

**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).

| <b>baseline</b> |  |                                      |                    |                |                |
|-----------------|--|--------------------------------------|--------------------|----------------|----------------|
| <b>GMM</b>      | <b>Module definition</b>                               | <b>HIER1</b>                         | <b>Enriched in</b> | <b>pvaluew</b> | <b>qvaluew</b> |
| MF0108          | glycerol degradation<br>(dihydroxyacetone pathway)     | lipid degradation                    | ConD               | 0,018          | 0,963          |
| MF0068          | glucarate degradation                                  | carbohydrate<br>degradation          | ConD               | 0,044          | 0,963          |
| MF0024          | methionine degradation<br>(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<br>degradation | amines and polyamines<br>degradation | MedD               | 0,049          | 0,963          |

## 4w

| 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  |

## 8w

| 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   |