# **Supplemental Table 8.** Bacterial species whose abundance at week 0 was significantly different between those reporting “better” (n = 16) and “about the same” overall health (n = 10) at week 4 after diet change.

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **Phylum** | **Class** | **Order** | **Family** | **Genus** | **Species** | **Relative abundance, in %****Median (IQR)** | **Better vs About the same health****Baseline** |
| **Better overall health****(n=16)** | **About the same overall health****(n=10)** | **Log 2 FC****mean ± SE** | **Adjusted** ***P*-value1** |
| **Higher in “better overall health” (5 species)** |
| Proteobacteria | Gammaproteobacteria | Enterobacterales | Enterobacteriaceae | Enterobacter | cloacae complex sp ECNIH7 | 0.00E+00 (0.00E+00 - 8.03E-05) | 0.00E+00 (0.00E+00 - 0.00E+00) | 21.45±3.03 | 6.93E-10 |
| Proteobacteria | Gammaproteobacteria | Enterobacterales | Hafniaceae | Edwardsiella | piscicida | 0.00E+00 (0.00E+00 - 0.00E+00) | 0.00E+00 (0.00E+00 - 0.00E+00) | 21.29±3.04 | 6.93E-10 |
| Proteobacteria | Deltaproteobacteria | Desulfovibrionales | Desulfovibrionaceae | Bilophila | wadsworthia | 0.00E+00 (0.00E+00 - 0.00E+00) | 0.00E+00 (0.00E+00 - 0.00E+00) | 20.03±3.04 | 8.59E-09 |
| Bacteroidetes | Bacteroidia | Bacteroidales | Bacteroidaceae | Bacteroides | vulgatus | 6.47E-03 (3.90E-04 - 8.89E-02) | 3.10E-03 (3.61E-04 - 7.29E-03) | 5.57±1.25 | 1.24E-03 |
| Bacteroidetes | Bacteroidia | Bacteroidales | Bacteroidaceae | Bacteroides | dorei | 1.03E-03 (6.93E-05 - 4.83E-03) | 2.16E-04 (2.39E-05 - 3.51E-04) | 4.85±1.27 | 1.13E-02 |
| **Lower in “better overall health” (3 species)** |
| Firmicutes | Clostridia | Clostridiales | Clostridiaceae | Clostridium | baratii | 1.05E-04 (0.00E+00 - 2.72E-04) | 2.40E-04 (0.00E+00 - 7.37E-03) | -5.51±1.39 | 7.48E-03 |
| Firmicutes | Clostridia | Clostridiales | Clostridiaceae | Clostridium | perfringens | 2.19E-02 (1.89E-03 - 5.18E-02) | 7.72E-02 (5.13E-03 - 2.92E-01) | -4.87±1.22 | 7.48E-03 |
| Firmicutes | Clostridia | Clostridiales | Peptostreptococcaceae | no data | no data | 9.39E-04 (1.44E-04 - 2.64E-03) | 1.45E-03 (1.05E-03 - 2.97E-03) | -2.64±0.77 | 4.48E-02 |

FC: fold change, SE: standard error, NS: not significant

1 p values were adjusted with false discovery rate for multiple comparisons