Supplementary Materials:

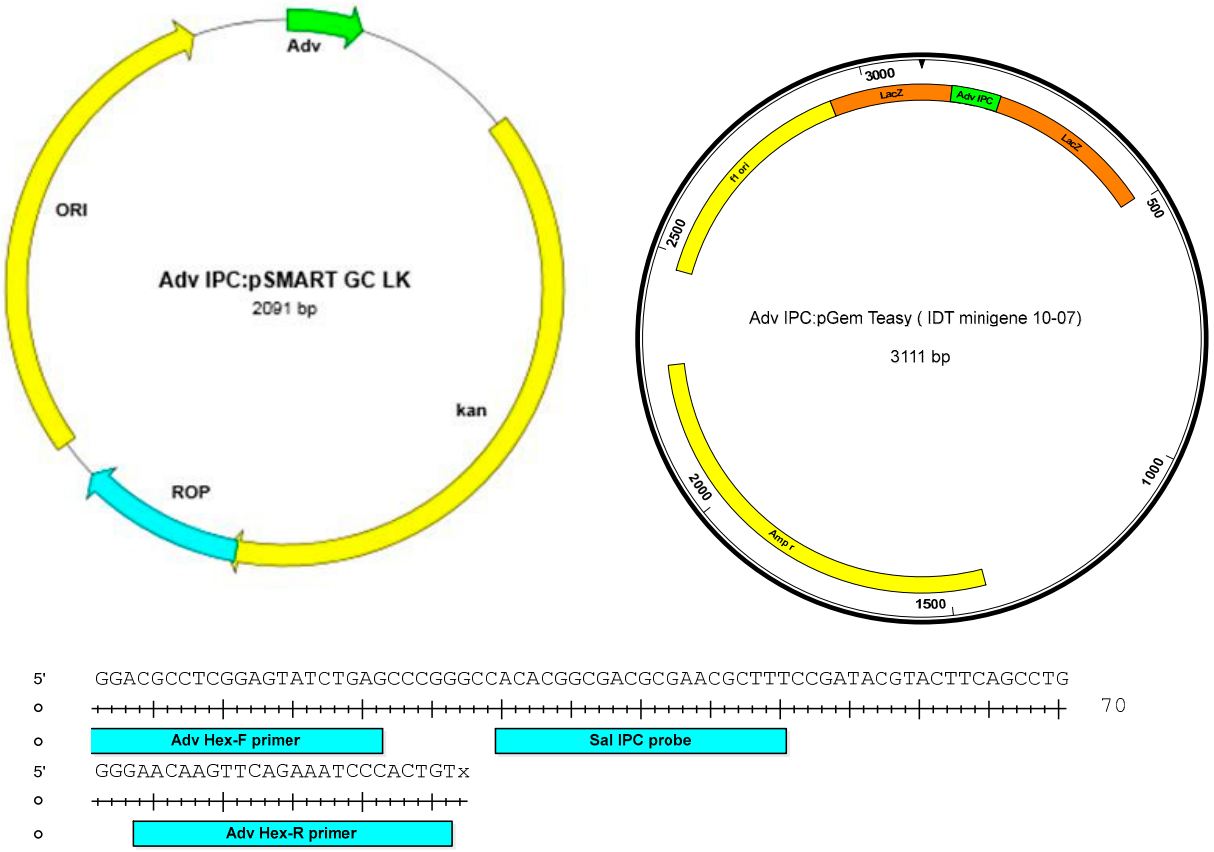

Figure S1. Graphical representation of the Adv IPC plasmids.

A synthetic DNA sequence, AdvIPC, was inserted into two different vectors: pSMART (left) and pGEM-Teasy plasmid (Right). The inserted sequence is shown below (bottom). The synthetic sequence consisted of the portion of the adenovirus hexon gene between nucleotides 17651 and 17746 of Adenovirus 41 Tak (NCBI accession number DQ315364) with nucleotides to 17679 to 17700 replaced with a probe sequence not found in nature [41].

Table S1. QPCR Parameters using the Roche LC480 Thermocycler

Target	Cycling Parameters	Number of Cycles	Temperature (°C)/Time (mm:ss)
blaSHV/TEM	Initial denaturation	1	95/01:00
	Denaturation of DNA	50	95/00:10
	Annealing and extension		60/00:45
sul1	Initial denaturation	1	
	Denaturation of DNA	50	95/00:10
	Annealing of primers/probe		50/00:15
	Extension		72/00:15
	Melt	1	60-95°C
Bacterial 16S rDNA	Initial denaturation	1	95/00:30
	Denaturation of DNA	45	95/00:10
	Annealing of primers/probe		50/01:00
	Extension		72/00:20
AdvIPC	Initial denaturation	1	95/02:00
	Denaturation of DNA	50	95/00:15
	Annealing and extension		65/00:30
Salmon SPC	Initial denaturation	1	95/10:00
	Denaturation of DNA	50	95/00:30
	Annealing and extension		60/00:60

Table S2. QPCR Parameters using the RotorGene Thermocycler

Target	Cycling Parameters	Number of Cycles	Temperature (°C)/Time (mm:ss)
Bacterial 16S rDNA	Initial denaturation	1	95/00:30
	Denaturation of DNA		95/00:10
	Annealing	45	50/01:00
	Extension		72/00:20
AdvIPC	Initial denaturation	1	95/01:00
	Denaturation of DNA		95/00:10
	Annealing	45	55/00:30
	Extension		68/00:20
Salmon SPC	Initial denaturation	1	95/10:00
	Denaturation of DNA		95/00:30
	Annealing and extension	45	60/00:60

The limit of detection (LOD) was determined for each qPCR according to rational provide by Bustin et. al. (2009) and Kralik et. al. (2017). At least ten replicate qPCRs were performed with ten-fold dilutions of plasmid standards. The lowest concentration that was detected in at least 90% of the assays was identified as the LOD. In addition, the efficiency and mean square error (LightCycler480) or r^2 (RotorGene) were compiled for each qPCR. Limit of quantification (LOQ) was also determined according to Kralik et. al. (2017) as the lowest detectable concentration with a coefficient of variation below 25%. The coefficient of variation for the *sul1*, *bla*$_{SHV/TEM}$, and *16S* qPCRs at the LOD concentrations were all below 25% indicating that there was no difference between the LOD and LOQ values.

The *bla*$_{SHV/TEM}$ hydrolysis probe qPCR was designed to detect a wide variety of SHV and TEM β-lactamase variants to increase the likelihood of detecting the resistance genes in the treatment matrices. Alignments of both TEM and SHV-class β-lactamase genes were performed using the DNASTAR software (Megalign application) and sequences downloaded from the NCBI sequence database. Eighteen SHV and 51 TEM-type β-lactamase genes were aligned and scanned manually for probable qPCR primers and probes. The target region identified as being most favorable for the detection of both SHV and TEM genes was between nucleotide 370 and 695 yielding a PCR product of 325 nucleotides (based on β-lactamase TEM-1 sequence accession number EF035622). The primers were examined *in silico* for specificity using the NCBI primer BLAST tool (https://blast.ncbi.nlm.nih.gov/Blast.cgi) and were shown to match only β-lactamase genes. Furthermore, DNA sequencing of fifteen amplicons from different wastewater matrices showed that all readable sequences matched β-lactamase genes in the NCBI Genbank sequence database.

The *bla*$_{SHV/TEM}$ qPCR was linear over eight orders of magnitude (Figure S2) and showed a limit of detection (LOD) of 70 copies/µl (positive in $\geq$95% of qPCRs) with an average efficiency of 95% $\pm$ 17% and error of 0.12 $\pm$ 0.18 (n=68).

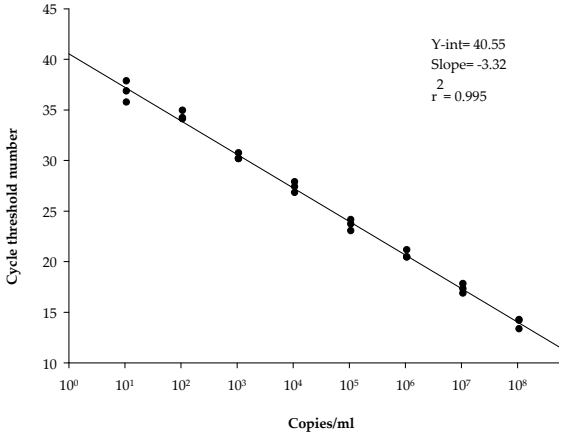

Figure S2. TEM-SHV β-lactamase qPCR characterization. Serial ten-fold dilutions of a plasmid containing a blaSHV/TEM gene were analyzed in triplicate with the blaSHV/TEM qPCR using the LightCycler480. The plot shows qPCR results from a single representative experiment. Linear regression statistics and the r^2 value are depicted in the box located in the upper right corner.

The *sul1* qPCR showed a LOD of 6 copies/µl (positive in ≥95% of qPCRs) with an average efficiency of 86% ± 6% (n=18) and error (calculated as mean square error not r^2) of 0.095.

Assessment of the total bacteria was done by a qPCR targeting a portion of the *16S* ribosomal DNA gene that is well conserved across a broad spectrum of bacteria, as described by Harms et. al. (2003). Samples were pretreated with a heat-labile dsDNase prior to addition of the template to reduce the amount of bacterial DNA in the commercial master mix preparation. The detection limit was determined to be 57 copies/µl (positive in ≥95% of qPCRs) with an average efficiency of 99% ± 5% (n= 17) using the Qiagen RotorGene thermocycler. The linearity was assessed using the r^2 metric resulting in an average of 0.99 (± 0.01).

The salmon SPC qPCR was performed as described previously 44]. The AdvIPC qPCR targeted an artificial DNA insert not found in nature. It demonstrated a detection limit of 10 copies/µl with an average efficiency of 97% ± 6% and an r^2 of 0.998 ± 0.002 (n=22).

Table S3. The quantity of *bla*$_{SHV/TEM}$, *sul1* and bacterial *16S* genes in full-scale WRP treatment processes: solids fraction.

WRP matrix [a]	*bla*$_{SHV/TEM}$ (copies/L)[b]	positive samples	*sul1* (copies/L)[b]	positive samples	16S rDNA (copies/L)[b]	positive samples
Raw	$1.41x10^{7}$ $\pm 3.31x10^{6}$	3/3	$7.61x10^{7}$ $\pm 4.43x10^{7}$	3/3	$6.58x10^{9}$ $\pm 5.14x10^{9}$	3/3
AS	$1.95x10^{7}$ $\pm 1.06x10^{7}$	9/9	$1.82x10^{10}$ $\pm 2.36x10^{10}$	9/9	$1.21x10^{12}$ $\pm 7.22x10^{11}$	9/9
SE	$1.09x10^{5}$ $\pm 9.24x10^{4}$	3/3	$3.03x10^{7}$ $\pm 1.85x10^{7}$	3/3	$5.77x10^{8}$ $\pm 1.74x10^{8}$	3/3
FE	$<5.30x10^{3}$	0/6	$7.89x10^{3}$ $\pm 9.18x10^{3}$	3/6	$4.57x10^{5}$ $\pm 6.30x10^{5}$	6/6
Filter backwash	$1.55x10^{6}$ $\pm 1.91x10^{6}$	5/5	ND	-	ND	-

[a] *Samples were collected from a full-scale tertiary WRP. Final effluent refers to tertiary-treated water that was chlorinated and de-chlorinated. Backwash was collected from the filtration tanks during the backwash cycle after approximately 24-hours of continuous use. SE and FE samples were concentrated by HFF. AS: activated sludge; SE: secondary effluent; FE: final effluent.*

[b] *Results are in qPCR copies per L of original matrix ± standard deviation. Final effluents were obtained as grab samples prior to entering the distribution piping. ND= Not done. Averages were calculated using the qPCR concentrations of positive samples and the limit of detection for all samples that were negative. "Less than" values denote all samples were negative and the concentration given represents the LOD for each assay.*

Table S4. The quantity of *bla*$_{SHV/TEM}$, *sul1* and bacterial *16S* genes in full-scale WRP treatment processes: dissolved fraction.

WRP matrix [a]	*bla*$_{SHV/TEM}$ (copies/L)[b]	positive samples	*sul1* (copies/L)[b]	positive samples	16S rDNA (copies/L)[b]	positive samples
Raw	6.31×10^{6} $\pm 2.32 \times 10^{6}$	3/3	1.04×10^{9} $\pm 1.70 \times 10^{9}$	3/3	6.22×10^{9} $\pm 3.03 \times 10^{9}$	3/3
AS	9.29×10^{5} $\pm 4.46 \times 10^{5}$	3/9	3.57×10^{7} $\pm 2.57 \times 10^{7}$	9/9	1.46×10^{9} $\pm 1.43 \times 10^{9}$	9/9
SE	9.17×10^{3} $\pm 4.55 \times 10^{2}$	3/3	1.88×10^{6} $\pm 1.39 \times 10^{6}$	3/3	3.60×10^{8} $\pm 2.43 \times 10^{8}$	3/3
FE	$<5.30 \times 10^{3}$	0/6	1.68×10^{4} $\pm 1.85 \times 10^{4}$	5/6	6.32×10^{5} $\pm 8.38 \times 10^{5}$	6/6
Filter backwash	3.29×10^{5} $\pm 2.16 \times 10^{5}$ [d]	2/5	ND	-	ND	-

[a] *Samples were collected from a full-scale WRP. Final effluent refers to tertiary-treated water that was chlorinated and de-chlorinated. Backwash was collected from the filtration tanks during the backwash cycle after approximately 24-hours of continuous use. SE and FE samples were concentrated by HFF. AS: activated sludge; SE: secondary effluent; FE: final effluent.*

[b] *Results are in qPCR copies per L of original matrix ± standard deviation. Final effluents were obtained as grab samples prior to entering the distribution piping. ND= Not done. Averages were calculated using the qPCR concentrations of positive samples and the limit of detection for all samples that were negative. "Less than" values denote all samples were negative and the concentration given represents the LOD for each assay.*

Table S5. The ratio of solids and dissolved fractions for different wastewater matrices.

Solids (SA) to dissolved (DF) ratios						
	16S	**St. Dev.**	**sul1**	**St. Dev.**	**bla$_{SHV/TEM}$**	**St. Dev.**
Raw (SA/DF)	1.94E+00		2.67E+00		3.96E+00	
	1.08E+00		1.48E+00		2.42E+00	
	1.65E-01		9.82E-03		1.28E+00	
Average=	1.06E+00	8.86E-01	1.38E+00	1.33E+00	2.55E+00	1.34E+00
AS (SA/DF) (collected with HFF FE samples)	1.01E+04		1.32E+03		1.09E+01	
	2.75E+03		7.61E+02		1.53E+01	
	3.84E+03		1.47E+03		8.85E+00	
	1.43E+04		3.77E+03		1.12E+01	
	1.75E+02		3.82E+02		2.31E+01	
	6.57E+02		6.19E+02		4.17E+00	
Average=	5.31E+03	5.68E+03	1.39E+03	1.24E+03	1.23E+01	6.44E+00
AS (SA/DF) (collected with HFF SE samples)	6.42E+02		9.38E+01		1.80E+02	
	6.21E+02		2.01E+02		1.57E+02	
	3.03E+02		7.33E+01		3.73E+01	
Average=	5.22E+02	1.90E+02	1.23E+02	6.84E+01	1.25E+02	7.67E+01
HFF SE (SA/DF)	2.31E+00		9.98E+00		7.42E+00	
	2.08E+00		2.09E+01		5.12E+00	
	1.18E+00		3.72E+01		2.26E+01	
Average=	1.86E+00	6.00E-01	2.27E+01	1.37E+01	1.17E+01	9.51E+00
HFF FE (SA/DF)	9.91E-01		5.25E-01		1.00E+00	
	7.29E-01		4.98E-01		1.00E+00	
	1.41E+00		8.37E-01		1.00E+00	
	4.69E-01		2.64E-01		1.00E+00	
	7.54E-02		1.73E+00		1.00E+00	
	5.06E-01		1.00E+00		1.00E+00	
Average=	6.96E-01	4.62E-01	8.09E-01	5.20E-01	1.00E+00	0.00E+00
Combined AS data						
Average=	3.71E+03	5.09E+03	9.65E+02	1.17E+03	4.98E+01	6.38E+01

Table S6. ANOVA statistical analysis of ARGs and 16S qPCR concentration between different water types.

Sample [a]	*bla*$_{SHV/TEM}$ vs *sul1* [b]	*bla*$_{SHV/TEM}$ vs 16S [b]	*sul1* vs 16S [b]	Number of samples
Raw to AS (SF)	1.00E-03	1.00E-03	1.88E-01	3
Raw to AS (DF)	>0.05	>0.05	>0.05	3
AS to SE HFF (SF)	>0.05	3.00E-03	1.00E-03	3
AS to SE HFF (DF)	>0.05	>0.05	>0.05	3
SE HFF to FE HFF (SF)	2.00E-03 [c]	2.00E-03 [c]	>0.05	6
SE HFF to FE HFF (DF)	2.00E-03 [c]	2.00E-03 [c]	>0.05	6
AS to FE HFF (SF)	2.00E-03 [c]	2.00E-03 [c]	>0.05	6
AS to FE HFF (DF)	3.00E-03 [c]	3.00E-03 [c]	>0.05	6
Raw to FE HFF (SF)	>0.05 [c]	1.00E-03 [c]	>0.05	3
Raw to FE HFF (DF)	8.00E-03 [c]	>0.05 [c]	>0.05	3

[a] *The qPCR data (copy/L) was log transformed and subtracted between two matrices to determine the log increase or decrease between two stages. The log difference data were compared via one way ANOVA (SigmaPlot) between the three gene targets.AS: activated sludge; SE: secondary effluent; FE final effluent; HFF: hollow fiber filtration concentrated; SF: solids associated fraction; DF: dissolved fraction. Where normality or equal variance tests failed the Kruskal-Wallis One Way Analysis of Variance on Ranks was used for statistical comparisons.*

[b] *ANOVA p-values listed. Statistically significant differences are indicated by p-values less than 0.05.*

[c] *Note that the bla*$_{SHV/TEM}$ *concentrations were below the LOD for all final effluent samples and the assay's LOD was used in these calculations however, the statistical relevance should be interpreted cautiously.*

Table S7. Statistical comparison of the *bla* or *sul1* to *16S* rDNA ratio between different water types.

	Solids-associated		Dissolved	
Water matrices [a]	bla:16S t-test [a]	Sul:16S t-test [a]	bla:16S t-test [a]	Sul:16S t-test [a]
Raw vs AS	0.015	0.244	0.035	0.807
AS vs SE	0.074	0.359	0.036	0.145
SE vs FE	0.018 [b]	0.005	0.044 [b]	0.016
Raw vs SE	0.004	0.358	0.035	0.807
Raw vs FE	0.671 [b]	0.006	0.499 [b]	0.077
AS vs FE	0.036 [b]	0.002	0.389 [b]	0.015

[a] *The qPCR concentrations (copies/L) for each gene target were log transformed and divided by the log transformed 16S concentrations. Each ratio was compared between different wastewater matrices via t-test (Microsoft Excel). Statistically significant differences are indicated by p-values less than 0.05. SE and FE samples were HFF concentrated. AS: activated sludge; SE: secondary effluent; FE final effluent; HFF: hollow fiber filtration concentrated; SF: solids associated fraction; DF: dissolved fraction.*

[b] *The red font denotes samples where the ARG was below LOD for all samples analyzed. The assay's LOD was used in these situations.*

Table S8. Reduction of exogenous plasmid DNA in tertiary filtration and chlorination processes.

Sample [a]	Dissolved fraction [b]	Dissolved fraction + chlorine [b]	Solids fraction [b]	Solids fraction + chlorine [b]
Pre-filtration	$1.23\times10^{8} \pm 1.17\times10^{8}$	$2.06\times10^{6} \pm 5.29\times10^{6}$	$8.79\times10^{6} \pm 1.39\times10^{7}$	$1.11\times10^{5} \pm 2.27\times10^{5}$
20 min. filtrate	$1.07\times10^{7} \pm 7.47\times10^{6}$	$2.84\times10^{2} \pm 9.10\times10^{1}$ [c]	$1.33\times10^{5} \pm 9.28\times10^{4}$	$<3.00\times10^{2}$
90 min. filtrate	$1.39\times10^{7} \pm 1.04\times10^{7}$	$<3.16\times10^{2}$	$1.60\times10^{6} \pm 1.56\times10^{6}$	$<3.00\times10^{2}$ [c]

[a] *Samples collected prior to filtration but after plasmid addition and at different times during the filtration. Filtrate refers to the water collected immediately after filtration. The last sample was taken after the last volume had entered the filter column.*

[b] *Data for the dissolved and solids-associated fractions represent the averages and standard deviations from eight independent filtration/disinfection experiment (seven for the solids fraction). Samples that were below the LOD were assigned the LOD. Units are copies per ml of original matrix.*

[c] *One of the eight experiments showed a positive qPCR signal but below the quantification limit of the assay and therefore the LOD value was assigned.*

Table S9. Comparison of plasmid concentrations between the solids-associated and dissolved fractions during filtration and disinfection.

Sample [a]	Average log difference (n=7)[b]	t-test p-value [c]	Rank sum test p-value [c]
Pre-filtration	1.39	0.028	0.021
Pre-filtration + chlorine	0.506	0.342	0.867
Post-filtration	1.17	0.007	0.014
Post-filtration + chlorine	-	Below LOD	Below LOD

[a] *Upon addition of the plasmid, samples were collected before and after filtration. Post-filtration refers to the 90 minute time point after filtration had begun.*

[b] *Each individual sample was log transformed and the difference calculated between both fractions. The average of the seven log differences is given.*

[c] *Two-tailed t-test was performed assuming unequal variance between the solids-associated and dissolved fractions of each type of sample using MS Excel (n=7). Rank sum performed on SigmaPlot version 11 (n=7). "Below LOD" signifies that seven of the data points were below LOD therefore accurate statistical determinations cannot be made.*

Table S10. Turbidity measurements on full-scale WRP waters prior to HFF concentration.

Sample date	Water type	Turbidity (NTU)
8/1/16	Secondary effluent	1.58
8/8/16	Secondary effluent	0.98
8/29/16	Secondary effluent	1.57
9/7/16	Tertiary, disinfected effluent	0.37
9/19/16	Tertiary, disinfected effluent	0.55
9/28/16	Tertiary, disinfected effluent	0.62
10/11/16	Tertiary, disinfected effluent	0.53
10/18/16	Tertiary, disinfected effluent	0.69
10/24/16	Tertiary, disinfected effluent	0.72

Table S11. Individual qPCR data from all full-scale WRP samples.

Raw qPCR data in copies/L (not log transformed)							
Units are qPCR copies/L of matrix	qPCR concentrations: Solids-associated fraction				qPCR concentrations: Dissolved fraction		
	16S	**sul1**	**bla**		**16S**	**sul1**	**bla**
Raw (SA)	8.48E+09	8.12E+07	1.47E+07	**Raw (DF)**	4.38E+09	3.04E+07	3.71E+06
	1.05E+10	1.18E+08	1.70E+07		9.73E+09	7.96E+07	7.05E+06
	7.54E+08	2.94E+07	1.05E+07		4.57E+09	3.00E+09	8.17E+06
Average=	**6.58E+09**	**7.61E+07**	**1.41E+07**	**Average=**	**6.22E+09**	**1.04E+09**	**6.31E+06**
AS (SA)	3.03E+12	7.98E+10	1.28E+07	**AS (DF)**	2.98E+08	6.05E+07	**1.18E+06**
	9.56E+11	1.38E+10	1.81E+07		3.48E+08	1.81E+07	**1.18E+06**
	6.00E+11	9.94E+09	1.04E+07		1.56E+08	6.78E+06	**1.18E+06**
	1.40E+12	1.15E+10	1.33E+07		9.77E+07	3.05E+06	**1.18E+06**
unconcentrated samples collected	7.48E+11	1.90E+10	2.73E+07	*unconcentrated samples collected*	4.28E+09	4.97E+07	**1.18E+06**
along with HFF FE	9.80E+11	7.44E+09	4.92E+06	*along with HFF FE*	1.49E+09	1.20E+07	**1.18E+06**
Average=	**1.28E+12**	**2.36E+10**	**1.45E+07**	**Average=**	**1.11E+09**	**2.50E+07**	**1.18E+06**
AS (SA)	1.14E+12	6.00E+09	3.23E+07	**AS (DF)**	1.78E+09	6.40E+07	1.79E+05
unconcentrated samples collected	1.17E+12	1.30E+10	1.94E+07	*unconcentrated samples collected*	1.88E+09	6.48E+07	1.23E+05
along with HFF SE	8.60E+11	3.09E+09	3.66E+07	*along with HFF SE*	2.84E+09	4.22E+07	9.80E+05
Average 3 samples above=	**1.06E+12**	**7.37E+09**	**2.94E+07**	**Average 3 samples above=**	**2.17E+09**	**5.70E+07**	**4.28E+05**
Average of all AS samples=	**1.21E+12**	**1.82E+10**	**1.95E+07**	**Average of all AS samples=**	**1.46E+09**	**3.57E+07**	**9.29E+05**
HFF SE (SA)	5.69E+08	2.97E+07	6.42E+04	**HFF SE (DF)**	2.46E+08	2.98E+06	8.66E+03
	4.07E+08	4.91E+07	4.78E+04		1.95E+08	2.35E+06	9.34E+03
	7.54E+08	1.20E+07	2.15E+05		6.40E+08	3.23E+05	9.52E+03
Average=	**5.77E+08**	**3.03E+07**	**1.09E+05**	**Average=**	**3.60E+08**	**1.88E+06**	**9.17E+03**
HFF FE (SA)	5.96E+05	2.14E+04	**5.30E+03**	**HFF FE (DF)**	6.01E+05	4.08E+04	**5.30E+03**
	1.68E+06	1.72E+04	**5.30E+03**		2.30E+06	3.45E+04	**5.30E+03**
	1.43E+05	**8.40E+02**	**5.30E+03**		1.02E+05	1.00E+03	**5.30E+03**
	1.90E+05	6.18E+03	**5.30E+03**		4.06E+05	2.34E+04	**5.30E+03**
	1.02E+04	**8.40E+02**	**5.30E+03**		1.35E+05	4.86E+02	**5.30E+03**
	1.25E+05	**8.40E+02**	**5.30E+03**		2.47E+05	**8.40E+02**	**5.30E+03**
Average=	**4.57E+05**	**7.89E+03**	**5.30E+03**	**Average=**	**6.32E+05**	**1.68E+04**	**5.30E+03**
	Red font indicates samples resulted in a negative qPCR and were assigned the assays LOD.						
Data set includes the AS data from the HFF FE and HFF SE samples. SE grab and FE grab data were omitted because of the high percentage of negative samples. HFF samples showed a higher rate of qPCR signals above LOD. The qPCR data for the AS(DF) samples collected with the HFF SE samples had a standard curve that detected one-log lower than the LOD resulting in positive concentrations that were below the LOD but are reported here because they were within the quantifiable range and above background.							

Table S12. Solids and dissolved plasmid qPCR data from pilot-scale media filtration experiments.

Units for all results are copies per ml matrix. Eluted in 30 ul EB						
Experiment Date	Chlorine Solution made	Diluted date	2nd Eff+DNA SN	2nd Eff+DNA SN+C	2nd Eff+DNA Pellet	2nd Eff+DNA P+C
7/26/2012	7/13/2012	7/26/2012	4.96E+07	7.39E+05	1.07E+06	1.26E+05
8/6/2012	7/13/2012	8/6/2012	3.66E+05	4.55E+02	--	--
9/5/2012	9/4/2012	9/5/2012	7.52E+07	3.16E+02	1.86E+06	7.14E+02
9/10/2012	9/7/2012	9/7/2012	1.17E+08	1.51E+07	3.60E+06	6.15E+05
Post-Shock Treatment 10/9/2012	10/9/2012	10/9/2012	3.51E+07	1.21E+02	7.77E+06	2.26E+04
Post-Shock Treatment 10/16/12	10/16/2012	10/16/2012	2.92E+08	1.40E+04	1.85E+06	9.63E+03
Post-Shock Treatment 10/22/12	10/22/2012	10/22/2012	3.12E+08	2.77E+05	3.99E+07	2.74E+03
Post-Shock Treatment 10/29/12	10/29/2012	10/29/2012	1.01E+08	2.07E+04	5.46E+06	3.00E+02
		average	1.23E+08	2.02E+06	8.79E+06	1.11E+05
		St. Dev.	1.17E+08	5.29E+06	1.39E+07	2.27E+05
		Note that the qPCR for the 8-6-12 pellet fractions did not meet the efficiency requirement and thus the data was not used.				
All data checked and valid as of 8-4-17. RR						
Legend. 2nd Eff= secondary effluent; +DNA= with AdvIPC plasmid added, P=pellet fraction; SN= supernatant fraction; C or Chl= chlorinated; copies= qPCR copies			Note that the limit of detection for this set of qPCR runs was 50 copies/PCR tube. 5ul template added per PCR tube. DNA extracted from 1ml matrix (0.95ml for SN) was eluted in 30ul			
Chlorine treated vs no chlorine	Copies/ml matrix	Copies/ml matrix	Conc in pellet vs SN	Copies/ml matrix	2nd Eff+DNA Pellet	2nd Eff+DNA P+C
Log difference (copy/ml)	2nd Eff+DNA Pellet	2nd Eff+DNA P+C	% of total		Log transformed	Log transformed
0.93	1.07E+06	1.26E+05	2.10	7/26/2012	6.03	5.10
--	--	--		8/6/2012		
3.42	1.86E+06	7.14E+02	2.42	9/5/2012	6.27	2.85
0.77	3.60E+06	6.15E+05	2.98	9/10/2012	6.56	5.79
2.54	7.77E+06	2.26E+04	18.14	Post-Shock Treatmer	6.89	4.35
2.28	1.85E+06	9.63E+03	0.63	Post-Shock Treatmer	6.27	3.98
4.16	3.99E+07	2.74E+03	11.35	Post-Shock Treatmer	7.60	3.44
4.26	5.46E+06	3.00E+02	5.11	Post-Shock Treatmer	6.74	2.48
2.62	8.79E+06	1.11E+05	6.11	Average difference	**2.62**	Pellet + Chlorine
1.42	1.39E+07	2.27E+05	6.36	St. Dev difference	**1.42**	

Chlorine treated										
Units for all results are copies per ml matrix. Eluted in 30 ul EB										
Experiment Date	Chlorine Solution made	Diluted date	20-min Pellet	20-min P+C	90-min Pellet	90-min P+C	20-min SN	20-min SN+C	90-min SN	90-min SN+C
7/26/2012	7/13/2012	7/26/2012	7.23E+04	3.00E+02	1.91E+05	5.76E+00	2.35E+07	5.84E+01	3.02E+07	3.16E+02
8/6/2012	7/13/2012	8/6/2012	--	--	--	--	4.26E+04	3.16E+02	7.71E+04	3.16E+02
9/5/2012	9/4/2012	9/5/2012	1.82E+05	3.00E+02	4.68E+05	3.00E+02	1.34E+07	3.16E+02	9.57E+06	3.16E+02
9/10/2012	9/7/2012	9/7/2012	8.61E+04	3.00E+02	1.47E+05	3.00E+02	1.26E+07	3.16E+02	6.44E+06	3.16E+02
Post-Shock Treatment 10/9/2012	10/9/2012	10/9/2012	1.43E+05	3.00E+02	4.44E+06	3.00E+02	2.74E+06	3.16E+02	4.48E+06	3.16E+02
Post-Shock Treatment 10/16/12	10/16/2012	10/16/2012	8.70E+04	3.00E+02	1.30E+06	3.00E+02	1.58E+07	3.16E+02	2.39E+07	3.16E+02
Post-Shock Treatment 10/22/12	10/22/2012	10/22/2012	4.32E+04	3.00E+02	2.49E+06	3.00E+02	1.07E+07	3.16E+02	1.82E+07	3.16E+02
Post-Shock Treatment 10/29/12	10/29/2012	10/29/2012	3.15E+05	3.00E+02	2.18E+06	3.00E+02	7.07E+06	3.16E+02	1.84E+07	3.16E+02
		Average cpy/ml	1.33E+05	3.00E+02	1.60E+06	3.00E+02	1.07E+07	2.84E+02	1.39E+07	3.16E+02
		St. Dev. cpy/ml	9.28E+04	0.00E+00	1.56E+06	1.11E+02	7.47E+06	9.10E+01	1.04E+07	6.08E-14
		Red font= below LOD.								
Less than values were given the value of the detection limit for the assay which is 50 copies/PCR										
Note that the 90 min P+C gave qPCR signal but beyond the detection limit of the assay.The raw data is shown but the detection limit of the assay was used for calculation purposes.										
	Log difference (copy/ml matrix)				20-min Pellet	20-min P+C	90-min Pellet	90-min P+C	2nd Eff P+C	
		Sample date		2nd Eff+DNA Pellet	Log transformed	Log transform	Log transforr	Log transforme	Log transformed	
1.07E+06	2.38	7/26/2012		6.03	4.86	2.48	5.28	0.76	5.10	
--	#VALUE!	8/6/2012								
1.86E+06	3.16	9/5/2012		6.27	5.26	2.48	5.67	2.48	2.85	
3.60E+06	2.22	9/10/2012		6.56	4.94	2.48	5.17	2.48	5.79	
7.77E+06	2.78	Post-Shock Treatment 10/9/2012		6.89	5.15	2.48	6.65	2.48	4.35	
1.85E+06	2.46	Post-Shock Treatment 10/16/12		6.27	4.94	2.48	6.11	2.48	3.98	
3.99E+07	1.97	Post-Shock Treatment 10/22/12		7.60	4.64	2.48	6.40	2.48	3.44	
5.46E+06	3.70	Post-Shock Treatment 10/29/12		6.74	5.50	2.48	6.34	2.48	2.48	
			Average difference		1.58	4.14	**0.68**	**4.39**	**2.62**	
			St. Dev difference		0.66	0.52	**0.47**	**0.60**	**1.42**	
					Log removal= log (2nd eff+DNA)-log(Sample + chlorine)					
	Log difference (copy/ml matrix)				20-min SN	20-min SN+C	90-min SN	90-min SN+C	2nd Eff+DNA SN	2nd Eff+DNA SN+C
2nd Eff+DNA Supernatant (cpy/ml matrix)		Sample date		2nd Eff+DNA Super	Log transformed	Log transformed	Log transformed	Log transformed	Log transformed	Log transformed
4.96E+07		7/26/2012		7.70	7.37	1.77	7.48	2.50	7.70	5.87
3.66E+05		8/6/2012		5.56	4.63	2.50	4.89	2.50	5.56	2.66
7.52E+07		9/5/2012		7.88	7.13	2.50	6.98	2.50	7.88	2.50
1.17E+08		9/10/2012		8.07	7.10	2.50	6.81	2.50	8.07	7.18
3.51E+07		Post-Shock Treatment 10/9/2012		7.54	6.44	2.50	6.65	2.50	7.54	2.08
2.92E+08		Post-Shock Treatment 10/16/12		8.47	7.20	2.50	7.38	2.50	8.47	4.15
3.12E+08		Post-Shock Treatment 10/22/12		8.49	7.03	2.50	7.26	2.50	8.49	5.44
1.01E+08		Post-Shock Treatment 10/29/12		8.01	6.85	2.50	7.26	2.50	8.01	4.32
			Average difference		1.00	5.31	**0.88**	**5.21**		**3.44**
			St. Dev difference		0.35	0.96	**0.34**	**0.93**		**1.61**

Units for all results are copies per ml matrix. Eluted in 30 ul EB						
Experiment Date	Chlorine Solution made	Diluted date	Post-Column BLANK SN	Post-Column BLANK SN+C	Post-Column BLANK Pellet	Post-Column BLANK P+C
7/26/2012	7/13/2012	7/26/2012	--	0.00E+00	0.00E+00	0.00E+00
8/6/2012	7/13/2012	8/6/2012	0.00E+00	0.00E+00	--	--
9/5/2012	9/4/2012	9/5/2012	0.00E+00	0.00E+00	0.00E+00	0.00E+00
9/10/2012	9/7/2012	9/7/2012	0.00E+00	0.00E+00	3.16E+03	0.00E+00
Post-Shock Treatment 10/9/2012	10/9/2012	10/9/2012	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Post-Shock Treatment 10/16/12	10/16/2012	10/16/2012	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Post-Shock Treatment 10/22/12	10/22/2012	10/22/2012	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Post-Shock Treatment 10/29/12	10/29/2012	10/29/2012	0.00E+00	0.00E+00	0.00E+00	0.00E+00
Post column blank= filtrate sample taken before the plasmid was added, negative control. BLANK= sample of the secondary effluent collected before the addition of the plasmid, negative control. Post shock treatment= after the filter matrix was treated with a high dose of chlorine to decrease bio-fouling						
Experiment Date	Chlorine Solution made	Diluted date	2nd Eff BLANK SN	2nd Eff BLANK SN+C	2nd Eff BLANK Pellet	2nd Eff BLANK P+C
7/26/2012	7/13/2012	7/26/2012	<50	<50	<50	<50
8/6/2012	7/13/2012	8/6/2012	<50	<50	--	--
9/5/2012	9/4/2012	9/5/2012	<50	<50	<50	<50
9/10/2012	9/7/2012	9/7/2012	<50	<50	<50	<50
Post-Shock Treatment 10/9/2012	10/9/2012	10/9/2012	<50	<50	<50	<50
Post-Shock Treatment 10/16/12	10/16/2012	10/16/2012	<50	<50	<50	<50
Post-Shock Treatment 10/22/12	10/22/2012	10/22/2012	<50	<50	<50	<50
Post-Shock Treatment 10/29/12	10/29/2012	10/29/2012	<50	<50	<50	<50