4. Article Two, B.5- Water Quality Monitoring ("WQM") Plan – Report on whether any of the semi-annual (or annual) WQM required under Article Two, B.5, was conducted during the quarter, and if so, in which sewer basins, and report the results of that monitoring (both BST and fecal coliform) for each such sewer basin.

The 2016 semi-annual sampling round was collected December 15, 2016, when twenty of the twenty-six sewer basins were sampled. Human source fecal bacteria were identified by Quantitative Polymerase Chain Reaction (qPCR) testing in one or more samples from eighteen sewer basins.

On October 3, 2016, justification for a change to the WQM Plan was submitted to the Regulators. On October 6, 2016, WSSC made a verbal request to MDE and EPA for an expedited review and approval of the requested changes. Per the verbal request, library-dependent BOX-PCR analysis for Microbial Source Tracking (MST), used previously, can no longer be supported by WSSC's contract laboratory due to extenuating circumstances. WSSC requested use of library-independent MST source tracking methods based on qPCR, effective immediately. MDE approved the justification on November 21, 2016, and EPA approved the justification on December 13, 2016. Human sources were analyzed using two specific qPCR markers, an EPA Developed Assay and *B. dorei*. Avian sources were analyzed for one specific qPCR marker, Bird Fecal ID<sup>TM</sup>. Canine sources were analyzed for one specific qPCR marker, Dog Bacteroides ID<sup>TM</sup>. Other animal sources (e.g., horse, bovine, general ruminant etc.) are still undergoing qPCR methods development.

The 2017 annual round of water quality sampling is planned between April and June, and results will be reported in the Third Quarter of 2017.

a.

Broad Creek-	BST Results: Fecal	<b>Bacteria Results</b>
	(gene copies/100mL) (Enteroce	occus CCE/100ml
	qPCR Source Determination:	
DDC001 down stresser	Human Bacteroides (EPA) = <loq< td=""><td>2</td></loq<>	2
BRC001 – downstream	Human Bacteroides (Dorei) = <b>840</b>	132
(Henson Creek)	Bird Fecal $ID^{TM} = ND$	
	Dog Bacteroides $ID^{TM} = ND$	
	qPCR Source Determination:	
BBC002 unstream	Human Bacteroides $(EPA) = ND$	
BRC002 – upstream (Henson Creek)	Human Bacteroides (Dorei) = <lo< td=""><td>Q 413</td></lo<>	Q 413
	Bird Fecal $ID^{TM} = \langle LOQ \rangle$	
	Dog Bacteroides $ID^{TM} = \langle LOQ \rangle$	

## **Basins Subject to Semi-Annual Monitoring and Reporting Requirements:**

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents

b.	Cabin John-	<b>BST Results:</b>		teria Results:
		(gene copies/100mL)	(Enterococcus	s CCE/100ml)
		qPCR Source Determination	on:	
		Human Bacteroides (EPA	A) = ND	
	CBJ001 – downstream	Human Bacteroides (Dor	ei) = ND	82
		Bird Fecal $ID^{TM} = ND$		
		Dog Bacteroides ID <sup>TM</sup> =	ND	
		qPCR Source Determination	on:	
		Human Bacteroides (EPA	A) = ND	
	CBJ002 – upstream	Human Bacteroides (Dor	ei) = <loq< td=""><td>99</td></loq<>	99
	_	Bird Fecal $ID^{TM} = ND$		
		Dog Bacteroides ID <sup>TM</sup> =	ND	

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents

c.	Horsepen-	<b>BST Results:</b>	Fecal Bac	teria Results:
		(gene copies/100mL)	(Enterococcus	s CCE/100ml)
		qPCR Source Determination	qPCR Source Determination:	
		Human Bacteroides (EPA	A) = ND	
	HSP001 – downstream	Human Bacteroides (Dor	ei) = ND	144
		Bird Fecal $ID^{TM} = ND$		
		Dog Bacteroides ID <sup>TM</sup> =	ND	
		qPCR Source Determination	on:	
		Human Bacteroides (EPA	A) = ND	
	HSP002 – upstream	Human Bacteroides (Dor	ei) = ND	186
		Bird Fecal $ID^{TM} = ND$		
		Dog Bacteroides ID <sup>TM</sup> =	ND	

d.

e.

Indian Creek-	BST Results: Fo	ecal Bacteria Results:
	(gene copies/100mL) (Ente	rococcus CCE/100ml)
	qPCR Source Determination:	
	Human Bacteroides (EPA) = $<$ I	LOQ
INC001 – downstream	Human Bacteroides (Dorei) = 1	<b>,090</b> 740
	Bird Fecal $ID^{TM} = 631$	
	Dog Bacteroides $ID^{TM} = ND$	
	qPCR Source Determination:	
	Human Bacteroides (EPA) = N	D
INC002 – upstream	Human Bacteroides (Dorei) = N	ND 257
_	Bird Fecal $ID^{TM} = \langle LOQ \rangle$	
	Dog Bacteroides $ID^{TM} = ND$	

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents

Little Falls-	<b>BST Results:</b>	Fecal Bac	teria Results:
	(gene copies/100mL)	(Enterococcus	s CCE/100ml)
	qPCR Source Determinatio	n:	
	Human Bacteroides (EPA	$A = \langle LOQ \rangle$	
LFS001 – downstream	Human Bacteroides (Dor	ei) = <b>1,180</b>	1,354
	Bird Fecal $ID^{TM} = \langle LOQ \rangle$		
	Dog Bacteroides ID <sup>TM</sup> =	<loq< td=""><td></td></loq<>	
	qPCR Source Determinatio	n:	
	Human Bacteroides (EPA	(A) = 380	
LFS002 – upstream	Human Bacteroides (Dor	ei) = <b>1,900</b>	6,236
	Bird Fecal $ID^{TM} = \langle LOQ \rangle$		
	Dog Bacteroides ID <sup>TM</sup> =	<loq< td=""><td></td></loq<>	

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents

Lower Anacostia-	<b>BST Results:</b>	Fecal Bact	teria Results:
	(gene copies/100mL)	(Enterococcus	CCE/100ml)
	qPCR Source Determination	on:	
	Human Bacteroides (EPA	A) = <b>1,550</b>	
ANA001 – downstream	Human Bacteroides (Dor	ei) = <b>23,500</b>	703
	Bird Fecal $ID^{TM} = 753$		
	Dog Bacteroides ID <sup>TM</sup> =	ND	
	qPCR Source Determination	on:	
	Human Bacteroides (EPA	A) = <b>2,580</b>	
ANA002 – upstream	Human Bacteroides (Dor	ei) = <b>27,500</b>	800
	Bird Fecal $ID^{TM} = 256$		
	Dog Bacteroides ID <sup>TM</sup> =	<loq< td=""><td></td></loq<>	

g.	Lower Beaverdam Creek	BST Results:	<b>Fecal Bac</b>	teria Results:
		(gene copies/100mL)	(Enterococcus	s CCE/100ml)
	LBD001 – downstream	qPCR Source Determination:		8,345
	LDD001 – downstream	Human Bacteroides (EPA	A) = <b>740</b>	0,545

h.

i.

	Human Bacteroides (Dorei) = $4,180$ Bird Fecal ID <sup>TM</sup> = $778$ Dog Bacteroides ID <sup>TM</sup> = ND	
LBD002 – upstream	qPCR Source Determination:Human Bacteroides (EPA) = NDHuman Bacteroides (Dorei) = $<$ LOQBird Fecal ID <sup>TM</sup> = 354Dog Bacteroides ID <sup>TM</sup> = ND	1,889

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents

Muddy Branch-	BST Results:	Fecal Bacteria Results:
-	(gene copies/100mL) (	Enterococcus CCE/100ml)
	qPCR Source Determination	:
	Human Bacteroides (EPA)	= ND
MDB001 – downstream	Human Bacteroides (Dorei	) = ND 40
	Bird Fecal $ID^{TM} = ND$	
	Dog Bacteroides $ID^{TM} = N$	D
	qPCR Source Determination	
	Human Bacteroides (EPA)	= ND
MDB002 – upstream	Human Bacteroides (Dorei	) = < LOQ 197
	Bird Fecal $ID^{TM} = \langle LOQ \rangle$	
	Dog Bacteroides $ID^{TM} = <$	LOQ

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents

Northeast Branch-	<b>BST Results:</b>	Fecal Bacteria Results
	(gene copies/100mL)	(Enterococcus CCE/100ml)
	qPCR Source Determinatio	on:
	Human Bacteroides (EPA	A) = <b>429</b>
NEB001 – upstream	Human Bacteroides (Dor	ei) = <b>5,950</b> 259
	Bird Fecal $ID^{TM} = \langle LOQ \rangle$	
	Dog Bacteroides ID <sup>TM</sup> =	<loq< td=""></loq<>
	qPCR Source Determinatio	on:
	Human Bacteroides (EPA	A) = 287
NEB002 – downstream	Human Bacteroides (Dor	ei) = <b>3,650</b> 188
	Bird Fecal $ID^{TM} = \langle LOQ \rangle$	
	Dog Bacteroides $ID^{TM} = $	<loq< td=""></loq<>

j.	Northwest Branch-	BST Results:	<b>Fecal Bac</b>	teria Results:
		(gene copies/100mL)	(Enterococcus	CCE/100ml)
		qPCR Source Determination:		
		Human Bacteroides (EPA)	) = 4,510	
	NWA001 – downstream	Human Bacteroides (Dore	i) = <b>40,800</b>	1,196
		Bird Fecal $ID^{TM} = \langle LOQ \rangle$		
		Dog Bacteroides ID <sup>TM</sup> = <	LOQ	
	NWA002 – upstream	qPCR Source Determination	n:	149

l.

Human Bacteroides (EPA) = ND	
Human Bacteroides (Dorei) = ND	
Bird Fecal $ID^{TM} = ND$	
Dog Bacteroides $ID^{TM} = \langle LOQ \rangle$	
	• 1 .

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents

k.	Oxon Run-	<b>BST Results:</b>	Fecal Bacteria Results:
		(gene copies/100mL)	(Enterococcus CCE/100ml)
		qPCR Source Determination	on:
	OXN001 – downstream	Human Bacteroides (EPA	(A) = 2,570
		Human Bacteroides (Dorei) = $44,900$	rei) = <b>44,900</b> 389
	(Oxon Run)	Bird Fecal $ID^{TM} = ND$	
		Dog Bacteroides ID <sup>TM</sup> =	<loq< td=""></loq<>
	OVN002 upstroom	qPCR Source Determination	on:
	OXN002 – upstream	Human Bacteroides (EPA	A) = <b>367</b>
	(Watts Branch,	Human Bacteroides (Dor	rei) = <b>1,590</b> 213
	tributary to	Bird Fecal $ID^{TM} = ND$	
	Anacostia River)	Dog Bacteroides ID <sup>TM</sup> =	874

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents

Paint Branch-	<b>BST Results:</b>	Fecal Bacte	eria Results
	(gene copies/100mL)	(Enterococcus (	CCE/100ml)
	qPCR Source Determination		
	Human Bacteroides (EPA)	= ND (ND)	
PNT001 – downstream	Human Bacteroides (Dorei	= ND (ND)	147 (113)
	Bird Fecal $ID^{TM} = ND$ (ND	))	
	Dog Bacteroides $ID^{TM} = N$	D (ND)	
	qPCR Source Determination		
	Human Bacteroides (EPA)	= 260	
PNT002 – upstream	Human Bacteroides (Dorei	) = 5,600	140
	Bird Fecal $ID^{TM} = \langle LOQ \rangle$		
	Dog Bacteroides $ID^{TM} = N$	D	

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents Note: Values in parentheses for station PNT001 are for field duplicate sample.

m.	Parkway-	<b>BST Results:</b>	<b>Fecal Bac</b>	teria Results:
		(gene copies/100mL)	(Enterococcus	r CCE/100ml)
		qPCR Source Determinatio	n:	
	PKY001 – downstream	Human Bacteroides (EPA	$A = \langle LOQ \rangle$	
		Human Bacteroides (Dore	ei) = <b>683</b>	125
	(Bear Branch)	Bird Fecal $ID^{TM} = 307$		
		Dog Bacteroides ID <sup>TM</sup> = 1	ND	
		qPCR Source Determinatio	n:	
	PKY002 – upstream	Human Bacteroides (EPA	A = ND	140
	(Walker Branch)	Human Bacteroides (Dore	ei) = ND	140
		Bird Fecal ID <sup>TM</sup> = ND		

0.

p.

	Dog Bacteroides $ID^{TM} = ND$	
$\overline{ND} = Not Detected, $	low limit of quantitation, CCE = Calibrator Cell Eq	uivalents

n.	Piscataway-	<b>BST Results:</b>	Fecal Bact	eria Results:
		(gene copies/100mL)	(Enterococcus	CCE/100ml)
	qPCR Source Determination:			
		Human Bacteroides (EPA	A = ND (ND)	
	PSW001 – downstream	Human Bacteroides (Dor	ei) = ND (ND)	111 (178)
		Bird Fecal $ID^{TM} = \langle LOQ (\langle LOQ \rangle) \rangle$		
		Dog Bacteroides ID <sup>TM</sup> =	ND (ND)	
		qPCR Source Determination	on:	
		Human Bacteroides (EPA	A) = ND	
	PSW002 – upstream	Human Bacteroides (Dorei) = ND		93
		Bird Fecal $ID^{TM} = \langle LOQ \rangle$		
		Dog Bacteroides ID <sup>TM</sup> =	ND	

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents Note: Values in parentheses for station PSW001 are for field duplicate sample.

Rock Creek-	BST Results:	<b>Fecal Bacte</b>	ria Results:
	(gene copies/100mL)	(Enterococcus CCE/100n	
	qPCR Source Determination	1:	
	Human Bacteroides (EPA)	) = 423 (410)	
RKC001 – downstream	Human Bacteroides (Dorei)	= 8,840 (9,070)	317 (248)
	Bird Fecal ID <sup>TM</sup> = $<$ LOQ ( $<$ LOQ)		```
	Dog Bacteroides $ID^{TM} = N$	teroides $ID^{TM} = ND (\langle LOQ \rangle)$	
	qPCR Source Determination	1:	
	Human Bacteroides (EPA)	) = ND	
RKC002 – upstream	Human Bacteroides (Dore	i) = ND	256
-	Bird Fecal $ID^{TM} = \langle LOQ \rangle$		
	Dog Bacteroides $ID^{TM} = N$	١D	

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents Note: Values in parentheses for station RKC001 are for field duplicate sample.

Seneca Creek-	BST Results:	Fecal Bacteria Resu	
	(gene copies/100mL)	(Enterococcus	CCE/100ml)
	qPCR Source Determination	n:	
SNC001 – downstream	Human Bacteroides (EPA	A = < LOQ	
	Human Bacteroides (Dor	ei) = <b>694</b>	48
(Seneca Creek)	Bird Fecal $ID^{TM} = ND$		
	Dog Bacteroides ID <sup>TM</sup> =	ND	
	qPCR Source Determination	n:	
SNIC002 unstraam	Human Bacteroides (EPA	$\Lambda$ ) = ND	
SNC002 – upstream	Human Bacteroides (Dor	ei) = ND	191
(Dry Seneca Creek)	Bird Fecal $ID^{TM} = ND$		
	Dog Bacteroides ID <sup>TM</sup> =	<loq< td=""><td></td></loq<>	

r.

q.	Sligo Creek-	BST Results: Fecal H	Bacteria Results:
		(gene copies/100mL) (Enterococ	<i>cus</i> CCE/100ml)
		qPCR Source Determination:	
		Human Bacteroides (EPA) = <loq< td=""><td></td></loq<>	
	SLC001 – downstream	Human Bacteroides (Dorei) = $2,480$	419
		Bird Fecal $ID^{TM} = \langle LOQ \rangle$	
		Dog Bacteroides $ID^{TM} = \langle LOQ \rangle$	
		qPCR Source Determination:	
		Human Bacteroides (EPA) = ND	
	SLC002 – upstream Human Bacteroides (Dorei) = <loq< td=""><td>282</td></loq<>		282
	-	Bird Fecal $ID^{TM} = ND$	
		Dog Bacteroides $ID^{TM} = ND$	

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents

Upper Beaverdam Creek-	BST Results: Fe	cal Bac	cteria Results:
	(gene copies/100mL) (Enter	ососси	s CCE/100ml)
	qPCR Source Determination:		
	Human Bacteroides (EPA) = <l< td=""><td>.OQ</td><td></td></l<>	.OQ	
UBD001 – downstream	Human Bacteroides (Dorei) = $4$ ,	010	3,625
	Bird Fecal $ID^{TM} = \langle LOQ \rangle$		
	Dog Bacteroides ID <sup>TM</sup> = ND		
	qPCR Source Determination:		
	Human Bacteroides (EPA) = $33$	6	
UBD002 – upstream	Human Bacteroides (Dorei) = <b>12,500</b>		1,316
	Bird Fecal $ID^{TM} = \langle LOQ \rangle$		
	Dog Bacteroides ID <sup>TM</sup> = ND		

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents

s.	Watts Branch-	<b>BST Results:</b>	Fecal Bact	eria Results:
		(gene copies/100mL)	(Enterococcus	CCE/100ml)
		qPCR Source Determination:		
	WTB001 – downstream	Human Bacteroides (EPA	A = ND	
		Human Bacteroides (Dore	ei) = <loq< td=""><td>139</td></loq<>	139
	(Watts Branch)	Bird Fecal $ID^{TM} = \langle LOQ \rangle$ Dog Bacteroides $ID^{TM} = ND$		
		qPCR Source Determination	n:	
	WTB002 upstroom	Human Bacteroides (EPA	A = ND (ND)	
	WTB002 – upstream (Sandy Branch)	Human Bacteroides (Dore	ei) = ND(ND)	(ND) (ND) 184 (97)
	(Salidy Branch)	Bird Fecal $ID^{TM} = ND (ND)$ Dog Bacteroides $ID^{TM} = ND (ND)$		

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents Note: Values in parentheses for station WTB002 are for field duplicate sample. 4<sup>th</sup> Quarter 2016 WSSC Consent Decree – Civil Action No. PJM-04-3679

Western Branch-	<b>BST Results:</b>	Fecal Bact	eria Results:
	(gene copies/100mL)	(Enterococcus	CCE/100ml)
	qPCR Source Determination:		
	Human Bacteroides (EPA	A) = <b>15,700</b>	
		(13,000)	10.000
WNB001 – downstream	Human Bacteroides (Dor	rei) = <b>171,000</b>	10,090
		(161,000)	(6,893)
	Bird Fecal $ID^{TM} = \langle LOQ \rangle$	Q ( <loq)< td=""><td></td></loq)<>	
	Dog Bacteroides ID <sup>TM</sup> =	<loq (<loq)<="" td=""><td></td></loq>	
	qPCR Source Determination	on:	
	Human Bacteroides (EPA	A) = ND	
WNB002 – upstream	B002 – upstream Human Bacteroides (Dorei) = <loq< td=""><td>238</td></loq<>		238
	Bird Fecal $ID^{TM} = \langle LOQ \rangle$		
	Dog Bacteroides ID <sup>TM</sup> =	ND	

ND = Not Detected, <LOQ = Below limit of quantitation, CCE = Calibrator Cell Equivalents Note: Values in parentheses for station WNB001 are for field duplicate sample.

## Basins Subject to Annual Monitoring and Reporting Requirements-

- a. Dulles Interceptor-
- b. Mattawoman-
- c. Monocacy-
- d. Patuxent Center-
- e. Patuxent North-
- f. Rock Run-