

Supplementary Table 7 List of contrasted GMM functional modules between ConD and MedD groups at each timepoint, their enrichment status and pvalues from Wilcoxon rank sum tests (pvaluew) and after adjustment for multiple comparisons using the Benjamini-Hochberg procedure (qvaluew).

baseline					
GMM	Module definition	HIER1	Enriched in	pvaluew	qvaluew
MF0108	glycerol degradation (dihydroxyacetone pathway)	lipid degradation	ConD	0,018	0,963
MF0068	glucarate degradation	carbohydrate degradation	ConD	0,044	0,963
MF0024	methionine degradation (mercaptan pathway)	amino acid degradation	MedD	0,036	0,963
MF0085	pyruvate:formate lyase	central metabolism	MedD	0,044	0,963
MF0005	acetylneuraminate and acetylmannosamine degradation	amines and polyamines degradation	MedD	0,049	0,963

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GMM	Module definition	HIER1	Enriched in	pvaluew	qvaluew
MF0112	acetate to acetyl-CoA	organic acid metabolism	ConD	0,0017	0,0182
MF0060	ribose degradation	carbohydrate degradation	ConD	0,0046	0,0382
MF0054	arabinose degradation	carbohydrate degradation	ConD	0,0067	0,0518
MF0033	cysteine degradation (mercaptopyruvate pathway)	amino acid degradation	ConD	0,0076	0,0559
MF0102	mucin degradation	glycoprotein degradation	ConD	0,0205	0,1290
MF0040	lysine degradation (cadaverine pathway)	amino acid degradation	MedD	0,0002	0,0125
MF0056	galactose degradation (Leloir pathway)	carbohydrate degradation	MedD	0,0003	0,0125
MF0114	acetyl-CoA to crotonyl-CoA	organic acid metabolism	MedD	0,0003	0,0125
MF0024	methionine degradation (mercaptan pathway)	amino acid degradation	MedD	0,0005	0,0125
MF0101	Sulfate reduction (assimilatory)	gas metabolism	MedD	0,0005	0,0125
MF0057	alpha-D-glucose and alpha-D-glucose 1-phosphate degradation	carbohydrate degradation	MedD	0,0006	0,0125
MF0058	fructose degradation	carbohydrate degradation	MedD	0,0007	0,0125
MF0001	ethanol production (formate pathway)	alcohol metabolism	MedD	0,0009	0,0145
MF0091	beta-D-glucuronide and D-glucuronate degradation	glycoprotein degradation	MedD	0,0011	0,0145
MF0043	arginine degradation (agmatinase pathway)	amino acid degradation	MedD	0,0011	0,0145
MF0085	pyruvate:formate lyase	central metabolism	MedD	0,0012	0,0145
MF0027	cysteine degradation	amino acid degradation	MedD	0,0020	0,0206
MF0111	triacylglycerol degradation	lipid degradation	MedD	0,0033	0,0314
MF0005	acetylneuraminate and acetylmannosamine degradation	amines and polyamines degradation	MedD	0,0040	0,0354
MF0013	glutamate degradation (crotonyl-CoA pathway)	amino acid degradation	MedD	0,0156	0,1082
MF0051	sucrose degradation (Actinobacteria)	carbohydrate degradation	MedD	0,0183	0,1205
MF0070	galactonate degradation	carbohydrate degradation	MedD	0,0322	0,1901
MF0030	threonine degradation (formate pathway)	amino acid degradation	MedD	0,0333	0,1901
MF0029	threonine degradation (glycine pathway)	amino acid degradation	MedD	0,0346	0,1901

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GMM	Module definition	HIER1	Enriched in	pvaluew	qvaluew
MF0019	proline degradation (aminopentanoate pathway)	amino acid degradation	ConD	0,008	0,584
MF0004	putrescine degradation	amines and polyamines degradation	ConD	0,024	0,584
MF0106	anaerobic fatty acid beta-oxidation	lipid degradation	ConD	0,026	0,584
MF0083	pyruvate dehydrogenase complex	central metabolism	ConD	0,027	0,584
MF0047	lactose and galactose degradation (PTS)	carbohydrate degradation	ConD	0,036	0,584
MF0043	arginine degradation (agmatinase pathway)	amino acid degradation	MedD	0,021	0,584
MF0113	acetyl-CoA to acetate	organic acid metabolism	MedD	0,023	0,584
MF0013	glutamate degradation (crotonyl-CoA pathway)	amino acid degradation	MedD	0,038	0,584
MF0005	acetylneuraminate and acetylmannosamine degradation	amines and polyamines degradation	MedD	0,040	0,584