Distinct metabolic capabilities of Marine Group II archaea adapted to low-salinity estuarine environments

 $L. Fan^{19}, B. Xu^{19}, Y. Liu^{29}, F. Li^1, M. Li^2. C. Zhang^{1*}$

¹Shenzhen Key Laboratory of Marine Archaea Geo-Omics, Department of Ocean Science and Engineering, Southern University of Science and Technology, Shenzhen 518055, China (*correspondence: zhangel@sustech.edu.cn)

²Institute for Advanced Study, Shenzhen University, Shenzhen 518055, China.

⁹Joint first authors

Marine Group II (MGII) archaea are among the most abundant archaeal populations in global oceans and are absent in freshwater ecosystems or salty lakes [1]. They are one of the key players of organic matter degradation in oceans [2]. However, their distribution and biogeochemical roles in lowsalinity zones in estuaries is unknown. Here we conducted metagenomic studies of MGII archaea at the Pearl River Estuary, China and identified two distinct patterns of distribution along salinity gradient. Some novel lineages of MGII-a archaea were found only in zones of salinity between 10 and 20 % (Figure 1). These lineages were distantly related to oceanic MGII archaea and possessed diverse functional mechanisms for adapting low salinity environment including magnesium transportation. Moreover, they had the potential to degrade distinct types of organic matters in estuarine lowsalinity zones. The discovery of these novel archaeal lineages captures an evolutionary process in which marine archaea explore new ecological niches where rivers meet the sea.

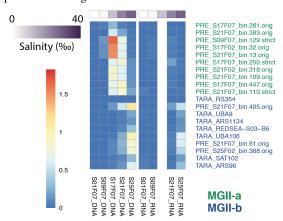


Figure 1: Distribution of MGII archaea along salinity gradient at the Pearl River Estuary, China. [1] Rinke (2018) *ISME J.* **13,** 663-675; [2] Tully (2019) *Nat. commun* **10,** 271.