

Réunion Bioinformatique

1^{er} mars 2016

Présentation de la nouvelle version du pipeline de diagnostique NGS (David Goudenège)

Présentation du projet MétaNutriNASH (Jerome Boursier)

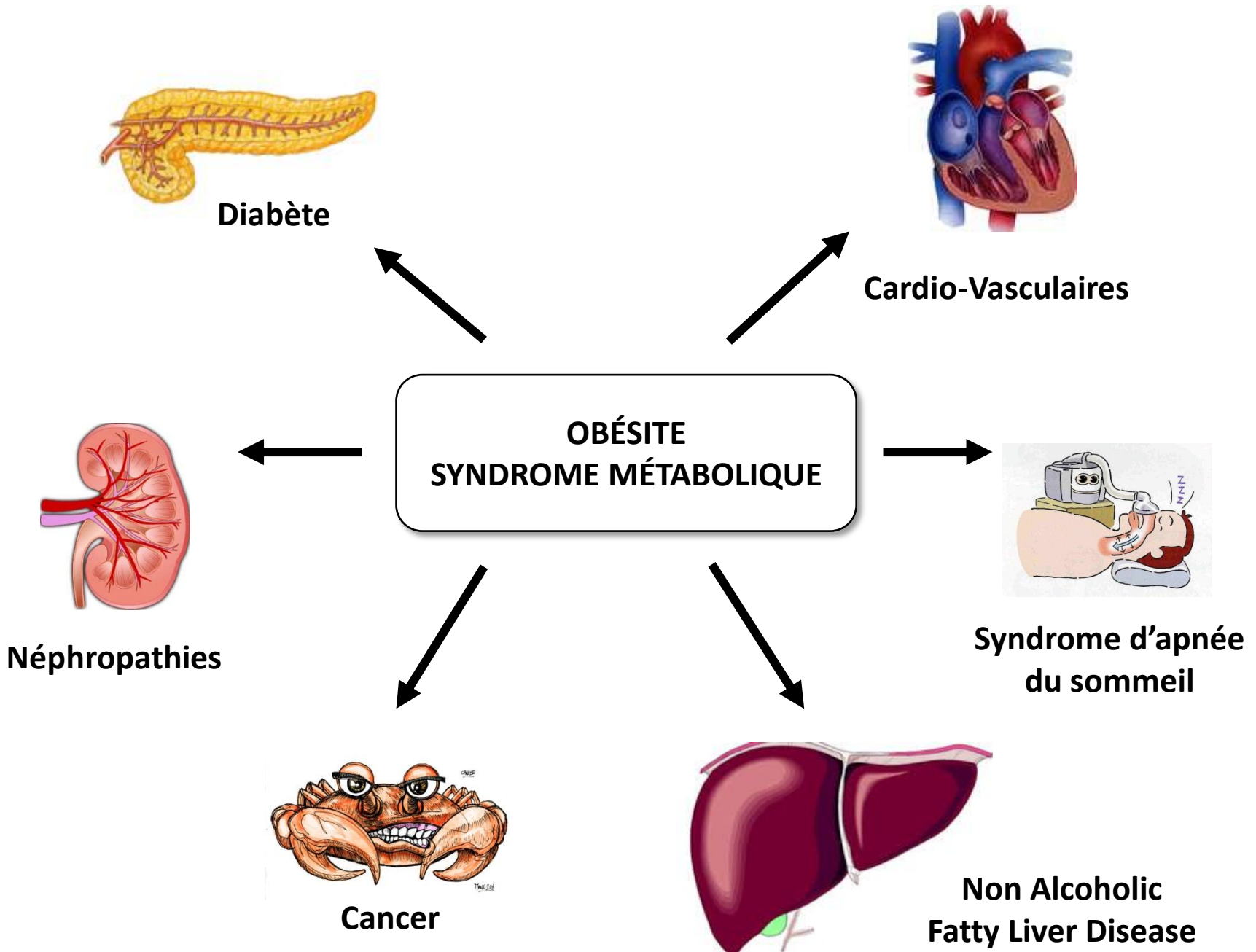
Présentation du « datacenter biomédecine » (Marc Ferré)

Présentation du "Big Data" vu par les informaticiens (Benoit Da Mota)

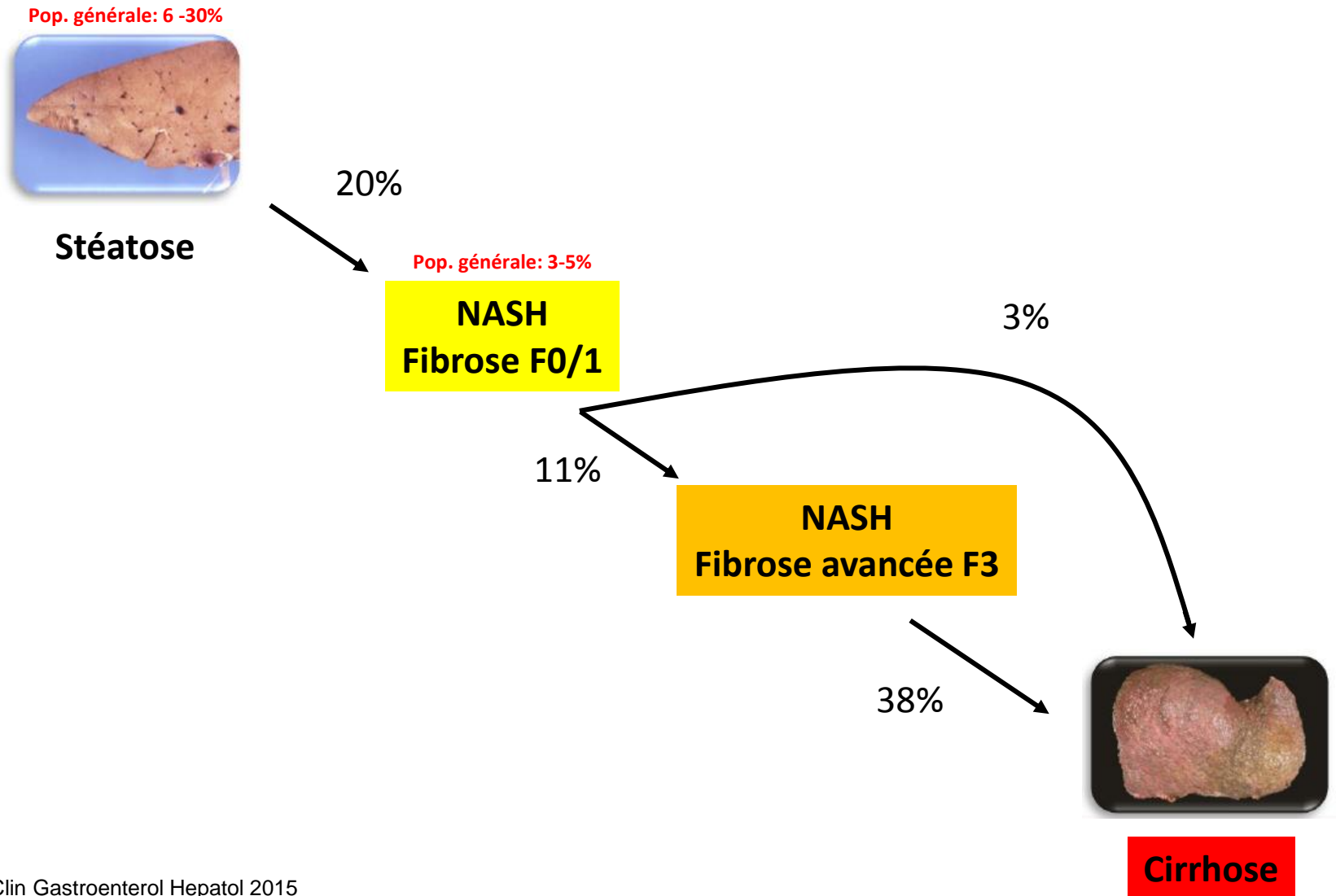
Mise en place de formation sur les outils et méthodes bioinfo/biostat

Discussion sur la mise en place d'une fiche plus détaillée sur les besoins, les moyens et les compétences bioinfo et biostats de chacun

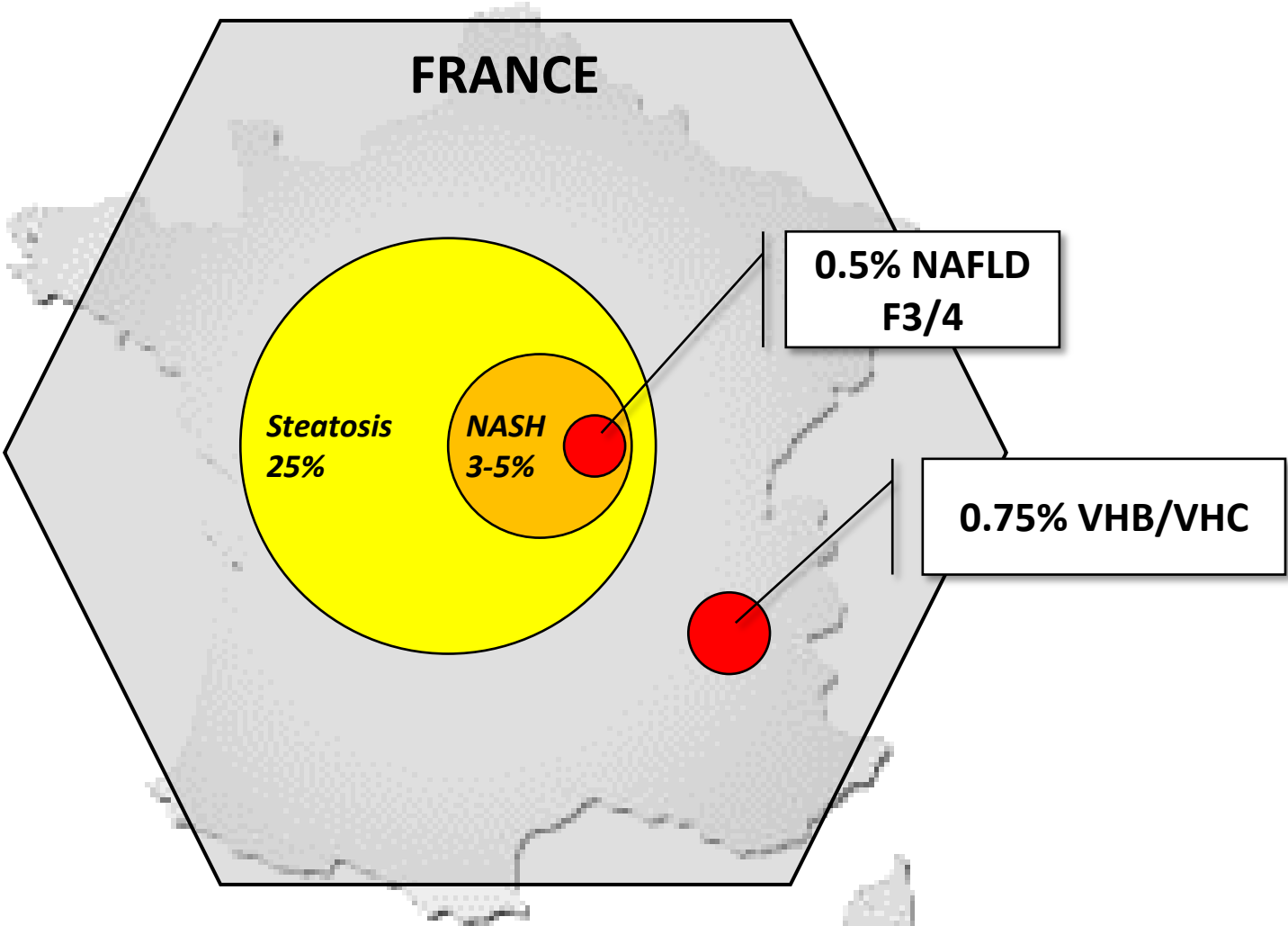
Projet MétaNutriNASH



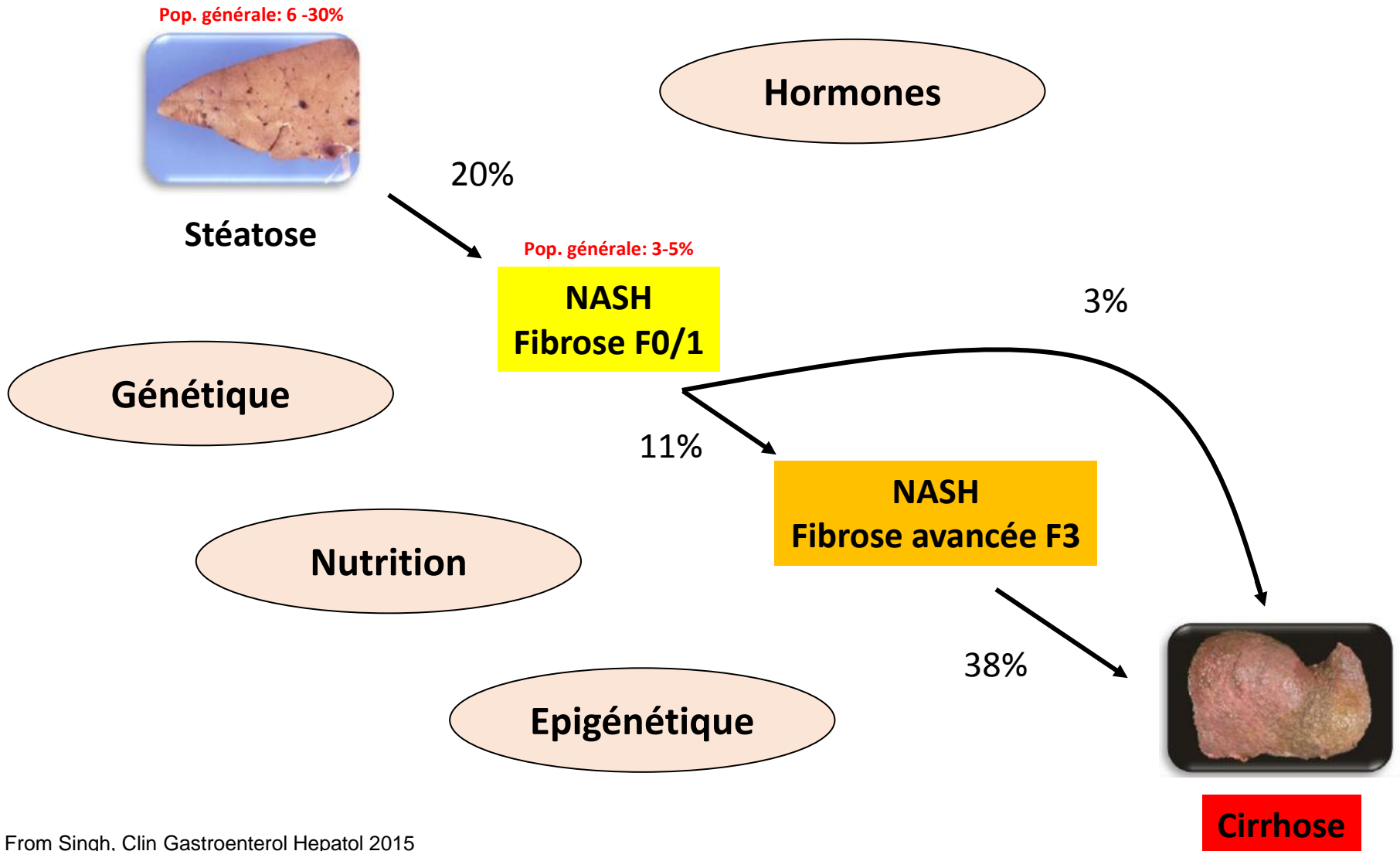
Histoire naturelle de la NAFLD



The burden of NAFLD disease

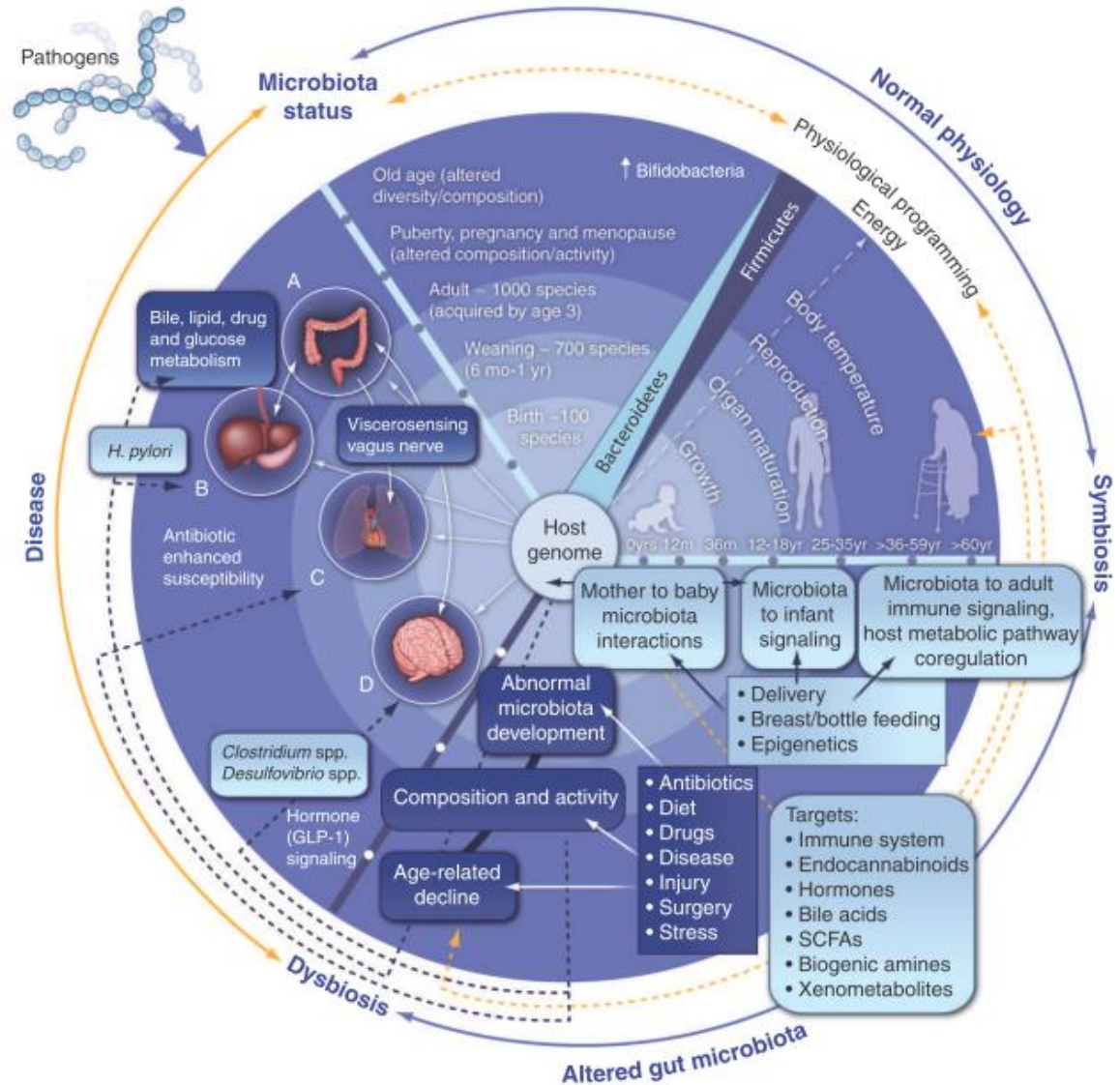


Histoire naturelle de la NAFLD

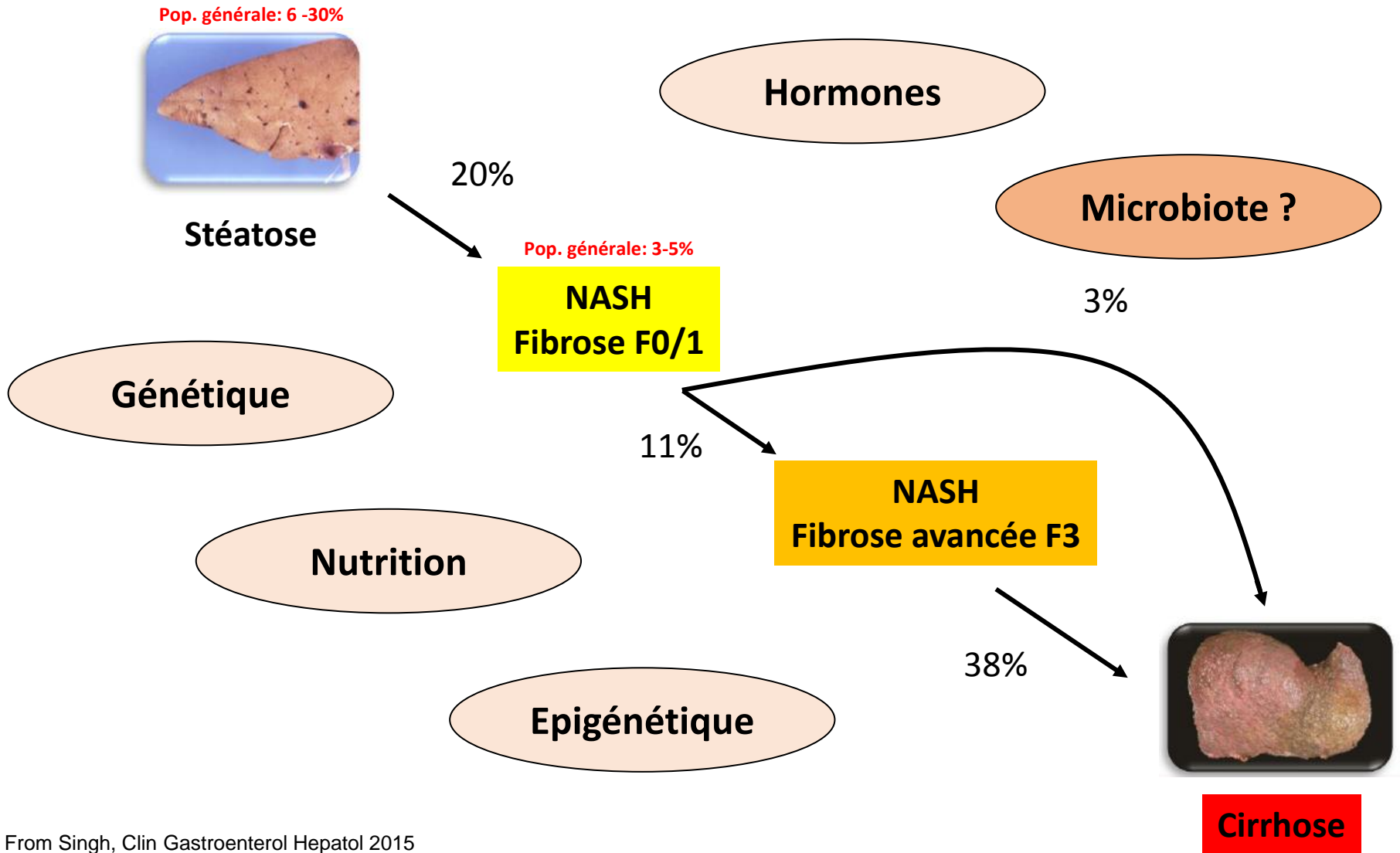


Host-Gut Microbiota Metabolic Interactions

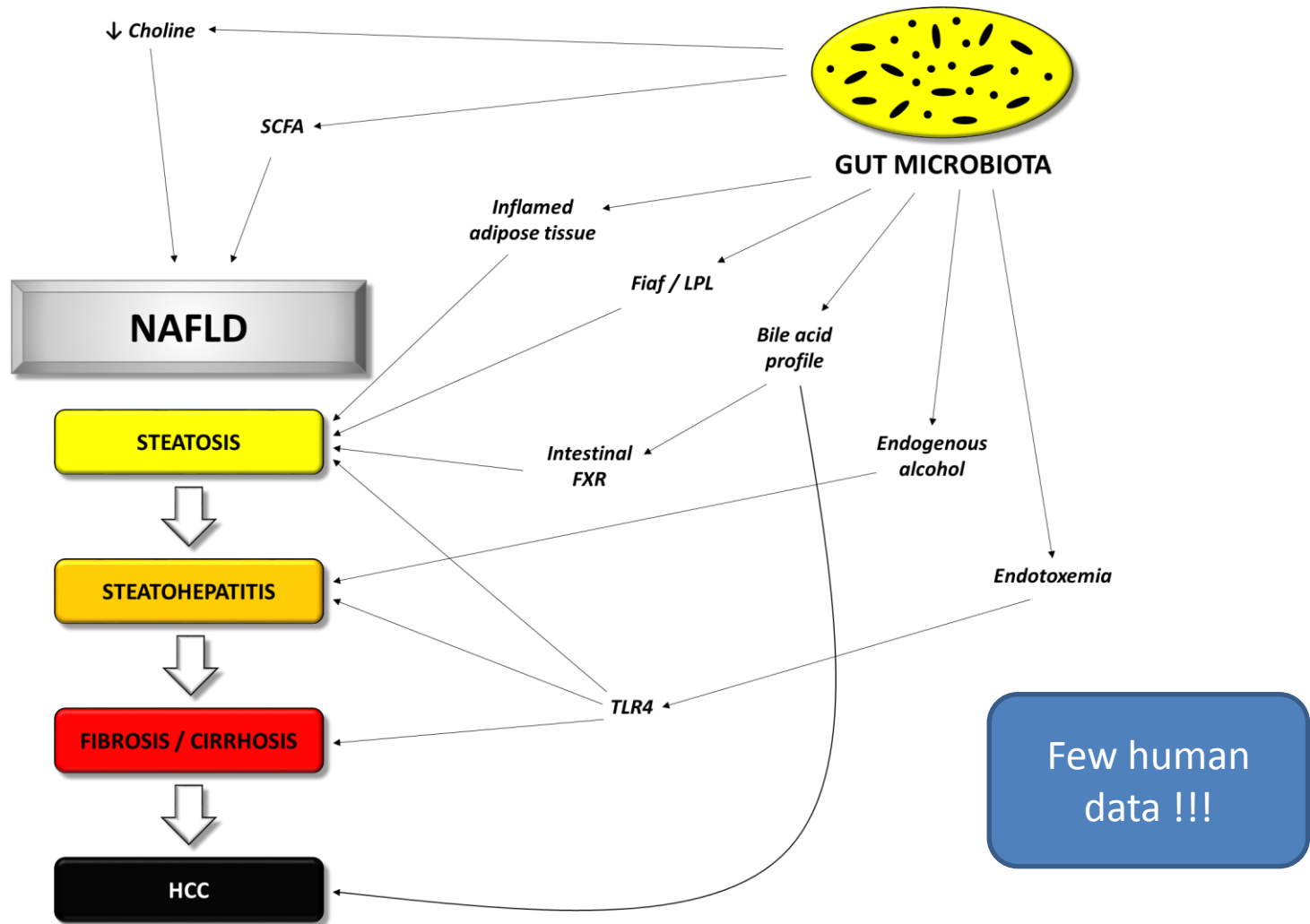
Jeremy K. Nicholson *et al.*
Science **336**, 1262 (2012);
DOI: 10.1126/science.1223813



Histoire naturelle de la NAFLD

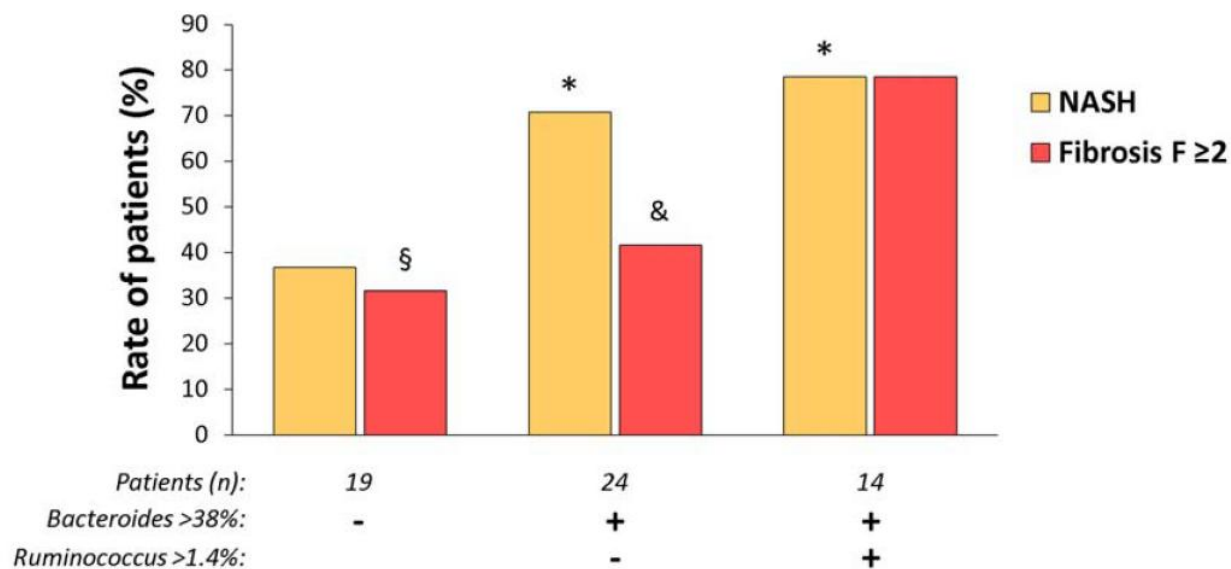


Microbiote intestinal et NAFLD



The Severity of Nonalcoholic Fatty Liver Disease Is Associated With Gut Dysbiosis and Shift in the Metabolic Function of the Gut Microbiota

Jérôme Boursier,^{1,2} Olaf Mueller,³ Matthieu Barret,⁴ Mariana Machado,⁵ Lionel Fizanne,² Felix Araujo-Perez,⁶ Cynthia D. Guy,⁷ Patrick C. Seed,^{3,6} John F. Rawls,³ Lawrence A. David,³ Gilles Hunault,² Frédéric Oberti,^{1,2} Paul Calès,^{1,2} and Anna Mae Diehl⁵



The Severity of Nonalcoholic Fatty Liver Disease Is Associated With Gut Dysbiosis and Shift in the Metabolic Function of the Gut Microbiota

Jérôme Boursier,^{1,2} Olaf Mueller,³ Matthieu Barret,⁴ Mariana Machado,⁵ Lionel Fizanne,² Felix Araujo-Perez,⁶ Cynthia D. Guy,⁷ Patrick C. Seed,^{3,6} John F. Rawls,³ Lawrence A. David,³ Gilles Hunault,² Frédéric Oberti,^{1,2} Paul Calès,^{1,2} and Anna Mae Diehl⁵

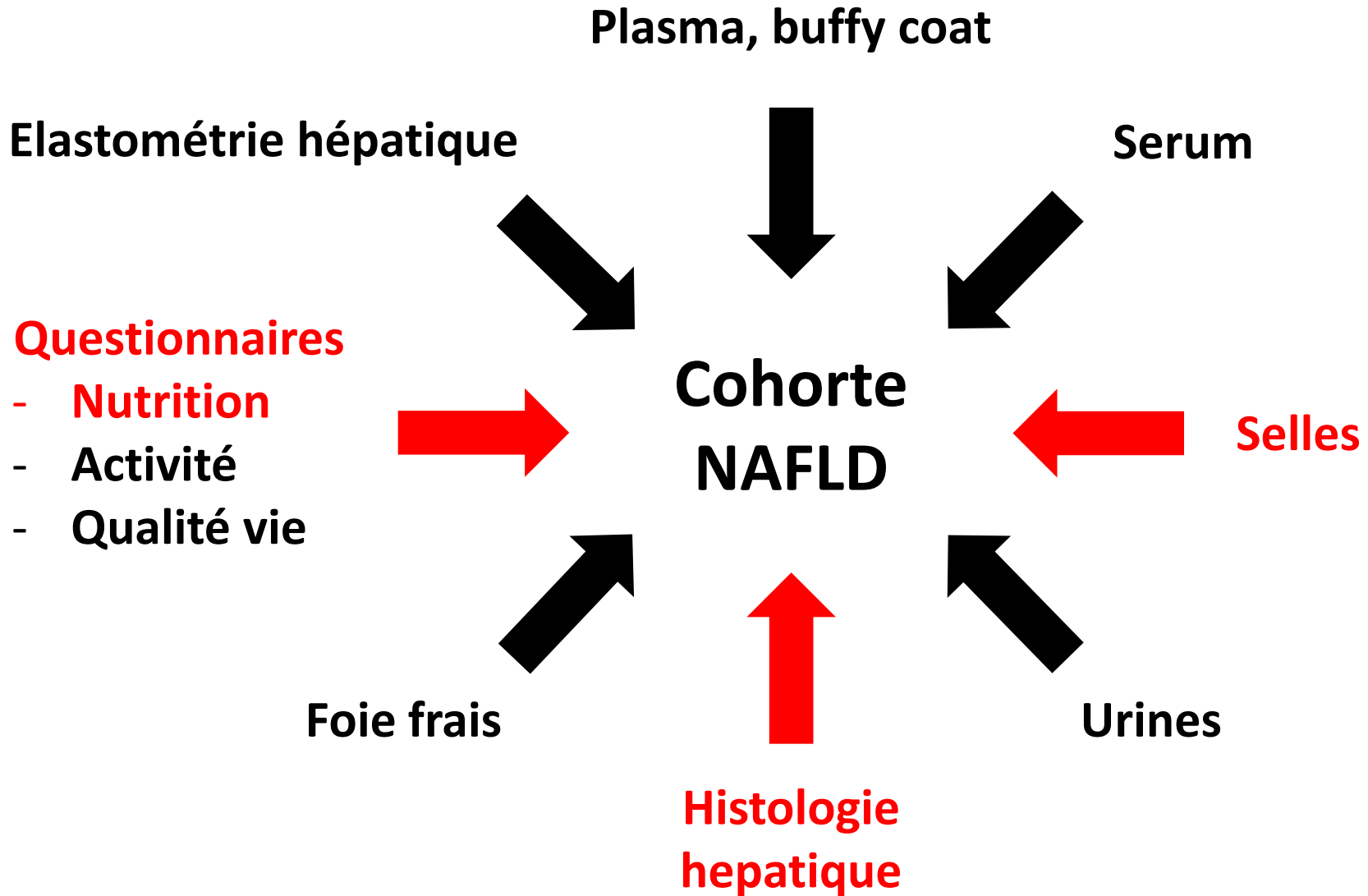
Table 4. Functional Profile of the Gut Microbiota From NASH or F_≥2 Patients

KO Functional Categories Level 2	Level 3	NASH vs. No NASH		F _≥ 2 vs. F0/F1	
		LDA	P Value	LDA	P Value
Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis	2.34	0.03	–	–
Carbohydrate metabolism	Glyoxylate and dicarboxylate metabolism	2.28	0.03	2.28	0.02
Carbohydrate metabolism	Pentose and glucuronate interconversions	–	–	2.74	0.02
Carbohydrate metabolism	Pentose phosphate pathway	–	–	2.44	0.01
Carbohydrate metabolism	Starch and sucrose metabolism	2.68	0.01	–	–
Carbohydrate metabolism	Unclassified	2.22	0.02	2.27	0.01
Lipid metabolism	Fatty acid biosynthesis	–	–	2.10	0.03
Lipid metabolism	Lipid biosynthesis proteins	–	–	2.07	0.03
Lipid metabolism	Sphingolipid metabolism	2.45	0.04	–	–
Metabolism of other amino acids	Cyanoamino acid metabolism	2.27	0.03	–	–
Translation	Translation factors	–	–	-2.25	0.05
Replication and repair	DNA replication proteins	–	–	-2.55	0.04

KEGG pathways were inferred from 16s rRNA gene sequences using PICRUSt. Functional categories significantly enriched or depleted in NASH patients or patients with F_≥2 fibrosis were assessed with LEfSE ($P \leq 0.05$; LDA, >2). NASH and F_≥2 fibrosis were associated with microbiota enrichment in KEGG categories related to metabolic functions.

Abbreviation: KO, KEGG orthology.

Etude MétaNutriNASH



Etude MétaNutriNASH

