

top ten

in gastroenterologia

14[^] EDIZIONE

24-25 NOVEMBRE 2023

BERGAMO

HOTEL EXCELSIOR SAN MARCO
Piazza della Repubblica, 6

A detailed microscopic image showing a cell with a prominent nucleus on the left, surrounded by a complex network of green, rod-like structures, likely representing the cytoskeleton or a specific organelle. The image is set against a dark background, highlighting the intricate details of the cell's internal structure.

**MICROBIOTA E RISPOSTA ALLE
TERAPIE**

MICROBIOTA E RISPOSTA ALLE TERAPIE

FARMACOMICROBIOMICA

PATRIZIA BRIGIDI

Dipartimento di Scienze Mediche e Chirurgiche

Università di Bologna

La sottoscritta Patrizia Brigidi

dichiara

che negli ultimi due anni ha avuto rapporti diretti di finanziamento con i seguenti soggetti portatori di interessi commerciali in campo sanitario:

- ***Roche***
- ***Alfasigma***

PHARMACOMICROBIOMICS

Pharmacogenomics: how human genome variations affect drug action

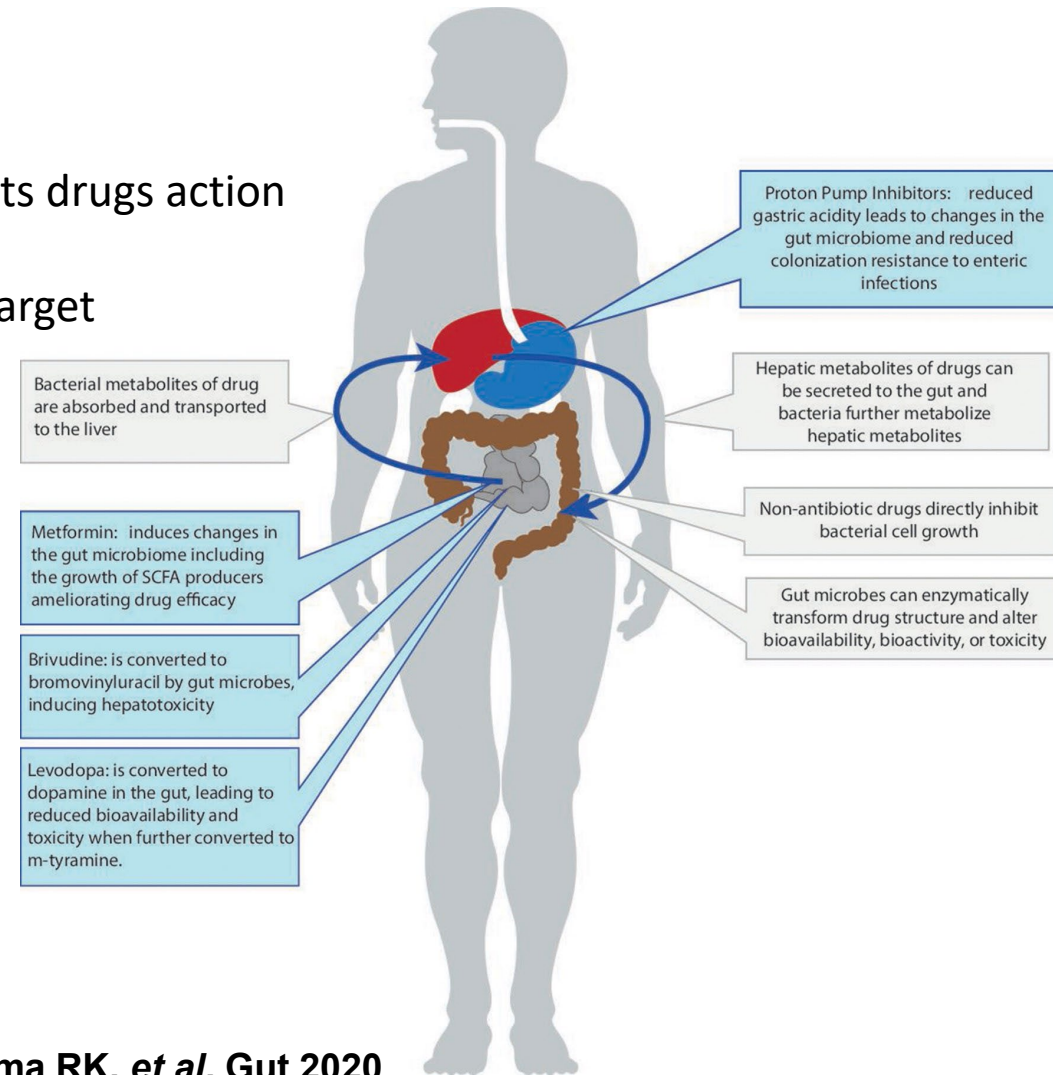
Pharmacomicrobiomics: how GM, as the second human genome, affects drugs action

Unlike human genetics, GM is modifiable ➡ attractive therapeutic target

Bidirectional interaction GM and commonly used non-antibiotic drugs

- **GM composition can be influenced by drugs**
- **GM can influence an individual's response to a drug by enzymatically transforming the drug's structure and altering its bioavailability, bioactivity or toxicity**

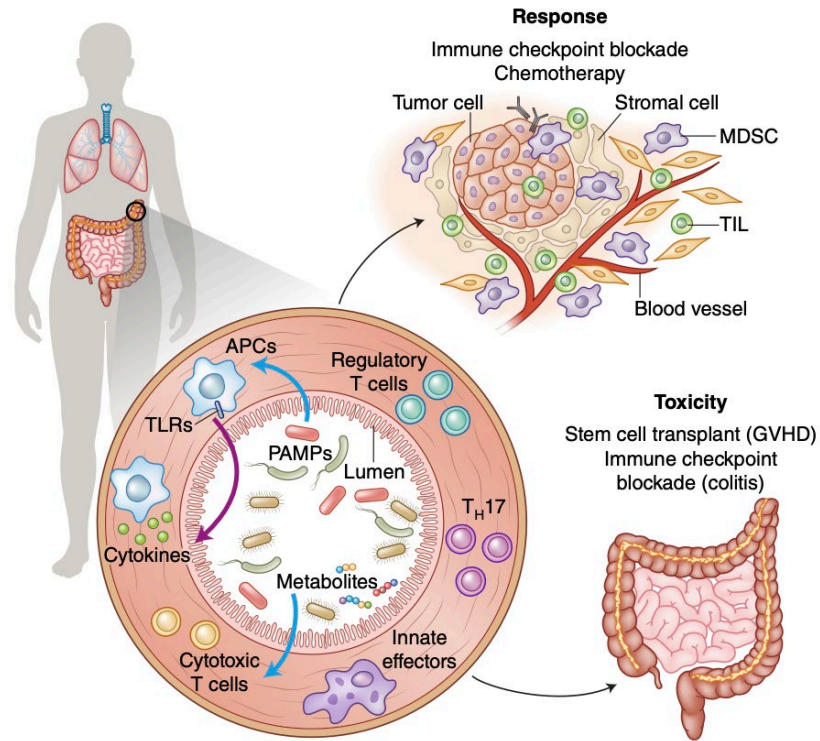
Large human cohort studies: associations between specific drugs and altered GM, including **PPIs, lipid-lowering statins, laxatives, metformin, beta-blockers and ACE inhibitors, and selective serotonin reuptake inhibitor antidepressants**



Weersma RK, *et al.* Gut 2020

PHARMACOMICROBIOMICS: EXPLOITING THE DRUG-GM INTERACTIONS IN ANTICANCER THERAPIES

GM is involved in modulating the clinical response to cancer therapy (chemotherapy and immunotherapy) and associated toxicities (colitis and GvHD)



Chemoresistance: GM metabolizes chemotherapeutic drugs into their inactive forms

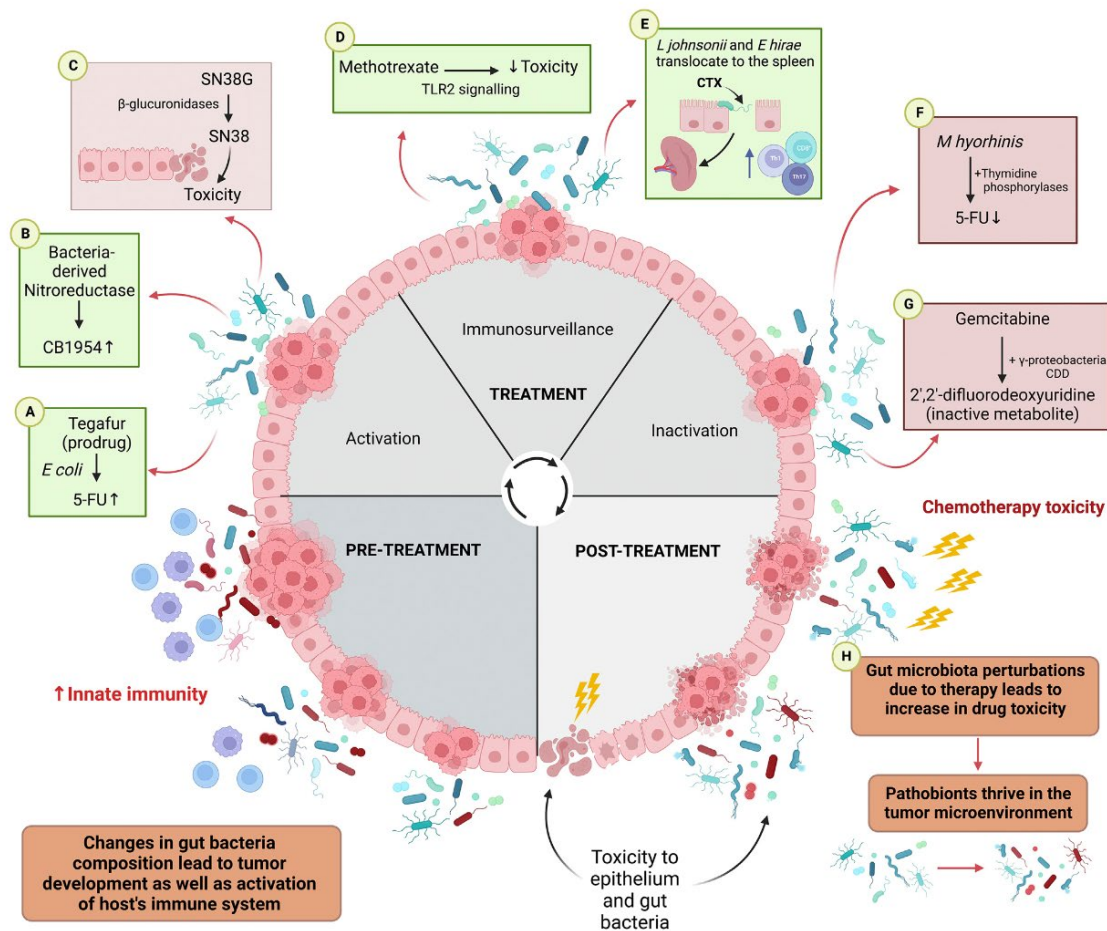
Immunotherapy resistance: GM supports the fine-tuning the general host immune status and subsequently antitumour activation of the immune system (immune checkpoint inhibition)

Toxicity: GM alters systemic immune function via local changes within the gut mucosa and gut-associated lymphoid tissue

GM SHAPES ONCOLOGIC OUTCOMES
↓
RESPONDERS NON RESPONDERS????

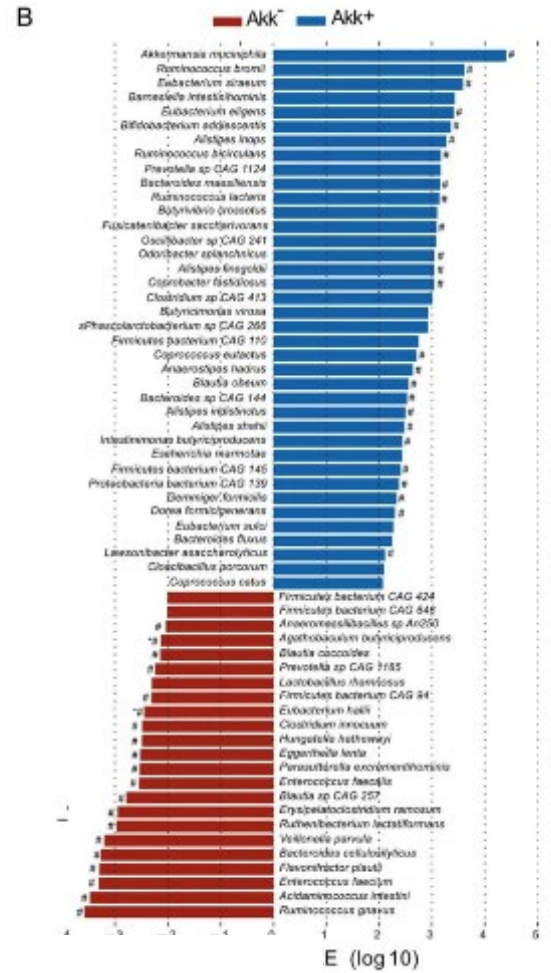
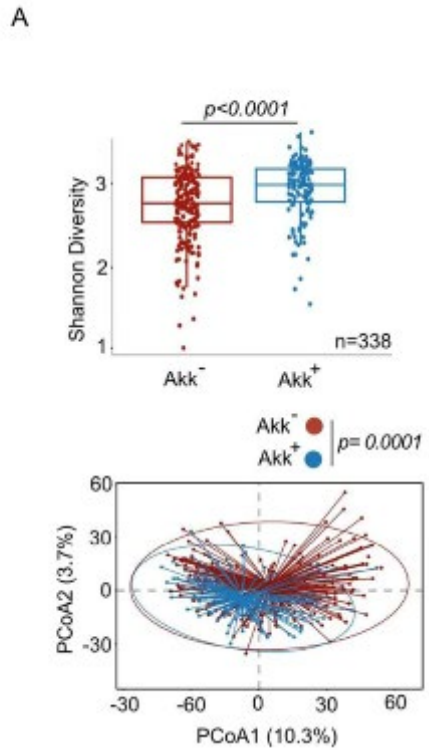
Helmink *et al.* Nat Med 2019; Bullman *et al.*, Science 2017; Spencer *et al.*, Science 2021

MECHANISMS OF HOST-ONCOMICROBIOME-THERAPY INTERACTIONS



Chrysostomou et al., Gastroenterology 2023

INTESTINAL *A. MUCINIPHILA* PREDICTS CLINICAL RESPONSE TO mAB ANTI-PD-1 IN NON-SMALL CELL LUNG CANCER PATIENTS



RESPONDERS

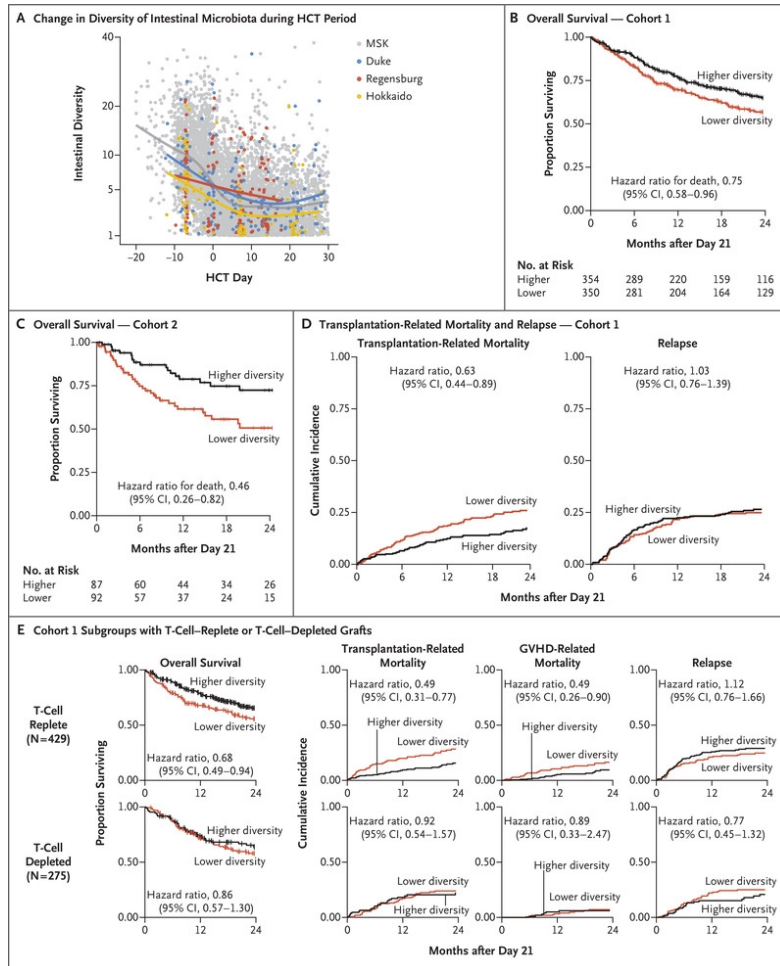
↑ Diversity, *A. muciniphila*, *Ruminococcaceae* (*R. bromii*, *R. bicirculans*, *R. lactaris*), *Lachnospiraceae* (*Eubacterium siraeum*, *E. eligens*) and *Alistipes* spp. (*A. inops*, *A. finegoldii*, *A. indistinctus*, *A. shahii*)

NON RESPONDERS

↓ *A. muciniphila*
 ↑ *Veillonella parvula*, *Actinomyces* and *Clostridium* (*C. innocuum*, *Hungatella hathewayi*)

Derosa et al., Nat Med 2022

GM AS PREDICTOR OF MORTALITY IN ALLOGENEIC HEMATOPOIETIC-CELL TRANSPLANTATION

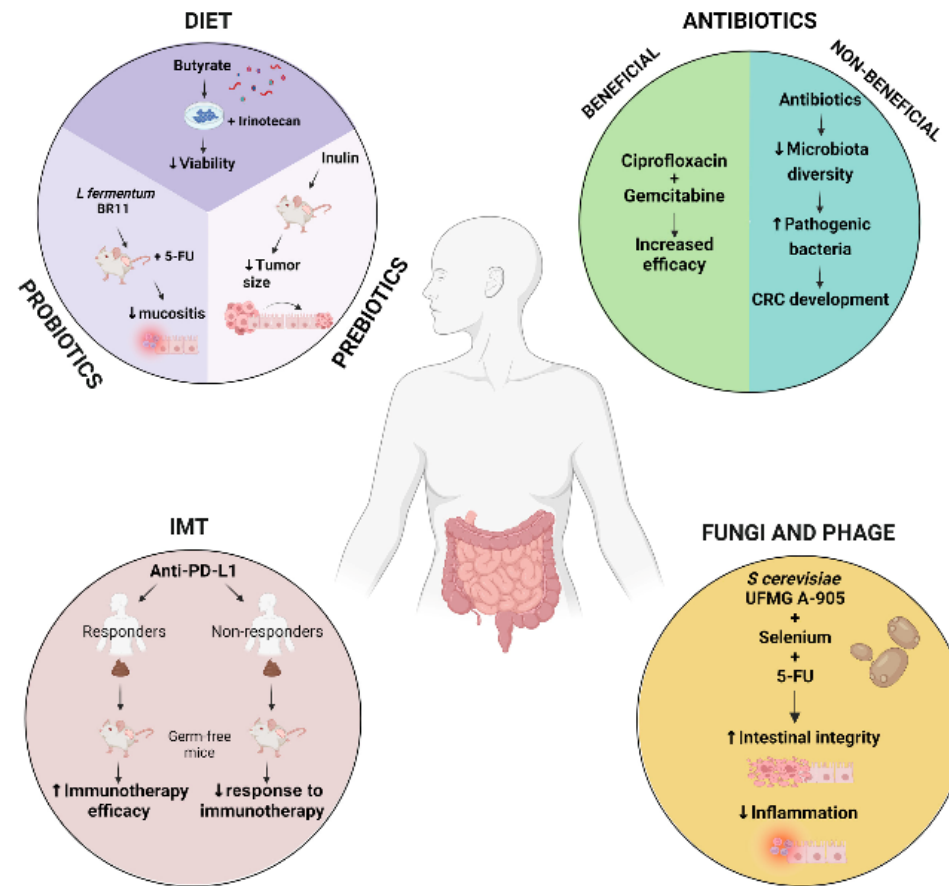


1,362 patients undergoing allogeneic hematopoietic-cell transplantation at four centers (New York, Germany, Japan and North Carolina) (8,767 fecal samples)

- **Patterns of microbiota disruption (diversity loss and domination by single taxa) are similar across transplantation centres**
- **Higher GM diversity at the time of neutrophil engraftment is associated with lower mortality**

Peled *et al.*, New Engl J Med 2020

THERAPY OUTCOMES CAN BE MODULATED BY RESHAPING THE MICROBIOME



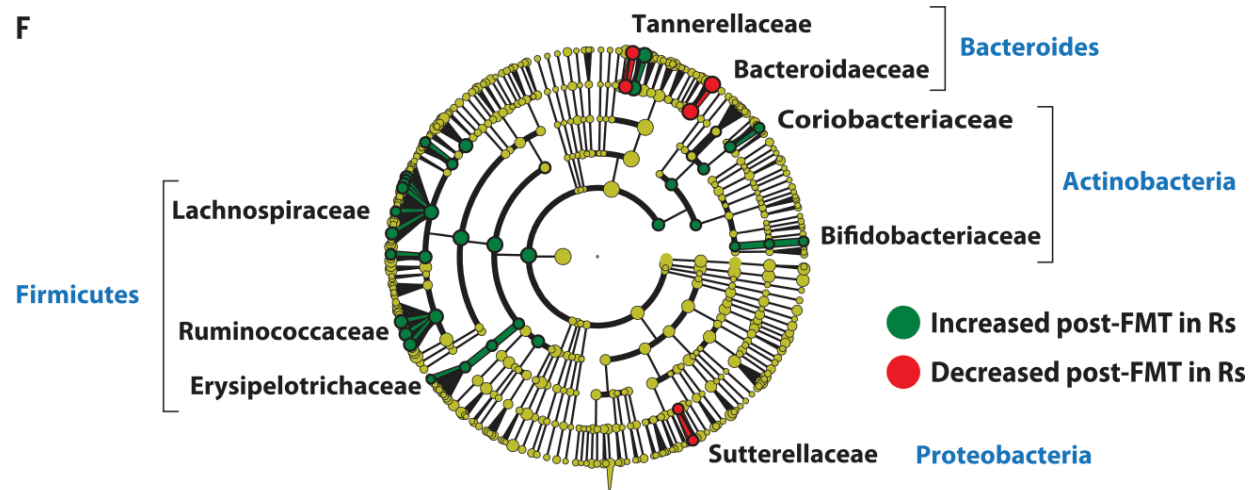
Chrysostomou *et al.*, Gastroenterology 2023

FMT OVERCOMES RESISTANCE TO mAbs anti-PD-1 THERAPY IN MELANOMA PATIENTS

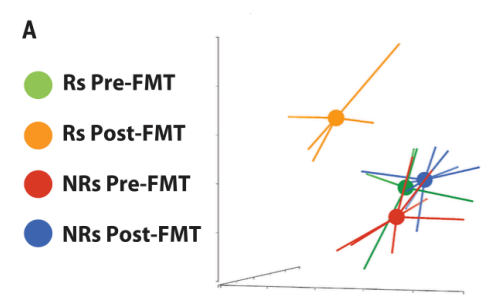
Immune checkpoint blockade with **mAbs anti-PD-1** provides long-term clinical benefits to nearly **40% of patients with advanced melanoma**

15 melanoma patients refractory to anti-PD-1 therapy, received FMT from patients demonstrated durable complete response

FMT: clinical benefit in 6 of 15 patients, and induced rapid and durable GM perturbation



SERUM CYTOKINES



- Responders exhibited:
- **increased abundance of taxa** associated with response to anti-PD-1
 - **increased CD8+ T cell activation**
 - **decreased frequency of IL-8–** expressing myeloid cells

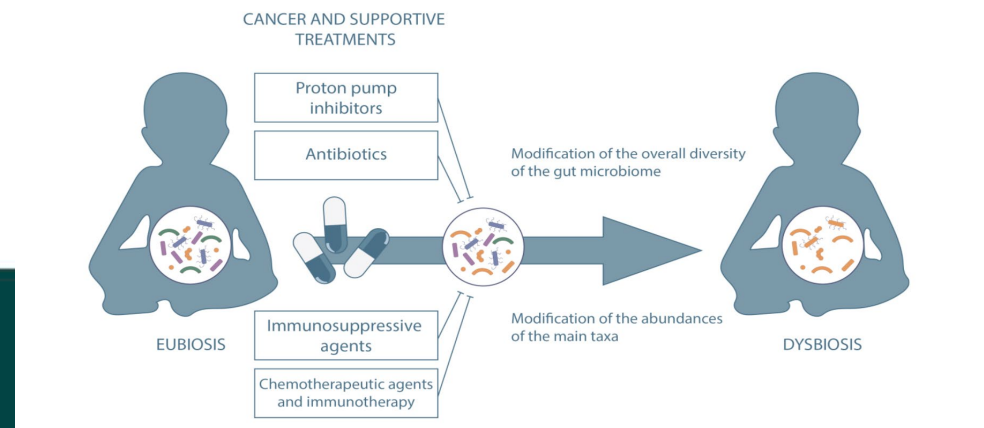
Davar *et al.*, Science 2021

HEMATOPOIETIC STEM CELL TRANSPLANTATION IN PEDIATRIC PATIENTS: GM ROLE

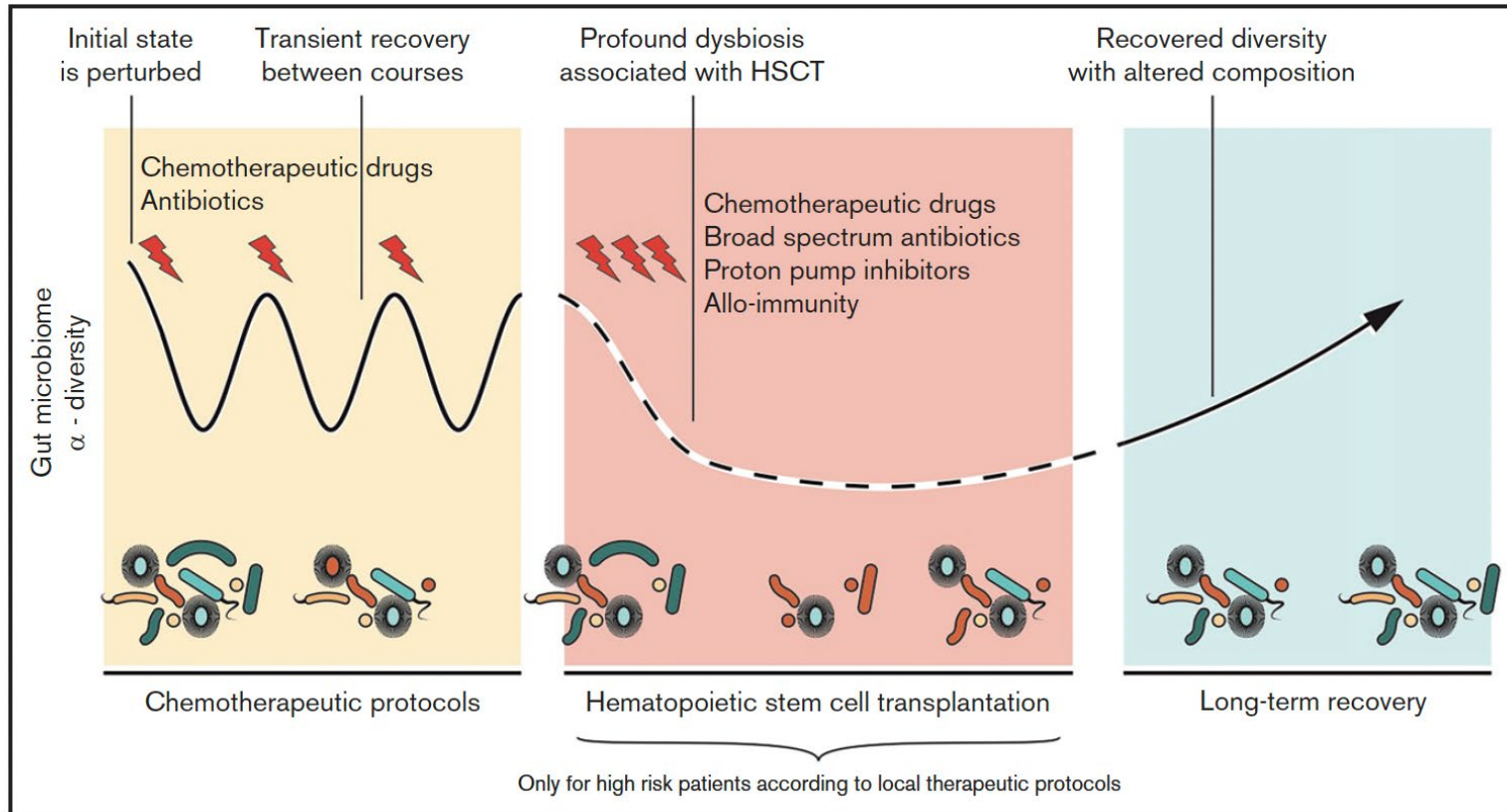
- **Leukemias and lymphomas** are the most frequent type of cancer in pediatric patients (acute leukemia, leading cause of childhood cancer-related deaths worldwide has an incidence rate of 10 to 50 cases per 100 000 per year)
- **These disorders reach the 80-90%** of long-term survival rates thanks to chemotherapy and/or immunotherapies
- **Aggressive treatment with several treatment-related complications**
- **Children GM different ecological properties** compared to adults

Hematopoietic stem cell transplantation (HSCT) is the strongest curative treatment for pediatric hematologic malignancies

In HSCT patients GM is severely injured



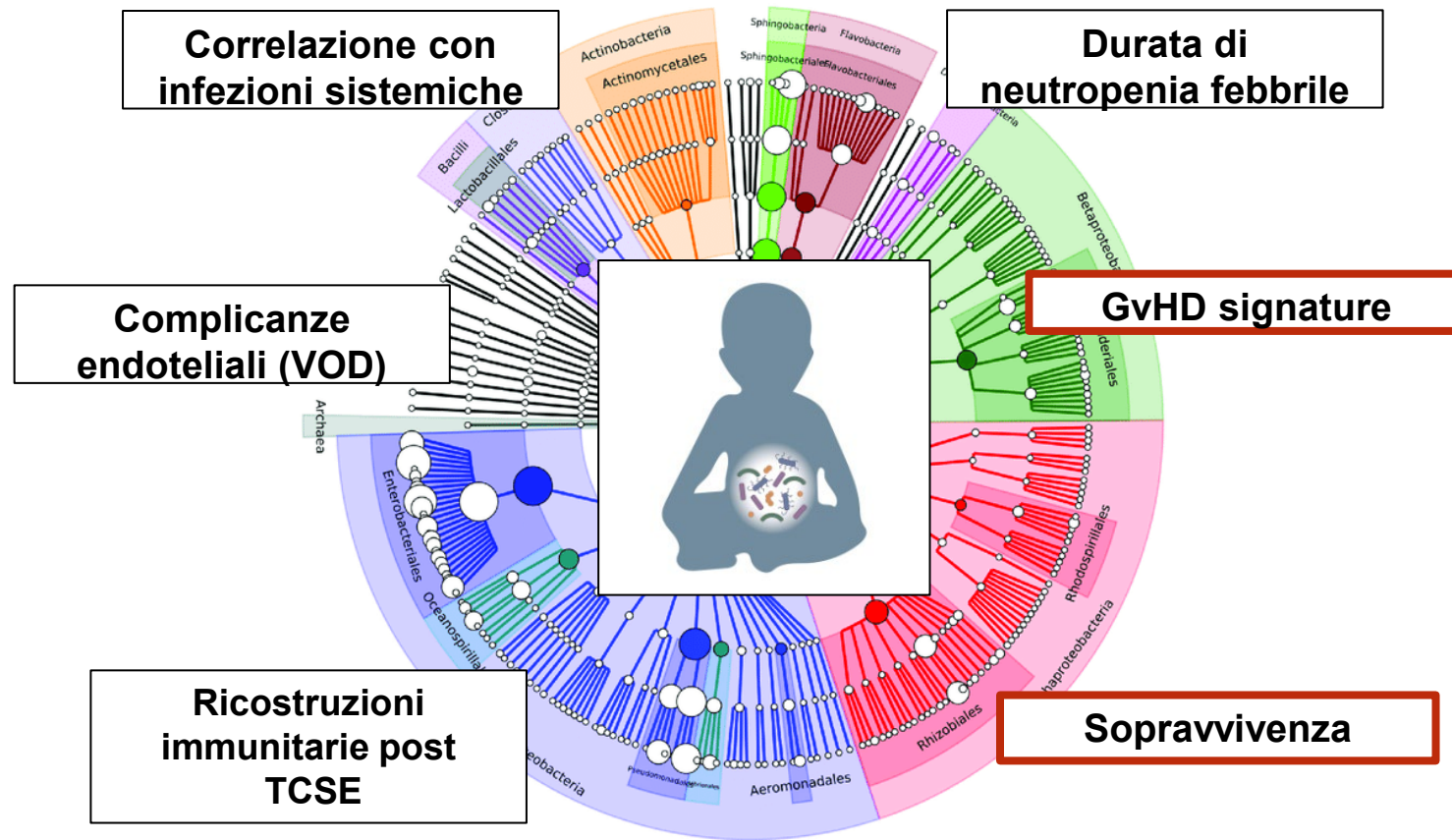
TRAJECTORY OF GM DURING THE THERAPEUTIC COURSE OF HSCT



- **Dramatic decrease of α diversity**
- **Loss of health-associated commensals**
- **Expansion of potentially pathogenic bacteria, with a predominance of Gram-negative Enterobacteria**
- **After 2-3 months the ecosystem partially recovers its initial richness and metabolic capacity**

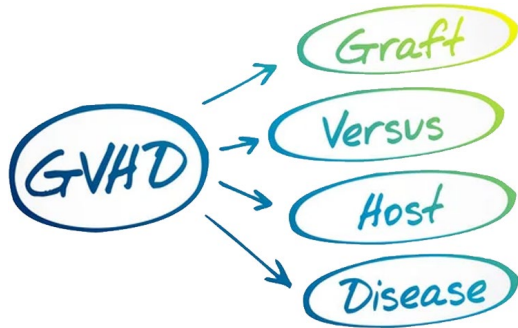
Masetti *et al.*, 2021 Blood Adv

DYNAMICS OF GM DIVERSITY AND CLINICAL OUTCOMES IN HSCT



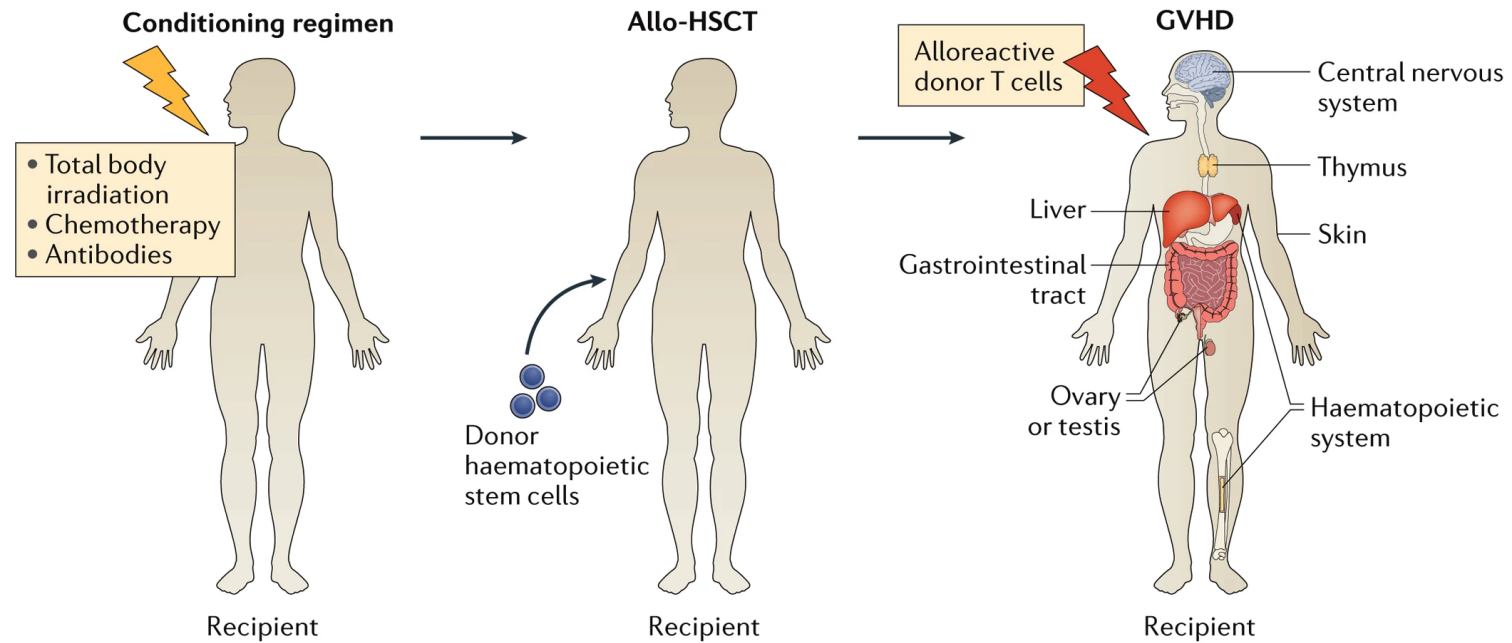
Biagi et al. 2015 *Bone marrow transplant*; Simms-Waldrup et al. 2017 *Bone marrow transplant*; Biagi et al. 2019 *BMC Med Genomics*; Ingham et al. 2019 *Microbiome*; Kelly et al. 2019 *Bone marrow transplantation*; D'Amico et al. 2019 *Nutrients*; Ingham et al. 2021 *Microbiome*; Zama et al. 2021 *Transplant Cell Ther*; Masetti et al. 2021 *Sci Rep*; Masetti et al. 2022 *Cancers*

DYNAMICS OF GM DIVERSITY AND GVHD SIGNATURE



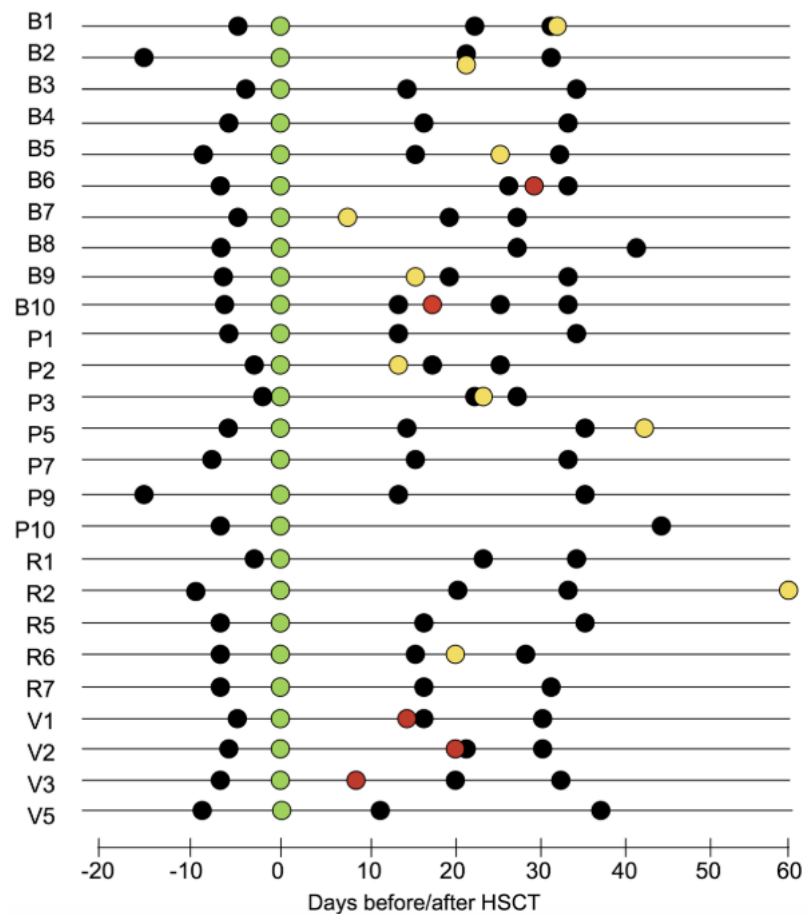
Reactivity of donor derived immune cells against allogenic recipient tissues

GVHD is one of the major complications of allo-HSCT



Nature Reviews | [Cancer](#)

EARLY GM SIGNATURES OF aGvHD IN CHILDREN UNDERGOING HSCT



Italian multicentric longitudinal study

36 children undergoing allogeneic HSCT at 4 centers (BO, OPBG, VR, PV)

> 130 samples (pre-HSCT, engraftment, post-HSCT fecal samples)

19/36 patients developed aGvHD

Biagi *et al.*, 2019 *BMC Medical Genomics*

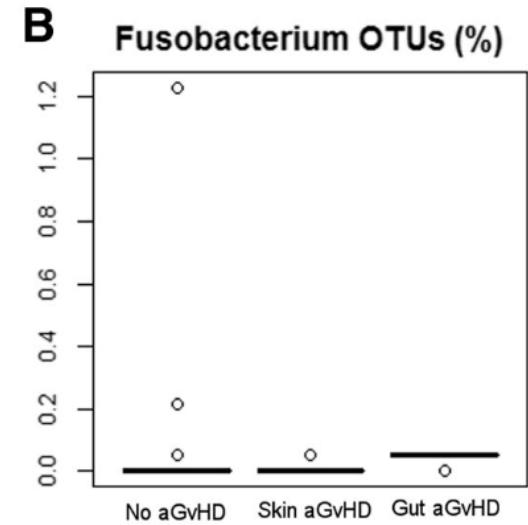
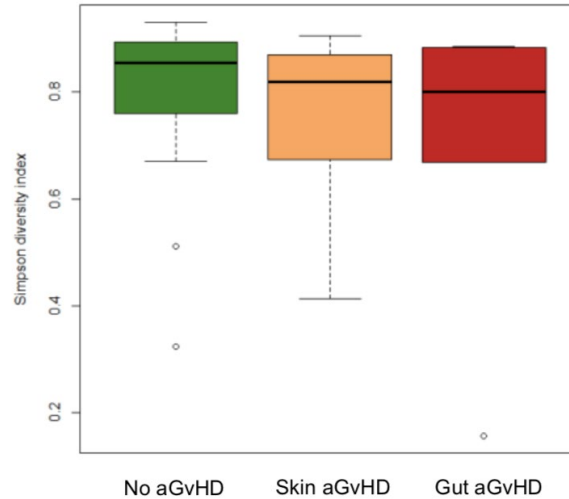
Early gut microbiota signature of aGvHD in children given allogeneic hematopoietic cell transplantation for hematological disorders

Elena Biagi^{1†*}, Daniele Zama^{2†}, Simone Rampelli¹, Silvia Turrone¹, Patrizia Brigidi¹, Clarissa Consolandi³, Marco Severgnini³, Eleonora Picotti², Pietro Gasperini², Pietro Merli⁴, Nunzia Decembrino⁵, Marco Zecca⁵, Simone Cesaro⁶, Maura Faraci⁷, Arcangelo Prete², Franco Locatelli⁴, Andrea Pession², Marco Candela^{1†} and Riccardo Masetti^{2†}

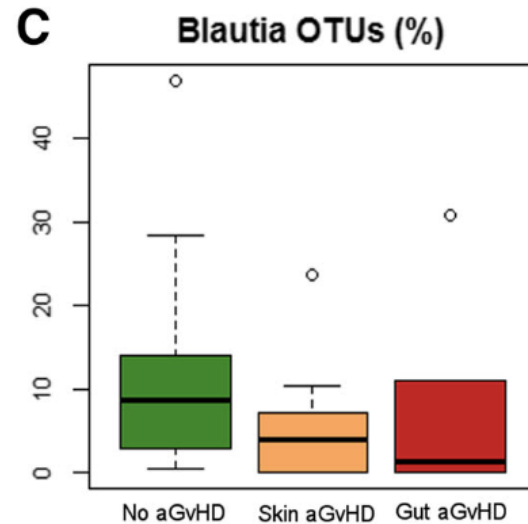
Higher pre-HSCT GM diversity associated to a lower incidence of intestinal aGvHD

High relative abundance of *Blautia* in pre-HSCT samples of NO aGvHD patients

High relative abundance of *Fusobacterium nucleatum* associated to severity of intestinal aGvHD

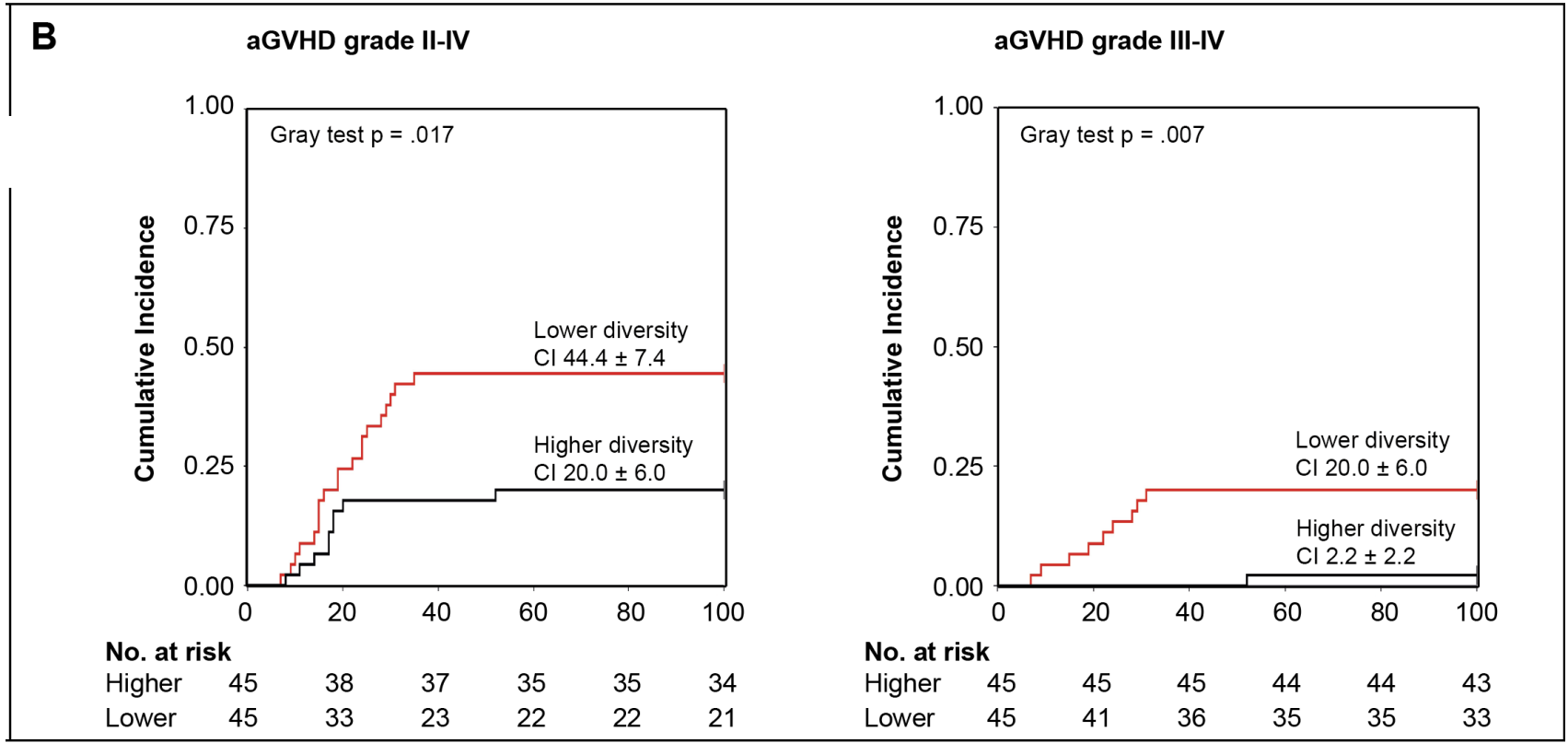


Pathobionts



SCFA producer:

- trophic effect on the intestinal barrier
- crosstalk between GM and host immune cells



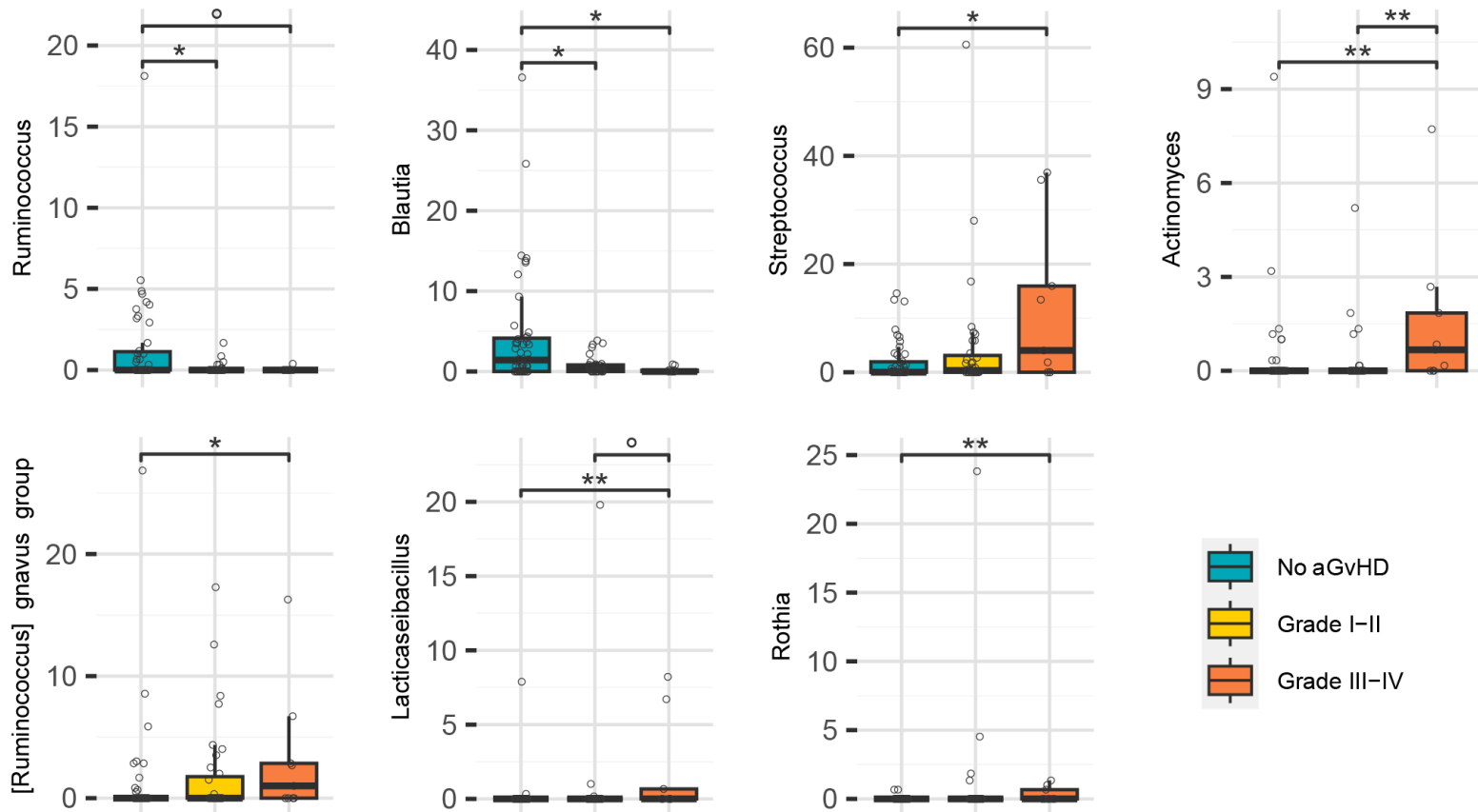
GM diversity of pre-HSCT of fecal samples predicts cumulative incidence of acute GvHD

Multicentric longitudinal study

90 patients undergoing HSCT at 5 centers (BO, OPBG, VR, PV, Wroclaw) (>300 fecal samples)

Higher pre-HSCT **GM diversity** associated to a **lower incidence of grade II-IV and grade III-IV aGVHD**

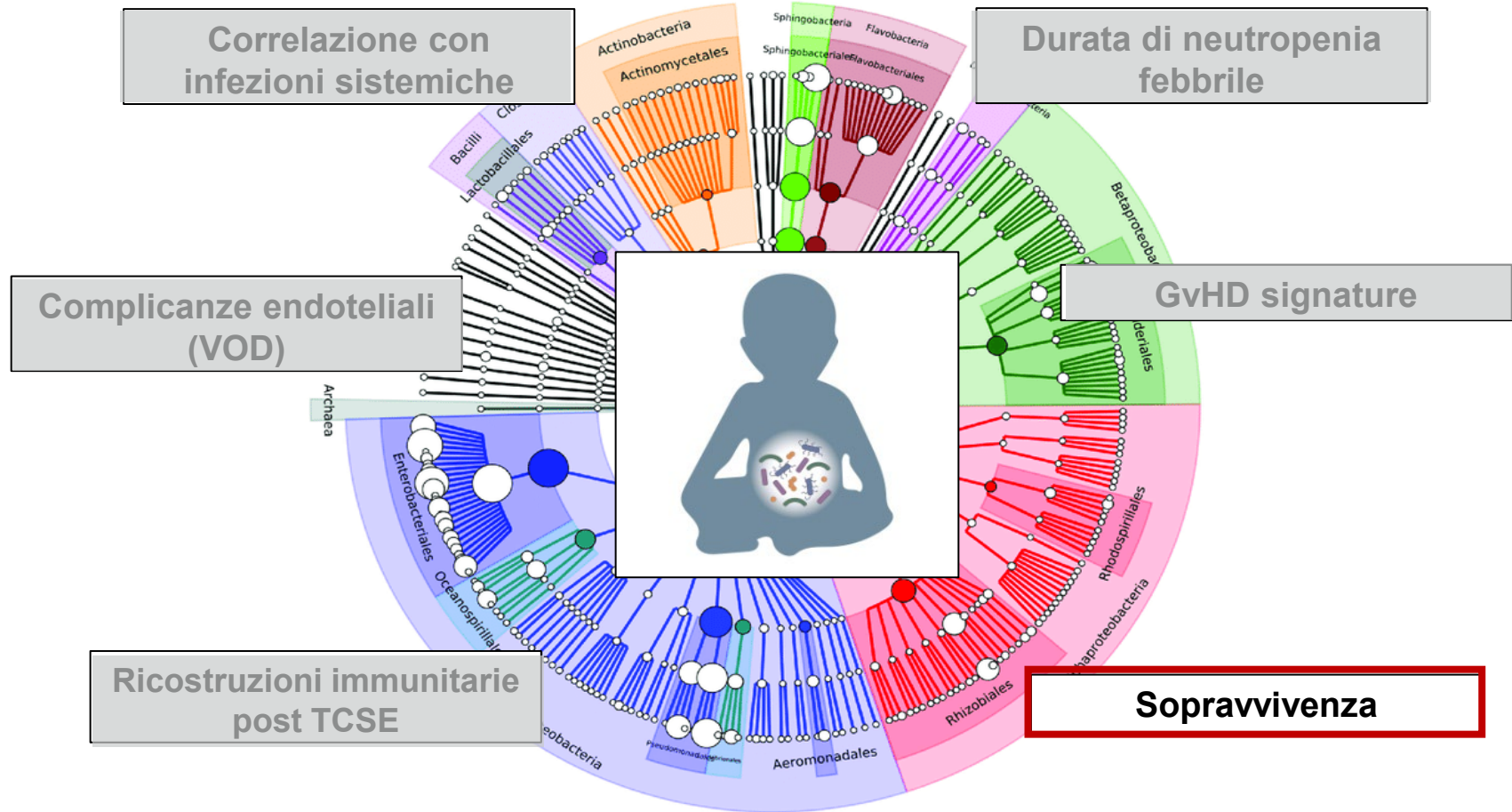
Masetti *et al.*, 2023 *Blood*



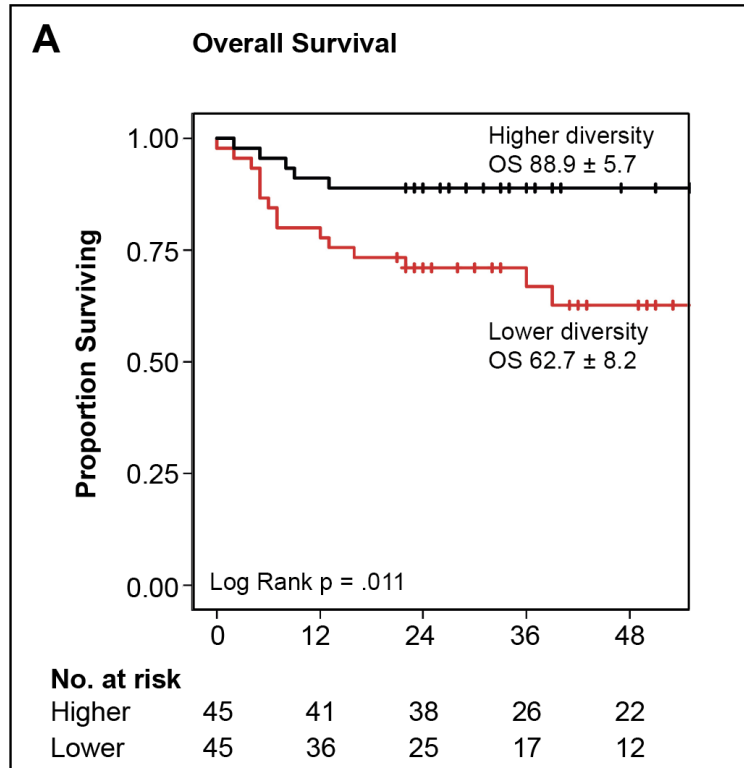
High abundance of *Blautia* and *Ruminococcus* ($p \leq 0.05$) in pre-HSCT is protective for the subsequent development of acute GvHD

Increased abundance of facultative aerobic pathobionts in pre-HSCT is associated with increased acute GvHD

Masetti et al., Blood 2023

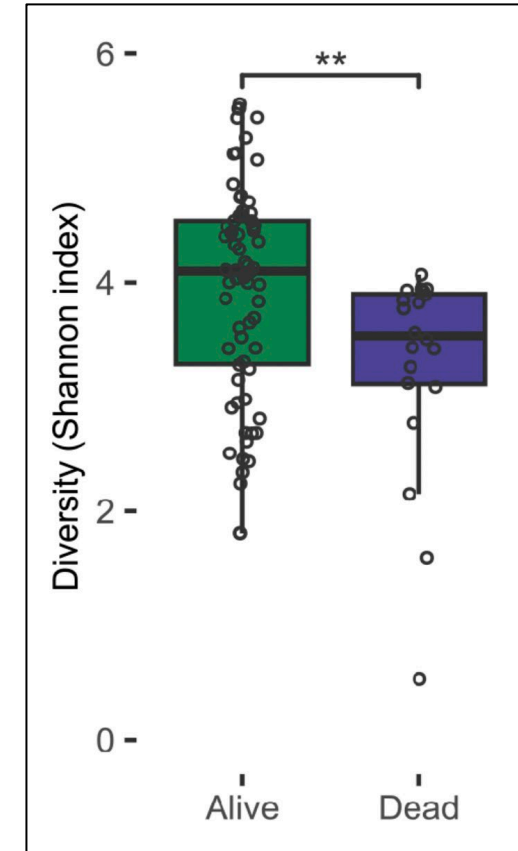


GM DIVERSITY AND SURVIVAL IN CHILDREN RECEIVING HSCT



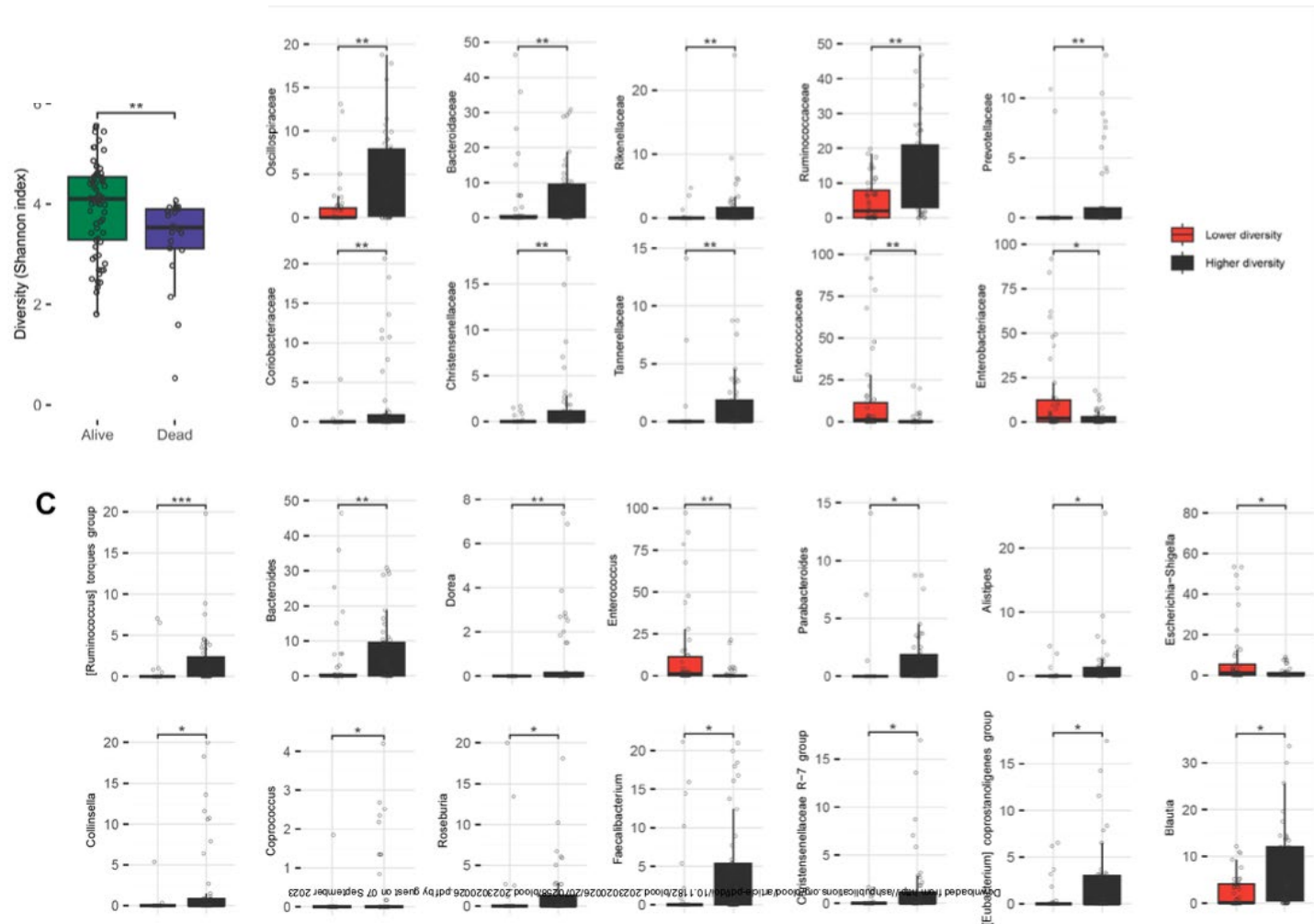
- **90 patients** undergoing HSCT at 5 centers (the largest pediatric cohort studied for GM composition in HSCT)
- Evaluation of **GM diversity before HSCT and at engraftment**
- Evaluated the impact of GM diversity on the survival post HSCT

GM diversity before HSCT



Masetti *et al.*, 2023 *Blood*

First evidence of an association between pre-transplantation lower GM diversity and poorer outcome in children undergoing allo-HSCT



Higher-diversity group composition:
 > abundances of health-related families, such as *Ruminococcaceae* and *Oscillospiraceae*, *Bacteroidaceae*, *Rikenellaceae*, *Prevotellaceae*, *Coriobacteriaceae*, *Christensenellaceae*, (**SCFAs producer genera** such as *Blautia*, *Faecalibacterium*, *Roseburia*, *Bacteroides*, ..)

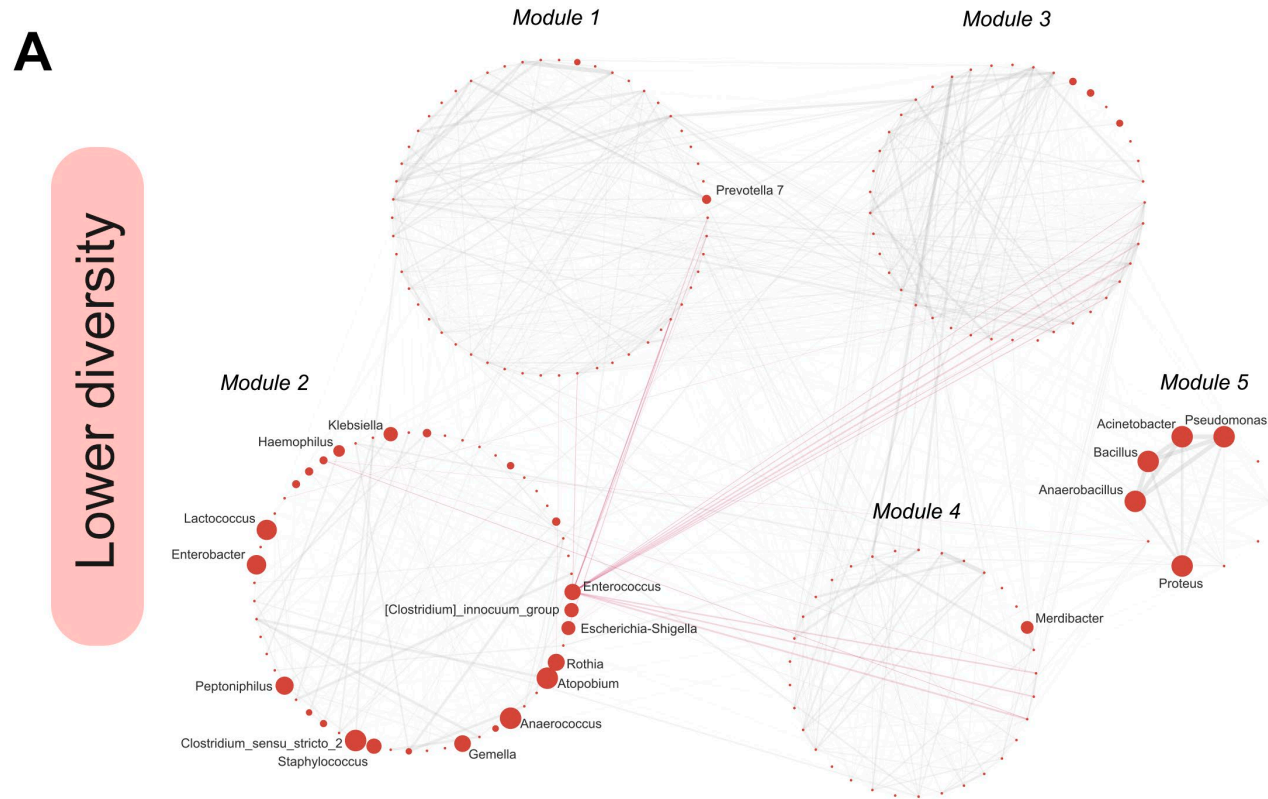
Lower-diversity group composition:
 overabundance of *Enterococcaceae* and *Enterobacteriaceae*, including **many facultative aerobic pathobionts** (*Enterococcus*, *Escherichia-Shigella* and *Enterobacter*)

GM diversity and composition before transplantation correlate with survival

GM NETWORKS OF THE LOWER-DIVERSITY GROUP

Differences between the higher- and lower-diversity groups in terms of network topology and network properties linked to potential ecological interactions within GM communities.

5 modules were detected, which were clearly differently populated in the two diversity groups.



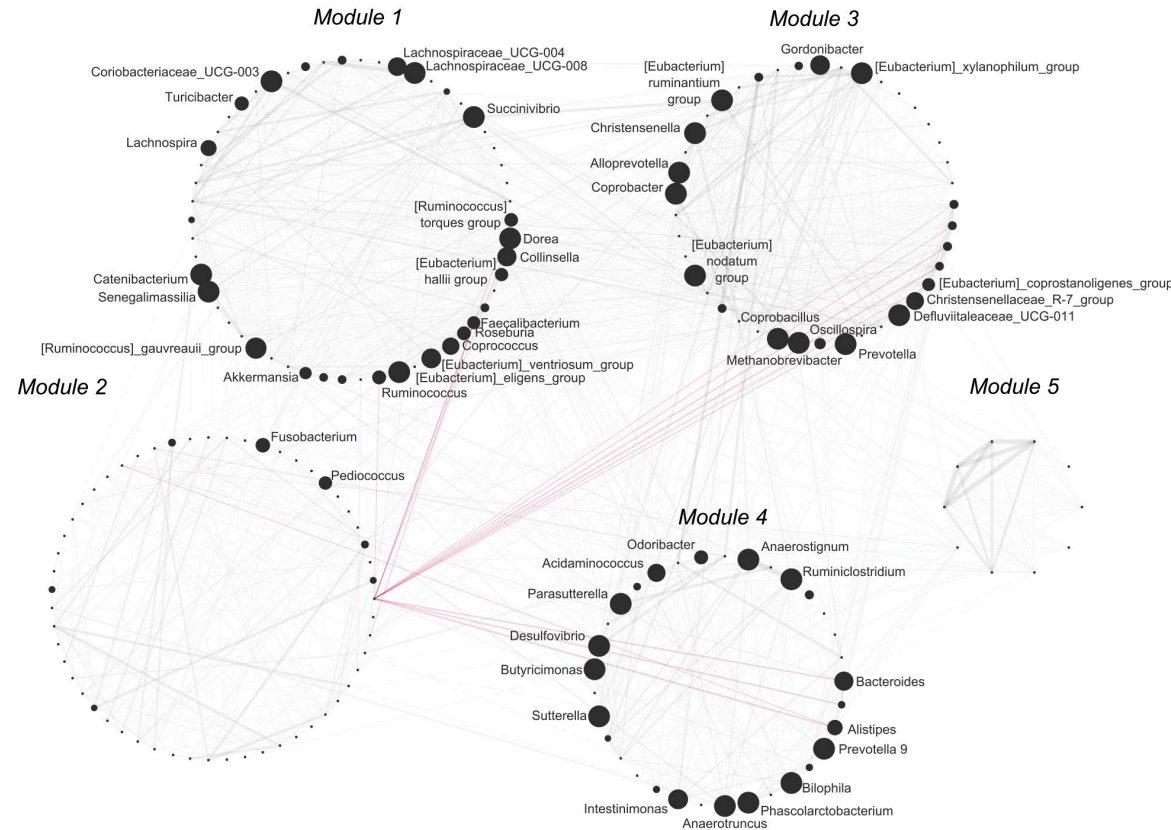
Before HSCT, GM network of patients belonging to the lower-diversity group showed enrichment in network modules:

#2, represented by *Enterococcus*, *Escherichia-Shigella*, *Rothia*, *Enterobacter*, *Anaerococcus* and *Klebsiella*

#5, with *Pseudomonas*, *Anaerobacillus*, *Bacillus*, *Proteus*, and *Acinetobacter*

GM NETWORKS OF THE HIGHER-DIVERSITY GROUP



Higher diversity

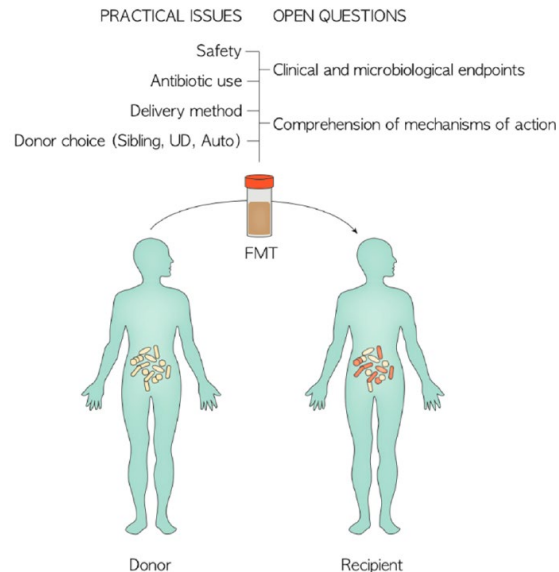


Before HSCT, GM network of patients belonging to the higher-diversity group showed enrichment in modules **#1, #3 and #4** containing several SCFAs producers (*i.e.*, *Bacteroides*, *Coprococcus*, *Roseburia*, *Oscillospira*, *Faecalibacterium*, *Ruminococcus*, and [*Eubacterium*] spp)

NEXT STEPS....

Pietro Merli,^{1*} Lorenza Putignani,^{2*} Annalisa Ruggeri,¹ Federica Del Chierico,³ Livia Gargiullo,⁴ Federica Galaverna,¹ Stefania Gaspari,¹ Daria Pagliara,¹ Alessandra Russo,³ Stefania Pane,⁵ Luisa Strocchio,¹ Mattia Algeri,¹ Francesca Rea,⁶ Erminia Francesca Romeo,⁶ Paola Bernaschi,⁷ Andrea Onetti Muda,⁸ Bruno Dallapiccola⁹ and Franco Locatelli¹⁰

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Decolonization of multi-drug resistant bacteria by fecal microbiota transplantation in five pediatric patients before allogeneic hematopoietic stem cell transplantation: gut microbiota profiling, infectious and clinical outcomes

Fecal microbiota transplantation for the treatment of steroid refractory GvHD in pediatric patients

PNRR BBMRI Microbiome Biobank

 **BBMRI.it**
Biobanking and BioMolecular Resources Research Infrastructure of Italy

Harnessing the Gut Microbiota to Potentiate the Efficacy of CAR T Cell Therapy

HemaSphere

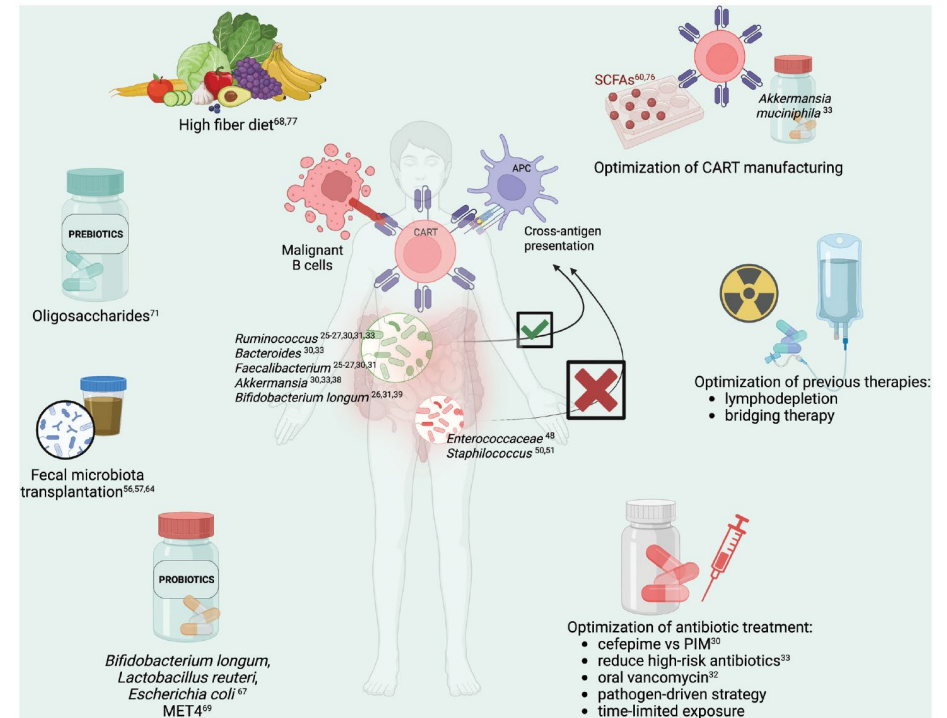
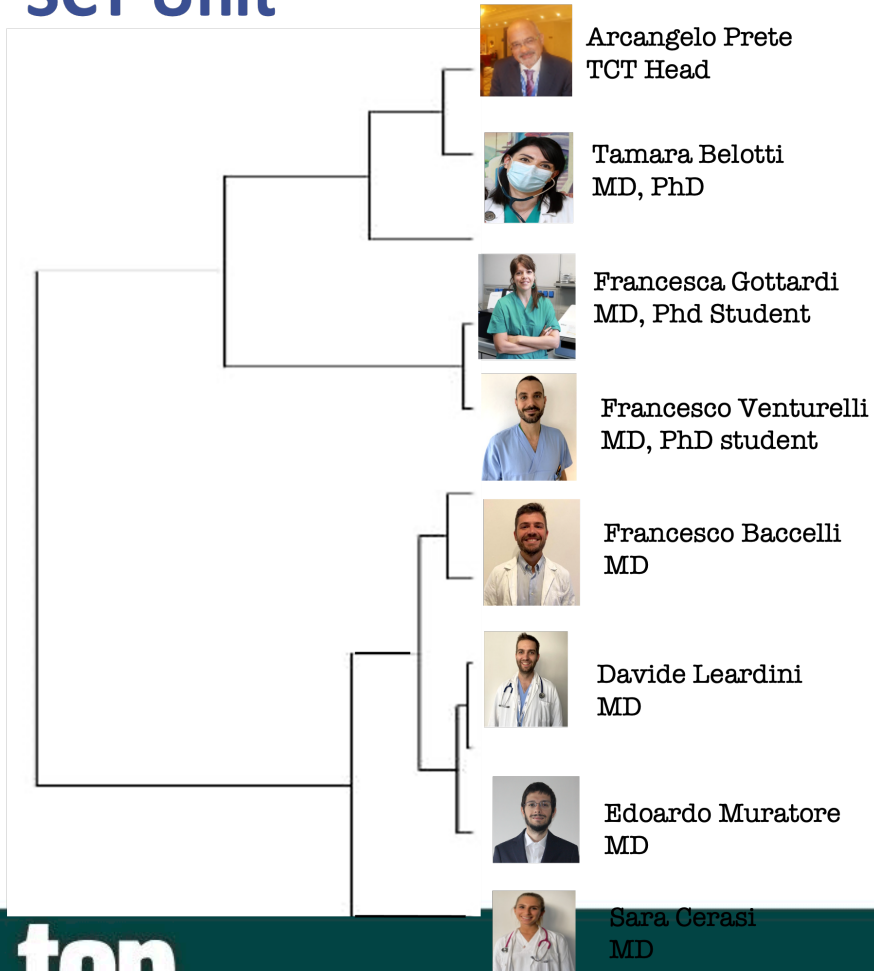


Figure 1. Possible strategies to enhance CART immunotherapy by modulating the gut microbiota. CART = chimeric antigen receptor T cell therapy; MET4 = Microbial Ecosystem Therapeutics; PIM = piperacillin-tazobactam, imipenem, meropenem; SCFAs = short-chain fatty acids.

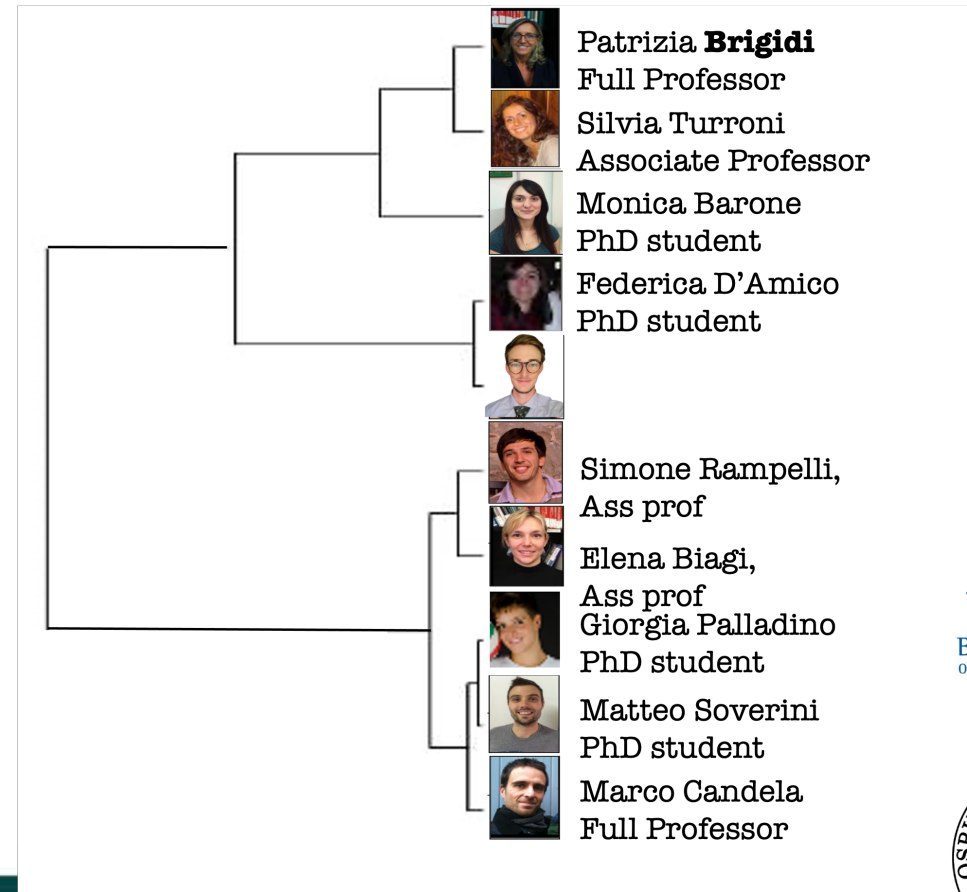
GRAZIE PER L'ATTENZIONE

Aknowledgments: dai diamanti non nasce niente.....

SCT Unit



Micro Unit



Dott.ssa Maura Faraci



Dott. Simone Cesaro



Dott. Pietro Merli
Prof. Franco Locatelli



Dott. Marco Zecca

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TOP TEN Slides

1

PHARMACOMICROBIOMICS

Pharmacogenomics: how human genome variations affect drug action

Pharmacomicrobiomics: how GM, as the second human genome, affects drugs action

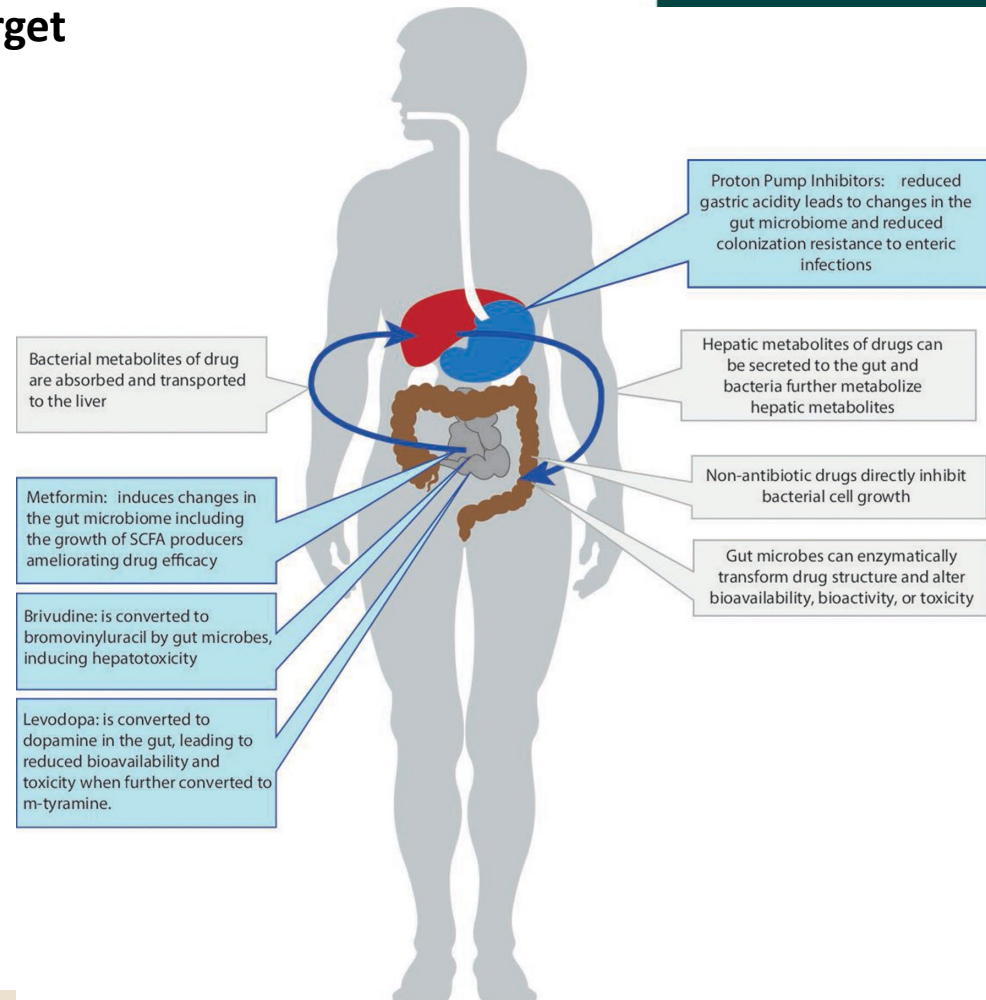
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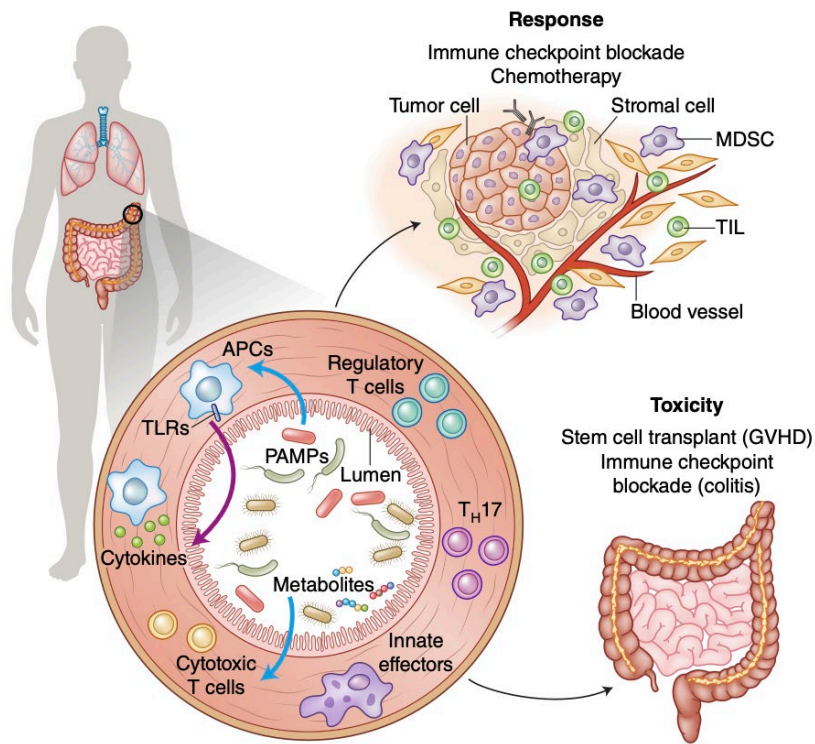
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Weersma RK, *et al.* Gut 2020



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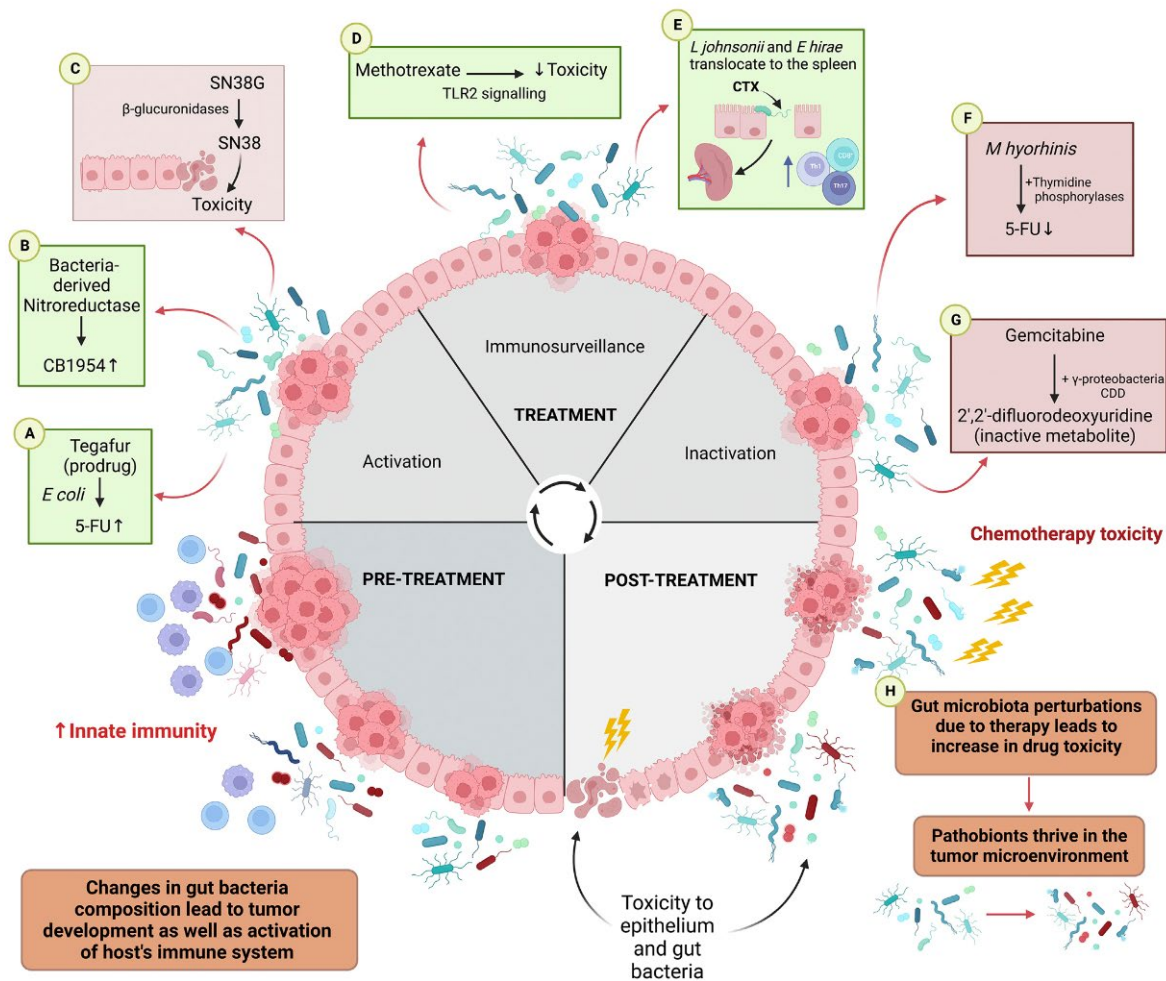
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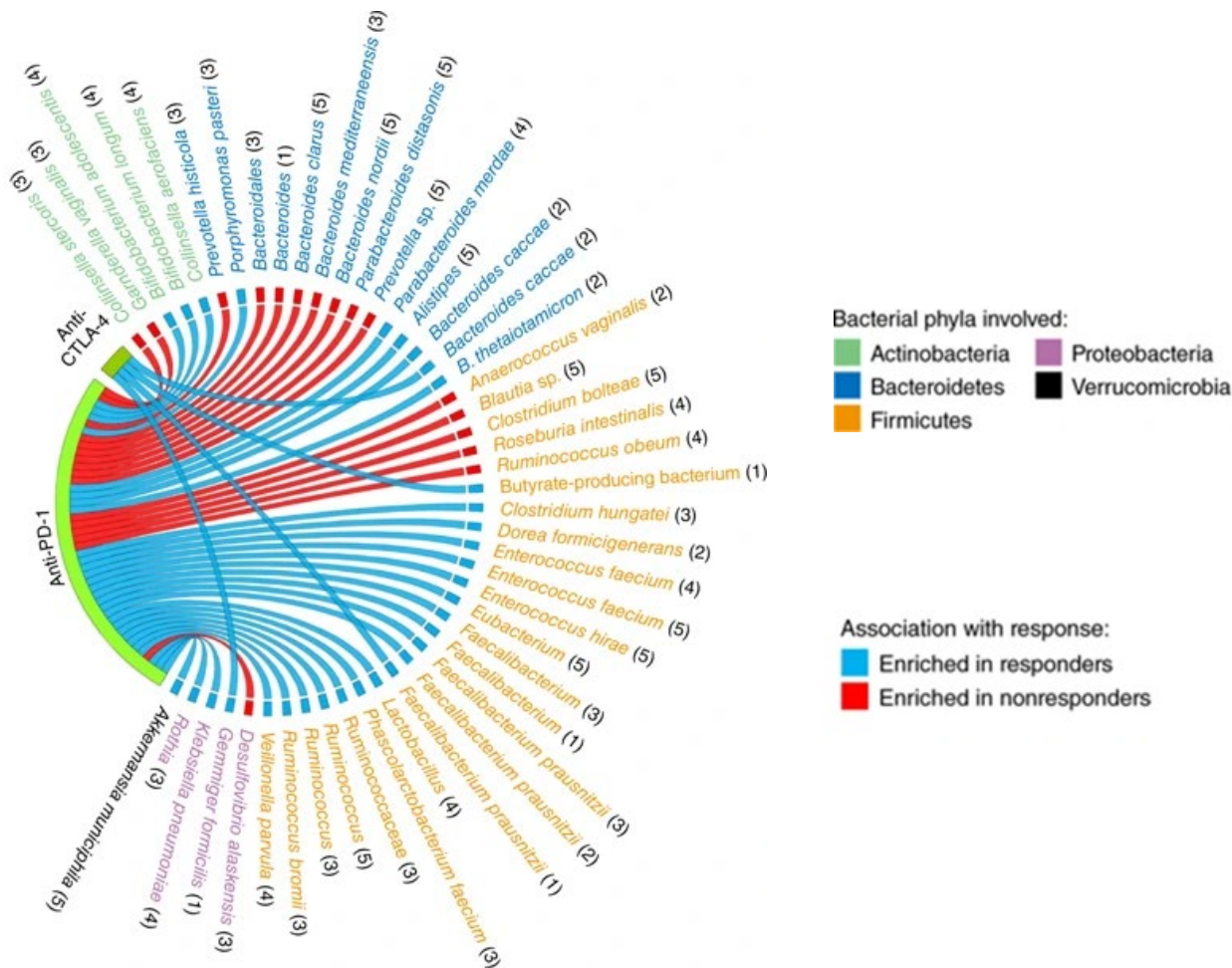
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MECHANISMS OF HOST-ONCOMICROBIOME-THERAPY INTERACTIONS



4

GM STRUCTURE IS PREDICTIVE OF RESPONSE TO IMMUNOTHERAPY



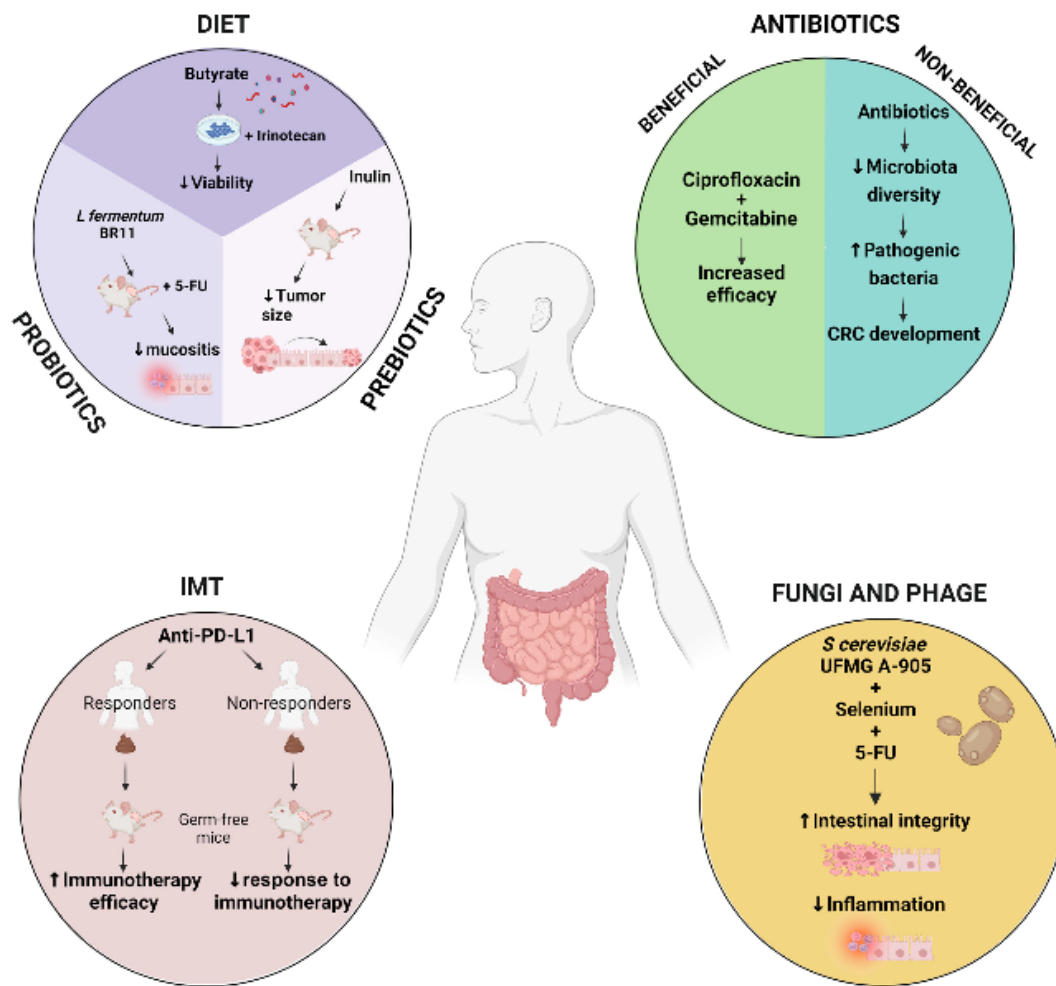
A positive response to mAbs targeting PD-1 in metastatic melanoma patients is associated with more “favourable” GM:

- higher diversity
- higher relative abundance of health-associated bacteria (*Ruminococcaceae*, *Lachnospiraceae*, *Bifidobacteriaceae* and *Coriobacteriaceae*)



Enhanced systemic and anti-tumour immune responses and improved effector T cell function

THERAPY OUTCOMES CAN BE MODULATED BY RESHAPING THE MICROBIOME

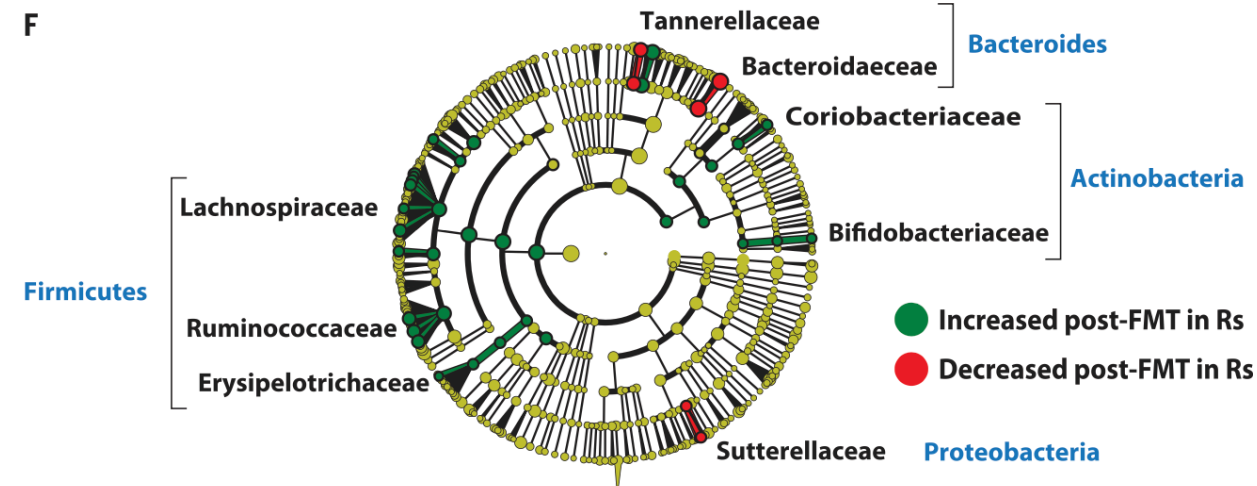


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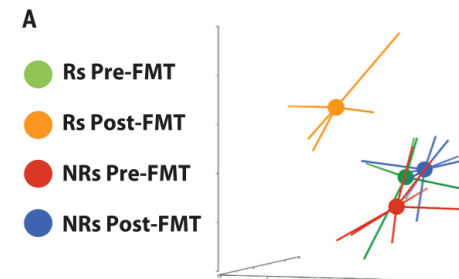
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SERUM CYTOKINES



Responders exhibited:

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DYNAMICS OF GM DIVERSITY AND GVHD SIGNATURE IN CHILDREN UNDERGOING HSCT

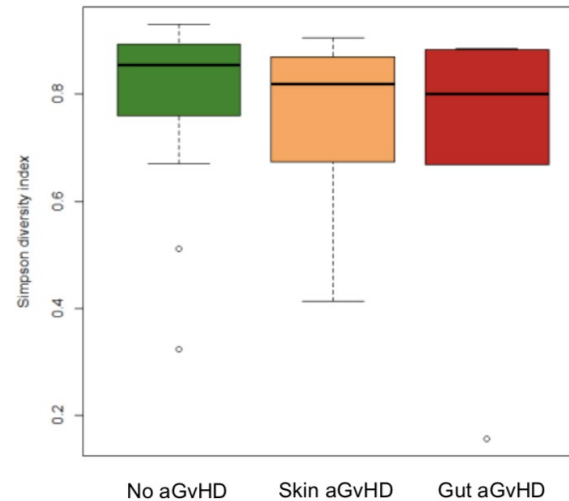
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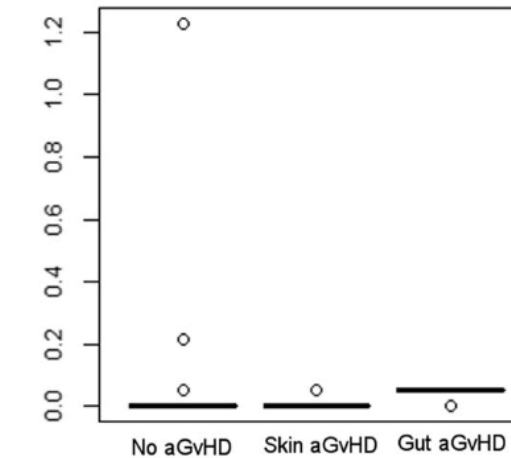
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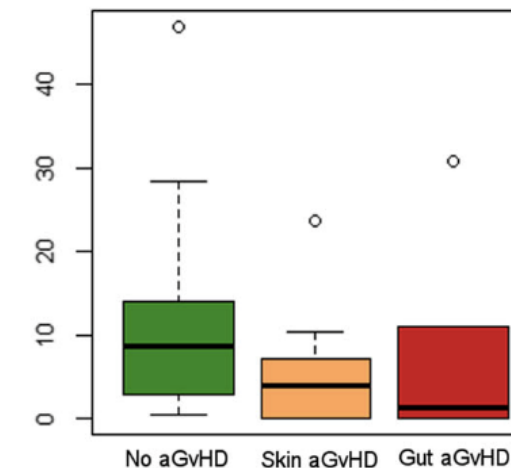
High relative abundance of *Fusobacterium nucleatum* associated to severity of intestinal aGvHD



B Fusobacterium OTUs (%)



C Blautia OTUs (%)



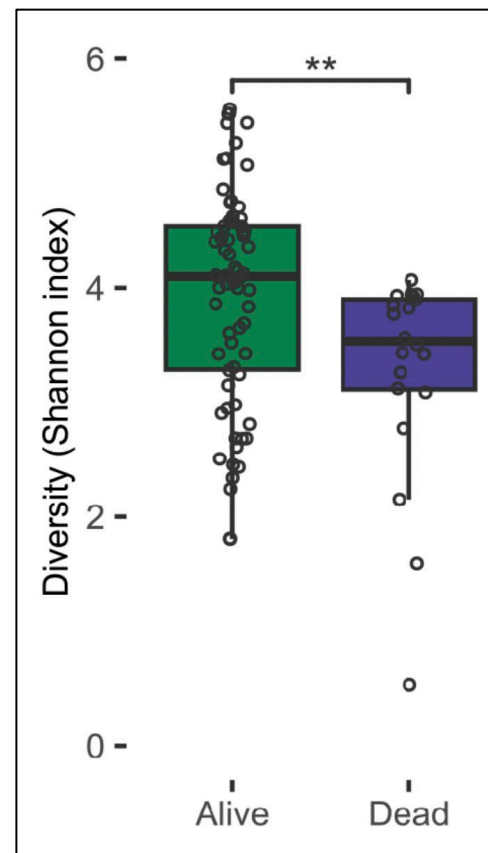
Pathobionts

SCFA producer:

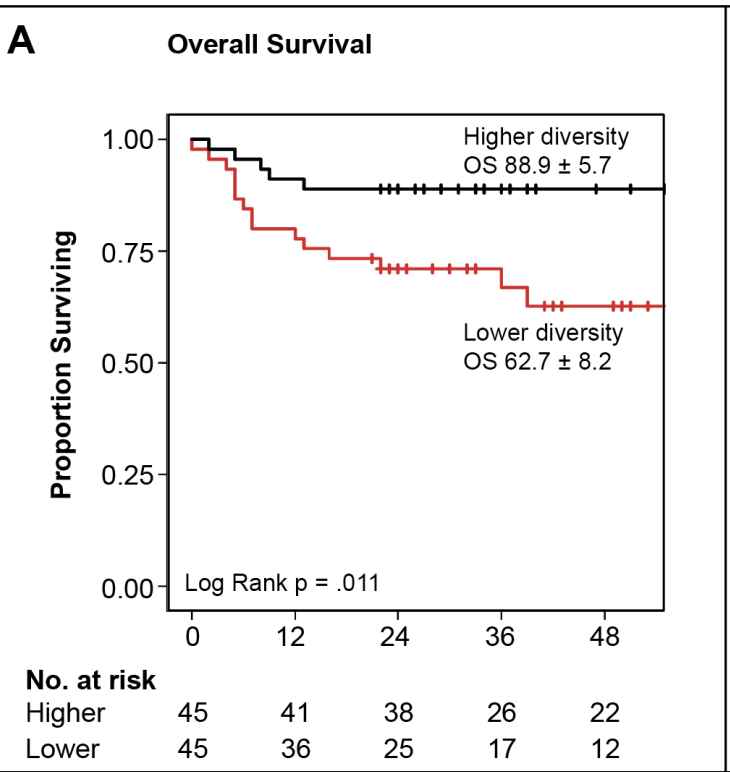
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- crosstalk between GM and host immune cells

GM DIVERSITY AND SURVIVAL IN CHILDREN RECEIVING HSCT

GM diversity before HSCT



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- Evaluation of **GM diversity before HSCT and at engraftment**
- Evaluated the impact of GM diversity on the survival post HSCT



First evidence of an association between pre-transplantation lower GM diversity and poorer outcome in children undergoing allo-HSCT

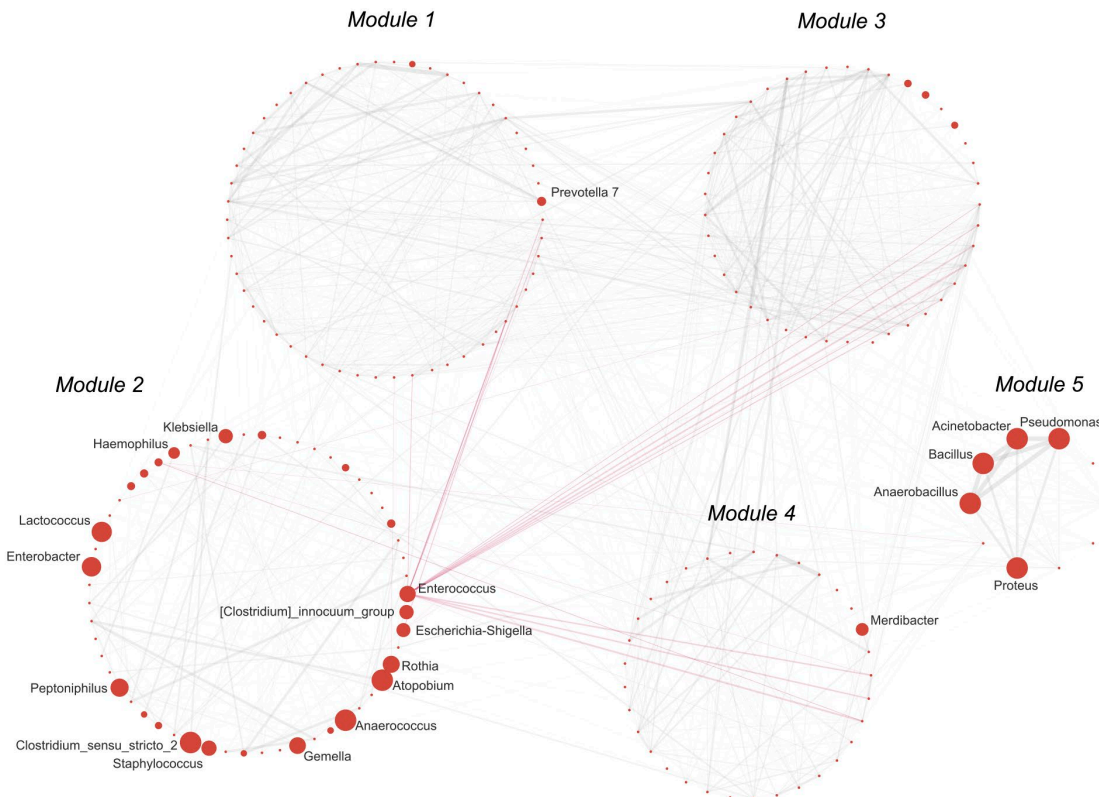
GM NETWORKS OF THE LOWER-DIVERSITY GROUP

Differences between the higher- and lower-diversity groups in terms of network topology and network properties linked to potential ecological interactions within GM communities

5 modules were detected, which were clearly differently populated in the two diversity groups

A

Lower diversity



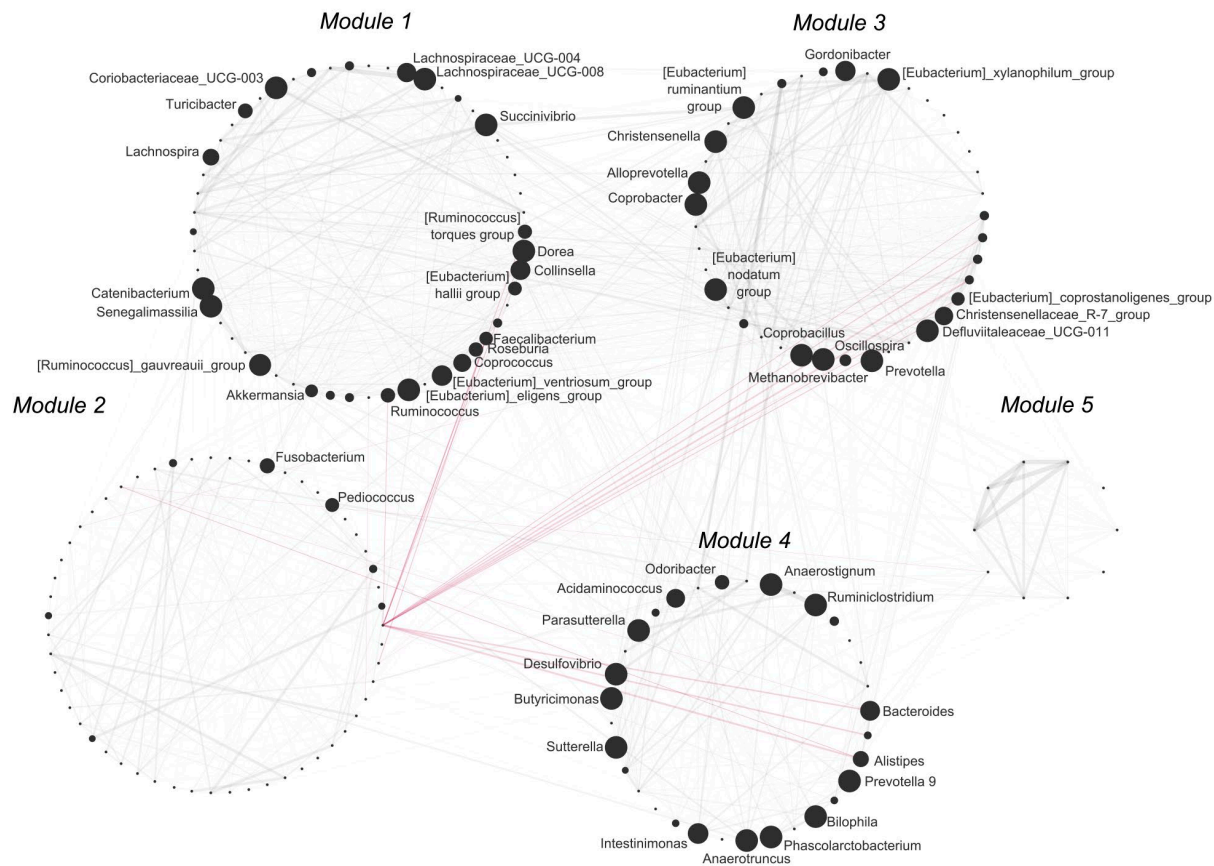
Before HSCT, GM network of patients belonging to the lower-diversity group showed enrichment in network modules:

#2, represented by *Enterococcus*, *Escherichia-Shigella*, *Rothia*, *Enterobacter*, *Anaerococcus* and *Klebsiella*

#5, with *Pseudomonas*, *Anaerobacillus*, *Bacillus*, *Proteus*, and *Acinetobacter*

GM NETWORKS OF THE HIGHER-DIVERSITY GROUP

Higher diversity



Before HSCT, GM network of patients belonging to the higher-diversity group showed enrichment in modules **#1**, **#3** and **#4** containing several SCFAs producers (*i.e.*, *Bacteroides*, *Coprococcus*, *Roseburia*, *Oscillospira*, *Faecalibacterium*, *Ruminococcus*, and *[Eubacterium]* spp)