Supporting Information

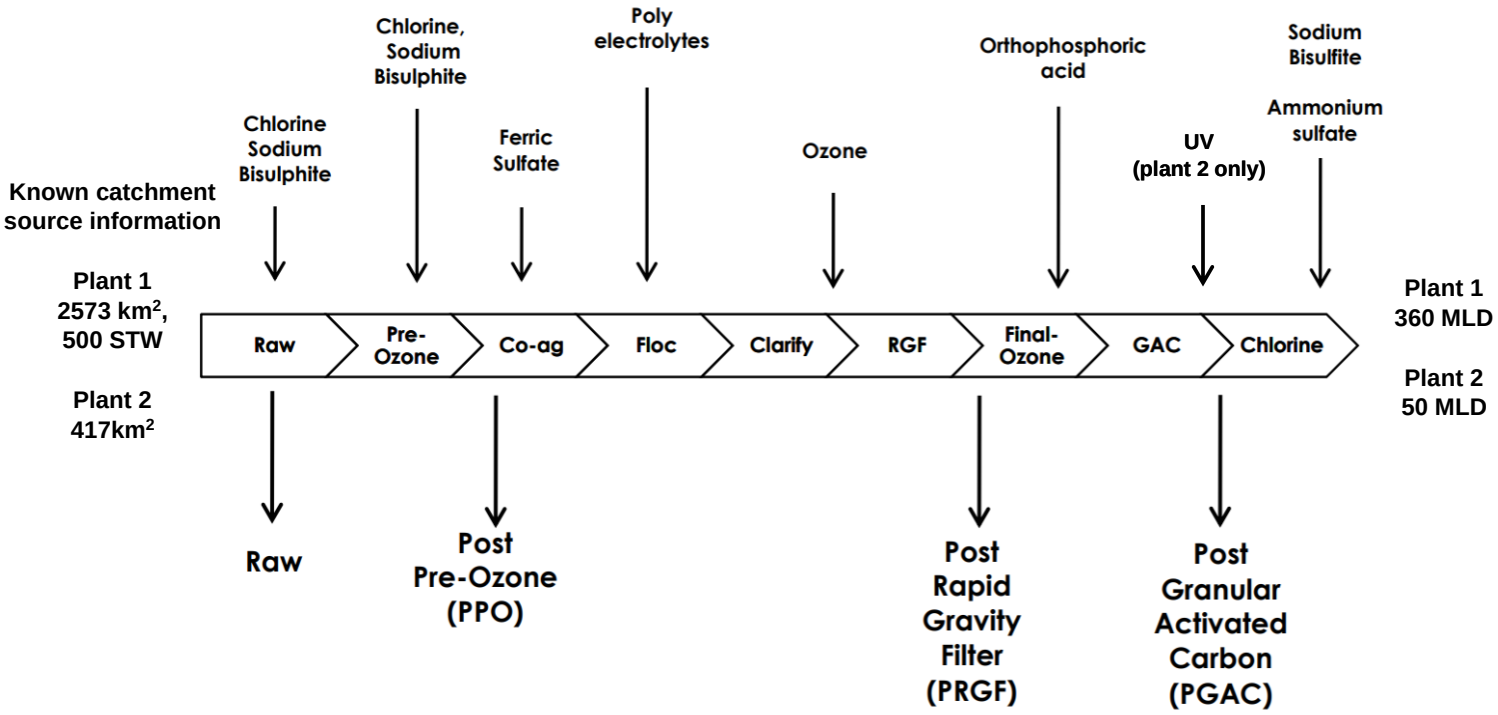


Figure S.1 - Schematic of the treatment processes of UK works providing samples. Plant 2 included a UV disinfection system prior to chlorination, but no post-UV pre-chlorination sample point. STW= Sewage Treatment Works.

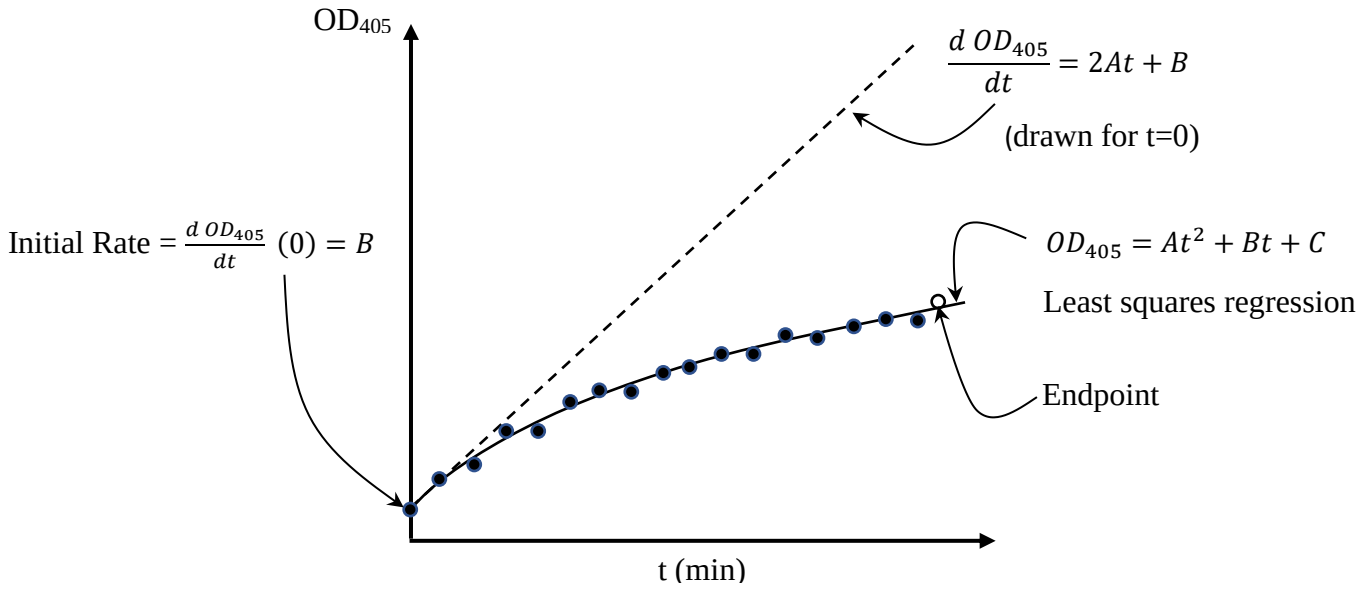


Figure S.2 – Initial rate vs endpoint analysis schemes.

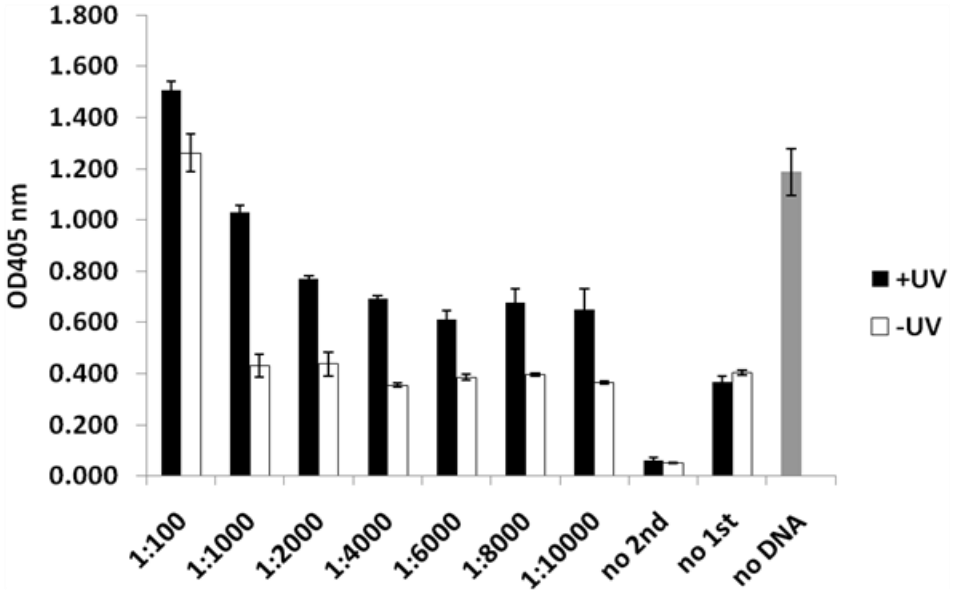
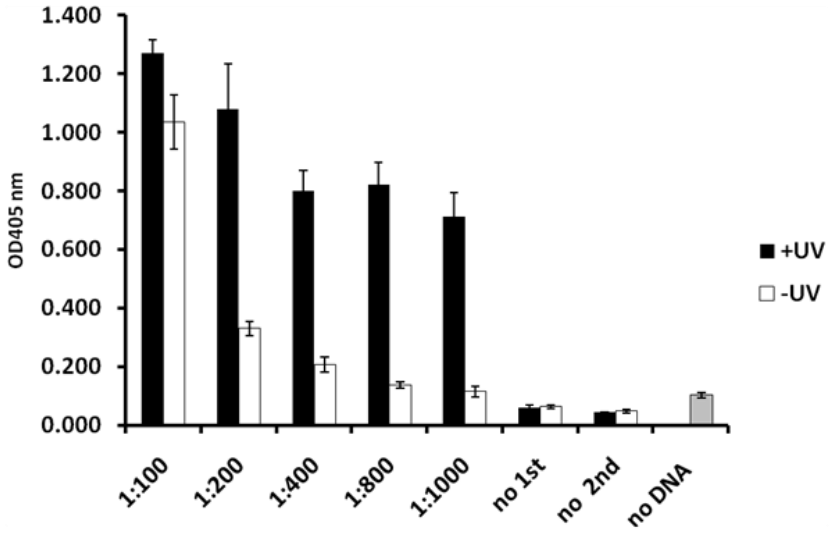
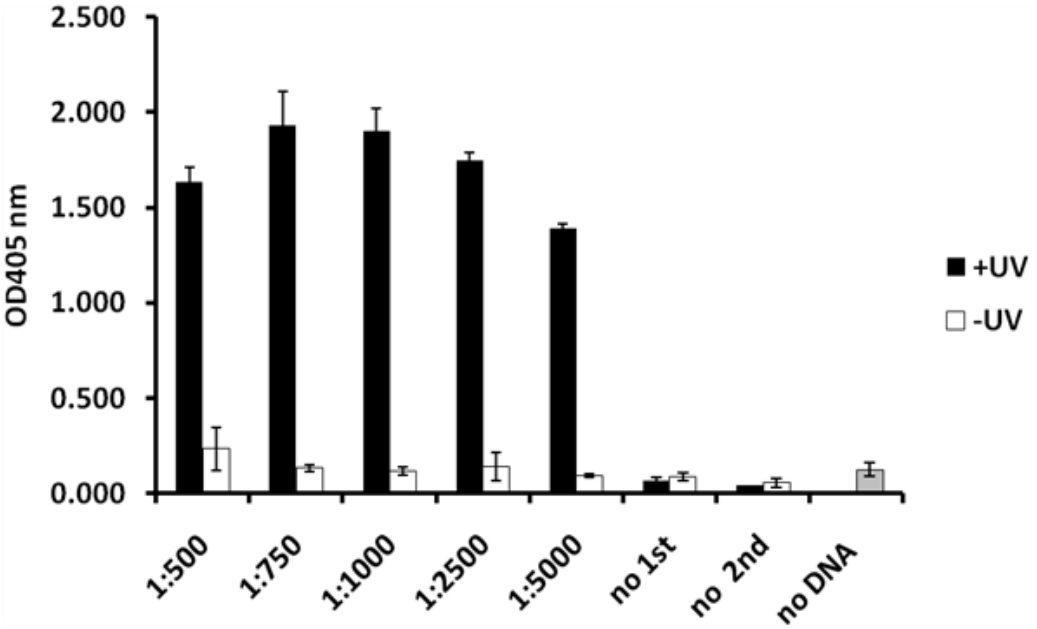


Figure S.3 - Primary antibody (H3Ab) dilution optimisation. Secondary antibody used at 1:500 dilution. Primary antibody used at 1:100 dilution for "no 2nd" and "no DNA" controls. ELISA development time t=50mins. Error bars are 1.96 × Standard Error.



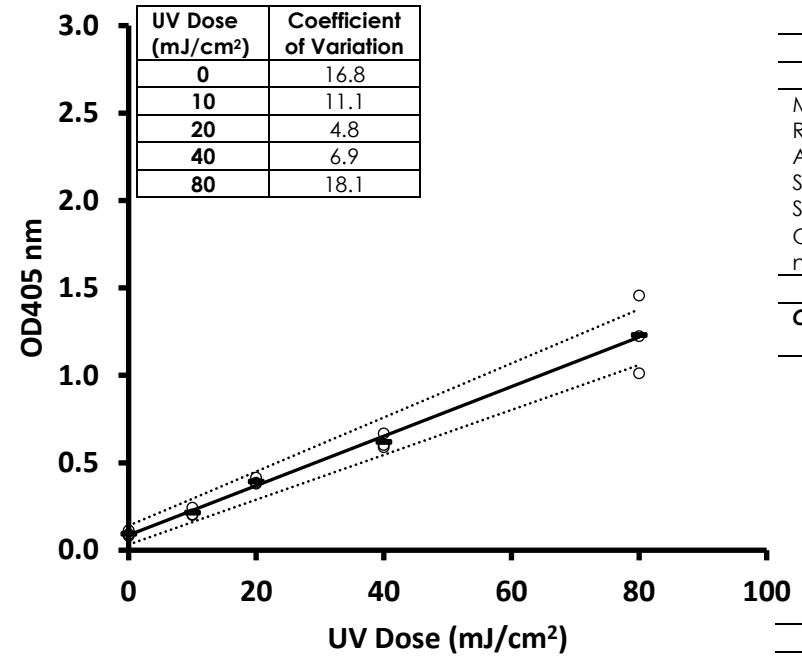
	1:100	1:200	1:400	1:800	1:1000	no 1st	no 2nd	no DNA
S/N	1.226	3.262	3.859	6.007	6.168	0.963	0.915	-

Figure S.4 - Further optimisation of H3Ab dilution with signal to noise ratio (S/N) for each condition. Secondary antibody used at 1:500 dilution. Primary antibody used at 1:1000 dilution for "no 2nd" and "no DNA" controls. ELISA development time t=50mins. Error bars are 1.96 × Standard Error.



	1:500	1:750	1:1000	1:2500	1:5000	no 1st	no 2nd	no DNA
S/N	6.986	14.582	16.286	12.526	14.690	0.775	0.746	-

Figure S.5 - Optimisation of secondary antibody (HRP) dilution with signal to noise ratio S/N. H3 clone primary antibody used at 1:1000 dilution. Secondary antibody used at 1:500 dilution for “no 1st" and “no DNA” controls. ELISA development time t=50mins. Error bars are 1.96 × Standard Error.



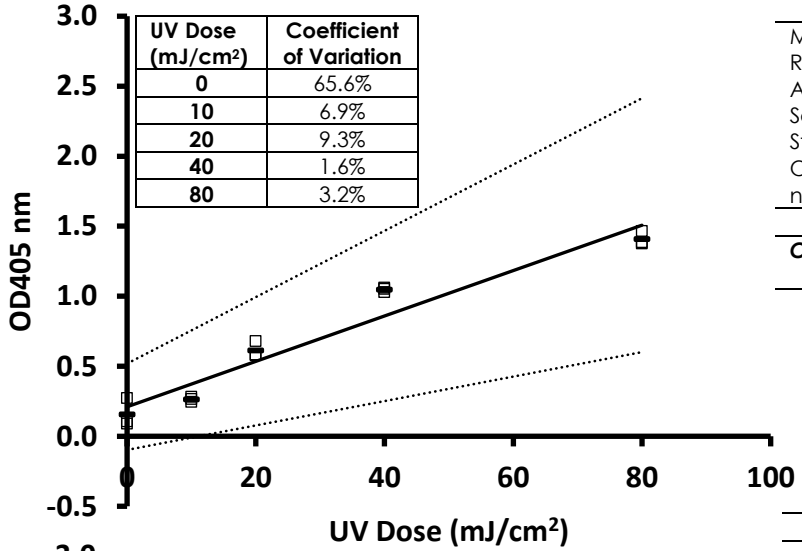
UV Dose (mJ/cm²)	Coefficient of Variation
0	16.8
10	11.1
20	4.8
40	6.9
80	18.1

C

Regression Statistics		y=mx+c	
Multiple R	0.9987	Intercept (c)	0.0864
R Square	0.9975	Gradient (m)	0.0142
Adjusted R Square	0.9966	p-value (c)	0.01479
Standard Error	0.0261	p-value (m)	0.0001
Observations	5.0000	t(min)	14
n	1		

Residuals

Observation	*Predicted*	*Residuals*	*Standard Residuals*
0	0.0864	0.0088	0.3903
10	0.2279	-0.0117	-0.5169
20	0.3694	0.0240	1.0633
40	0.6525	-0.0332	-1.4711
80	1.2186	0.0121	0.5343



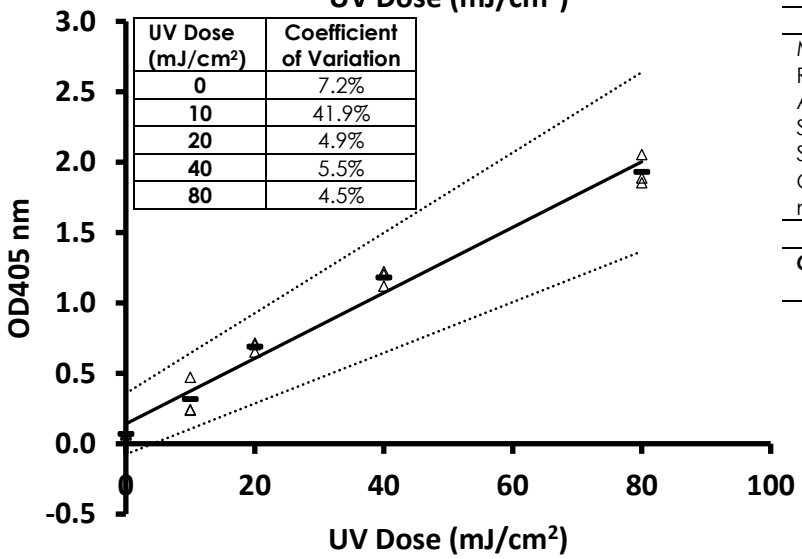
UV Dose (mJ/cm²)	Coefficient of Variation
0	65.6%
10	6.9%
20	9.3%
40	1.6%
80	3.2%

B

Regression Statistics		y=mx+c	
Multiple R	0.9699	Intercept (c)	0.2107
R Square	0.9407	Gradient (m)	0.0162
Adjusted R Square	0.9210	p-value (c)	0.1179
Standard Error	0.1486	p-value (m)	0.0062
Observations	5.0000	t(min)	8
n	1		

Residuals

Observation	*Predicted*	*Residuals*	*Standard Residuals*
0	0.2107	-0.0561	-0.4357
10	0.3728	-0.1098	-0.8535
20	0.5349	0.0781	0.6067
40	0.8591	0.1872	1.4550
80	1.5075	-0.0994	-0.7725



UV Dose (mJ/cm²)	Coefficient of Variation
0	7.2%
10	41.9%
20	4.9%
40	5.5%
80	4.5%

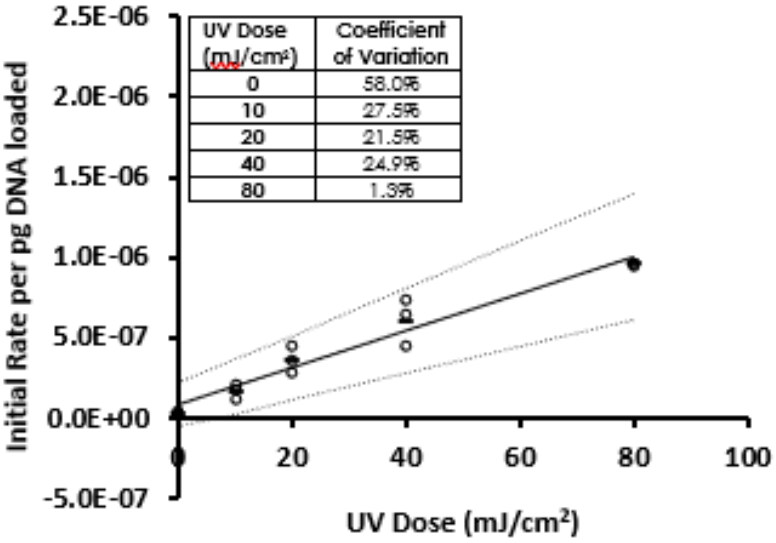
A

Regression Statistics		y=mx+c	
Multiple R	0.9926	Intercept (c)	0.1408
R Square	0.9852	Gradient (m)	0.0233
Adjusted R Square	0.9802	p-value (c)	0.1299
Standard Error	0.1042	p-value (m)	0.0008
Observations	5.0000	t(min)	26
n	1		

Residuals

Observation	*Predicted*	*Residuals*	*Standard Residuals*
0	0.1408	-0.0710	-0.7871
10	0.3735	-0.0554	-0.6135
20	0.6062	0.0854	0.9461
40	1.0716	0.1109	1.2287
80	2.0024	-0.0699	-0.7742

Figure S.6 - *E. coli* gDNA optimised UV Dose response based on endpoint OD 405nm data for each replicate experiment.. Open shapes (□ ○ Δ) are data points from replicates, solid bar (**—**) is mean value. Light dotted line represents the 95% confidence interval of the linear regression.



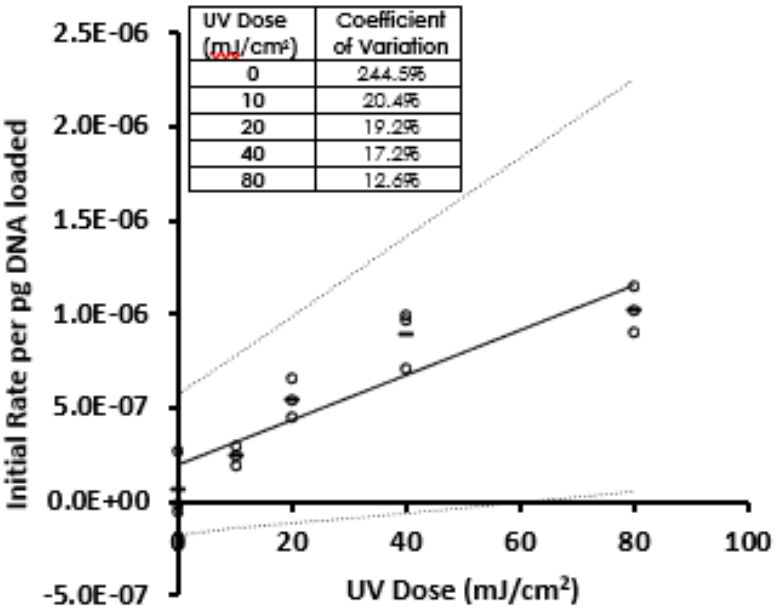
UV Dose (mJ/cm²)	Coefficient of Variation
0	58.0%
10	27.5%
20	21.5%
40	24.9%
80	1.3%

C

Regression Statistics		y=mx+c	
Multiple R	0.9884	Intercept (c)	8.22E-08
R Square	0.9769	Gradient (m)	1.15E-08
Adjusted R Square	0.9692	p-value (c)	0.1467
Standard Error	6.47E-08	p-value (m)	0.0015
Observations	5.0000	t(min)	14
n	1		

Residuals

Observation	Predicted	Residuals	Standard Residuals
0	8.22E-08	-5.3E-08	-0.9518
10	1.97E-07	-2.4E-08	-0.4216
20	3.13E-07	5.55E-08	0.9896
40	5.43E-07	6.49E-08	1.1572
80	1E-06	-4.3E-08	-0.7733



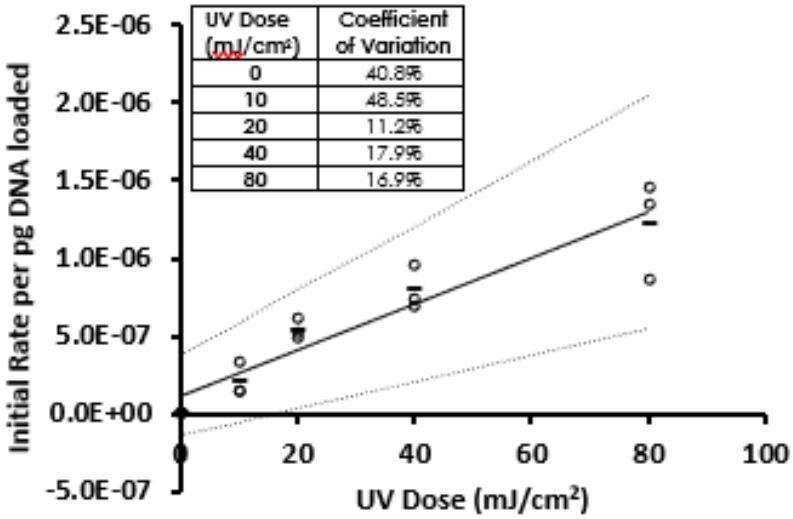
UV Dose (mJ/cm²)	Coefficient of Variation
0	244.5%
10	20.4%
20	19.2%
40	17.2%
80	12.6%

B

Regression Statistics		y=mx+c	
Multiple R	0.9238	Intercept (c)	1.98E-07
R Square	0.8535	Gradient (m)	1.19E-08
Adjusted R Square	0.8046	p-value (c)	0.1893
Standard Error	1.80E-07	p-value (m)	0.0249
Observations	5.0000	t(min)	8
n	1		

Residuals

Observation	Predicted	Residuals	Standard Residuals
0	1.98E-07	-1.3E-07	-0.8196
10	3.17E-07	-7.4E-08	-0.4740
20	4.36E-07	1.12E-07	0.7222
40	6.73E-07	2.16E-07	1.3854
80	1.15E-06	-1.3E-07	-0.8140



UV Dose (mJ/cm²)	Coefficient of Variation
0	40.8%
10	48.5%
20	11.2%
40	17.9%
80	16.9%

A

Regression Statistics		y=mx+c	
Multiple R	0.9751	Intercept (c)	1.18E-07
R Square	0.9509	Gradient (m)	1.48E-08
Adjusted R Square	0.9345	p-value (c)	0.2381
Standard Error	1.23E-07	p-value (m)	0.0047
Observations	5.0000	t(min)	26
n	1		

Residuals

Observation	Predicted	Residuals	Standard Residuals
0	1.18E-07	-1.1E-07	-1.0023
10	2.65E-07	-4.5E-08	-0.4210
20	4.13E-07	1.3E-07	1.2223
40	7.09E-07	9.65E-08	0.9079
80	1.3E-06	-7.5E-08	-0.7069

Figure S.7 - *E. coli* gDNA optimised UV Dose response based on endpoint OD 405nm data for each replicate experiment. Open circles (○) are data points from replicates, solid bar (—) is mean value. Light dotted line represents the 95% confidence interval of the linear regression.

		Initial Rate	Initial Rate Ratio	Endpoint	End Point Ratio
A-B	**std err**	3.02E-09	1.22E-03	2.39E-03	8.21E-04
	t	-0.118	2.051	-0.862	-0.924
	df	6	6	6	6
	p-value	**0.910**	**0.086**	**0.422**	**0.391**
A-C	**std err**	2.19E-09	1.08E-03	1.70E-03	5.47E-04
	t	-1.490	0.132	-5.367	-4.840
	df	6	6	6	6
	p-value	**0.187**	**0.899**	0.002	0.003
B-C	**std err**	3.44E-09	1.38E-03	2.87E-03	9.66E-04
	t	-0.846	-1.712	-2.460	-1.957
	df	6	6	6	6
	p-value	**0.430**	**0.138**	0.049	**0.098**

Table S.1 – Pairwise t-Test based (Real-Stats SlopesTest) significance testing (t-test) of slope of replicate assays A-C. Level of significance 95% significance testing of the slopes of individual replicates A-C by initial rate, initial rate ratio, endpoint and endpoint ratio. Ratio data are the ratio of endpoints or initial rates for 0, 10, 20, 40, and 80 mJ/cm^2 *in vivo* treated *E.coli* gDNA to a 500mJ/cm^2 treated naked *E.coli* gDNA control.

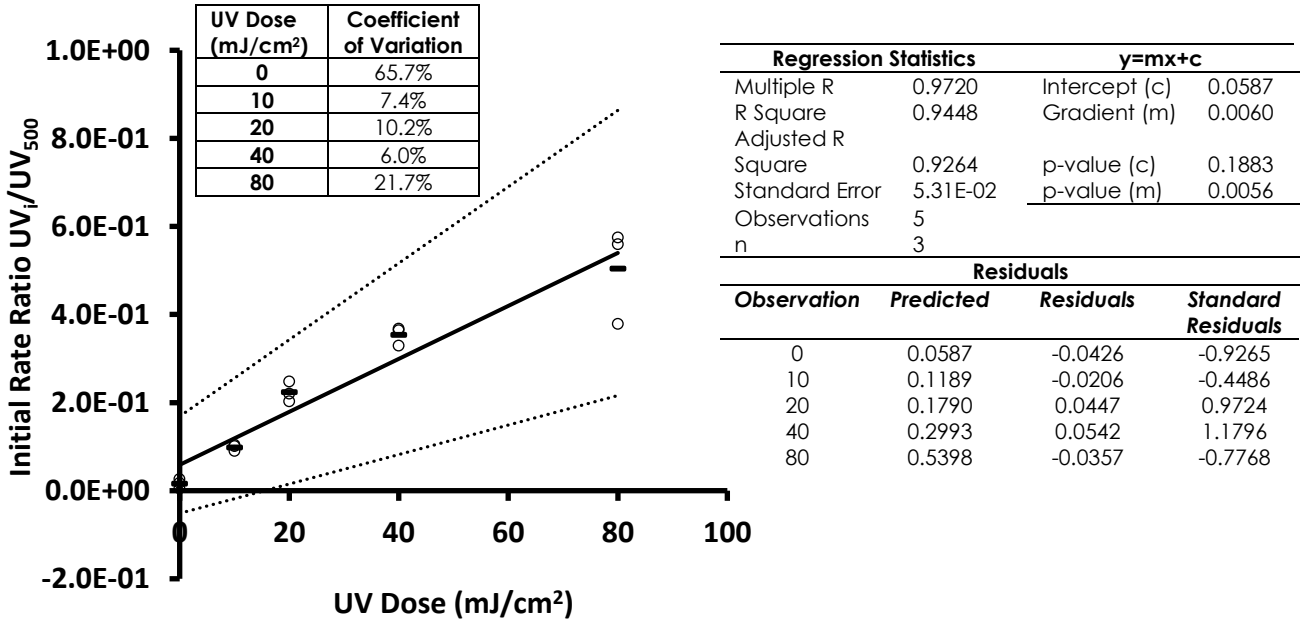
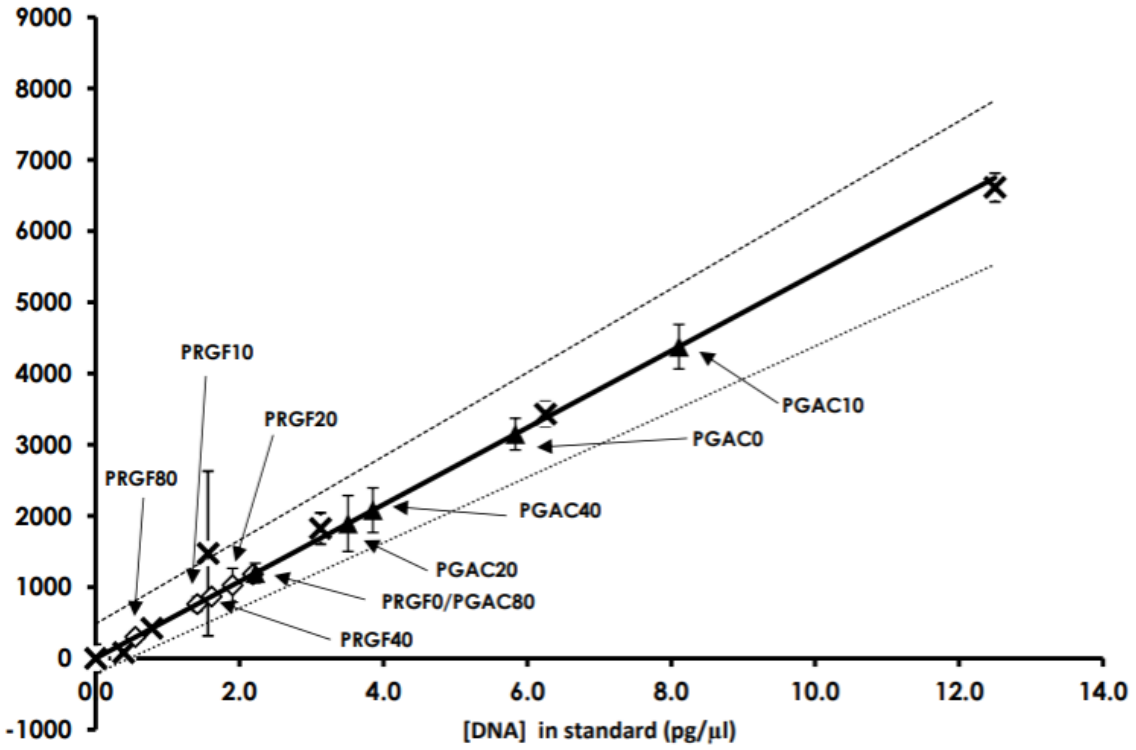


Figure S.8 - ***E. coli* gDNA Optimised UV Dose response based on initial rate data as a ratio of the initial rate for 500mJ/cm^2 treated naked *E.coli* gDNA (Ratio: Initial Rates UV_i/UV_{500}) for three replicate experiments.**(○) are the means of the three replicates A-C from figures data points from three replicate experiments, solid bar (**—**) is mean value. Light dotted line represents the 95% confidence interval of the linear regression.



Sample Point	UV Dose (mJ/cm²)	Picogreen OD_{520}	pg/ul Sample
PRGF *diamonds*	0	1179	13.51
	10	762	8.73
	20	1027	11.76
	40	870	9.96
	80	298	3.42
PGAC *triangles*	0	3148	36.06
	10	4376	50.12
	20	1893	21.69
	40	2080	23.83
	80	1198	13.31

Regression Statistics		y=mx+c	
Multiple R	0.9944	Intercept (c)	135.045
R Square	0.9888	Gradient (m)	523.812
Adjusted R Square	0.9865	p-value (c)	0.366
Standard Error	275.235	p-value (m)	4.535E-6
Observations	7		

Residuals			
Observation	*Predicted OD405*	*Residuals*	*Standard Residuals*
0.0000	135	-135	-0.537
0.3906	340	-260	-1.033
0.7813	544	-125	-0.496
1.5625	954 1	519	2.065
3.1250	1772	51	0.204
6.2500	3409	22	0.087
12.5000	6683	-73	-0.289

Figure S.9- PicoGreen DNA concentration determination from PRGF and PGAC samples. Linear regression of DNA standards at concentrations of 0, 0.391, 0.781, 1.563, 3.125, 6.250, 12.500 pg/µl shown as (✕). Sample concentration calculated by (Fluorescence Intensity 520/Gradient of standard curve) / dilution of sample relative to standards in PicoGreen assay (0.1667). 95% confidence interval of the regression shown dotted. Error bars are 1.96 × Standard Error.