

**Table S6: Dilution-based qPCR inhibition assessment on selected wastewater samples using the tetM gene.** Undiluted extracts were compared to a 5× diluted aliquot, for which an expected Cq shift of 2.32 cycles is anticipated in the absence of PCR inhibition. Deviations from this expected shift were used as an indicative measure of inhibition, where smaller-than-expected  $\Delta Cq$  values or large Cq reductions upon dilution suggest the presence of inhibitory compounds.  $\Delta Cq$  values that are within the range of  $2.32 \pm 0.5$  are highlighted in green. Samples labeled as “spike” refer to wastewater aliquots processed in parallel but not spiked for tetM, and are therefore expected to show comparable behavior to non-spiked samples. This assessment was exploratory and limited in scope, and results should be interpreted qualitatively to support discussion of method-dependent inhibition rather than as a comprehensive inhibition characterization.

Time Points	Spiked?	Concentration method	Extraction Method	Target	Undiluted Cq	Cq after 5x dilution	$\Delta Cq$ (expected $\Delta Cq = 2.32$ )
T3	No	INNOV	RN	tetM	25,53	28,15	2,62
		NANO	RN	tetM	23,17	24,09	0,92
		Prec	QIA	tetM	38,04	24,20	-13,85
		Prec	RN	tetM	20,40	22,65	2,25
		UltraC	RN	tetM	21,42	23,46	2,04
		Zymo	Zymo	tetM	26,41	28,12	1,71
	Yes	INNOV	RN	tetM	27,67	29,52	1,85
		NANO	RN	tetM	23,09	25,26	2,17
		Prec	QIA	tetM	22,75	24,14	1,39
		Prec	RN	tetM	20,34	22,39	2,05
		UltraC	RN	tetM	22,59	24,35	1,77
		Zymo	Zymo	tetM	22,38	25,10	2,72
	No	INNOV	RN	tetM	25,73	27,60	1,87
		NANO	RN	tetM	22,49	23,91	1,42
		Prec	QIA	tetM	29,32	24,49	-4,82
		Prec	RN	tetM	28,59	30,14	1,55
		UltraC	RN	tetM	21,12	23,31	2,19
		Zymo	Zymo	tetM	24,59	27,04	2,45
	Yes	INNOV	RN	tetM	25,36	27,43	2,07
		NANO	RN	tetM	21,17	22,88	1,70
		Prec	QIA	tetM	0,00	24,87	24,87

		<b>Prec</b>	<b>RN</b>	tetM	21,40	23,56	2,16
		<b>UltraC</b>	<b>RN</b>	tetM	20,52	22,38	1,86
		<b>Zymo</b>	<b>Zymo</b>	tetM	22,25	24,40	2,16