Supplemental Table S3. Differential microbial abundance in the fecal microbiomes of NB patients after 4 cycles of therapy or the ones from healthy children.

NB patients after 4 cycles of therapy [6] *vs* HC-Controls [17]	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 the end of therapy or lower abundance in the ones of healthy children's samples (HC-Controls)								
p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Bacteroidaceae; ***g_Bacteroides; s_xylanisolvens***			6.1531	0.0021				
p_Bacillota	4.1877	0.0496	4.1877	1.4E-8				
p_Bacillota; ***c_Bacilli***			12.492	1.8E-15				
p_Bacillota; c_Bacilli; ***o_Lactobacillales***			9.9159	3.3E-11				
p_Bacillota; c_Bacilli; o_Lactobacillales; ***f_Enterococcaceae***			17.503	1.2E-14				
p_Bacillota; c_Bacilli; o_Lactobacillales; f_Enterococcaceae; ***g_Enterococcus***			13.524	2.4E-11				
p_Bacillota; c_Bacilli; o_Lactobacillales; ***f_Streptococcaceae***			9.0566	2.2E-9	4.3344	0.0100		
p_Bacillota; c_Bacilli; o_Lactobacillales; f_Streptococcaceae; ***g_Streptococcus***			6.8355	6.4E-7				
p_Bacillota; c_Bacilli; o_Lactobacillales; f_Streptococcaceae; ***g_Streptococcus; s_thermophilus***			8.3448	3.3E.4				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Clostridiaceae; ***g_Clostridium; s_paraputrificum***			5.2546	0.0233				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Lachnospiraceae; ***g_Enterocloster***			3.7105	0.0386				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Lachnospiraceae; g_Enterocloster ***; s_clostridioformis***			4.5914	0.0084				
p_Bacillota; c_Erysipelotrichia; o_Erysipelotrichales; f_Coprobabillaceae; ***g_Thomasclavelia; s_spiroformis***			4.4034	0.0050				
p_Pseudomonadota; ***c_Deltaproteobacteria***	2.2086	11.0535						
p_Pseudomonadota; c_Deltaproteobacteria; o_Desulfovibrionales; f_Desulfovibrionaceae; ***g_Bilophila; s_wadsworthia***			5.5002	0.0260				
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; f_Enterobacteriaceae; ***g_Kosakonia***			5.5432	0.0014				
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; f_Enterobacteriaceae; ***g_Kosakonia; s_sacchari***			6.0017	0.0021				
Higher abundance in the fecal microbiomes healthy children's samples (HC-Controls) or lower abundance in the ones of NB patients at the end of therapy								
p_Actinomycetota			-3.0847	0.0389				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Lachnospiraceae; ***g_Roseburia; s_inulinivorans***			-7.8959	0.0332				
p_*Bacillota; c_Clostridia; o_Eubacteriales; f_Lachnospiraceae;* ***g_Dorea***	-7.3729	0.0121			-30.0	2.7E-21		
p_Bacillota; c_Erysipelotrichia; o_Erysipelotrichales; f_Coprobacillaceae; ***g_Thomasclavelia; s_ramosa***			-4.6923	0.0332				
p_Bacillota; c_Erysipelotrichia; o_Erysipelotrichales; f_Turicibacteraceae; ***g_Turicibacter***	-7.1817	0.0121						
p_Psedomonadota; ***c_Alphaproteobacteria***	-6.5252	13.0631			-27.331	1.3E-15		
p_Pseudomonadota; c_Alphaproteobacteria; ***o_Hyphomicrobiales***	-7.6444	0.0011			-26.277	3.7E-15		
p_Pseudomonadota; c_Alphaproteobacteria; o_Hyphomicrobiales; ***f_Hyphomicrobiaceae***	-7.0950	0.0023			-30.0	1.0E-21		
p_Pseudomonadota; c_Gammaproteobacteria; o_Pasteurellales; f_Pasteurellaceae; ***g_Haemophilus; s_sputorum***			-7.3858	0.0332				
p_Verrucomicrobiota; c_Verrucomicrobiia; o_Verrucomicrobiales; f_Akkermansiaceae; ***g_Akkermansia***	-6.5777	0.0121			-29.84	2.2E-22		

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.