



Supplementary Figure S6 Length-dependent gene abundances pervasively influence the quantification of microbial function. (A) Identification of KEGG Orthologs (KOs) with significant differences (adjusted p-value < 0.05) using relative gene abundances (B) Comparison of the relative gene abundance values of K08480 in two different cyanobacterial cultures using the 'contig mapping' method proposed in this study. (C) Comparison of the relative gene abundance values of K08480 in two cyanobacterial cultures using Salmon. Asterisk in **B** indicate adjusted p-value < 0.05.