Supplementary Material

Comparable SAR11 and *Prochlorococcus* light enhanced uptake in the North Atlantic subtropical gyre

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Supplementary Table 1: Oligonucleotide probes used in this study

Probe name	Target organism	Sequence 5' ->3'	Position[-]	FA %	Reference
EUB338*	*Bacteria*	GCTGCCTCCCGTAGGAGT	338	35	Amann et al. 1990
EUB338-II*	Supplement to EUB338	GCAGCCACCCGTAGGTGT	338	35	Daims et al. 1999
EUB338-III*	Supplement to EUB338	GCTGCCACCCGTAGGTGT	338	35	Daims et al. 1999
PRO405	*Prochlorococcus*	AGAGGCCTTCGTCCCTCA	405	40	West et al. 2010
SAR11-152R **	SAR11	TTAGCACAAGTTTCCYCGTGT	152	25	Morris et al. 2002
SAR11-441R **	SAR11	TACAGTCATTTTCTTCCCCGAC	441	25	Morris et al. 2002
SAR11-441Rmod **	SAR11	TAC**C**GTCATTTTCTTCCCCGAC	441	25	Morris et al., 2002. Modified, this study[+]
SAR11-542R **	SAR11	TCCGAACTACGCTAGGTC	542	25	Morris et al. 2002
SAR11-732R **	SAR11	GTCAGTAATGATCCAGAAAGYTG	732	25	Morris et al. 2002
SAR11-487 **	SAR11	CGGACCTTCTTATTCGGG	487	25	This study
SAR11-487-h3 **	SAR11	CGGCTGCTGGCACGAAGTTAGC	505	25	This study

Footnote:

Abbreviations: h, unlabelled helper oligonucleotide probe; FA, formamide concentration (v/v) in hybridization buffer

- Position in 16S rRNA according to *E. coli* numbering

* , ** probes applied together

[+] SAR11-Rmod has a one-base modification (shown underlined) from SAR11-441R to account variance in SAR11 clade sequences.

References

Amann RI, Binder BJ, Olson RJ, Chisholm SW, Devereux R, Stahl DA (1990). Combination of 16s ribosomal-Rna-targeted oligonucleotide probes with flow-cytometry for analyzing mixed microbial-populations. *Appl Environ Microb* **56:** 1919-1925.

Daims H, Bruhl A, Amann R, Schleifer KH, Wagner M (1999). The domain-specific probe EUB338 is insufficient for the detection of all Bacteria: Development and evaluation of a more comprehensive probe set. *Syst Appl Microbiol* **22:** 434-444.

Morris RM, Rappe MS, Connon SA, Vergin KL, Siebold WA, Carlson CA *et al* (2002). SAR11 clade dominates ocean surface bacterioplankton communities. *Nature* **420:** 806-810.

West NJ, Schonhuber WA, Fuller NJ, Amann RI, Rippka R, Post AF *et al* (2001). Closely related *Prochlorococcus* genotypes show remarkably different depth distributions in two oceanic regions as revealed by *in situ* hybridization using 16S rRNA-targeted oligonucleotides. *Microbiology* **147:** 1731-1744.

Legends to figures

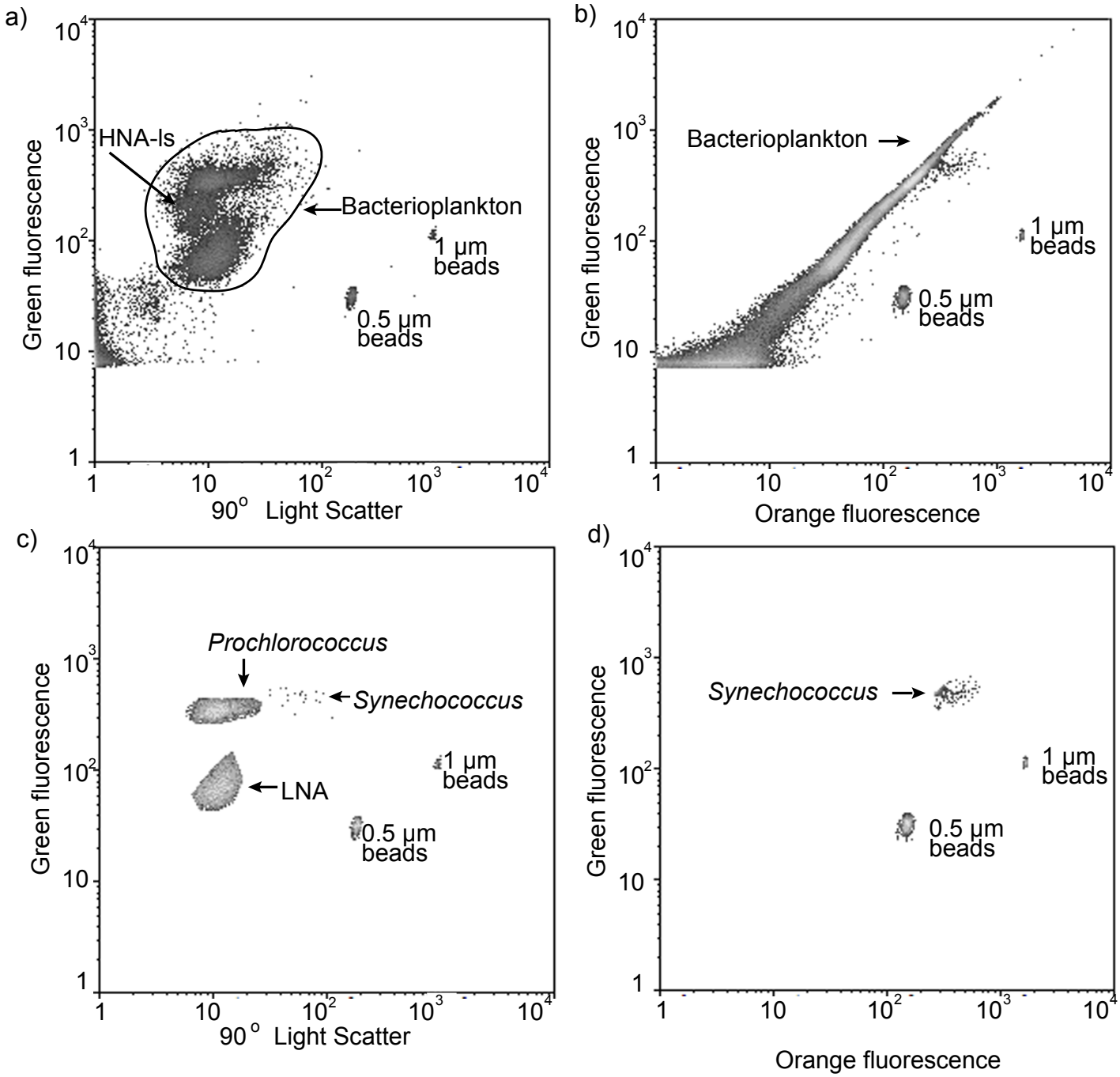
Supplementary Figure 1: (a, b) Characteristic flow cytometric density plot signatures of SYBR Green – DNA stained bacterioplankton and **(c, d)** Flow-sorted groups of LNA containing cells, *Prochlorococcus* cells and *Synechococcus* cells, and singlet reference beads. Axis represents SYBR Green I DNA-stained green fluorescence, and (a, c) 90° light scatter or (c, d) phycoerythirn orange auto-fluorescence characteristic of *Synechococcus*.

Supplementary Figure 2: Time course total microbial uptake of ^{3}H-ATP in the light (white symbols) and in the dark (dark grey symbols) in different experiments as shown in Figure 1. Same symbols represent paired light and dark experiments.

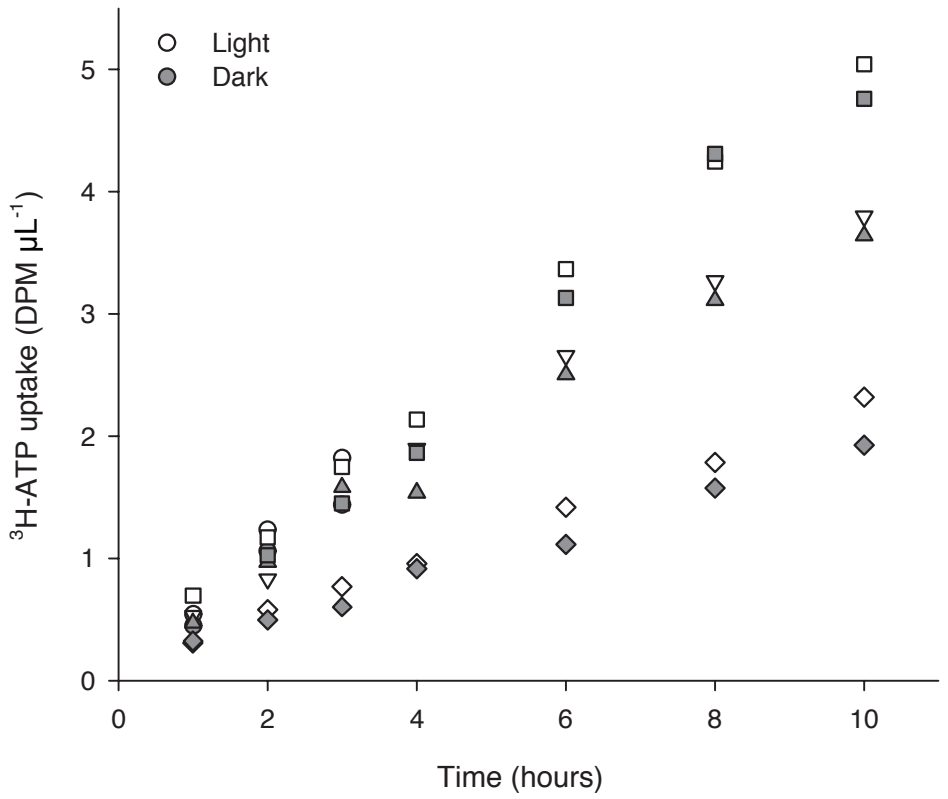
Supplementary Figure 3: Scatter plot comparison of **(a)** total ^{33}P-ATP and **(b)** total methionine microbial uptake retained in particulate material (total) versus flow sorted bacterioplankton (Bpl) uptake. No statistically significant difference was detected between measurements for both substrates. ATP: t-test p=0.55, methionine t-test p=0.17, f-statistic higher than f-critical for both substrates. Scatter plot comparison of **(c)** ^{33}P-ATP and **(d)** methionine total bacterioplankton (Bpl) uptake versus sum of *Prochlorococcus* (Pro) and SAR11 uptake. Total group uptake was calculated as the uptake of an average flow-sorted cell by the abundance of the group in the corresponding experiment.

Supplementary Figure 4: Bioassay estimation of ATP ambient concentration and uptake rate with ^{3}H-ATP and ^{33}P-ATP showing relationship between added ATP concentration and uptake time.

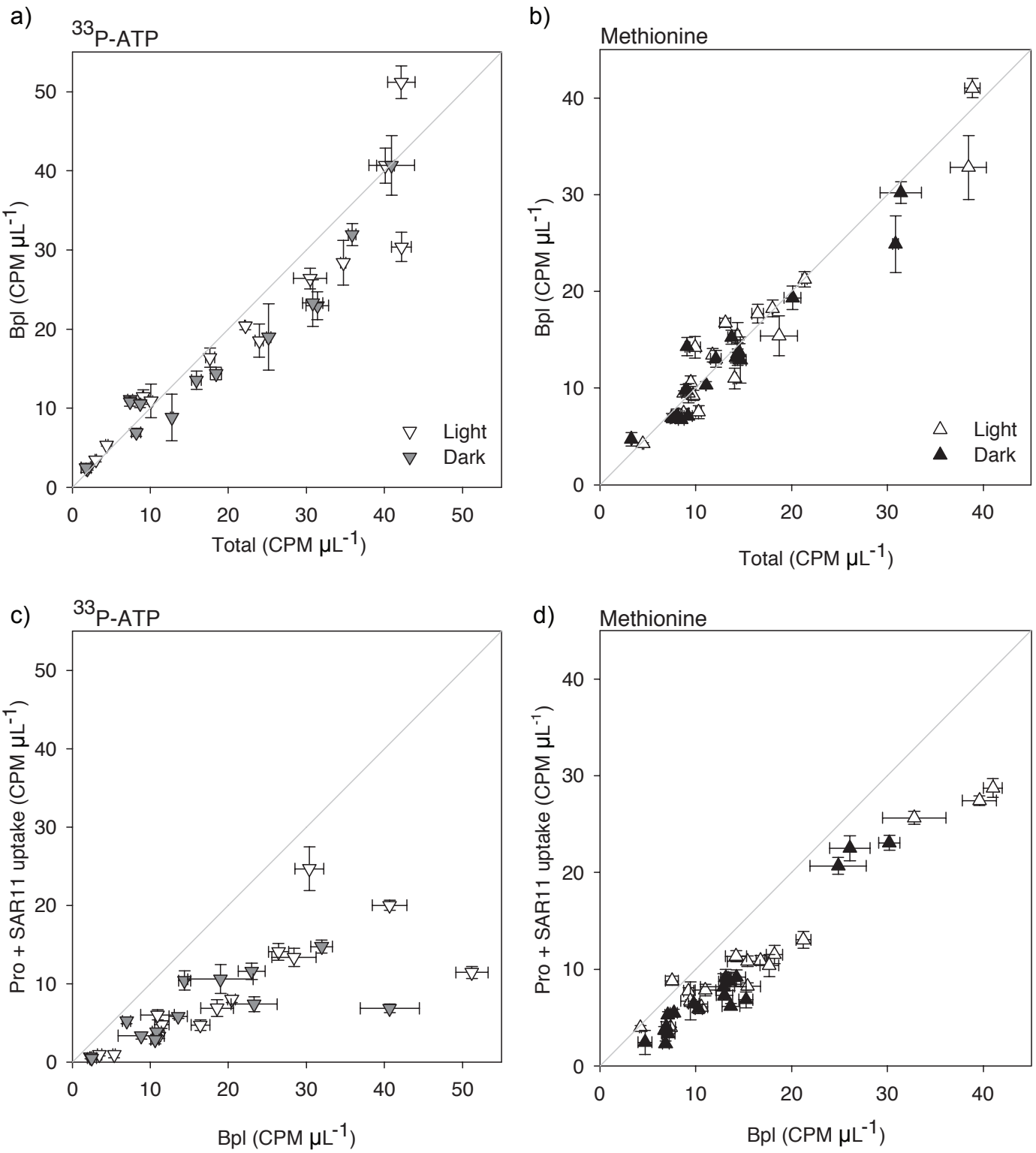
Supplementary Figure 5: Scatter plot comparison of **(a)** ^{33}P-ATP and **(b)** methionine uptake in dark versus light incubations of high-nucleic acid containing bacterioplankton (HNA-ls) estimated by subtracting the sum of *Prochlorococcus* and SAR11 population uptake from the total microbial uptake. Paired t-test for both substrates $p>0.05$.



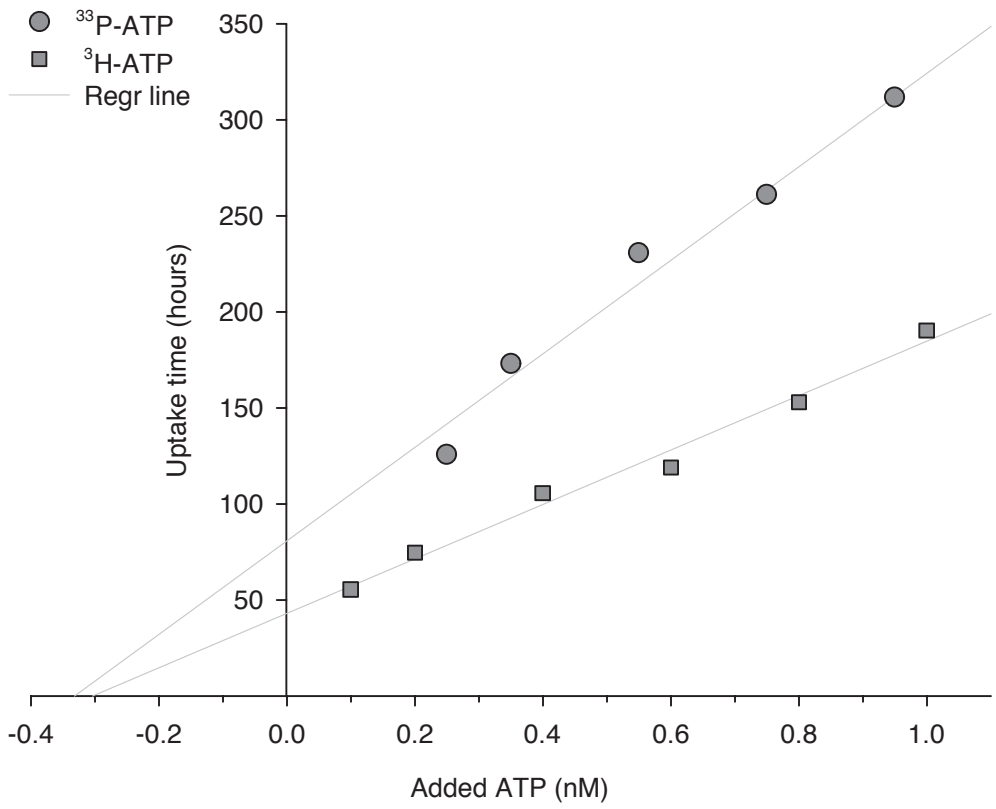
Supplementary Figure 1



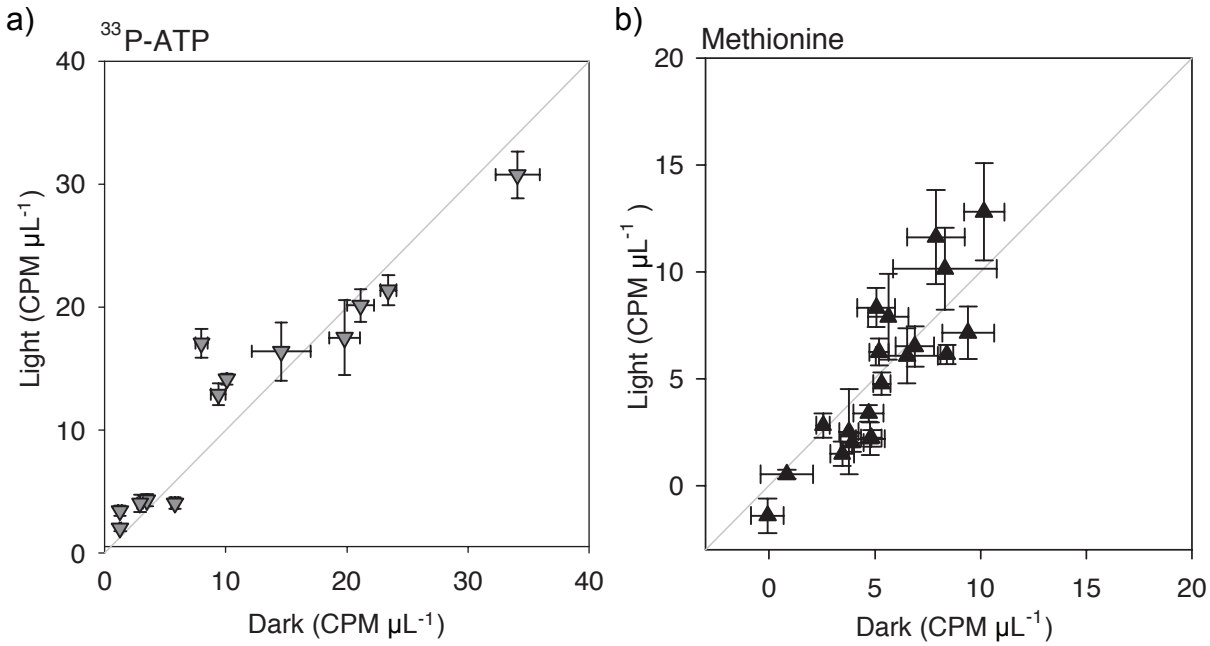
Supplementary Figure 2



Supplementary Figure 3



Supplementary Figure 4



Supplementary Figure 5