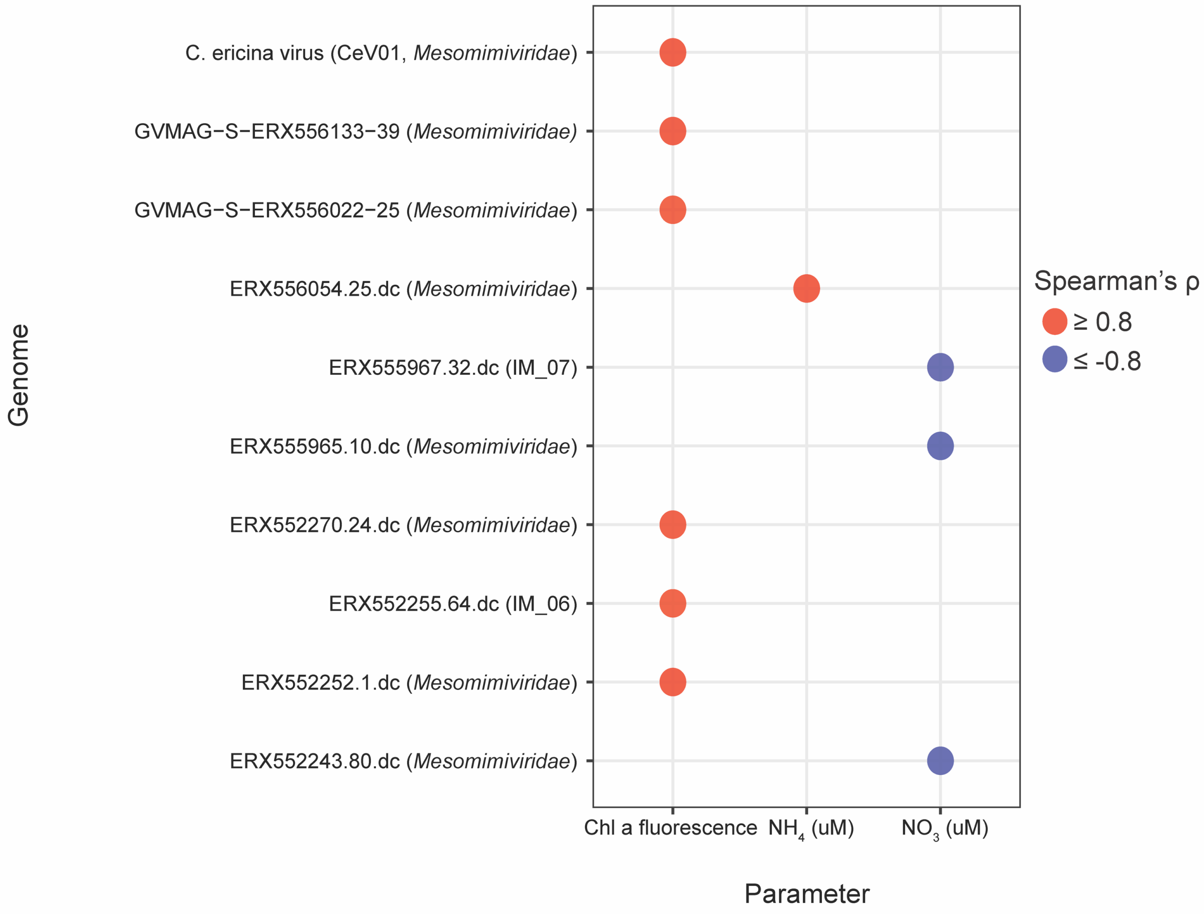

Supplementary Figure 7. Spearman's correlations between environmental parameters (CTD and nutrient data) and summed transcript abundances of each giant virus genome/MAG across the in situ dataset. Only correlations with Spearman's rho (ρ) ±0.8 with an adjusted p-value (Holm method) of ≤0.1 are shown. The Family-level assignment of each genome is shown in parentheses next to its ID.