“Investigation of bacterial communities within the digestive organs of the hydrothermal vent shrimp *Rimicaris exoculata* provide insights into holobiont geographic clustering” - Dominique A. Cowart, Lucile Durand, Marie-Anne Cambon-Bonavita, Sophie Arnaud-Haond (corresponding author : sophie.arnaud@ifremer.fr)

QIIME workflows and commands

For processing samples and assigning taxonomy

1. validate\_mapping\_file.py (use original 454 fna/qual files and metadata file)

2. split\_libraries.py (removes short and low quality sequences, adds barcodes names) 🡪 seqs.fna

3. identify\_chimeric\_seqs.py (input seqs.fna and 454.fna [to ID chimeras based on parent sequences] files) 🡪 chimeras.txt

4. pick\_otus.py (input seqs.fna to pick otus denovo, without reference file) 🡪 seqs\_otus.txt

5. pick\_rep\_set.py (input seqs\_otus.txt) 🡪 rep\_set.fna

6. assign\_taxonomy (input rep\_set.fna; reference database: GreenGenes 2013, RDP classifier method) 🡪 rep\_set\_tax\_assignment.txt

7. make\_otu\_table.py (input rep\_set\_tax\_assign.txt. This otu table includes taxonomic assignments) 🡪 otu\_table.biom

8. filter\_otus\_from\_otu\_table.py (input otu\_table.biom. Remove sequences appearing < 3 times pass –n 3) 🡪 no\_singletons.biom

9. filter\_otus\_from\_otu\_table.py (input no\_singletons.biom and chimeras.txt [step 4]. Removes chimeras) 🡪 no\_chimeras.biom

10. convert\_biom.py (input no\_chimeras.biom. Converts to text file if pass –b –header\_key\_taxonomy) 🡪 otu\_taxa\_assign.txt

For Network Analyses

1. filter\_fasta.py (input .txt file list of sequence names to filter from seqs.fna [step 2 above]) 🡪 filtered\_seqs.fna

2. align\_seqs.py (input filtered\_seqs.fna to use PYNAST method to align sequences) 🡪 filtered\_seqs\_aligned.fasta

3. filter\_aignment.py (input filtered\_seqs\_aligned.fasta file to filter alignment) 🡪 filtered\_seqs\_aligned\_pfiltered.fasta

For taxonomic comparisons across phyla and class

1. summarize\_taxa\_through\_plots.py (input otu table no\_chimeras.biom [step 9 above] and metadata file [step 1 above] to generate plots based on a category specified in the metadata file. Add –c and name of category to specify separation by that category [i.e. vents, molt size, etc.] 🡪 per\_study\_otu\_tables.biom