

Fig. S1. Rarefaction analysis of the amplicon data obtained from three sponge samples.

Rarefaction curves were constructed based on OTUs clustered at 98% sequence identity across different samples.

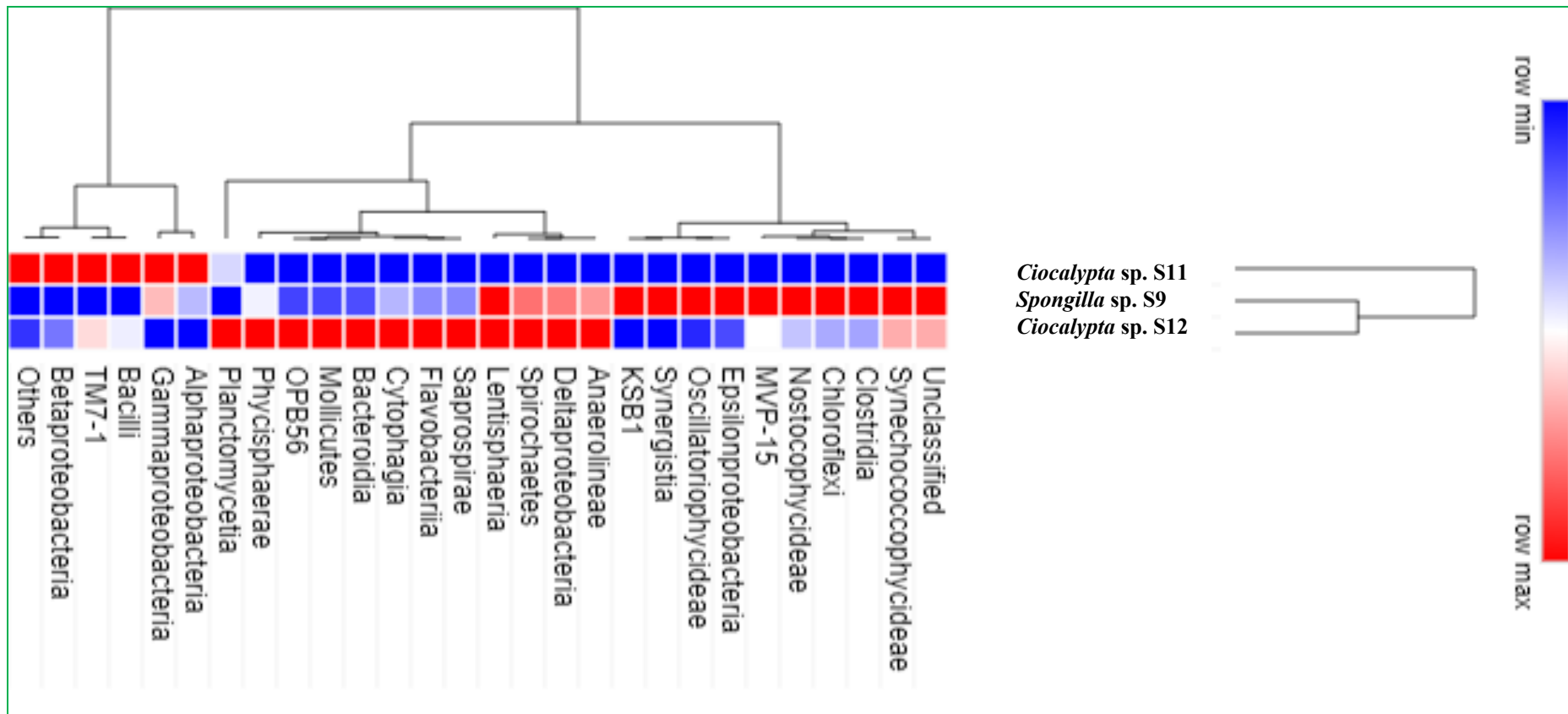


Fig. S2. Heat map showing Class-level comparison of bacterial community structure obtained from amplicon metagenome of three sponge samples; *Spongilla* sp. S9, *Ciocalypta* sp. S11 and *Ciocalypta* sp. S12.

The relative abundance is represented as the percentage of each class to the total effective bacterial sequences of each sample. Classes with greater than 0.5% of abundance in atleast two samples (28 out of 89 classes of bacteria) were shown here. The class Alphaproteobacteria is most abundant and present in all samples. *Anaerolineae* was the next dominant and absent in *Ciocalypta* sp. S11

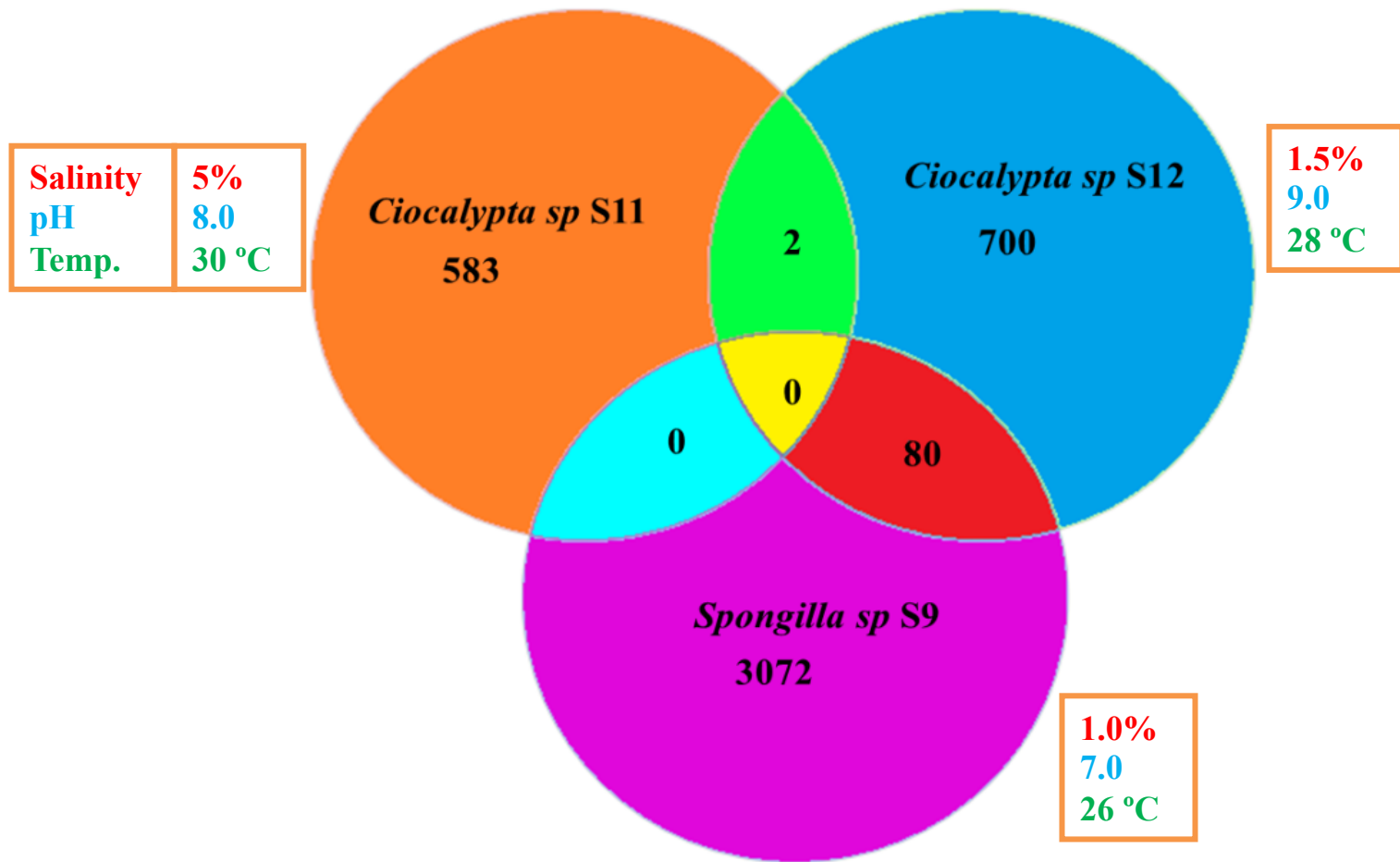


Fig. S3. Venn diagram representing diversity of core and shared OTUs with in the three sponge samples *Spongilla sp. S9*, *Ciocalypta sp. S11* and *Ciocalypta sp. S12*.

The number in the overlapping zone indicates how many OTUs were shared between sponge samples, and the numbers in the non-overlapping zone indicate how many OTUs were exclusively found in each sponge. The overlapping zone of three circles represent the shared OTUs between three sponges.

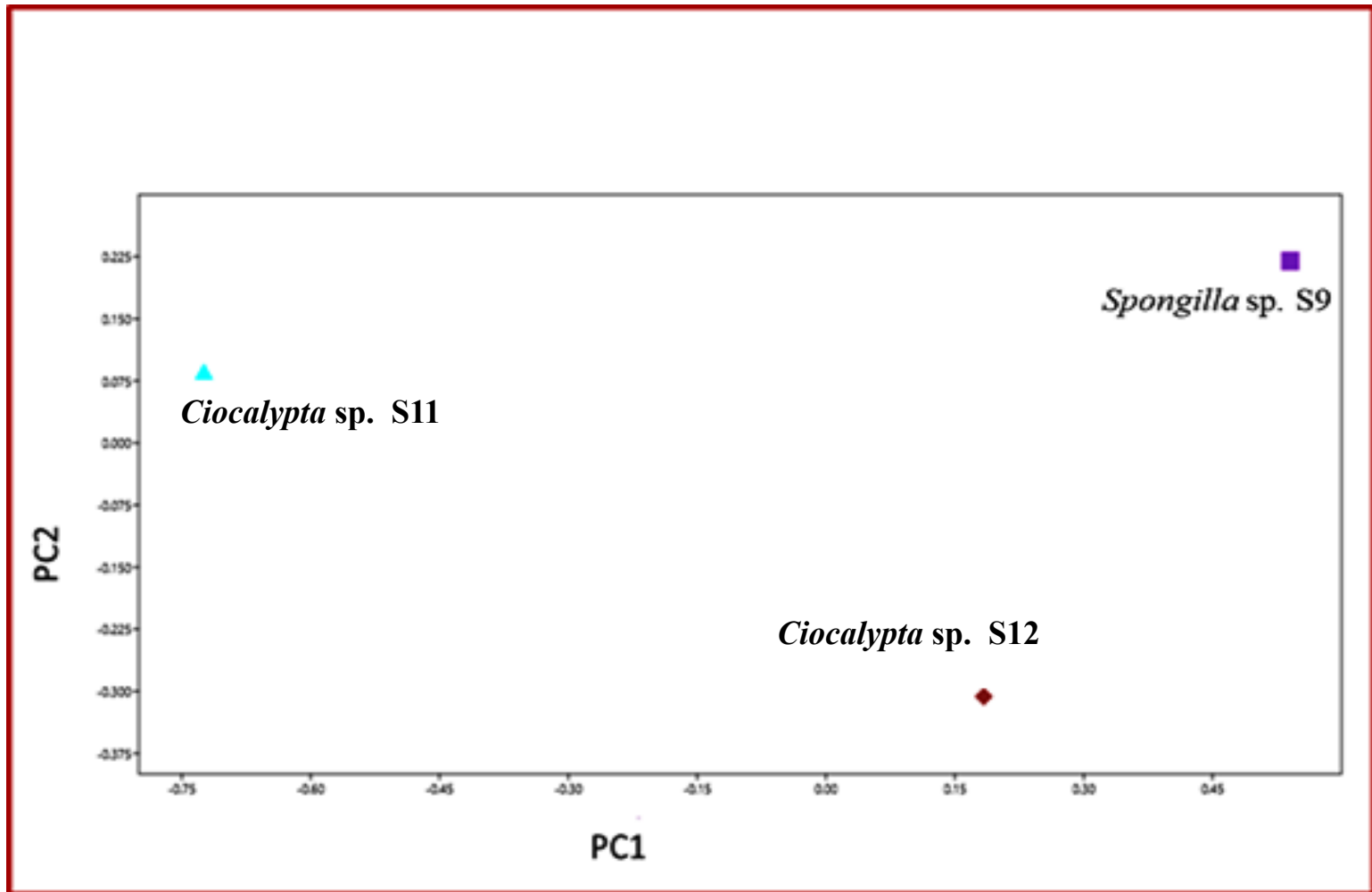


Fig. S4. Non-metric multidimensional scaling (nMDS) plot representing the diversity based on Bay-curtis distance among three sponge samples *Spongilla* sp. S9, *Ciocalypta* sp. S11 and *Ciocalypta* sp. S12.

The plot is constructed based on the abundance of OTUs found in sponge sample at phylum level. The distance between the sample demonstrates the difference in diversity. The three sponge samples are distantly related and shared less OTUs.

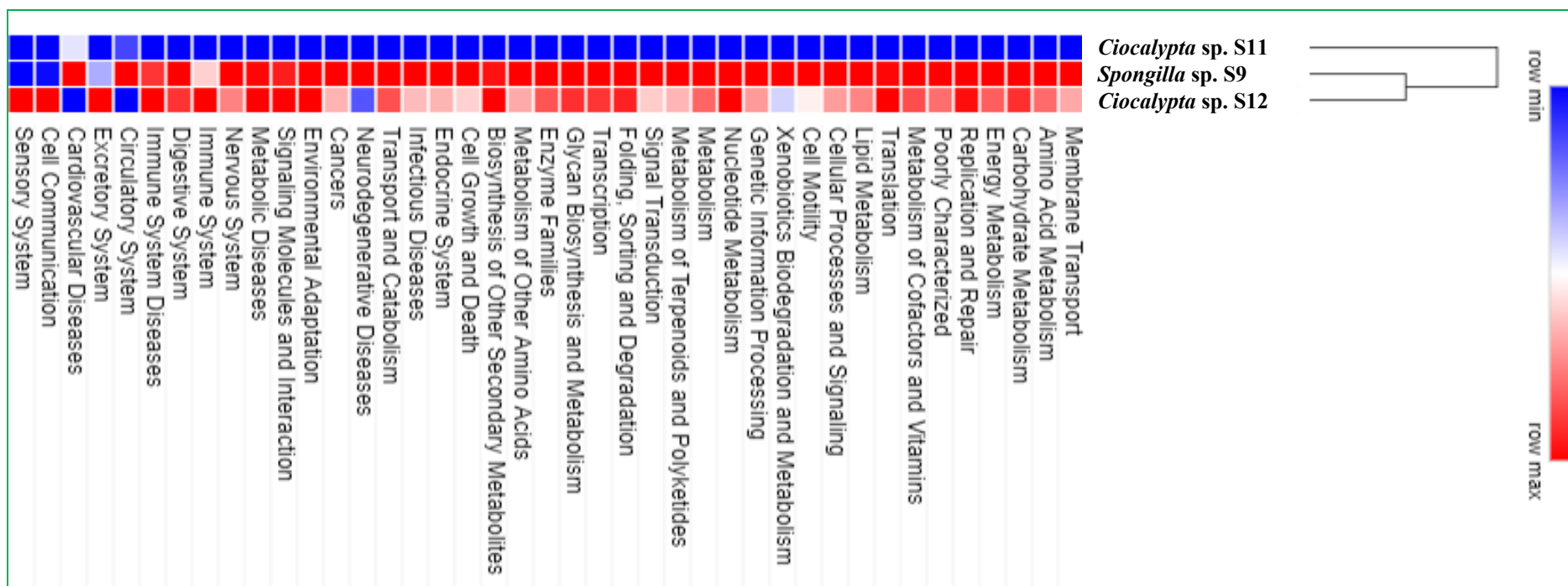


Fig. S5 Heat map showing difference in relative abundances of KEGG pathways between three sponge samples *Spongilla* sp. S9, *Ciocalypta* sp. S11 and *Ciocalypta* sp. S12.

Heat map is constructed based on relative abundances of KEGG pathways at level 2 between three sponge samples and clustered hierarchically in one direction. The horizontal axis denotes the relative abundance of KEGG pathways and the vertical axis refers to sponge samples. KEGG: Kyoto Encyclopaedia of Genes and Genomes

Cut-off	Sponge Sample ID	Number of Sequences	Shannon (H)	Inverse Simpson	Observed Richness
98%	<i>Ciocalypta</i> sp. S11	4828	4.8 ± 0.0	44.5 ± 0.0	585 ± 0.0
	<i>Ciocalypta</i> sp. S12	4828	5.7 ± 0.0	121.1 ± 4.4	778.7 ± 16.9
	<i>Spongilla</i> sp. S9	4828	8.2 ± 0.0	425.2 ± 26.3	3146.6 ± 26.4
97%	<i>Ciocalypta</i> sp. S11	4826	4.8 ± 0.0	44.4 ± 0.0	613 ± 0.0
	<i>Ciocalypta</i> sp. S12	4826	5.6 ± 0.0	111.7 ± 4.0	685.6 ± 15.5
	<i>Spongilla</i> sp. S9	4826	7.9 ± 0.0	376.2 ± 20.4	2908.2 ± 27.1

Table. S1. Comparison of microbial community richness and diversity indices of three sponge samples *Spongilla* sp S9, *Ciocalypta* sp. S11 and *Ciocalypta* sp. S12.

All statistical diversity indices and estimators were performed under 1000 iterations and by rarefying the OUT table to 4828 sequences. The results of statistical analyses for bacterial communities show that *Spongilla* sp. S9 has higher OTUs, species richness, and diversity compared to other two sponge samples. (a). Shannon: Shannon diversity index (>0 , higher, more diverse). (b). Inverse Simpson is the reciprocal of Simpson diversity index where higher the value, the greater the diversity (c). Observed Richness (sobs) is a richness estimator that returns number of observed OTUs from observed definition.