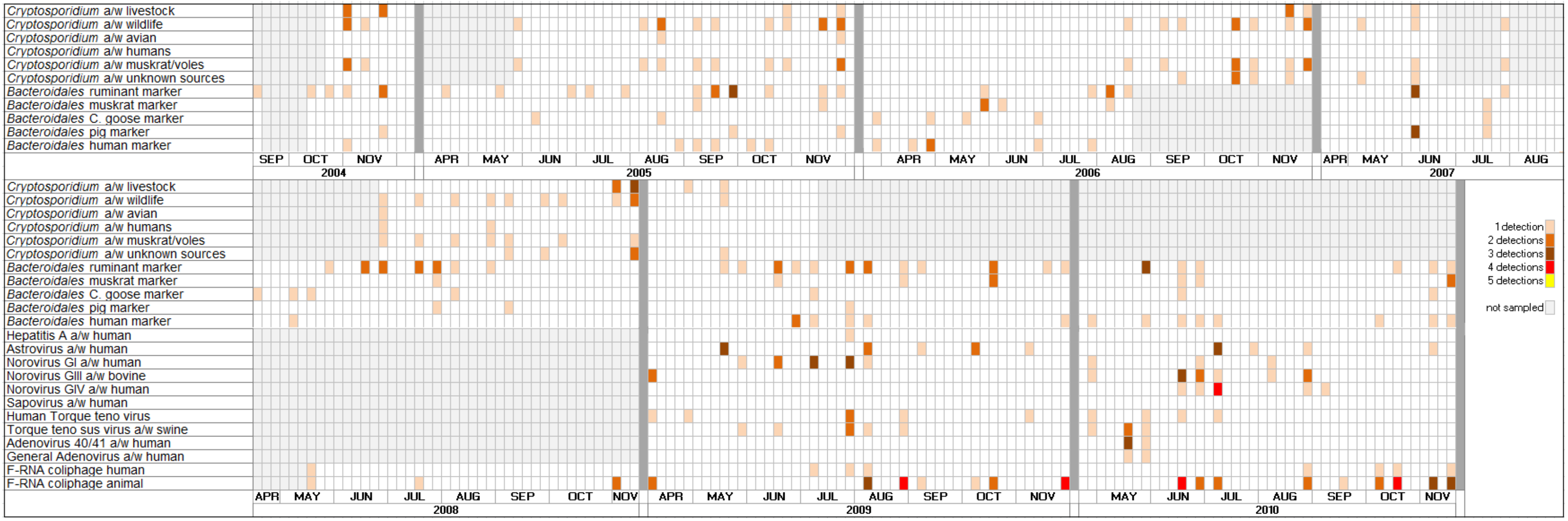
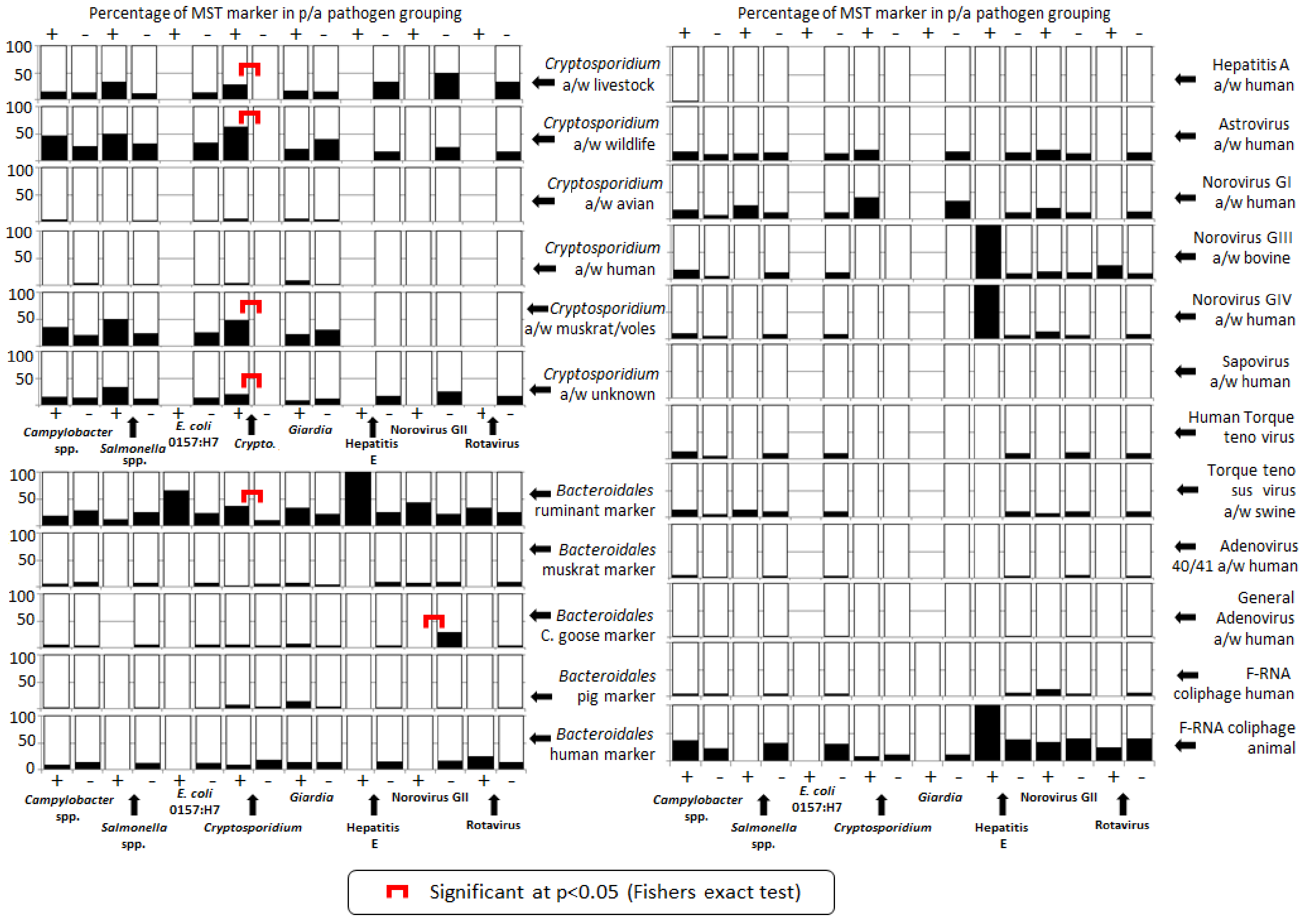
Supplemental Figure 1. Heat map of the number of detections of *Cryptosporidium* species/genotypes assigned to broad host classes, the detection of *Bacteroidales* source markers, DNA and RNA virus detections (with associated hosts), and coliphage host marker detections for all sites in 10 day intervals through time from 2004 to 2010 for AAD. A/w, associated with.





Supplemental Figure 2. Samples of host markers (y-axis) when a pathogen is present or absent (x-axis) using AAD. Significant difference in occurrence as observed by Fisher's exact test (p<0.05). A/w, associated with.

Supplementary Table 1A. Number of TCD collected at RCA_{in}; RCA_{out}\URCA_{in}; and URCA_{out}. And number of TCD collected for parasite analysis collected at RCA_{in}; URCA_{out}. A/w, associated with.

		All data	spring	summer	fall	high	low	no flow
Microbial source tracking end point	Site	N	N	N	N	N	N	N
Cryptosporidium a/w livestock	RCA_{in}	37	6	19	12	15	11	11
Cryptosporidium a/w livestock	URCA_{out}	37	6	19	12	15	11	11
Cryptosporidium a/w wildlife	RCA_{in}	37	6	19	12	15	11	11
Cryptosporidium a/w wildlife	URCA_{out}	37	6	19	12	15	11	11
Cryptosporidium a/w avian	RCA_{in}	37	6	19	12	15	11	11
Cryptosporidium a/w avian	URCA_{out}	37	6	19	12	15	11	11
Cryptosporidium a/w humans	RCA_{in}	37	6	19	12	15	11	11
Cryptosporidium a/w humans	URCA_{out}	37	6	19	12	15	11	11
Cryptosporidium a/w muskrat/voles	RCA_{in}	37	6	19	12	15	11	11
Cryptosporidium a/w muskrat/voles	URCA_{out}	37	6	19	12	15	11	11
Cryptosporidium a/w unknown sources	RCA_{in}	37	6	19	12	15	11	11
Cryptosporidium a/w unknown sources	URCA_{out}	37	6	19	12	15	11	11
Bacteroidales ruminant marker	RCA_{in}	64	26	23	15	26	27	11
Bacteroidales ruminant marker	RCA_{out}\URCA_{in}	64	26	23	15	26	27	11
Bacteroidales ruminant marker	URCA_{out}	64	26	23	15	26	27	11
Bacteroidales muskrat marker	RCA_{in}	67	29	23	15	27	28	12
Bacteroidales muskrat marker	RCA_{out}\URCA_{in}	67	29	23	15	27	28	12
Bacteroidales muskrat marker	URCA_{out}	67	29	23	15	27	28	12
Bacteroidales C. goose marker	RCA_{in}	67	29	23	15	27	28	12
Bacteroidales C. goose marker	RCA_{out}\URCA_{in}	67	29	23	15	27	28	12
Bacteroidales C. goose marker	URCA_{out}	67	29	23	15	27	28	12
Bacteroidales pig marker	RCA_{in}	67	29	23	15	27	28	12
Bacteroidales pig marker	RCA_{out}\URCA_{in}	67	29	23	15	27	28	12
Bacteroidales pig marker	URCA_{out}	67	29	23	15	27	28	12
Bacteroidales human marker	RCA_{in}	67	29	23	15	27	28	12
Bacteroidales human marker	RCA_{out}\URCA_{in}	67	29	23	15	27	28	12
Bacteroidales human marker	URCA_{out}	67	29	23	15	27	28	12
Hepatitis A a/w human	RCA_{in}	27	9	9	9	11	13	3
Hepatitis A a/w human	RCA_{out}\URCA_{in}	27	9	9	9	11	13	3
Hepatitis A a/w human	URCA_{out}	27	9	9	9	11	13	3
Astrovirus a/w human	RCA_{in}	27	9	9	9	11	13	3
Astrovirus a/w human	RCA_{out}\URCA_{in}	27	9	9	9	11	13	3
Astrovirus a/w human	URCA_{out}	27	9	9	9	11	13	3
Norovirus GI a/w human	RCA_{in}	27	9	9	9	11	13	3
Norovirus GI a/w human	RCA_{out}\URCA_{in}	27	9	9	9	11	13	3
Norovirus GI a/w human	URCA_{out}	27	9	9	9	11	13	3
Norovirus GIII a/w bovine	RCA_{in}	27	9	9	9	11	13	3
Norovirus GIII a/w bovine	RCA_{out}\URCA_{in}	27	9	9	9	11	13	3
Norovirus GIII a/w bovine	URCA_{out}	27	9	9	9	11	13	3
Norovirus GIV a/w human	RCA_{in}	27	9	9	9	11	13	3
Norovirus GIV a/w human	RCA_{out}\URCA_{in}	27	9	9	9	11	13	3
Norovirus GIV a/w human	URCA_{out}	27	9	9	9	11	13	3
Sapovirus a/w human	RCA_{in}	27	9	9	9	11	13	3
Sapovirus a/w human	RCA_{out}\URCA_{in}	27	9	9	9	11	13	3
Sapovirus a/w human	URCA_{out}	27	9	9	9	11	13	3
Human Torque teno virus	RCA_{in}	27	9	9	9	11	13	3
Human Torque teno virus	RCA_{out}\URCA_{in}	27	9	9	9	11	13	3
Human Torque teno virus	URCA_{out}	27	9	9	9	11	13	3
Torque teno sus virus a/w swine	RCA_{in}	27	9	9	9	11	13	3
Torque teno sus virus a/w swine	RCA_{out}\URCA_{in}	27	9	9	9	11	13	3
Torque teno sus virus a/w swine	URCA_{out}	27	9	9	9	11	13	3
Adenovirus 40/41 a/w human	RCA_{in}	27	9	9	9	11	13	3

		All data	spring	summer	fall	high	low	no flow
Microbial source tracking end point	Site	N	N	N	N	N	N	N
Adenovirus 40/41 a/w human	$RCA_{out}\backslash URCA_{in}$	27	9	9	9	11	13	3
Adenovirus 40/41 a/w human	$URCA_{out}$	27	9	9	9	11	13	3
General Adenovirus a/w human	RCA_{in}	27	9	9	9	11	13	3
General Adenovirus a/w human	$RCA_{out}\backslash URCA_{in}$	27	9	9	9	11	13	3
General Adenovirus a/w human	$URCA_{out}$	27	9	9	9	11	13	3
F-RNA coliphage human	RCA_{in}	38	13	15	10	16	19	3
F-RNA coliphage human	$RCA_{out}\backslash URCA_{in}$	38	13	15	10	16	19	3
F-RNA coliphage human	$URCA_{out}$	38	13	15	10	16	19	3
F-RNA coliphage animal	RCA_{in}	38	13	15	10	16	19	3
F-RNA coliphage animal	$RCA_{out}\backslash URCA_{in}$	38	13	15	10	16	19	3
F-RNA coliphage animal	$URCA_{out}$	38	13	15	10	16	19	3

Supplementary Table 1B. Number of samples collected for AAD. A/w, associated with.

Microbial source tracking end point	Site	All data	spring	summer	fall	high	low	no flow
Cryptosporidium a/w livestock	RCA$_{\text{in}}$	40	7	19	14	15	11	14
Cryptosporidium a/w livestock	RCA$_{\text{out}}$\URCA$_{\text{in}}$	8	0	6	2	4	4	0
Cryptosporidium a/w livestock	URCA$_{\text{mid}}$	0	0	0	0	0	0	0
Cryptosporidium a/w livestock	URCA$_{\text{out}}$	58	17	22	19	25	21	12
Cryptosporidium a/w wildlife	RCA$_{\text{in}}$	40	7	19	14	15	11	14
Cryptosporidium a/w wildlife	RCA$_{\text{out}}$\URCA$_{\text{in}}$	8	0	6	2	4	4	0
Cryptosporidium a/w wildlife	URCA$_{\text{mid}}$	0	0	0	0	0	0	0
Cryptosporidium a/w wildlife	URCA$_{\text{out}}$	58	17	22	19	25	21	12
Cryptosporidium a/w avian	RCA$_{\text{in}}$	40	7	19	14	15	11	14
Cryptosporidium a/w avian	RCA$_{\text{out}}$\URCA$_{\text{in}}$	8	0	6	2	4	4	0
Cryptosporidium a/w avian	URCA$_{\text{mid}}$	0	0	0	0	0	0	0
Cryptosporidium a/w avian	URCA$_{\text{out}}$	58	17	22	19	25	21	12
Cryptosporidium a/w humans	RCA$_{\text{in}}$	40	7	19	14	15	11	14
Cryptosporidium a/w humans	RCA$_{\text{out}}$\URCA$_{\text{in}}$	8	0	6	2	4	4	0
Cryptosporidium a/w humans	URCA$_{\text{mid}}$	0	0	0	0	0	0	0
Cryptosporidium a/w humans	URCA$_{\text{out}}$	58	17	22	19	25	21	12
Cryptosporidium a/w muskrat/voles	RCA$_{\text{in}}$	40	7	19	14	15	11	14
Cryptosporidium a/w muskrat/voles	RCA$_{\text{out}}$\URCA$_{\text{in}}$	8	0	6	2	4	4	0
Cryptosporidium a/w muskrat/voles	URCA$_{\text{mid}}$	0	0	0	0	0	0	0
Cryptosporidium a/w muskrat/voles	URCA$_{\text{out}}$	58	17	22	19	25	21	26
Cryptosporidium a/w unknown sources	RCA$_{\text{in}}$	40	7	19	14	15	11	14
Cryptosporidium a/w unknown sources	RCA$_{\text{out}}$\URCA$_{\text{in}}$	8	0	6	2	4	4	0
Cryptosporidium a/w unknown sources	URCA$_{\text{mid}}$	0	0	0	0	0	0	0
Cryptosporidium a/w unknown sources	URCA$_{\text{out}}$	58	17	22	19	25	21	12
Bacteroidales ruminant marker	RCA$_{\text{in}}$	83	29	34	20	30	29	24
Bacteroidales ruminant marker	RCA$_{\text{out}}$\URCA$_{\text{in}}$	68	28	25	15	28	29	11
Bacteroidales ruminant marker	URCA$_{\text{mid}}$	48	23	15	10	21	24	3
Bacteroidales ruminant marker	URCA$_{\text{out}}$	83	29	30	24	33	35	15
Bacteroidales muskrat marker	RCA$_{\text{in}}$	86	32	34	20	31	30	25
Bacteroidales muskrat marker	RCA$_{\text{out}}$\URCA$_{\text{in}}$	71	31	25	15	29	30	12
Bacteroidales muskrat marker	URCA$_{\text{mid}}$	48	23	15	10	21	24	3
Bacteroidales muskrat marker	URCA$_{\text{out}}$	83	29	30	24	33	35	15
Bacteroidales C. goose marker	RCA$_{\text{in}}$	86	32	34	20	31	30	25
Bacteroidales C. goose marker	RCA$_{\text{out}}$\URCA$_{\text{in}}$	71	31	25	15	29	30	12
Bacteroidales C. goose marker	URCA$_{\text{mid}}$	48	23	15	10	21	24	3
Bacteroidales C. goose marker	URCA$_{\text{out}}$	83	29	30	24	33	35	15
Bacteroidales pig marker	RCA$_{\text{in}}$	86	32	34	20	31	30	25
Bacteroidales pig marker	RCA$_{\text{out}}$\URCA$_{\text{in}}$	71	31	25	15	29	30	12
Bacteroidales pig marker	URCA$_{\text{mid}}$	48	23	15	10	21	24	3
Bacteroidales pig marker	URCA$_{\text{out}}$	83	29	30	24	33	35	15
Bacteroidales human marker	RCA$_{\text{in}}$	86	32	34	20	31	30	25
Bacteroidales human marker	RCA$_{\text{out}}$\URCA$_{\text{in}}$	71	31	25	15	29	30	12
Bacteroidales human marker	URCA$_{\text{mid}}$	48	23	15	10	21	24	3
Bacteroidales human marker	URCA$_{\text{out}}$	83	29	30	24	33	35	15
Hepatitis A a/w human	RCA$_{\text{in}}$	31	9	13	9	11	15	5
Hepatitis A a/w human	RCA$_{\text{out}}$\URCA$_{\text{in}}$	27	9	9	9	11	13	3
Hepatitis A a/w human	URCA$_{\text{mid}}$	23	6	8	9	9	11	3
Hepatitis A a/w human	URCA$_{\text{out}}$	27	9	9	9	11	13	3
Astrovirus a/w human	RCA$_{\text{in}}$	31	9	13	9	11	15	5
Astrovirus a/w human	RCA$_{\text{out}}$\URCA$_{\text{in}}$	27	9	9	9	11	13	3
Astrovirus a/w human	URCA$_{\text{mid}}$	23	6	8	9	9	11	3
Astrovirus a/w human	URCA$_{\text{out}}$	27	9	9	9	11	13	3
Norovirus GI a/w human	RCA$_{\text{in}}$	31	9	13	9	11	15	5
Norovirus GI a/w human	RCA$_{\text{out}}$\URCA$_{\text{in}}$	27	9	9	9	11	13	3
Norovirus GI a/w human	URCA$_{\text{mid}}$	23	6	8	9	9	11	3

Microbial source tracking end point	Site	All data	spring	summer	fall	high	low	no flow
Norovirus GI a/w human	URCA$_{out}$	27	9	9	9	11	13	3
Norovirus GIII a/w bovine	RCA$_{in}$	31	9	13	9	11	15	5
Norovirus GIII a/w bovine	RCA$_{out}$\URCA$_{in}$	27	9	9	9	11	13	3
Norovirus GIII a/w bovine	URCA$_{mid}$	23	6	8	9	9	11	3
Norovirus GIII a/w bovine	URCA$_{out}$	27	9	9	9	11	13	3
Norovirus GIV a/w human	RCA$_{in}$	31	9	13	9	11	15	5
Norovirus GIV a/w human	RCA$_{out}$\URCA$_{in}$	27	9	9	9	11	13	3
Norovirus GIV a/w human	URCA$_{mid}$	23	6	8	9	9	11	3
Norovirus GIV a/w human	URCA$_{out}$	27	9	9	9	11	13	3
Sapovirus a/w human	RCA$_{in}$	31	9	13	9	11	13	5
Sapovirus a/w human	RCA$_{out}$\URCA$_{in}$	27	9	9	9	11	11	3
Sapovirus a/w human	URCA$_{mid}$	23	6	8	9	9	13	3
Sapovirus a/w human	URCA$_{out}$	27	9	9	9	11	13	3
Human Torque teno virus	RCA$_{in}$	31	9	13	9	11	15	5
Human Torque teno virus	RCA$_{out}$\URCA$_{in}$	27	9	9	9	11	13	3
Human Torque teno virus	URCA$_{mid}$	23	6	8	9	9	9	3
Human Torque teno virus	URCA$_{out}$	27	9	9	9	11	13	3
Torque teno sus virus a/w swine	RCA$_{in}$	31	9	13	9	11	15	5
Torque teno sus virus a/w swine	RCA$_{out}$\URCA$_{in}$	27	9	9	9	11	13	3
Torque teno sus virus a/w swine	URCA$_{mid}$	23	6	8	9	9	9	3
Torque teno sus virus a/w swine	URCA$_{out}$	27	9	9	9	11	13	3
Adenovirus 40/41 a/w human	RCA$_{in}$	31	9	13	9	11	15	5
Adenovirus 40/41 a/w human	RCA$_{out}$\URCA$_{in}$	27	9	9	9	11	13	3
Adenovirus 40/41 a/w human	URCA$_{mid}$	23	6	8	9	9	9	3
Adenovirus 40/41 a/w human	URCA$_{out}$	27	9	9	9	11	13	3
General Adenovirus a/w human	RCA$_{in}$	31	9	13	9	11	15	5
General Adenovirus a/w human	RCA$_{out}$\URCA$_{in}$	27	9	9	9	11	13	3
General Adenovirus a/w human	URCA$_{mid}$	23	6	8	9	9	9	3
General Adenovirus a/w human	URCA$_{out}$	27	9	9	9	11	13	3
F-RNA coliphage human	RCA$_{in}$	44	13	18	13	16	20	8
F-RNA coliphage human	RCA$_{out}$\URCA$_{in}$	39	13	15	11	17	19	3
F-RNA coliphage human	URCA$_{mid}$	31	8	13	10	14	16	1
F-RNA coliphage human	URCA$_{out}$	39	13	15	11	17	19	3
F-RNA coliphage animal	RCA$_{in}$	44	13	18	13	16	20	8
F-RNA coliphage animal	RCA$_{out}$\URCA$_{in}$	39	13	15	11	17	19	3
F-RNA coliphage animal	URCA$_{mid}$	31	8	13	10	14	16	1
F-RNA coliphage animal	URCA$_{out}$	39	13	15	11	17	19	3

Supplementary Table 1C. *Salmonella* serovars isolated and observed at water sampling sites for study.

Site	Year	*Salmonella* serovar	Observations
RCA_{in}	2006	Kentucky	3
		Mbandaka	2
RCA_{out}\$URCA_{in}$	2005	Bovismorbificans	3
	2006	Kentucky	3
		Mbandaka	1
	2009	I:4,5,12:b:-	9
$URCA_{mid}$	2009	I:4,5,12:b:-	3
	2010	I:4,5,12:b:-	2
$URCA_{out}$	2006	Kentucky	2
	2008	I:4,5,12:b:-	3
	2009	I:4,5,12:b:-	5

Supplementary Table 2A. Median (ME) and mean absolute deviation (MAD) of source *Bacteroidales* (number copies 100 mL^{-1}) for TCD under seasonal and flow conditions with accompanying significant Kruskal–Wallis (KW) and Mann-Whitney U (W) tests amongst sites and site pairs, respectively. Significant differences between sites (identified by site number) are indicated in median column and are bolded (p<0.05). High flow ≥ 0.018 m^3 s^{-1}; low flow ≥ 0.002 m^3 s^{-1} and < 0.018 m^3 s^{-1}; and no flow < 0.002 m^3 s^{-1}.

		All data		spring		summer		fall		high		low		no flow	
Microbial source tracking endpoint	Site (#)	MAD	ME	MAD	ME	MAD	ME	MAD	ME	MAD	ME	MAD	ME	MAD	ME
Bacteroidales ruminant marker	RCA$_{in}$ (18)	1265	0	981	0	1081	0	2087	0	389	$\mathbf{0}_{(15W)}$	1644	0	2038	0
Bacteroidales ruminant marker	RCA$_{out}$\URCA$_{in}$(22)	51627	$\mathbf{0}_{(15W)}$	124147	0	849	0	1157	0	400	0	751	$\mathbf{0}_{(15W)}$	277286	0
Bacteroidales ruminant marker	URCA$_{out}$ (15)	38345	$\mathbf{0}_{(22W)}$	1826	0	97223	0	7834	0	1364	$\mathbf{0}_{(18W)}$	81312	$\mathbf{0}_{(22W)}$	16828	0
Bacteroidales muskrat marker	RCA$_{in}$ (18)	136	$\mathbf{0}^{KW}$	0	$\mathbf{0}^{KW}_{(22W)}$	304	0	117	0	0	$\mathbf{0}^{KW}$	136	0	414	0
Bacteroidales muskrat marker	RCA$_{out}$\URCA$_{in}$(22)	513	$\mathbf{0}^{KW}_{(15W)}$	710	$\mathbf{0}^{KW}_{(18W;15W)}$	356	0	358	0	258	$\mathbf{0}^{KW}$	916	0	0	0
Bacteroidales muskrat marker	URCA$_{out}$ (15)	310	$\mathbf{0}^{KW}_{(22W)}$	0	$\mathbf{0}^{KW}_{(22W)}$	878	0	0	0	0	$\mathbf{0}^{KW}$	727	0	0	0
Bacteroidales C. goose marker	RCA$_{in}$ (18)	211	$\mathbf{0}^{KW}_{(22W)}$	0	$\mathbf{0}^{KW}_{(22W)}$	597	0	0	0	0	$\mathbf{0}^{KW}_{(22W)}$	494	0	0	0
Bacteroidales C. goose marker	RCA$_{out}$\URCA$_{in}$(22)	4943	$\mathbf{0}^{KW}_{(18W;15W)}$	7817	$\mathbf{0}^{KW}_{(18W;15W)}$	3594	0	139	0	3168	$\mathbf{0}^{KW}_{(18W)}$	8436	$\mathbf{0}_{(15W)}$	0	0
Bacteroidales C. goose marker	URCA$_{out}$ (15)	575	$\mathbf{0}^{KW}_{(22W)}$	1302	$\mathbf{0}^{KW}_{(22W)}$	0	0	0	0	1395	$\mathbf{0}^{KW}$	0	$\mathbf{0}_{(22W)}$	0	0
Bacteroidales pig marker	RCA$_{in}$ (18)	1525	0	166	0	2168	$\mathbf{0}^{KW}$	2993	0	3078	$\mathbf{0}_{(15W)}$	443	0	0	0
Bacteroidales pig marker	RCA$_{out}$\URCA$_{in}$(22)	589	0	1333	0	0	$\mathbf{0}^{KW}$	0	0	1428	0	0	0	0	0
Bacteroidales pig marker	URCA$_{out}$ (15)	652	0	0	0	0	$\mathbf{0}^{KW}$	2759	0	0	$\mathbf{0}_{(18W)}$	1527	0	0	0
Bacteroidales human marker	RCA$_{in}$ (18)	3271	$\mathbf{0}^{KW}_{(22W;15W)}$	1899	0	7081	$\mathbf{0}_{(22W)}$	0	0	0	$\mathbf{0}^{KW}_{(22W;15W)}$	1962	0	13006	0
Bacteroidales human marker	RCA$_{out}$\URCA$_{in}$(22)	159125	$\mathbf{0}^{KW}_{(18W)}$	309772	0	75443	$\mathbf{0}_{(18W)}$	22232	0	30486	$\mathbf{0}^{KW}_{(18W)}$	353246	0	2813	0
Bacteroidales human marker	URCA$_{out}$ (15)	18854	$\mathbf{0}^{KW}_{(18W)}$	17127	0	23256	0	15324	0	16506	$\mathbf{0}^{KW}_{(18W)}$	10597	0	38375	0

Supplementary Table 2B. Mean (M) source *Bacteroidales* (copies 100 mL^{-1}), number of samples (N), and standard deviation (SD) for TCD under different season and flow conditions. See Suppl. 2A for flow regime definition.

		All data			Spring			summer			fall			high			low			no flow		
Microbial source tracking endpoint	Site	N	M	SD	N	M	SD	N	M	SD	N	M	SD	N	M	SD	N	M	SD	N	M	SD
Bacteroidales ruminant marker	RCA$_{\mathrm{in}}$	64	764	2378	26	607	1338	23	655	2001	15	1204	3959	26	211	761	27	1057	3036	11	1353	2965
Bacteroidales ruminant marker	RCA$_{\mathrm{out}}$\URCA$_{\mathrm{in}}$	64	26672	209789	26	64813	329176	23	514	1205	15	668	2155	26	226	644	27	406	1657	11	153651	505813
Bacteroidales ruminant marker	URCA$_{\mathrm{out}}$	64	21182	140951	26	1187	3342	23	54548	234284	15	4678	16264	26	981	2483	27	45293	216110	11	9747	30718
Bacteroidales muskrat marker	RCA$_{\mathrm{in}}$	67	71	372	29	0	0	23	166	601	15	63	244	27	0	0	28	73	271	12	226	783
Bacteroidales muskrat marker	RCA$_{\mathrm{out}}$\URCA$_{\mathrm{in}}$	67	292	1126	29	412	1522	23	195	776	15	207	584	27	145	461	28	558	1661	12	0	0
Bacteroidales muskrat marker	URCA$_{\mathrm{out}}$	67	157	1289	29	0	0	23	459	2200	15	0	0	27	0	0	28	377	1994	12	0	0
Bacteroidales C. goose marker	RCA$_{\mathrm{in}}$	67	107	877	29	0	0	23	312	1497	15	0	0	27	0	0	28	256	1357	12	0	0
Bacteroidales C. goose marker	RCA$_{\mathrm{out}}$\URCA$_{\mathrm{in}}$	67	2825	10589	29	4928	14005	23	1968	8656	15	75	289	27	1908	5797	28	4921	15257	12	0	0
Bacteroidales C. goose marker	URCA$_{\mathrm{out}}$	67	292	2389	29	674	3631	23	0	0	15	0	0	27	724	3763	28	0	0	12	0	0
Bacteroidales pig marker	RCA$_{\mathrm{in}}$	67	824	3738	29	86	464	23	1247	3975	15	1603	6209	27	1807	5678	28	230	1217	12	0	0
Bacteroidales pig marker	RCA$_{\mathrm{out}}$\URCA$_{\mathrm{in}}$	67	299	2446	29	690	3718	23	0	0	15	0	0	27	742	3854	28	0	0	12	0	0
Bacteroidales pig marker	URCA$_{\mathrm{out}}$	67	331	2709	29	0	0	23	0	0	15	1478	5724	27	0	0	28	792	4190	12	0	0
Bacteroidales human marker	RCA$_{\mathrm{in}}$	67	1712	10785	29	1020	4614	23	3701	17750	15	0	0	27	0	0	28	1057	4695	12	7094	24574
Bacteroidales human marker	RCA$_{\mathrm{out}}$\URCA$_{\mathrm{in}}$	67	91228	573338	29	165815	864303	23	47617	146426	15	13895	29582	27	19598	40050	28	198673	883917	12	1688	4612
Bacteroidales human marker	URCA$_{\mathrm{out}}$	67	10797	32690	29	9552	30671	23	13518	39997	15	9033	24973	27	9389	30191	28	5818	21172	12	25583	53390

Supplementary Table 3A. Median (ME) and mean absolute deviation (MAD) of source *Bacteroidales* (copies 100 mL^{-1}) for AAD under seasonal and flow conditions with accompanying significant Kruskal–Wallis (KW) and Mann-Whitney U (W) tests amongst sites and site pairs, respectively. Significant differences between sites (identified by site number) are indicated in median column and are bolded (p<0.05). See Suppl.2A for flow regime definition.

		All data		spring		summer		fall		high		low		no flow	
Microbial source tracking end point	Site (Site #)	MAD	ME	MAD	ME	MAD	ME	MAD	ME	MAD	ME	MAD	ME	MAD	ME
Bacteroidales ruminant marker	RCA$_{in}$ (18)	1165	**$0^{KW}_{(15W)}$**	901	0	1138	**$0^{KW}_{(23W)}$**	1626	**$0^{KW}_{(15W)}$**	341	**$0^{KW}_{(15W)}$**	1561	0^{KW}	1562	0
Bacteroidales ruminant marker	RCA$_{out}$\URCA$_{in}$(22)	48636	**$0^{KW}_{(15W)}$**	115608	0	794	**$0^{KW}_{(23W)}$**	1157	**$0^{KW}_{(15W)}$**	417	**$0^{KW}_{(15W)}$**	703	**$0^{KW}_{(23W;15W)}$**	277286	0
Bacteroidales ruminant marker	URCA$_{mid}$ (23)	6829	**0^{KW}**	1327	0	14940	**$4898^{KW}_{(18W;22W)}$**	0	**$0^{KW}_{(15W)}$**	3627	**0^{KW}**	9646	**$0^{KW}_{(22W)}$**	4961	0
Bacteroidales ruminant marker	URCA$_{out}$ (15)	30346	**$0^{KW}_{(18W;22W)}$**	1688	0	75952	**0^{KW}**	7193	**$875^{KW}_{(18W;22W;23W)}$**	1496	**$0^{KW}_{(18W;22W)}$**	63769	**$0^{KW}_{(22W)}$**	16894	0
Bacteroidales muskrat marker	RCA$_{in}$ (18)	210	0	0	**$0^{KW}_{(22W)}$**	456	0	90	0	0	0	128	0	544	0
Bacteroidales muskrat marker	RCA$_{out}$\URCA$_{in}$(22)	488	**$0_{(15W)}$**	671	**$0^{KW}_{(18W;15W)}$**	330	0	358	0	242	0	867	0	0	0
Bacteroidales muskrat marker	URCA$_{mid}$ (23)	531	0	133	**0^{KW}**	0	0	1920	**$0_{(15W)}$**	317	0	772	0	0	0
Bacteroidales muskrat marker	URCA$_{out}$ (15)	251	**$0_{(22W)}$**	0	**$0^{KW}_{(22W)}$**	680	0	0	**$0_{(23W)}$**	0	0	586	0	0	0
Bacteroidales C. goose marker	RCA$_{in}$ (18)	1113	**0^{KW}**	882	**$0^{KW}_{(22W)}$**	1910	0	0	0	0	**$0^{KW}_{(22W)}$**	463	**0^{KW}**	3028	0
Bacteroidales C. goose marker	RCA$_{out}$\URCA$_{in}$(22)	4700	**$0^{KW}_{(23W;15W)}$**	7436	**$0^{KW}_{(18W)}$**	3331	0	139	0	2985	**$0^{KW}_{(18W;23W)}$**	7961	**$0^{KW}_{(15W)}$**	0	0
Bacteroidales C. goose marker	URCA$_{mid}$ (23)	0	**$0^{KW}_{(22W)}$**	0	**0^{KW}**	0	0	0	0	0	**$0^{KW}_{(22W)}$**	0	**0^{KW}**	0	0
Bacteroidales C. goose marker	URCA$_{out}$ (15)	465	**$0^{KW}_{(22W)}$**	1302	**0^{KW}**	0	0	0	0	1149	**0^{KW}**	0	**$0^{KW}_{(22W)}$**	0	0
Bacteroidales pig marker	RCA$_{in}$ (18)	1384	0	151	0	1942	**0^{KW}**	2284	0	2741	0	415	0	672	0
Bacteroidales pig marker	RCA$_{out}$\URCA$_{in}$(22)	556	0	1250	0	0	**0^{KW}**	0	0	1333	0	0	0	0	0
Bacteroidales pig marker	URCA$_{mid}$ (23)	83	0	168	0	0	**0^{KW}**	0	0	184	0	0	0	0	0
Bacteroidales pig marker	URCA$_{out}$ (15)	592	0	0	0	0	**0^{KW}**	1923	0	177	0	1231	0	0	0
Bacteroidales human marker	RCA$_{in}$ (18)	2575	**$0^{KW}_{(22W;15W)}$**	1733	0	4860	**$0^{KW}_{(22W)}$**	0	**$0^{(22W)}$**	0	**$0^{KW}_{(22W;15W)}$**	1841	0	6538	0
Bacteroidales human marker	RCA$_{out}$\URCA$_{in}$(22)	150884	**$0^{KW}_{(18W;23W)}$**	290477	0	70627	**$0^{KW}_{(18W;23W)}$**	22232	**$0^{(18W)}$**	28943	**$0^{KW}_{(18W;23W)}$**	332345	**$0_{(23W)}$**	2813	0
Bacteroidales human marker	URCA$_{mid}$ (23)	0	**$0^{KW}_{(22W;15W)}$**	0	0	0	**$0^{KW}_{(22W)}$**	0	0	0	**$0^{KW}_{(22W)}$**	0	**$0_{(22W)}$**	0	0
Bacteroidales human marker	URCA$_{out}$ (15)	16217	**$0^{KW}_{(18W;23W)}$**	17127	0	18461	**0^{KW}**	12406	0	13815	**$0^{KW}_{(18W)}$**	10304	0	32747	0

Supplementary Table 3B. Mean (M) source *Bacteroidales* (copies 100 mL^{-1}) and number of samples (N) and standard deviation (SD) for AAD under season and flow conditions.   See Suppl.2A for flow regime definition.

		All data			spring			summer			fall			high			low			no flow		
Microbial source tracking endpoint	Site	N	M	SD	N	M	SD	N	M	SD	N	M	SD	N	M	SD	N	M	SD	N	M	SD
Bacteroidales ruminant marker	RCA$_{in}$	83	681	2244	29	544	1278	34	667	2066	20	903	3440	30	183	710	29	984	2938	24	937	2510
Bacteroidales ruminant marker	RCA$_{out}$\URCA$_{in}$	68	25116	203527	28	60217	317199	25	473	1163	15	668	2155	28	243	636	29	378	1600	11	153651	505813
Bacteroidales ruminant marker	URCA$_{mid}$	48	4495	13153	23	727	2465	15	13271	21235	10	0	0	21	2240	7064	24	6566	17243	3	3721	6445
Bacteroidales ruminant marker	URCA$_{out}$	83	17709	123795	29	1064	3179	30	43939	205087	24	5033	13325	33	1192	2462	35	36170	189778	15	10969	27156
Bacteroidales muskrat marker	RCA$_{in}$	86	110	598	32	0	0	34	250	927	20	47	211	31	0	0	30	69	262	25	296	1062
Bacteroidales muskrat marker	RCA$_{out}$\URCA$_{in}$	71	275	1095	31	385	1474	25	179	745	15	207	584	29	135	445	30	521	1609	12	0	0
Bacteroidales muskrat marker	URCA$_{mid}$	48	283	1331	23	70	334	15	0	0	10	1200	2791	21	167	764	24	421	1752	3	0	0
Bacteroidales muskrat marker	URCA$_{out}$	83	127	1158	29	0	0	30	352	1927	24	0	0	33	0	0	35	301	1784	15	0	0
Bacteroidales C. goose marker	RCA$_{in}$	86	584	2921	32	455	2576	34	1047	3911	20	0	0	31	0	0	30	239	1311	25	1720	5119
Bacteroidales C. goose marker	RCA$_{out}$\URCA$_{in}$	71	2666	10303	31	4610	13586	25	1811	8306	15	75	289	29	1776	5608	30	4593	14774	12	0	0
Bacteroidales C. goose marker	URCA$_{mid}$	48	0	0	23	0	0	15	0	0	10	0	0	21	0	0	24	0	0	3	0	0
Bacteroidales C. goose marker	URCA$_{out}$	83	236	2146	29	674	3631	30	0	0	24	0	0	33	593	3404	35	0	0	15	0	0
Bacteroidales pig marker	RCA$_{in}$	86	744	3424	32	78	442	34	1101	3562	20	1202	5377	31	1574	5322	30	215	1175	25	350	1749
Bacteroidales pig marker	RCA$_{out}$\URCA$_{in}$	71	282	2376	31	646	3596	25	0	0	15	0	0	29	690	3718	30	0	0	12	0	0
Bacteroidales pig marker	URCA$_{mid}$	48	42	292	23	88	422	15	0	0	10	0	0	21	96	442	24	0	0	3	0	0
Bacteroidales pig marker	URCA$_{out}$	83	303	2452	29	0	0	30	0	0	24	1049	4540	33	91	523	35	633	3748	15	0	0
Bacteroidales human marker	RCA$_{in}$	86	1334	9530	32	924	4396	34	2504	14599	20	0	0	31	0	0	30	986	4538	25	3405	17026
Bacteroidales human marker	RCA$_{out}$\URCA$_{in}$	71	86088	557119	31	155117	836022	25	43808	140811	15	13895	29582	29	18246	38922	30	185428	854381	12	1688	4612
Bacteroidales human marker	URCA$_{mid}$	48	0	0	23	0	0	15	0	0	10	0	0	21	0	0	24	0	0	3	0	0
Bacteroidales human marker	URCA$_{out}$	83	9168	29790	29	9552	30671	30	10364	35319	24	7208	20970	33	7682	27461	35	5726	19785	15	20467	48496

Supplementary Table 4: Presence and absence of microbial source tracking endpoints associated with final CART classification model criteria based on site, season and flow regime using TCD. High flow ≥ 0.018 m^{3} s^{-1}; low flow ≥ 0.002 m^{3} s^{-1} and < 0.018 m^{3} s^{-1}; and no flow < 0.002 m^{3} s^{-1}. A/w, associated with.

Microbial source tracking endpoints	CART Classification Criteria	Presence	Absence	Percent presence	Percent absence
Cryptosporidium a/w livestock	All data	8	66	11	89
Cryptosporidium a/w livestock	(Spring) and (summer)	0	50	0	100
Cryptosporidium a/w livestock	(Fall) AND (low flow) AND (no flow)	0	2	0	100
Cryptosporidium a/w livestock	(Fall) AND (high flow)	8	14	36	64
Cryptosporidium a/w wildlife	All data	29	45	39	61
Cryptosporidium a/w wildlife	(Spring) and (summer)	14	36	28	72
Cryptosporidium a/w wildlife	(Fall) AND (low flow) AND (No flow)	0	2	0	100
Cryptosporidium a/w wildlife	(Fall) AND (high flow)	15	7	68	32
Cryptosporidium a/w avian	All data	3	71	4	96
Cryptosporidium a/w avian	(Low flow)	0	22	0	100
Cryptosporidium a/w avian	(High flow) AND (no flow)	3	49	6	94
Cryptosporidium a/w human	-	-	-	-	-
Cryptosporidium a/w muskrat	All data	23	51	31	69
Cryptosporidium a/w muskrat	(Spring)	1	11	8	92
Cryptosporidium a/w muskrat	(Summer) AND (fall)	22	40	35	65
Cryptosporidium a/w unknown	All data	8	66	11	89
Cryptosporidium a/w unknown	(Spring) AND (summer)	2	48	4	96
Cryptosporidium a/w unknown	(Fall)	6	18	25	75
Bacteroidales ruminant marker	All data	40	152	21	79
Bacteroidales ruminant marker	(URCA$_{\text{out}}$)	20	44	31	69
Bacteroidales ruminant marker	(RCA$_{\text{in}}$) AND (RCA$_{\text{out}}$\URCA$_{\text{in}}$) AND (high flow) AND (low flow)	13	93	12	88
Bacteroidales ruminant marker	(RCA$_{\text{in}}$) AND (RCA$_{\text{out}}$\URCA$_{\text{in}}$) AND (no flow)	7	15	32	68
Bacteroidales muskrat marker	All data	12	189	6	94
Bacteroidales muskrat marker	(RCA$_{\text{in}}$) AND (URCA$_{\text{out}}$)	4	130	3	97
Bacteroidales muskrat marker	(RCA$_{\text{out}}$\URCA$_{\text{in}}$) AND (no flow)	0	12	0	100
Bacteroidales muskrat marker	(RCA$_{\text{out}}$\URCA$_{\text{in}}$) AND (high flow) AND (low flow)	8	47	15	85
Bacteroidales C. goose marker	All data	11	190	5	95
Bacteroidales C. goose marker	(RCA$_{\text{in}}$) AND (URCA$_{\text{out}}$)	2	132	1	99
Bacteroidales C. goose marker	(RCA$_{\text{out}}$\URCA$_{\text{in}}$)	9	58	13	87
Bacteroidales pig marker	All data	7	194	3	97
Bacteroidales pig marker	(RCA$_{\text{in}}$)	5	62	7	93
Bacteroidales pig marker	(RCA$_{\text{out}}$\URCA$_{\text{in}}$) AND (URCA$_{\text{out}}$)	2	132	1	99
Bacteroidales human marker	All data	26	175	13	87
Bacteroidales human marker	(RCA$_{\text{in}}$)	3	64	4	96
Bacteroidales human marker	(RCA$_{\text{out}}$\URCA$_{\text{in}}$) AND (URCA$_{\text{out}}$) AND (spring)	6	52	10	90
Bacteroidales human marker	(RCA$_{\text{out}}$\URCA$_{\text{in}}$) AND (URCA$_{\text{out}}$) AND (summer) AND (fall)	17	59	22	78

Microbial source tracking endpoints	CART Classification Criteria	Presence	Absence	Percent presence	Percent absence
Hepatitis A a/w human	-	-	-	-	-
Astrovirus a/w human	-	-	-	-	-
Astrovirus a/w human	All data	10	71	12	88
Astrovirus a/w human	(High flow)	1	32	3	97
Astrovirus a/w human	(Low flow) AND (no flow)	9	39	19	81
Norovirus GI a/w human	All data	11	70	14	86
Norovirus GI a/w human	(Fall)	0	27	0	100
Norovirus GI a/w human	(Spring) AND (summer) AND (no flow)	0	9	0	100
Norovirus GI a/w human	(Spring) AND (summer) AND (high flow) AND (low flow)	11	34	24	76
Norovirus GIII a/w bovine	All data	9	72	11	89
Norovirus GIII a/w bovine	(Fall)	0	27	0	100
Norovirus GIII a/w bovine	(Spring) AND (summer) AND (no flow)	0	9	0	100
Norovirus GIII a/w bovine	(Spring) AND (summer) AND (high flow) AND (low flow)	9	36	20	80
Norovirus GIV a/w human	All data	6	75	7	93
Norovirus GIV a/w human	(High flow) AND (no flow)	0	42	0	100
Norovirus GIV a/w human	(Low flow)	6	33	15	85
Sapovirus a/w human	-	-	-	-	-
Human Torque teno virus	All data	7	74	9	91
Human Torque teno virus	(RCA$_{in}$) AND (RCA$_{out}$\URCA$_{in}$)	3	51	6	94
Human Torque teno virus	(URCA$_{out}$) AND (spring) AND (summer)	4	14	22	78
Human Torque teno virus	(URCA$_{out}$) AND (fall)	0	9	0	100
Torque teno sus virus a/w swine	All data	6	75	7	93
Torque teno sus virus a/w swine	(RCA$_{in}$)	0	27	0	100
Torque teno sus virus a/w swine	(RCA$_{out}$\URCA$_{in}$) AND (URCA$_{out}$) AND (fall)	0	18	0	100
Torque teno sus virus a/w swine	(RCA$_{out}$\URCA$_{in}$) AND (URCA$_{out}$) AND (spring) AND (summer)	6	30	17	83
Adenovirus 40/41 a/w human	All data	3	78	4	96
Adenovirus 40/41 a/w human	(High flow) AND (low flow)	0	72	0	100
Adenovirus 40/41 a/w human	(No flow)	3	6	33	67
General Adenovirus a/w human	-	-	-	-	-
F-RNA coliphage human	All data	5	109	4	96
F-RNA coliphage human	(Spring) AND (fall)	2	67	3	97
F-RNA coliphage human	(Summer) AND (RCA$_{out}$\URCA$_{in}$)	0	15	0	100
F-RNA coliphage human	(Summer) AND (RCA$_{in}$) AND (URCA$_{out}$)	3	27	10	90
F-RNA coliphage animal	All data	35	79	31	69
F-RNA coliphage animal	(Spring) AND (summer)	19	65	23	77
F-RNA coliphage animal	(Fall)	16	14	53	47

Supplementary Table 5A. Cross tabulation of source co-occurrence for samples collected at the same site and time for AAD.

		Cryptosporidium a/w livestock		*Cryptosporidium* a/w wildlife		*Cryptosporidium* a/w avian		*Cryptosporidium* a/w humans		*Cryptosporidium* a/w muskrat/voles		*Cryptosporidium* a/w unknown sources		*Bacteroidales* ruminant marker		*Bacteroidales* muskrat marker		*Bacteroidales* C. goose marker		*Bacteroidales* pig marker		*Bacteroidales* human marker		Hepatitis A a/w human		Astrovirus a/w human		Norovirus GI a/w human		Norovirus GIII a/w bovine		Norovirus GIV a/w human		Sapovirus a/w human		Human Torque teno virus		Torque teno sus virus a/w swine		Adenovirus 40/41 a/w human		F-RNA coliphage human		F-RNA coliphage animal	
		+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-
Cryptosporidium a/w wildlife	+	10	28																																										
	-	7	61																																										
Cryptosporidium a/w avian	+	1	2	3	0																																						
	-	16	87	35	68																																						
Cryptosporidium a/w humans	+	0	2	0	2	0	2																																				
	-	17	87	38	66	3	101																																				
Cryptosporidium a/w muskrat/voles	+	8	21	29	0	3	26	0	29																																		
	-	9	68	9	68	0	77	2	75																																		
Cryptosporidium a/w unknown sources	+	5	7	12	0	0	12	0	12	7	5																																
	-	12	82	26	68	3	91	2	92	22	72																																
Bacteroidales ruminant marker	+	4	16	7	13	0	20	1	19	6	14	1	19																														
	-	8	56	18	46	2	62	1	63	11	52	6	58																														
Bacteroidales muskrat marker	+	0	3	0	3	0	3	0	3	0	3	0	3	0	11																												
	-	12	69	25	56	2	79	2	79	17	64	7	74	59	207																												
Bacteroidales C. goose marker	+	0	3	1	2	0	3	0	3	0	3	0	3	0	14	2	12																										
	-	12	69	24	57	2	79	2	79	17	64	7	74	64	204	14	260																										
Bacteroidales pig marker	+	2	2	2	2	1	3	0	4	2	2	1	3	5	5	1	9	1	9																								
	-	10	70	23	57	1	79	2	78	15	65	6	74	59	213	15	263	13	265																								
Bacteroidales human marker	+	1	10	3	8	0	11	0	11	3	8	0	11	6	20	3	24	4	23	0	27																						
	-	11	62	22	51	2	71	2	71	14	59	7	66	58	198	13	248	19	251	10	251																						
Hepatitis A a/w human	+	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	1	0	1	0	1																						
	-	2	4	1	5	0	6	0	6	0	6	1	5	23	73	8	92	3	97	1	99	14	86																						
Astrovirus a/w human	+	1	0	1	0	0	1	0	1	0	1	1	0	2	12	0	14	0	14	0	14	1	13	0	15																				
	-	1	4	0	5	0	5	0	5	0	5	0	5	22	61	9	79	3	84	1	86	13	74	1	92																				
Norovirus GI a/w human	+	0	2	0	2	0	2	0	2	0	2	0	2	5	8	0	13	1	12	1	12	3	10	1	12	1	12																		
	-	2	2	1	3	0	4	0	4	0	4	1	3	19	65	8	80	2	86	0	88	11	77	0	95	14	81																		
Norovirus GIII a/w bovine	+	0	0	0	0	0	0	0	0	0	0	0	1	2	7	1	9	0	10	0	10	2	8	0	12	2	10	2	10																
	-	2	4	1	5	0	6	0	6	0	6	0	5	22	66	7	84	3	88	1	90	12	79	1	95	13	83	11	85																
Norovirus GIV a/w human	+	0	0	0	0	0	0	0	0	0	0	0	0	1	6	0	7	0	7	0	7	1	6	0	8	4	4	1	7	4	4														
	-	2	4	1	5	0	6	0	6	0	6	1	5	23	67	8	86	3	91	1	93	13	81	1	99	11	89	12	88	8	92														
Sapovirus a/w human	+	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												
	-	2	4	1	5	0	6	0	6	0	6	1	5	24	73	8	93	3	98	1	100	14	87	1	107	15	92	13	95	12	96	8	100												
Human Torque teno virus	+	0	0	0	0	0	0	0	0	0	0	0	0	2	8	0	10	0	10	0	10	0	10	1	9	2	8	2	8	3	7	1	9	0	10										
	-	2	4	1	5	0	6	0	6	0	6	1	5	22	65	8	83	3	88	1	90	14	77	0	98	13	85	11	87	9	89	7	91	0	98										
Torque teno sus virus a/w swine	+	0	0	0	0	0	0	0	0	0	0	0	0	2	6	0	10	0	10	0	10	1	9	1	9	1	9	3	7	0	10	0	10	0	10	2	8								
	-	2	4	1	5	0	6	0	6	0	6	1	5	22	67	8	83	3	88	1	90	13	78	0	98	14	84	10	88	12	86	8	90	0	98	8	90								
Adenovirus 40/41 a/w human	+	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	4	0	4	0	4	1	3	0	4	0	4	0	4	0	4	0	4	0	4	0	4	1	3						
	-	2	4	1	5	0	6	0	6	0	6	1	5	23	71	8	89	3	94	1	96	13	84	1	103	15	89	13	91	12	92	8	96	0	104	10	94	9	95						
General Adenovirus a/w human	+	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	2	0	2	0	2	0	2	0	2	0	2	0	2	0	2	0	2	0	2	0	2	0	2	1	1				
	-	2	4	1	5	0	6	0	6	0	6	1	5	23	72	8	91	3	96	1	98	14	85	1	105	15	91	13	93	12	94	8	98	0	106	10	96	10	96	3	103				
F-RNA coliphage human	+	0	0	0	0	0	0	0	0	0	0	0	0	2	5	1	6	0	7	0	7	1	6	0	7	2	5	1	6	1	6	1	6	0	7	1	6	1	6	0	7	0	7		
	-	7	26	11	22	1	32	2	31	7	26	5	28	33	103	7	133	5	135	3	137	13	127	1	95	13	83	11	85	10	86	7	89	0	96	9	87	8	88	4	92	2	94		
F-RNA coliphage animal	+	1	2	1	2	0	3	0	3	0	3	0	3	9	32	4	37	3	38	0	41	7	34	0	41	5	36	2	39	8	33	5	36	0	41	3	38	2	39	0	41	0	41	4	41
	-	6	24	10	20	1	29	2	28	7	23	5	25	26	76	4	102	2	104	3	103	7	99	1	61	10	52	10	52	3	59	3	59	0	62	7	55	7	55	4	58	2	60	4	104

Supplementary Table 5B: Odds ratio (OR) estimates for co-occurrence of microbial source tracking endpoints for AAD. Significant results bolded.

		Cryptosporidium a/w						*Bacteroidales*					Virus										
Microbial Source Tracking Endpoint	Estimate	livestock	wildlife	avian	humans	muskrat/voles	unknown sources	ruminant marker	muskrat marker	C. goose marker	pig marker	human marker	Hepatitis A a/w human	Astrovirus a/w human	Norovirus GI a/w human	Norovirus GIII a/w bovine	Norovirus GIV a/w human	Sapovirus a/w human	Human Torque teno virus	Torque teno sus virus a/w swine	Adenovirus 40/41 a/w human	General Adenovirus a/w human	F-RNA coliphage human
Cryptosporidium a/w wildlife	Lower 95% CI OR	0.9																					
	Odds Ratio	3.1																					
	Upper 95% CI OR	10.6																					
Cryptosporidium a/w avian	Lower 95% CI OR	0.0	0.8																				
	Odds Ratio	2.7	∞																				
	Upper 95% CI OR	54.4	∞																				
Cryptosporidium a/w humans	Lower 95% CI OR	0.0	0.0	0.0																			
	Odds Ratio	0.0	0.0	0.0																			
	Upper 95% CI OR	28.4	9.6	215.4																			
Cryptosporidium a/w muskrat/voles	Lower 95% CI OR	0.8	**42.8**	**1.1**	0.0																		
	Odds Ratio	2.8	**∞**	**∞**	0.0																		
	Upper 95% CI OR	9.5	**∞**	**∞**	14.2																		
Cryptosporidium a/w unknown sources	Lower 95% CI OR	**1.0**	**6.5**	0.0	0.0	**1.1**																	
	Odds Ratio	**4.8**	**∞**	0.0	0.0	**4.5**																	
	Upper 95% CI OR	**21.0**	**∞**	19.9	43.0	**19.9**																	
Bacteroidales ruminant marker	Lower 95% CI OR	0.3	0.4	0.0	0.0	0.5	0.0																
	Odds Ratio	1.7	1.4	0.0	3.3	2.0	0.5																
	Upper 95% CI OR	7.6	4.5	17.3	263.7	7.3	4.7																
Bacteroidales muskrat marker	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	0.0															
	Odds Ratio	0.0	0.0	0.0	0.0	0.0	0.0	0.0															
	Upper 95% CI OR	15.2	5.7	169.0	169.0	9.8	29.2	1.4															
Bacteroidales C. goose marker	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	**0.0**	0.3														
	Odds Ratio	0.0	1.2	0.0	0.0	0.0	0.0	**0.0**	3.1														
	Upper 95% CI OR	15.2	23.8	169.0	169.0	9.8	29.2	**1.0**	16.1														
Bacteroidales pig marker	Lower 95% CI OR	0.4	0.2	0.3	0.0	0.3	0.1	0.8	0.0	0.0													
	Odds Ratio	6.7	2.4	22.9	0.0	4.2	4.0	3.6	1.9	2.3													
	Upper 95% CI OR	102.8	35.7	2044.1	119.3	62.8	59.9	16.2	15.8	18.6													
Bacteroidales human marker	Lower 95% CI OR	0.0	0.1	0.0	0.0	0.2	0.0	0.3	0.4	0.5	0.0												
	Odds Ratio	0.6	0.9	0.0	0.0	1.6	0.0	1.0	2.4	2.3	0.0												
	Upper 95% CI OR	4.8	4.1	36.5	36.5	7.7	4.8	2.8	9.5	7.7	4.4												
Hepatitis A a/w human	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0											
	Odds Ratio	0.0	0.0	0.0	0.0	0.0	0.0	∞	0.0	0.0	0.0	0.0											
	Upper 95% CI OR	∞	∞	∞	∞	∞	∞	∞	450.2	1249.2	3676.0	241.4											
Astrovirus a/w human	Lower 95% CI OR	0.1	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0										
	Odds Ratio	∞	∞	0.0	0.0	0.0	∞	0.5	0.0	0.0	0.0	0.4	0.0										
	Upper 95% CI OR	∞	∞	∞	∞	∞	∞	2.4	3.2	15.6	241.4	3.5	240.9										

		Cryptosporidium a/w						*Bacteroidales*					Virus											
Microbial Source Tracking Endpoint	Estimate	livestock	wildlife	avian	humans	muskrat/voles	unknown sources	ruminant marker	muskrat marker	C. goose marker	pig marker	human marker	Hepatitis A a/w human	Astrovirus a/w human	Norovirus GI a/w human	Norovirus GIII a/w bovine	Norovirus GIV a/w human	Sapovirus a/w human	Human Torque teno virus	Animal Torque teno virus a/w swine	Adenovirus 40/41 a/w human	Adenovirus General V a/w human	F-RNA coliphage human
Norovirus GI a/w human	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.1	0.2	0.3	0.2	0.0									
	Odds Ratio	0.0	0.0	0.0	0.0	0.0	0.0	2.1	0.0	3.5	∞	2.1	∞	0.5									
	Upper 95% CI OR	11.8	77.9	∞	∞	∞	77.9	8.4	4.1	72.6	∞	10.0	∞	3.8									
Norovirus GIII a/w bovine	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.2	0.0	0.1	0.1								
	Odds Ratio	0.0	0.0	0.0	0.0	0.0	0.0	0.9	1.3	0.0	0.0	1.6	0.0	1.3	1.5								
	Upper 95% CI OR	∞	∞	∞	∞	∞	∞	5.0	12.5	23.4	352.9	9.7	310.5	7.1	8.8								
Norovirus GIV a/w human	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	**1.3**	0.0	**1.7**							
	Odds Ratio	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	1.0	0.0	**7.8**	1.0	**11.0**							
	Upper 95% CI OR	∞	∞	∞	∞	∞	∞	4.4	9.0	35.8	519.5	9.7	483.8	**48.8**	9.4	**72.1**							
Sapovirus a/w human	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0						
	Odds Ratio	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0						
	Upper 95% CI OR	∞	∞	∞	∞	∞	∞	∞	∞	∞	∞	∞	∞	∞	∞	∞	∞						
Human Torque teno virus	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.3	0.2	0.2	0.6	0.0	0.0					
	Odds Ratio	0.0	0.0	0.0	0.0	0.0	0.0	0.7	0.0	0.0	0.0	0.0	∞	1.6	2.0	4.2	1.4	0.0					
	Upper 95% CI OR	∞	∞	∞	∞	∞	∞	4.1	5.7	23.4	352.9	2.8	∞	9.5	11.8	22.7	13.5	∞					
Torque teno sus virus a/w swine	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.3	0.0	0.5	0.0	0.0	0.0	0.2				
	Odds Ratio	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.7	∞	0.7	3.7	0.0	0.0	0.0	2.8				
	Upper 95% CI OR	∞	∞	∞	∞	∞	∞	6.2	5.7	23.4	352.9	5.6	∞	5.5	19.8	3.7	6.2	∞	17.8				
Adenovirus 40/41 a/w human	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1			
	Odds Ratio	0.0	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	0.0	2.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.5			
	Upper 95% CI OR	∞	∞	∞	∞	∞	∞	30.8	19.5	71.4	932.0	29.0	998.2	9.8	11.6	12.8	21.0	∞	16.0	48.5			
General Adenovirus V a/w human	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3		
	Odds Ratio	0.0	0.0	0.0	0.0	0.0	0.0	3.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	29.9		
	Upper 95% CI OR	∞	∞	∞	∞	∞	∞	248.5	65.0	204.8	1874.0	33.9	2002.4	33.8	40.0	43.9	69.9	∞	54.2	54.2	2639.1		
F-RNA coliphage human	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
	Odds Ratio	0.0	0.0	0.0	0.0	0.0	0.0	1.2	3.1	0.0	0.0	1.6	0.0	2.5	1.3	1.4	2.1	0.0	1.6	1.8	0.0	0.0	
	Upper 95% CI OR	∞	∞	∞	∞	∞	∞	8.1	32.3	25.2	53.6	15.1	530.4	17.5	12.3	13.8	21.8	∞	15.8	18.4	23.4	77.3	
F-RNA coliphage animal	Lower 95% CI OR	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.5	0.4	0.0	0.8	0.0	0.2	0.0	**1.0**	0.5	0.0	0.1	0.0	0.0	0.0	0.4
	Odds Ratio	2.0	1.0	0.0	0.0	0.0	0.0	0.8	2.7	4.1	0.0	2.9	0.0	0.7	0.3	**4.7**	2.7	0.0	0.6	0.4	0.0	0.0	2.5
	Upper 95% CI OR	43.8	21.5	387.6	61.7	9.5	15.1	2.1	15.5	50.3	6.3	10.4	58.9	2.6	1.4	**29.3**	18.5	∞	2.9	2.3	2.3	8.1	14.2

Supplementary Table 5C: Fisher’s exact test p-values for co-occurrence of microbial source tracking endpoints for AAD. Significant results (p<0.05) bolded. A/w, associated with.

	Cryptosporidium a/w						*Bacteroidales*					Virus										
	livestock	wildlife	avian	humans	muskrat/voles	unknown sources	ruminant marker	muskrat marker	C. goose marker	pig marker	human marker	Hepatitis A a/w human	Astrovirus a/w human	Norovirus GI a/w human	Norovirus GIII a/w bovine	Norovirus GIV a/w human	Sapovirus a/w human	Human Torque teno virus	Torque teno sus virus a/w swine	Adenovirus 40/41 a/w human	General Adenovirus a/w human	F-RNA coliphage human
Cryptosporidium a/w wildlife	0.051																					
Cryptosporidium a/w avian	0.411	0.044																				
Cryptosporidium a/w humans	1.000	0.536	1.000																			
Cryptosporidium a/w muskrat/voles	0.072	**2.20E-16**	0.019	1.000																		
Cryptosporidium a/w unknown sources	**0.023**	**1.23E-06**	1.000	1.000	**0.017**																	
Bacteroidales ruminant marker	0.467	0.583	1.000	0.422	0.339	1.000																
Bacteroidales muskrat marker	1.000	0.551	1.000	1.000	1.000	1.000	0.128															
Bacteroidales C. goose marker	1.000	1.000	1.000	1.000	1.000	1.000	**0.045**	0.178														
Bacteroidales pig marker	0.096	0.579	0.094	1.000	0.181	0.299	0.051	0.441	0.397													
Bacteroidales human marker	1.000	1.000	1.000	1.000	0.687	0.587	1.000	0.180	0.143	0.606												
Hepatitis A a/w human	1.000	1.000	1.000	1.000	1.000	1.000	0.247	1.000	1.000	1.000	1.000											
Astrovirus a/w human	0.333	0.167	1.000	1.000	1.000	0.167	0.506	0.355	1.000	1.000	0.685	1.000										
Norovirus GI a/w human	0.467	1.000	1.000	1.000	1.000	1.000	0.298	0.592	0.342	0.129	0.384	0.120	0.689									
Norovirus GIII a/w bovine	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.580	1.000	1.000	0.626	1.000	0.672	0.636								
Norovirus GIV a/w human	1.000	1.000	1.000	1.000	1.000	1.000	0.677	1.000	1.000	1.000	1.000	1.000	**0.012**	1.000	**0.005**							
Sapovirus a/w human	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000						
Human Torque teno virus	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.350	0.093	0.627	0.345	0.081	0.553	1.000					
Torque teno sus virus a/w swine	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.093	1.000	0.100	0.598	1.000	1.000	0.232				
Adenovirus 40/41 a/w human	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.455	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.326			
General Adenovirus a/w human	1.000	1.000	1.000	1.000	1.000	1.000	0.436	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.073		
F-RNA coliphage human	1.000	1.000	1.000	1.000	1.000	1.000	0.680	0.330	1.000	1.000	0.511	1.000	0.269	0.592	0.558	0.442	1.000	0.522	0.483	1.000	1.000	
F-RNA coliphage animal	0.524	1.000	1.000	1.000	1.000	1.000	0.830	0.219	0.133	0.560	0.064	1.000	0.777	0.118	**0.024**	0.260	1.000	0.736	0.311	0.149	0.516	0.235