

Supplementary Materials: Current Status of Marker Genes of *Bacteroides* and Related Taxa for Identifying Sewage Pollution in Environmental Waters

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Table S1. Detection of *Bacteroides* 16S rRNA HF183 marker in human fecal and wastewater samples reported in the research literature.

Number of Samples Tested (Sample Type)	Positive	Negative	References
58 (raw sewage)	58	0	[1]
4 (raw sewage)	4	0	[2]
50 (raw sewage)	50	0	[3]
15 (raw sewage)	15	0	[4]
25 (human feces)	12	13	[5]
13 (human feces)	11	2	[6]
5 (raw sewage)	4	1	[7]
14 (raw sewage)	14	0	[8]
54 (raw sewage)	54	0	[9]
33 (raw sewage)	23	10	[10]
37 (raw sewage)	37	0	[11]
32 (raw sewage)	32	0	[12]
8 (raw sewage)	8	0	[13]
10 (raw sewage)	10	0	[14]
22 (raw sewage)	50	0	[15]
33 (raw sewage)	33	0	[16]
5 (raw sewage)	5	0	[17]
40 (raw sewage)	20	20	[18]
24 (raw sewage)	24	0	[19]
16 (raw sewage)	12	4	[20]
6 (septic wastewater)	6	0	[21]
7 (human feces)	6	1	[2]
44 (human feces)	43	1	[22]
104 (human feces)	89	15	[23]
20 (raw sewage)	20	0	[5]
3 (raw sewage)	3	0	[6]
12 (human feces)	7	5	[7]
15 (human feces)	13	2	[24]
16 (human feces)	6	10	[9]
26 (human feces)	3	23	[10]
20 (human feces)	16	4	[11]
54 (human feces)	51	3	[13]
8 (human feces)	5	3	[14]
1 (human feces)	1	0	[25]
30 (human feces)	5	25	[17]
24 (human feces)	13	11	[26]
24 (human feces)	15	9	[27]
5 (human feces)	5	0	[21]
12 (septic wastewater)	12	0	[4]

Table S1. Cont.

Number of Samples Tested (Sample Type)	Positive	Negative	References
3 (septic wastewater)	2	1	[14]
3 (septic wastewater)	3	0	[15]
15 (pit toilet wastewater)	7	8	[19]
20 (septic wastewater)	1	19	[19]
6 (raw sewage)	6	0	[21]
10 (septic wastewater)	4	6	[28]
15 (secondary eluent)	15	0	[4]
10 (treated effluent)	10	0	[4]
22 (secondary effluent)	22	0	[11]
17 (secondary effluent)	17	0	[27]
5 (Treated effluent)	5	0	[21]
46 (secondary effluent)	40	6	[29]
1 (raw wastewater)	1	0	[30]
4 (Septic wastewater)	4	0	[30]
39 (raw wastewater)	39	0	[31]
37 (secondary effluent)	37	0	[31]
18 (human feces)	11	7	[32]
16 (raw sewage)	14	0	[32]
Total	1033	209	All studies

Table S2. Detection of *Bacteroides* 16S rRNA HF134 marker in human fecal and wastewater samples reported in the research literature.

Number of Samples Tested (Sample Type)	Positive	Negative	References
40 (raw sewage)	12	28	[18]
54 (raw sewage)	54	0	[9]
16 (human feces)	15	1	[9]
3 (raw sewage)	1	2	[6]
15 (raw sewage)	15	0	[4]
13 (human feces)	6	5	[6]
44 (human feces)	37	7	[22]
1 (human feces)	1	0	[25]
12 (septic wastewater)	12	0	[4]
10 (septic wastewater)	4	6	[28]
15 (secondary effluent)	15	0	[4]
10 (treated effluent)	9	1	[4]
Total	181	50	All studies

Table S3. Detection of *Bacteroides* 16S rRNA HuBac marker in human fecal and wastewater samples reported in the research literature.

Number of Samples Tested (Sample Type)	Positive	Negative	References
9 (raw sewage)	0	0	[33]
50 (raw sewage)	50	0	[3]
6 (human feces)	6	0	[34]
1 (human feces)	1	0	[25]
18 (human feces)	16	2	[32]
14 (raw sewage)	14	0	[32]
Total	87	2	All studies

Table S4. Detection of *Bacteroides* 16S rRNA BacHum-UCD marker in human fecal and wastewater samples reported in the research literature.

Number of Samples Tested (Sample Type)	Positive	Negative	References
14 (raw sewage)	14	0	[32]
45 (raw sewage)	45	0	[31]
5 (raw sewage)	0	5	[7]
5 (raw sewage)	5	0	[17]
50 (raw sewage)	50	0	[3]
10 (raw sewage)	10	0	[14]
18 (human feces)	12	6	[32]
8 (human feces)	8	0	[14]
61 (human feces)	53	8	[35]
1 (human feces)	1	0	[25]
12 (human feces)	3	9	[7]
30 (human feces)	12	18	[17]
45 (secondary effluent)	45	0	[31]
3 (septic wastewater)	3	0	[14]
12 (raw sewage)	12	0	[36]
Total	273	46	All studies

Table S5. Detection of *Bacteroides* 16S rRNA BacH marker in human fecal and wastewater samples reported in the research literature.

Number of Samples Tested (Sample Type)	Positive	Negative	References
20 (raw sewage)	20	0	[37]
5 (raw sewage)	2	3	[17]
6 (raw sewage)	6	0	[38]
50 (raw sewage)	50	0	[3]
21 (human feces)	20	1	[37]
61 (human feces)	47	14	[35]
30 (human feces)	4	26	[17]
25 (human feces)	22	3	[38]
1 (human feces)	1	0	[25]
11 (septic wastewater)	7	4	[39]
Total	179	51	All studies

Table S6. Detection of *Bacteroides* 16S rRNA HumanBac1 marker in human fecal and wastewater samples reported in the research literature.

Number of Samples Tested (Sample Type)	Positive	Negative	References
50 (raw sewage)	50	0	[3]
4 (human feces)	2	2	[40]
5 (raw sewage)	5	0	[41]
5 (Secondary effluent)	5	0	[41]
5 (Tertiary effluent)	5	0	[41]
Total	67	2	All studies

Table S7. Detection of *Bacteroides* non-16S rRNA HumM2 marker in human fecal and wastewater samples reported in the research literature.

Number of Samples Tested (Sample Type)	Positive	Negative	References
16 (human feces)	16	0	[42]
20 (raw sewage)	20	0	[42]
5 (raw sewage)	5	0	[17]
30 (human feces)	12	18	[17]
Total	53	18	All studies

Table S8. Detection of *Bacteroides* non-16S rRNA HumM3 marker in human fecal and wastewater samples reported in the research literature.

Number of Samples Tested (Sample Type)	Positive	Negative	References
16 (human feces)	16	0	[42]
20 (raw sewage)	20	0	[42]
Total	36	0	All studies

Table S9. Detection of *Bacteroides* non-16S rRNA *Bacteroides thetaiotaomicron* marker in human fecal and wastewater samples reported in the research literature.

Number of Samples Tested (Sample Type)	Positive	Negative	References
18 (secondary effluent)	18	0	[43]
54 (Primary effluent)	54	0	[43]
54 (raw sewage)	54	0	[43]
18 (secondary effluent, pre-chlorination)	18	0	[43]
54 (secondary effluent, post-chlorination)	54	0	[43]
24 (septic wastewater)	24	0	[43]
24 (treated septic wastewater)	24	0	[43]
20 (raw sewage)	20	0	[44]
5 (raw sewage)	5	0	[41]
5 (Secondary effluent)	5	0	[41]
5 (Tertiary effluent)	5	0	[41]
54 (raw sewage)	52	2	[9]
16 (human feces)	0	16	[9]
Total	333	18	All studies

Table S10. Detection of *Bacteroides* non-16S rRNA *gyrB* marker in human fecal and wastewater samples reported in the research literature.

Number of Samples Tested (Sample Type)	Positive	Negative	References
10 (fecal samples)	10	0	[45]
Total	10	0	All studies

Table S11. Detection of *Bacteroides* 16S rRNA HF183 marker in non-human fecal samples reported in the research literature.

Number of Non-Human Samples	Negative	Positive	References
19	18	1	[2]
136	135	1	[3]
86	81	11	[22]
180	174	6	[23]
73	62	11	[5]
27	27	0	[6]

Table S11. Cont.

Number of Non-Human Samples	Negative	Positive	References
25	25	0	[7]
30	28	2	[24]
119	119	0	[10]
214	201	13	[11]
50	49	1	[12]
211	211	0	[13]
36	35	1	[14]
316	303	13	[15]
4	1	3	[25]
230	163	67	[41]
155	155	0	[4]
85	85	0	[26]
73	52	21	[18]
77	77	0	[19]
340	340	0	[20]
98	97	1	[27]
29	26	3	[21]
173	172	1	[28]
133	133	0	[29]
41	38	3	[32]
Total	2807	159	All studies

Table S12. Detection of *Bacteroides* 16S rRNA HF134 marker in non-human fecal samples reported in the research literature.

Number of Non-Human Samples	Negative	Positive	References
72	58	14	[18]
155	148	7	[4]
173	161	12	[28]
86	85	1	[22]
4	4	0	[25]
Total	456	34	All studies

Table S13. Detection of *Bacteroides* 16S rRNA HuBac marker in non-human fecal samples reported in the research literature.

Number of Non-Human Samples	Negative	Positive	References
4	4	0	[25]
28	20	8	[34]
136	86	50	[3]
41	25	16	[32]
Total	135	74	All studies

Table S14. Detection of *Bacteroides* 16S rRNA BacHum-UCD marker in non-human fecal samples reported in the research literature.

Number of Non-Human Samples	Negative	Positive	References
41	40	1	[32]
25	25	0	[7]
4	3	1	[25]
219	148	71	[35]
136	130	6	[3]
36	14	22	[14]
Total	360	101	All studies

Table S15. Detection of *Bacteroides* 16S rRNA BacH marker in non-human fecal samples reported in the research literature.

Number of Non-Human Samples	Negative	Positive	References
302	301	1	[37]
4	1	3	[25]
361	361	0	[38]
219	116	103	[35]
136	128	8	[3]
Total	907	115	All studies

Table S16. Detection of *Bacteroides* 16S rRNA HumanBac1 marker in non-human fecal samples reported in the research literature.

Number of Non-Human Samples	Negative	Positive	References
12	2	10	[40]
70	0	70	[41]
136	107	29	[3]
Total	109	109	All studies

Table S17. Detection of *Bacteroides* non-16S rRNA HumM2 marker in non-human fecal samples reported in the research literature.

Number of Non-Human Samples	Negative	Positive	References
249	247	2	[42]
Total	247	2	All studies

Table S18. Detection of *Bacteroides* non-16S rRNA HumM3 marker in non-human fecal samples reported in the research literature.

Number of Non-Human Samples	Negative	Positive	References
249	242	7	[42]
Total	242	7	All studies

Table S19. Detection of *Bacteroides* non-16S rRNA *Bacteroides thetaiotaomicron* marker in non-human fecal samples reported in the research literature.

Number of Non-Human Samples	Negative	Positive	References
230	223	7	[41]
16	16	0	[44]
Total	239	7	All studies

Table S20. Detection of *Bacteroides* 16S rRNA *gyrB* marker in non-human fecal samples reported in the research literature.

Number of Non-Human Samples	Negative	Positive	References
30	29	1	[45]
Total	29	1	All studies

References

- Green, H.C.; Haugland, R.A.; Verma, M.; Millen, H.T.; Borchardt, M.A.; Field, K.G.; Walters, W.A.; Knight, R.; Kelty, C.A.; Shanks, O.C. Improved HF183 quantitative real-time PCR assay for characterization of human fecal pollution in ambient surface water samples. *Appl. Environ. Microbiol.* **2014**, *80*, 3086–3094.
- Seurinck, S.; Defoirdt, T.; Verstraete, W.; Siciliano, S.D. Detection and quantification of human-specific HF183 *Bacteroides* 16S rRNA genetic marker with real-time PCR for assessment of human faecal pollution. *Environ. Microbiol.* **2005**, *7*, 249–259.
- Ahmed, W.; Goonetilleke, A.; Powell, D.; Gardner, T. Evaluation of multiple sewage-associated *Bacteroides* PCR markers for sewage pollution tracking. *Water Res.* **2009**, *43*, 4872–4877.
- Ahmed, W.; Stewart, J.; Powell, D.; Gardner, T. Evaluation of *Bacteroides* markers for the detection of human faecal pollution. *Lett. Appl. Microbiol.* **2008**, *46*, 237–242.
- Carson, C.A.; Christiansen, J.M.; Yampara-Iquise, H.; Benson, V.W.; Baffaut, C.; Davis, J.V.; Broz, R.R.; Kurtz, W.B.; Rogers, W.M.; Fales, W.H. Specificity of a *Bacteroides thetaiotaomicron* marker for human feces. *Appl. Environ. Microbiol.* **2005**, *71*, 4945–4949.
- Bernhard, A.E.; Field, K.G. A PCR assay to discriminate human and ruminant feces on the basis of host differences in *Bacteroides-Prevotella* genes encoding 16S rRNA. *Appl. Environ. Microbiol.* **2000**, *66*, 4571–4574.
- Jenkins, M.W.; Tiwari, S.; Lorente, M.; Gichaba, C.M.; Wuertz, S. Identifying human and livestock sources of fecal contamination in Kenya with host-specific *Bacteroidales* assays. *Water Res.* **2009**, *43*, 4956–4966.
- Haugland, R.A.; Varma, M.; Kelty, C.A.; Peed, L.; Sivaganesan, M.; Shanks, O.C. Evaluation of genetic markers from the 16S rRNA gene V2 region for use in quantitative detection of selected *Bacteroidales* species and human fecal waste by real-time PCR. *Syst. Appl. Microbiol.* **2010**, *33*, 348–357.
- Shanks, O.C.; White, K.; Kelty, C.A.; Sivaganesan, M.; Blannon, J.; Meckes, M.; Varma, M.; Haugland, R.A. Performance of PCR-based assays targeting *Bacteroides* genetic markers of human fecal pollution in sewage and fecal samples. *Environ. Sci. Technol.* **2010**, *44*, 6281–6288.
- Dorai-raj, S.; O’Grady, J.; Collieran, E. Specificity and sensitivity evaluation of novel and existing *Bacteroidales* and *Bifidobacteria*-specific PCR assays on feces and sewage samples and their application for microbial source tracking in Ireland. *Water Res.* **2009**, *43*, 4980–4988.
- Ahmed, W.; Masters, N.; Toze, S. Consistency in the host specificity and host sensitivity of the *Bacteroides* HF183 marker for sewage pollution tracking. *Lett. Appl. Microbiol.* **2012**, *55*, 283–289.
- Ahmed, W.; Goonetilleke, A.; Powell, D.; Chauhan, K.; Gardner, T. Comparison of molecular markers to detect fresh sewage in environmental waters. *Water Res.* **2009**, *43*, 4908–4917.
- Fremaux, B.; Gritzfeld, J.; Boa, T.; Yost, C.K. Evaluation of host-specific *Bacteroidales* 16S rRNA gene markers as a complementary tool for detecting fecal pollution in a prairie watershed. *Water Res.* **2009**, *43*, 4838–4849.
- Van De Werfhorst, L.C.; Sercu, B.; Holden, P. Comparison of the host specificities of two *Bacteroidales* quantitative PCR assays used for tracking human fecal contamination. *Appl. Environ. Microbiol.* **2011**, *77*, 6258–6260.
- Harwood, V.J.; Brownell, M.; Wang, S.; Lepo, J.; Ellender, R.D.; Ajidahun, A.; Hellein, K.N.; Kennedy, E.; Ye, X.; Flood, C. Validation and field testing of library-independent microbial source tracking methods in the Gulf of Mexico. *Water Res.* **2009**, *43*, 4812–4819.
- Ahmed, W.; Sidhu, J.P.S.; Smith, K.; Beale, D.; Gyawali, P.; Toze, S. Distributions of fecal markers in wastewater from varying climatic zones for human fecal pollution tracking in Australian surface waters. *Appl. Environ. Microbiol.* **2016**, *82*, 1316–1323.
- Odagiri, M.; Schriewer, A.; Hanley, K.; Wuertz, S.; Misra, P.R.; Panigrahi, P.; Jenkins, M.W. Validation of *Bacteroidales* quantitative PCR assays targeting human and animal fecal contamination in the public and domestic domains in India. *Sci. Total Environ.* **2015**, *502*, 462–470.

18. Ballesté, E.; Bonjoch, X.; Belanche, L.A.; Blanch, A.R. Molecular indicators used in the development of predictive models for microbial source tracking. *Appl. Environ. Microbiol.* **2010**, *76*, 1789–1795.
19. Johnston, C.; Byappanahalli, M.N.; Gibson, M.D.; Ufnar, J.A.; Whitman, R.L.; Stewart, J.R. Probabilistic analysis showing that a combination of *Bacteroides* and *Methanobrevibacter* source tracking markers is effective for identifying waters contaminated by human fecal pollution. *Environ. Sci. Technol.* **2013**, *47*, 13621–13628.
20. Toledo-Hernandez, C.; Ryu, H.; Gonzalez-Nieves, J.; Huertas, E.; Toranzos, G.A.; Santo Domingo, J.W. Tracking the primary sources of fecal pollution in a tropical watershed in a one year-study. *Appl. Environ. Microbiol.* **2013**, *79*, 1689–1696.
21. Stea, E.C.; Hansen, L.T.; Jamieson, R.C.; Yost, C.K. Fecal contamination in the surface waters of a rural and an urban source-watershed. *J. Environ. Qual.* **2015**, *44*, 1556–1567.
22. Gourmelon, M.; Caparis, M.P.; Segura, R.; Menec, C.L.; Lozach, S.; Piriou, J.Y.; Rince, R.A. Evaluation of two library-independent microbial source tracking methods to identify sources of fecal contamination in French estuaries. *Appl. Environ. Microbiol.* **2007**, *73*, 4857–4866.
23. Gawler, A.H.; Beecher, J.E.; Brandão, J.; Carroll, N.M.; Falcão, L.; Gourmelon, M.; Masterson, B.; Nunes, B.; Porter, J.; Rince, A.; *et al.* Validation of host-specific *Bacteroidales* 16S rRNA genes as markers to determine the origin of fecal pollution in Atlantic Rim countries of the European Union. *Water Res.* **2007**, *41*, 3780–3784.
24. Ahmed, W.; Yusuf, R.; Hasan, I.; Goonetilleke, A.; Gardner, T. Quantitative PCR assay of sewage-associated *Bacteroides* markers to assess sewage pollution in an urban lake in Dhaka, Bangladesh. *Can. J. Microbiol.* **2010**, *56*, 838–845.
25. McLain, J.E.T.; Ryu, H.; Kabir-Badr, L.; Rock, C.M.; Abbaszadegan, M. Lack of specificity for PCR assays targeting human *Bacteroides* 16S rRNA gene: Cross-amplification with fish feces. *FEMS Microbiol. Lett.* **2009**, *299*, 38–43.
26. Mieszkina, S.; Furet, J.-P.; Corthier, G.; Gourmelon, M. Estimation of pig fecal contamination in a river catchment by real-time PCR using two pig-specific *Bacteroidales* 16S rRNA genetic markers. *Appl. Environ. Microbiol.* **2009**, *75*, 3045–3054.
27. Mauffret, A.; Caparis, M.P.; Gourmelon, M. Relevance of *Bacteroidales* and F-specific RNA bacteriophages for efficient fecal contamination tracking at the level of a catchment in France. *Appl. Environ. Microbiol.* **2012**, *78*, 5143–5152.
28. Lamendella, R.; Santo Domingo, J.W.; Oerther, D.B.; Vogel, J.R.; Stoeckel, D.M. Assessment of fecal pollution sources in a small northern-plains watershed using PCR and phylogenetic analyses of *Bacteroidetes* 16S rRNA gene. *FEMS Microbiol. Ecol.* **2006**, *59*, 651–660.
29. Edge, T.A.; Hill, S.; Seto, P.; Marsalek, J. Library-dependent and library-independent microbial source tracking to identify spatial variation in faecal contamination source along a Lake Ontario Beach (Ontario, Canada). *Water Sci. Technol.* **2010**, *62*, 719–727.
30. Nshimiyimana, J.P.; Ekklesia, E.; Shanahan, P.; Chua, L.H.C.; Thomson, J.R. Distribution and abundance of human-specific *Bacteroides* and relation to traditional indicators in an urban tropical catchment. *J. Appl. Microbiol.* **2014**, *116*, 1369–1383.
31. Mayer, R.E.; Bofill-Mas, S.; Egle, L.; Reischer, G.H.; Schade, M.; Fernandez-Cassi, X.; Fuchs, W.; Mach, R.L.; Linder, G.; Kirschner, A.; *et al.* Occurrence of human-associated *Bacteroidetes* genetic source tracking markers in raw and treated wastewater of municipal and domestic origin and comparison to standard and alternative indicators of faecal pollution. *Water Res.* **2016**, *90*, 265–276.
32. Kildare, B.J.; Leutenegger, C.; McSwain, B.S.; Bambi, D.G.; Rajal, V.B.; Wuertz, S. 16S rRNA-based assays for quantitative detection of universal, human-, cow-, and dog-specific fecal *Bacteroidales*: A Bayesian approach. *Water Res.* **2007**, *41*, 3701–3715.
33. Coakley, T.; Brion, G.M.; Fryar, A.E. Prevalence of and relationship between two human-associated DNA biomarkers for *Bacteroides* in an urban watershed. *J. Environ. Qual.* **2015**, *44*, 1694–1698.
34. Layton, A.; McKay, L.; Williams, D.; Garrett, V.; Gentry, R.; Sayler, G. Development of *Bacteroides* 16S rRNA gene TaqMan-based real-time PCR assays for estimation of total, human, and bovine fecal pollution in water. *Appl. Environ. Microbiol.* **2006**, *72*, 4214–4224.
35. Reischer, G.H.; Edbon, J.E.; Bauer, J.M.; Schuster, N.; Ahmed, W.; Åström, J.; Blanch, A.R.; Blöschl, G.; Byamukama, D.; Coakley, T.; *et al.* Performance characteristics of qPCR assays targeting human- and ruminant-associated *Bacteroidetes* for microbial source tracking across sixteen countries on six continents. *Environ. Sci. Technol.* **2013**, *47*, 8548–8556.

36. Silkie, S.S.; Nelson, K.L. Concentrations of host-specific and genetic fecal markers measured by quantitative PCR in raw sewage and fresh animal feces. *Water Res.* **2009**, *43*, 4860–4871.
37. Reischer, G.H.; Kasper, D.C.; Steinborn, R.; Farnleitner, A.H.; Mach, R.L. A quantitative real-time PCR assay for the highly sensitive and specific detection of human faecal influence in spring water from a large alpine catchment area. *Lett. Appl. Microbiol.* **2007**, *44*, 351–356.
38. Tambalo, D.D.; Fremaux, B.; Boa, T.; Yost, C.K. Persistence of host-associated *Bacteroidales* gene markers and their quantitative detection in an urban and agricultural mixed prairie watershed. *Water Res.* **2012**, *46*, 2891–2904.
39. Ridley, C.M.; Jamieson, R.C.; Hansen, L.T.; Yost, C.K.; Bezanson, G.S. Baseline and storm event monitoring of Bacteroidales marker concentrations and enteric pathogen presence in a rural Canadian watershed. *Water Res.* **2014**, *60*, 278–288.
40. Okabe, S.; Okayama, N.; Savichtcheva, O.; Ito, T. Quantification of host-specific *Bacteroides-Prevotella* 16S rRNA genetic markers for assessment of fecal pollution in freshwater. *Appl. Microbiol. Biotechnol.* **2007**, *74*, 890–901.
41. Aslan, A.; Rose, J.B. Evaluation of the host-specificity of *Bacteroides thetaiotaomicron* alpha-1-6, mannanase gene as a sewage marker. *Lett. Appl. Microbiol.* **2012**, *56*, 51–56.
42. Shanks, O.C.; Kelty, C.A.; Sivaganesan, M.; Varma, M.; Haugland, R.A. Quantitative PCR for genetic markers of human fecal pollution. *Appl. Environ. Microbiol.* **2009**, *75*, 5507–5513.
43. Srinivasan, S.; Aslan, A.; Xagorarakis, I.; Alocilja, E. *Escherichia coli*, enterococci and *Bacteroides thetaiotaomicron* qPCR signals through wastewater and septage treatment. *Water Res.* **2011**, *45*, 2561–2572.
44. Lee, C.S.; Lee, J. Evaluation of new *gyrB*-based real-time PCR system for the detection of *B. fragilis* as an indicator of human-specific fecal contamination. *J. Microbiol. Methods* **2010**, *82*, 311–318.
45. Yampara-Iquise, H.; Zheng, G.; Jones, J.E.; Carson, C.A. Use of a *Bacteroides thetaiotaomicron*-specific α -1-6, mannanase quantitative PCR to detect human faecal pollution in water. *J. Appl. Microbiol.* **2008**, *105*, 1686–1693.