Supplemental data

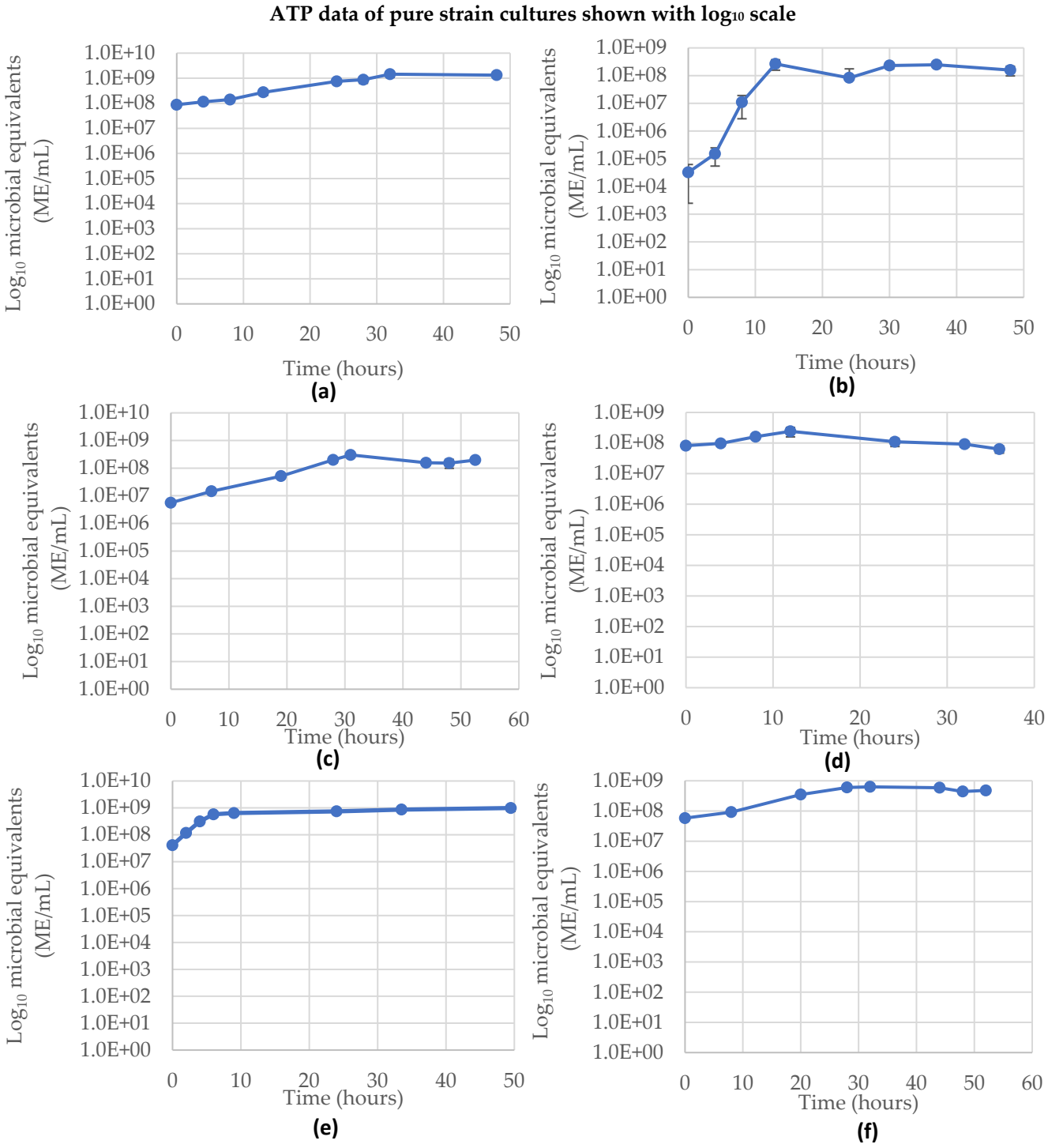


Figure S1: Microbial equivalents per milliliter time course as determined using luciferase-based ATP assay for each species plotted on a log10 scale for: **(a)** *A. woodii*; **(b)** *B. subtilis*; **(c)** *D. vulgaris*; **(d)** *G. subterraneus*; **(e)** *P. putida*; **(f)** *T. aromatica*. Blue lines are the species growth curves (n=3).

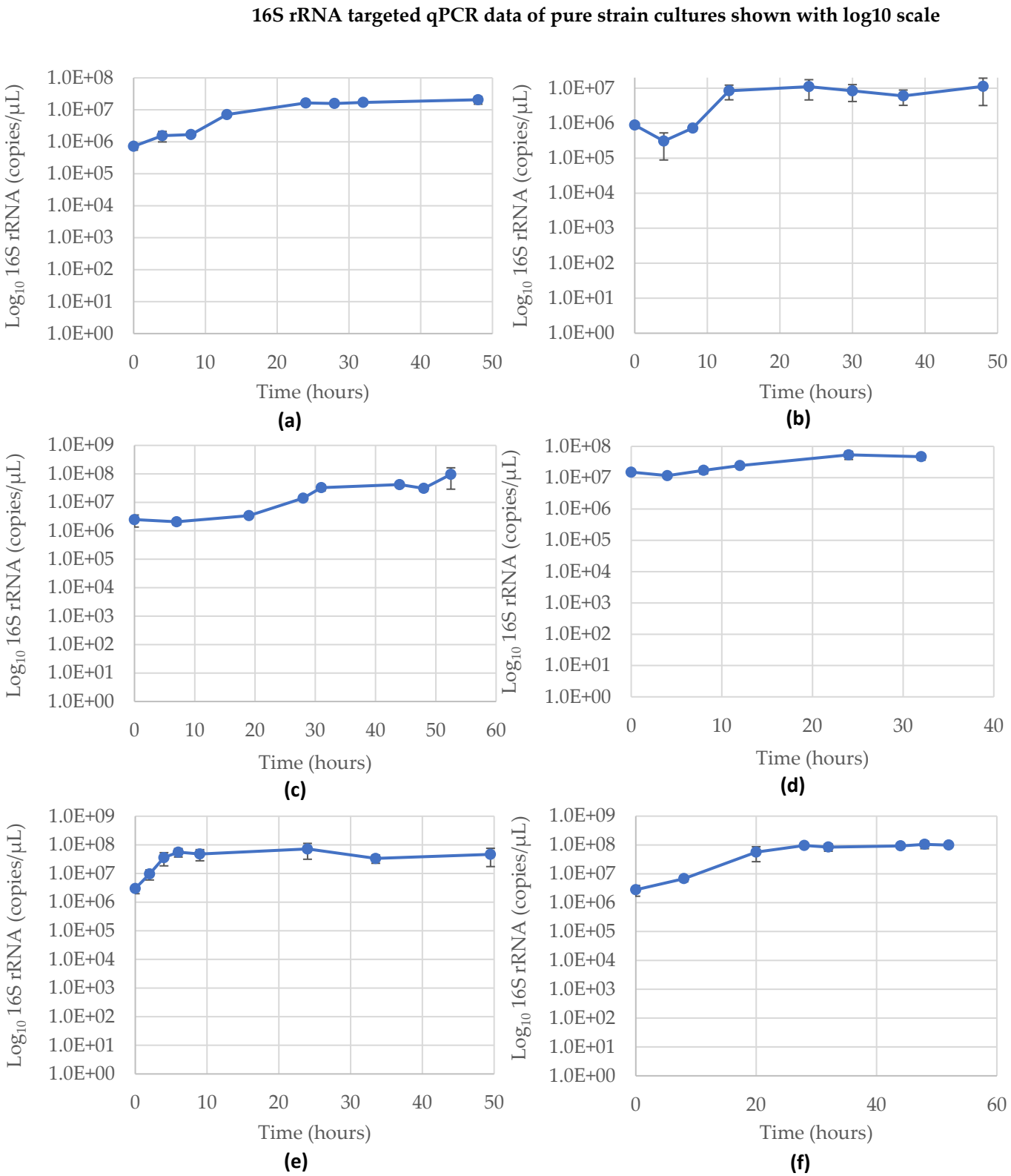


Figure S2: 16S rRNA copies per microliter as detected by qPCR on a log10 scale over a time course of: **(a)** *A. woodii*; **(b)** *B. subtilis*; **(c)** *D. vulgaris*; **(d)** *G. subterraneus*; **(e)** *P. putida*; **(f)** *T. aromatica*. Blue lines are the species growth curves (n=6, three biological each with two technical replicates).

XY scatter plots used to calculate correlation values between monitoring methods.

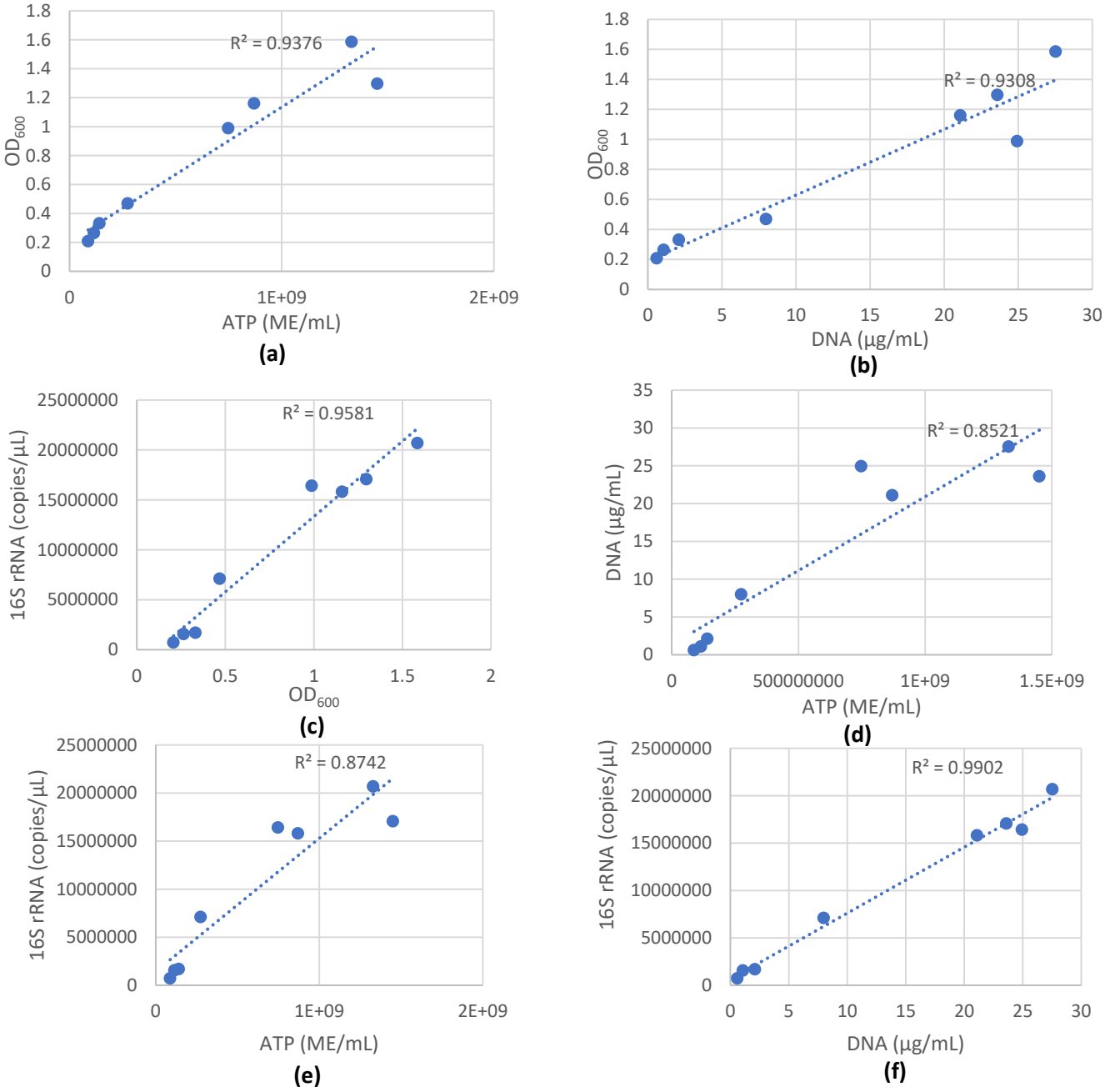


Figure S3: XY scatter plots of all four monitoring methods from *A. woodii* used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; **f)** DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

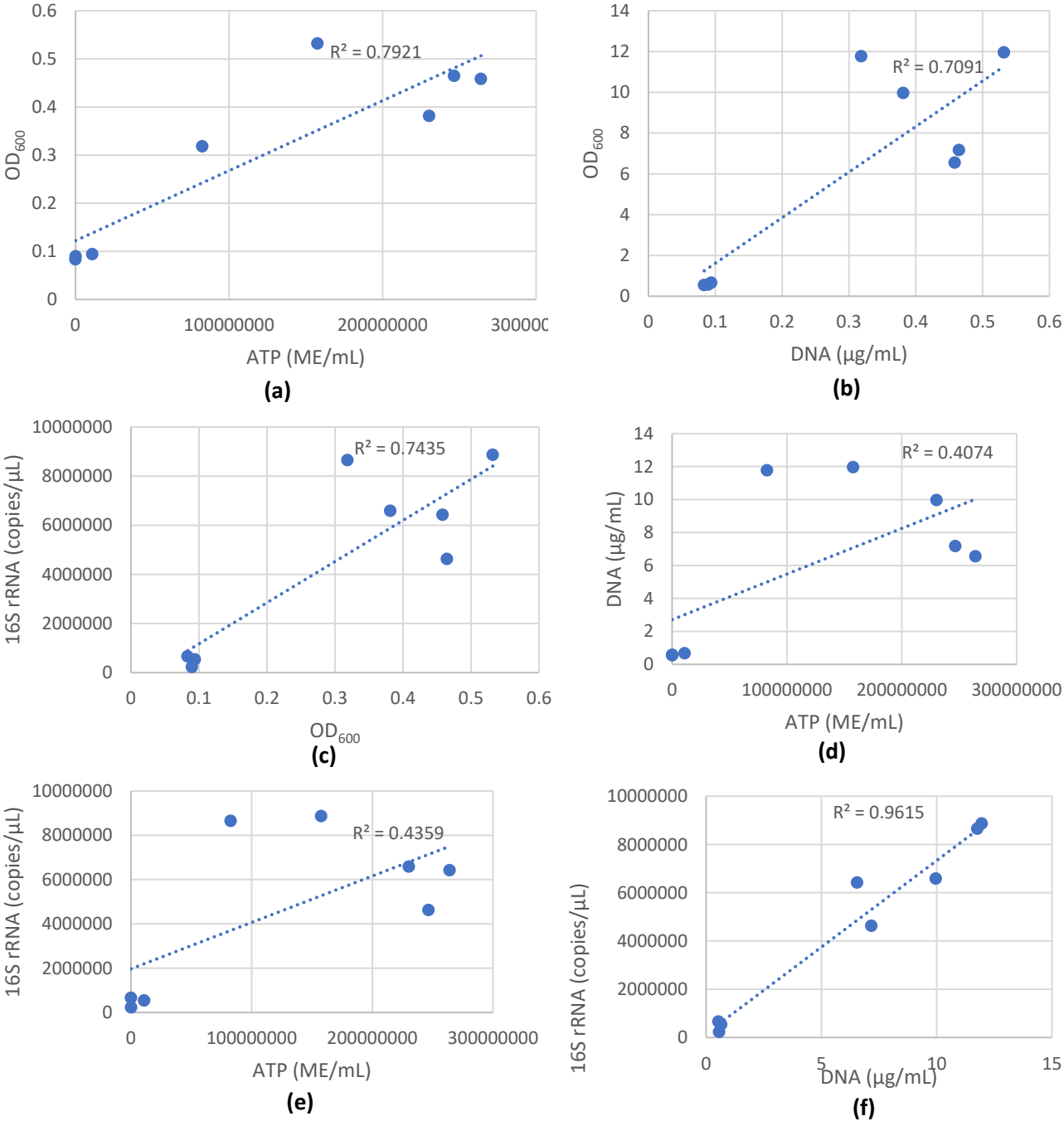


Figure S4: XY scatter plots of all four monitoring methods from *B. subtilis* used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; **f)** DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

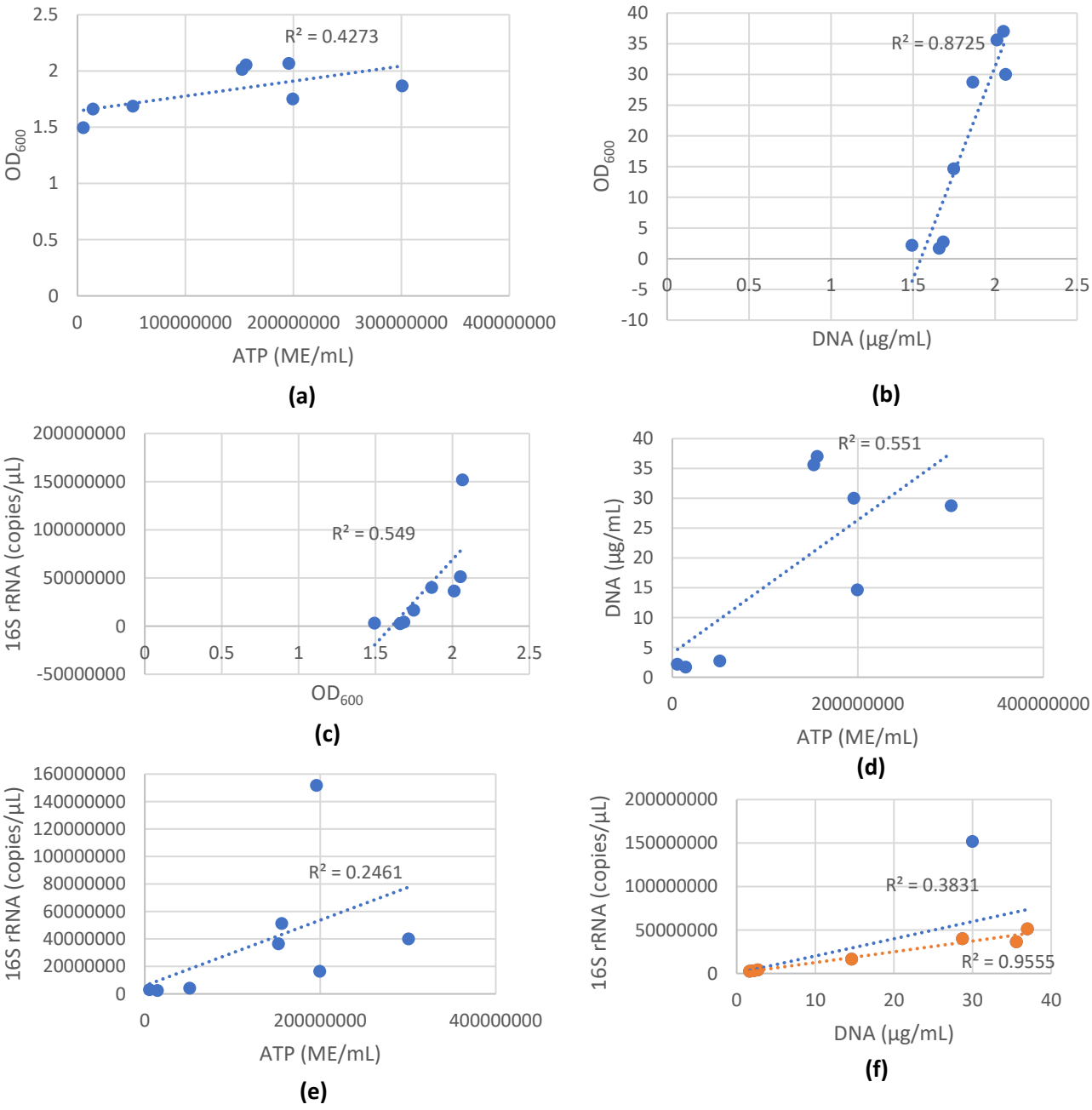


Figure S5: XY scatter plots of all four monitoring methods from *D. vulgaris* used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; **f)** DNA and 16S rRNA. Modified DNA and 16S rRNA correlation to exclude the final 16S (and corresponding DNA) time point is shown in orange. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

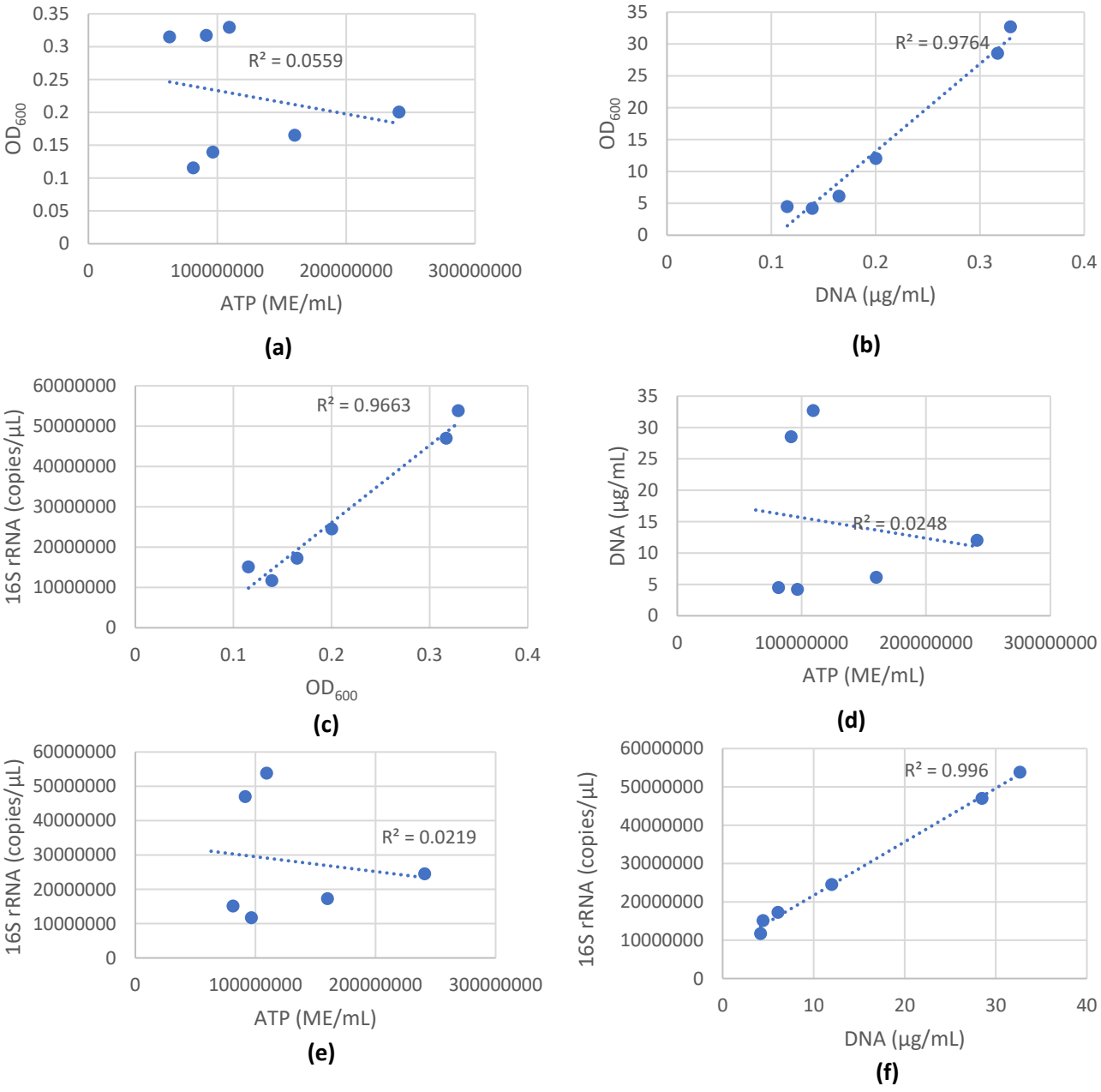


Figure S6: XY scatter plots of all four monitoring methods from *G. subterraneus* used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; **f)** DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

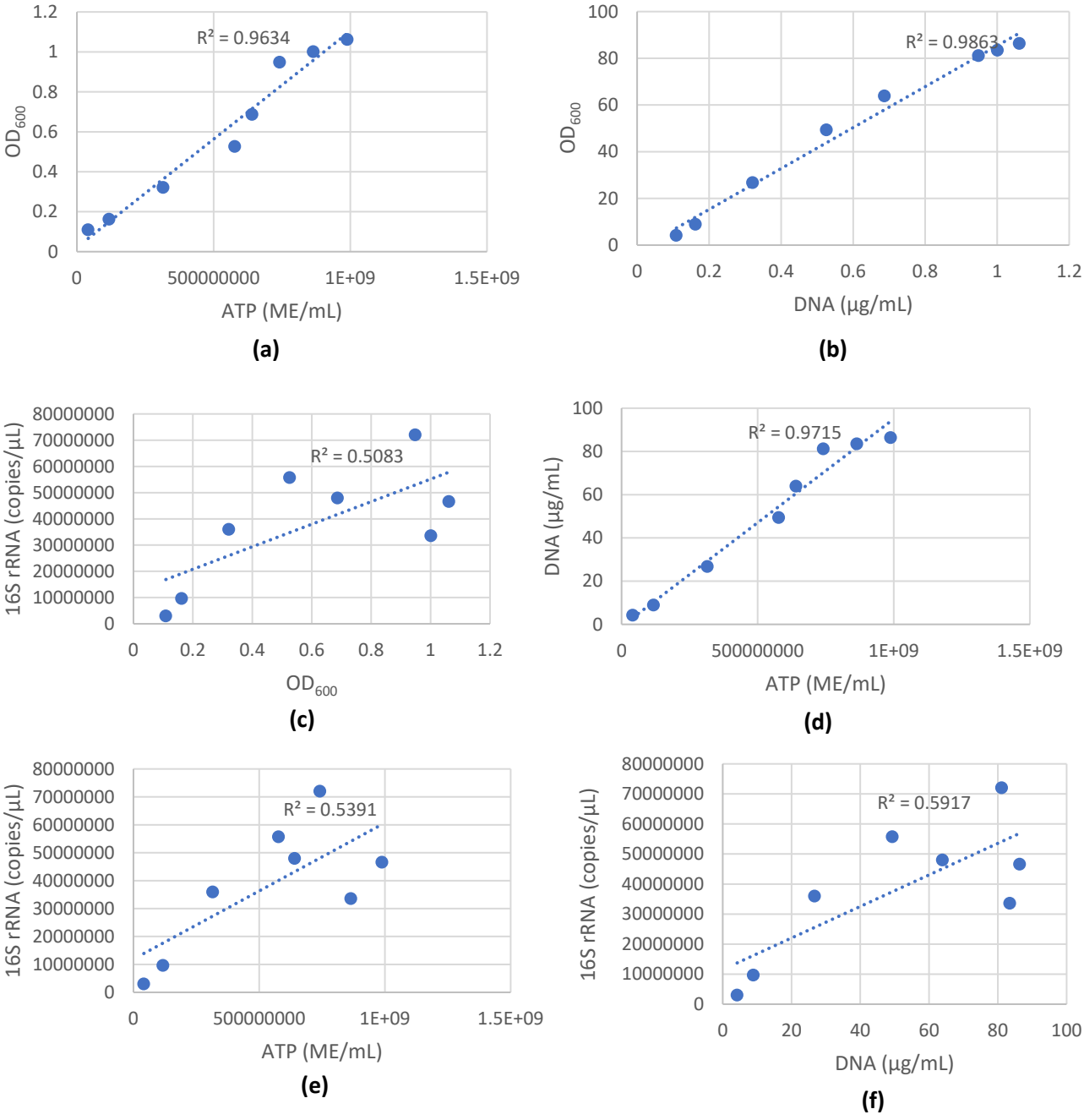


Figure S7: XY scatter plots of all four monitoring methods from *P. putida* used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; **f)** DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

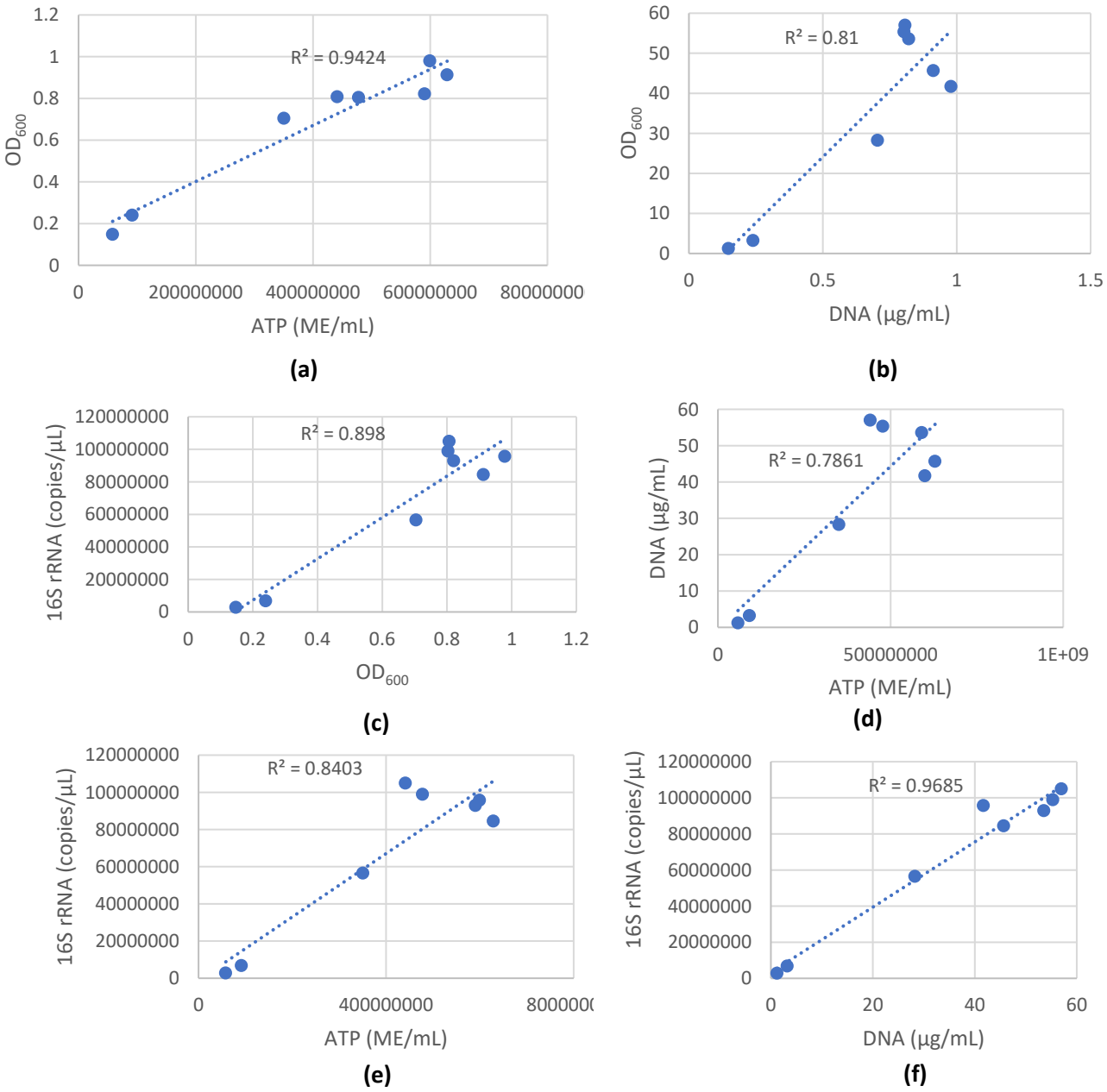


Figure S8: XY scatter plots of all four monitoring methods from *T. aromatica* used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; **f)** DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

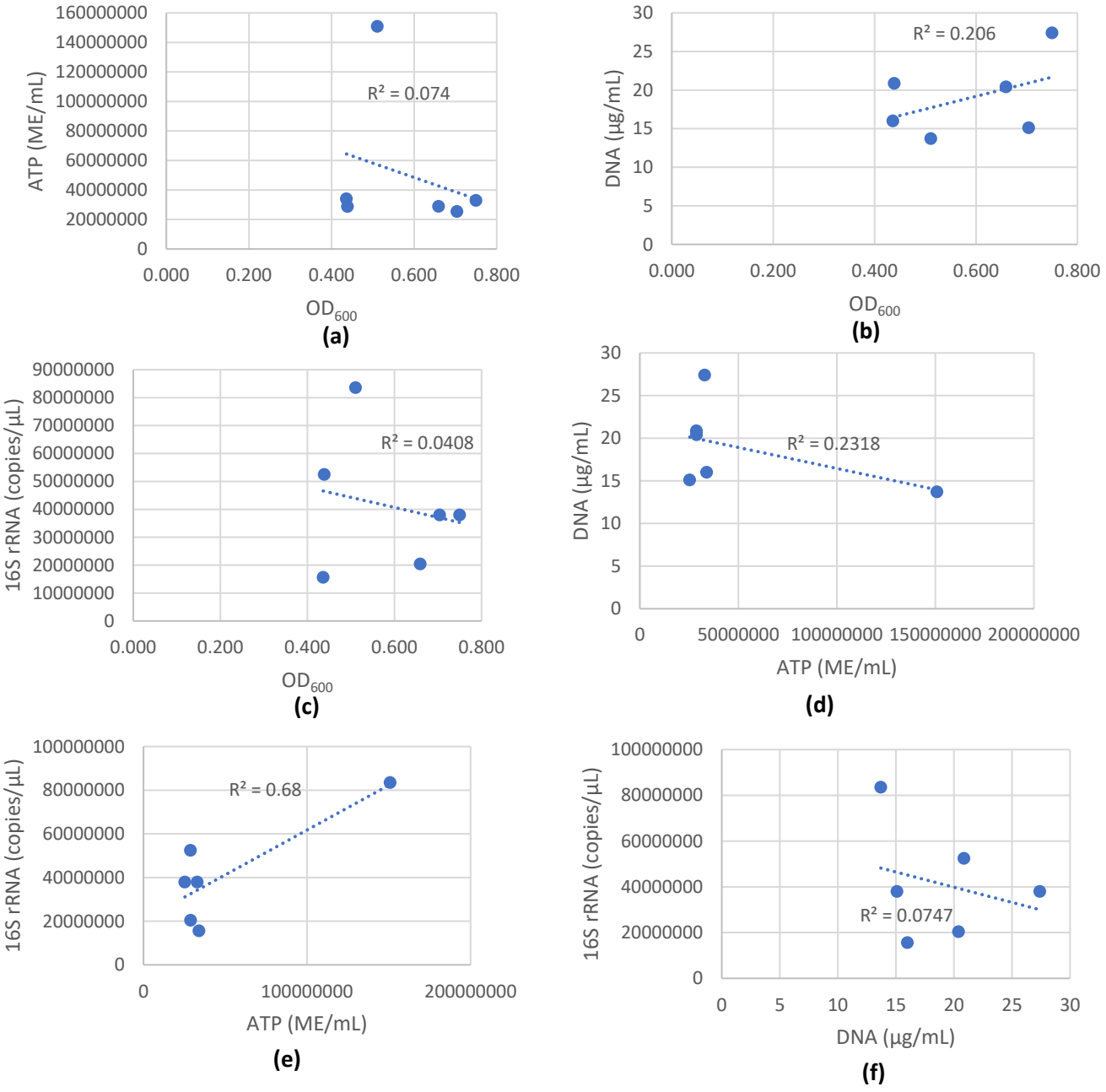


Figure S9: XY scatter plots of all four monitoring methods from the planktonic cells from the CBR exposed to THPS used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; **f)** DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

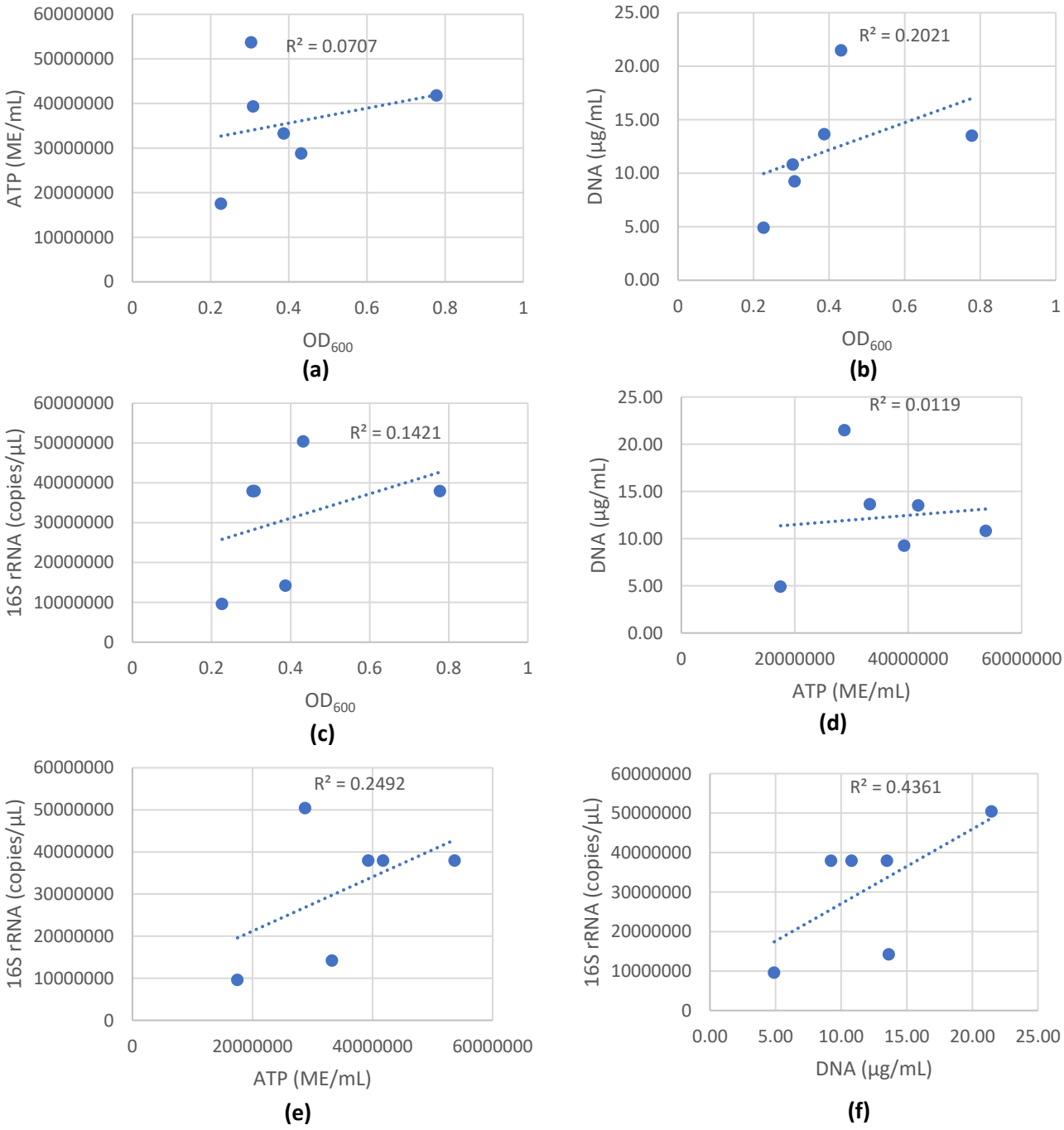


Figure S10: XY scatter plots of all four monitoring methods from the planktonic cells from the CBR not exposed to THPS used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; **f)** DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

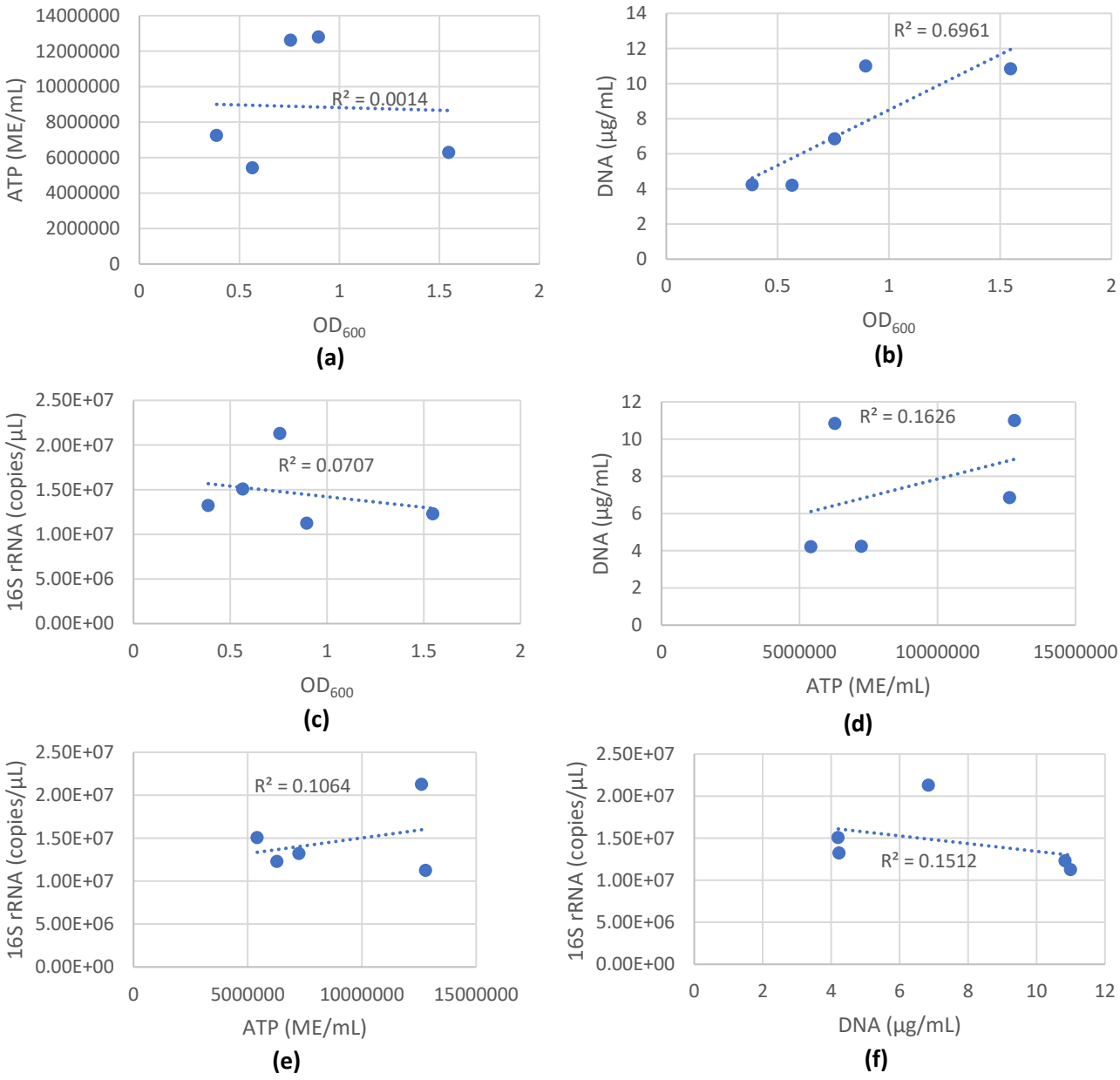


Figure S11: XY scatter plots of all four monitoring methods from the sessile cells from the CBR exposed to THPS used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; **f)** DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

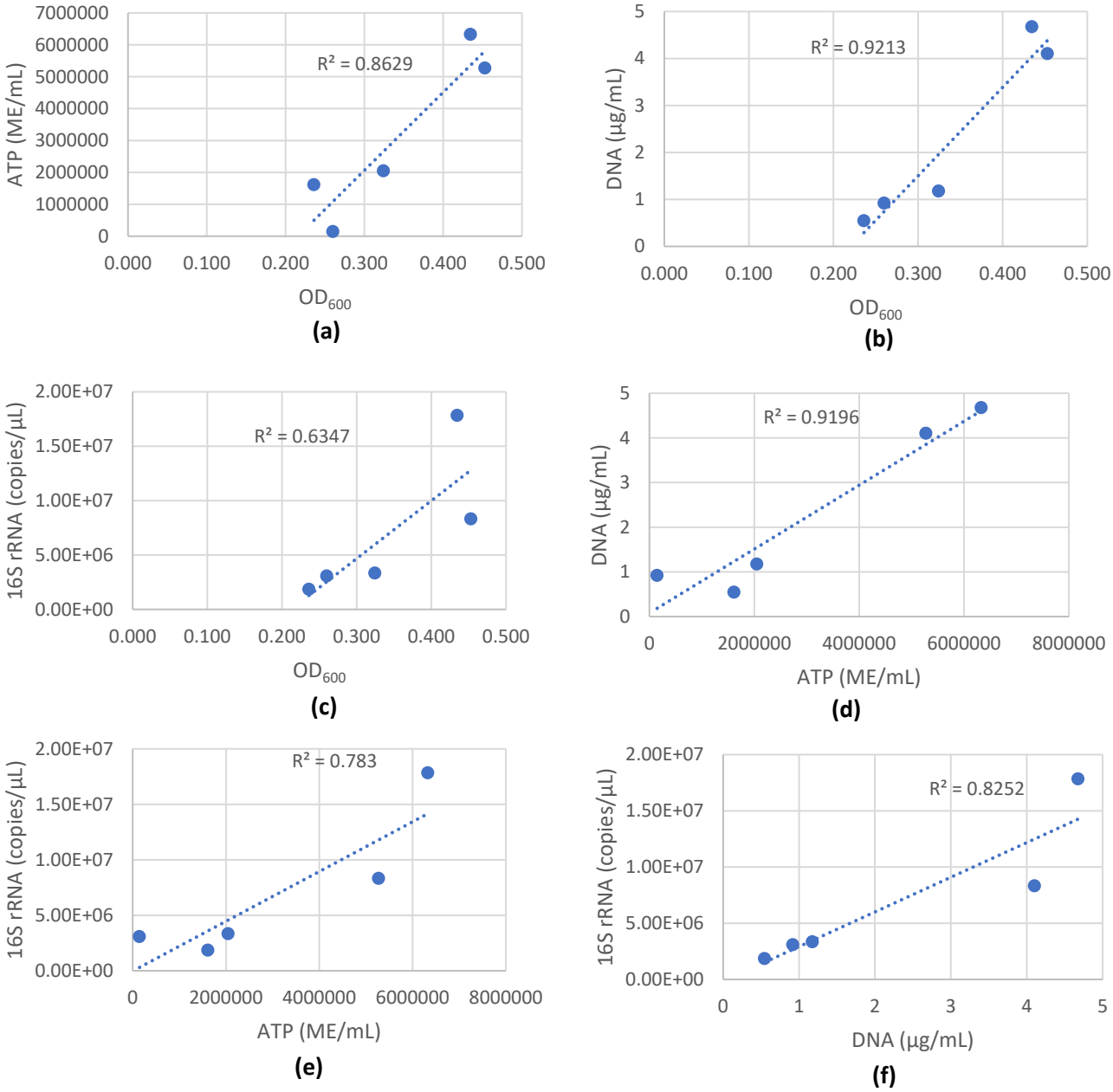


Figure S12: XY scatter plots of all four monitoring methods from the sessile cells from the CBR not exposed to THPS used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; f) DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

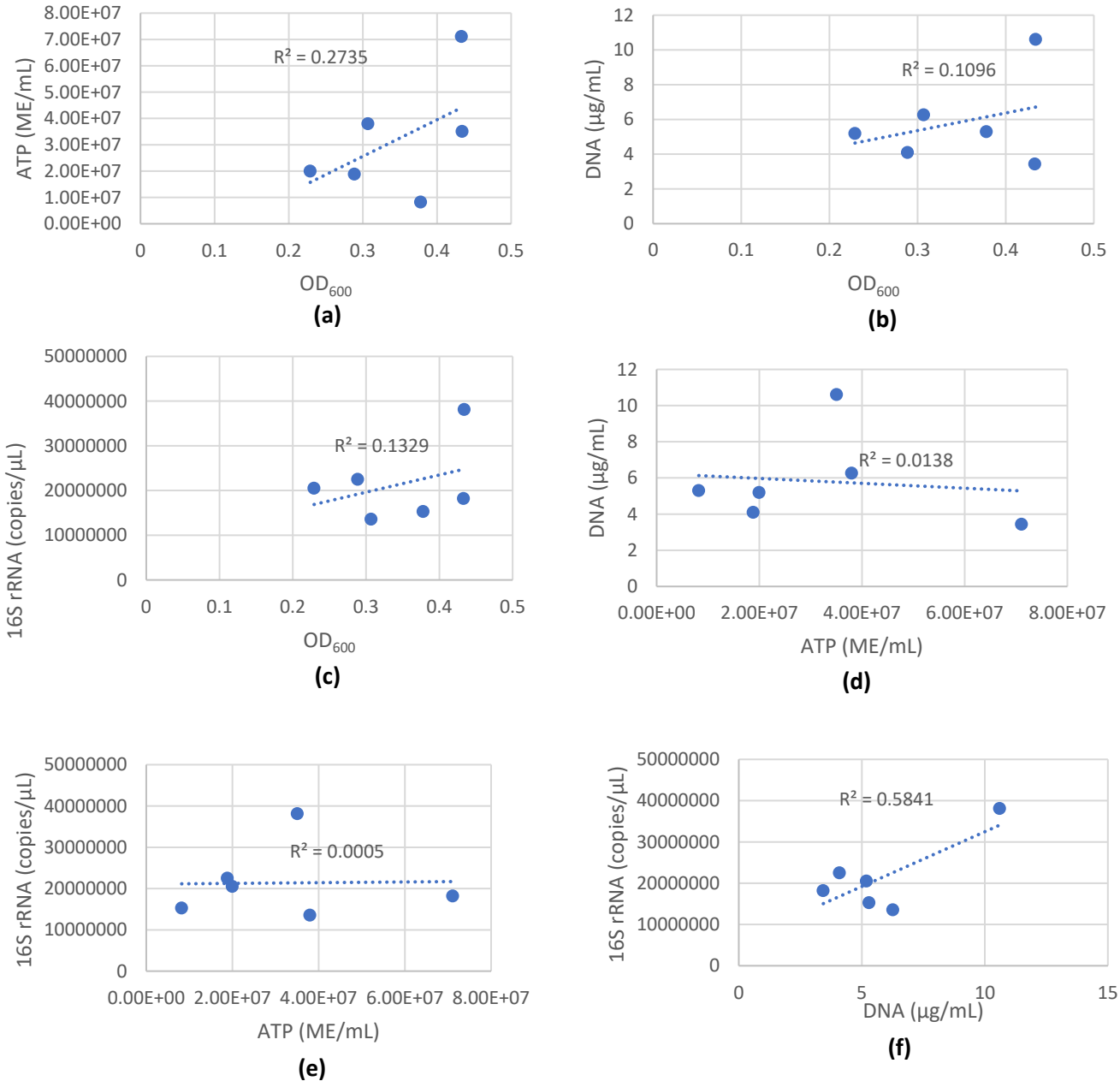


Figure S13: XY scatter plots of all four monitoring methods from the planktonic cells from the CBR exposed to BAC used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; f) DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

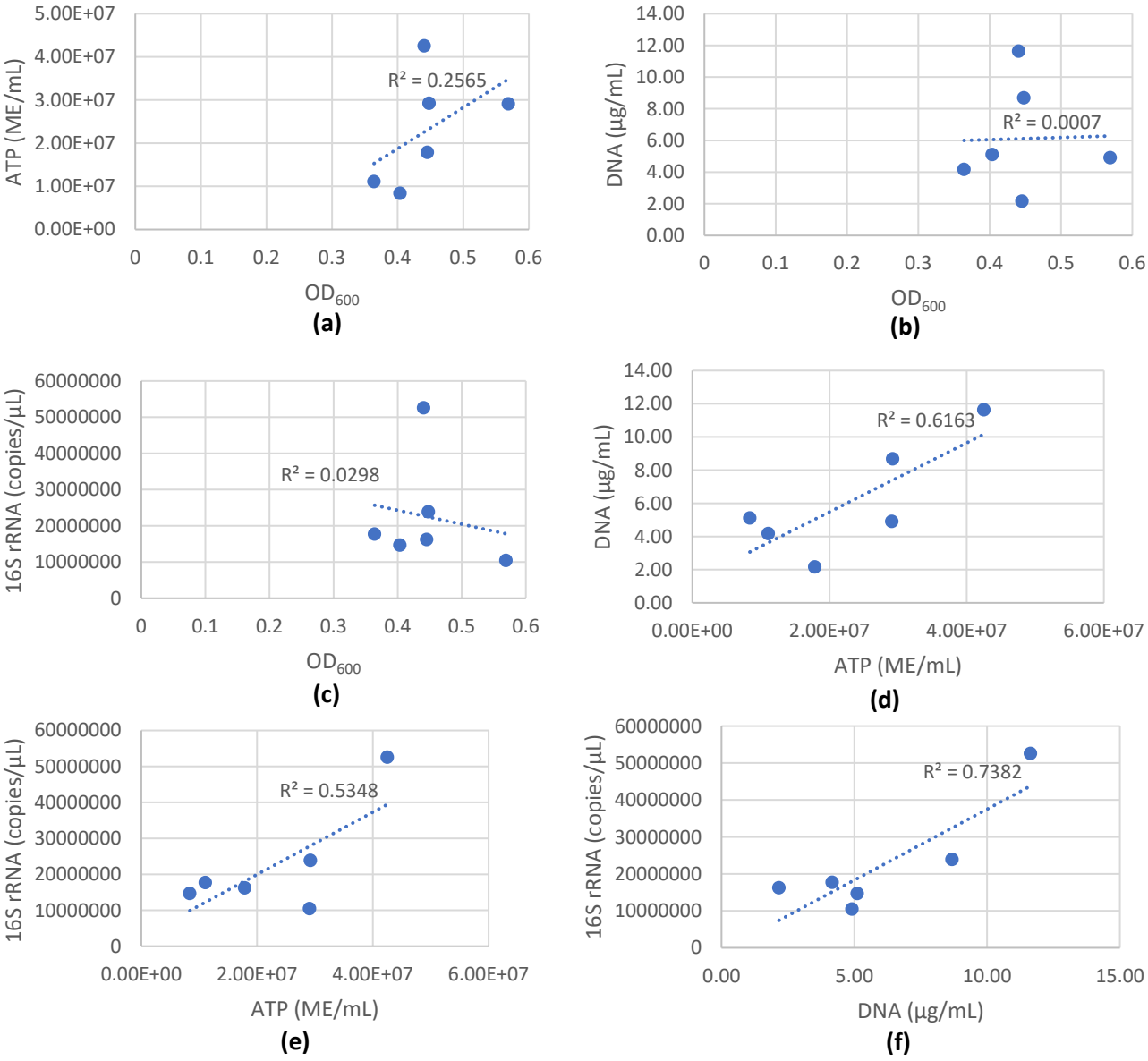


Figure S14: XY scatter plots of all four monitoring methods from the planktonic cells from the CBR not exposed to BAC used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; f) DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

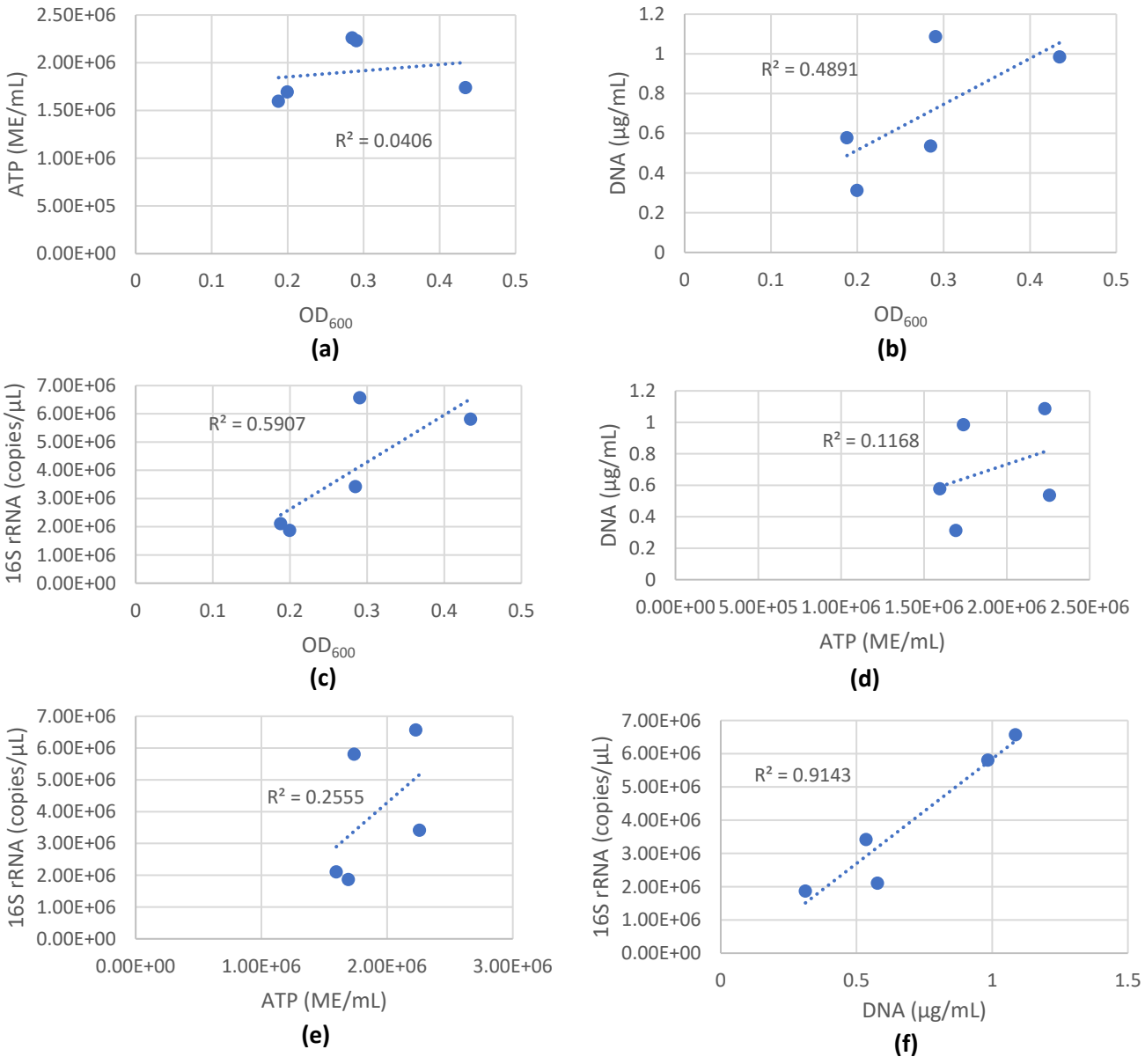


Figure S15: XY scatter plots of all four monitoring methods from the sessile cells from the CBR exposed to BAC used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; f) DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

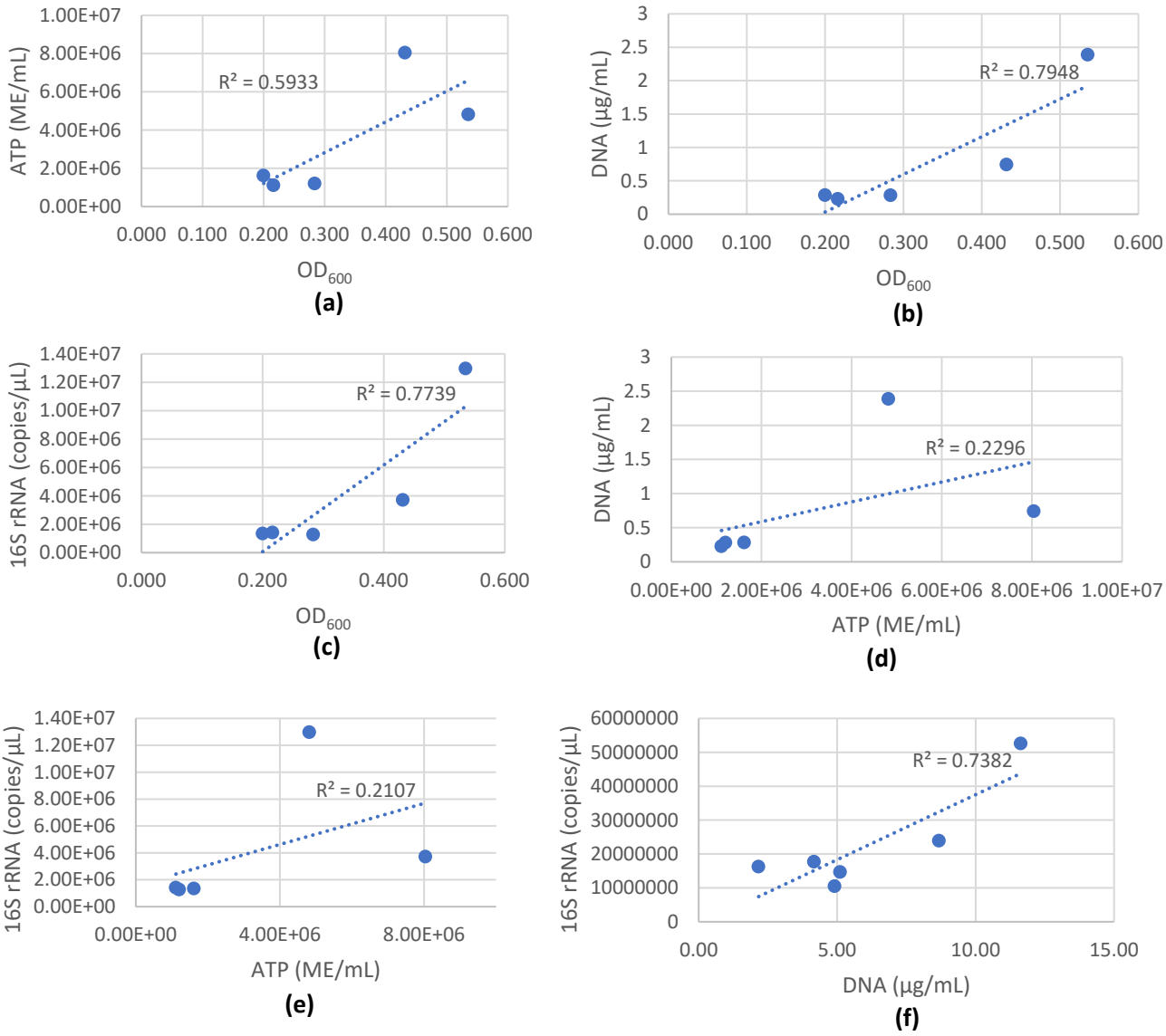


Figure S16: XY scatter plots of all four monitoring methods from the sessile cells from the CBR not exposed to BAC used to determine the correlation values (R values) between **a)** OD_{600} and ATP; **b)** OD_{600} and DNA; **c)** OD_{600} and 16S rRNA; **d)** ATP and DNA; **e)** ATP and 16S rRNA; f) DNA and 16S rRNA. R values were calculated by taking the square root of the R^2 value from the linear trendlines.

Preliminary data used for proper time point sampling of each pure strain culture

Table S1 Tabulated data of OD_{600}, ATP and DNA methods used to determine proper sampling time points

Species	Time point (hours)	OD_{600}			ATP (ME/mL)	DNA (μg/mL)
A. woodii	Inoculant	0.443	0.436	0.420	18464132.1	22.4
	0	0.053	0.054	0.052	148353206	0.20
	4	0.132	0.139	0.138	153662741	0.06
	24	0.258	0.265	0.263	944771926	5.71
	28	0.281	0.286	0.285	1085024459	7.32
	48	0.344	0.369	0.359	1280022005	6.83
	72	0.402	0.415	0.416	405683780	11.9
B. subtilis	Inoculant	-0.001	-0.005	-0.001	3267689.6	0.21
	0	0.002	0.000	-0.001	1646305.71	0.00
	4	0.053	0.054	0.052	3550989.73	0.00
	24	0.093	0.094	0.095	94891705.6	3.29
	28	0.106	0.108	0.109	115769729	1.40
	48	0.082	0.085	0.085	72515616.1	3.37
	72	0.063	0.065	0.064	21028258.6	1.89
D. vulgaris	Inoculant	1.399	1.286	1.372	5523846.76	24.0
	0	0.508	0.451	0.478	1835906.96	0.14
	4	0.903	0.946	0.964	5436732.65	0.43
	24	1.067	1.081	1.123	56788087.6	1.47
	28	1.177	1.267	1.250	106486584	2.33
	48	1.438	1.477	1.519	223674759	11.7
	72	1.484	1.519	1.546	68422350.4	14.3
G. subterraneus	Inoculant	0.109	0.100	0.100	80174941.4	29.7
	0	0.008	0.019	0.011	25474003.1	1.27
	4	0.060	0.062	0.061	166534202	1.53
	24	0.147	0.154	0.154	82235622.3	26.2
	28	0.146	0.150	0.152	51172577.5	32.3
	48	0.142	0.148	0.148	62980550.8	28.0
	72	0.155	0.151	0.163	47872959.5	26.9
P. putida	Inoculant	0.089	0.100	0.094	306912138	24.1
	0	0.014	0.014	0.012	37671520.7	4.50
	4	0.101	0.104	0.103	114483588	21.2
	24	0.111	0.110	0.112	190658791	13.3
	28	0.125	0.126	0.129	203596504	21.8
	48	0.122	0.128	0.129	312392817	19.7
	72	0.129	0.136	0.136	216840262	20.6
T. aromatica	Inoculant	0.192	0.195	0.211	694631059	37.7
	0	0.022	0.023	0.034	65662138.4	3.90
	4	0.086	0.086	0.086	120465046	5.08
	24	0.294	0.292	0.291	301583805	14.4
	28	0.402	0.410	0.404	497318538	35.9
	48	0.349	0.353	0.352	1045147643	57.0
	72	0.317	0.329	0.325	709747004	46.7

Calculated cell count equivalents from OD_{600}, ATP, DNA concentrations and 16S rRNA targeted qPCR

Table S2 Summary of the calculated cell counts per milliliter from each monitoring method at the initial time point, mid log phase and stationary phase for all species tested

Species	Time point (hours)	Testing method			
		Converted CFU/mL from OD_{600}	ATP (ME/mL)	Calculated cells from average DNA (cells/mL)	Calculated cells from 16S rRNA (cells/mL)
A. woodii	0	$4.55 \times 10^7 \pm 6.60 \times 10^5$	$8.77 \times 10^7 \pm 8.29 \times 10^6$	$3.02 \times 10^8 \pm 2.16 \times 10^7$	$1.45 \times 10^8 \pm 3.48 \times 10^7$
	13	$9.77 \times 10^7 \pm 8.77 \times 10^6$	$2.74 \times 10^8 \pm 7.05 \times 10^7$	$3.99 \times 10^9 \pm 6.71 \times 10^8$	$1.42 \times 10^9 \pm 1.96 \times 10^8$
	32	$2.63 \times 10^8 \pm 1.12 \times 10^7$	$1.45 \times 10^9 \pm 3.74 \times 10^8$	$1.18 \times 10^{10} \pm 1.35 \times 10^9$	$3.41 \times 10^9 \pm 2.92 \times 10^8$
B. subtilis	0	$2.07 \times 10^7 \pm 4.99 \times 10^5$	$3.23 \times 10^4 \pm 2.98 \times 10^4$	$2.71 \times 10^8 \pm 6.29 \times 10^7$	$8.85 \times 10^7 \pm 1.79 \times 10^7$
	13	$9.57 \times 10^7 \pm 2.08 \times 10^7$	$2.64 \times 10^8 \pm 1.08 \times 10^8$	$3.28 \times 10^9 \pm 1.79 \times 10^9$	$8.44 \times 10^8 \pm 3.79 \times 10^8$
	30	$8.03 \times 10^7 \pm 4.76 \times 10^6$	$2.30 \times 10^8 \pm 5.61 \times 10^7$	$4.98 \times 10^9 \pm 2.40 \times 10^9$	$8.40 \times 10^8 \pm 4.24 \times 10^8$
D. vulgaris	0	$3.03 \times 10^8 \pm 2.26 \times 10^7$	$5.59 \times 10^6 \pm 9.61 \times 10^4$	$1.08 \times 10^9 \pm 2.41 \times 10^8$	$7.24 \times 10^8 \pm 3.32 \times 10^8$
	28	$3.54 \times 10^8 \pm 3.88 \times 10^7$	$2.00 \times 10^8 \pm 4.28 \times 10^7$	$7.32 \times 10^9 \pm 8.65 \times 10^8$	$4.08 \times 10^9 \pm 8.04 \times 10^8$
	48	$4.06 \times 10^8 \pm 2.96 \times 10^7$	$1.53 \times 10^8 \pm 5.43 \times 10^7$	$1.78 \times 10^{10} \pm 1.10 \times 10^9$	$9.08 \times 10^9 \pm 1.93 \times 10^9$
G. subterraneus	0	$2.71 \times 10^7 \pm 9.43 \times 10^4$	$8.15 \times 10^7 \pm 8.02 \times 10^6$	$2.23 \times 10^9 \pm 2.24 \times 10^8$	$3.77 \times 10^9 \pm 4.51 \times 10^8$
	12	$4.41 \times 10^7 \pm 2.19 \times 10^6$	$2.41 \times 10^8 \pm 8.28 \times 10^7$	$6.00 \times 10^9 \pm 7.82 \times 10^8$	$6.12 \times 10^9 \pm 6.02 \times 10^8$
	32	$6.74 \times 10^7 \pm 4.81 \times 10^6$	$9.16 \times 10^7 \pm 1.75 \times 10^7$	$1.43 \times 10^{10} \pm 2.95 \times 10^9$	$1.17 \times 10^{10} \pm 2.62 \times 10^9$
P. putida	0	$2.58 \times 10^7 \pm 1.63 \times 10^5$	$4.12 \times 10^7 \pm 2.55 \times 10^6$	$2.09 \times 10^9 \pm 1.21 \times 10^8$	$4.29 \times 10^8 \pm 1.47 \times 10^8$
	6	$1.09 \times 10^8 \pm 1.61 \times 10^7$	$5.77 \times 10^8 \pm 1.08 \times 10^8$	$2.47 \times 10^{10} \pm 5.26 \times 10^9$	$7.96 \times 10^9 \pm 2.59 \times 10^9$
	33.5	$2.04 \times 10^8 \pm 4.39 \times 10^7$	$8.65 \times 10^8 \pm 1.46 \times 10^8$	$4.17 \times 10^{10} \pm 1.02 \times 10^{10}$	$4.79 \times 10^9 \pm 1.55 \times 10^9$
T. aromatica	0	$3.35 \times 10^7 \pm 1.39 \times 10^6$	$5.81 \times 10^7 \pm 2.97 \times 10^6$	$6.11 \times 10^8 \pm 1.11 \times 10^8$	$7.01 \times 10^8 \pm 2.83 \times 10^8$
	20	$1.45 \times 10^8 \pm 6.38 \times 10^6$	$3.51 \times 10^8 \pm 2.64 \times 10^7$	$1.41 \times 10^{10} \pm 1.53 \times 10^9$	$1.41 \times 10^{10} \pm 7.54 \times 10^9$
	48	$1.65 \times 10^8 \pm 2.30 \times 10^6$	$4.41 \times 10^8 \pm 2.90 \times 10^7$	$2.85 \times 10^{10} \pm 1.08 \times 10^9$	$2.62 \times 10^{10} \pm 7.66 \times 10^9$