

Supplementary Table S2. Combinations of parameters tested for the nemabiome data analysis

Maximal Error Rate (forward, reverse)	Truncation length (bp)	BAND_SIZE	ASV with at least 50% bootstrap support	Fraction of ASVs passing bootstrap support cut-off	Total number of ASVs	Fraction with missing taxonomy	Taxonomy method	False positive	False negative
2,5	217	-1	92	0,8363636	110	0,1636364	ldtaxa	0	1
2,5	217	16	90	0,8181818	110	0,1818182	ldtaxa	0	1
2,5	217	32	89	0,8090909	110	0,1909091	ldtaxa	0	1
2,5	200	16	108	0,8059701	134	0,1940299	ldtaxa	0	1
2,5	200	32	106	0,7910448	134	0,2089552	ldtaxa	0	1
2,5	200	-1	102	0,761194	134	0,238806	ldtaxa	0	1
1,1	217	32	83	0,7830189	106	0,2169811	ldtaxa	0	1
1,1	200	16	105	0,7720588	136	0,2279412	ldtaxa	0	1
1,1	217	16	81	0,7641509	106	0,2358491	ldtaxa	0	1
1,1	200	32	103	0,7573529	136	0,2426471	ldtaxa	0	1
1,1	217	-1	80	0,754717	106	0,245283	ldtaxa	0	1
1,1	200	-1	102	0,75	136	0,25	ldtaxa	0	1
2,5	217	-1	97	0,8818182	110	0,1181818	Assigntaxa	1	1
2,5	200	16	118	0,880597	134	0,119403	Assigntaxa	1	1
2,5	200	32	118	0,880597	134	0,119403	Assigntaxa	1	1
2,5	200	-1	117	0,8731343	134	0,1268657	Assigntaxa	1	1
2,5	217	16	96	0,8727273	110	0,1272727	Assigntaxa	1	1
2,5	217	32	96	0,8727273	110	0,1272727	Assigntaxa	1	1
1,1	217	16	89	0,8396226	106	0,1603774	Assigntaxa	1	1
1,1	217	32	89	0,8396226	106	0,1603774	Assigntaxa	1	1
1,1	217	-1	88	0,8301887	106	0,1698113	Assigntaxa	1	1
1,1	200	16	112	0,8235294	136	0,1764706	Assigntaxa	1	1
1,1	200	-1	111	0,8161765	136	0,1838235	Assigntaxa	1	1
1,1	200	32	110	0,8088235	136	0,1911765	Assigntaxa	1	1