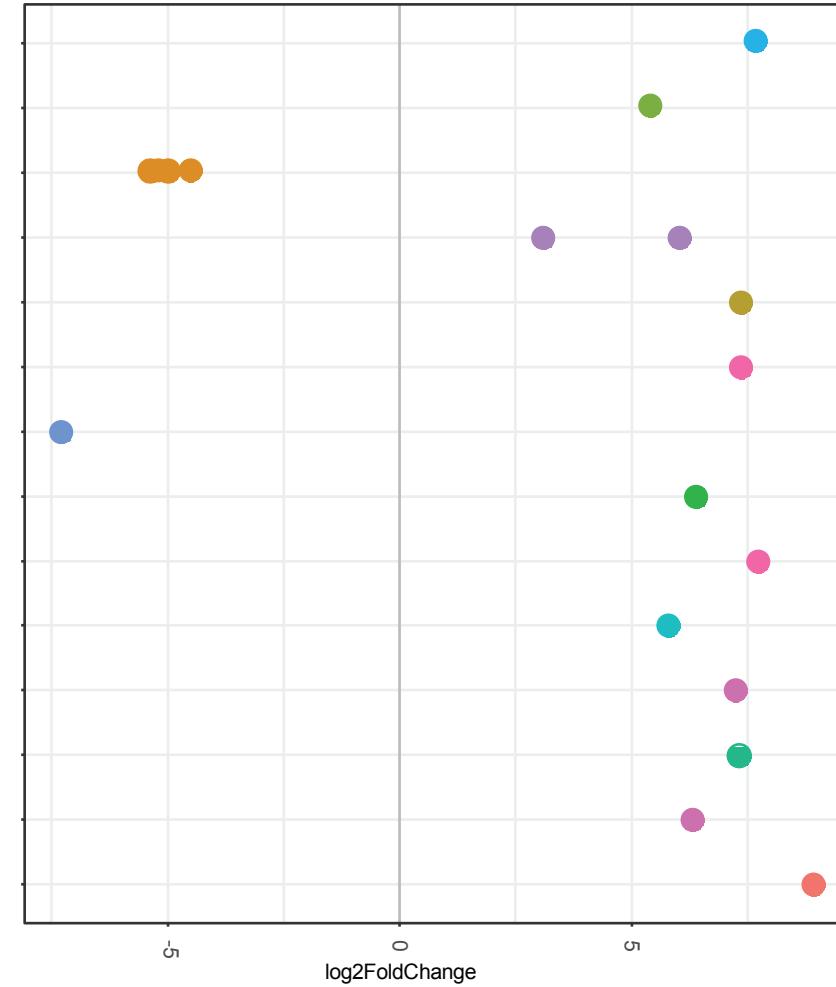


P_Verrucomicrobia; C_Verrucomicrobiae; O_Verrucomicrobales; F_Rubritaleaceae; G_Rubritalea
P_Proteobacteria; C_Gammaproteobacteria; O_Oceanospirillales; F_Oleophilaceae; G_Oleophilus
P_Proteobacteria; C_Gammaproteobacteria; O_Oceanospirillales; F_Hahellaceae; G_Endozoicomonas
P_Proteobacteria; C_Gammaproteobacteria; O_Alteromonadales; F_Colwelliaceae; G_Thalassotalea
P_Proteobacteria; C_Deltaproteobacteria; O_Myxococcales; F_Haliangiaceae; G_Haliangium
P_Proteobacteria; C_Alphaproteobacteria; O_Rickettsiales; F_LWSR-14; G_uncultured bacterium
P_Proteobacteria; C_Alphaproteobacteria; O_Rhodospirillales; F_Rhodospirillaceae; G_Thalassospira
P_Proteobacteria; C_Alphaproteobacteria; O_Rhodobacterales; F_Rhodobacteraceae; G_Paracoccus
P_Proteobacteria; C_Alphaproteobacteria; O_DB1-14; F_uncultured bacterium; G_uncultured bacterium
P_Cyanobacteria; C_Cyanobacteria; O_SubsectionIV; F_FamilyII; G_Rivularia
P_Cyanobacteria; C_Cyanobacteria; O_SubsectionIII; F_FamilyI; G_uncultured
P_Cyanobacteria; C_Cyanobacteria; O_SubsectionIII; F_FamilyI; G_Planktothricoides
P_Bacteroidetes; C_Sphingobacteriia; O_Sphingobacteriales; F_Chitinophagaceae; G_uncultured
P_Bacteroidetes; C_Cytophagia; O_Cytophagales; F_Flammeovirgaceae; G_Candidatus Amoebophilus



Supplementary Figure S1 - Differential abundance coral-associated OTUs between summer and winter. OTUs identified as differentially abundant following analysis using DESeq2 and Benjamini-Hochberg FDR corrections, are represented as circles. Each colour indicates a different genus. Positive log₂ fold-change values indicate OTUs with abundances higher in summer than in winter, while negative values indicate OTUs which were more abundant in winter compared with summer. Levels of taxonomy are indicated as P (phylum), C (Class), O (Order), F (Family) and G (Genus). This is a graphical presentation of the DESeq2 results listed in Supplementary File S1.