

**Raw sequence reads**

297 million reads



**After Quality Control, Read trimming, Adapter removal**

264 million reads (88.89%)

Trimmomatic (Bolger et al. 2014), fastq-mcf (Aronesty 2011)



**Removal of Aiptasia host, algal endosymbiont, PhiX, 28S rRNA sequences**

8.6 million reads (2.89%)

BBsplit from BBmap (Bushnell 2016)



**Paired-end read pairs based taxonomic classification**

38,090 annotated sequences (bacteria, archaea, viruses)

CLARK (Ounit 2015)



**Virus community: taxonomic composition and structure**

3,293 sequences,  
116 distinct viral taxa of 40 families

MetagenomeSeq (Paulson et al. 2013) & R package vegan (Oksanen et al. 2017)



— Aiptasia — *Symbiodinium* — Bacteria & Archaea — Virus