**Supplemental Table S4. Differential abundance in the fecal microbiomes of NB patients after 4 cycles of therapy and of NB patients at onset.**

| NB patients at the end of therapy [6] *vs.* NB patients at onset [15] | zero-inflated Gaussian fit | | EdgeR | | DESeq2 | | LDA | |
|---|---|---|---|---|---|---|---|---|
| Taxonomy | log2FC | FDR | log2FC | FDR | log2FC | FDR | LDA-SCORE | FDR |
| **Higher abundance in the fecal microbiomes of NB patients at end of therapy or lower in the ones of NB patients at the onset** | | | | | | | | |
| *p_Actinomycetota; c_Actinomycetes;* ***o_Actinomycetales*** | | | 6.4431 | 0.0016 | | | | |
| *p_Actinomycetota; c_Actinomycetes; o_Micrococcales;* ***f_Micrococcaceae*** | | | 4.7143 | 0.0296 | | | | |
| | | | | | | | | |
| *p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Bacteroidaceae;* ***g_Bacteroides; s_ovatus*** | 4.6411 | 0.0170 | 4.6411 | 0.0041 | 9.186 | 0.0332 | | |
| | | | | | | | | |
| ***p_Bacillota*** | | | 5.2692 | 1.5E-8 | | | | |
| *p_Bacillota;* ***c_Bacilli*** | | | 11.829 | 3.1E-10 | | | | |
| *p_Bacillota; c_Bacilli;* ***o_Lactobacillales*** | | | 9.3106 | 1.2E-8 | 5.0486 | 7.1E-4 | | |
| *p_Bacillota; c_Bacilli; o_Lactobacillales;* ***f_Enterococcaceae*** | | | 9.7544 | 9.4E-5 | | | | |
| *p_Bacillota; c_Bacilli; o_Lactobacillales; f_Enterococcaceae;* ***g_Enterococcus*** | | | 9.0494 | 2.5E-4 | | | | |
| *p_Bacillota; c_Bacilli; o_Lactobacillales;* ***f_Streptococcaceae*** | | | 5.5173 | 0.0104 | 5.9089 | 0.0119 | | |
| *p_Bacillota; c_Bacilli; o_Lactobacillales; f_Streptococcaceae;* ***g_Streptococcus*** | | | 5.3874 | 0.0165 | | | | |
| *p_Bacillota; c_Bacilli; o_Lactobacillales; f_Streptococcaceae;* ***g_Streptococcus; s_thermophilus*** | 12.638 | 0.0143 | 12.638 | 7.4E-8 | 13.366 | 9.9E-4 | | |
| *p_Bacillota; c_Clostridia; o_Eubacteriales;* ***f_Eubacteriaceae*** | | | 6.8077 | 9.4E-5 | | | | |
| *p_Bacillota; c_Clostridia; o_Eubacteriales; f_Eubacteriaceae;* ***g_Eubacterium*** | | | 5.6969 | 0.0012 | | | | |
| *p_Bacillota; c_Clostridia; o_Eubacteriales; f_Lachnospiraceae;* ***g_Lachnospira; s_eligens*** | 7.3422 | 0.0170 | 7.3422 | 6.5E-4 | 9.9892 | 0.0215 | | |
| *p_Bacillota; c_Clostridia; o_Eubacteriales; f_Lachnospiraceae;* ***g_Blautia; s_wexlerae*** | | | 4.2355 | 0.0330 | | | | |
| *p_Bacillota; c_Clostridia; o_Eubacteriales;* ***f_Oscillospiraceae*** | | | 3.7018 | 0.0280 | | | | |
| *p_Bacillota; c_Clostridia; o_Eubacteriales; f_Oscillospiraceae;* ***g_Faecalibacterium; s_prausnitzii*** | 0.5812 | 0.0482 | | | | | | |
| *p_Bacillota; c_Clostridia; o_Eubacteriales; f_Oscillospiraceae;* ***g_Gemminger*** | -5.377 | 0.0035 | | | | | | |
| *p_Bacillota; c_Clostridia; o_Eubacteriales; f_Oscillospiraceae;* ***g_Gemminger; s_formicilis*** | -8.9181 | 0.0137 | -8.9181 | 0.0330 | | | | |
| | | | | | | | | |
| *p_Pseudomonadota;* ***c_Betaproteobacteria*** | 1.6073 | 0.0286 | | | | | | |
| **Higher abundance in NB samples at onset or lower in the ones of NB patients at end of therapy** | | | | | | | | |
| *p_Actinomycetota; c_Actinomycetes; o_Bifidobacteriales; f_Bifidobacteriaceae;* ***g_Bifidobacterium; s_breve*** | -7.2717 | 0.0078 | -7.2717 | 0.0330 | -8.6188 | 0.0215 | | |
| *p_Actinomycetota; c_Actinomycetes; o_Bifidobacteriales; f_Bifidobacteriaceae;* ***g_Bifidobacterium; s_longum*** | -8.5872 | 0.0087 | -8.5872 | 0.0273 | | | | |
| | | | | | | | | |
| *p_Bacillota; c_Clostridia; o_Eubacteriales; f_Peptostreptococcaceae;* ***g_Clostridioides; s_difficile*** | | | -5.5242 | 0.0444 | | | | |
| *p_Bacillota; c_Clostridia; o_Eubacteriales; f_Clostridiaceae;* ***g_Hungatella; s_hathewayi*** | | | -11.006 | 0.0273 | | | | |
| *p_Bacillota; c_Clostridia; o_Eubacteriales; f_Clostridiaceae;* ***g_Clostridium; s_neonatale*** | -12.448 | 2.9E-4 | -12.448 | 0.0151 | -28.765 | 1.8E-16 | | |
| *p_Bacillota; c_Erysipelotrichia; o_Erysipelotrichales; f_Coprobacillaceae;* ***g_Thomasclavelia s_ramosum*** | -3.4354 | 0.0482 | | | | | | |
| *p_Bacillota; c_Negativicutes; o_Veillonellales; Veillonellaceae;* ***g_Veillonella; s_atypica*** | -7.3498 | 0.0482 | | | | | | |
| *p_Bacillota; c_Negativicutes; o_Veillonellales; Veillonellaceae;* ***g_Veillonella; s_parvula*** | | | -7.5665 | 0.0330 | | | | |
| | | | | | | | | |
| ***p_Pseudomonadota*** | | | -8.577 | 0.0158 | | | | |
| *p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; f_Enterobacteriaceae;* ***g_Pseudescherichia; s_vulneris*** | -1.9753 | 0.0482 | | | | | | |
| *p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; f_Enterobacteriaceae;* ***g_Leclercia*** | -12.909 | 0.0394 | -12.909 | 0.0217 | -29.304 | 2.2E-17 | | |

The number in square brackets indicates the number of patients in each group. The columns represent the statistical analyses using four algorithms (the zero-inflated Gaussian Fit, the EdgeR, the DESeq2, and the LDA). All statistical analyses showed the FDR (False Discovery Rate) that indicates the p-value after adjustment for multiple comparisons. FDR equal to or less than 0.05 was considered statistically significant. The taxonomy is shown as p_Phylum; c_Class; o_Order; f_Family; g_Genus; s_Specie. The base two logarithmic value of fold changes (log2FC) represents the increase (+) or decrease (-) in the abundance of a particular taxon between the two groups. The LDA-Score represents the effect size of each abundant taxa.