

Figure F1. Downhole DNA concentration profiles extracted for metagenomic sequencing of bacteria and archaea, Holes U1545B, U1546D, and U1547B. Temperature values represent in situ measurements (Teske et al., 2021b, 2021d). Extractions give consistent results across different sample sets, as shown by initial DNA extractions by G. Ramírez and D. Bojanova.

Figure F2. Downhole DNA concentration profiles extracted for PCR amplification of 16S rRNA genes and functional genes (Table T2), Holes U1545B–U1552B.

Figure F3. Direct cell counts with SYBR Green as DNA-staining fluorophore in Guaymas Basin sediment samples from selected Expedition 385 drill sites (Mor-

ono et al., 2022). Data points correspond to samples used for 16S rRNA gene and functional gene surveys of bacteria and archaea (Table T2).

Figure F4. DNA concentration profiles for surficial hydrothermal sediments (*Alvin* Dive 4872; 24 December 2016) extracted manually by a combined freeze-thawing, enzymatic lysis, and organic extraction protocol (Zhou et al., 1996) and cleaned using Amicon purification columns (Table T4). Core 1 was obtained from warm sediment without microbial mat cover, Core 6 from hot hydrothermal sediment covered with a white *Beggiatoaceae* mat, and Core 14 from very hot hydrothermal sediment covered with an orange *Beggiatoaceae* mat. For final DNA concentrations per milligram of sediment, the extract concentrations are multiplied by factor 100.