

Supplementary Table 5. Differential pathways in the gut microbiome between NASH patients and controls^a

Pathway ^b	Abundance ^c	State ^d	LDA score (log10) ^e	P value ^f
Transcription factors	4.2405	Control	3.1130	0.0021
Bisphenol degradation	2.9400	Control	2.0850	0.0211
Glycolysis,Gluconeogenesis	4.0528	Control	2.6145	0.0001
Germination	2.7262	Control	2.1170	0.0002
Glycerolipid metabolism	3.5951	Control	2.5566	0.0003
Porphyrin and chlorophyll metabolism	4.0370	Control	2.8661	0.0031
Signal transduction mechanisms	3.6936	Control	2.4495	0.0101
Benzoate degradation	3.3370	Control	2.4952	0.0130
C5-Branched dibasic acid metabolism	3.5664	Control	2.6241	0.0001
Lysine biosynthesis	3.9658	Control	2.7877	0.0005
Bacterial chemotaxis	3.5144	Control	2.6144	0.0065
Phenyl propanoid biosynthesis	3.2117	Control	2.2986	0.0060
Pyruvate metabolism	4.0346	Control	2.6934	0.0021
RNA transport	3.1924	Control	2.1309	0.0019
Fatty acid elongation in mitochondria	0.1111	Control	2.2405	0.0311
Arginine and proline metabolism	4.1243	Control	2.9697	0.0002
Nitrotoluene degradation	3.0510	Control	2.1979	0.0153
Cytoskeleton proteins	3.6129	Control	2.4521	0.0001
Tetracycline biosynthesis	3.2321	Control	2.3235	0.0031
Xylene degradation	2.8083	Control	2.0001	0.0041
ABC transporters	4.5428	Control	3.5453	0.0019
Atrazine degradation	2.4896	Control	2.0454	0.0003
Chloroalkane and chloroalkene degradation	3.3350	Control	2.6168	0.0000
Fructose and mannose metabolism	4.0242	Control	2.6166	0.0180
Fatty acid biosynthesis	3.6964	Control	2.1085	0.0413
Phenylalanine,tyrosine and tryptophan biosynthesis	3.9617	Control	2.7138	0.0006
Sporulation	3.9492	Control	3.2963	0.0002
Pentose phosphate pathway	3.9613	Control	2.5966	0.0021
Starch and sucrose metabolism	4.0440	Control	2.8980	0.0003
Valine,leucine and isoleucine biosynthesis	3.9218	Control	3.0072	0.0000
Pantothenate and CoA biosynthesis	3.8347	Control	2.4599	0.0001
Transporters	4.8492	Control	3.8774	0.0007
Methane metabolism	4.1509	Control	2.8710	0.0050
Glycosaminoglycan degradation	3.0727	NASH	2.4027	0.0287
Pertussis	2.6665	NASH	2.2059	0.0004
Ubiquinone and other terpenoid,quinone biosynthesis	3.4063	NASH	2.8570	0.0004
Vitamin B6 metabolism	3.3398	NASH	2.1716	0.0045
Purine metabolism	4.3835	NASH	3.0163	0.0002
Glycosyl transferases	3.6155	NASH	2.7060	0.0000
Cellular antigens	2.8885	NASH	2.3846	0.0003
Glycine,serine and threonine metabolism	3.9467	NASH	2.0796	0.0054
Carbon fixation in photosynthetic organisms	3.8374	NASH	2.3654	0.0228
Citratecycle(TCA cycle)	3.8644	NASH	2.9492	0.0002

Folate biosynthesis	3.6814	NASH	2.6058	0.0000
Valine,leucineand isoleucine degradation	3.3389	NASH	2.0561	0.0008
Lysosome	3.2242	NASH	2.4532	0.0385
Homologous recombination	3.9948	NASH	2.5726	0.0085
Peroxisome	3.2940	NASH	2.1046	0.0180
General function prediction only	4.5748	NASH	2.8008	0.0003
Nitrogen metabolism	3.8805	NASH	2.4369	0.0028
Pyrimidine metabolism	4.2988	NASH	2.9902	0.0028
Energy metabolism	3.9804	NASH	2.7569	0.0002
Carbon fixation pathways in prokaryotes	4.0602	NASH	2.8986	0.0001
Glutathione metabolism	3.3891	NASH	2.5713	0.0002
Huntingtons disease	2.5136	NASH	2.0044	0.0002
RNA degradation	3.7000	NASH	2.3636	0.0010
Function unknown	4.1099	NASH	2.7177	0.0444
DNA replication	3.8408	NASH	2.4472	0.0195
Glycan biosynthesis and metabolism	2.6174	NASH	2.0970	0.0005
Prenyl transferases	3.5569	NASH	2.4847	0.0017
Inorganic ion transport and metabolism	3.3427	NASH	2.3311	0.0228
Glycosphingolipid biosynthesis-ganglio series	2.9656	NASH	2.3378	0.0141
Lipopolysaccharide biosynthesis proteins	3.7170	NASH	3.1659	0.0001
Peptidases	4.3036	NASH	2.8211	0.0130
Drug metabolism-other enzymes	3.5617	NASH	2.3586	0.0017
Otherion-coupled transporters	4.1523	NASH	2.8750	0.0008
Cell motility and secretion	3.2602	NASH	2.4125	0.0003
Translation factors	3.7595	NASH	2.4290	0.0228
Protein digestion and absorption	2.6948	NASH	2.2083	0.0008
Vibrio cholerae pathogenic cycle	2.9208	NASH	2.1480	0.0002
Protein folding and associated processing	3.8473	NASH	2.5427	0.0006
Bacterial secretion system	3.7739	NASH	2.4927	0.0228
Arachidonic acid metabolism	2.7012	NASH	2.2787	0.0002
Membrane and intracellular structural molecules	3.8592	NASH	3.1293	0.0001
Oxidative phosphorylation	4.1024	NASH	2.6713	0.0008
DNA replication proteins	4.1189	NASH	2.7596	0.0166
Chaperones and folding catalysts	4.0651	NASH	2.9453	0.0001
Toluene degradation	3.1063	NASH	2.3290	0.0002
Nicotinate and nicotinamide metabolism	3.6907	NASH	2.5111	0.0050
Taurine and hypotaurine metabolism	3.0882	NASH	2.0020	0.0003
Riboflavin metabolism	3.4798	NASH	2.5463	0.0000
Lipopolysaccharide biosynthesis	3.5725	NASH	3.0927	0.0001
One carbon pool by folate	3.8422	NASH	2.6821	0.0054
Pores ion channels	3.6983	NASH	3.0405	0.0001
Chromosome	4.2122	NASH	2.7941	0.0246

LDA, linear discriminant analysis.

^aLDA was performed with LEfSe. (<http://huttenhower.sph.harvard.edu/galaxy>).

^bKEGG pathways that are differentially represented in the gut microbiome between NASH patients and controls.

^cThe logarithm mean of pathway abundance in the higer presented group.

^dThe disease state with the higer abundance of the pathways.

^elogarithmic LDA score. LDA score is equal or larger than 2 to be considered as discriminative pathways.

^fKruskall-Wallis test.