Supplemental Table S5. Differential abundance in the fecal microbiomes of NB patients after 4 and 2 cycles of therapy.

NB patients after 4 cycles of therapy [5] *vs.* NB patients after 2 cycles of drugs treatment [6]	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 after 4 cycles of therapy or lower in the ones of NB patients after 2 cycles of therapy								
p_Actinomycetota; c_Actinomycetes; o_Bifidobacteriales; f_Bifidobacteriaceae; ***g_Bifidobacterium; s_bifidum***			6.4199	0.0380				
p_Actinomycetota; c_Actinomycetes; o_Bifidobacteriales; f_Bifidobacteriaceae; ***g_Bifidobacterium; s_pseudocatenulatum***			6.3698	0.0380				
p_*Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Bacteroidaceae;* ***g_Bacteroides; s_uniformis***			8.5738	0.0380				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Clostridiaceae; ***g_Clostridium; s_butyricum***			9.529	0.0380				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Clostridiaceae; ***g_Clostridium; s_innocuum***			6.3895	0.0380				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Clostridiaceae; ***g_Clostridium; s_paraputrificum***			8.9336	0.0398				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Lachnospiraceae; ***g_Anaerostipes; s_hadrus***			6.4286	0.0499				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Lachnospiraceae; ***g_Blautia; s_producta***			5.7424	0.0380				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Lachnospiraceae; ***g_Blautia; s_wexlerae***			10.678	0.0339	26.305	1.5E-16		
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Lachnospiraceae; ***g_Roseburia; s_faecis***			7.7252	0.0339				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Oscillospiraceae; ***g_Ruminococcus; s_bromii***			10.09	0.0339				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Oscillospiraceae; ***g_Ruminococcus; s_torques***	8.0091	0.0031	8.0091	0.0339	24.066	3.6E-14		
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Oscillospiraceae; ***g_Flavonifractor; s_plautii***			7.5719	0.0380				
p_Bacillota; c_Negativicutes; o_Acidaminococcales; ***f_Acidaminococcaceae***			8.3712	0.0315	25.839	1.6E-16		
p_Pseudomonadota; c_Deltaproteobacteria; o_Desulfovibrionales; f_Desulfovibrionaceae; ***g_Bilophila; s_wadsworthia***			7.7555	0.0380				
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; f_Enterobacteriaceae; ***g_Kosakonia; s_sacchari***			7.6877	0.0380				
Higher abundance in the fecal microbiomes of NB patients after 2 cycles of therapy or lower in the ones of NB patients after 4 cycles of therapy								
*p_Actinomycetota; c_Actinomycetes; o_Micrococcales; f_* ***Micrococcaceae***					-8.9935	0.0132		
p_Actinomycetota; c_Actinomycetes; o_Micrococcales s; f_Micrococcaceae; ***g_Rothia***					-8.4708	0.0403		
p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; ***f_Prevotellaceae***	-3.6094	0.0042			-28.799	1.7E-20		
p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Prevotellaceae; ***g_Prevotella***			-27.418	3.2E-18	-28.725	5.3E-20		
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Clostridiaceae; ***g_Clostridium; s_disporicum***			-5.8843	0.0380				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Lachnospiraceae; ***g_Roseburia; s_intestinalis***	-6.3531	0.0055						
p_Bacillota; c_Erysipelotrichia; o_Erysipelotrichales; f_Turicibacteraceae; ***g_Turicibacter; s_sanguinis***					-25.412	7.3E-16		
p_Bacillota; c_Negativicutes; o_Veillonellales; f_Veillonellaceaea; ***g_Veillonella; s_atypica***			-5.6708	0.0380	-8.7678	0.0049		
p_Pseudomonadota; ***c_Epsilonproteobacteria***	-7.7298	5.7E-5	-7.7298	0.0304	-26.281	3.4E-17		
p_Pseudomonadota; c_Epsilonproteobacteria; ***o_Campylobacterales***	-8.8736	4.6E-4	-8.8736	0.0375	-28.171	1.4E-19		
*p_Pseudomonadota; c_Epsilonproteobacteria; o_Campylobacterales****; f_Campylobacteraceae***	-7.6404	0.0042			-30.0	6.7E-22		
p_Pseudomonadota; c_Epsilonproteobacteria; o_Campylobacterales; f_Campylobacteraceae; ***g_Campylobacter***					-27.162	3.5E-18		
p_Pseudomonadota; c_Epsilonproteobacteria; o_Campylobacterales; f_Campylobacteraceae; ***g_Campylobacter; s_concisus***			-9.4906	0.0297	-26.772	4.1E-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.