



Microbiota and its role for response to immunotherapy



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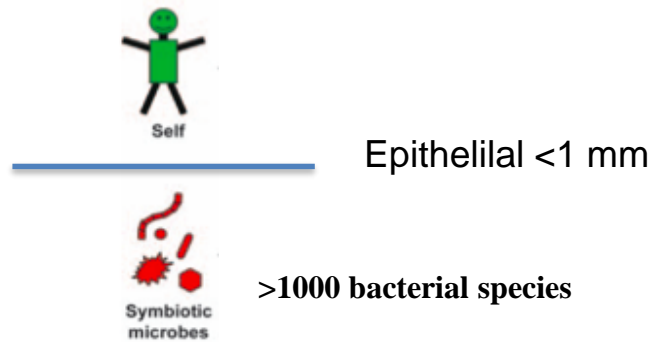




**I'M
NOT
DANGEROUS**



From forgotten to superorganism

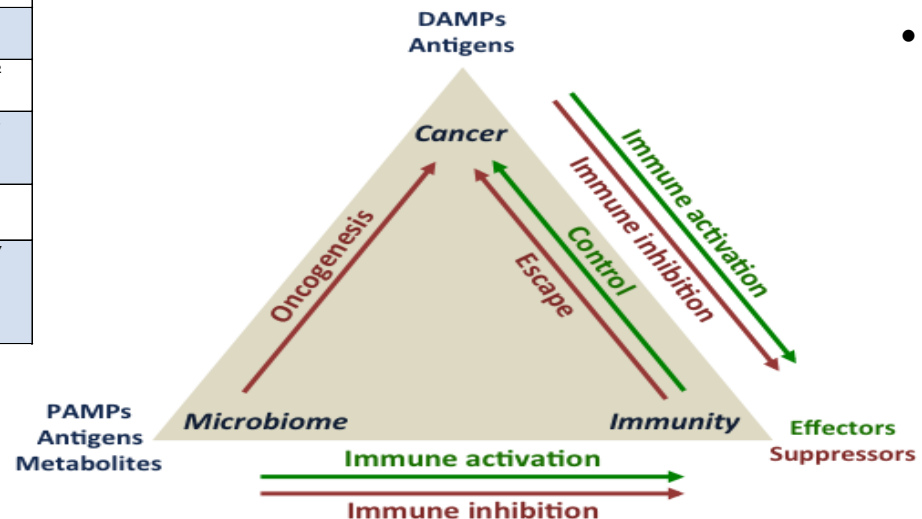


Epidemiological associations between commensals and cancer



- Process nutrients
- Produce vitamins
- Protects from new microbes
- Shape the immune system

Cancer	Analyzed specimens	Association	Ref (PMID)
HNSCC	Saliva	The total abundance of genus <i>Streptococcus</i> , <i>Dialister</i> , and <i>Veillonella</i> can be used to discriminate patients with tumor from controls.	27259999
ALL	Feces	Lower abundance of <i>Anaerostipes</i> , <i>Coprococcus</i> , <i>Roseburia</i> in the ALL group compared with siblings	27527070
Pancreas	Oral wash	<i>Porphyromonas gingivalis</i> and <i>Aggregatibacter actinomycetemcomitans</i> , were associated with higher risk of pancreatic cancer	27742762
HPV cancer	Cervical mucus	When comparing CIN2+ vs CIN1: <i>L. iners</i> and unclassified <i>Lactobacillus spp</i> was associated with CIN 2+	26935422
Breast cancer	Normal (or tumor) breast tissue versus healthy breast	BC healthy tissue associated with higher relative abundances of <i>Bacillus</i> , <i>Enterobacteriaceae</i> and <i>Staphylococcus</i>	27342554
GU cancer	Urine	<i>Streptococcus</i> abundance was nearly zero in most normal samples but significantly elevated in patient samples	25126590
Lung cancer	Sputum and buccal samples	Burning coal exposed never smoking chinese females in sputum and not in buccal samples compared to controls: <i>Granulicatella</i> (6.1 vs. 2.0%), <i>Abiotrophia</i> (1.5 vs. 0.085%), and <i>Streptococcus</i> (40.1 vs. 19.8%) were enriched in cases compared with controls	24895247

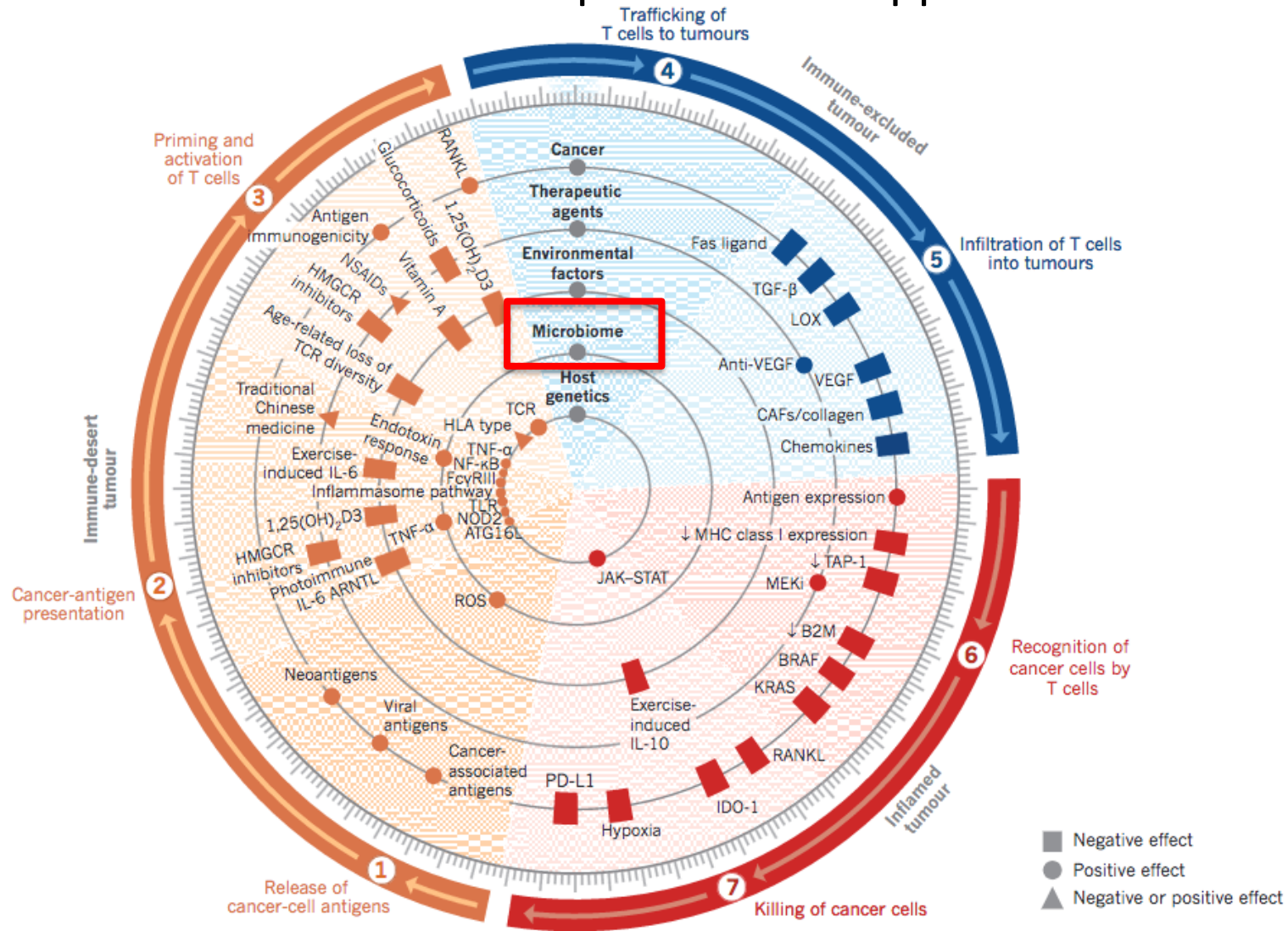


Sender R. *BioRxiv* 2016

Zitvogel L. *Cell* 2016 and *Nat Rev* 2017

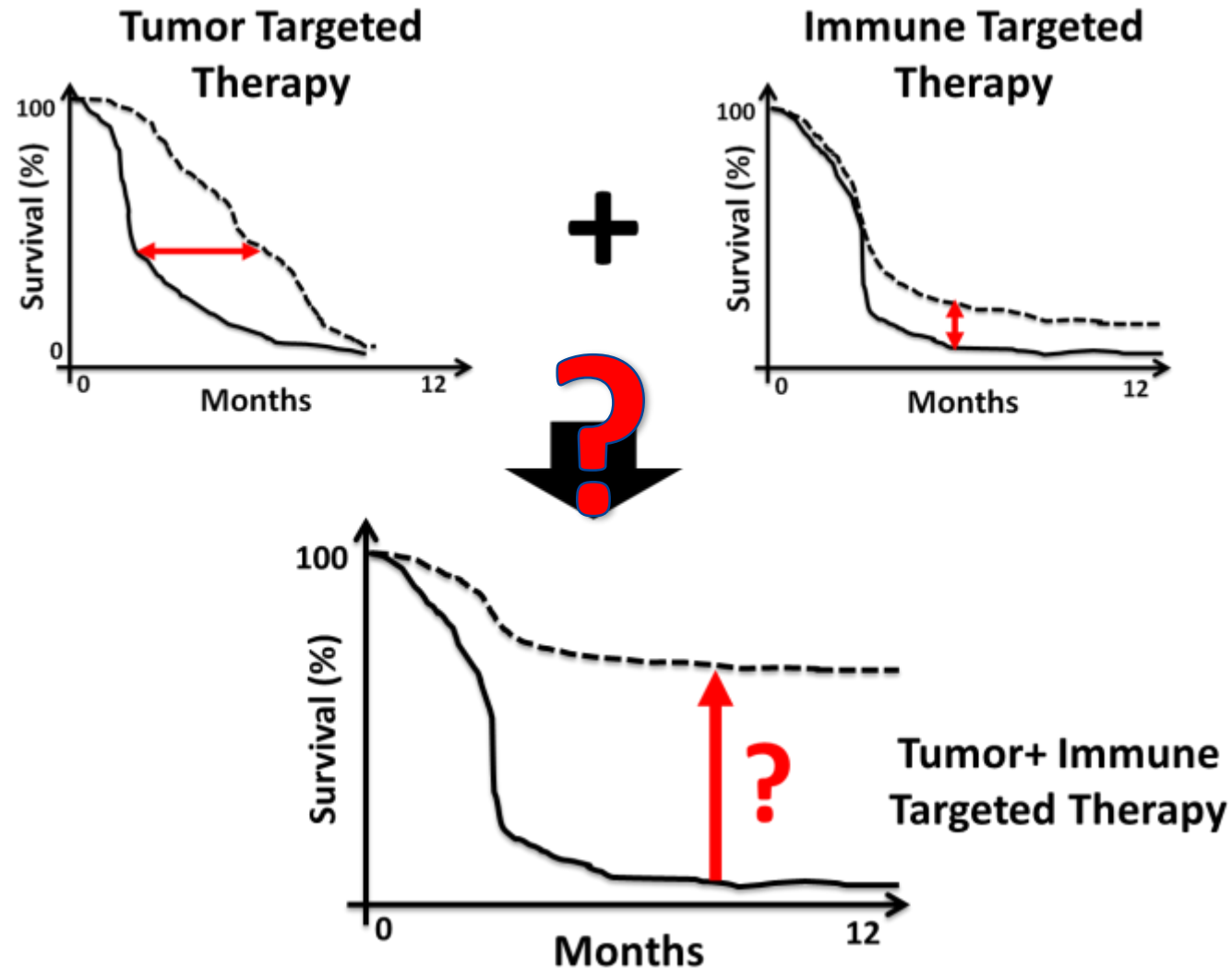
The cancer-immune set point:

the equilibrium between the factors that promote or suppress anticancer immunity



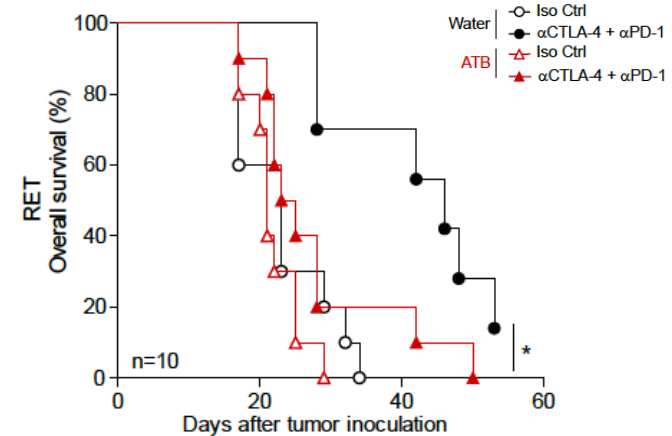
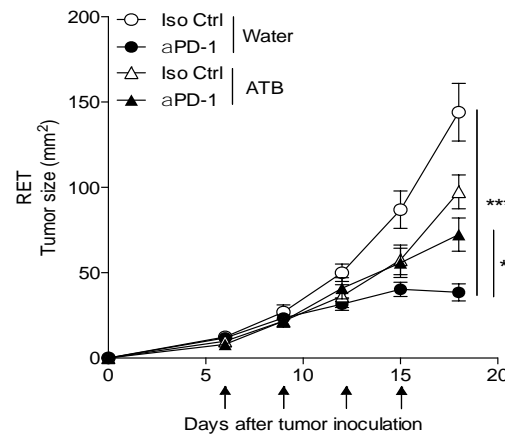
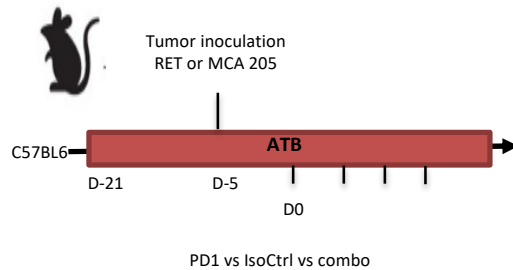
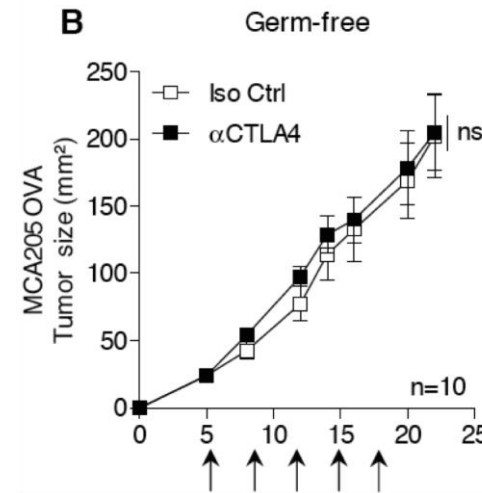
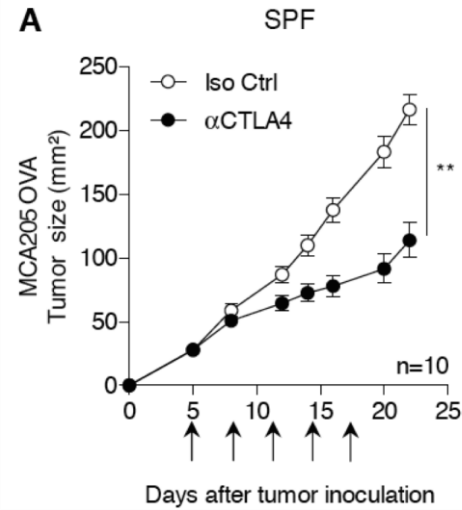
Future of Immuno-Oncology:

Could a « minimalist microbiome » normalize the cancer-immune set point?



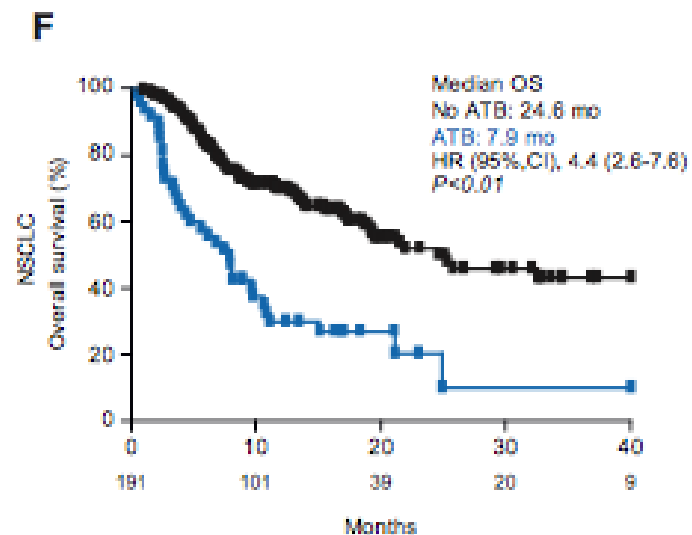
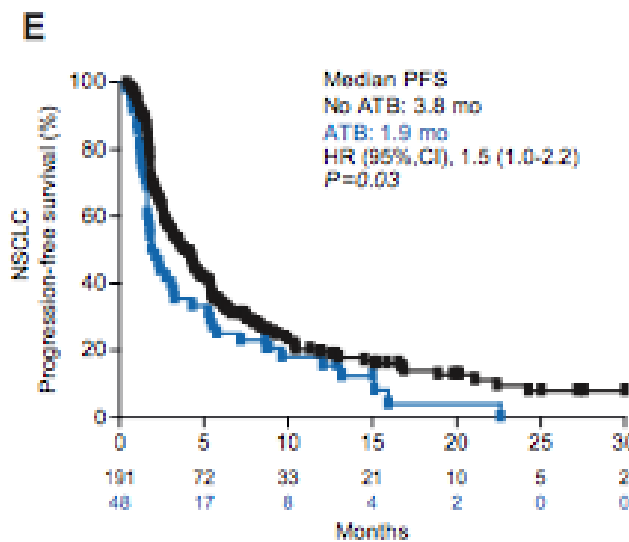
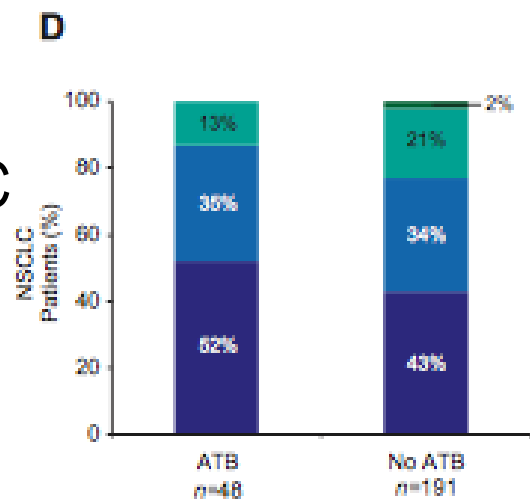
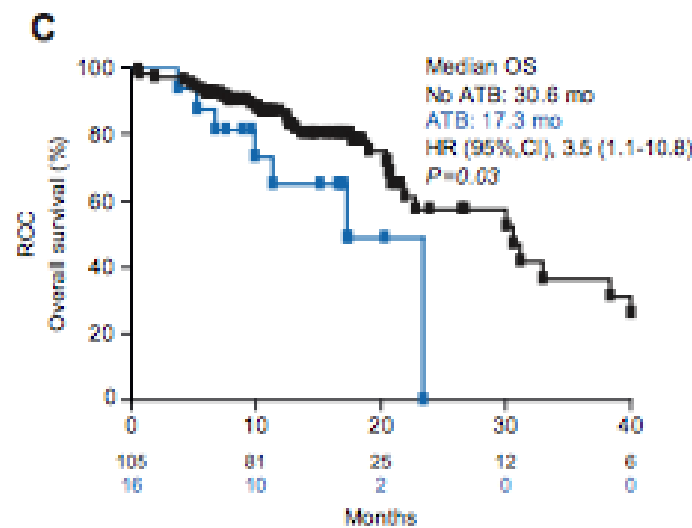
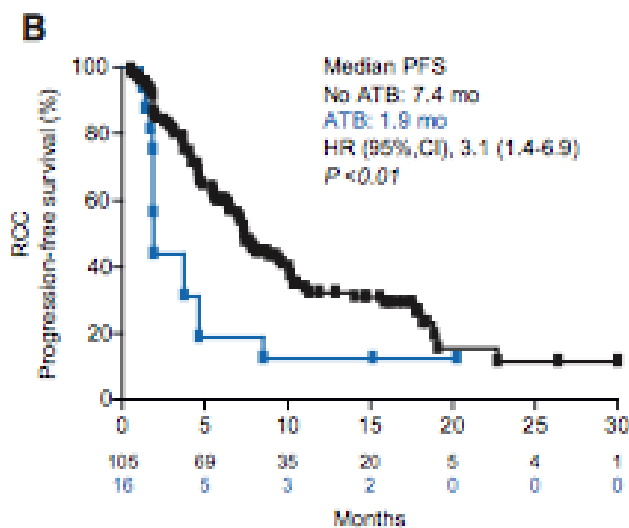
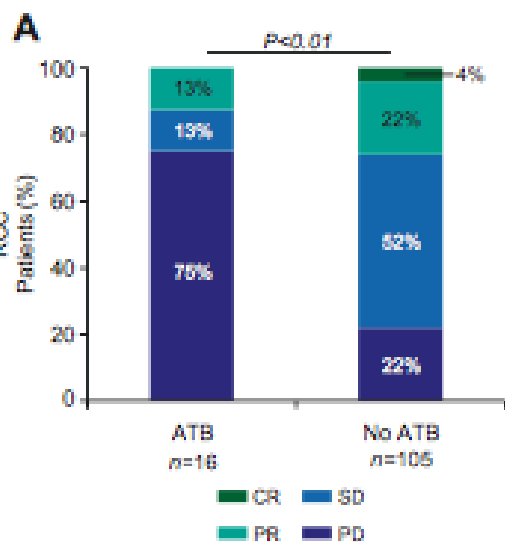


The antitumor efficacy of anticancer immunotherapy requires gut bacteria



Similar results using cyclophosphamide, platinum salts, IL-10R
(Vétizou 2015, Iida Science 2013, Viaud Science 2013, Routy 2017).

In 2 cohorts of patients, RCC and NSCLC, prior ATB was associated with worse outcomes with ICI



*Derosa L., Annals Oncol 2018
ASCO GU 2017 Merit Award*

ATB remained independently associated with worse PFS or OS in multivariate analysis

Several reports are confirming the detrimental impact of ATB

	CANCER TYPE	ATB WINDOW	OUTCOME
Routy Science 2018	NSCLC n =140 RCC n= 67 UC= 32	2 months PRE or 1 month POST	↓ PFS ↓ OS
Derosa Annals 2018	NSCLC n=239 RCC n=121	1 month PRE	↑ PD ↓ PFS ↓ OS
Huemer Oncotarget 2018	NSCLC n=30	1 month PRE or 1 month POST	↓ PFS ↓ OS
Kaderbhai Anticancer Res 2017	NSCLC n=74	3 months PRE	No change in PFS ↓ OS (not published)
Elkief (In press)	Melanoma n=74	1 month PRE	↓ PFS ↓ OS
Lalani ASCO GU 2018	RCC n=146	2 months PRE or 1 month POST	↓ ORR ↓ PFS
Tinsley ASCO 2018	Melanoma n=201 NSCLC n=58 RCC n=46	14 days PRE or 42 days POST	↓ PFS ↓ OS
Do ASCO 2018	NSCLC n=109	1 month PRE or 1 month POST	↓ OS
Rubio IASLC 2018	NSCLC n = 168	2 months PRE or 1 month POST	↓ PFS ↓ OS
Galli IASLC 2018	NSCLC n=157	ATB for an average of 9 days	↓ PFS ↓ OS
Ouaknine IASLC 2018	NSCLC n=72	2 months PRE or 1 month POST	↓ OS

n= 1744

Elkief, Derosa et al. submitted to Annals

Working hypothesis

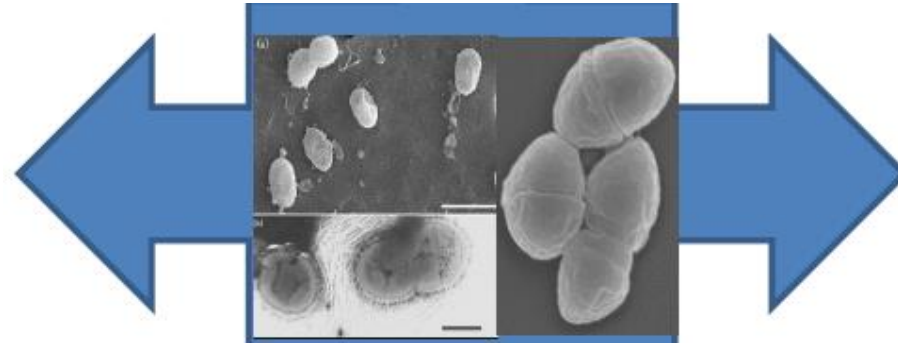
- ATB can change the composition of the gut microbiome (at least in a transient way)
- We speculated that :
- dysbiosis (gut microbiome alteration)
- and ultimately the composition of microbiome might affect the therapeutic efficacy of ICBs

Gut microbiome can predict the efficacy of PD-1/PD-L1 blockade?



How to decipher the clinical relevance of the composition of the gut microbiome?

Avatar platform



Metagenomics
Shotgun DNA Seq



NR

R

R: responders; NR: non responders



The “GRCC Cacathèque” – Stoolbank-

a dynamic analyses in a paired fashion (before 1st inj, (after 2 inj.), after 8 inj., after 6 months)

NSCLC



RCC

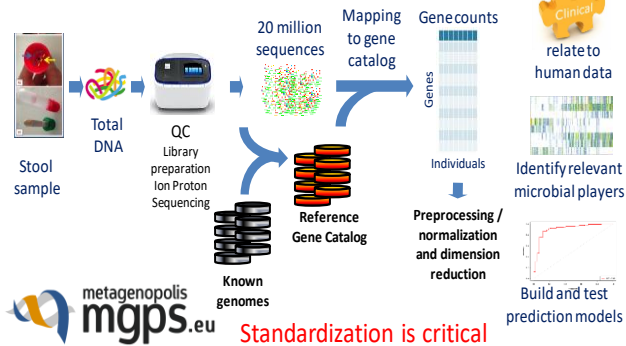


n=100 Discovery cohort
n=53 Validation cohort

- Clinical data on PD-1
- Toxicities
- Responses (CT scan)

Taking into account ATB uptake

Quantitative metagenomics



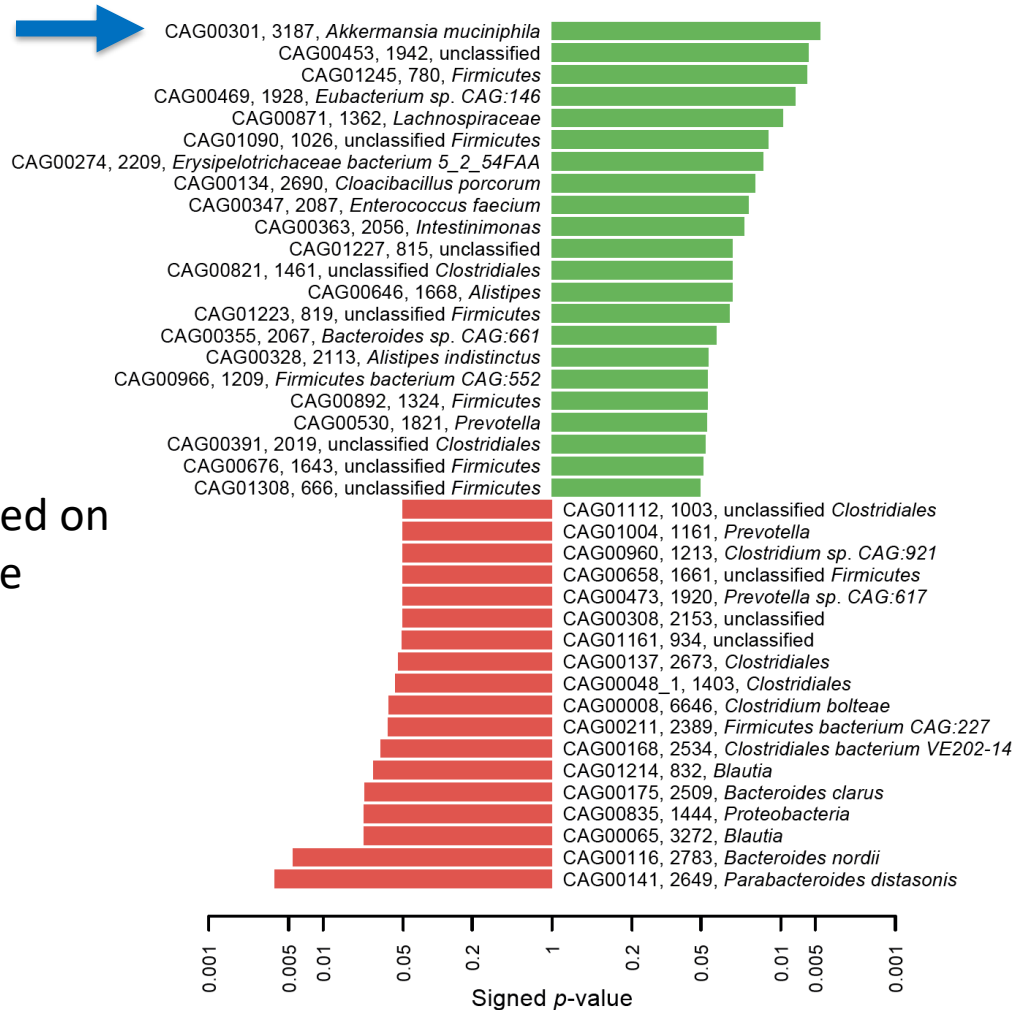
We explored the composition of the gut using quantitative metagenomics analyses by shotgun sequencing



E. LeChâtelier

Akkermansia muciniphila : most significantly associated with favorable clinical outcome

■ Enriched in R: Objective response (PR and SD)
■ Enriched in NR: Objective response (PD or death)



R

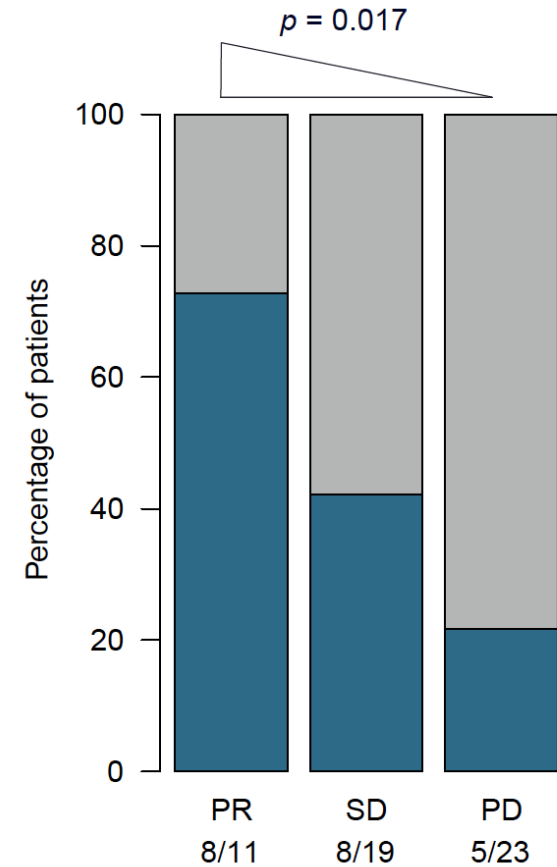
2 different signatures, based on baseline sample



NR

Discovery cohort n =100 (60 NSCLC + 40 RCC)

■ *Akkermansia*
■ No *Akkermansia*



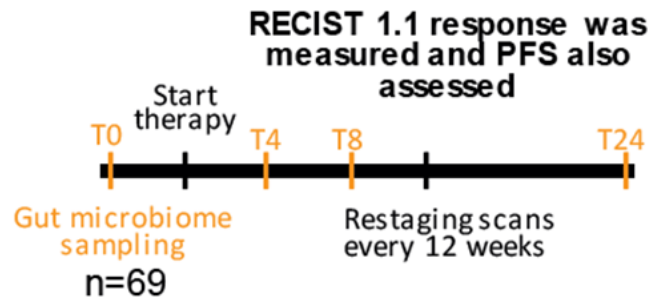
Validation cohort n=53 (27 NSCLC +26 RCC)

(Routy, Le-Chatelier, Derosa et al; Science, 2018).

Specific microbiota fingerprint signature in RCC

NIVOREN trial
NCT03013335

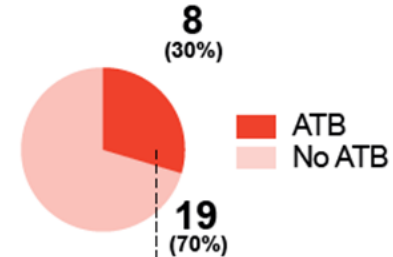
n=85



'Primary resistant'
PD, SD less than 6 months



27
(39%)



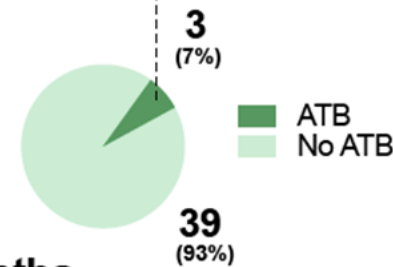
Recent ATB was associated with increased rate of primary PD

N=85 patients with mRCC going onto aPD-1 (Nivoren trial, Gustave Roussy) were enrolled onto protocol and gut microbiome was profiled (n=69)

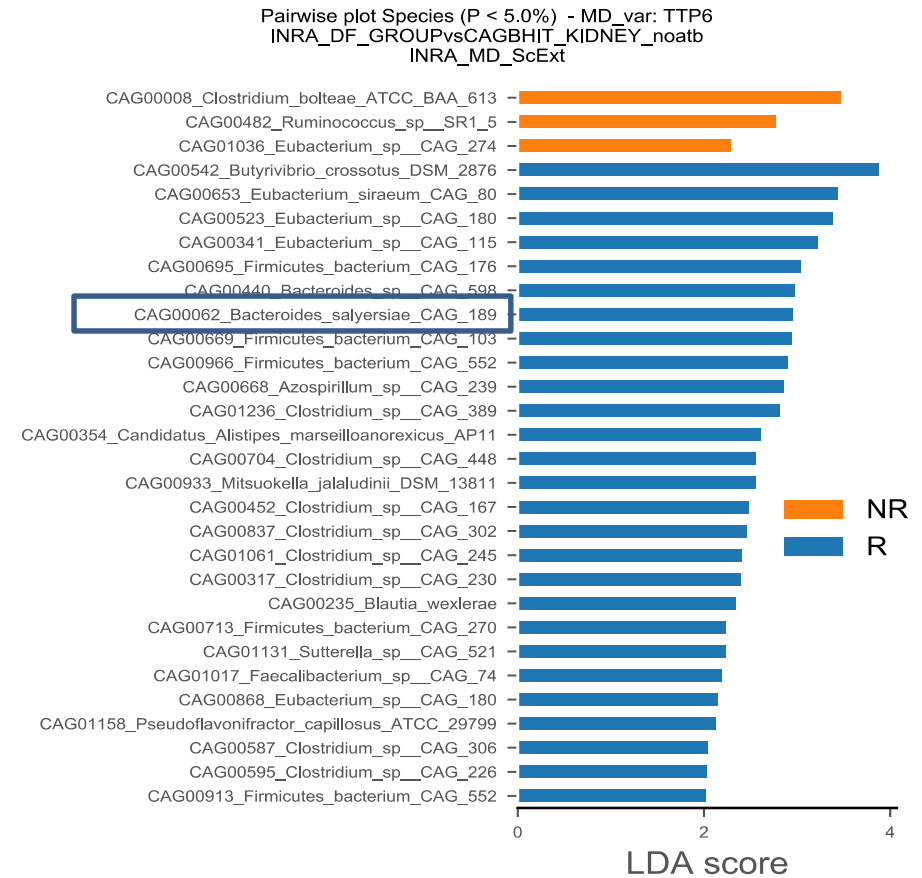
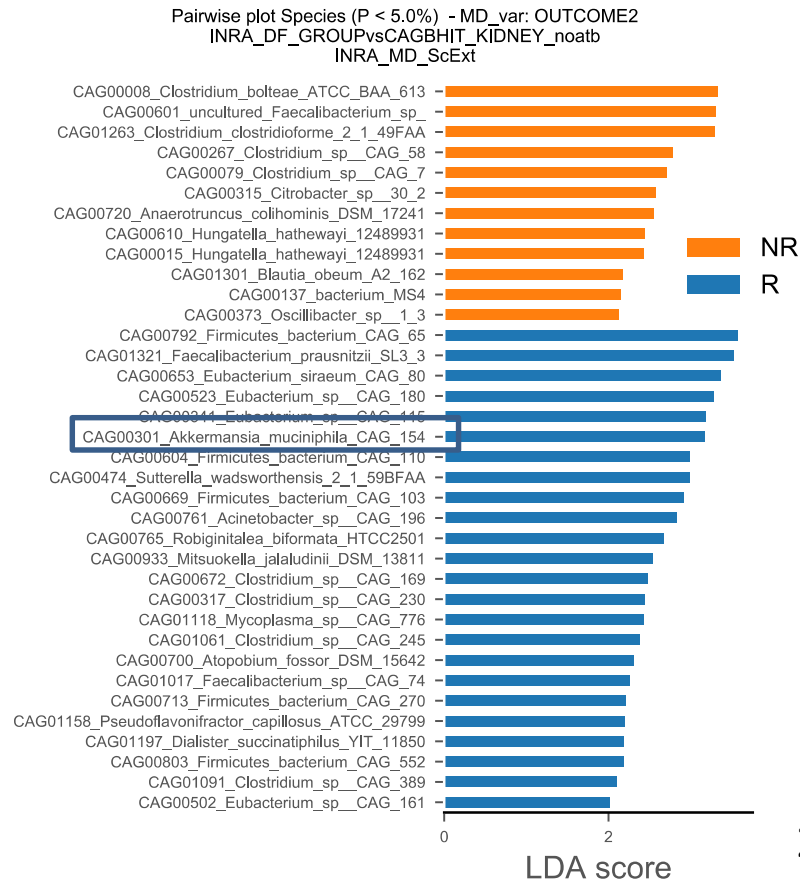
'Non- PD'
CR, PR, SD for at least 6 months



42
(61%)

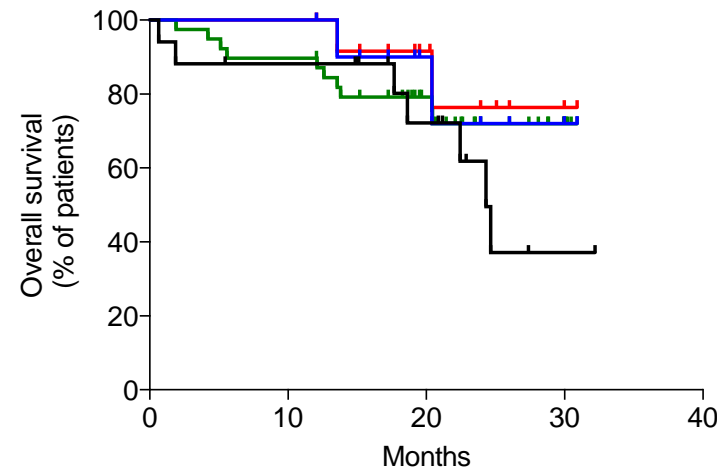
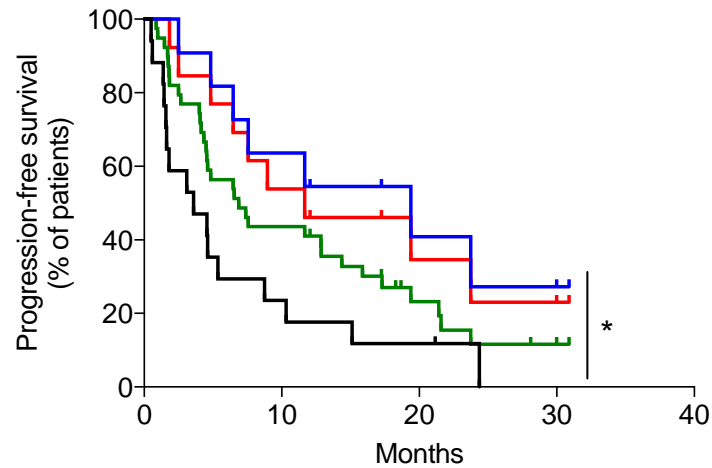
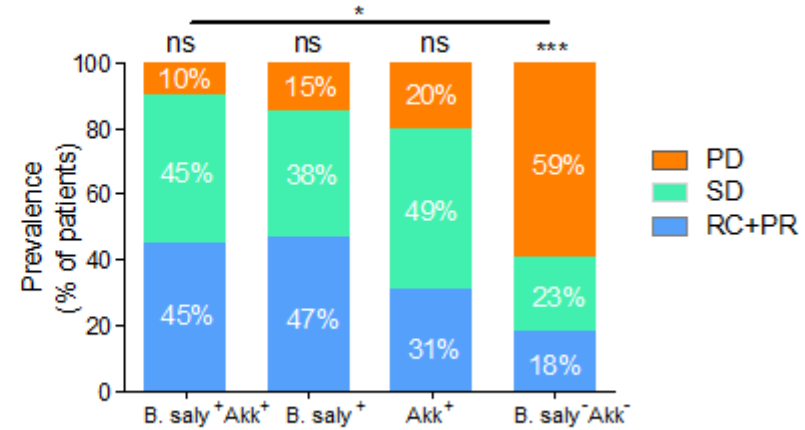
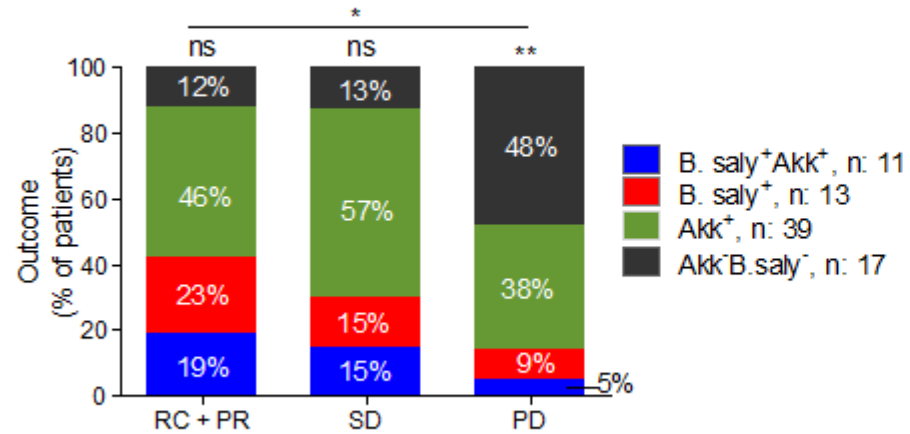


A. muciniphila and *B. salyersiae* were more abundant in R (FR of 2.65 ($p = 0.01$) and 27.09 ($p = 0.05$), respectively)



2 different signatures, based on baseline sample

The co-absence of *A. muciniphila* and *B. salyersiae* was a predictor of primary resistance



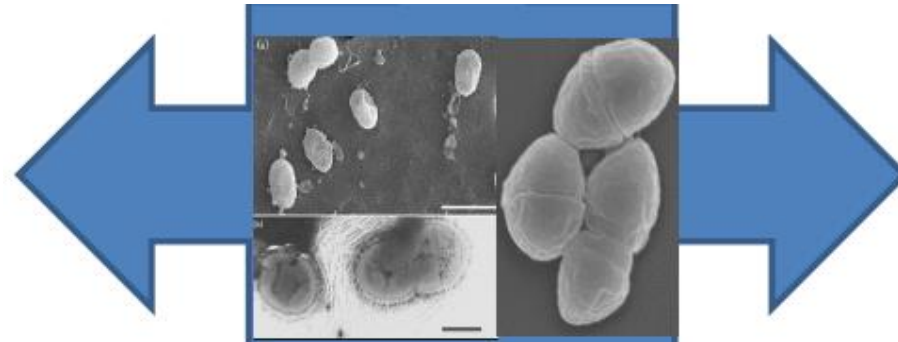
— *B. saly*⁺*Akk*⁺, mPFS: 19.39 months
— *B. saly*⁺, mPFS: 11.67 months
— *Akk*⁺, mPFS: 6.87 months
— *B. saly*⁻*Akk*⁻, mPFS: 3.58 months

— *B. saly*⁺*Akk*⁺, mOS: Undefined
— *B. saly*⁺, mOS: Undefined
— *Akk*⁺, mOS: Undefined
— *B. saly*⁻*Akk*⁻, mOS: 24.32 months

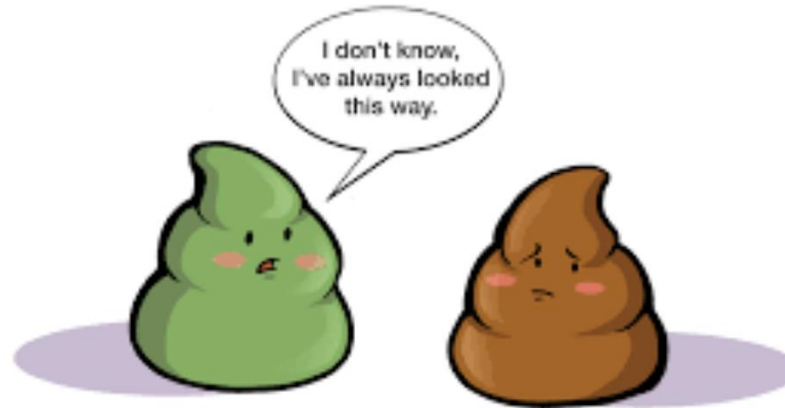
NB: random bacteria from Lefse
Butyvirbio crosotus or
Eubacterium spp
 did not increase PFS

How to decipher the clinical relevance of the composition of the gut microbiome?

Avatar platform



Metagenomics
Shot gun DNA Seq



NR

R

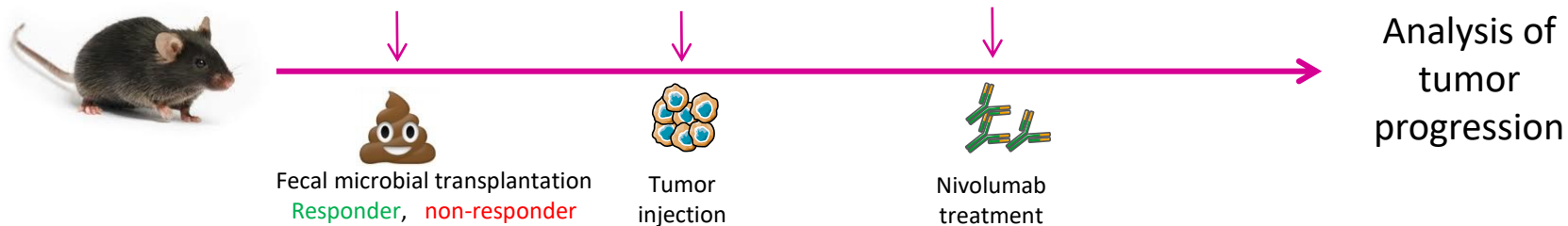
R: responders; NR: non responders





NSCLC Fecal microbial transplantation in « Avatar » mice

We recolonized ATB treated mice with FMT of stools from lung cancer patients

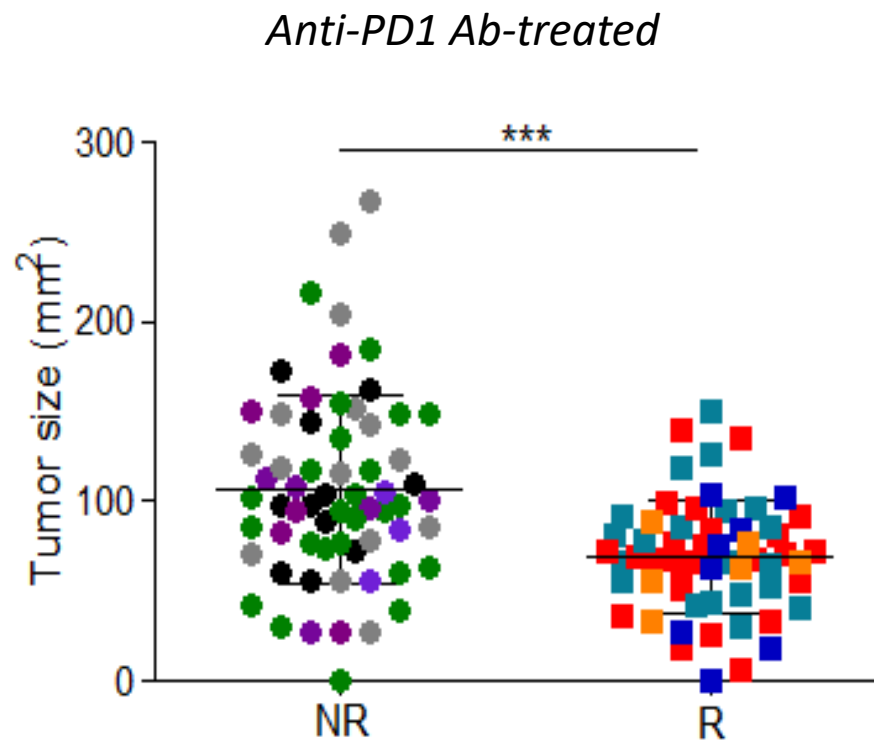
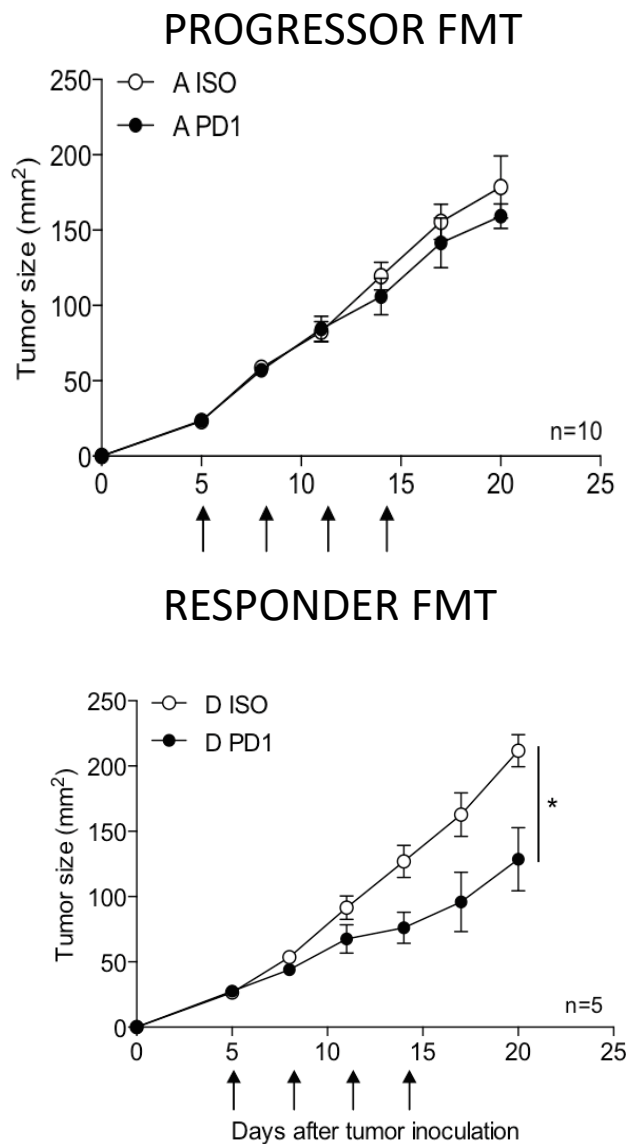


FMT	Patient characteristics							
All patients (n=7)	Non responders				Responders			
	A	B	E	F	C	D	H	I
Age-yr	67	76	77	48	61	73	66	53
Gender	Male	Male	Female	Male	Male	Male	Female	Male
Smoking status	Former	Former	Former	Current	Current	Former	Non smoker	Former
Histology	Non-squamous	Non-squamous	Non-squamous	Squamous	Non-squamous	Non-squamous	Non-squamous	Non-squamous
Mutation status	KRAS positive	Negative	Negative	Negative	Negative	Negative	EGFR positive	Negative
Number of metastatic sites	3	1	1	1	1	1	1	2
Brain metastasis	Yes	No	No	No	No	No	No	No
Number of prior systemic regimens	2	2	1	2	1	4	3	1
Time to Progression-months	2,4	1,3	1,6	1,4	4,5	5	4,3	5,1

(Routy, Le-Chatelier, Derosa et al; Science, 2018).



Feces composition influences the antitumor efficacy of anti-PD1 Abs in avatar mice

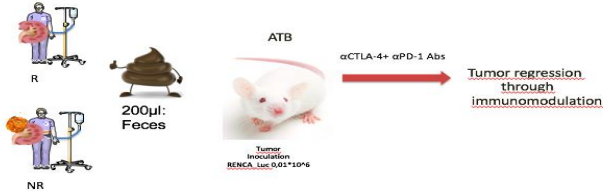


Non responders : A, B, E, F, NSCLC pt (RECIST criteria at 3 months)
Responders : C, D, H, I, NSCLC pt (RECIST criteria at 3 months)

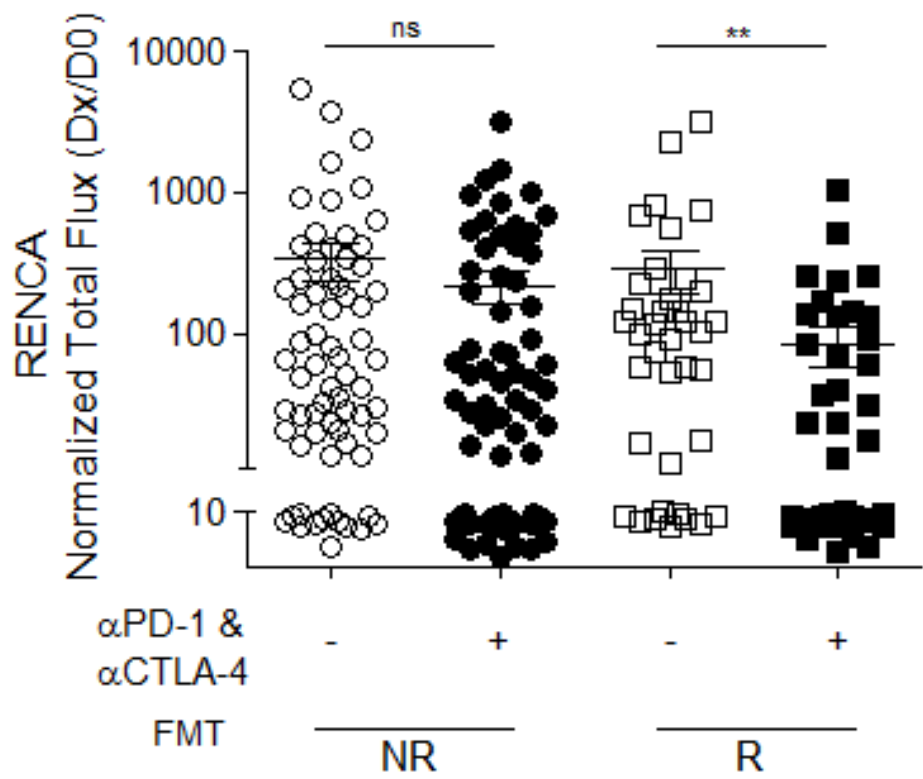
Stools from responders conferred sensitivity

(Routy, Le-Chatelier, Derosa et al; Science, 2018).

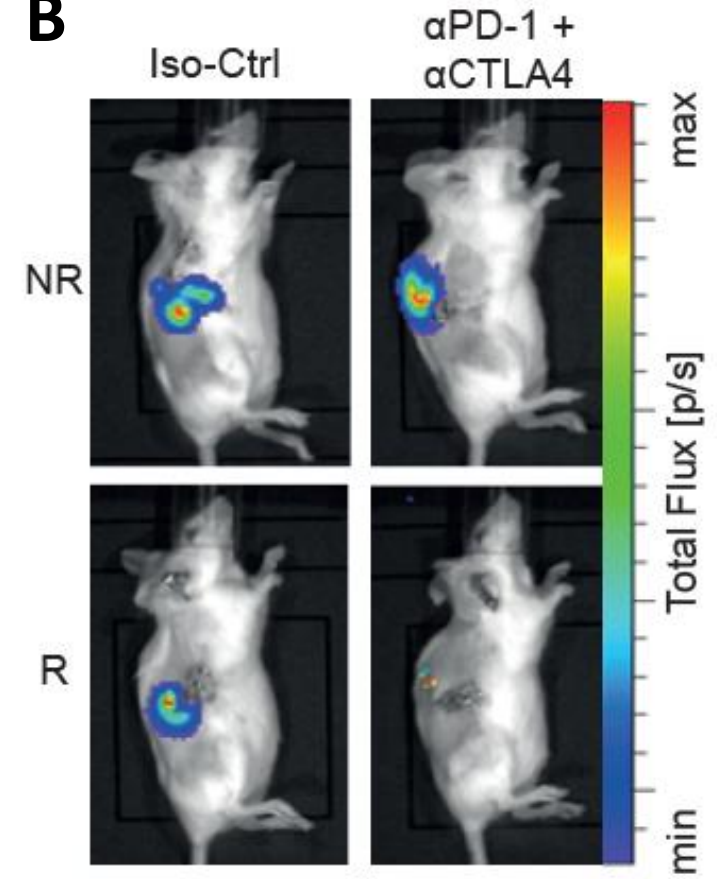
Fecal microbial transplantation in the context of kidney cancer: RCC cancer feces into ATB avatar RENCA mice



A



B



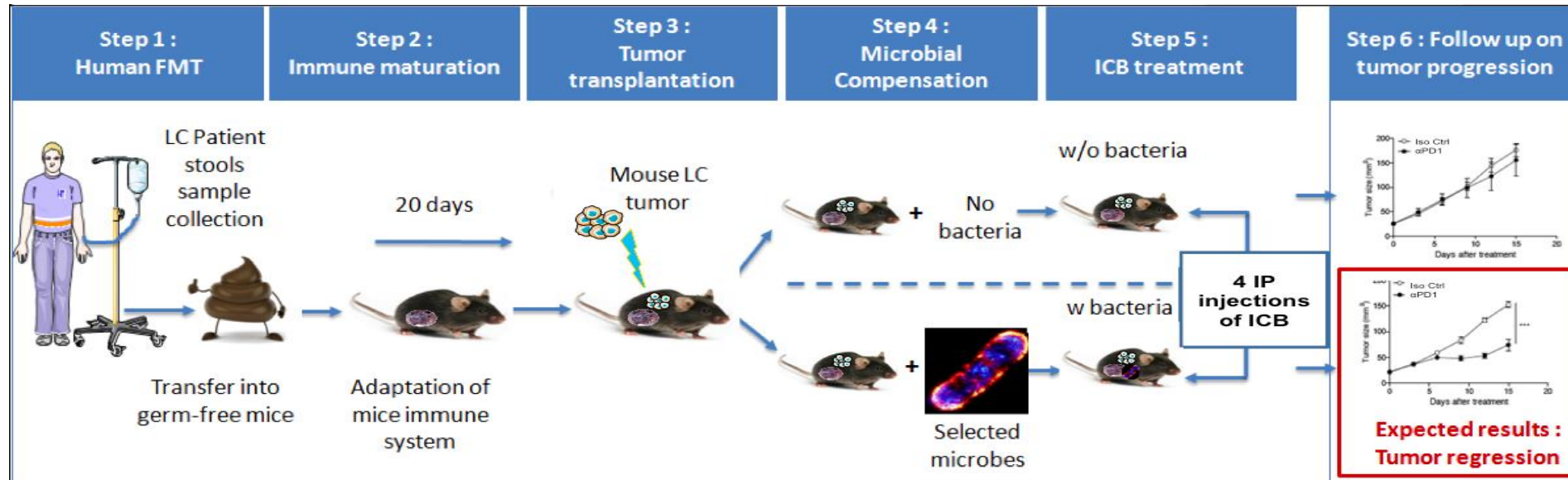
n: 131

FMT of 5 RCC NR and 5 RCC R

R: responders; NR: non responders

(Modified from Routy, Le-Chatelier, Derosa et al; Science, 2018).

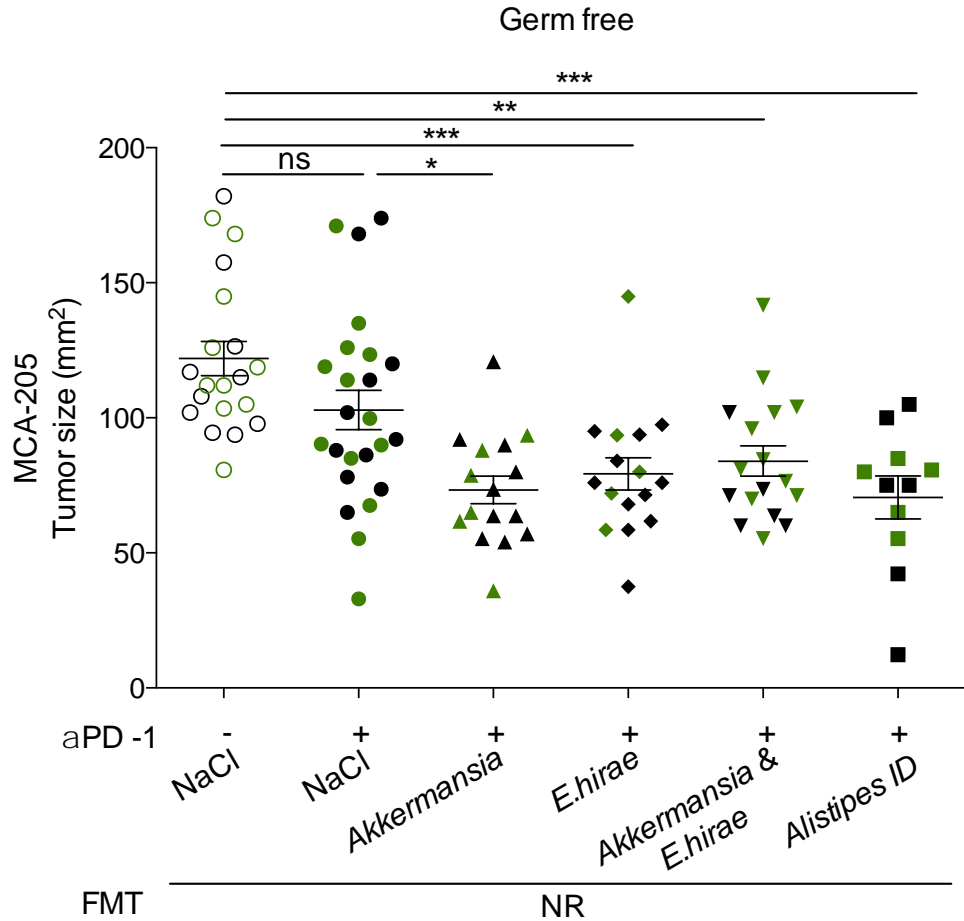
Avatar model to compensate non responder feces into good feces with oncomicrobiotics



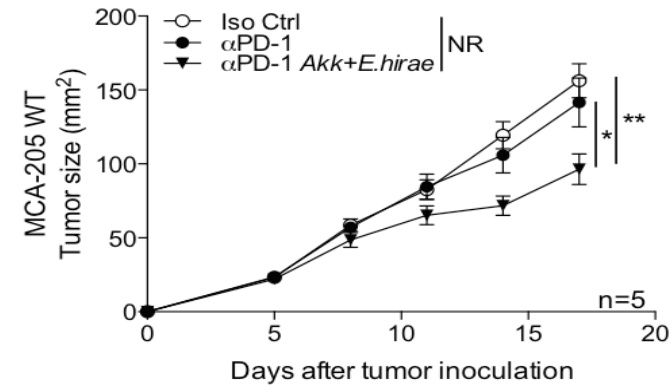
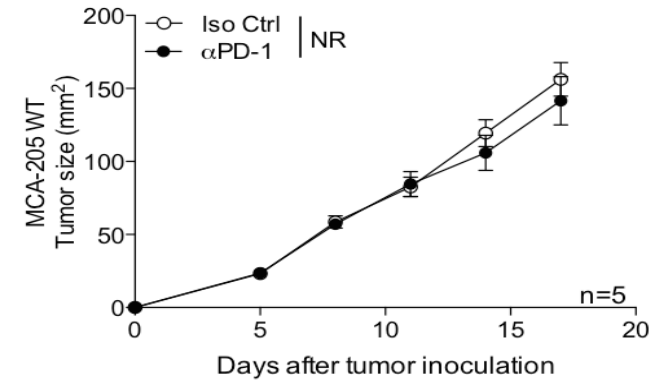
To validate the biological significance of the commensal species identified in the metagenomic analysis of patients with a favorable clinical outcome, we mono- or bi-colonized mouse intestines with *A. muciniphila* alone or combined with other commensals (oncoBax) in several conditions of gut dysbiosis



FMT-induced dysbiosis: Restoration of aPD1 Abs efficacy with anticancer probiotics

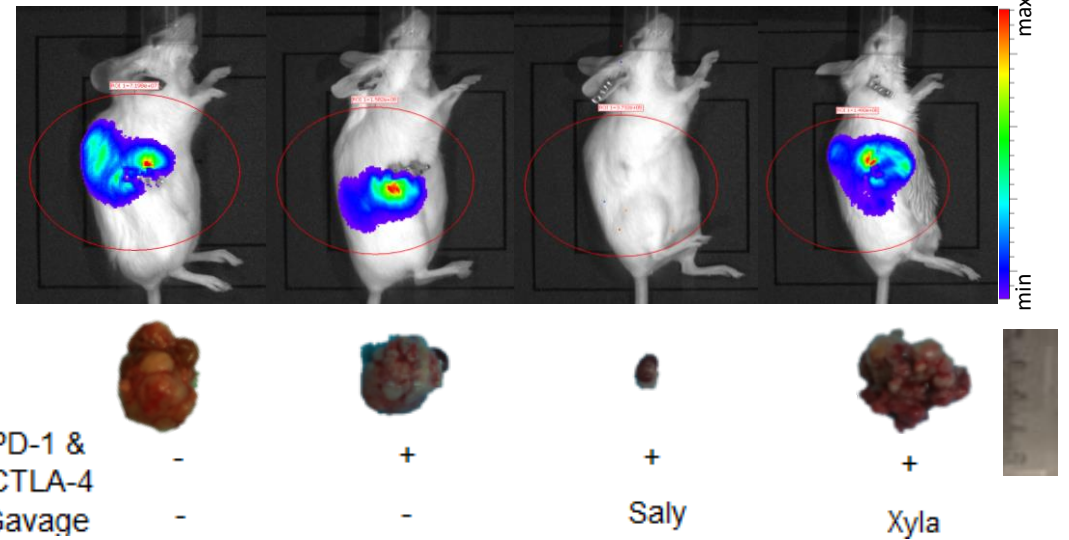
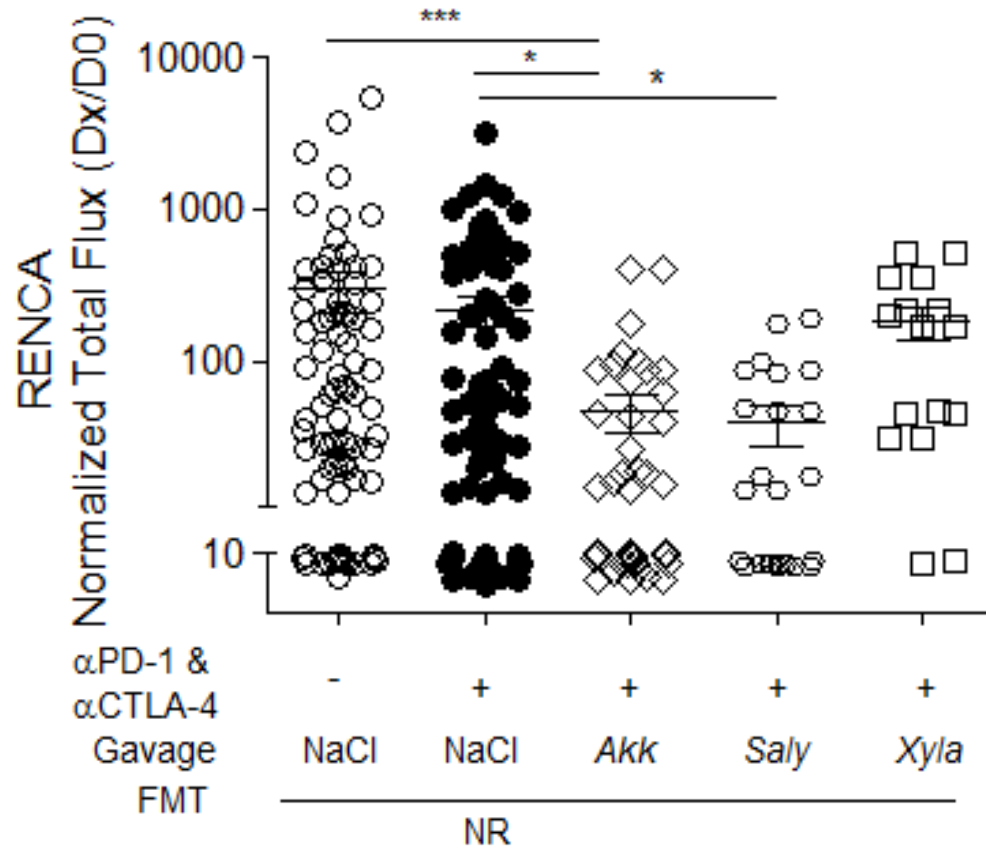


NB: random bacteria *E. faecalis* or *B. nordii* did not compensate the dysbiosis



(Modified from Routy, Le-Chatelier, Derosa et al; Science, 2018).

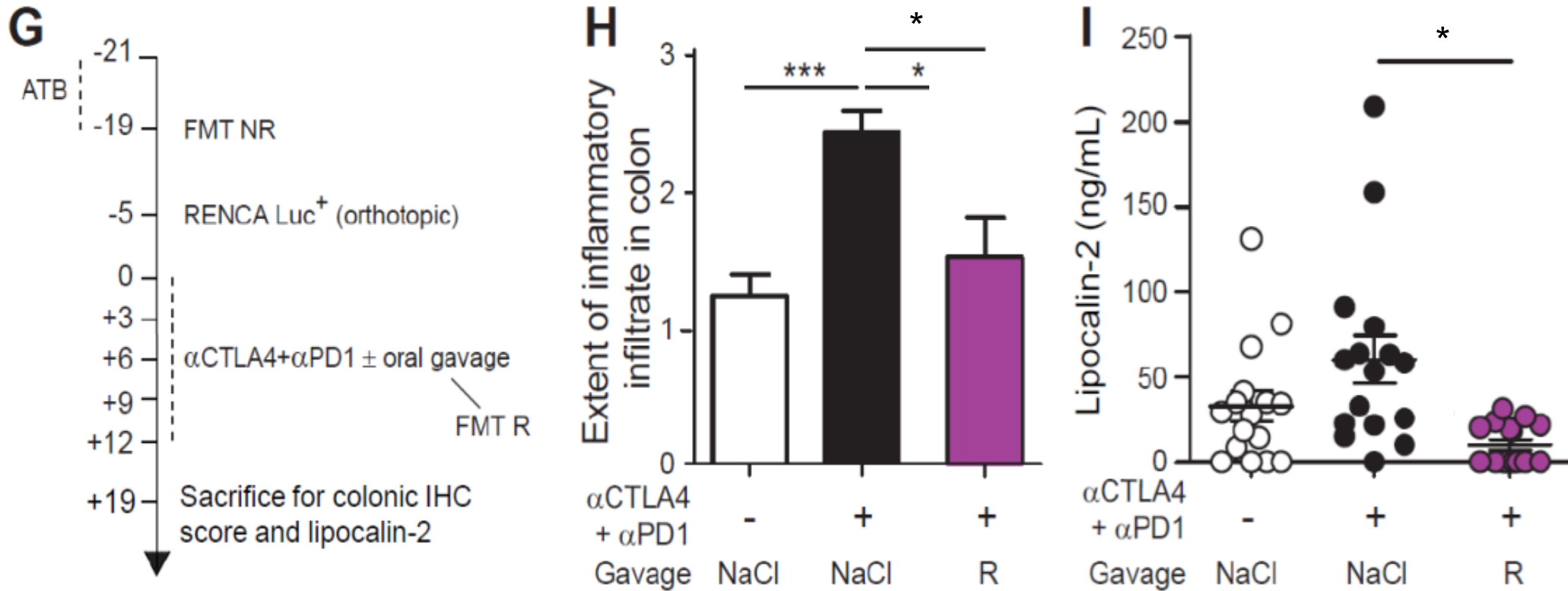
Next, in RENCA model oral supplementation with *A. muciniphila* or *B. salyersiae* (but not *B. xylanosolvens*) post-FMT with NR feces restored the efficacy of PD-1/CTLA-4 co-blockade



Tumor free: Dx/D0 < 10

Modified from Derosa L. ASCO 2018 Merit Award

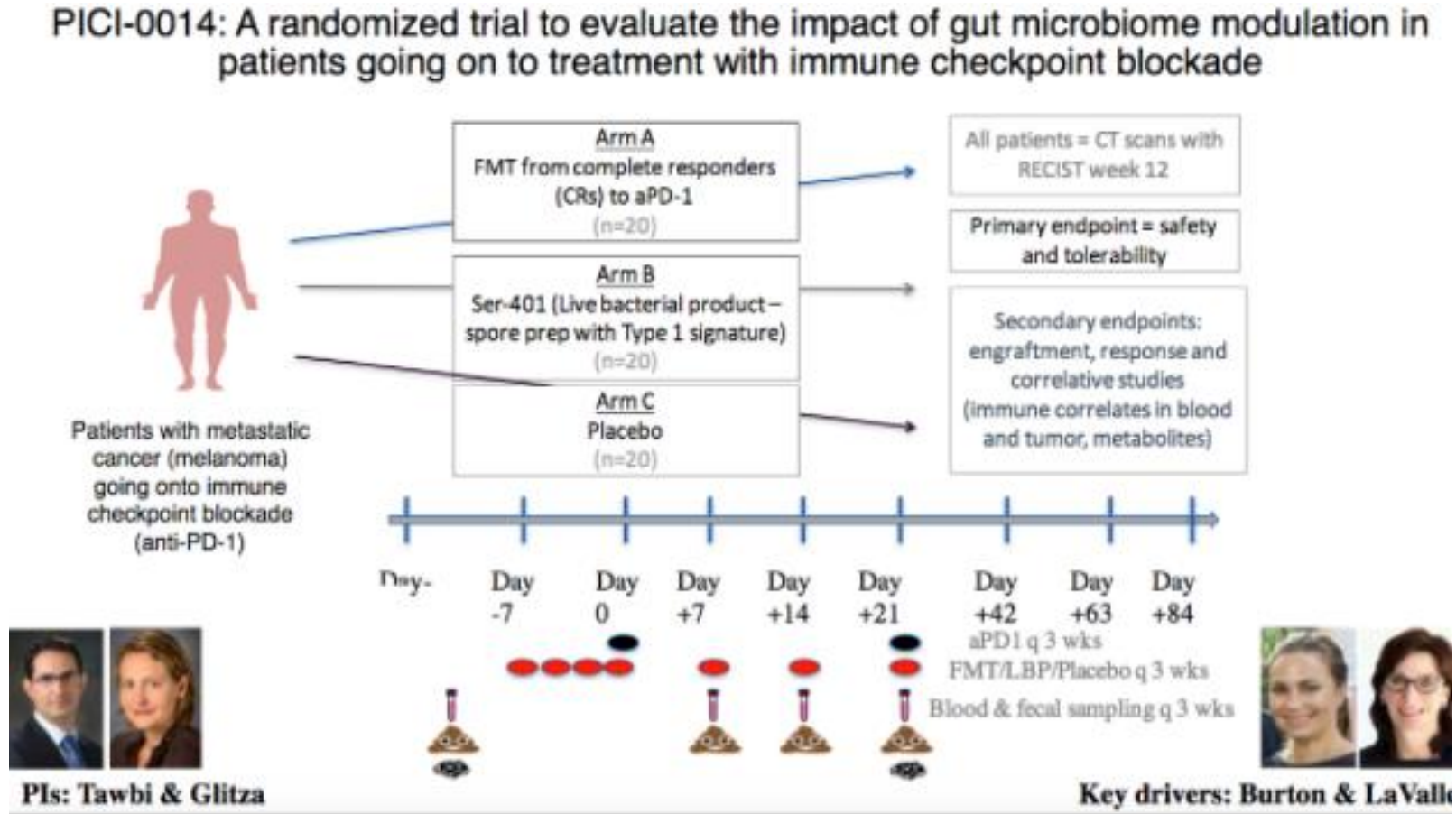
Combo treatment results in gut toxicity but oral gavage with R feces conferred protection against toxicity



Gavage with R feces:

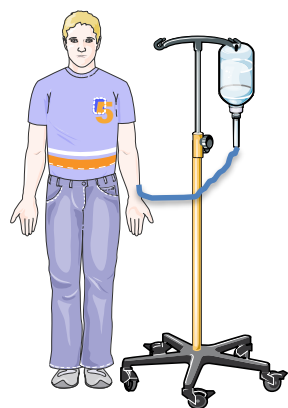
48,5% increase in the prevalence of tumor free mice

Fecal microbiota transplant and administration of bacterial consortia are being used experimentally in cancer



There are considerable questions regarding the selection of the most appropriate donor or the optimal composition of bacterial formulation

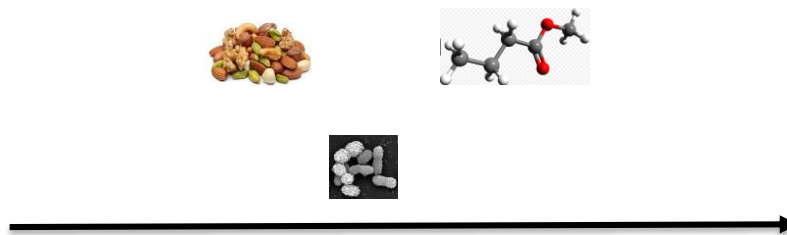
Modulating the microbiome to improve therapeutic response: Ready for clinical trials?



Diagnostic Kit



Unfavorable feces



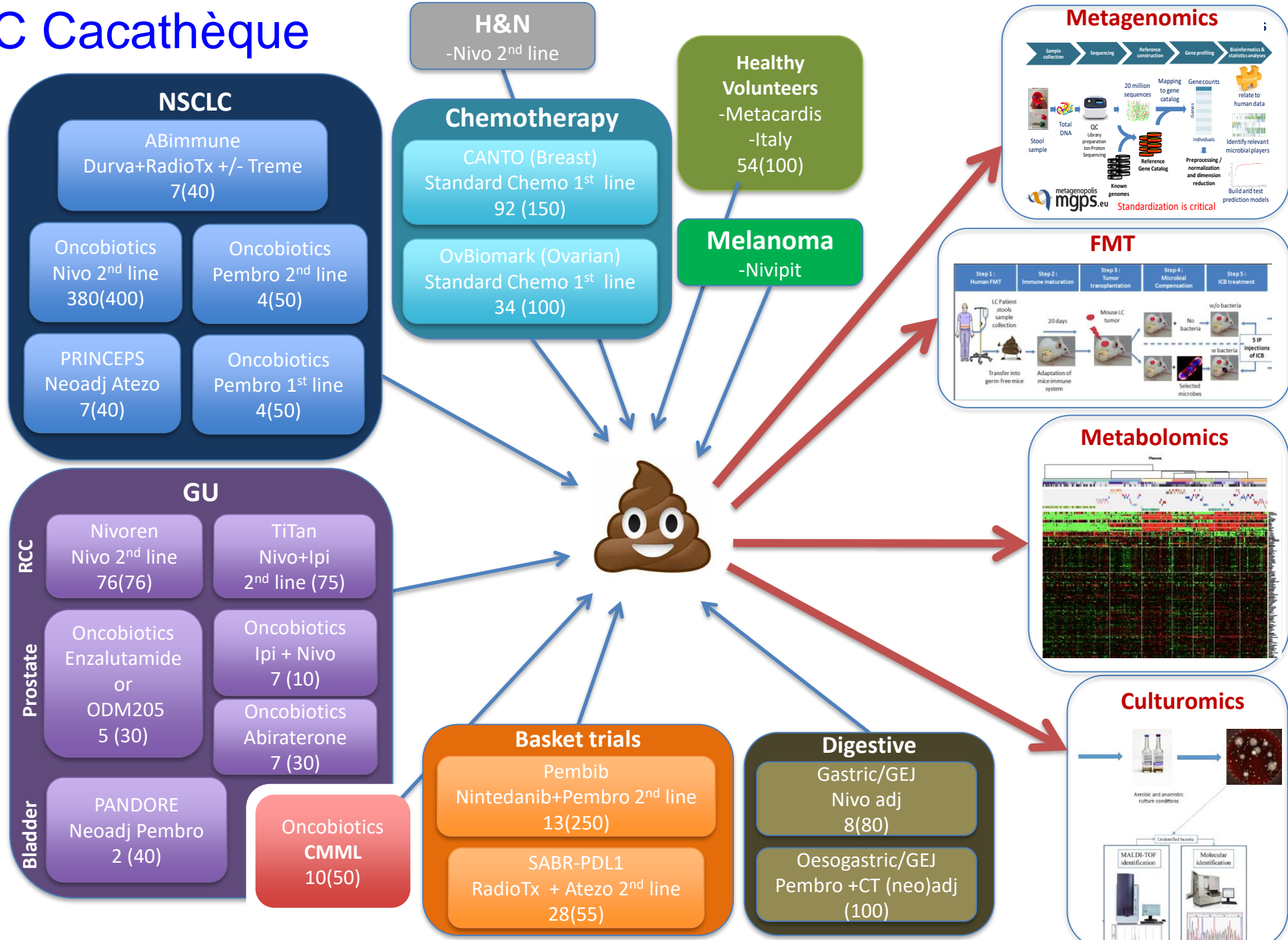
Favorable feces

Modalities that may modify the patient microbiome:

- Fecal transplant (R or HV stools?)
 - Diet
- Bacteria (single vs consortia)
 - Antibiotics
 - Prebiotics
 - Metabolites

GRCC Cacathèque

Network 1 (RHU): LUMIERE



ACRONYM: ONCOBIOME**‘European’ Cacathèque****List of participants**

Participant No	Participant organisation name	Country
1 (Coord)	Gustave Roussy Cancer Center (GRCC)	France
2	National Institute for Health & Medical Research (INSERM)	France
3	University of Trento (UNITN)	Italy
4	Fondazione IRCCS Istituto Nazionale dei Tumori (INT)	Italy
5	Masaryk University (MU)	Czech Republic
6	Universitätsklinikum Erlangen (UKER)	Germany
7	Radboud University (RU)	Netherlands
8	Italian Institute for Genomic Medicine (IIGM)	Italy
9	University of Cambridge (UCAM)	UK
10	Karolinska Institute (NKI)	Sweden
11	University Hospital of Montreal (CRCHUM)	Canada
12	Unicancer (UNI)	France
13	La Charité-UniversitätsMedezin Berlin (CHA)	Germany
14	German Breast Group (GBG)	Germany
15	HalioDx (HDX)	France
16	EverImmune (EVI)	France
17	Algoé Consultants (ALG)	France

ONCOBIOME project has received funding from the European Union’s Horizon 2020 research and innovation programme

ONCOBIOME endpoints

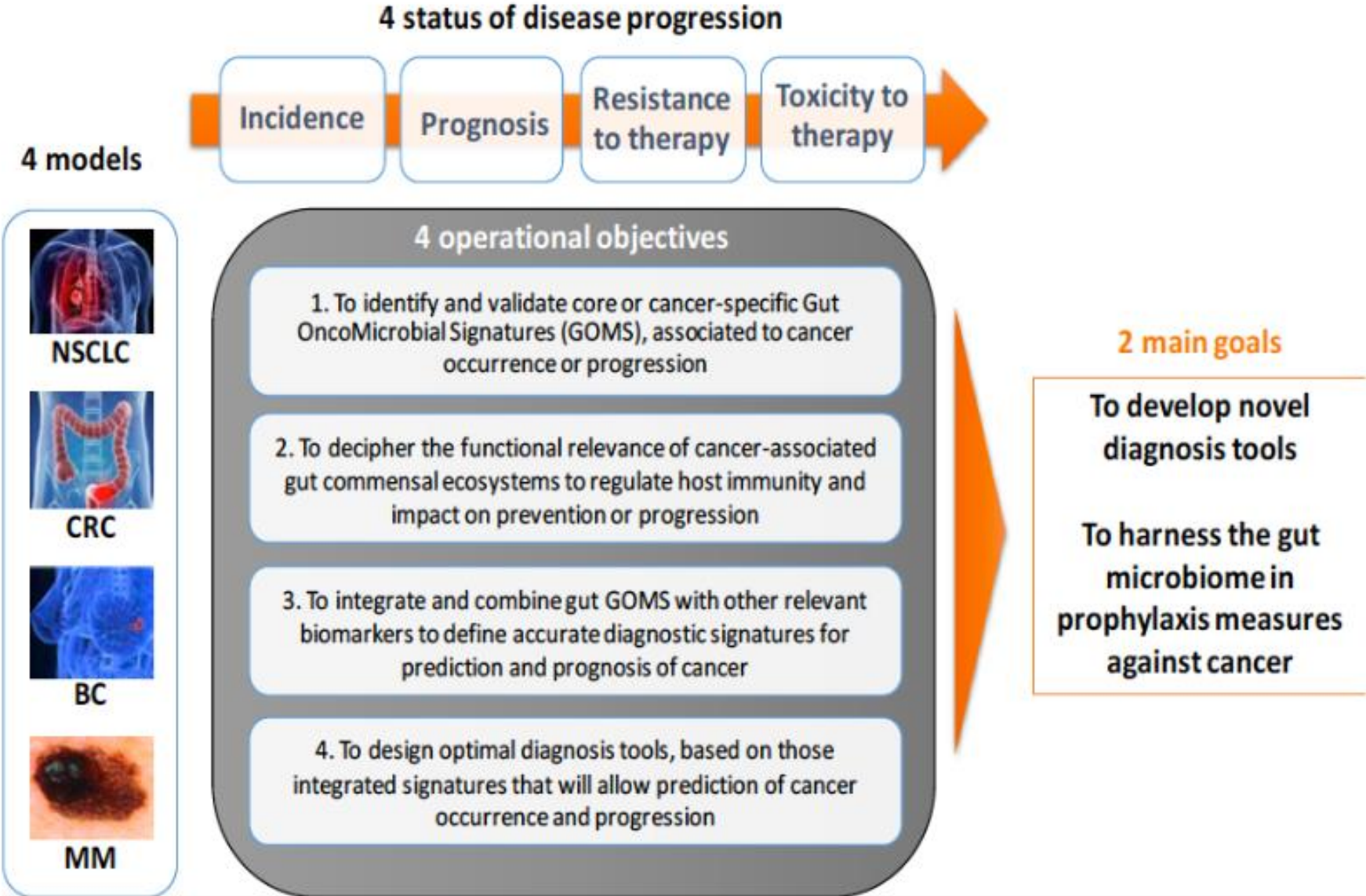
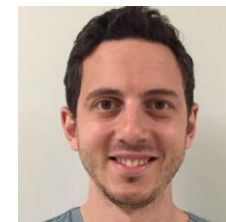


Figure 1: ONCOBIOME objectives

Conclusion and future perspectives

- Microbiota affects immunity and therapeutic response in cancer
- Mouse model suggest that modulation of the microbiome can enhance responses to ICI and prevent toxicity
- Ready for interventional studies?
 - Life stile/diet randomized trial are challenging!
- Paradigm shift in oncology
 - From tumor cells
 - To immune system
 - To host and its environment

In GUT (bacteria), we trust!



Memorial Sloan Kettering
Cancer Center



If You Trust Gut (Microbiota), Please Contact Me For Collaborations

lisa.derosa@gustaveroussy.fr