

## 1 **Supplementary figure legends**

2 **Fig. S1** Transmission electron microscopy of OM43 cells from the Red Sea growing at 28 °C in  
3 low-nutrient media. Bar size: 200 nm.

4 **Fig. S2** Growth measurements at 28 °C of the Red Sea isolate MBRS-H7 in the presence  
5 (squares) or absence (circles) of 100 µM methanol.

6 **Fig. S3** Maximum-likelihood (n=1000 bootstraps) phylogenetic comparison of the 16S rRNA  
7 gene versus the 23S rRNA gene classification of main methylotrophic bacterial groups. Isolates  
8 MBRS-F5 and MBRS-G12 which are almost identical to MBRS-H7 are also shown. Red: H-RS;  
9 Bold black: Freshwater *Ca. Methylopumilus* strains; Green: other *Methylophylaceae*.

10 **Fig. S4** Maximum-likelihood (n=1000 bootstraps) phylogeny of xanthorhodopsin proteins based  
11 on the classification by Vollmers *et al.*, 2013, including members of the OM43 clade and *Ca.*  
12 *Methylopumilus* strains. The relationship with other divergent rhodopsin-like proteins is also  
13 shown. Isolates MBRS-F5 and MBRS-G12 which are virtually identical to MBRS-H7 are also  
14 shown.

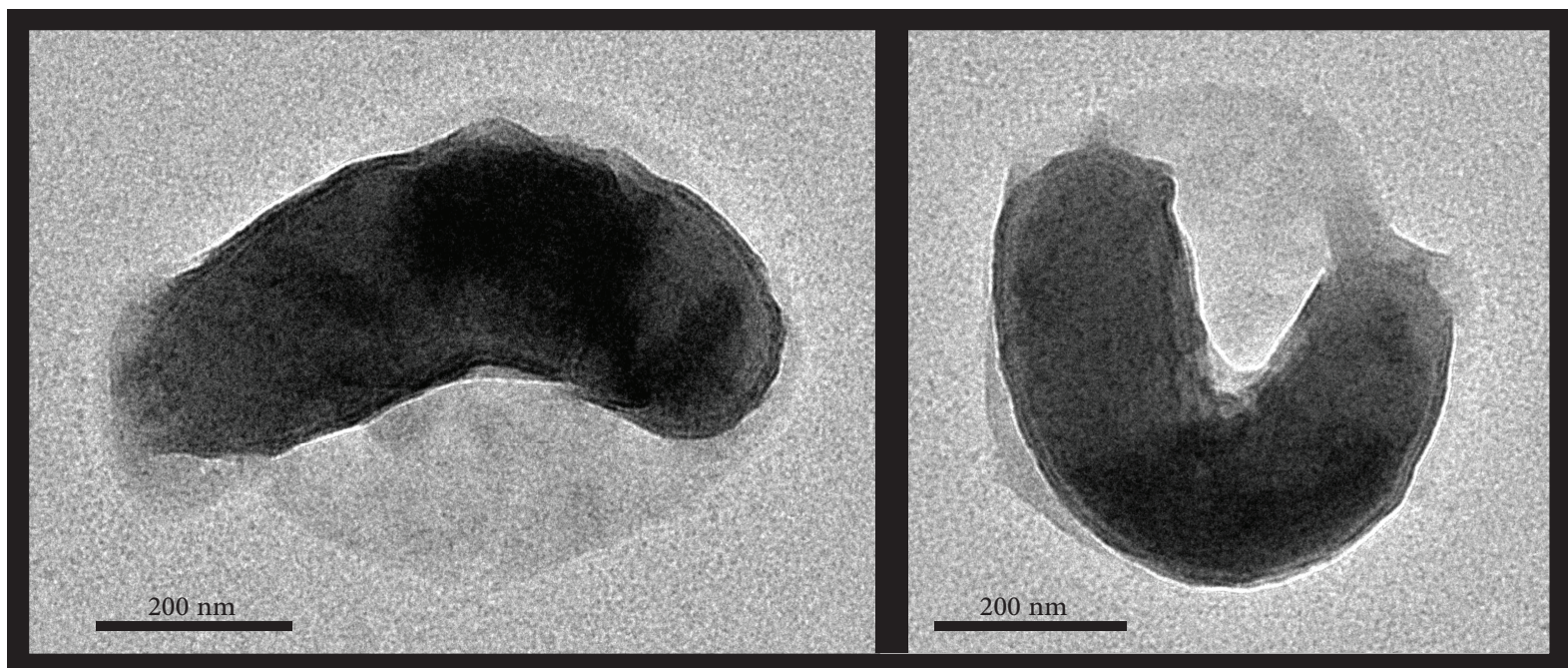
15 **Fig. S5** Fragment recruitment analysis comparing HTCC2181, KB13 and MBRS-H7 against  
16 metagenomes from the Red Sea, East Tropical South Pacific (ETSP), Hawaii Ocean Time Series  
17 (HOT), and Bermuda Atlantic Time Series (BATS), at different seasons and depths.

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## References

**Vollmers J, Voget S, Dietrich S, Gollnow K, Smits M, Meyer K, Brinkhoff T, Simon M, Daniel R.** 2013. Poles apart: Arctic and Antarctic Octadecabacter strains share high genome plasticity and a new type of xanthorhodopsin. PLoS One **8**:e63422.



**Figure S1.**

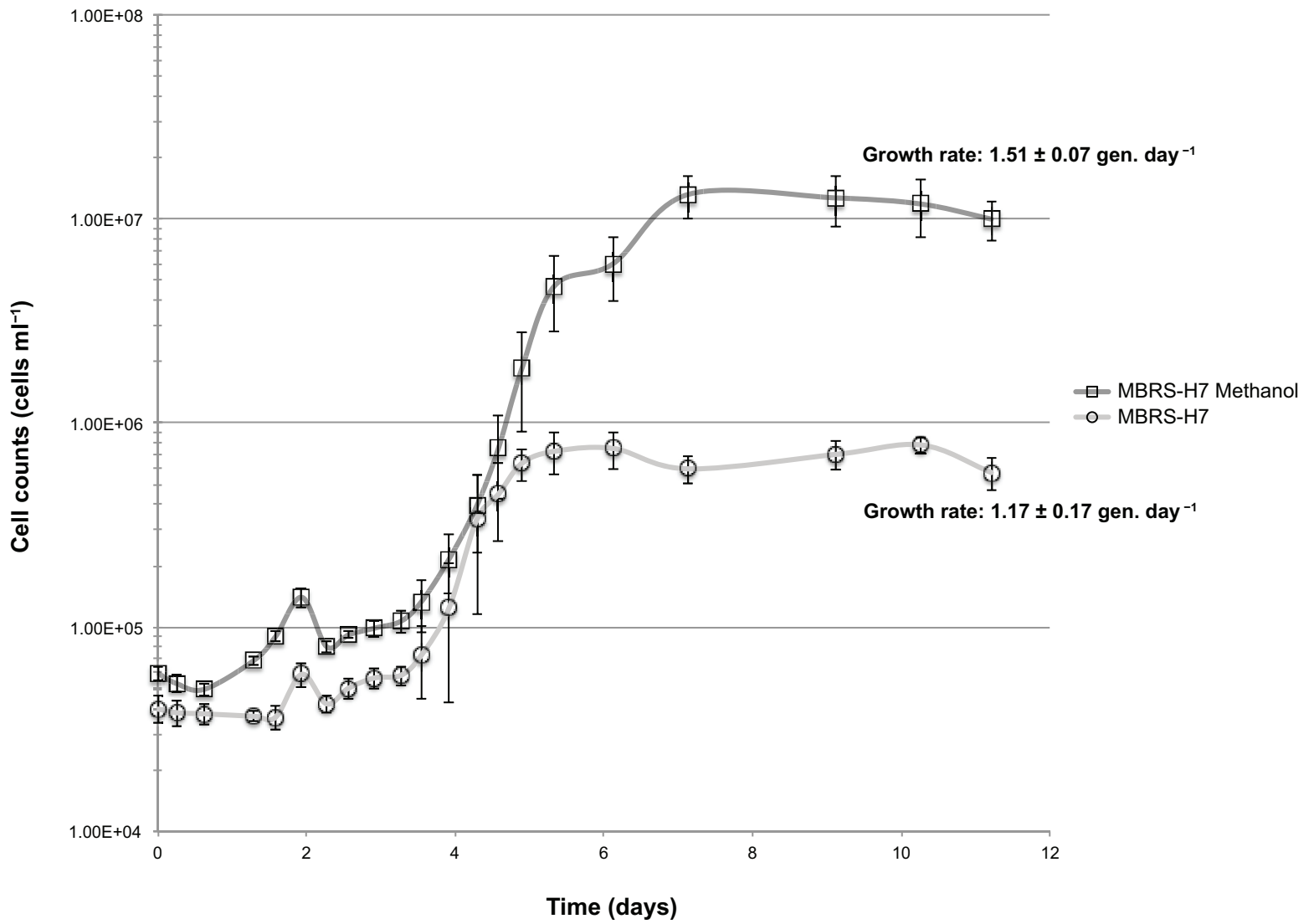


Figure S2.

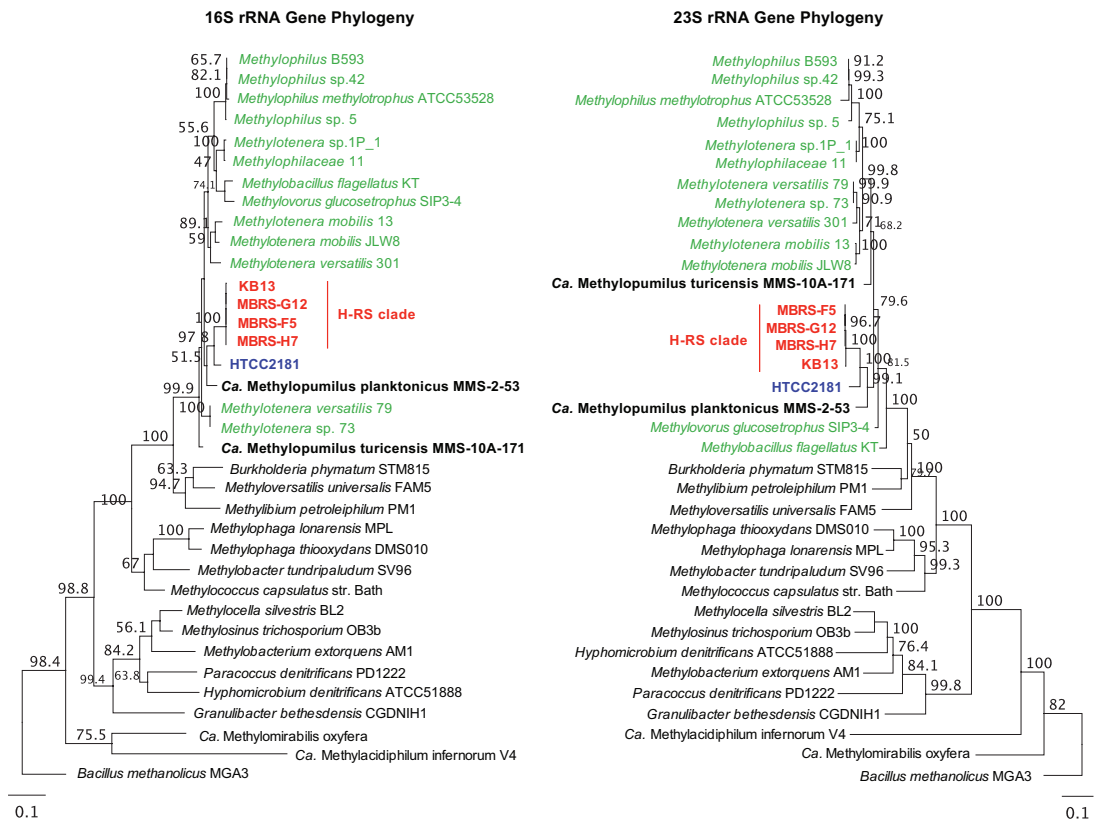


Figure S3

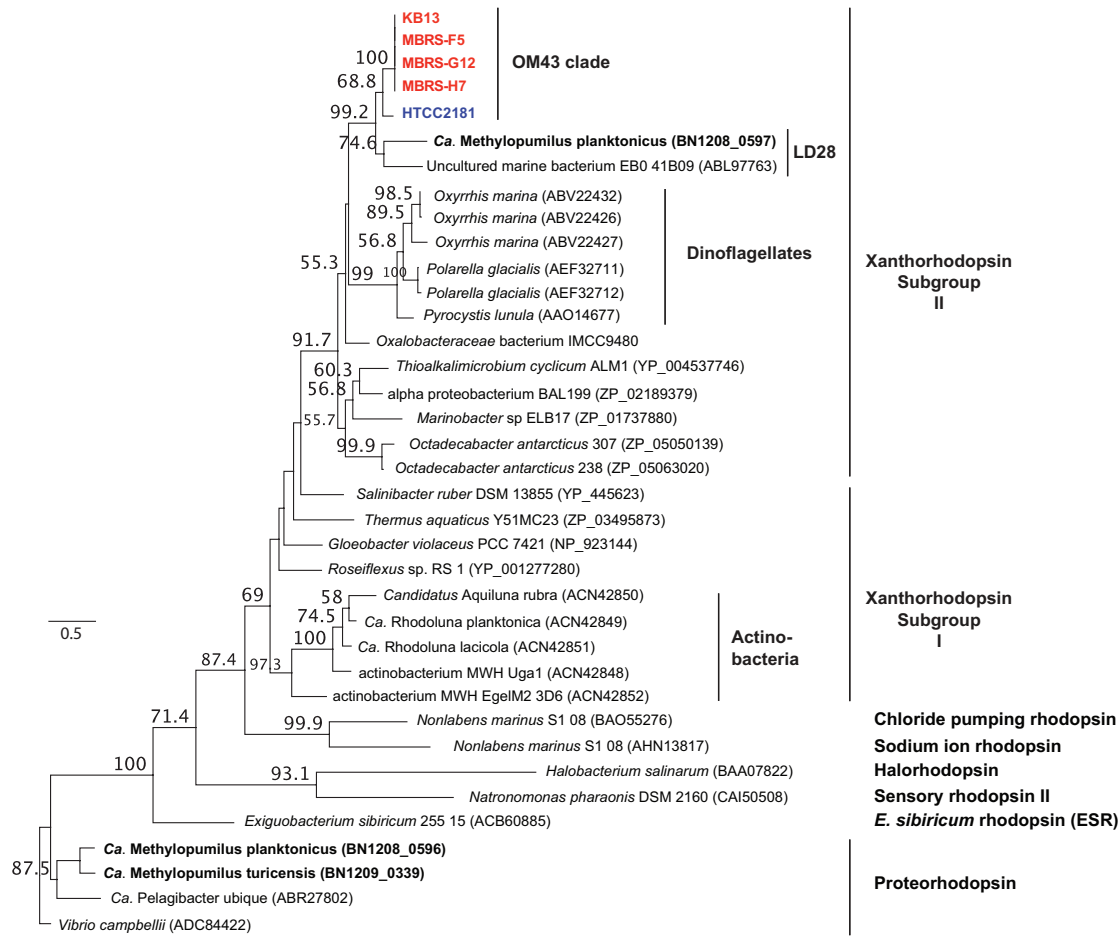
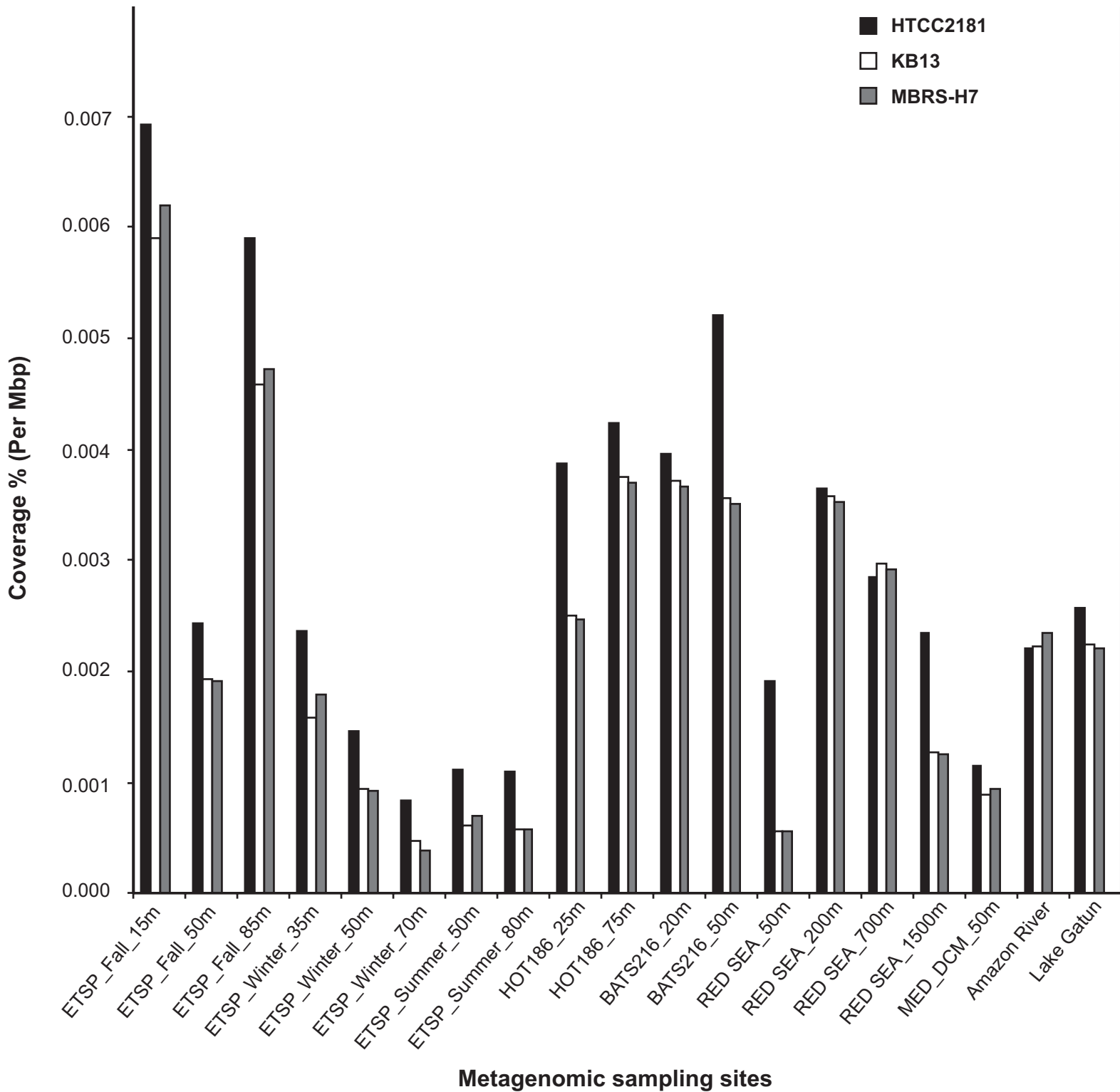


Figure S4



**Figure S5.**