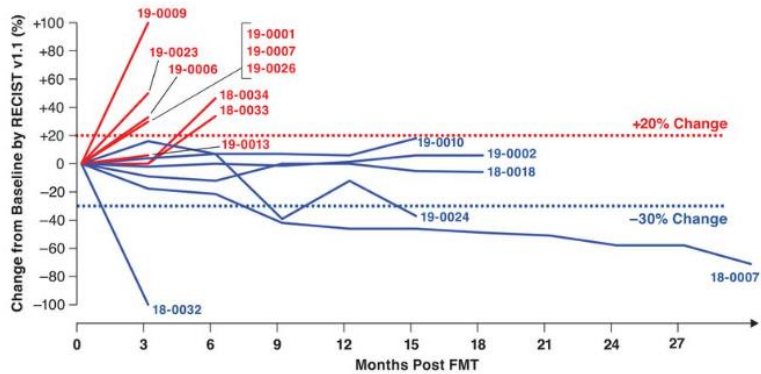
# Modulating the Microbiome: Fecal Microbiome Transplant (FMT)



Primary progression on PD-1 inhibitor for melanoma



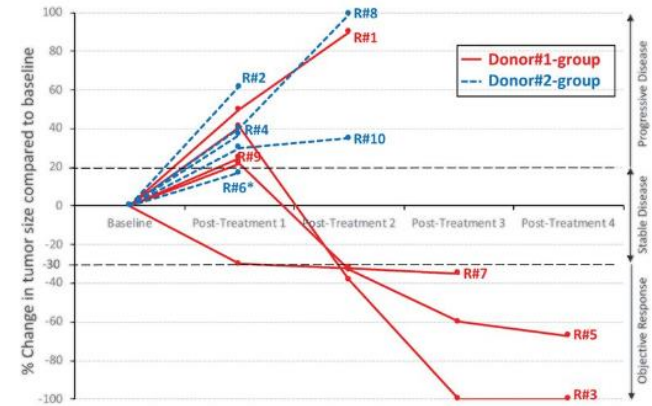
Rechallenge with PD-1 inhibitor + FMT from responder



Progression on PD-1 inhibitor for melanoma



Rechallenge with PD-1 inhibitor + FMT from responder



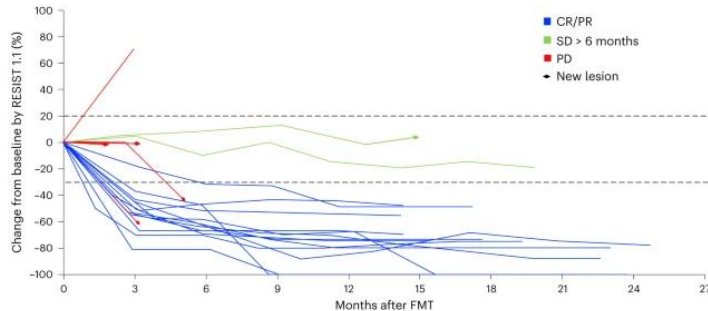
# Modulating the Microbiome: Fecal Microbiome Transplant (FMT)



Treatment naïve advanced melanoma



PD-1 inhibitor + Healthy Donor FMT

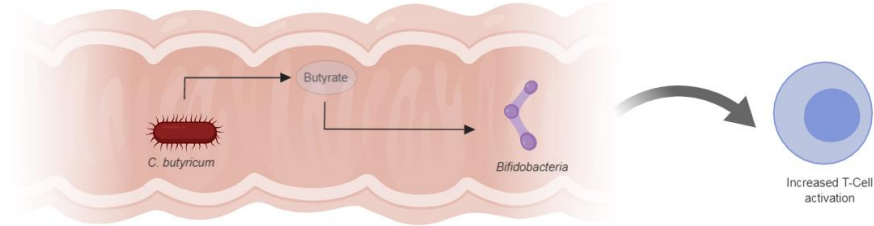


Challenges to FMT

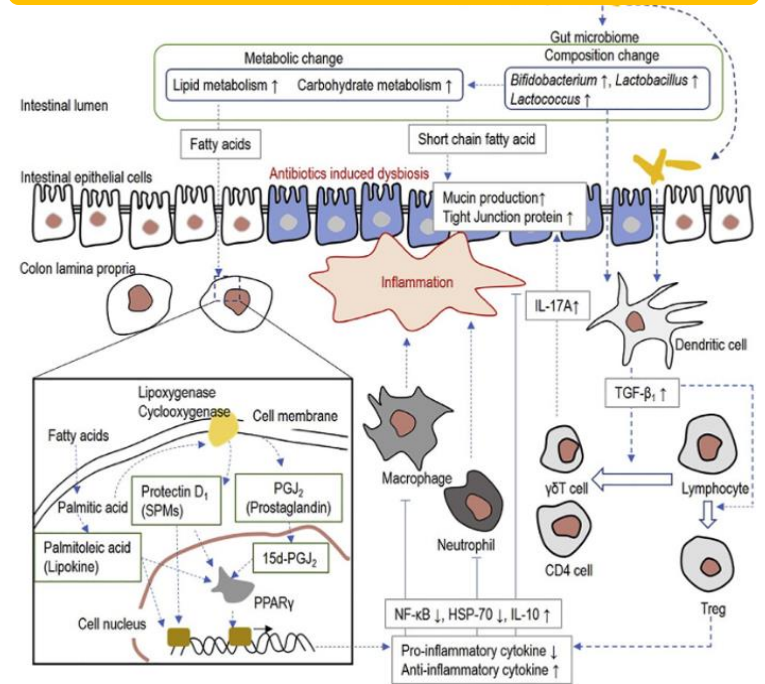
- Requires substantial resources/ infrastructure
- Challenging to ensure sourcing and consistency of product
- Potential safety risks (e.g., pathogenic transmission)
- Unknown what optimal FMT product constitutes (e.g., healthy donor or responder?)

# Modulating the Microbiome: Live Bacterial Products

## Simple



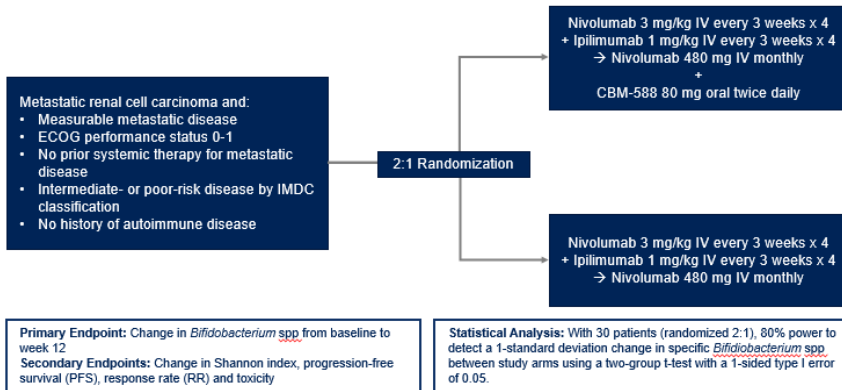
## Complicated



# Modulating the Microbiome: Live Bacterial Products

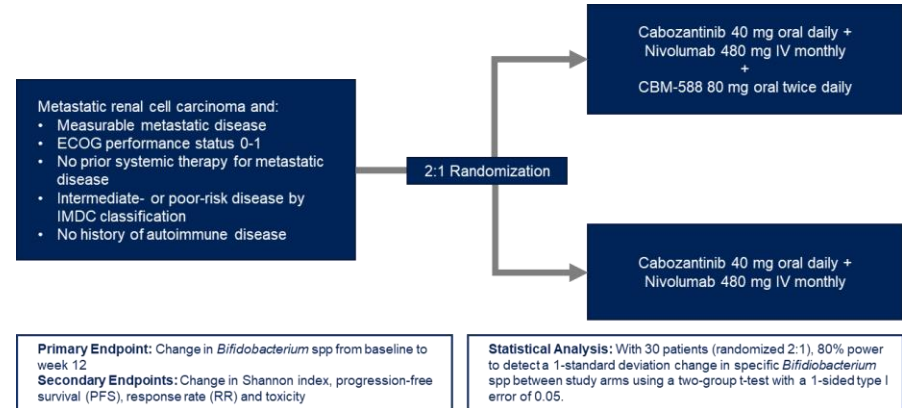


## Nivolumab/Ipilimumab +/- CBM588



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## Cabozantinib/Nivolumab +/- CBM588

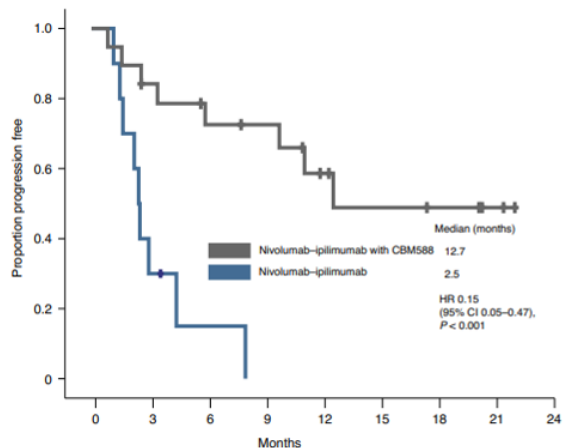


Ebrahimi *et al*/ Nature Medicine 2024

# Modulating the Microbiome: Live Bacterial Products



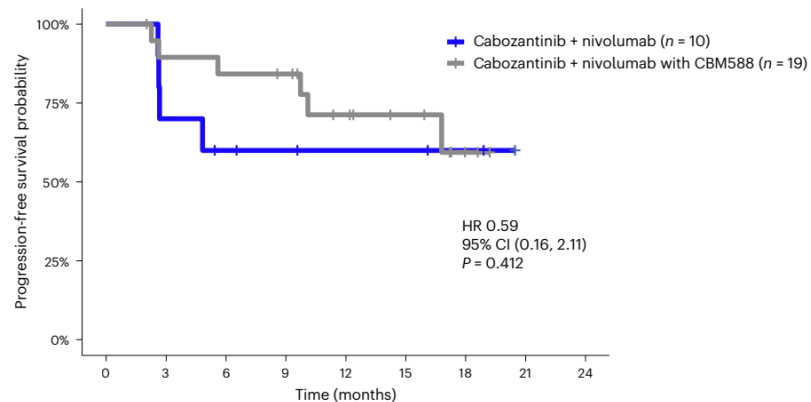
## Nivolumab/Ipilimumab +/- CBM588



Number at risk	0	3	6	9	12	15	18	21	24
Nivo-ipi-CBM588	19	15	12	11	7	5	4	2	0
Nivo-ipi	10	3	1	0	0	0	0	0	0

Dizman *et al* Nature Medicine 2022

## Cabozantinib/Nivolumab +/- CBM588



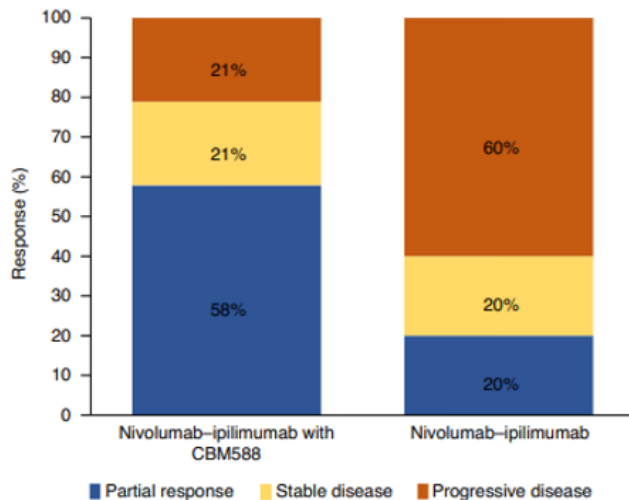
Number at risk	0	3	6	9	12	15	18	21	24
Cabozantinib + nivolumab	10	7	5	4	3	3	2	0	0
Cabozantinib + nivolumab + CBM588	20	17	16	15	10	7	2	0	0

Ebrahimi *et al* Nature Medicine 2024

# Modulating the Microbiome: Live Bacterial Products

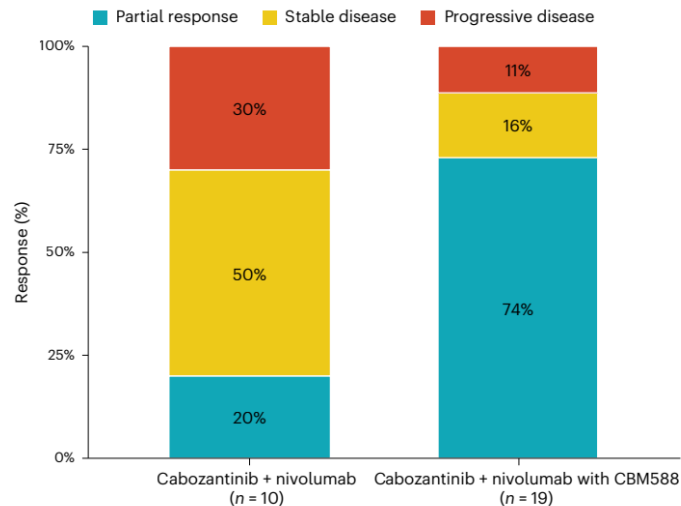


## Nivolumab/Ipilimumab +/- CBM588



Dizman *et al* / Nature Medicine 2022

## Cabozantinib/Nivolumab +/- CBM588



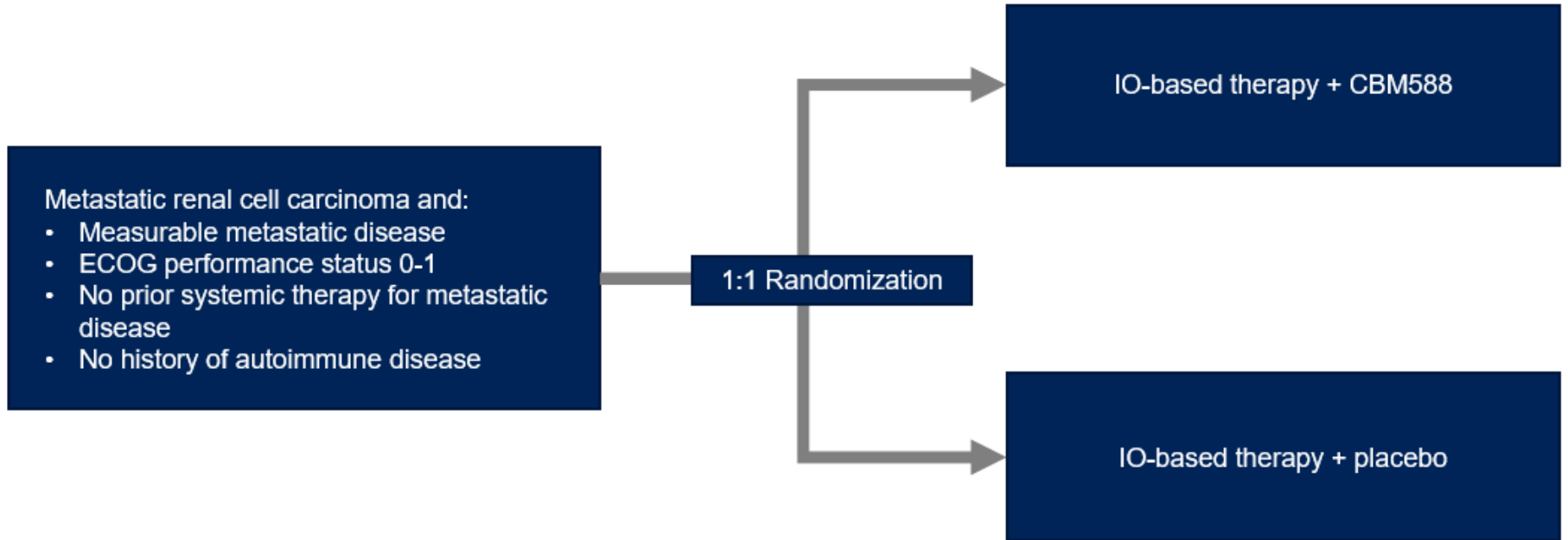
Ebrahimi *et al* / Nature Medicine 2024



# Modulating the Microbiome: Live Bacterial Products



## SWOG Proposal: A Definitive Study Assessing CBM588



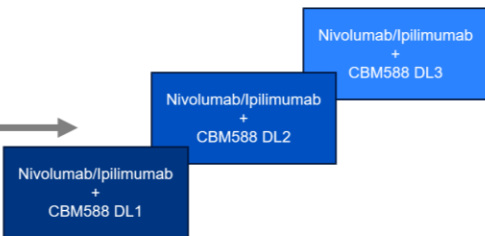
PIs: Barata/Pal/Vaishampayan

# Ongoing Microbiome/RCC Studies at City of Hope



## Nivolumab/ipilimumab + CBM588

- Metastatic renal cell carcinoma and:
- Measurable metastatic disease
  - ECOG performance status 0-1
  - No prior systemic therapy for metastatic disease
  - Intermediate- or poor-risk disease by IMDC classification
  - No history of autoimmune disease

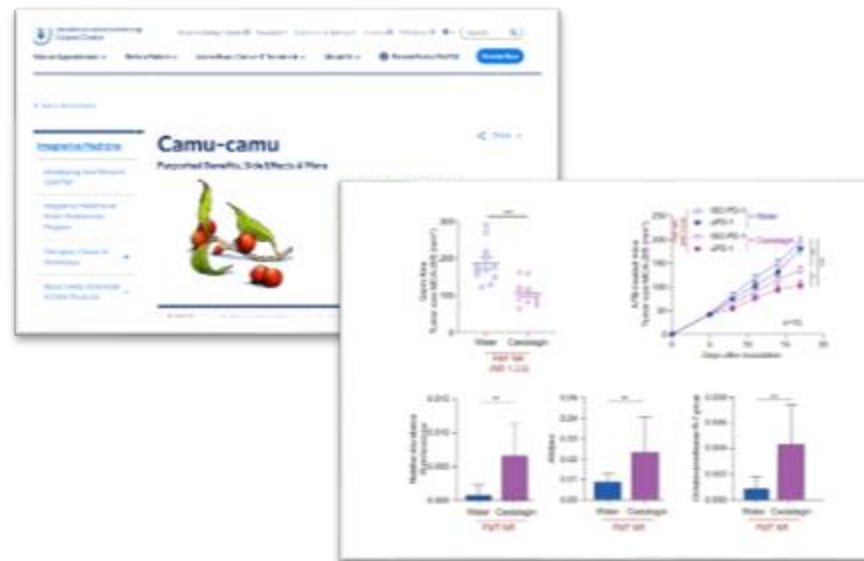


**Primary Endpoint:** Safety of novel CBM588 formulation  
**Secondary Endpoints:** Change in Shannon index, progression-free survival (PFS), response rate (RR) and toxicity

**Statistical Analysis:** Classical 3+3 design

PI: Alexander Chehrazi-Raffle, MD

## Nivolumab/ipilimumab +/- Camu Camu



PI: Regina Barragan-Carrillo, MD

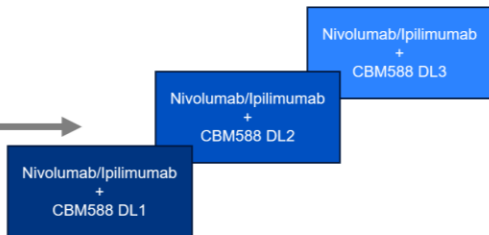


# Ongoing Microbiome/RCC Studies at City of Hope



## Nivolumab/Ipilimumab + CBM588

- Metastatic renal cell carcinoma and:
- Measurable metastatic disease
  - ECOG performance status 0-1
  - No prior systemic therapy for metastatic disease
  - Intermediate- or poor-risk disease by IMDC classification
  - No history of autoimmune disease



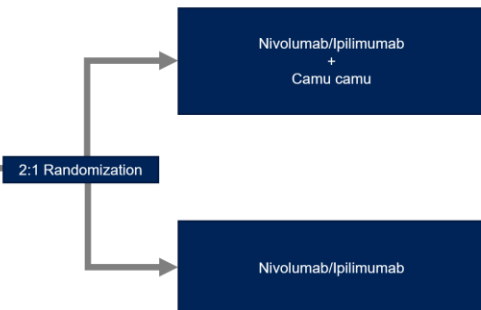
**Primary Endpoint:** Safety of novel CBM588 formulation  
**Secondary Endpoints:** Change in Shannon index, progression-free survival (PFS), response rate (RR) and toxicity

**Statistical Analysis:** Classical 3+3 design

PI: Alexander Chehrazi-Raffle, MD

## Nivolumab/Ipilimumab +/- Camu Camu

- Metastatic renal cell carcinoma and:
- Measurable metastatic disease
  - ECOG performance status 0-1
  - No prior systemic therapy for metastatic disease
  - Intermediate- or poor-risk disease by IMDC classification
  - No history of autoimmune disease

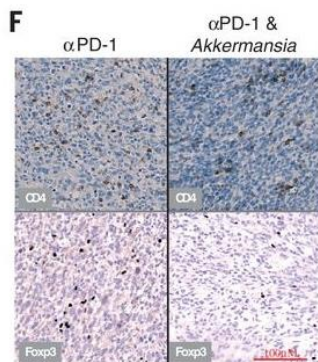
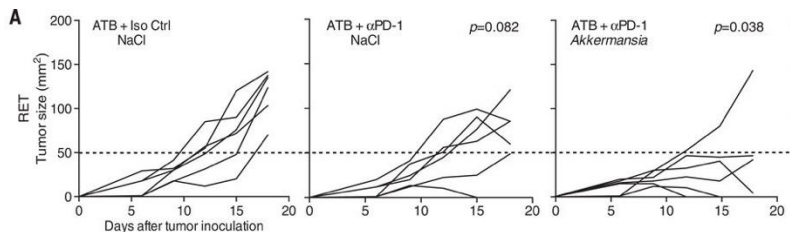


**Primary Endpoint:** Change in *Ruminococcus* spp from baseline to week 12  
**Secondary Endpoints:** Change in Shannon index, progression-free survival (PFS), response rate (RR) and toxicity

**Statistical Analysis:** With 30 patients (randomized 2:1), 80% power to detect a 1-standard deviation change in specific *Ruminococcus* spp between study arms using a two-group t-test with a 1-sided type I error of 0.05.

PI: Regina Barragan-Carrillo, MD

# On the Horizon: Oncobax AK



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## A Study of Oncobax®-AK in Patients With Advanced Solid Tumors

The safety and scientific validity of this study is the responsibility of the study sponsor and investigators. Listing a study does not mean it has been evaluated by the U.S. Federal Government. [Know the risks and potential benefits](#) of clinical studies and talk to your health care provider before participating. Read our [disclaimer](#) for details.

ClinicalTrials.gov Identifier: NCT05885730

Recruitment Status : Recruiting

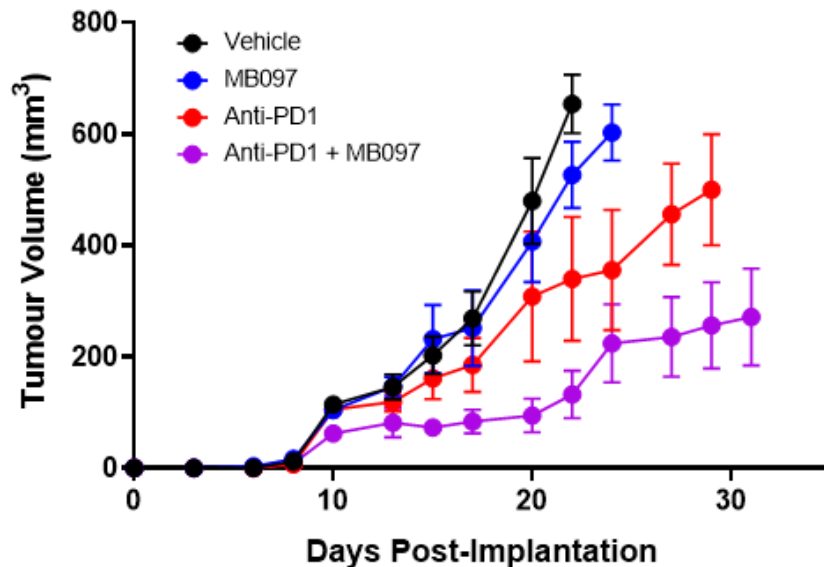
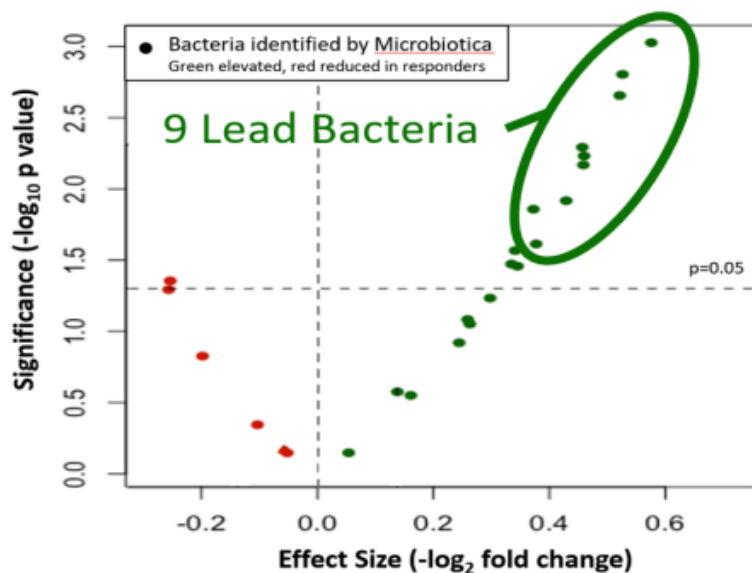
First Posted : May 19, 2023

Last Update Posted : May 19, 2023

See [Contacts and Locations](#)

[View this study on the modernized ClinicalTrials.gov](#)

# On the Horizon: MB097



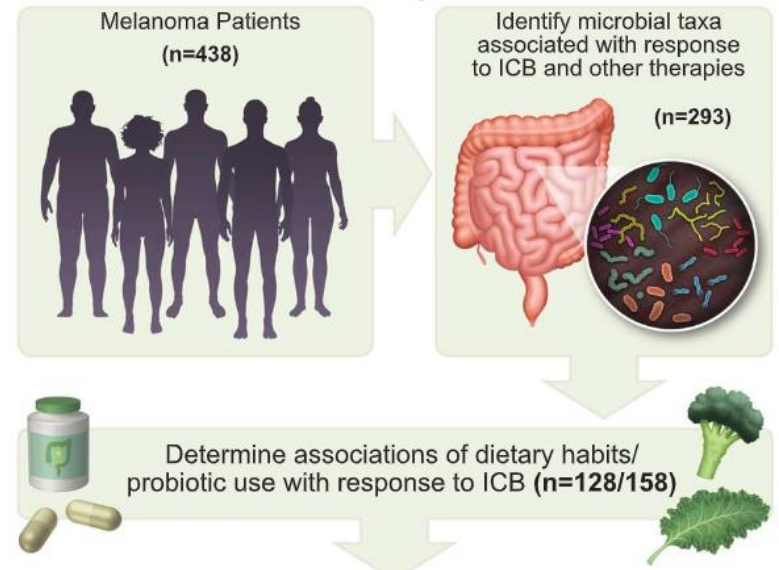
# Other Interesting Data: Interplay of Diet?

## IMMUNOTHERAPY

### Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response

Christine N. Spencer<sup>1†‡</sup>, Jennifer L. McQuade<sup>2†</sup>, Vancheswaran Gopalakrishnan<sup>1†§</sup>, John A. McCulloch<sup>3†</sup>, Marie Vetizou<sup>3†</sup>, Alexandria P. Cogdill<sup>1,4†¶</sup>, Md A. Wadud Khan<sup>1</sup>, Xiaotao Zhang<sup>5</sup>, Michael G. White<sup>1</sup>, Christine B. Peterson<sup>6</sup>, Matthew C. Wong<sup>1</sup>, Golnaz Morad<sup>1</sup>, Theresa Rodgers<sup>2</sup>, Jonathan H. Badger<sup>3</sup>, Beth A. Helmink<sup>1#</sup>, Miles C. Andrews<sup>1,7</sup>, Richard R. Rodrigues<sup>8</sup>, Andrey Morgun<sup>9</sup>, Young S. Kim<sup>10</sup>, Jason Roszik<sup>2</sup>, Kristi L. Hoffman<sup>11</sup>, Jiali Zheng<sup>5,\*</sup>, Yifan Zhou<sup>4</sup>, Yusra B. Medik<sup>4</sup>, Laura M. Kahn<sup>4,12</sup>, Sarah Johnson<sup>1</sup>, Courtney W. Hudgens<sup>13</sup>, Khalida Wani<sup>13</sup>, Pierre-Olivier Gaudreau<sup>14</sup>, Angela L. Harris<sup>15</sup>, Mohamed A. Jamal<sup>16</sup>, Erez N. Baruch<sup>17</sup>, Eva Perez-Guijarro<sup>18</sup>, Chi-Ping Day<sup>18</sup>, Glenn Merlino<sup>18</sup>, Barbara Pazdrak<sup>2</sup>, Brooke S. Lochmann<sup>2</sup>, Robert A. Szczepaniak-Sloane<sup>1</sup>, Reetakshi Arora<sup>1</sup>, Jaime Anderson<sup>2</sup>, Chrystia M. Zobniw<sup>2</sup>, Eliza Posada<sup>2</sup>, Elizabeth Sirmans<sup>2</sup>, Julie Simon<sup>1</sup>, Lauren E. Haydu<sup>1</sup>, Elizabeth M. Burton<sup>1</sup>, Linghua Wang<sup>16</sup>, Minghao Dang<sup>16</sup>, Karen Clise-Dwyer<sup>19,20</sup>, Sarah Schneider<sup>19</sup>, Thomas Chapman<sup>1</sup>, Nana-Ama A. S. Anang<sup>4</sup>, Sheila Duncan<sup>1</sup>, Joseph Toker<sup>21,22</sup>, Jared C. Malke<sup>1</sup>, Isabella C. Glitza<sup>2</sup>, Rodabe N. Amaria<sup>2</sup>, Hussein A. Tawbi<sup>2</sup>, Adi Diab<sup>2</sup>, Michael K. Wong<sup>2</sup>, Sapna P. Patel<sup>2</sup>, Scott E. Woodman<sup>2</sup>, Michael A. Davies<sup>2</sup>, Merrick I. Ross<sup>1</sup>, Jeffrey E. Gershenwald<sup>1</sup>, Jeffrey E. Lee<sup>1</sup>, Patrick Hwu<sup>2††</sup>, Vanessa Jensen<sup>23</sup>, Yardena Samuels<sup>24</sup>, Ravid Straussman<sup>24</sup>, Nadim J. Ajami<sup>16</sup>, Kelly C. Nelson<sup>25</sup>, Luigi Nezi<sup>26</sup>, Joseph F. Petrosino<sup>11</sup>, P. Andrew Futreal<sup>16</sup>, Alexander J. Lazar<sup>12,16,27</sup>, Jianhua Hu<sup>28</sup>, Robert R. Jenq<sup>16,29</sup>, Michael T. Tetzlaff<sup>30</sup>, Yan Yan<sup>31</sup>, Wendy S. Garrett<sup>32</sup>, Curtis Huttenhower<sup>31,33,34,35</sup>, Padmanee Sharma<sup>4,36,37</sup>, Stephanie S. Watowich<sup>4</sup>, James P. Allison<sup>4,37</sup>, Lorenzo Cohen<sup>38††</sup>, Giorgio Trinchieri<sup>3,\*††</sup>, Carrie R. Daniel<sup>5,\*††</sup>, Jennifer A. Wargo<sup>1,16,\*††</sup>

#### A Overall schema for current study: to assess gut microbiota profiles, dietary habits and probiotic use with outcomes in melanoma patients



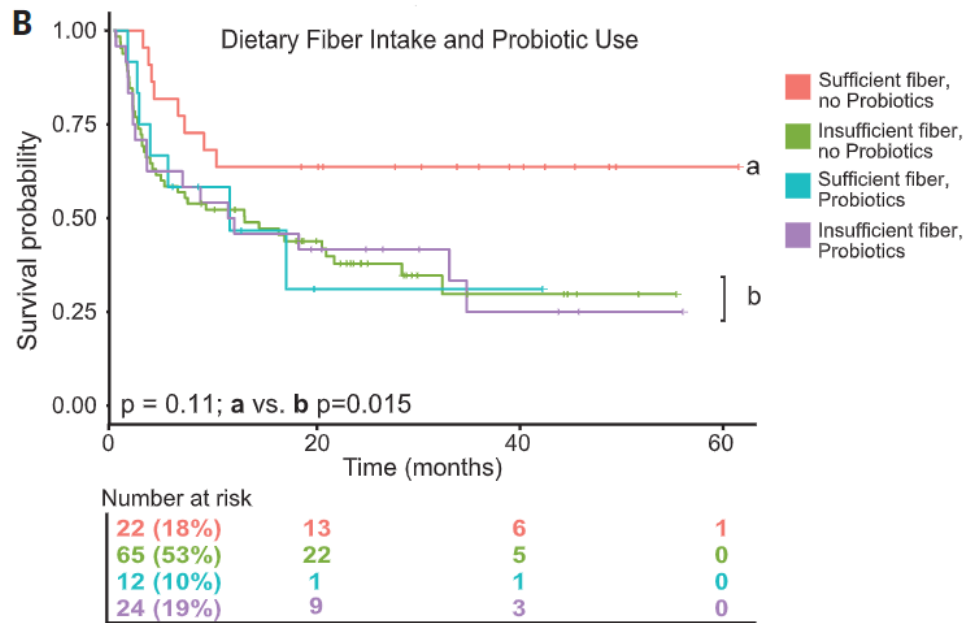
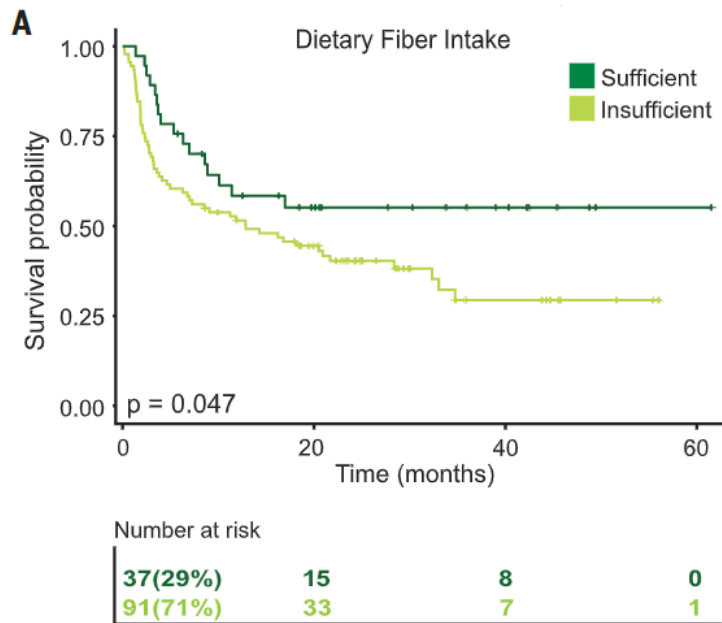
## Other Interesting Data: Interplay of Diet?

**Table 1. Associations of baseline probiotic supplement use and dietary fiber intake in late-stage melanoma patients treated with ICB and followed for tumor response and progression-free survival.** Dashes indicate not applicable. HR, hazard ratio; CI, confidence interval; OR, odds ratio; N/R, not reached; ref, referent group.

Comparison	n	Progression-free survival					Odds of response to ICB			
		Events	Median months	HR*	95% CI	P value†	Responder n (%)	OR*	95% CI	P value‡
<i>Probiotic supplement use</i>										
Total	158	85	-	-	-	-	65%	-	-	-
No	109	56	23	1.00	ref	-	74 (68%)	1.00	ref	-
Yes	49	29	17	1.30	0.82, 2.07	0.27	29 (59%)	0.79	0.37, 1.66	0.52
<i>Dietary fiber intake</i>										
Total	128	73	-	-	-	-	65%	-	-	-
Per 5 g/day increase	-	-	-	0.71	0.52, 0.98	0.04	-	1.70	0.97, 3.00	0.06
Insufficient	91	57	13	1.00	ref	-	55 (60%)	1.00	ref	-
Sufficient	37	16	N/R	0.59	0.33, 1.04	0.07	28 (76%)	2.20	0.86, 5.61	0.10
<i>Dietary fiber intake + probiotic supplement use</i>										
Total	123	72	-	-	-	-	63%	-	-	-
Sufficient fiber + no probiotics	22	8	N/R	0.44	0.21, 0.92	0.03	18 (82%)	2.94	0.87, 9.94	0.08
Other‡	101	64	13	1.00	ref	-	60 (59%)	1.00	ref	-

\*HR and 95% CI estimated using Cox proportional hazards regression. OR and 95% CI estimated using logistic regression. All models include multivariable adjustment for subtype, stage, lactate dehydrogenase level, and BMI. †P value by Wald test. ‡Other category includes patients who either reported insufficient fiber intake or probiotic use.

# Other Interesting Data: Interplay of Diet?





## Other Interesting Data: How Do We Assess Diet?

Notably, all 26 items corresponding to foods or food groups assessed in the NCI-DSQ contribute to the derivation of dietary fiber and calcium intake; thus, patients with 2 or more missing responses to any query on the DSQ were excluded ( $n=38$ ), while imputation by mode was applied for 4 patients with only 1 missing response. The threshold of 20 grams per day used to define “sufficient” versus “insufficient” dietary fiber intake (and other categorical dietary variables) was selected based on the statistical distribution within our cohort (Fig. S10).

While the NCI-DSQ was validated against 24-hour recalls (17), it is not a measure of an individual’s absolute or true intake. For example, portion size is estimated using national survey data, not individual level data. Thus, to define sufficient vs. insufficient fiber intake categories our approach was informed by the NCI-DSQ evaluation and validation work by Thompson *et al.* in comparison to 24-hour recalls within a nationally representative sample (NHANES). Given that so few meet the U.S. dietary guidelines (i.e., ~14 g per 1,000 kcal daily based on sex, age and energy needs), these recommended levels are often in the lower or upper tails of the distribution of actual intake in a population. Similarly, we considered threshold values in the top quartile (25<sup>th</sup> percentile) or tertile (33<sup>rd</sup> percentile) of estimated usual intake to provide more accurate classifications when using the DSQ (17). As this threshold met by ~30% of our patients is not a specific recommendation, the value of 20 g/day should not be over-interpreted. Results are also presented in the context of an incremental 5 g/day increase with patient outcomes; a unit change that was informed by the standard deviation or sigma (Fig. S10).

# Other Interesting Data: The definition of a healthy gut?





Cell



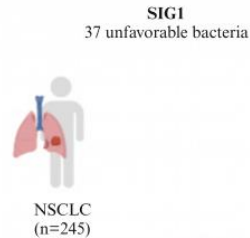
Volume 187, Issue 13, 20 June 2024, Pages 3373-3389.e16

Article

## Custom scoring based on ecological topology of gut microbiota associated with cancer immunotherapy outcome

[Lisa Derosa](#)<sup>1,2,3,4,45,46</sup>  , [Valerio Iebba](#)<sup>1,5,45</sup>, [Carolina Alves Costa Silva](#)<sup>1,2,3,45</sup>, [Gianmarco Piccinno](#)<sup>6</sup>, [Guojun Wu](#)<sup>7,8,9</sup>, [Leonardo Lordello](#)<sup>1,3</sup>, [Bertrand Routy](#)<sup>10,11</sup>, [Naisi Zhao](#)<sup>12</sup>, [Cassandra Thelemaque](#)<sup>1,3</sup>, [Roxanne Birebent](#)<sup>1,2,3</sup>, [Federica Marmorino](#)<sup>13,14</sup>, [Marine Fidelle](#)<sup>1,2,3</sup>, [Meriem Messaoudene](#)<sup>11</sup>, [Andrew Maltez Thomas](#)<sup>6</sup>, [Gerard Zalcman](#)<sup>15</sup>, [Sylvie Friard](#)<sup>16</sup>, [Julien Mazieres](#)<sup>17</sup>, [Clarisse Audigier-Valette](#)<sup>18</sup>, [Denis Moro-Sibilot](#)<sup>19</sup>, [François Goldwasser](#)<sup>20,21,22...</sup>, [Laurence Zitvogel](#)<sup>1,2,3,44</sup>  

Immunotherapy

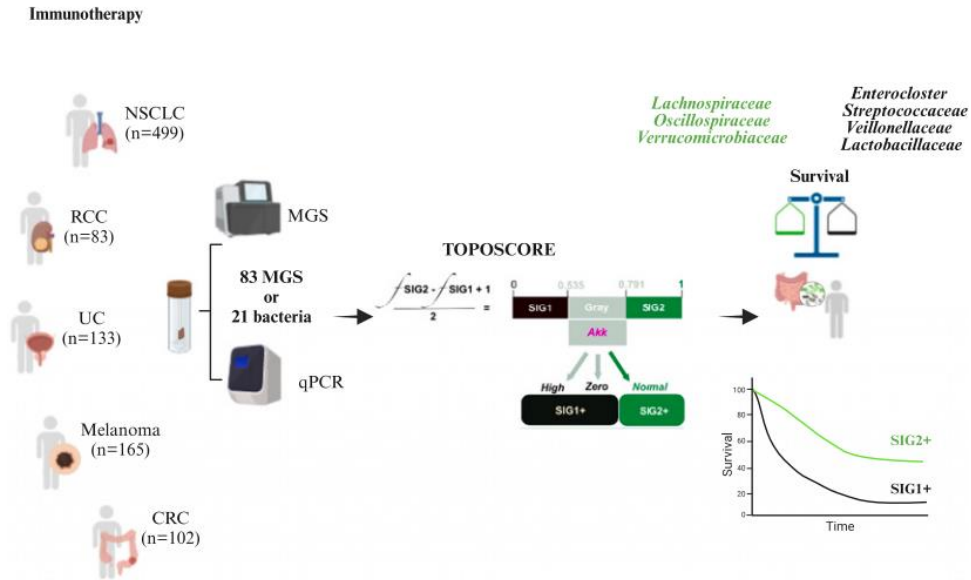


Species interacting groups (SIGs)

**SIG1**  
37 unfavorable bacteria

**SIG2**  
45 favorable bacteria

# Other Interesting Data: The definition of a healthy gut?



# Acknowledgements



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