Supplemental Table S1. Differential microbial abundance in the fecal microbiomes of NB patients at onset and the ones of Healthy Controls.

NB patient samples at onset [15] *vs* Healthy Controls (HC) [17]	zero-inflated Gaussian fit		EdgeR		DESeq2		LDA	
Taxonomy	log2FC	FDR	log2FC	FDR	log2FC	FDR	LDA-SCORE	FDR
Higher abundance in fecal microbiomes of NB patients at onset or lower abundance in the ones of Healthy Controls (HC).								
p_Actinomycetota; c_Actinomycetes; o_Bifidobacteriales; ***f_Bifidobacteriaceae***			3.5387	4.9E-4				
p_Actinomycetota; c_Actinomycetes; o_Bifidobacteriales; f_Bifidobacteriaceae; ***g_Bifidobacterium; s_breve***	1.9716	0.0077						
*p_Actinomycetota; c_Coriobacteriia; o_Eggetherellales; f_* ***Eggerthellaceae; g_Eggerthella***	1.3651	0.0309						
p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; ***f_Phorphyromonadaceae***			5.8994	2.8E-4				
p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Tannerellaceae; ***g_Parabacteroides***			3.9185	0.0162				
p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Tannerellaceae; ***g_Parabacteroides; s_distasonis***			4.3262	0.0293				
p_Bacillota; c_Bacilli; ***o_Lactobacillales***			2.4418	0.0036				
p_Bacillota; c_Bacilli; o_Lactobacillales; ***f_Enterococcaceae***	8.1650	0.0023	8.165	3.6E-8	5.1819	0.0086		
*p_Bacillota; c_Bacilli; o_Lactobacillales; f_Enterococcaceae****; g_Enterococcus***	5.3209	0.0025	5.3209	2.0E-4	4.9228	0.0315		
p_Bacillota; c_Bacilli; o_Lactobacillales; ***f_Lactobacillaceae***			3.8121	0.0089				
p_Bacillota; c_Bacilli; o_Lactobacillales; ***f_Streptococcaceae***			5.2513	8.1E-6				
p_Bacillota; c_Bacilli; o_Lactobacillales; f_Streptococcaceae; ***g_Streptococcus***			2.579	0.0211				
p_Bacillota; c_Clostridia; ***o_Clostridiales***			3.1396	0.0014				
p_Bacillota; c_Clostridia; o_Eubacteriales; ***f_Clostridiaceae***			5.5979	5.7E-7	2.1357	0.0405		
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Clostridiaceae; ***g_Clostridium***			2.559	0.0162	2.2537	0.0243		
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Clostridiaceae; ***g_Clostridium; s_hathewayi***			5.6751	0.0014				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Clostridiaceae; ***g_Clostridium; s_paraputrificum***	3.8399	0.0342	3.8399	0.0388				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Clostridiaceae; ***g_Hungatella; s_hathewayi***			4.0714	0.0095				
p_Bacillota; c_Clostridia; o_Eubacteriales; ***f_Peptostreptococcaceae***			4.6151	2.8E-4				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Oscillospiraceae; ***g_Anaerotruncus***			4.3168	7.5E-4				
p_Bacillota; c_Clostridia; o_Eubacteriales; f_Oscillospiraceae; ***g_Anaerotruncus; s_colihominis***			4.9874	4.5E-4				
p_Bacillota; c_Negativicutes; ***o_Selenomonadales***			3.0082	0.0036				
p_Bacillota; c_Negativicutes; o_Veillonellales; ***f_Veillonellaceae***			4.258	4.0E-4				
p_Bacillota; c_Negativicutes; o_Veillonellales; f_Veillonellaceae; ***g_Veillonella; s_dispar***	2.0306	0.0450						
p_Bacillota; c_Negativicutes; o_Veillonellales; f_Veillonellaceae; ***g_Veillonella; s_tobetsuensis***	2.7349	0.0473						
p_Pseudomonadota	12.5145	4.2E-4	12.515	2.3E-11	1.1757	0.0384	4.58	5.1E-4
p_Pseudomonadota; ***c_Deltaproteobacteria***			4.3561	0.0056				
p_Pseudomonadota; c_Deltaproteobacteria; ***o_Desulfovibrionales***			4.3371	0.0036				
p_Pseudomonadota; c_Deltaproteobacteria; o_Desulfovibrionales; ***f_Desulfovibrionaceae***	3.8919	0.0124	3.8919	0.0029				
p_Pseudomonadota; c_Deltaproteobacteria; o_Desulfovibrionales; f_Desulfovibrionaceae; ***g_Bilophila***	4.7545	0.0034	4.7545	0.0021				
p_Pseudomonadota; c_Deltaproteobacteria; o_Desulfovibrionales; f_Desulfovibrionaceae; ***g_Bilophila; s_wadsworthia***			4.004	0.0170				
p_Pseudomonadota; ***c_Gammaproteobacteria***	10.7774	0.0042	10.777	5.0E-11	1.5154	0.0040	4.58	0.0037
p_Pseudomonadota; c_Gammaproteobacteria; ***o_Enterobacterales***	9.8523	0.0014	9.8523	2.2E-12	1.7234	0.0054	4.59	0.0022
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; ***f_Enterobacteriaceae***	8.1018	0.0012	8.1018	3.7E-11	2.3116	0.0012	4.59	0.0042
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; f_Enterobacteriaceae; ***g_Enterobacter***	7.5888	0.0056	7.5888	1.3E-5				
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; f_Enterobacteriaceae; ***g_Enterobacter; s_asburiae***	6.9146	0.0016	6.9146	8.4E-5				
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; f_Enterobacteriaceae; ***g_Escherichia***			4.8581	4.4E-4				
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; f_Enterobacteriaceae; ***g_Escherichia; s_coli***	4.6945	0.0450	4.6945	0.0012				
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; f_Enterobacteriaceae; ***g_Klebsiella***			3.5546	0.0211				
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; f_Enterobacteriaceae; ***g_Klebsiella; s_variicola***			3.4136	0.0464	7.2882	0.0046		
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacterales; f_Enterobacteriaceae; ***g_Leclercia***	9.6192	8.0E-4	9.6192	6.9E-6	6.1166	0.0243		
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacteriales; f_Enterobacteriaceae; ***g_Leclercia; s_adecarboxylata***	8.001	0.0104	8.001	1.4E-4	5.9222	0.0346		

p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacteriales; f_Enterobacteriaceae; ***g_Salmonella***			7.2654	8.1E-5				
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacteriales; f_Enterobacteriaceae; ***g_Salmonella; s_enterica***	6.9432	0.0137	6.9432	1.4E-4				
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacteriales; f_Enterobacteriaceae; ***g_Trabulsiella***			3.2494	0.0021				
p_Pseudomonadota; c_Gammaproteobacteria; o_Enterobacteriales; f_Enterobacteriaceae; ***g_Trabulsiella; s_odontotermitis***			2.9425	0.0119				
Higher abundance in fecal microbiome of Healthy Control (HC) or lower abundance in the ones of NB patients at onset								
p_Actinomycetota; c_Actinomycetes; o_Bifidobacteriales; f_Bifidobacteriaceae; ***g_Bifidobacterium; s_bifidum***	-1.4016	0.0138						
p_Actinomycetota; c_Actinomycetes; o_Bifidobacteriales; f_Bifidobacteriaceae; ***g_Bifidobacterium; s_pseudocatenulatum***			-3.4336	0.0422				
p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Bacteroidaceae; ***g_Bacteroides; s_ovatus***	-5.1499	2.2E-4	-5.1499	0.0012				
p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Bacteroidaceae; ***g_Bacteroides; s_uniformis***	-2.0185	0.0054						
p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Bacteroidaceae; ***g_ Phocaeicola; s_vulgatus***	-3.7246	0.0077						
p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; ***f_Prevotellaceae***	-4.1366	0.0012	-4.1366	0.0129				
p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; f_Prevotellaceae; ***g_Prevotella***	-5.1257	0.0029	-5.1257	0.0048	-6.9818	0.0243		
p_Bacteroidota; c_Bacteroidia; o_Bacteroidales; ***f_Rikenellaceae***			-3.5311	0.0075	-5.0811	0.0402		
p_Bacillota; c_Bacilli; o_Lactobacillales; f_Lactobacillaceae; ***g_Lactobacillus; s_rogosae***	-7.1605	3.5E-6	-7.1605	1.4E-4	-9.1528	0.0046		
p_Bacillota; c_Bacilli; o_Lactobacillales; f_Streptococcaceae; ***g_Streptococcus; s_thermophillus***	-4.6113	0.0054	-4.6113	0.0015				
p_Bacillota; c_Clostridia; o_Eubateriales; f_Clostridiaceae; ***g_Clostridium; s_aldenense***	-3.4019	0.0450	-3.4019	0.0109				
p_Bacillota; c_Clostridia; o_Eubateriales; ***f_Eubacteriaceae***	-3.9262	0.0305	-3.9262	4.0E-4	-3.793	0.0221	-3.18	0.0311
p_Bacillota; c_Clostridia; o_Eubateriales; f_Eubacteriaceae; ***g_Eubacterium***	-5.773	8.6E-5	-5.773	4.2E-5	-4.5786	0.0118	-3.41	0.0271
p_Bacillota; c_Clostridia; o_Eubateriales; f_Eubacteriaceae; ***g_Eubacterium; s_eligens***	-8.5301	2.1E-4	-8.5301	9.5E-6	-8.0194	0.0046		
p_Bacillota; c_Clostridia; o_Eubateriales; f_Lachnospiraceae; ***g_Anaerostipes***	-3.7797	0.0191	-3.7797	8.1E-4	-6.6597	0.0168		
p_Bacillota; c_Clostridia; o_Eubateriales; f_Lachnospiraceae; ***g_Dorea***			-5.3419	5.8E-4				
p_Bacillota; c_Clostridia; o_Eubateriales; f_Eubacteriaceae; ***g_ Eubacterium; s_hadrum***	-5.2008	2.2E-4	-5.2008	0.0012				
p_Bacillota; c_Clostridia; o_Eubateriales; f_Lachnospiraceae; ***g_Roseburia***	-4.7214	0.0309	-4.7214	4.0E-4			-3.15	0.0343
p_Bacillota; c_Clostridia; o_Eubateriales; f_Lachnospiraceae; ***g_Roseburia; s_faecis***	-2.6713	0.0137			-5.5196	0.0209		
p_Bacillota; c_Clostridia; o_Eubateriales; f_Lachnospiraceae; ***g_Roseburia; s_intestinalis***	-2.4941	0.0080						
p_Bacillota; c_Clostridia; o_Eubateriales; f_Lachnospiraceae; ***g_Roseburia; s_inulinivorans***	-4.365	0.0327	-4.365	0.0119	-7.1539	0.0080		
p_Bacillota; c_Clostridia; o_Eubateriales; f_Oscillospiraceae; ***g_Faecalibacterium; s_prausnitzii***	-2.9448	0.0342						
p_Bacillota; c_Clostridia; o_Eubateriales; f_Oscillospiraceae; ***g_Ruminococcus; s_bromii***	-4.7206	9.0E-4	-4.7206	0.0012	-7.5374	0.0080		
p_Bacillota; c_Clostridia; o_Eubateriales; f_Oscillospiraceae; ***g_Ruminococcus; s_gauvreauii***	-1.0176	0.0328						
p_Bacillota; c_Negativicutes; o_Veillonellales; f_Veillonellaceaea; ***g_Dialister***	-4.2034	0.0191	-4.2034	0.0050				
p_Bacillota; c_Negativicutes; o_Veillonellales; f_Veillonellaceaea; ***g_Dialister; s_invisus***	-3.08	2.2E-4						
p_Bacillota; c_Erysipelotrichia; o_Erysipelotrichales; f_Turicibacteraceae; ***g_Turicibacter***	-4.4245	0.0061	-4.4245	0.0029	-7.3208	0.0118		
p_Bacillota; c_Erysipelotrichia; o_Erysipelotrichales; f_ Turicibacteraceae; ***g_Turicibacter; s_sanguinis***	-3.2298	0.0422	-3.2298	0.0320				
p_Pseudomonadota; ***c_Betaproteobacteria***	-1.8199	0.0021						
p_Pseudomonadota; c_Betaproteobacteria; ***o_Burkholderiales***	-1.6084	0.0380						
p_Pseudomonadota; c_Betaproteobacteria; o_Burkholderiales; ***f_Sutterellaceae***	-1.9243	0.0392			-6.7015	0.0020		
p_Pseudomonadota; c_Gammaproteobacteria; ***o_Pasteurellales***					-3.5573	0.0317	-3.22	0.0265
p_Pseudomonadota; c_Gammaproteobacteria; o_Pasteurellales; ***f_Pasteurellaceae***							-3.22	0.0338
p_Pseudomonadota; c_Gammaproteobacteria; o_Pasteurellales; f_Pasteurellaceae; ***g_Haemophilus***	-1.6309	0.0472						
p_Pseudomonadota; c_Gammaproteobacteria; o_Pasteurellales; f_Pasteurellaceae; ***g_Haemophilus; s_parainfluenzae***	-1.1812	0.0450						
p_Pseudomonadota a; c_Gammaproteobacteria; o_Pasteurellales; f_Pasteurellaceae; ***g_Haemophilus; s_sputorum***	-3.3546	0.0042	-3.3546	0.0412	-7.9367	0.0046		
p_Pseudomonadota; c_Gammaproteobacteria; o_Pasteurellales; f_Pasteurellaceae; ***g_Mannheimia***	-1.7943	0.0449						
p_Pseudomonadota; c_Gammaproteobacteria; o_Pasteurellales; f_Pasteurellaceae; ***g_Mannheimia; s_varigena***	-1.4604	0.0342						

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. All statistical analyses adjust the data for

imbalanced class distribution (under-sampling) and dataset sparsity. 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.