Supplementary Table S1. Summary of sequencing output and Kraken2 taxonomic classification by sample. Percentages are calculated relative to the total reads in each sample.

Sample	Total reads	Classified reads (%)	Unclassified reads (%)	Sequencing yield (Mb)	Read N50 (bp)	Mean QScore (sd)
F13	844,933	79.78	20.22	332.04	862	22,2 ± 3,64
F62	260,191	98.40	1.60	488.27	2,198	21,8 ± 3,29
F75	142,434	91.06	8.94	279.08	2,407	20,5 ± 3,14
F76	14,343	40.84	59.16	8.39	772	22,4 ± 3,64
F78	135,636	56.95	43.05	85.76	1,168	23,4 ± 3,59
F79	10,250	87.05	12.95	5.38	999	22,1 ± 3,66