



Association of coral algal symbionts with a diverse viral community responsive to heat shock

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Raw data

795 million sequence reads



Read trimming & adapter removal

609 million sequence reads retained (76.59%)

trimmomatic

min. length: 35 bp; leading 30; trailing 30; headcrop 6

fastq-mcf

l:50, q=20, qual_mean=20

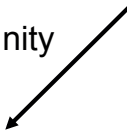


PhiX174 & algal host sequence removal

123 million sequence reads retained (15.46%)

BBSplit

Viral community



Taxonomic classification

263,878 read pairs retained
(bacteria, archaea, viruses)

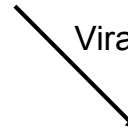
CLARK



Virus taxonomy

41 families, 144 taxa
49,557 read pairs

Viral gene expression



De novo assembly & annotation

56,064 contig (N50 = 1,462bp)

4,856 contigs w/ viral genes

rnaSPAdes & Prokka



Read mapping to assembly

(paired & unpaired reads)

Kallisto-0.42.5

paired reads: -b 10; single reads: -l 70 -s 18



Differential gene expression

43 diff. exp. viral contigs

metagenomeSeq