Procura por marcadores

A Microbial signature for CRC classification

No neoplasia (N = 61) | Small Adenoma (N = 27) | CRC (stages I / II N = 22, III / IV N = 31)

	Median control rel. abundance	Contribution to model
Fusobacterium nucleatum subsp. *vincentii*	1E–06	23.3%
Fusobacterium nucleatum subsp. *animalis*	1E–06	12.3%
Peptostreptococcus stomatis	2E–06	9.4%
Porphyromonas asaccharolytica	1E–06	6.4%
Clostridium symbiosum	4E–06	5.7%
Clostridium hylemonae	1E–06	2.3%
Bacteroides fragilis	1E–04	1.3%
Lactobacillus salivarius	1E–06	1.2%
Fusobacterium gonidiaformans	1E–06	0.8%
Lactobacillus ruminis	1E–06	0.5%
Eubacterium rectale	0.02	0.7%
Bacteroides caccae	0.002	0.8%
Eubacterium ventriosum	0.002	0.8%
Clostridium scindens	6E–06	1.2%
Eubacterium eligens	0.007	1.4%
Bifidobacterium angulatum	1E–05	1.5%
Methanosphaera stadtmanae	1E–06	1.5%
Dorea formicigenerans	0.002	1.6%
Butyrivibrio crossotus	1E–05	1.7%
Phascolarctobacterium succinatutens	1E–05	2.9%
unclassified *Ruminococcus sp.*	0.01	5.5%
Streptococcus salivarius	9E–04	9.1%

−2 0 2

Mean log–odds ratio

% of total absolute weight

CRC progression

Metagenomic test score

FOBT Hemoccult

Wif-1 gene methylation test

Relative abundance change over controls

0.001 0.01 0.1 0 10 100 1000

depleted in CRC ↔ enriched in CRC

Metagenomic test score CRC predicted

0 0.25 0.5 0.75 1

decision boundary = 0.275

Other test results: negative, positive, NA

CRC progression (AJCC staging): No neoplasia, Adenoma, CRC 0 / I / II, CRC III / IV

Association with CRC: Enriched in controls, Enriched in CRC patients

B Internal cross validation

FPR = 0.08

TPR = 0.72

TPR = 0.58

TPR = 0.49

*

Metagenomic test combined with FOBT (AUC = 0.87)

Metagenomic test (AUC = 0.84)

*

FOBT Hemoccult

Wif-1 methylation test

True positive rate

False positive rate

C External validation

FPR = 0.08

TPR = 0.52

Metagenomic test (AUC = 0.85)

False positive rate

D Early detection

study population

F G

N = 22 N = 31 N = 26 N = 12

CRC stage I / II

CRC stage III / IV

CRC stage 0 / I / II

CRC stage III / IV

True positive rate

E Changes along CRC progression

F. nucleatum subsp. *vincentii* rho = 0.43 **

F. nucleatum subsp. *animalis* rho = 0.39 **

Peptostreptococcus stomatis rho = 0.23 *

Porphyromonas asaccharolytica rho = 0.33 *

1E–6 1E–5 1E–4 0.001 0.01

Relative abundance (log-scale)

Potential of fecal microbiota for early-stage detection of colorectal cancer

Georg Zeller, Julien Tap, Anita Y Voigt, Shinichi Sunagawa, Jens Roat Kultima, Paul I Costea, Aurélien Amiot, Jürgen Böhm, Francesco Brunetti, Nina Habermann, Rajna Hercog, Moritz Koch, Alain Luciani, Daniel R Mende, Martin A Schneider, Petra Schrotz-King, Christophe Tournigand, Jeanne Tran Van Nhieu, Takuji Yamada, Jürgen Zimmermann, Vladimir Benes, Matthias Kloor, Cornelia M Ulrich, Magnus von Knebel Doeberitz, Iradj Sobhani, Peer Bork

Intestinal microbiota metabolism of L-carnitine, a nutrient in red meat, promotes atherosclerosis

Robert A Koeth[1,2], Zeneng Wang[1,2], Bruce S Levison[1,2], Jennifer A Buffa[1,2], Elin Org[3], Brendan T Sheehy[1], Earl B Britt[1,2], Xiaoming Fu[1,2], Yuping Wu[4], Lin Li[1,2], Jonathan D Smith[1,2,5], Joseph A DiDonato[1,2], Jun Chen[6], Hongzhe Li[6], Gary D Wu[7], James D Lewis[6,8], Manya Warrier[9], J Mark Brown[9], Ronald M Krauss[10], W H Wilson Tang[1,2,5], Frederic D Bushman[5], Aldons J Lusis[3] & Stanley L Hazen[1,2,5]

ARTICLE

doi:10.1038/nature09922

Gut flora metabolism of phosphatidylcholine promotes cardiovascular disease

Zeneng Wang[1,2], Elizabeth Klipfell[1,2], Brian J. Bennett[3], Robert Koeth[1], Bruce S. Levison[1,2], Brandon DuGar[1], Ariel E. Feldstein[1,2], Earl B. Britt[1,2], Xiaoming Fu[1,2], Yoon-Mi Chung[1,2], Yuping Wu[4], Phil Schauer[5], Jonathan D. Smith[1,6], Hooman Allayee[7], W. H. Wilson Tang[1,2,6], Joseph A. DiDonato[1,2], Aldons J. Lusis[3] & Stanley L. Hazen[1,2,6]

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Procura por marcadores

Instituto René Rachou
FIOCRUZ MINAS

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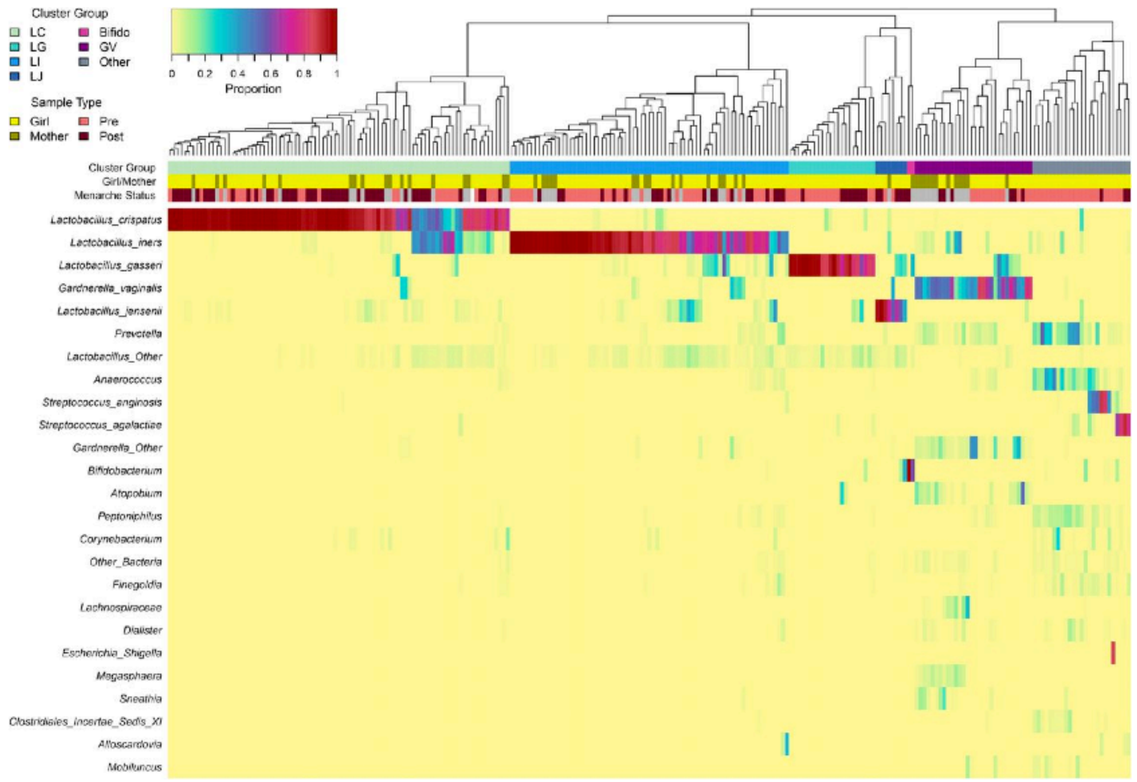
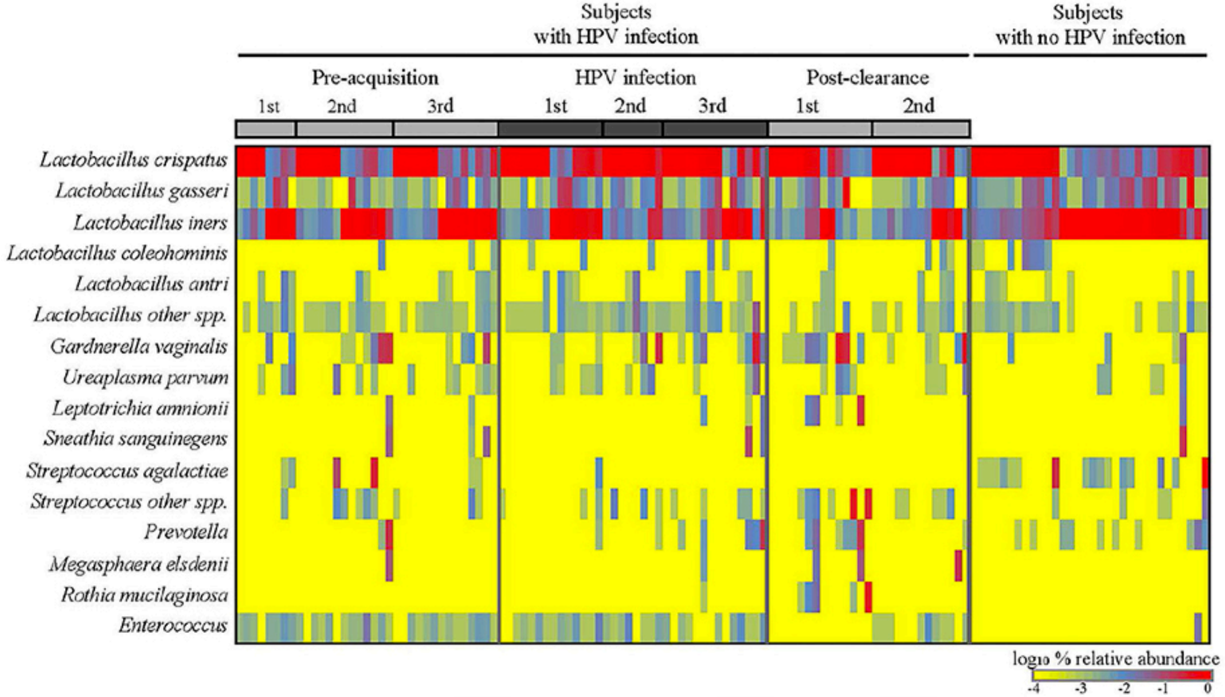
Tem padrão?



Vaginal Microbiota of Adolescent Girls Prior to the Onset of Menarche Resemble Those of Reproductive-Age Women

Roxana J. Hickey[a,b], Xia Zhou[a,*], Matthew L. Settles[a,b], Julie Erb[c], Kristin Malone[c], Melanie A. Hansmann[c], Marcia L. Shew[d], Barbara Van Der Pol[e], J. Dennis Fortenberry[d], Larry J. Forney[a,b]



Cervical-Vaginal Microbiome and Associated Cytokine Profiles in a Prospective Study of HPV 16 Acquisition, Persistence, and Clearance

Anna-Barbara Moscicki[1], Baochen Shi[2], Hazel Huang[2], Emma Barnard[2] and Huiying Li[2]*