Marine Group II Archaea are significant players of carbon cycling in estuaries and coastal seas

 $\begin{array}{c} C. \ Zhang^{1*}, W. \ Xie^1, S. \ Murugapiran^2,\\ J. \ A. \ Dodsworth^3, H. \ Luo^4, Y. \ Sun^4, S. \ Chen^1,\\ P. \ Wang^1, B. \ P. \ Hedlund^2 \ and \ T. \ J. \ Phelps^5 \end{array}$

¹Tongji University, Shanghai, China

(Correspondance:archaeazhang_1@tongji.edu.cn) ²University of Nevada, Las Vegas, Nevada, USA ³California State University, San Bernardino, CA, USA ⁴Chinese University of Hong Kong, Hong Kong, China ⁵University of Tennessee, Knoxville, Tennessee, USA

Marine Group I (MG I) and Marine Group II (MG II) were the first two groups of planktonic archaea discovered in the marine environment about two decades ago. While MG I has been known to play significant roles in carbon and nitrogen cycles in global oceans, the role of MG II has remained ambiguous. Here we report a seasonal pattern of MG II in the Pearl River Estuary and the coastal South China Sea and provide genomic information that reveals the novelty of a new subgroup (MG IIc) containing metabolic pathways previously unidentified in planktonic archaea. The abundance of MG II gradually increases from fresh river water to the estuary (representing up to >95% of total archaea) but drops significantly in the open marine water, suggesting that the estuary may be a favored environment for the growth of MG II. MG IIc is identified by metagenomic analysis from the more saline location in the estuary, and is distantly related to MG IIa and MG IIb. In agreement with MG IIa and MG IIb, MG IIc contains an abundance of enzymes for protein degradation. All MG II organisms identified so far are heterotrophs; however, the exact pathway of carbon metabolism by this mysterious group has been elusive. This study narrows this knowledge gap and suggests that MG II may have an important role in secondary production in estuaries and coastal seas. The MG II organisms may also be significant sources of archaeal lipid biomarkers in the marine environment, which may help us address the uncertainties of TEX₈₆ proxies potentially caused by changes in archaeal community structure.