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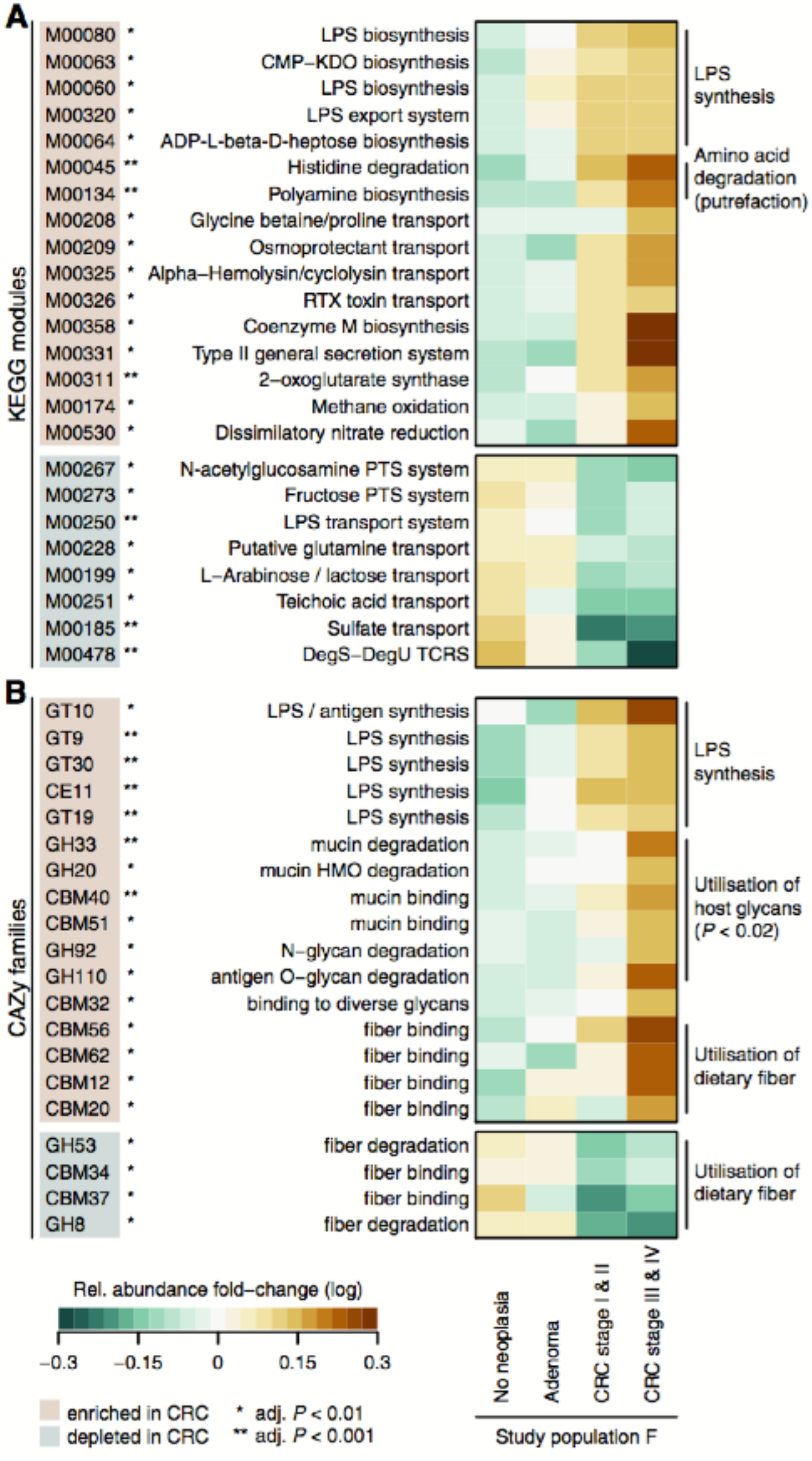
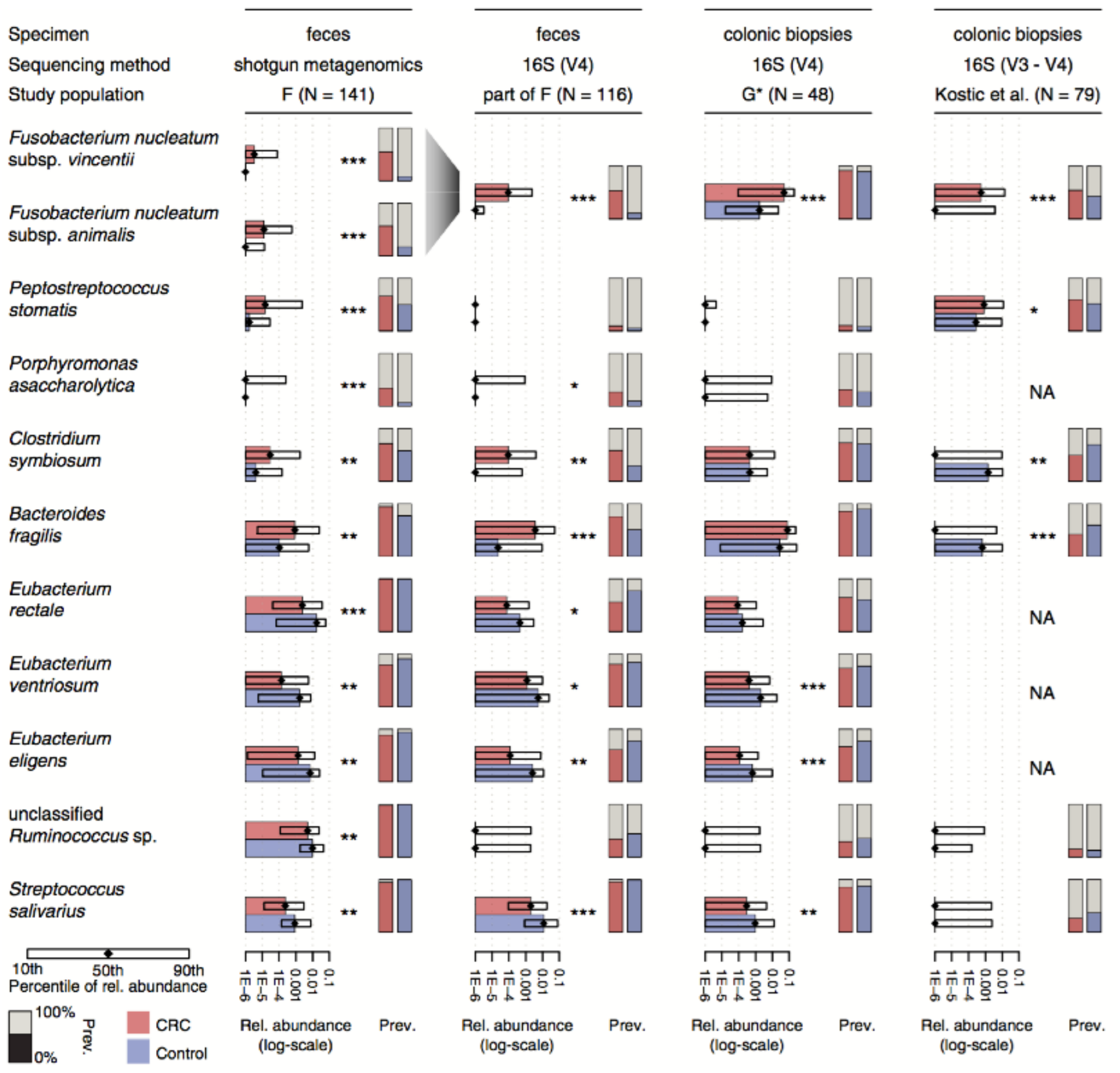
Article

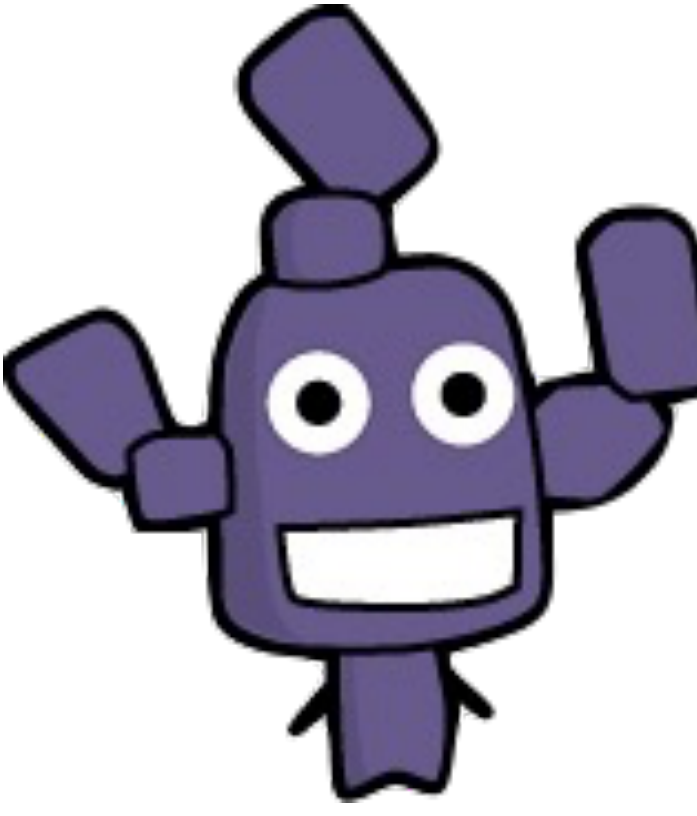
molecular systems biology

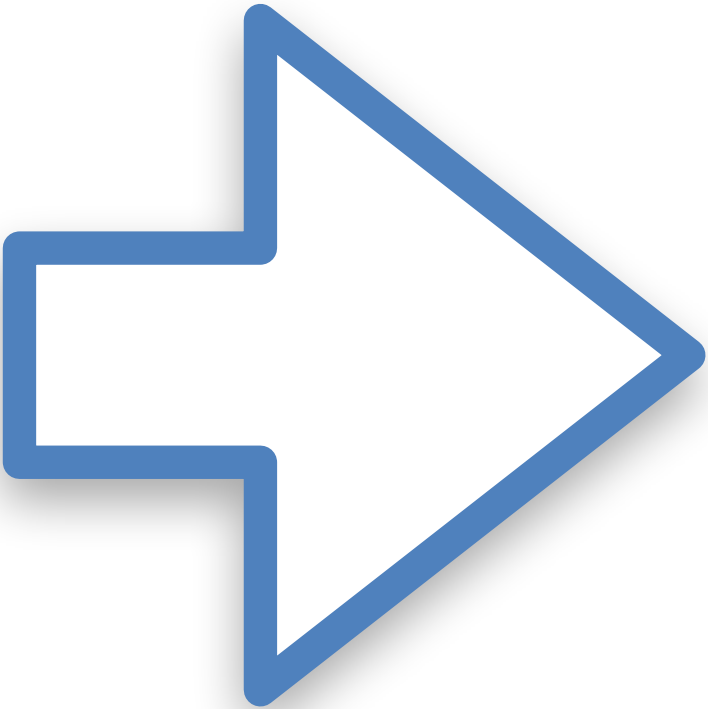
Potential of fecal microbiota for early-stage detection of colorectal cancer

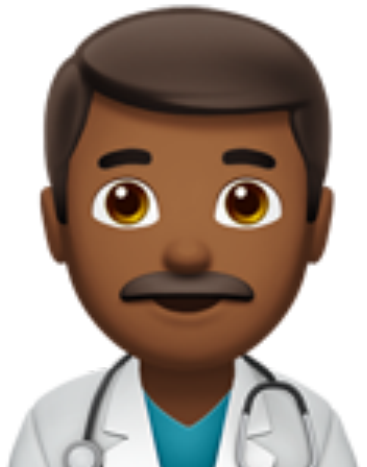
Georg Zeller[1,†], Julien Tap[1,2,†], Anita Y Voigt[1,3,4,5,†], Shinichi Sunagawa[1], Jens Roat Kultima[1], Paul I Costea[1], Aurélien Amiot[2], Jürgen Böhm[6,7], Francesco Brunetti[8], Nina Habermann[6,7], Rajna Hercog[9], Moritz Koch[10,‡], Alain Luciani[11], Daniel R Mende[1], Martin A Schneider[10], Petra Schrotz-King[6,7], Christophe Tournigand[12], Jeanne Tran Van Nhieu[13], Takuji Yamada[14], Jürgen Zimmermann[9], Vladimir Benes[9], Matthias Kloor[3,4,5], Cornelia M Ulrich[6,7,15], Magnus von Knebel Doeberitz[3,4,5], Iradj Sobhani[2,*] & Peer Bork[1,5,16,**]


A
KEGG modules
M00080 * LPS biosynthesis
M00063 * CMP−KDO biosynthesis
M00060 * LPS biosynthesis
M00320 * LPS export system
M00064 * ADP-L-beta-D-heptose biosynthesis
M00045 ** Histidine degradation
M00134 ** Polyamine biosynthesis
M00208 * Glycine betaine/proline transport
M00209 * Osmoprotectant transport
M00325 * Alpha−Hemolysin/cyclolysin transport
M00326 * RTX toxin transport
M00358 * Coenzyme M biosynthesis
M00331 * Type II general secretion system
M00311 ** 2−oxoglutarate synthase
M00174 * Methane oxidation
M00530 * Dissimilatory nitrate reduction
M00267 * N-acetylglucosamine PTS system
M00273 * Fructose PTS system
M00250 ** LPS transport system
M00228 * Putative glutamine transport
M00199 * L−Arabinose / lactose transport
M00251 * Teichoic acid transport
M00185 ** Sulfate transport
M00478 ** DegS−DegU TCRS
LPS synthesis
Amino acid degradation (putrefaction)
B
CAZy families
GT10 * LPS / antigen synthesis
GT9 ** LPS synthesis
GT30 ** LPS synthesis
CE11 ** LPS synthesis
GT19 ** LPS synthesis
GH33 ** mucin degradation
GH20 * mucin HMO degradation
CBM40 ** mucin binding
CBM51 * mucin binding
GH92 * N−glycan degradation
GH110 * antigen O−glycan degradation
CBM32 * binding to diverse glycans
CBM56 * fiber binding
CBM62 * fiber binding
CBM12 * fiber binding
CBM20 * fiber binding
GH53 * fiber degradation
CBM34 * fiber binding
CBM37 * fiber binding
GH8 * fiber degradation
LPS synthesis
Utilisation of host glycans (P < 0.02)
Utilisation of dietary fiber
Utilisation of dietary fiber
Rel. abundance fold−change (log)
−0.3 −0.15 0 0.15 0.3
enriched in CRC
depleted in CRC
* adj. P < 0.01
** adj. P < 0.001
No neoplasia
Adenoma
CRC stage I & II
CRC stage III & IV
Study population F


Specimen
feces
feces
colonic biopsies
colonic biopsies
Sequencing method
shotgun metagenomics
16S (V4)
16S (V4)
16S (V3 - V4)
Study population
F (N = 141)
part of F (N = 116)
G* (N = 48)
Kostic et al. (N = 79)
Fusobacterium nucleatum subsp. vincentii
Fusobacterium nucleatum subsp. animalis
Peptostreptococcus stomatis
Porphyromonas asaccharolytica
Clostridium symbiosum
Bacteroides fragilis
Eubacterium rectale
Eubacterium ventriosum
Eubacterium eligens
unclassified Ruminococcus sp.
Streptococcus salivarius
NA
10th
50th
90th
Percentile of rel. abundance
100%
0%
Prev.
CRC
Control
1E−6
1E−5
1E−4
0.001
0.01
0.1
Rel. abundance (log-scale)
Prev.







Diagnóstico

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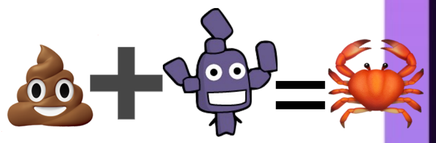
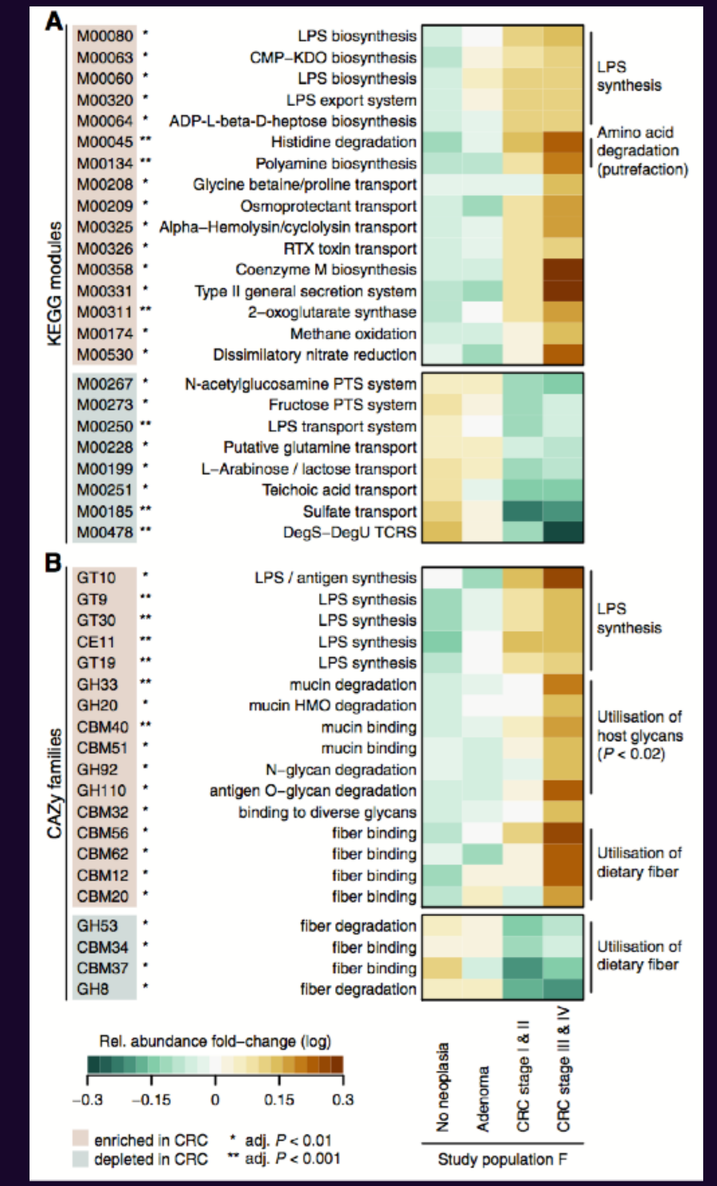
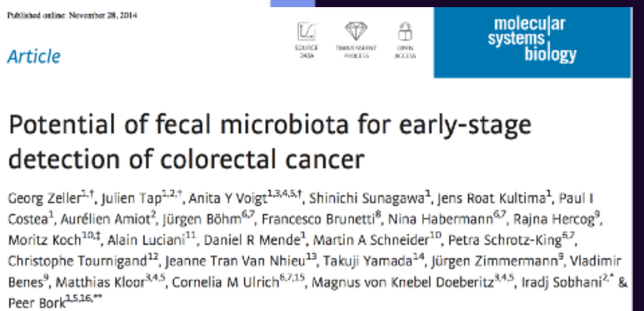
Diagnóstico



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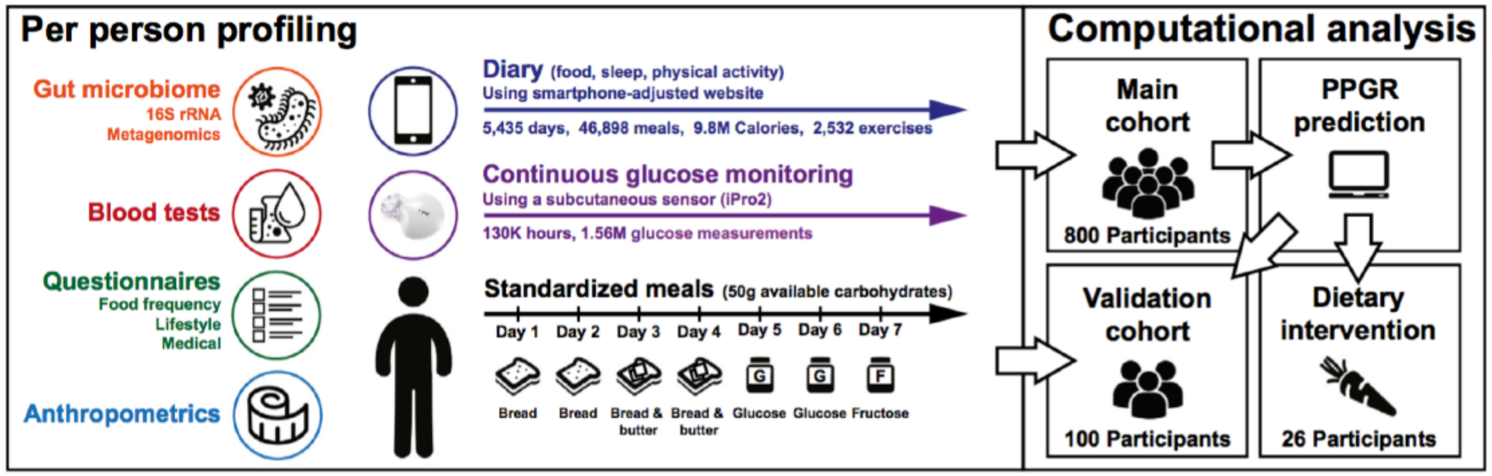
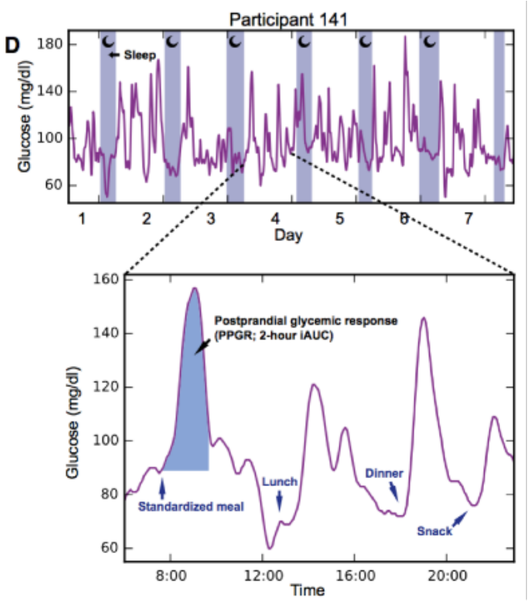
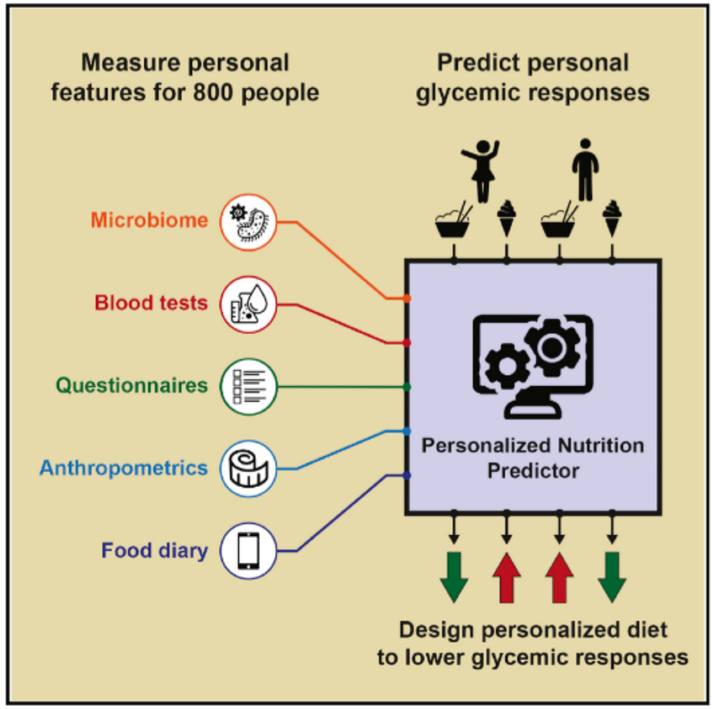
Personalized nutrition



Personalized Nutrition by Prediction of Glycemic Responses

David Zeevi,[1,2,8] Tal Korem,[1,2,8] Niv Zmora,[3,4,5,8] David Israeli,[6,8] Daphna Rothschild,[1,2] Adina Weinberger,[1,2] Orly Ben-Yacov,[1,2] Dar Lador,[1,2] Tali Avnit-Sagi,[1,2] Maya Lotan-Pompan,[1,2] Jotham Suez,[3] Jemal Ali Mahdi,[3] Elad Matot,[1,2] Gal Malka,[1,2] Noa Kosower,[1,2] Michal Rein,[1,2] Gili Zilberman-Schapira,[3] Lenka Dohnalová,[3] Meirav Pevsner-Fischer,[3] Rony Bikovsky,[1,2] Zamir Halpern,[5,7] Eran Elinav,[3,9,*] and Eran Segal[1,2,9,*]