

1 **Supplemental Material**

2 **Quantifying the Relative Contributions of Environmental Sources to the Microbial**
3 **Community in an Urban Stream under Dry and Wet Weather Conditions**

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9 Running Head: Relative Contribution of Sources to Microbes in Stream

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18 **TABLES**

19 Table S1: Summary of α -diversity indices.

Category	Sample Type (# of samples)	α -Diversity, mean (standard deviation)		
		Chao1	Shannon	observed OTUs
Environmental samples	Dry Weather Water (43)	534 (122)	6.0 (0.9)	343 (77)
	Rising Limb (15)	772 (133)	6.8 (0.6)	508 (100)
	Peak Flow (32)	753 (127)	6.9 (0.6)	509 (98)
	Declining Limb (19)	715 (127)	6.7 (0.6)	478 (91)
	Streambed Sediment (45)	729 (119)	7.1 (0.6)	523 (95)
	Holmes Lake Water (19)	400 (100)	5.6 (0.6)	265 (51)
	Storm Drain Outfall Water (24)	685 (139)	6.5 (0.9)	456 (101)
	Street Sweepings (3)	693 (46)	7.3 (0.3)	511 (17)
	Erodible Soil (20)	670 (115)	7.7 (0.6)	519 (71)
	Embankment Soil (49)	634 (100)	7.8 (0.4)	511 (72)
Fecal samples	Sanitary Sewage (7)	259 (38)	4.8 (0.2)	179 (19)
	Duck Feces (4)	234 (83)	3.7 (0.9)	143 (59)
	Pigeon Feces (3)	223 (66)	3.8 (0.6)	136 (50)
	Goose Feces (5)	190 (88)	4.3 (0.4)	114 (49)
	Horse Feces (4)	185 (41)	5.9 (0.3)	140 (13)
	Small Mammal Feces (4)	176 (73)	4.1 (0.7)	121 (50)
	Swallow Feces (6)	157 (75)	3.2 (1)	94 (35)
	Dog Feces (4)	115 (81)	3.6 (0.5)	80 (51)

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21 Table S2: Summary of water quality parameters for water collected from Antelope Creek.

Water Quality Parameters	Dry Weather ¹ (n = 43)	Wet Weather ¹		
		Rising Limb (n = 15)	Peak Flow (n = 32)	Declining Limb (n = 19)
NH ₃ -N (mg/L)	0.08 (0.09)	0.30 (0.30)	0.40 (0.20)	0.20 (0.30)
TKN (mg/L)	1.0 (0.4)	4.0 (2)	3.0 (1)	2.0 (0.5)
NO ₃ -N (mg/L)	0.6 (0.8)	0.6 (0.1)	0.6 (0.1)	0.5 (0.4)
SRP (mg/L)	0.2 (0.1)	0.2 (0.1)	0.2 (0.09)	0.2 (0.1)
TP (mg/L)	0.30 (0.10)	0.80 (0.50)	0.60 (0.20)	0.30 (0.09)
<i>E. coli</i> (CFU/100 mL)	2,000 (3,000)	50,000 (40,000)	70,000 (50,000)	60,000 (90,000)
Turbidity (NTU)	20 (10)	70 (60)	80 (40)	30 (10)
Chloride (mg/L)	20 (20)	10 (8)	8 (4)	10 (4)
TSS (mg/L)	30 (90)	400 (300)	300 (200)	40 (40)
COD (mg/L)	20 (10)	60 (40)	70 (50)	40 (30)

22 ¹Mean (Standard Deviation)

23 Table S3: Summary of the relative abundance of major families (i.e., relative abundance $\geq 0.1\%$) in various sample types.

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)
Dry Weather Water	Actinobacteria	Actinobacteria	Actinomycetales	ACK-M1	6.4
	Bacteroidetes	[Saprosirae]	[Saprosirales]	Chitinophagaceae	4.9
		Bacteroidia	Bacteroidales	Other	0.1
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	4.3
	Cyanobacteria	Oscillatoriothycideae	Chroococcales	Microcystaceae	5.1
	Firmicutes	Bacilli	Bacillales	[Exiguobacteraceae]	0.2
		Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	0.4
	Other	Other	Other	Other	0.9
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	0.3
			Rhodobacterales	Rhodobacteraceae	2.4
		Betaproteobacteria	Burkholderiales	Comamonadaceae	10.3
				Oxalobacteraceae	1.5
			Rhodocyclales	Rhodocyclaceae	1.4
		Deltaproteobacteria	Myxococcales	Other	0.1
		Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	0.9
		Gammaproteobacteria	Aeromonadales	Aeromonadaceae	0.6
			Alteromonadales	[Chromatiaceae]	9.9
				Alteromonadaceae	0.5
			Enterobacteriales	Enterobacteriaceae	0.2
			Pseudomonadales	Moraxellaceae	0.6
Pseudomonadaceae				2.0	

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)
Rising Limb Water	Actinobacteria	Actinobacteria	Actinomycetales	ACK-M1	0.3
		Thermoleophilia	Gaiellales	Gaiellaceae	0.1
	Bacteroidetes	[Saprosirae]	[Saprosirales]	Chitinophagaceae	1.8
		Bacteroidia	Bacteroidales	Other	0.1
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	2.1
	Cyanobacteria	Oscillatoriothycideae	Chroococcales	Microcystaceae	0.2
	Firmicutes	Bacilli	Bacillales	[Exiguobacteraceae]	4.4
				Paenibacillaceae	0.8
		Erysipelotrichi	Erysipelotrichales	Enterococcaceae	0.3
				Erysipelotrichaceae	0.2
	Other	Other	Other	Other	2.0
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	0.7
			Rhodobacterales	Rhodobacteraceae	7.1
		Betaproteobacteria	Burkholderiales	Comamonadaceae	8.7
				Oxalobacteraceae	7.8
			Rhodocyclales	Rhodocyclaceae	0.9
		Deltaproteobacteria	Myxococcales	Other	0.3
		Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	0.3
		Gammaproteobacteria	Aeromonadales	Aeromonadaceae	1.2
				[Chromatiaceae]	2.6
			Alteromonadales	Alteromonadaceae	0.4
Enterobacteriales				Enterobacteriaceae	3.4
Pseudomonadales			Moraxellaceae	9.9	
			Pseudomonadaceae	4.5	

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)
Peak Flow Water	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	0.2
	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	1.3
		Bacteroidia	Bacteroidales	Other	0.1
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	2.4
	Cyanobacteria	Oscillatoriothyriceae	Chroococcales	Microcystaceae	0.2
	Firmicutes	Bacilli	Bacillales	[Exiguobacteraceae]	1.0
				Paenibacillaceae	1.1
		Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	0.2
	Other	Other	Other	Other	0.9
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	0.7
			Rhodobacterales	Rhodobacteraceae	5.0
		Betaproteobacteria	Burkholderiales	Comamonadaceae	12.0
				Oxalobacteraceae	8.2
			Rhodocyclales	Rhodocyclaceae	1.1
		Deltaproteobacteria	Myxococcales	Other	0.3
		Epsilonproteobacteria	Campylobacteriales	Campylobacteraceae	0.4
		Gammaproteobacteria	Aeromonadales	Aeromonadaceae	4.7
				[Chromatiaceae]	3.8
			Alteromonadales	Alteromonadaceae	0.7
			Enterobacteriales	Enterobacteriaceae	6.9
Pseudomonadales			Moraxellaceae	9.5	
	Pseudomonadaceae	7.4			

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)		
Declining Limb Water	Actinobacteria	Actinobacteria	Actinomycetales	ACK-M1	3.1		
	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	2.9		
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	5.4		
	Cyanobacteria	Oscillatorioophycideae	Chroococcales	Microcystaceae	1.0		
	Firmicutes	Bacilli	Bacillales	[Exiguobacteraceae]	1.4		
				Paenibacillaceae	0.5		
	Other	Other	Other	Other	0.5		
	Proteobacteria	Alphaproteobacteria		Rhizobiales	Hyphomicrobiaceae	0.5	
				Rhodobacterales	Rhodobacteraceae	3.9	
		Betaproteobacteria		Burkholderiales	Comamonadaceae	22.5	
					Oxalobacteraceae	6.3	
				Rhodocyclales	Rhodocyclaceae	2.3	
		Deltaproteobacteria		Myxococcales	Other	0.5	
		Epsilonproteobacteria		Campylobacterales	Campylobacteraceae	0.7	
		Gammaproteobacteria			Aeromonadales	Aeromonadaceae	3.3
					Alteromonadales	[Chromatiaceae]	1.9
						Alteromonadaceae	0.9
	Enterobacteriales				Enterobacteriaceae	2.2	
Pseudomonadales	Moraxellaceae				2.9		
	Pseudomonadaceae	3.2					

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)		
Storm Drain Outfall Water	Actinobacteria	Actinobacteria	Actinomycetales	ACK-M1	0.3		
		Thermoleophilia	Gaiellales	Gaiellaceae	0.1		
	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	1.5		
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	4.4		
	Cyanobacteria	Chloroplast	Streptophyta	Other	0.1		
		Oscillatoriothycideae	Chroococcales	Microcystaceae	0.2		
	Firmicutes	Bacilli	Bacillales	[Exiguobacteraceae]	0.2		
				Paenibacillaceae	0.4		
	Other	Other	Other	Other	1.7		
	Proteobacteria	Alphaproteobacteria		Rhizobiales	Hyphomicrobiaceae	0.7	
				Rhodobacterales	Rhodobacteraceae	5.0	
		Betaproteobacteria		Burkholderiales	Comamonadaceae	11.4	
					Oxalobacteraceae	8.3	
					Rhodocyclales	Rhodocyclaceae	0.9
		Deltaproteobacteria		Myxococcales	Other	0.3	
		Epsilonproteobacteria		Campylobacterales	Campylobacteraceae	1.5	
		Gammaproteobacteria			Aeromonadales	Aeromonadaceae	1.4
					Alteromonadales	[Chromatiaceae]	1.4
						Alteromonadaceae	0.4
					Enterobacteriales	Enterobacteriaceae	6.2
Pseudomonadales					Moraxellaceae	5.7	
	Pseudomonadaceae	17.0					

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)	
Street Sweeping	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	0.2	
	Bacteroidetes	[Saprosirae]	[Saprosirales]	Chitinophagaceae	1.7	
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	1.2	
	Cyanobacteria	Chloroplast	Streptophyta	Other	5.9	
	Firmicutes	Bacilli	Bacillales	[Exiguobacteraceae]	0.6	
				Paenibacillaceae	0.9	
			Lactobacillales	Enterococcaceae	0.2	
				Streptococcaceae	0.3	
	Other	Other	Other	Other	2.8	
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	1.3	
			Rhodobacterales	Rhodobacteraceae	8.1	
		Betaproteobacteria	Burkholderiales	Comamonadaceae	7.3	
				Oxalobacteraceae	7.0	
			Rhodocyclales	Rhodocyclaceae	1.3	
		Deltaproteobacteria	Myxococcales	Other	2.2	
		Gammaproteobacteria		Aeromonadales	Aeromonadaceae	0.4
				Alteromonadales	Alteromonadaceae	0.4
Enterobacteriales				Enterobacteriaceae	7.3	
Pseudomonadales				Moraxellaceae	1.2	
	Pseudomonadaceae	4.7				

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)
Holmes Lake	Actinobacteria	Actinobacteria	Actinomycetales	ACK-M1	6.4
	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	6.3
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	1.9
	Cyanobacteria	Oscillatorioophycideae	Chroococcales	Microcystaceae	8.9
	Firmicutes	Bacilli	Bacillales	[Exiguobacteraceae]	0.2
		Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	0.4
	Other	Other	Other	Other	0.5
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	0.2
			Rhodobacterales	Rhodobacteraceae	3.9
		Betaproteobacteria	Burkholderiales	Comamonadaceae	10.7
				Oxalobacteraceae	4.4
			Rhodocyclales	Rhodocyclaceae	1.1
		Deltaproteobacteria	Myxococcales	Other	1.3
		Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	0.4
		Gammaproteobacteria	Aeromonadales	Aeromonadaceae	0.3
			Alteromonadales	[Chromatiaceae]	0.6
			Enterobacteriales	Enterobacteriaceae	0.1
Pseudomonadales	Moraxellaceae		0.1		
	Pseudomonadaceae		0.9		

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)	
Streambed Sediment	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	0.2	
	Bacteroidetes	[Saprosirae]	[Saprosirales]	Chitinophagaceae	3.1	
		Bacteroidia	Bacteroidales	Other	1.8	
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	1.3	
	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	0.4	
	Other	Other	Other	Other	1.5	
	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacterales	Hyphomicrobiaceae	1.4
			Rhodocyclales	Rhodocyclales	Rhodobacteraceae	8.5
		Betaproteobacteria	Burkholderiales	Burkholderiales	Comamonadaceae	17.2
			Rhodocyclales	Rhodocyclales	Oxalobacteraceae	0.4
			Rhodocyclales	Rhodocyclales	Rhodocyclaceae	8.1
		Deltaproteobacteria	Myxococcales	Myxococcales	Other	0.9
		Gammaproteobacteria	Aeromonadales	Aeromonadales	Aeromonadaceae	0.2
			Alteromonadales	Alteromonadales	[Chromatiaceae]	0.1
				Alteromonadales	Alteromonadales	Alteromonadaceae
			Pseudomonadales	Pseudomonadales	Moraxellaceae	1.2
	Pseudomonadales	Pseudomonadales	Pseudomonadales	Pseudomonadaceae	0.3	
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	0.2		

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)		
Erodible Soil	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	1.4		
	Bacteroidetes	[Saprosirae]	[Saprosirales]	Chitinophagaceae	3.9		
		Bacteroidia	Bacteroidales	Other	0.7		
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	0.6		
	Cyanobacteria	Chloroplast	Streptophyta	Other	0.4		
	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	0.2		
				Peptostreptococcaceae	0.1		
	Other	Other	Other	Other	0.3		
	Proteobacteria	Alphaproteobacteria		Rhizobiales	Hyphomicrobiaceae	3.3	
				Rhodobacterales	Rhodobacteraceae	1.4	
		Betaproteobacteria		Burkholderiales	Comamonadaceae	4.5	
					Oxalobacteraceae	0.8	
					Rhodocyclales	Rhodocyclaceae	1.3
		Deltaproteobacteria		Myxococcales	Other	6.0	
		Gammaproteobacteria			Aeromonadales	Aeromonadaceae	0.1
					Alteromonadales	Alteromonadaceae	0.4
					Enterobacteriales	Enterobacteriaceae	0.1
Pseudomonadales					Moraxellaceae	0.2	
	Pseudomonadaceae				0.4		

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)
Embankment Soil	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	5.3
	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	3.7
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	0.1
	Cyanobacteria	Chloroplast	Streptophyta	Other	0.5
	Other	Other	Other	Other	0.1
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	5.3
			Rhodobacterales	Rhodobacteraceae	1.1
		Betaproteobacteria	Burkholderiales	Comamonadaceae	3.6
				Oxalobacteraceae	1.5
			Rhodocyclales	Rhodocyclaceae	0.2
		Deltaproteobacteria	Myxococcales	Other	3.0
		Gammaproteobacteria	Alteromonadales	Alteromonadaceae	0.1
			Pseudomonadales	Moraxellaceae	0.2
	Pseudomonadaceae			0.6	

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)
Sanitary Sewage	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	2.5
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	0.6
	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	3.4
				Streptococcaceae	4.3
		Clostridia	Clostridiales	Clostridiaceae	0.2
				Lachnospiraceae	1.5
				Peptostreptococcaceae	0.6
				Ruminococcaceae	2.4
				Veillonellaceae	0.2
	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	0.3	
	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	0.1
				Leptotrichiaceae	6.9
	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	0.5
		Betaproteobacteria	Burkholderiales	Comamonadaceae	8.3
			Rhodocyclales	Rhodocyclaceae	1.9
		Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	23.2
		Gammaproteobacteria	Aeromonadales	Aeromonadaceae	5.7
Enterobacteriales				Enterobacteriaceae	1.5
Pseudomonadales				Moraxellaceae	17.4
	Pseudomonadaceae			1.5	

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)
Dog Feces	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	5.5
	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	10.9
	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	0.5
				Lactobacillaceae	0.1
				Streptococcaceae	11.9
		Clostridia	Clostridiales	Clostridiaceae	12.0
				Lachnospiraceae	15.9
				Peptostreptococcaceae	3.3
				Ruminococcaceae	8.9
	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	9.1	
	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	0.1
	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	2.4
			Legionellales	Coxiellaceae	7.3
			Pseudomonadales	Moraxellaceae	4.8
Pseudomonadaceae	0.1				
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	1.0	

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)
Duck Feces	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	0.3
	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	0.6
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	0.1
	Cyanobacteria	Chloroplast	Streptophyta	Other	0.1
	Firmicutes	Bacilli	Bacillales	[Exiguobacteraceae]	0.2
				Other	0.5
				Paenibacillaceae	0.1
			Lactobacillales	Enterococcaceae	3.1
			Lactobacillaceae	0.3	
			Streptococcaceae	0.7	
		Clostridia	Clostridiales	Clostridiaceae	14.4
				Lachnospiraceae	3.5
				Peptostreptococcaceae	6.9
				Ruminococcaceae	0.7
		Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	2.2
	Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae	1.6
	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	0.4
		Betaproteobacteria	Burkholderiales	Comamonadaceae	2.9
			Rhodocyclales	Rhodocyclaceae	0.6
		Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	4.4
Gammaproteobacteria		Aeromonadales	Aeromonadaceae	2.4	
		Enterobacteriales	Enterobacteriaceae	27.6	
		Legionellales	Coxiellaceae	6.0	
		Pseudomonadales	Moraxellaceae	7.7	
Pseudomonadaceae	0.3				

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)
Horse Feces	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	1.6
				Other	34.1
	Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	6.9
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	0.2
				Streptococcaceae	0.7
		Clostridia	Clostridiales	Clostridiaceae	0.9
				Lachnospiraceae	0.9
				Ruminococcaceae	9.3
				Veillonellaceae	0.6
	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	0.3	
	Other	Other	Other	Other	2.6
	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	0.3
			Pseudomonadales	Moraxellaceae	1.4
	Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	17.0
Verrucomicrobia	Verruco-5	WCHB1-41	RFP12	10.0	

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)	
Pigeon Feces	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	5.3	
	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	0.3	
	Cyanobacteria	Chloroplast	Streptophyta	Other	0.7	
	Firmicutes	Bacilli	Bacillales	[Exiguobacteraceae]	0.2	
				Other	0.1	
				Paenibacillaceae	6.1	
			Lactobacillales	Enterococcaceae	8.8	
			Lactobacillaceae	17.5		
			Clostridia	Clostridiales	Veillonellaceae	8.0
			Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	0.8
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	0.8	
			Rhodobacterales	Rhodobacteraceae	0.5	
		Betaproteobacteria	Burkholderiales	Comamonadaceae	1.5	
				Oxalobacteraceae	4.1	
		Gammaproteobacteria		Alteromonadales	Alteromonadaceae	1.3
Enterobacteriales				Enterobacteriaceae	15.7	
Pseudomonadales				Moraxellaceae	12.2	
	Pseudomonadaceae	1.0				

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)
Goose Feces	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	2.4
	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	0.4
		Bacteroidia	Bacteroidales	Bacteroidaceae	2.9
		Other			1.2
	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	0.4	
	Cyanobacteria	Chloroplast	Streptophyta	Other	0.4
	Firmicutes	Bacilli	Bacillales	[Exiguobacteraceae]	0.3
				Paenibacillaceae	0.6
			Lactobacillales	Enterococcaceae	5.5
				Streptococcaceae	0.2
		Clostridia	Clostridiales	Clostridiaceae	9.1
				Lachnospiraceae	2.9
				Peptostreptococcaceae	9.0
				Ruminococcaceae	16.4
		Veillonellaceae	0.4		
		Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	4.3
	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	3.4
	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	2.1
		Betaproteobacteria	Burkholderiales	Comamonadaceae	0.7
				Oxalobacteraceae	0.2
		Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	1.0
Gammaproteobacteria		Aeromonadales	Aeromonadaceae	1.1	
			Enterobacteriales	Enterobacteriaceae	6.6
		Pseudomonadales	Moraxellaceae	7.5	
			Pseudomonadaceae	0.6	

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)		
Swallow Feces	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	0.6		
	Bacteroidetes	Bacteroidia	Bacteroidales	Other	0.2		
	Cyanobacteria	Chloroplast	Streptophyta	Other	1.0		
	Firmicutes	Bacilli		Bacillales	Other	14.4	
				Lactobacillales	Enterococcaceae	10.7	
		Lactobacillaceae	1.6				
		Streptococcaceae	0.9				
		Clostridia		Clostridiales	Clostridiaceae	0.9	
					Lachnospiraceae	0.4	
					Ruminococcaceae	0.7	
	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	0.1			
	Other	Other	Other	Other	11.8		
	Proteobacteria	Betaproteobacteria		Burkholderiales	Comamonadaceae	0.1	
					Oxalobacteraceae	0.3	
		Gammaproteobacteria			Alteromonadales	Alteromonadaceae	1.9
					Enterobacteriales	Enterobacteriaceae	25.6
Legionellales					Coxiellaceae	0.8	
Pseudomonadales					Moraxellaceae	2.2	
	Pseudomonadaceae	3.9					

Sample Type	Phylum	Class	Order	Family	Relative Abundance (%)		
Small Mammal Feces	Bacteroidetes	[Saprospirae]	[Saprospirales]	Chitinophagaceae	0.2		
		Bacteroidia	Bacteroidales	Bacteroidaceae	10.3		
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	0.5		
	Firmicutes	Bacilli		Bacillales	[Exiguobacteraceae]	5.2	
				Lactobacillales	Enterococcaceae	0.8	
		Clostridia		Clostridiales		Streptococcaceae	0.1
						Clostridiaceae	7.0
						Lachnospiraceae	4.5
						Peptostreptococcaceae	2.3
						Veillonellaceae	0.3
	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	9.8		
	Other	Other	Other	Other	1.0		
	Proteobacteria	Alphaproteobacteria		Rhizobiales	Hyphomicrobiaceae	1.2	
				Rhodobacterales	Rhodobacteraceae	1.7	
		Betaproteobacteria		Burkholderiales	Comamonadaceae	3.9	
		Epsilonproteobacteria		Campylobacterales	Campylobacteraceae	1.8	
		Gammaproteobacteria			Aeromonadales	Aeromonadaceae	2.4
					Alteromonadales	[Chromatiaceae]	1.3
						Alteromonadaceae	13.6
					Enterobacteriales	Enterobacteriaceae	5.9
Pseudomonadales					Moraxellaceae	1.9	
		Pseudomonadaceae	2.4				

25 Table S4: Families with notable contributions (i.e., relative contribution > 0.50%) to the dry weather water in Antelope Creek.

Source	Phylum	Class	Order	Family	Relative Contribution (%)			
Holmes Lake	Actinobacteria	Actinobacteria	Actinomycetales	ACK.M1	5.77			
				Microbacteriaceae	1.92			
				Other	1.04			
	Bacteroidetes	Saprospirae.	Saprospirales.	Saprospirales.	Chitinophagaceae	3.60		
					Cytophagia	Cytophagales	Cytophagaceae	1.53
					Flavobacteriia	Flavobacteriales	Flavobacteriaceae	2.74
					Cryomorphaceae	1.19		
					Sphingobacteriia	Sphingobacteriales	Other	1.83
	Cyanobacteria	Chloroplast	Stramenopiles	Other	Other	2.00		
					Oscillatoriothycideae	Chroococcales	Microcystaceae	2.82
	Proteobacteria	Alphaproteobacteria		Rhodobacterales	Rhodobacteraceae	1.14		
				Sphingomonadales	Sphingomonadaceae	0.81		
		Betaproteobacteria			Burkholderiales	Comamonadaceae	6.42	
						Oxalobacteraceae	0.92	
						Alcaligenaceae	0.85	
						Methylophilales	Methylophilaceae	0.91
						Rhodocyclales	Rhodocyclaceae	0.56
Gammaproteobacteria				Alteromonadales	Chromatiaceae.	1.68		
					Pseudomonadales	Pseudomonadaceae	0.60	
					Xanthomonadales	Xanthomonadaceae	1.46	
Streambed Sediment	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	0.51			

26

27 Table S5: Families with notable contribution (i.e., relative contribution > 0.50%) to the rising limb of wet weather water in Antelope
 28 Creek.

Source	Phylum	Class	Order	Family	Relative Contribution (%)
Storm Drain Outfall Water	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	2.75
				Microbacteriaceae	0.86
				Geodermatophilaceae	0.80
				Nocardiaceae	0.59
	Bacteroidetes	Saprospirae	Saprospirales	Chitinophagaceae	0.85
				Cytophagia	Cytophagales
		Flavobacteriia	Flavobacteriales	Weeksellaceae.	1.13
				Flavobacteriaceae	0.70
	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	3.37	
	Firmicutes	Bacilli	Bacillales	Exiguobacteraceae	1.31
				Paenibacillaceae	0.59
	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	1.08
				Rhizobiales	Rhizobiaceae
			Rhodobacterales	Hyphomicrobiaceae	0.57
				Rhodobacteraceae	6.26
				Acetobacteraceae	0.80
			Rhodospirillaceae	0.61	
		Sphingomonadales	Sphingomonadaceae	2.92	
		Betaproteobacteria	Burkholderiales	Oxalobacteraceae	5.74
				Comamonadaceae	5.13
		Gammaproteobacteria	Alteromonadales	Chromatiaceae.	0.89
Enterobacteriales				Enterobacteriaceae	2.88
Pseudomonadales			Moraxellaceae	8.47	
			Pseudomonadaceae	3.29	
Xanthomonadales	Xanthomonadaceae		0.98		
Unassigned	Unassigned	Unassigned	Unassigned	1.39	

29

30 Table S6: Families with notable contribution (i.e., relative contribution > 0.50%) the peak flow of wet weather water in Antelope
 31 Creek.

Source	Phylum	Class	Order	Family	Relative Contribution (%)			
Storm Drain Outfall Water	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	1.58			
				Microbacteriaceae	0.53			
	Bacteroidetes				Saprospirae.	Saprospirales	Chitinophagaceae	0.88
					Cytophagia	Cytophagales	Cytophagaceae	1.62
					Flavobacteriia	Flavobacteriales	Flavobacteriaceae	1.97
					Weeksellaceae.	0.79		
		Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	1.88			
	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	1.07			
	Proteobacteria	Alphaproteobacteria			Caulobacterales	Caulobacteraceae	0.80	
					Rhizobiales	Rhizobiaceae	1.18	
					Rhodobacterales	Rhodobacteraceae	3.41	
					Sphingomonadales	Sphingomonadaceae	2.57	
		Betaproteobacteria				Burkholderiales	Comamonadaceae	9.55
						Oxalobacteraceae	8.16	
						Neisseriales	Neisseriaceae	0.67
			Rhodocyclales	Rhodocyclaceae	0.70			
		Gammaproteobacteria				Aeromonadales	Aeromonadaceae	3.05
						Chromatiaceae.	2.44	
						Alteromonadaceae	0.54	
						Enterobacteriales	Enterobacteriaceae	5.94
						Pseudomonadales	Moraxellaceae	7.77
							Pseudomonadaceae	7.06
						Xanthomonadales	Xanthomonadaceae	0.99
Unassigned		Unassigned	Unassigned	Unassigned	0.69			

32

33 Table S7: Families with notable contribution (i.e., relative contribution > 0.50%) to the declining limb of wet weather water in
 34 Antelope Creek.

Source	Phylum	Class	Order	Family	Relative Contribution (%)	
Storm Drain Outfall Water	Bacteroidetes	Saprospirae.	Saprospirales.	Chitinophagaceae	1.04	
		Cytophagia	Cytophagales	Cytophagaceae	1.17	
		Flavobacteriia	Flavobacteriales	Flavobacteriaceae	5.71	
		Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	1.68	
	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadales	Sphingomonadaceae	2.66
			Rhodobacterales	Rhodobacterales	Rhodobacteraceae	1.70
			Rhizobiales	Rhizobiales	Rhizobiaceae	1.11
			Caulobacterales	Caulobacterales	Caulobacteraceae	0.80
		Betaproteobacteria	Rhodocyclales	Rhodocyclales	Rhodocyclaceae	0.83
			Burkholderiales	Comamonadaceae	Comamonadaceae	18.65
				Oxalobacteraceae	Oxalobacteraceae	5.05
			Gammaproteobacteria	Pseudomonadales	Pseudomonadales	Pseudomonadaceae
					Moraxellaceae	2.18
		Enterobacteriales		Enterobacteriales	Enterobacteriaceae	1.72
		Alteromonadales		Alteromonadales	Chromatiaceae.	1.51
		Aeromonadales		Alteromonadaceae	Alteromonadaceae	0.55
Aeromonadaceae	Aeromonadaceae		1.27			
Streambed Sediment	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	0.77	
Holmes Lake	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	1.24	

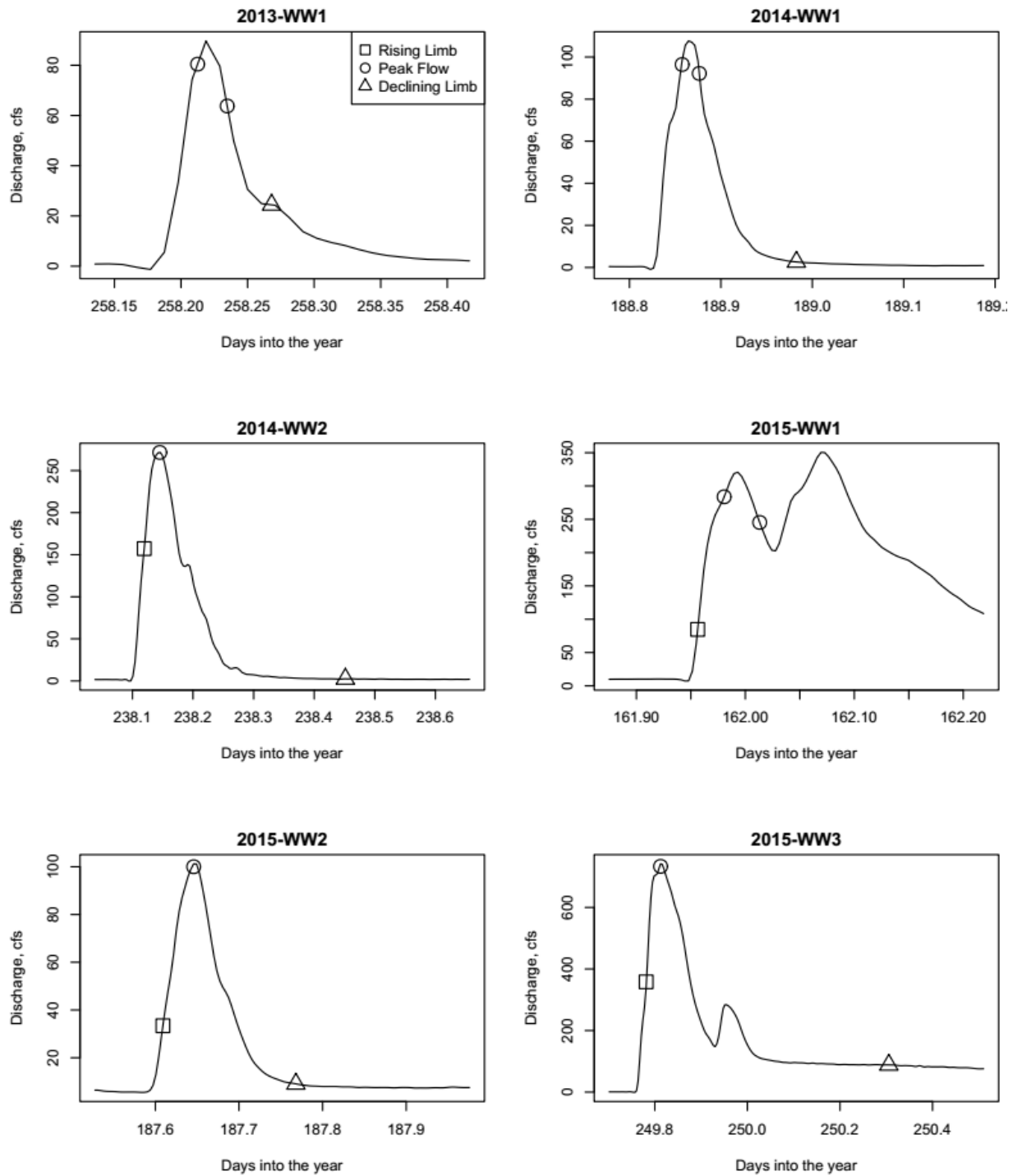
35

36 Table S8: Families with notable contribution (i.e., relative contribution > 0.50%) to the storm drain outfall water.

Kingdom	Phylum	Class	Order	Family	Relative Contribution (%)							
Street Sweepings	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	0.79							
				Geodermatophilaceae	0.61							
	Bacteroidetes				.Saprosirae.	Saprosirales	Chitinophagaceae	0.55				
					Cytophagia	Cytophagales	Cytophagaceae	1.05				
					Flavobacteriia	Flavobacteriales	Flavobacteriaceae	1.18				
					Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	1.60				
	Proteobacteria	Alphaproteobacteria			Caulobacterales	Caulobacteraceae	0.69					
					Rhizobiales	Rhizobiaceae	1.34					
						Hyphomicrobiaceae	0.60					
						Rhodobacterales	Rhodobacteraceae	4.07				
					Sphingomonadales	Sphingomonadaceae	2.17					
					Betaproteobacteria	Burkholderiales	Oxalobacteraceae	6.66				
							Comamonadaceae	5.62				
					Gammaproteobacteria				Enterobacteriales	Enterobacteriaceae	3.15	
									Pseudomonadales	Pseudomonadaceae	7.78	
	Moraxellaceae	1.79										
	Xanthomonadales	Xanthomonadaceae	0.58									
Unassigned	Unassigned	Unassigned	Unassigned	Unassigned	0.63							
Sanitary Sewage	Proteobacteria			Betaproteobacteria	Burkholderiales	Comamonadaceae	1.02					
				Gammaproteobacteria	Pseudomonadales	Moraxellaceae	0.87					
Unknown Source(s)	Bacteroidetes				.Saprosirae.	Saprosirales	Chitinophagaceae	0.52				
					Cytophagia	Cytophagales	Cytophagaceae	1.23				
					Flavobacteriia	Flavobacteriales	Flavobacteriaceae	0.90				
					Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	0.85				
	Proteobacteria	Alphaproteobacteria				Sphingomonadales	Sphingomonadaceae	0.77				
						Betaproteobacteria	Burkholderiales	Comamonadaceae	0.84			
								Oxalobacteraceae	0.73			
						Gammaproteobacteria				Alteromonadales	Chromatiaceae	0.76
										Pseudomonadales	Pseudomonadaceae	1.11
Moraxellaceae	0.98											

37

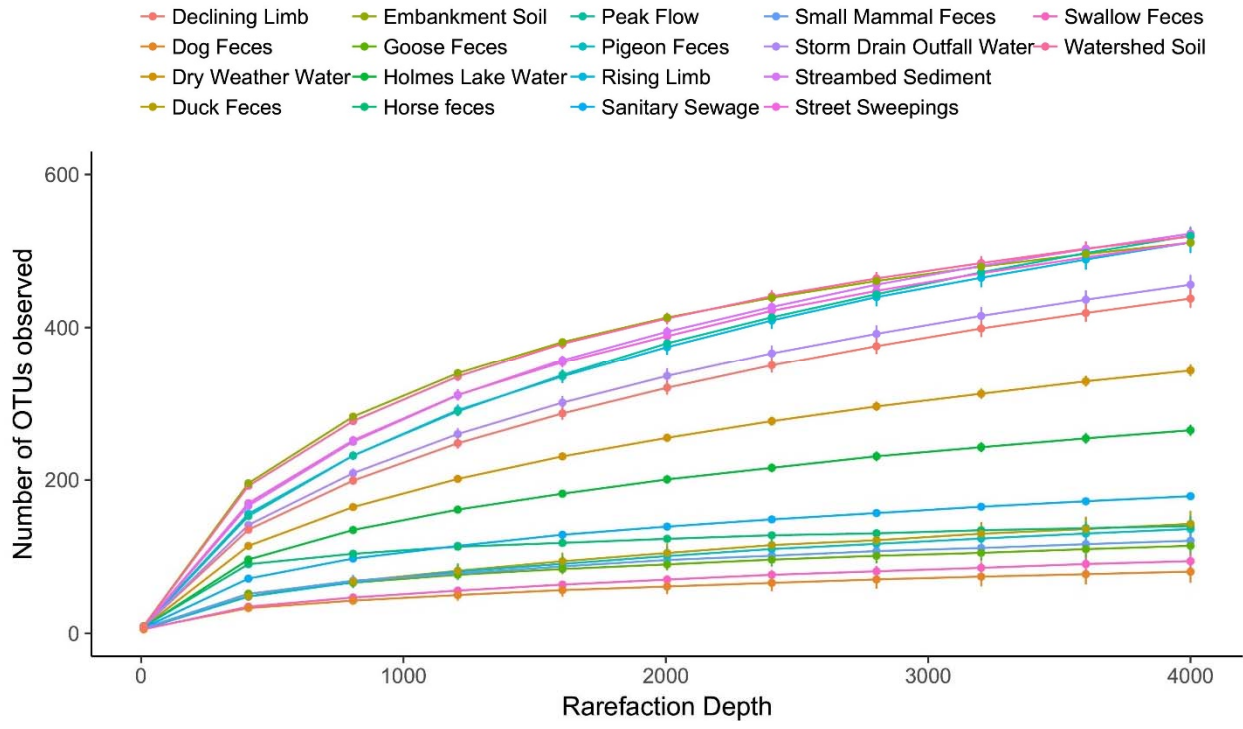
38 **FIGURES**



39

40 Figure S1: Hydrographs showing the times of sampling during the six wet weather events, one in

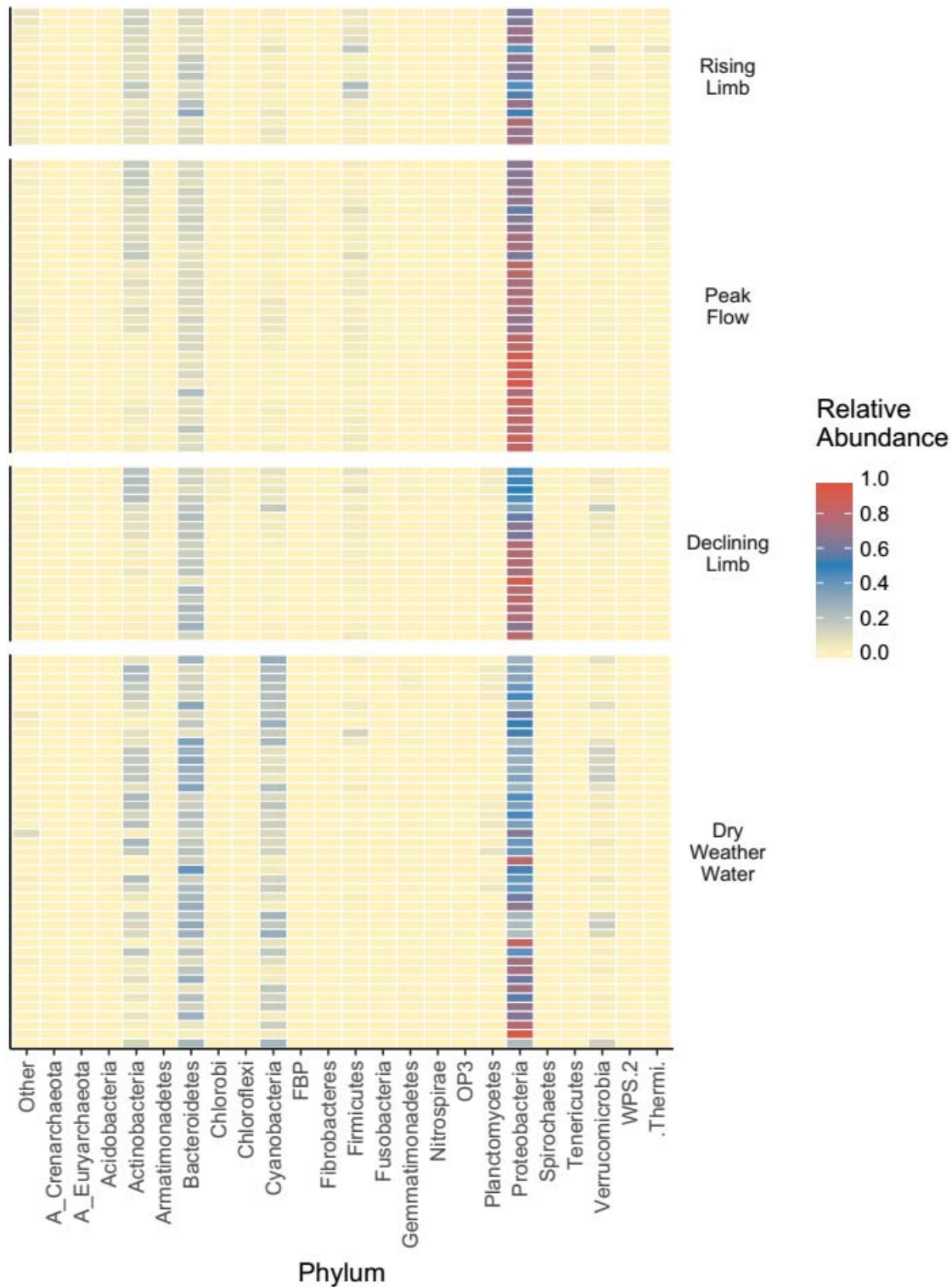
41 2013, two in 2014, and three in 2015.



42

43 Figure S2: Rarefaction curve showing the number of OTUs observed at different rarefaction

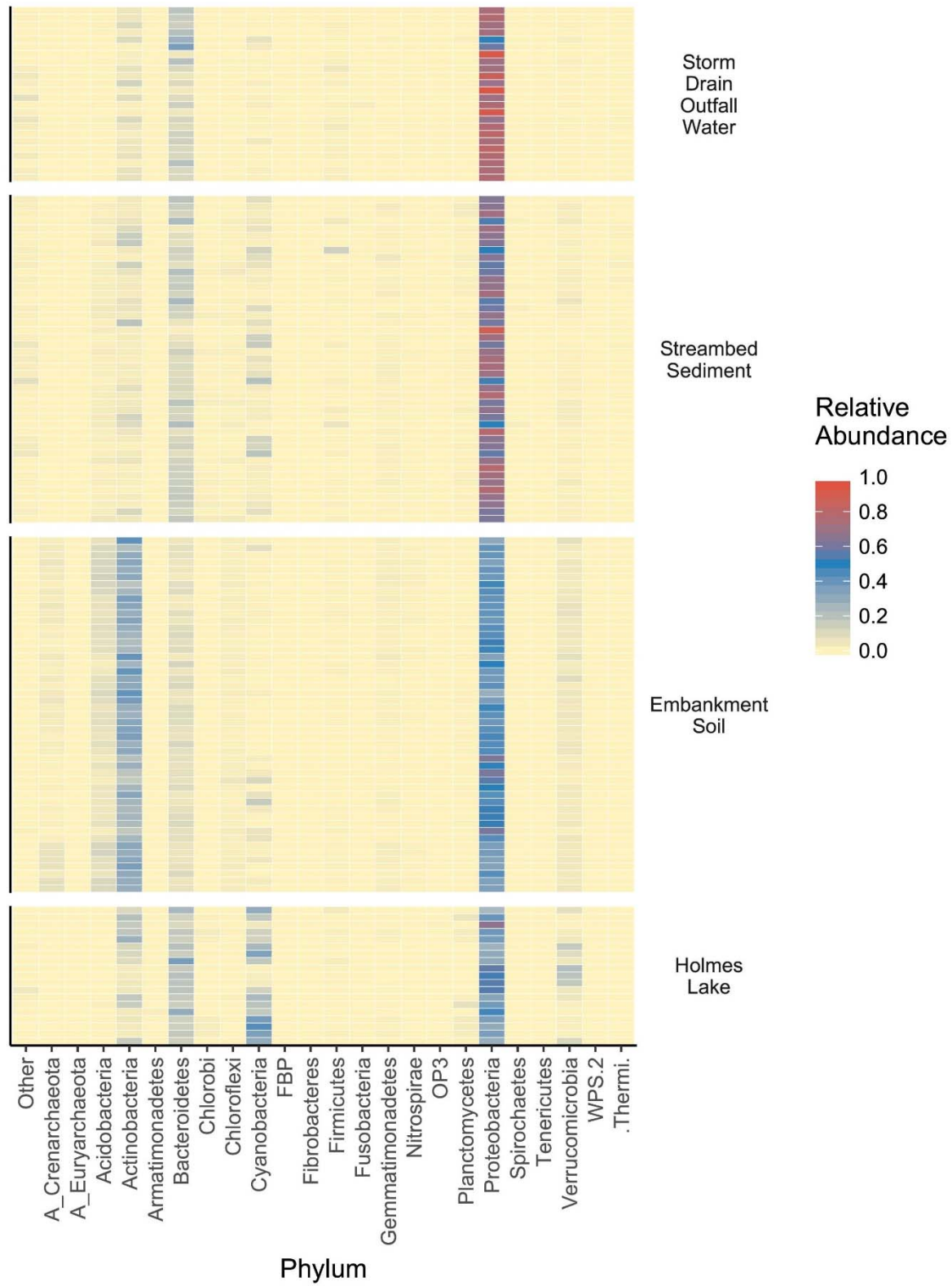
44 depths. Error bars represent 95% confidence interval.



45

46 Figure S3: Heat map showing the relative abundance of major phyla in individual dry and wet

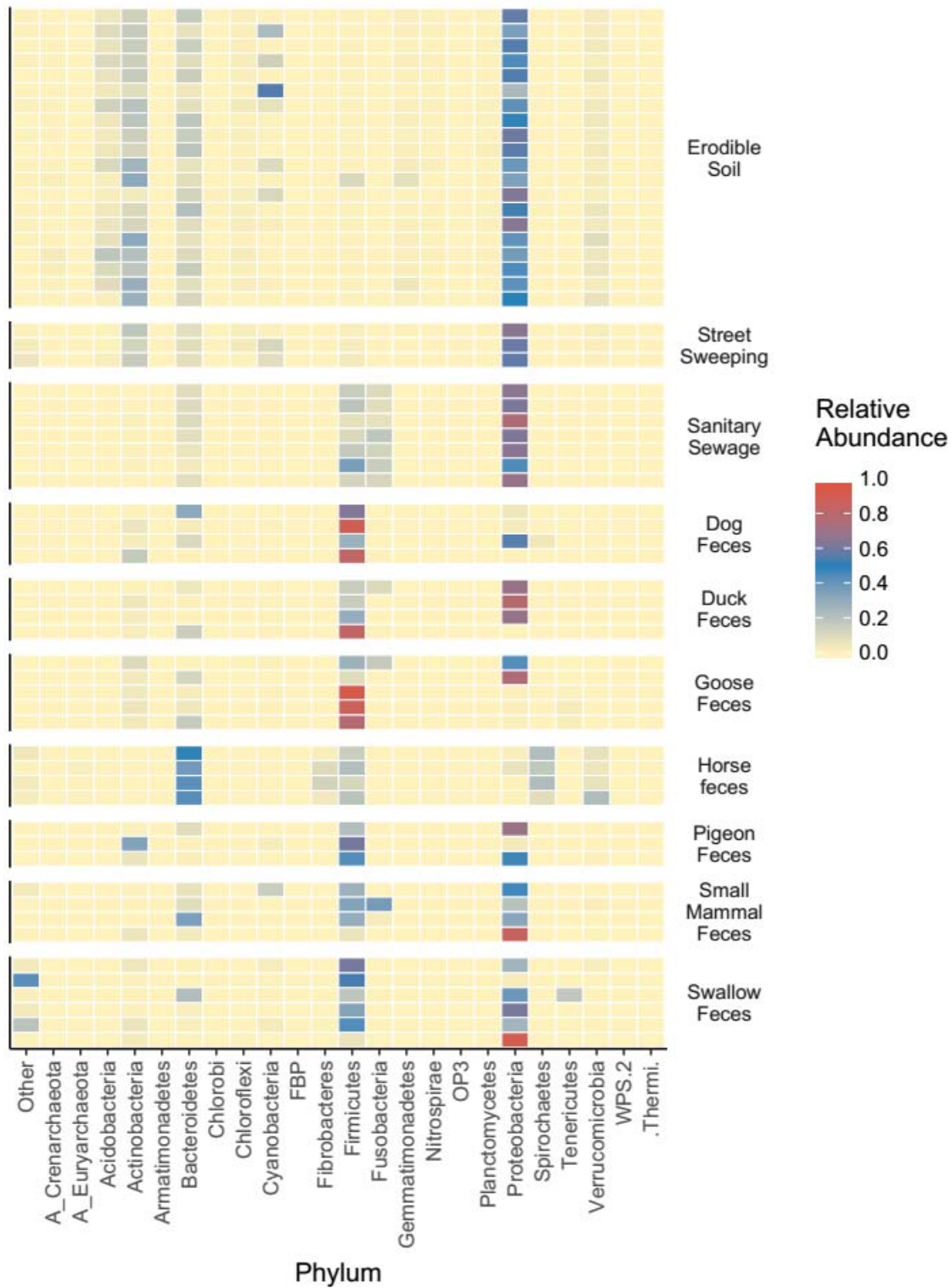
47 weather water samples.



48

49 Figure S4: Heat map showing the relative abundance of major phyla in individual storm drain

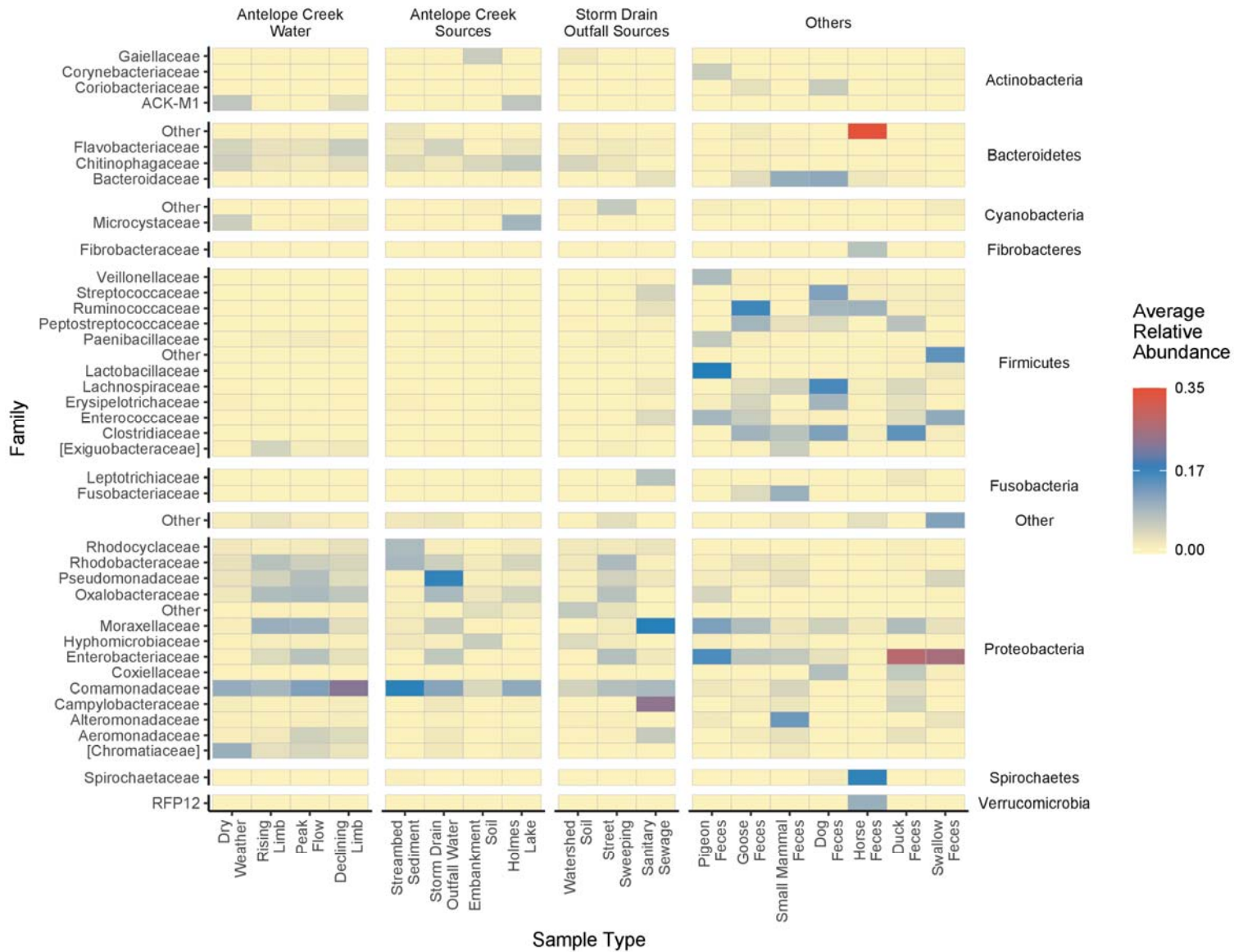
50 outfall, streambed sediment, embankment soil, and Holmes Lake samples.



51

52 Figure S5: Heat map showing the relative abundance of major phyla in individual erodible soil,

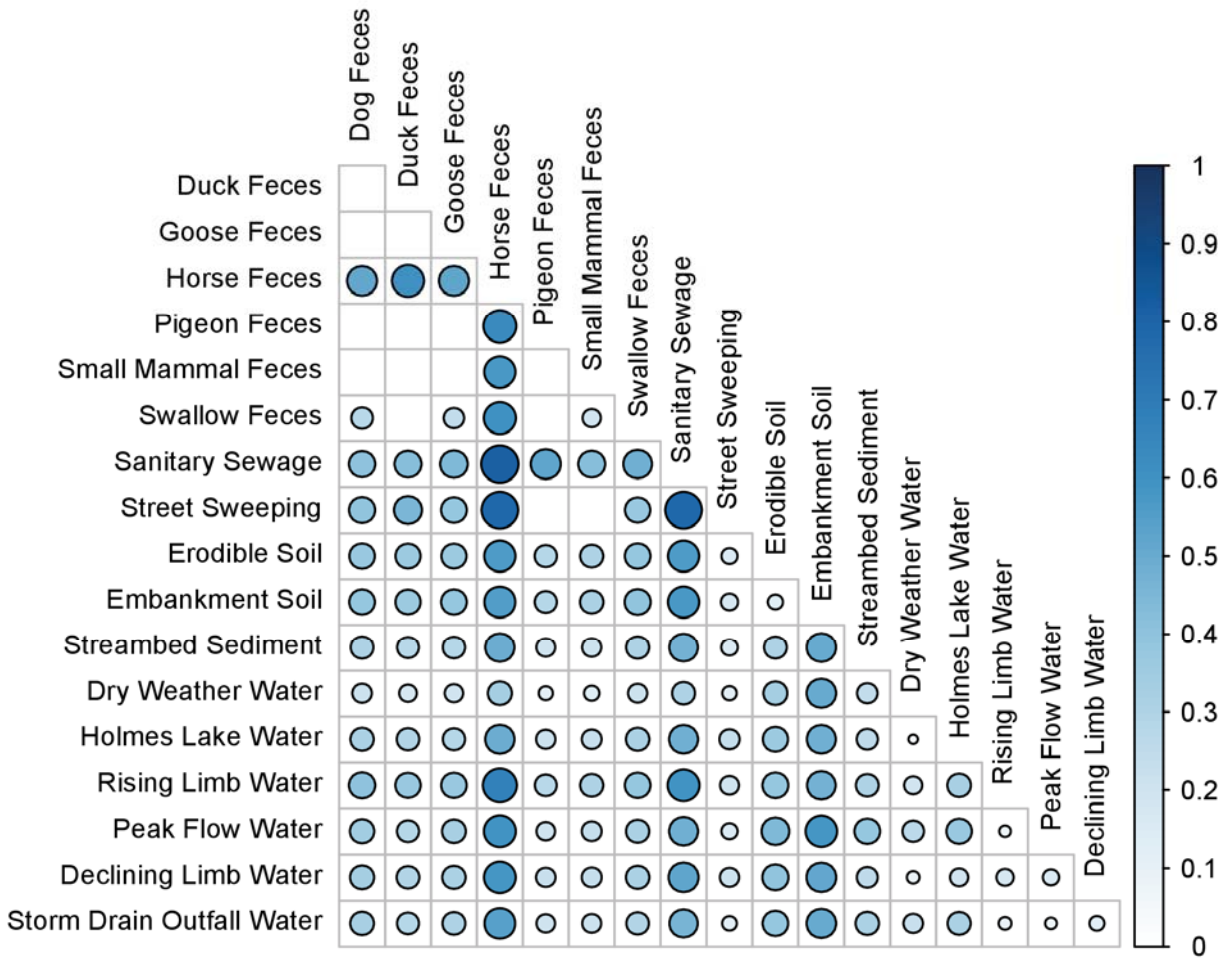
53 street sweeping and fecal samples.



54

55

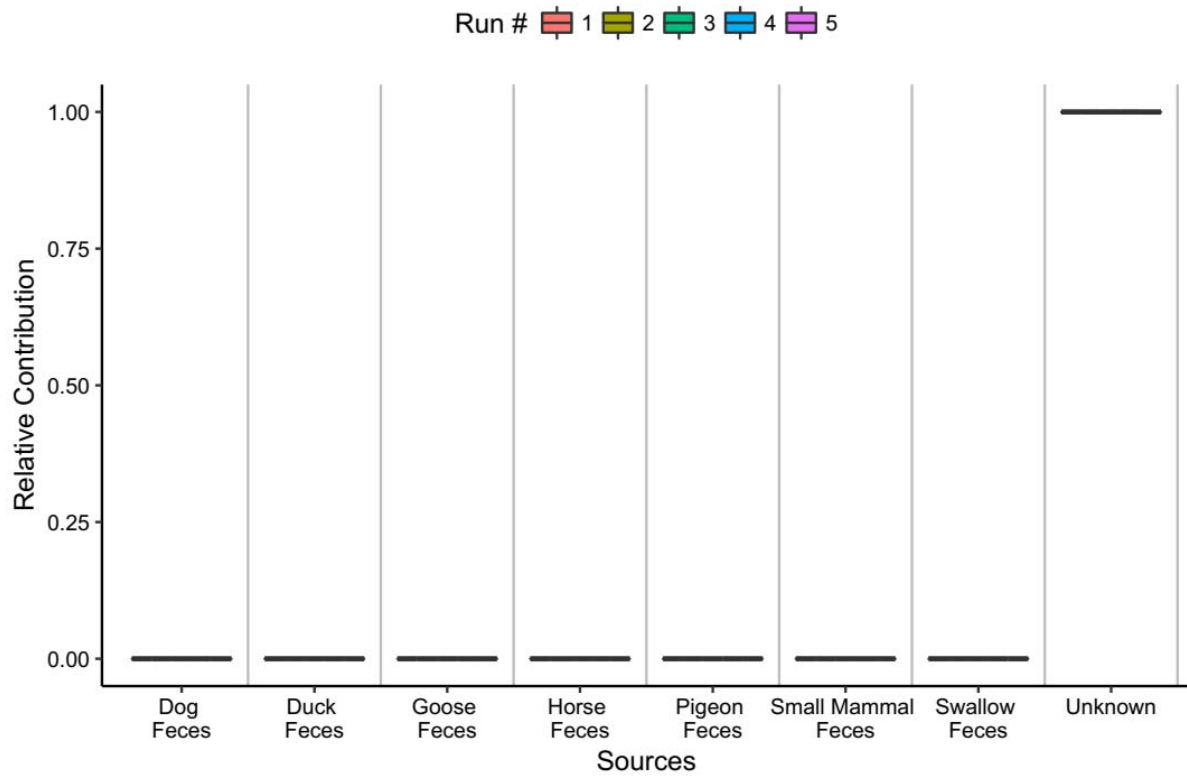
Figure S6: Heat map showing the families with relative abundance $\geq 0.5\%$ in at least one sample type.



56

57 Figure S7: Results of PERMANOVA based on weighted UniFrac distance showing the
 58 comparison of microbial composition between different sample types. Size and color of the
 59 circles both represent R^2 value. Circles are shown only for significant R^2 (Benjamini &
 60 Hochberg adjusted $p < 0.05$).

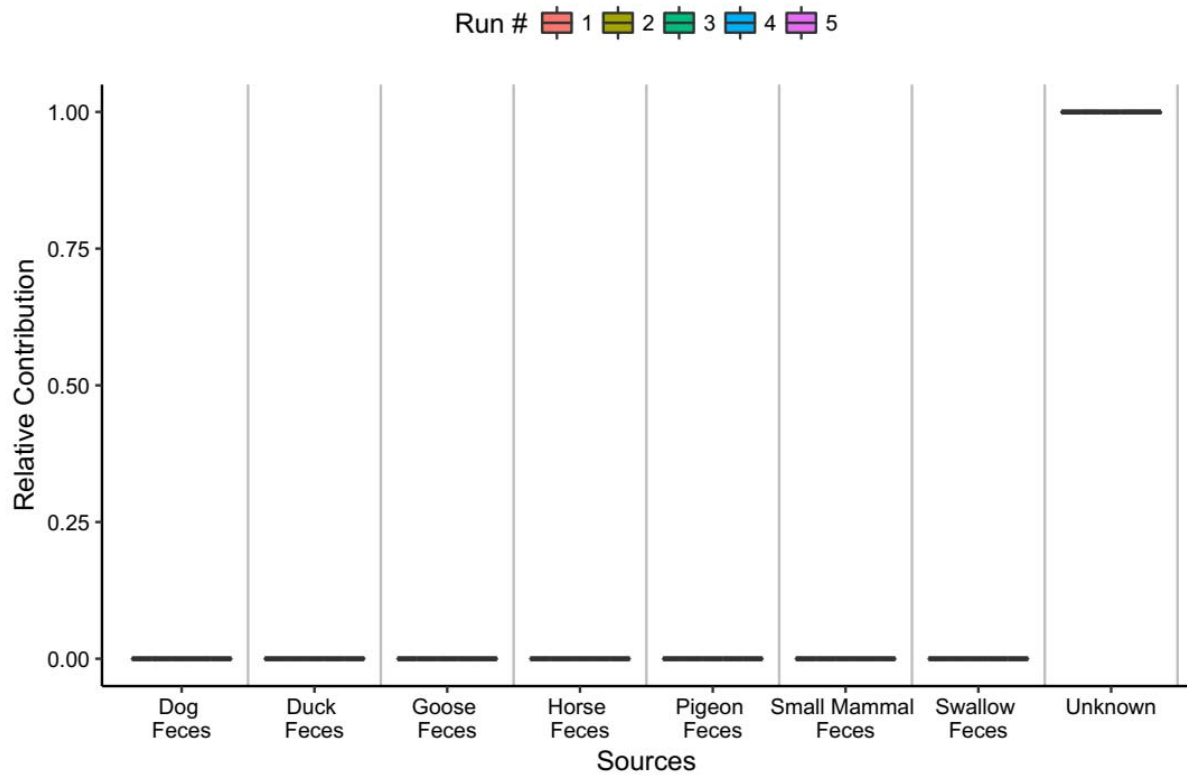
Embankment Soil



61

62 Figure S8: Five runs of SourceTracker analysis showing the relative contributions of potential
63 fecal sources to the overall microbial community in embankment soil.

Erodible Soil

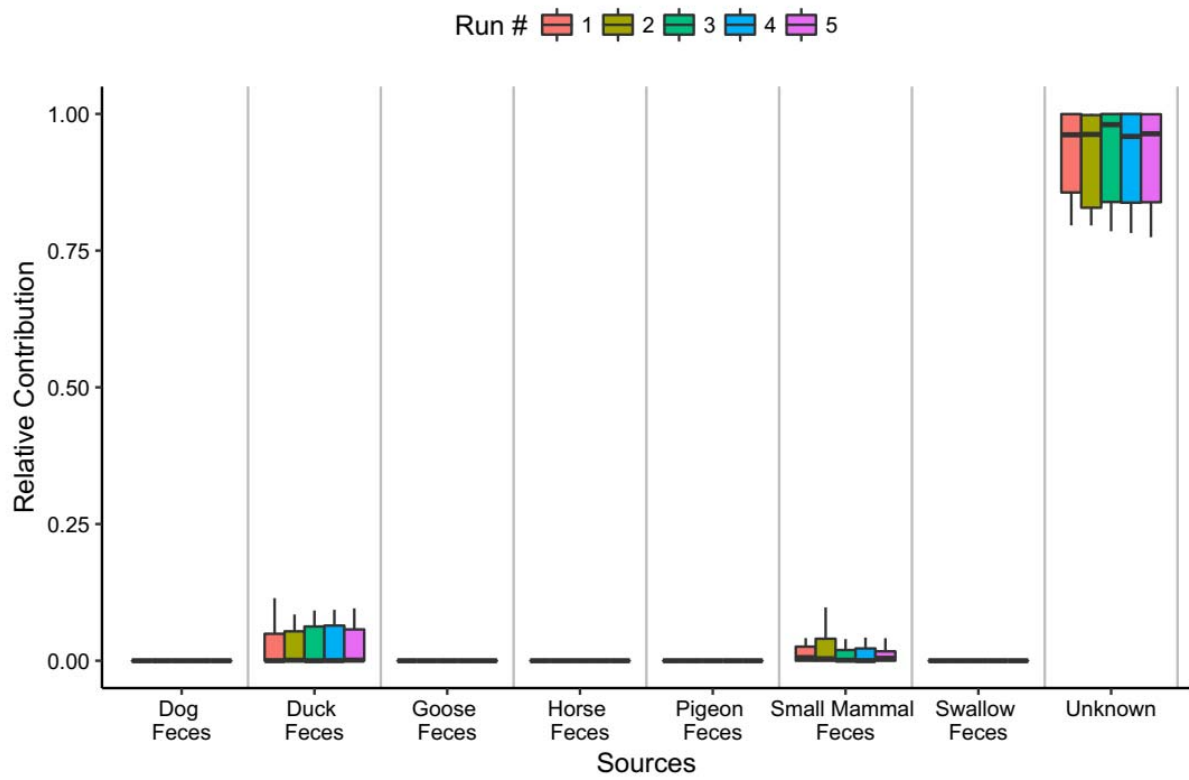


64

65 Figure S9: Five runs of SourceTracker analysis showing the relative contributions of potential

66 fecal sources to the overall microbial community in erodible soil.

Holmes Lake

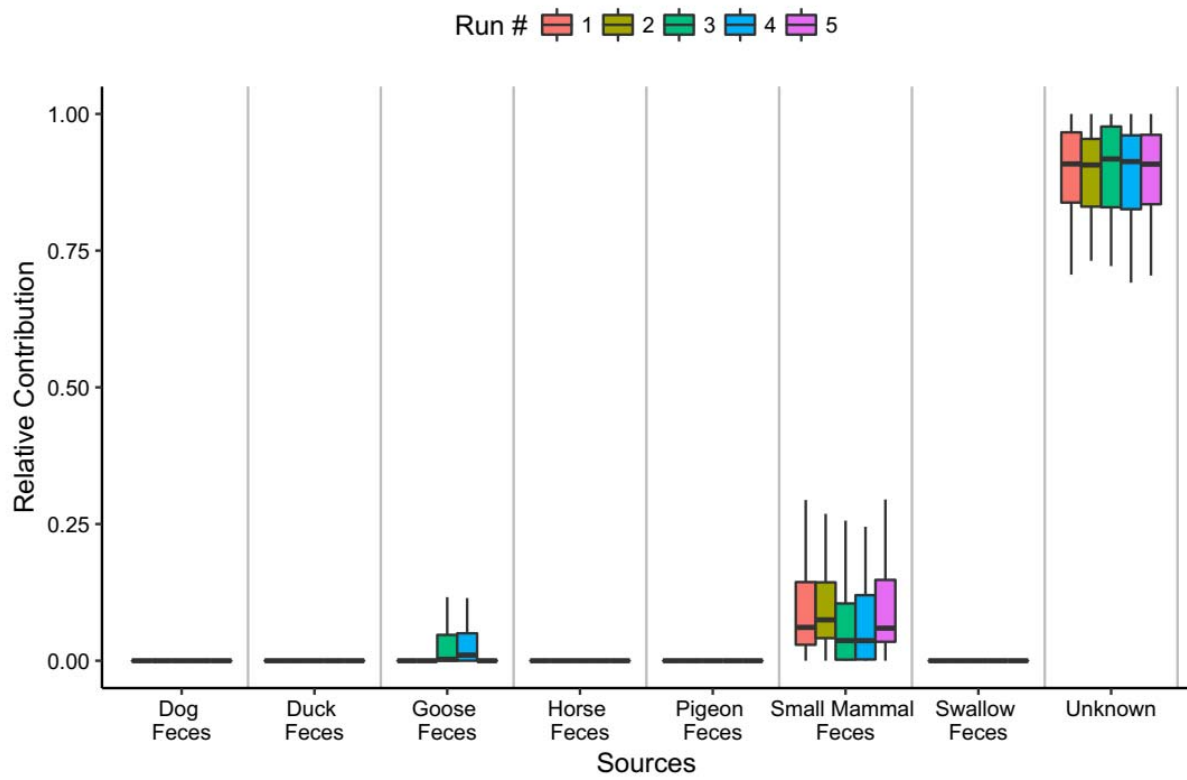


67

68 Figure S10: Five runs of SourceTracker analysis showing the relative contributions of potential

69 fecal sources to the overall microbial community in Holmes Lake.

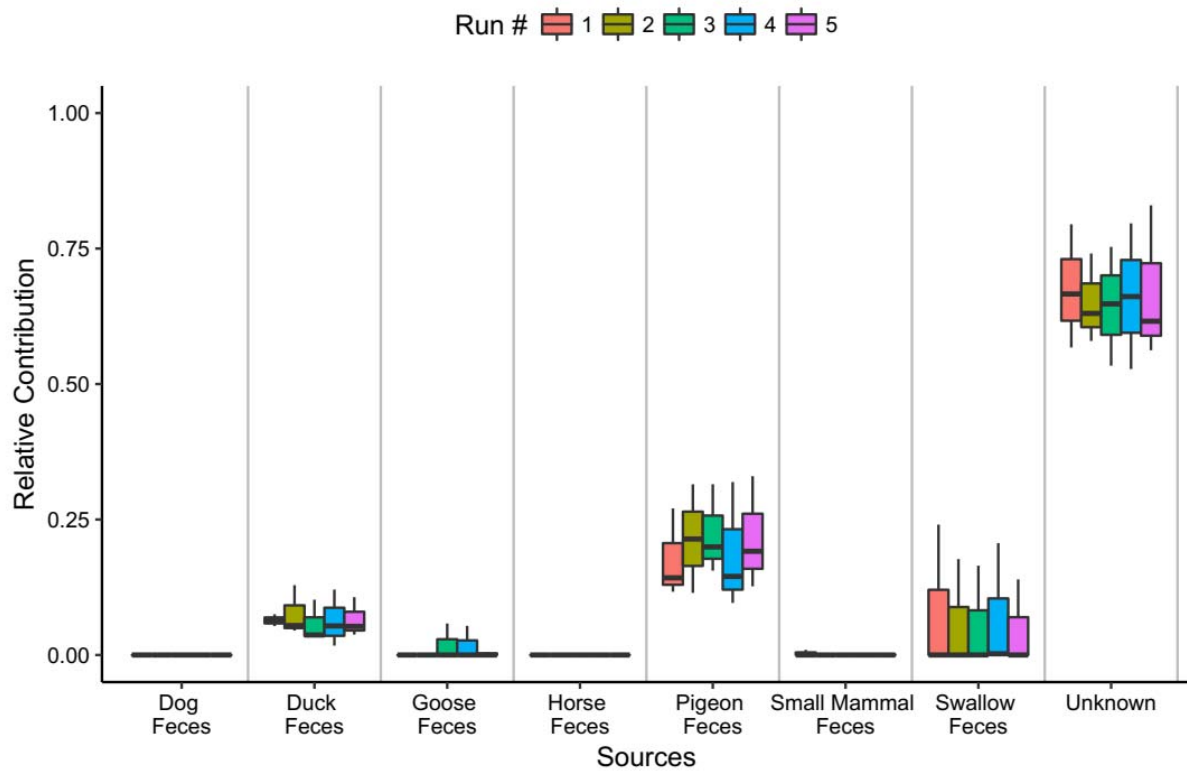
Streambed Sediment



70

71 Figure S11: Five runs of SourceTracker analysis showing the relative contributions of potential
72 fecal sources to the overall microbial community in streambed sediment.

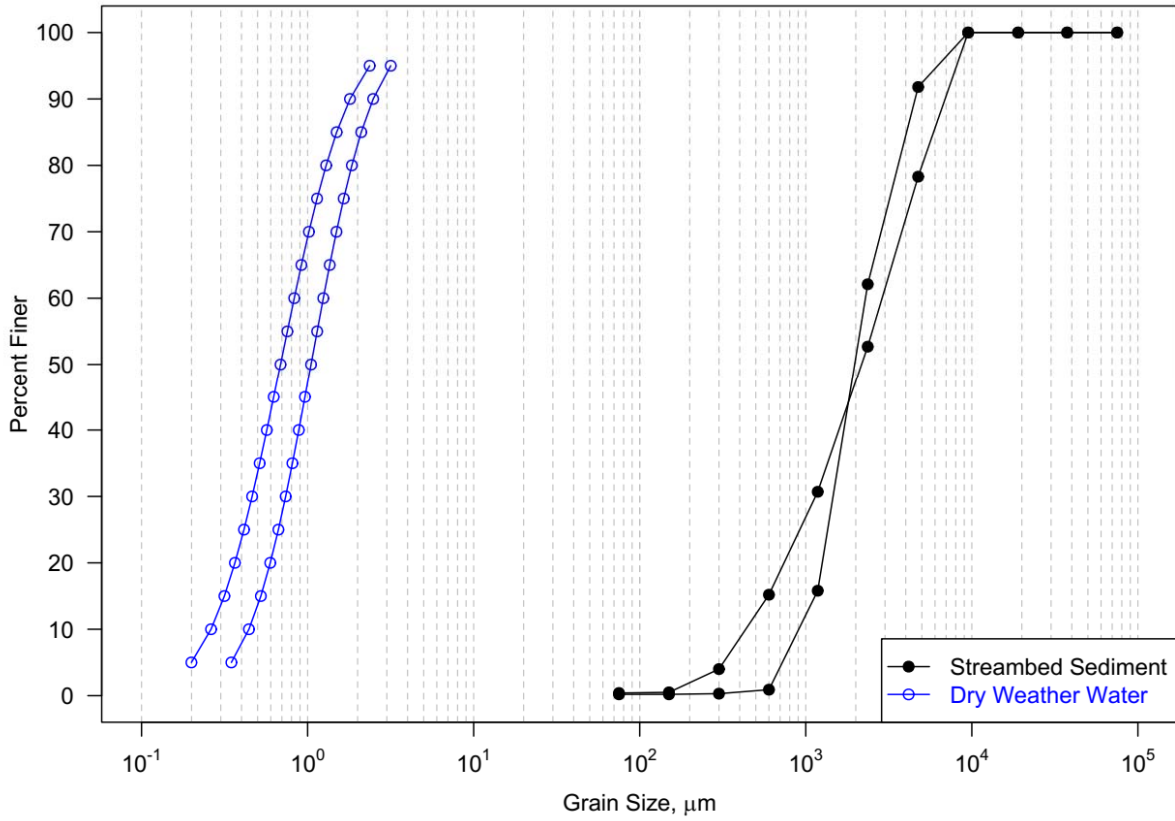
Street Sweepings



73

74 Figure S12: Five runs of SourceTracker analysis showing the relative contributions of potential

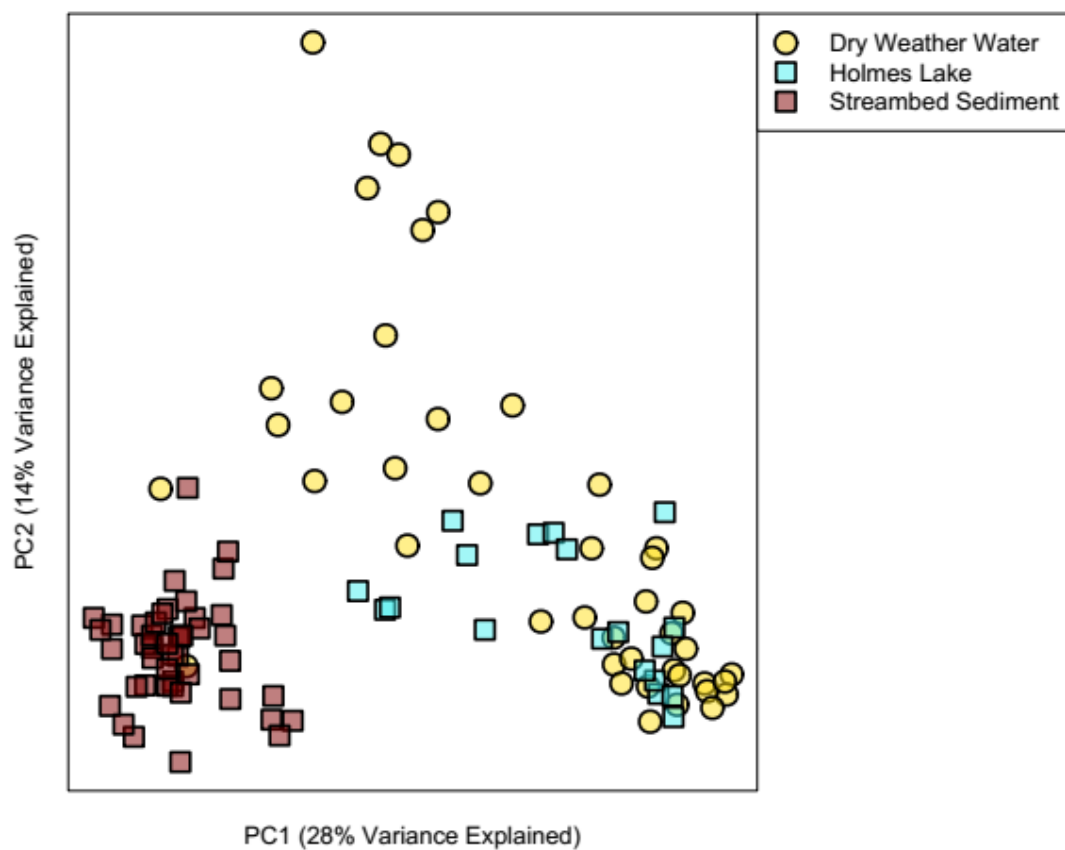
75 fecal sources to the overall microbial community in street sweeping.



76

77 Figure S13: Particle size analysis for typical dry weather water and streambed sediment samples

78 from Antelope Creek.



79

80 Figure S14: Principal coordinate analysis plot based on weighted UniFrac distance showing the
 81 relationship among the microbial communities in one sink environment (dry weather water) and
 82 two source environments (upstream reservoir Holmes Lake and streambed sediment).