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**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]

The NEW ENGLAND JOURNAL of MEDICINE

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# Intestinal Microbial Metabolism of Phosphatidylcholine and Cardiovascular Risk

W.H. Wilson Tang, M.D., Zeneng Wang, Ph.D., Bruce S. Levison, Ph.D., Robert A. Koeth, B.S., Earl B. Britt, M.D., Xiaoming Fu, M.S., Yuping Wu, Ph.D., and Stanley L. Hazen, M.D., Ph.D.

# A busca pelos marcadores

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Gut flora metabolism of phosphatidylcholine promotes cardiovascular disease

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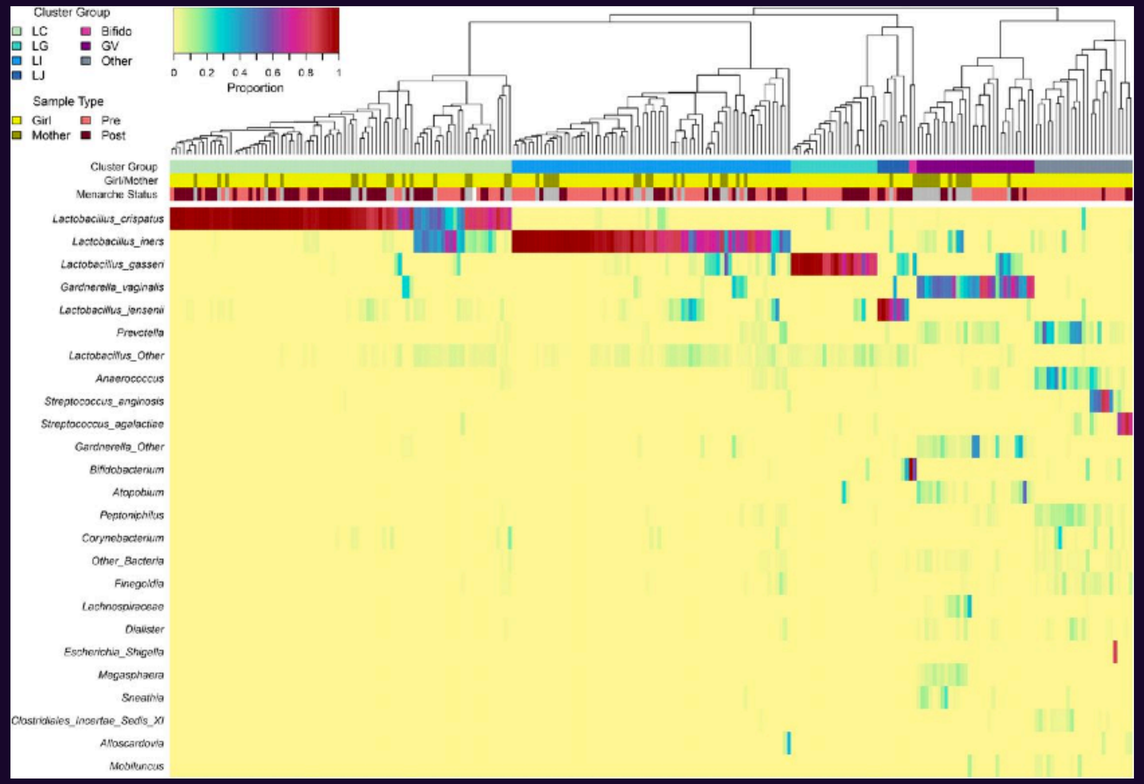
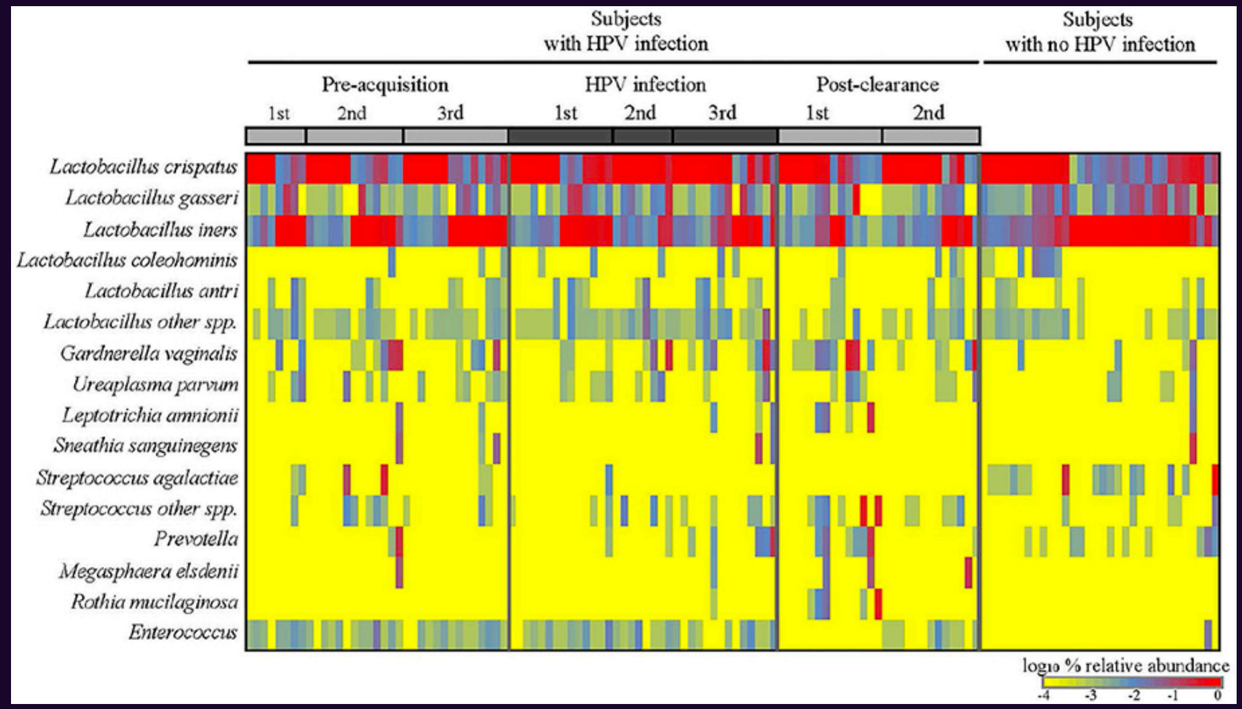
# Existe um padrão?




**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]*